Ancient Celts: A reconsideration of Celtic Identity through dental nonmetric trait analysis.

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Abstract

The Celts are a collection of tribes and/or populations that inhabited much of Central Europe during the Iron Age and are still something of an enigma. The relationship among the spread of their material culture, the application of Celtic ethnicity, movements among the diverse populations possessing Iron Age Hallstatt and La Tène artefacts throughout Central Europe believed to have been spread by Celtic people, and/or spoken languages identified as Celtic have long been questioned by researchers. However, previous research has primarily focused only on chronological and typological descriptions and documentation of diachronic change. Diverse populations throughout Europe have been intrinsically linked based on perceived similarities in burial practice, art styles and material culture. Subsequently, these associations have resulted in the creation of the so-called La Tène=Celtic paradigm. Under this paradigm, the presence of La Tène artefacts designate a population as Celtic, which is still prevalent in the field of Celtic studies regardless of documented regional differences.

The underlying biological diversity among presumed Celtic populations and processes driving the observed variation in artefacts, art styles and burial practices throughout the core and expansion regions (i.e., where the Hallstatt and La Tène material cultures initially developed versus those into which they subsequently spread during the 4th and 3rd centuries BC) are not well understood. The present study helps fill the void in the current understanding of underlying biological diversity among these populations in several ways. First, 36 morphological traits in 586 dentitions from 11 regional samples, from Britain and Europe, were collected using the Arizona State University Dental Anthropological System (ASUDAS). The above samples represent the core and expansion regions, along with a comparative European Iron Age sample outside the known range of Celtic expansion. Frequencies of occurrence for each dental and osseous nonmetric trait were recorded by sample. Second, the suite of traits was compared among samples using principal components analysis, (PCA) and the mean measure of divergence (MMD) distance statistic. Multidimensional scaling was subsequently employed on the symmetric MMD matrix to illustrate graphically inter-sample relationships. Phenetic patterns of overall biological similarity and dissimilarity among individuals and populations based on morphological traits were determined. MMD distances were then compared with geographic distances among samples, under the assumption that genetic affinity is inverse to spatial distance.

The biological distance estimates suggest the following. First, populations in the expansion regions exhibit less biological diversity than those within the core. Specifically, two samples within these regions are biologically indistinguishable, the remaining two are biologically distinct, and all samples within the core are phenetically diverse. Thus, populations in the expansion regions are genetically distinct from those in the core and were likely acculturated, not genetically influenced by these groups. Limited intra-and-extra regional gene flow and genetic isolation explain the population structure within the above regions. Second, overall phenetic heterogeneity, biological diversity, and population discontinuity are indicated, as the majority of the samples within both regions are biologically distinct from one another. This diversity may also reflect genetic and linguistic boundaries among the samples. Third, waves of migration from the core during the 4th and 3rd centuries BC were not likely responsible for diachronic changes in material culture within the expansion regions. Fourth, the separation of populations and material culture into the core and expansion regions, and the application of Celtic ethnicity to diverse populations possessing artefacts and a spoken language(s) identified as Celtic may be a nominal association, i.e., in name only. Simply put, the comparative results suggest that these groups represent biologically distinct populations.

These findings were compared with published archaeological, linguistic, genetic and bioarchaeological information to test for concordance between dental and other evidence. The present study does not support findings of previous studies and suggests there is more genetic diversity than previously assumed under the La Tène=Celtic paradigm. Thus, a combination of genetic isolation by distance, limited intra-and-extra-regional gene flow, trade, cultural diffusion and/or assimilation is likely responsible for the observed art style, burial practice, archaeological, genetic and linguistic diversity among populations possessing Hallstatt and La Tène artefacts and/or language(s). These diverse populations may have lost their cultural autonomy after being subsumed into a greater Celtic identity. Thus, the contemporary concept of Celts is likely a modern construct that has hindered understanding of the extent of regional diversity and cultural autonomy among diverse populations throughout Iron Age Europe.

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Chapter 1: Introduction

The Celts are a collection of tribes and/or populations that inhabited much of Central Europe during the Iron Age and are still something of a conundrum to archaeologists and historians. These groups are linguistically defined as an assemblage of populations who spoke languages identified as Celtic, which are categorized as a branch of Indo-European (IE) languages common throughout Europe and Asia. Descendant languages spoken today include Irish and Scottish Gaelic, Manx, Welsh, Cornish, and Breton. The term Celt has been applied to various groups and/or cultures since 700 BC and has been used to describe populations at various levels of specificity (See page 91). Populations and/or tribes throughout Europe that possessed similar cultures and spoken languages have been described by the Greeks and Romans as Keltoi/Celtae and Galli/Gallia. The Romans and Greeks habitually used these terms interchangeably, as we do today (Chapman, 1992; Collis, 1996, 1997, 2003; Cunliffe, 1997, 2018; Karl, 2002, 2004, 2007, 2010, 2012; Moore, 2012; Rankin, 1995).

In this thesis, the term Celt is used to refer to populations associated with the Hallstatt and La Tène cultures; which constitute Iron Age material cultures found throughout Central Europe and are believed to have been spread by Celtic people. Artefacts considered to be characteristic of these periods include brooches (fibulae) and neck rings (torcs). Diverse populations and/or groups throughout Europe have been intrinsically linked with the Celts based on perceived similarities in burial practice (e.g., chariot burials and square barrows), art styles and the jewellery and dress accessorizes described above. Subsequently, these associations have led to the creation of the so-called La Tène=Celtic paradigm, under which the presence of La Tène material culture designates a population as Celtic (See page 19) (Collis, 2003; Cunliffe, 1997, 2009, 2018; Giles, 2012; Koch, 2006). This concept is still prevalent in the field of Celtic studies regardless of any documented regional differences. The theoretical frameworks that surround modern Celtic scholarship are derived from interpretations of ethnicity, interpopulation connectivity, population history and the contextualization of material culture using a culture history approach, where past societies are categorized simply on such associations (Jones, 1996; Trigger, 2006). This concept has been gradually superseded by the advent of new theoretical and methodological frameworks via processual and post-processual archaeological approaches. However, the application of Celtic ethnicity is still largely dependent on material evidence described and classified on the basis of a culture history epistemology (See page 54) (Clark, 2014; Jones, 1996, 1997; Johnson, 2011). Furthermore, the relationship between Celtic ethnicity, ancestry, and any subsequent diachronic changes to these social identities are also primarily derived from and dependent on the above evidence.

Ancestry and ethnicity are interrelated social and cultural phenomena. In the literature, these terms have been used interchangeably referring to the social or cultural descent and history of a population or group. Consequently, the concepts of ancestry and ethnicity have become conflated and are ubiquitous in modern society, as explored in the 2015 ‘Celts: Art an Identity’ exhibition at the British Museum and National Museum of Scotland (National Museums Scotland, 2020). Furthermore, this may have also resulted in the diminished notion of ethnic, or ancestral, plurality (the notion of diverse cultures and customs co-existing in one society or population), within some regions (Blanton, 2015; Hill, 1994; Larsson, 1994; Ningsheng, 1994). Therefore, in this work, it is necessary to provide a working definition of both ancestry and ethnicity. Ancestry can be defined as a line of decent either familial, ethnic or genetic. Ethnicity can be loosely defined as a set of social and psychological phenomena that create a group, or groups, which are distinct from other neighbouring groups (See page 54) (Barth, 1969; Bálint, 1994; De Vos and Romanucci-Ross, 1975; Jones, 1997; Renfrew, 1994a, b; Trigger, 2006). Archaeologically, these phenomena will be evident in several ways, including differences in burial practices and material culture. Ethnic groups are fluid self-defining systems that are not regionally bounded. Although ancestral homelands may represent specific bounded regions, ancestry may also be influenced by and related to diachronic changes in ethnic identity. However, modern notions of ancestry often refer specifically to biological or genetic descent (Blanton, 2015; Bonacchi et al., 2016, 2018; Hingley, 2018; Hingley et al., 2018; Hofmann, 2015; Reich, 2018; Rothman, 2015). Consequently, the complex relationship between ancestry, ethnicity, and the social aspects of both among past populations has been minimized. Ethnicity and ancestry must also be distinguished from spatial continuity and discontinuity, as they often refer to self-conscious identification with a particular group of people (De Vos and Romanucci-Ross, 1975; Jones, 1997; Shennan, 1989).

Furthermore, modern perceptions of ethnic and ancestral identities may be derived from cultural contact and interaction (Barth, 1998, 2010; Bonacchi et al., 2016, 2018; Derks and Roymans, 2009; Eriksen, 1993; Hingley et al., 2018; Jones, 1997; Knapp, 2001; Shennan, 1989). Thus, the production of material culture may vary qualitatively and quantitatively in different contexts. Ethnic and perceived ancestral identity may vary in different social contexts, opposed to the discrete cultural entities that are visible archaeologically (See page 54) (Barth, 1969, 1998, 2010; Jones, 1997; Patterson, 1975;

Renfrew, 1993, 1994a, b; Shennan, 1989; Trigger, 2006). Therefore, it is necessary to interpret the role of these identities in forming distinct cultural traditions, artefacts, defining group interactions and the impact these contacts, and exchanges, have on the local customs and material culture (Bourdieu, 1977; Comaroff and Comaroff, 1992; Jones, 1997; Renfrew, 1993, 1994a, b; Manzanilla, 2015; Rothman, 2015). Moreover, it is necessary to take into consideration the dynamics of change in multiethnic societies, where diverse ethnic groups, or identities, and ancestral lineages are present within one population or community and maintain distinction over time (Bálint, 1994; Bonacchi et al., 2016, 2018; Lightfoot, 2015; Manzanilla, 2015). The cohabitation of diverse ethnic identities may have subsequently created new forms of social relationships, cultural practices and *in-situ* diachronic changes through time (Bonacchi et al., 2016, 2018; Hingley, 2018; Hingley et al., 2018; Lightfoot, 2015; Manzanilla, 2015). These changes may not be viable archaeologically, e.g., changes in clothing or customs. Thus, the social and cultural diversity within multiethnic societies may be minimized (See page 54) (Bálint, 1994; Larsson, 1994; Lightfoot, 2015; Rothman, 2015). However, changes in material culture may also represent diachronic changes from external influence, e.g., migrants, cultural contact and interaction (Dolukhanov, 1994; Lightfoot, 2015; Ningsheng, 1994; Rothman, 2015). Therefore, the co-occurrence of different types of artefacts or designs, i.e., Celtic fibulae or diverse art styles, within one population may indicate trade, *in-situ* change, the presence of out of group slaves or captives, external influence or migration (Larsson, 1994; Osborn, 1994; Rothman, 2015). However, the presence of multiethnic societies and diverse ethnic and ancestral groups living within the same population cannot be ruled out. In this instance, artefact diversity may represent a symbolic identity utilized by diverse groups to retain and keep their ethnicities or identities visible (Dolukhanov, 1994; Lightfoot, 2015; Rothman, 2015). The presence of regional diversity may imply a degree of self-awareness and suggest the presence of multiethnic societies (Frangipane, 2015; Larsson, 1994; Manzanilla, 2015; Ningsheng, 1994).

The creation of new ethnicities and multiethnic societies may derive from several processes, including transculturation (the subsequent creation of new cultural phenomena after the merging and converging of different cultures), hybridity (the maintenance of diverse practices, values and customs among two or more cultures), and ethnogenesis (the formation and development of ethnic groups or identities that are distinctive from other indigenous ethnicities) (Acheraïou, 2011; Anderson, 1999; Dolukhanov, 1994; Hermann, 2007; Hill, 1996). However, in areas shared by multiple diasporic communities, those populations or groups with diverse regional origins such as trading centres, multiethnicity may involve the maintenance and/or accentuation of several ethnic identities that coexist in close proximity (See page 54) (Frangipane, 2015; Hill, 1994; Lightfoot, 2015; Manzanilla, 2015; Rothman, 2015). Ethnic pluralism and immigration may also have resulted in the creation of new social relationships, cultural practices and sociopolitical organizations over time (Frangipane, 2015; Hill, 1994; Lightfoot, 2015; Manzanilla, 2015; Rothman, 2015). Initially, migrants may have represented a distinct and ethnically identifiable group within local populations. However, over time they may have begun to assimilate into the local culture and subsequently adopted new cultural practices. Alternatively, migrant communities may have integrated their cultural practices with those of the local population. Immigrant groups may also have maintained or had continuous contact with their ancestral homelands, e.g., through trade, resulting in transculturation and ethnogenesis within both regions (Bonacchi et al., 2016, 2018; Blanton, 2015; Frangipane, 2015; Hingley, 2018; Hingley et al., 2018; Lightfoot, 2015; Ningsheng, 1994).

Consequently, the above interactions facilitated the creation of new cultural phenomena, and new and distinct ethnic identities within one community. Furthermore, the compositions of the above groups were likely dynamic and changed over time due to inter-ethnic cohabitation, marriage and immigration from diverse regions (Lightfoot, 2015; Manzanilla, 2015; Osborn, 1994; Rothman, 2015). Migrants from diverse cultural backgrounds likely overcame heterogeneity to build coalescent social formations through the creation of new modes of social integration (Blanton, 2015; Bonacchi et al., 2016, 2018; Frangipane, 2015; Larsson, 1994; Ningsheng, 1994). Thus, the concept of ethnic and ancestral identity are not immutable; rather, they are historically and culturally contingent, and are defined more by social solidarity than either genealogy or geography (See page 54) (Dietler, 1994; Goldstein, 2015; Hill, 1994; Osborn, 1994; Rothman, 2015). However, constructed and perceived identities have also played a role in discourses of ethnicity and ancestral heritage (Blanton, 2015; Bonacchi et al., 2016, 2018; Frangipane, 2015; Goldstein, 2015; Grufludd et al., 1999; Hingley, 2018; Hingley et al., 2018; Lightfoot, 2015; Manzanilla, 2015; Rothman, 2015). The complex and interrelated nature of ethnic and ancestral identity, the processes through which they are created and influenced in multiethnic societies, make their application to archaeologically derived groups, such as the Celts, difficult. Moreover, the notion of highly mobile populations and/or large-scale migrations associated with the Celts further complicate the application of a specific ethnic or ancestral identity to these groups (See page 54).

After a period of migrations and population expansion during the 4th and 3rd centuries BC, Hallstatt and La Tène artefacts were spread throughout continental and non-continental Europe and incorporated into the cultures of various regional populations (Collis, 2003; Cunliffe, 1997, 2009, 2018; Giles, 2012; James, 1999; Koch, 2006, 2007; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). These populations subsequently lost their cultural autonomy and were subsumed into a greater Celtic identity. However, the exact nature of this movement and the extent of interactions with neighbouring populations is unknown. All the primary written sources are consistent in that the migrations involved large populations leaving their Central European homelands and spreading throughout Europe (See page 61) (Collis, 2003; Cunliffe, 1979, 1997, 2018; Tomaschitz, 2002). The underlying biological diversity among presumed Celtic populations and the processes driving the observed variation in artefacts, art styles and burial practices throughout the core and expansion regions (i.e., where Hallstatt and La Tène material cultures initially developed versus those into which they subsequently spread during the 4th and 3rd centuries BC) are not well understood (Anctil, 2016).

The centre and periphery, or core and expansion, model is a spatial association that describes and attempts to explain the relationship between advanced metropolitan, or urban, centres and less developed periphery regions within either a particular country or geographic area. However, this model is more commonly applied to the relationship between capitalist and developing societies (Champion, 1989; Frankenstein and Rowlands 1978; Hall et al., 2011; Harding, 2013b; Renfrew, 1986; Rowlands et al., 1987; Wallerstein, 1974). The centre and periphery are not likely to have represented a single urban location (e.g., town, urban centres, city or state), and may likely have encompassed those within a larger geographic area (e.g., multiple towns or urban centres within on country) (Champion, 1989; Frankenstein and Rowlands et al., 1987; Gotimann, 1980; Hall et al., 2011; Harding, 2013b; Paynter, 1982). Thus, the contrast between these regions is both spatial and cultural. The application of this model to past societies (from any period) and temporal periods (e.g., Iron Age Europe), attempts to explain spatially how economic, political and cultural authority is dispersed in the centre and surrounding peripheral or semi-peripheral, areas that can be described as, and are interpreted to have been either core or peripheral regions (See page 19) (Champion, 1989; Frankenstein and Rowlands et al., 1987; Hall et al., 2011; Harding, 2013b; Paynter, 1982). The processes of long-term social change, the social consequences of long-distance interaction and the complex relationships that exist among social, cultural, ethnic identity and development between the above regions are also a central focus of this model (Champion, 1989; Cherry, 1987; Frankenstein and Rowlands et al., 1987; Hall et al., 2011; Harding, 2013b; Paynter, 1982; Strassoldo, 1980).

The centre is described and interpreted as a group of urban locations, typically with technological advancements, wealth or in control of a viable commodity (i.e., salt), and of trade routes, or access to diverse and multiple exchange networks with other wealthy areas (Champion, 1989; Frankenstein and Rowlands et al., 1987; Hall et al., 2011; Hedeager, 1987; Hirth, 1978). These regions are also perceived to have been in a position to extract surplus and goods from the periphery. Conversely, the periphery regions are interpreted to have been correspondingly weak, with little economic influence and were used and regarded as a source of raw materials (Champion, 1989; Frankenstein and Rowlands et al., 1987; Gotimann, 1980; Hall et al., 2011; Harding, 2013b; Hirth, 1978; Paynter, 1982; Strassoldo, 1980; Wells, 1980). The semi-periphery areas are believed to have formed a link between the centre and periphery, whilst also acting as a buffer between these regions. The semi-periphery also facilitated the integration of the above regions both economically and geographically. However, it is difficult to identify the centre, semi-periphery and periphery in past societies and archaeological cultures, a recurring assemblage of artefacts from a specific time and place that may constitute the material culture of a particular culture and/or society (Champion, 1989; Frankenstein and Rowlands et al., 1987; Hall et al., 2011; Jones, 1997; Paynter, 1982; Renfrew, 1993, 1994a, b). Their description is often based on a presumption of economic and/or cultural influence and standing, due in part to the presence and amount of trad and prestige goods. The presumed relationships among populations inhabiting these areas and their interactions also influence the designation of these regions (See page 32) (Champion, 1989; Cherry, 1987; Frankenstein and Rowlands et al., 1987; Hirth, 1978; Hall et al., 2011; Harding, 2013b; Strassoldo, 1980; Wells, 1980).

Further, the presence of regional copies of trade items is not commonly taken into consideration when designating the centre and periphery regions. Spatial, temporal, and economic shifts in power within either region, and/or the semi-periphery, are not likely to have been static. In all likelihood, these regions did not remain stable with respect to one another, but may have exchanged roles, i.e., peripheries may become centres and vice versa, over diverse historical development trajectories (Champion, 1989; Frankenstein and Rowlands et al., 1987; Hall et al., 2011; Hedeager, 1987; Hirth, 1978; Paynter, 1982; Wells, 1980). Therefore, the nature and scale of the cultural interaction among these areas are dynamic and fluid. Consequently, the designation of a region as a centre, periphery or semi-periphery is also likely to have changed through time, due to economic hardship or the breakdown and restructuring of trade routes. While the centre regions are interpreted to affect the semi-periphery and periphery the influence of the latter regions on the former cannot be ruled out. Further, it is unknown if the periphery or semi-periphery may have superseded the centre. Thus, the diverse and fluid relationships among these regions may have subsequently altered the extent, nature and directionality of the cultural interaction and influence among these regions (Champion, 1989; Frankenstein and Rowlands et al., 1987; Hall et al., 2011; Harding, 2013b; Hall et al., 2011).

The nature of any centre and periphery, and semi-periphery relationship is also likely to have been based on intangible elements and social interaction, such as perceived trade or prestige goods and cultural assimilation, or on exclusively economic factors (Appadurai, 1986; Champion, 1989; Frankenstein and Rowlands et al., 1987; Hall et al., 2011; Harding, 2013b; Hirth, 1978; Hall et al., 2011; Paynter, 1982; Wells, 1980). Although the movement of trade and prestige items can be identified and described throughout the centre and periphery regions, it is unknown whether these items represent the extent of exchange between these areas, as descriptions and identification of these items are only based on those preserved, identified and described in the archaeological record. Quantifying the volume of trade and prestige goods may also be difficult due to the above issues (See page 32) (Appadurai, 1986; Champion, 1989; Frankenstein and Rowlands et al., 1987; Hall et al., 2011; Harding, 2013b; Wells, 1980). Comparisons and identification of the extent of inequalities in the exchange among centre and periphery regions may be difficult as well. Moreover, the presence of regional reproductions of trade items is not often taken into consideration when determining or establishing the presence and influence of a centre or periphery. Social change, a key element of the centre-periphery model, can also be influenced and created through external relationships (Champion, 1989; Frankenstein and Rowlands et al., 1987; Hall et al., 2011; Harding, 2013b; Hirth, 1978; Paynter, 1982; Wells, 1980).

Thus, the presence of trade and/or prestige items may not necessarily designate a region as either a centre or periphery. Rather, the presence of these items may indicate long-distance relationships between areas in either region, which may or may not influence social change. The presence of a trade item does not necessarily indicate extensive outside influence leading to social change (Appadurai, 1986; Champion, 1989; Frankenstein and Rowlands et al., 1987; Hall et al., 2011; Harding, 2013b; Wells, 1980). Instead, the presence of these items may indicate access to long-distance trade networks or the movement of people (Nash, 1984). Further, these external relationships were likely involved in initiating and/or maintaining internal processes of social and cultural development through a shared set of political or ideological values, cultural assimilation, breakdown and creation of new alliances among and within regions (Champion, 1989; Frankenstein and Rowlands et al., 1987; Harding, 2013b; Wells, 1980). These factors may have resulted in similar socio-economic development among and within populations that shared certain social practices, which would have been differentially incorporated into diverse regional cultures. Consequently, the extent of the interaction between the above regions is unknown. Thus, the application of this model to past societies and periods should be interpreted with a degree of caution.

Furthermore, the nature of a centre and periphery relationship in Iron Age Europe, or any past or modern-day societies and/or regions, is not likely to have been static regarding membership of its constituent groups, those regions that make up either the centre or periphery. Rather the relationship between these areas is more likely to have been dynamic and multidirectional concerning the exchange of goods and migrants from a presumed centre to a presumed periphery and vice versa. The nature of the peripheries, and the items and people being exchanged and moving were variable, and the composition of these regions was likely heterogeneous (See pages 19 and 32) (Champion, 1989; Frankenstein and Rowlands et al., 1987; Hall et al., 2011; Harding, 2013b; Wells, 1980). Therefore, the patterns of trade and influence between these areas and other peripheries, semi-peripheries and centre regions will be too. Thus, this model operates within a framework of social organization that can generate its own internal patterns of social, cultural and/or ethnic change, for example, through cultural assimilation (Champion, 1989; Frankenstein and Rowlands et al., 1987; Hall et al., 2011; Harding, 2013b; Wells, 1980). Consequently, there is no simple distinction between a centre and a periphery. These limitations make the application of this model to past societies and temporal periods (i.e., Iron Age Europe) difficult at best.

Celtic studies still use the centre and periphery model, but refer to it as the core and expansion model (Collis, 2003; Cunliffe, 1997, 2018; Scheeres, 2014a; Scheeres et al., 2014b). This difference reflects the use and application of this model as a geographic designation for populations possessing Celtic artefacts, languages and/or culture. The nature and scale of the interactions among and within the above regions are unknown, and has not been the focus of much research (See pages 19 and 32) (Anctil, 2016; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). This model as applied to Celtic populations is also specifically related to discussions and debates about the spread of the Hallstatt and La Tène material cultures during the 4th and 3rd centuries BC. Consequently, these broad geographic designations may encompass numerous populations and/or cultures. Further, the presence of the Hallstatt and La Tène material cultures are interpreted to represent the actual movement of people rather than trade, exchange or *in-situ* regional development. Although stable isotope analyses do not appear to support this notion, it is still central to and utilized in the field of Celtic studies (See page 61) (Collis, 2003; Koch, 2006).

Regional differences in Celtic artefacts, the complex social and cultural interactions among and within populations possessing Hallstatt and La Tène material culture are not a focus of this model as applied within the field of Celtic studies research (Anctil, 2016; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). Neither is the complex nature and interactions among the core and expansion regions, trade or exchange within these areas, and the difficulties with the application of this model and the term Celtic to past societies are not taken in to consideration. Further, the exact geographic distribution of populations possessing Celtic artefacts and languages is unknown. Few studies have attempted to determine the biological and cultural variation among populations within the core and expansion regions (Anctil, 2016; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). Consequently, the extent of the interactions, cultural, social and/or biological, among these regions is still largely unknown. Previous archaeological research indicates that the proposed migrations were more complex than simple one-way movement into the expansion regions (Anctil, 2016; Collis, 1996, 2003; Maxová et al., 2011; Scheeres, 2014a). Maintenance of trade networks may have been the catalyst for changes in burial practices and the abundant presence of Hallstatt and La Tène artefacts throughout the expansion regions (See page 61) (Collis 1996, 2003; Cunliffe, 1997, 2018; Koch, 2006, 2007; Tomaschitz, 2002). In such contexts, the debate about the biological diversity among populations possessing Hallstatt and La Tène artefacts has increased (Anctil, 2016; Maxová et al., 2011; Scheeres, 2014a).

In the Celtic core and expansion regions, the focus of this thesis, few limited biological and dental anthropological analyses have been employed (Anctil, 2016; Maxová et al., 2011). However, modern scholarship has recently begun to focus on Celtic population history through these frameworks (Anctil, 2016; Maxová et al., 2011; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). Previous work by the author (2016) examined the variation in dental nonmetric traits among proto-Celtic and Celtic groups possessing Hallstatt and La Tène artefacts in Iron Age Britain and continental Europe. This analysis was conducted to determine whether there was any evidence of biological affinity between these groups, an indication of population continuity among the samples analysed (Anctil, 2016). These results suggest that migration, cultural diffusion and/or assimilation throughout regions possessing Hallstatt and La Tène material culture are far more complex than assumed by archaeological and linguistic theoretical and methodological frameworks (Collis, 2003; Cunliffe, 1979, 1997, 2018; Demoule, 1999; Gleirscher, 1996; Karl, 2010; Koch, 2006; Macaulay, 1992; Stead, 1991a, b, d). This research also suggested that Celtic ethnic identity associated with these populations may not adequately reflect biological affinity, interpopulation relationships and population history throughout Iron Age Europe (Anctil, 2016). Indeed, the findings of the author support those of others, which show greater levels of biological diversity within regions than previously indicated, and that the intrinsic link between Celtic ethnicity and artefacts may be a nominal association, i.e., in name only (Anctil, 2016; Giles, 2012; Scheeres, 2014a; Scheeres et al., 2013b, Scheeres et al., 2014b). Scholars have begun to debate whether the association between the presence of Hallstatt and La Tène artefacts and Celtic identity adequately reflect the ethnic identities of these diverse populations (Anctil, 2016; Anthoons, 2011; Maxová et al., 2011; Scheeres, 2014a; Scheeres et al., 2013b, 2014b).

The relationship among the spread of Hallstatt and La Tène material culture, the application of Celtic ethnicity, and movements among these diverse populations have long been questioned by researchers (Anctil, 2016; Anthoons, 2011; Collis, 2003; Cunliffe, 1979, 1997, 2018; Demoule, 1999; Gleirscher, 1996; Karl, 2010; Koch, 2006; Macaulay, 1992; Scheeres, 2014a; Scheeres et al., 2013b, 2014b; Stead, 1991a). However, earlier research primarily focused on chronological and typological descriptions and documentation of diachronic change (See pages 19 and 32) (Anthoons, 2011; Collis, 2003; Cunliffe, 1979, 1997, 2018; Koch, 2006; Scheeres, 2014a; Scheeres et al., 2013b, 2014b; Stead, 1991a). The underlying biological, linguistic and cultural relationships within and among populations possessing the above cultures remain uncertain. Very few dental anthropology studies have examined the distribution of these traits among the diverse populations associated with the Celts, as most have focused on regional patterns rather than broader questions of ethnicity (Anctil, 2016; Coppa et al., 2007; Coppa et al., 1998; Cucina et al., 1999; Maxová et al., 2011; Scott et al., 2013b). Although previous work by the author examined the distribution of nonmetric dental and cranial traits among some of these populations, biological affinity among the groups has been largely ignored by Celtic scholars (Anctil, 2016).

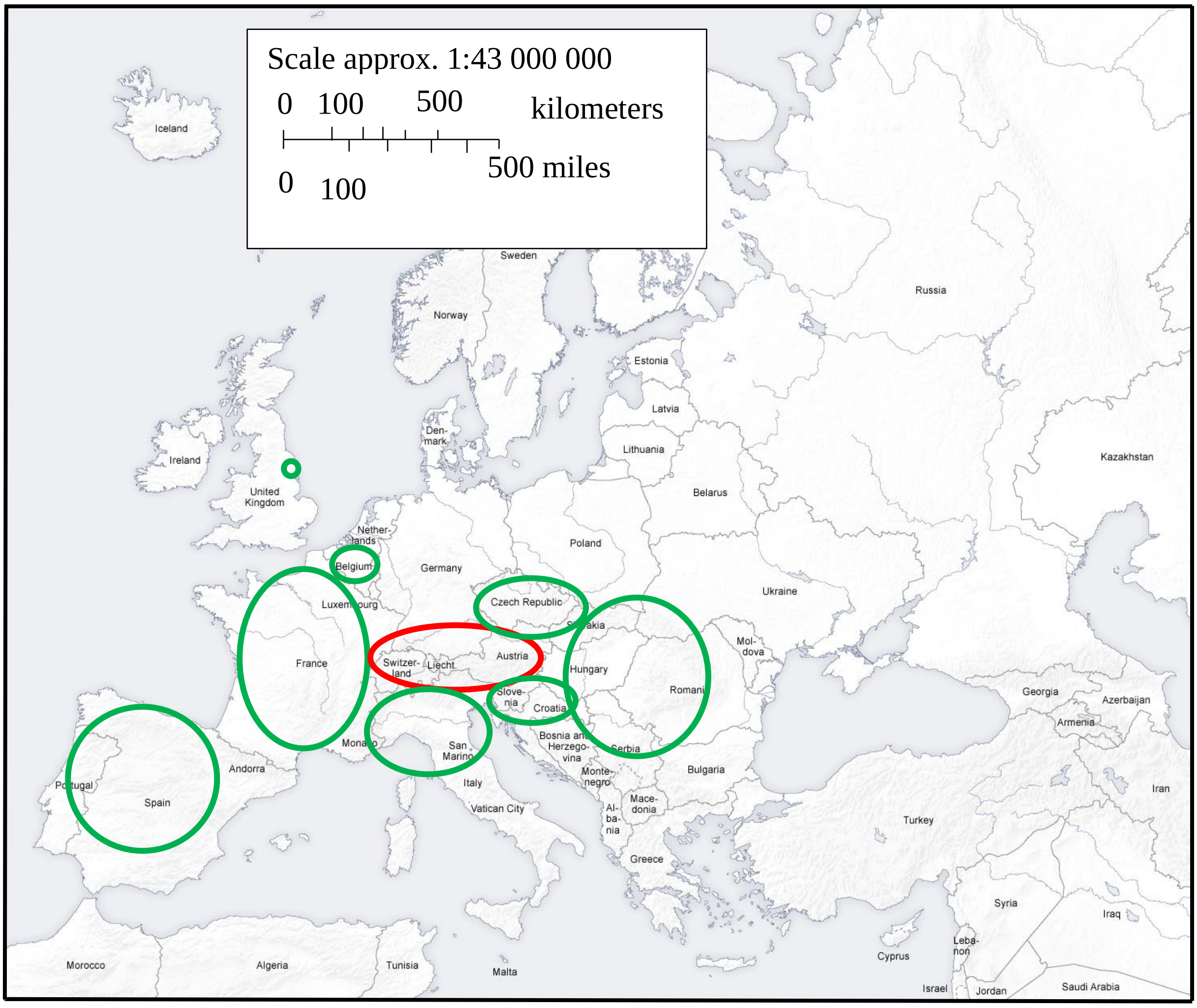
Biological affinity between and within human populations can be determined through biological distance analysis, which reflects both genetic and environmental differences (See pages 113, 118 and 119) (e.g., Bunimovitz, 1990; Buikstra, 1977; Buikstra et al., 1990; Coppa et al., 2007; Godde, 2009; Irish, 1993, 2006, 2016; Irish et al., 2018; Mizoguchi, 2013). Biological distance, or biodistance, is an analytical method for measuring the relative divergence within and between populations. Data generally include morphological (e.g., dental and cranial morphological markers) and metric (e.g., geometric morphometric, odontometric and craniometric analysis) features in bones or teeth that can be used as proxies for genetic data (Anctil, 2016; Bunimovitz, 1990; Buikstra et al., 1990; Hanihara, 2010; Hillson, 1996; Irish, 1993, 2016; Irish et al., 2014, 2018; Irish and Scott, 2017; Larsen, 2015; Turner, 1983a, b, 1984, 1985a, b, 1987; Turner et al., 1991). Biological distances based on genetic data and those obtained from dental morphology have been shown to have a strong relationship, indicated by an r-value of >0.5, positive correlation (r=0.500, p=.021) (See page 135) (Cohen, 1988; Hubbard, 2012; Hubbard et al., 2015) and higher, i.e., r=0.700 to 0.800 (p=.000) (Irish et al., 2020). As detailed in Hubbard's research, both morphometric and metric distance matrices indicate that diverse populations who are commonly believed to represent one ethnic group (i.e., Bantu, sub-Saharan Africa, farmers) are actually genetically closer, whilst populations believed to represent different ethnic groups are more genetically divergent. Thus, comparisons of genetic and dental morphological data suggest that both analyses are equally capable of identifying ethnic and biological differences among populations (See pages 119, 118 and 131) (Anctil, 2016; Black, 2014; Godde, 2009; Hubbard, 2012; Hubbard et al., 2015; Irish, 2010, 2016; Irish et al., 2018, 2020). Conversely, dental metric data does not have a strong correlation with genetic data and are therefore, not as viable for identifying the above differences (Anctil, 2016; Black, 2014; Godde, 2009; Hubbard, 2012; Hubbard et al., 2015; Irish, 1997, 1998a, b, c, 2005, 2006, 2008, 2013, 2010, 2016; Irish et al., 2018, 2020).

Dental morphological (or nonmetric) traits are suitable for biological distance analyses as they are largely independent of age, sex, and one another. Further, these traits have a high genetic component in expression (40-80%) and a high degree of intergroup variation in trait frequencies (See pages 119 and 125) (Hughes and Townsend, 2013; Irish, 1993, 2005, 2010, 2016; Irish et al., 2014, 2018; Larsen, 2015; Scott, 1973; Scott and Turner, 1997). Affinity studies are an effective tool for establishing close biological relationships, or the lack thereof, between and within populations in numerous studies (e.g., Black, 2014; Coppa et al., 1998, 1999, 2007; Cucina et al., 1999; Hubbard, 2012; Irish, 1993, 1997, 1998a, b, c, 2005, 2006, 2008, 2013, 2016, Irish et al., 2014, 2018, 2020; Irish and Turner, 1989,1990; Matsumura et al., 2009; Vargiu et al., 2009).

Data were collected using the Arizona State University Dental Anthropological System (ASUDAS). The standardized ASUDAS system consists of >100 nonmetric crown and root traits, for permanent teeth, scored with the assistance of 24 reference plaques. A subset of 36 traits based on the work of Irish (1993), has also been used in this study (See page 181, Figures 51-53 and Appendix I). Nonmetric dental traits (including mandibular and maxillary torus and rocker jaw) were scored following the ASUDAS procedures outlined in Turner et al (1991). Dental traits were recorded in 586 individuals, adults and sub-adults, aged 17 and older, with permanent dentitions from 11 regional samples. The samples represent the core and expansion regions, along with a comparative European Iron Age sample. Frequencies of occurrence for all dental and osseous nonmetric traits were recorded for each sample. The suite of traits was compared using principal components analysis (PCA) and the mean measure of divergence (MMD) distance statistic. Multidimensional scaling (MDS) was employed on the symmetric MMD distance matrix to graphically illustrate relationships among samples. Cluster analysis based upon this same matrix was used to further illustrate the distances among the samples. Phenetic patterns of overall biological similarity and dissimilarity among individuals and populations based on morphological traits are based on distances from the MMD, which were then compared to geographic distances among samples, under the assumption that genetic affinity is inverse to spatial distance (Cox and Cox, 1994; Harris and Sjøvold, 2004; Irish, 1993, 1997, 2005, 2006, 2007, 2010, 2016; Irish et al., 2014, 2018; Kruskal and Wish, 1978; Sjøvold, 1973, 1977; Relethford, 2004; Smouse et al., 1986; Wright, 1943).

The samples representing the core regions are: Nebringen (Stuttgart, Germany), Pottenbrunn (Austria), Münsingen-Rain (Switzerland), Hallstatt D (Austria), Dürrnberg (Austria) and a German pooled sample (Stuttgart, Germany). Samples representing the expansion regions are comprised of: Radovesice (Czech Republic), Kutná-Hora-Karlov (Czech Republic), Wetwang Slack (east Yorkshire, Britain) and Rudston Makeshift (east Yorkshire, Britain). A temporally contemporaneous sample from outside the known range of Celtic expansion, Pontecagnano (southern Italy), was also analysed for comparative purposes (Figure 1). The cemetery populations listed above have been subject to numerous osteological and dental analyses, as well as funerary and stable isotope studies, since their excavation and recovery, however, these analyses have primarily focused only on chronological and typological descriptions and documentation of diachronic change (See pages 138, 141, 143, 145, 149, 152, 155, 164, 168, 172, 177 and 179) (Anthoons, 2007, 2011; Collis, 1973, 2003; Cunliffe, 1984, 1991, 1994, 1997, 2009; Dent, 1982, 1985, 1995; Giles, 2012; Hodson, 1964, 1968, 1990; Scheeres, 2014a; Scheeres et al., 2013b, Scheeres et al., 2014b; Stead, 1991a). Biological affinity analyses have yet to be conducted on the skeletal material recovered from the majority of these cemeteries (Anctil, 2016; Maxová et al., 2011).

Figure 1. Map of Europe indicating the approximate geographic spread of Celtic material culture, not including isolated finds within the core and expansion regions, circled in red and green respectively (figure modified from generic mapping tools).



Research questions

The following research questions will be addressed in this thesis.

1. Do Celtic populations within the expansion regions exhibit more phenetic diversity than those within the core?
2. Were populations in the expansion regions acculturated, genetically influenced by the arriving Celts, and/or replaced?

3. Are the observed morphological differences among the samples within the core and expansion regions explained by an isolation by distance model?

Hypotheses

To address the preceding questions, the following hypotheses were tested using PCA, MMD, and isolation by distance analyses to determine whether there are significant differences in 36 dental nonmetric traits among the samples (See page 181).

1. H_0: There is no difference in nonmetric trait frequencies among Celtic populations in the expansion compared to the core regions.
H_a: There is a greater difference in nonmetric trait frequencies among Celtic populations in the expansion compared to the core regions, which would suggest less diversity in the expansion regions.
2. H_0: There is no significant difference in nonmetric trait frequencies among Celtic populations within the core and expansion regions.
H_a: There is a significant difference in nonmetric trait frequencies among Celtic populations within the core and expansion regions, which would suggest population discontinuity among these regions.
3. H_0: There is no significant relationship between nonmetric traits and geographic distances among Celtic populations throughout the core and expansion regions; which suggests that isolation by distance was not likely to be the primary process driving the observed variation.
H_a: There is a significant relationship between nonmetric traits and geographic distances among Celtic populations throughout the core and expansion regions.

Significance

This thesis will provide a greater understanding of the diverse biological and intercultural interactions among Celtic populations within the core and expansion regions. The research will also contribute to broader discussions and debates about intercultural interactions within these regions, and discourse on the contextualization of Hallstatt and La Tène artefacts and their integration into other cultures. In addition to discussions and debates about biological diversity among Celtic populations, Celtic population history, and the application of Celtic ethnicity to diverse populations (Cunliffe 1997, 20009; Koch 2006). The thesis also contributes to broad debates about the application and associations of archaeologically derived ethnicity, and how these associations can impact our understanding of population history and intercultural interaction. Through a multi-regional comparison of samples within the core and expansion regions, the biological affinity and movements of presumed Celtic populations can be improved. Although few archaeological studies have begun to dispute their presumed biological relationship, no biological affinity study has yet been conducted on populations from these regions (Collis, 2003; Cunliffe, 1997, 2009; Giles, 2012; Koch, 2006; Kruta, 2004). This thesis will move beyond the La Tène=Celtic paradigm regarding population history within the core and expansion regions.

The thesis will also help fill a void in the current knowledge and understanding of regional variation in nonmetric traits within Iron Age Europe. Despite research establishing which traits are commonly observed during this period, little is known about their regional distribution. Research into this distribution within Europe has been largely reported through population-specific analyses (Coppa et al., 1998, 2000, 2007; Hsu et al., 1999; Hallgrímsson et al., 2004; Khudaverdyan, 2013; Maxová et al., 2011; Pacelli and Márquez-Grant, 2010; Scott et al., 2013b; Vargiu et al., 2009; Weets, 2004; Zubova, 2014). Few previous studies have documented this variation; as a result, the nature of the variation in dental nonmetric traits and their regional patterning is relatively unknown (Adler, 2005; Anctil, 2016; Coppa et al., 1998, 1999, 2000, 2007; Cucini et al., 1999; Hallgrímsson et al., 2004; Henneberg, 1998; Hsu et al., 1999; Khudaverdyan, 2013; Maxová et al., 2011; Mcilvaine et al., 2014; Pacelli and Márquez-Grant, 2010; Rathmann et al., 2016, 2019; Scott et al., 2013b; Thorson, 2018; Vargiu et al., 2009; Zubova, 2014). However, the author’s first study (2016) indicated the presence of a greater degree of variation in dental nonmetric traits in European Iron Age populations, associated with and without the Celts, than previously presumed.

The samples used in this thesis represent groups that have thus far not been the focus of many dental analyses. The collected data can help serve as a building block for further research into geographically neglected regions within Europe during the Iron Age. Furthermore, the results of this study will serve as a foundation for future research into the biological affinity, and Celtic population history throughout Europe (See Armit et al., 2020, for information about the social and biological relationships between Iron Age Britons and populations in continental Europe). This thesis will provide the first evidence as to the presence of the biological affinity and diversity among Celtic populations within and throughout the core and expansion regions; and whether the application of the term Celt to these diverse populations and regions is nominal.

Organization of the thesis

Chapter 2 presents the historical and archaeological background of Celtic populations within and throughout the core and expansions regions. The association between archaeological culture and ethnicity is described. Evidence supporting the contention that the application of Celtic ethnicity to diverse populations within these regions may be nominal is provided. A chronology of the archaeological cultures associated with the Celts in the above regions is described. The archaeological background and dispersal of the proto-Celtic Hallstatt and fully Celtic La Tène culture is presented, followed by evidence supporting their associations with the Celts. Finally, evidence of cultural continuity between the Hallstatt and La Tène cultures is presented. This chapter provides a baseline for the archaeological, chronological, and cultural continuity concerning the Celts, while also providing a baseline for their specific cultural associations to contextualize the population-specific information in the next chapter to a greater extent.

Chapter 3 provides evidence for Celtic migration from and within the core and expansion regions, and whether the presence of Hallstatt and La Tène artefacts there within suggests demic diffusion, migration, trade and/or cultural assimilation. The linguistic and modern European genetic evidence about the presence and movements of the Celts and proto-Celts is provided. Intra-and-extra-regional genetic variation among populations within these regions is also presented. This chapter describes Celtic population history within each region.

Chapter 4 provides the methodological background regarding dental nonmetric trait affinity analyses using model-free and model-bound approaches, biodistance, population history and structure, the heritability of traits, and the Arizona State University Dental Anthropological System (ASUDAS). The assumption underlying biodistance and population structure analysis is provided.

Chapter 5 describes the statistical methods and the rationale for their use. The background information for all samples and dental traits used in this study are presented.

Chapter 6 includes a series of tables and graphs that display results of the biodistance analysis, results from a Wilcoxon signed-rank test for inter-observer repeatability, the results from PCA, MMD, MDS, cluster analyses and isolation by distance as, determined via a pairwise comparison of the symmetric MMD and geographic distance matrices using linear regression. A brief explanation of the results is given.

Chapter 7 provides an in-depth discussion of the results and subsequent interpretations. Each research question is discussed in turn, and is followed by conclusions of the study. Possible future work concerning the data and additional analyses are also considered.

Appendix I. Includes the ASUDAS scoring procedures for nonmetric traits as outlined in Turner et al (1991). The trait scoring sheets are also provided.

Appendix II. Presents the inter-trait correlations as determined by the Kendall's tau-b correlation coefficient.

Appendix III. Describes the Disadvantages and advantages of using teeth as a research tool.

Appendix IV. Presents the remaining two-dimensional sample scatterplots.

Appendix V. Provides the Varimax rotation of the PCA data or the first 2 components.

Appendix VI. Provides the PCA component loadings, eigenvalues and variance for the first 3 components explained for the samples. Varimax rotation of the first 3 components and a Three-dimensional scatterplot of the PCA data among the samples are also provided.

Appendix VII. Presents the Three-dimensional MDS graphs of the MMD distances among the samples.

Appendix VIII. Summarises information about the individuals excavated and the methods used by the recording osteologist to determine age-at-death and estimate sex. The number of individuals included or excluded from this analysis, and sample demography is also provided.

Chapter 2: Hallstatt archaeological background, location, and spread

The Hallstatt culture is named after its type site, Hallstatt in Stiermarken, Austria which is typologically dated from 1,200-475 BC. Excavations began in 1846 by Johann Georg Ramsauer, who eventually uncovered 1,045 burials (Hodson, 1990; Karl, 2006b). The cemetery is one of the richest known sites of its kind; a wide range of weapons, brooches, pins, and pottery have been recovered as well as imported Italian bronze vessels, that have been used to establish chronology (Hodson, 1990). The cemetery, and subsequently the culture, are divided into four periods; Hallstatt A (HaA) 1,200-1,000 BC; Hallstatt B (HaB) 1,000-800 BC; Hallstatt C (HaC) 800-650 BC and Hallstatt D (HaD) 650-475 BC based on chronological differences in artefact types (Collis, 2004; Hodson, 1990; Koch, 2006; Kristinsson, 2010). However, these chronological divisions did not consider the extent of regional variation and distribution of artefacts. Further, the distribution of Hallstatt material culture may have been region-specific and may not have been present in all the regions it is found at a similar date (Collis, 2003; Koch, 2006). Therefore, the above periods represent the earliest possible divisions chronological divisions for this culture (Collis, 2003; Hodson, 1990; Koch, 2006; Kristinsson, 2010).

This culture has been found throughout much of Central Europe including the core and expansion regions. The former is defined as the regions in which Celtic material culture initially developed and include Austria, Switzerland and southern Germany (Collis, 2003; Koch, 2006; Kruta, 1991). The latter are defined as those into which it subsequently spread during the 4th and 3rd centuries BC. It includes Britain, France, Slovakia, Slovenia, Croatia, Hungary, Serbia, Romania, Belgium, the Iberian Peninsula and the Czech Republic (Almagro-Gorbea, 1991; Almássy, 2009; Cunliffe, 1979, 1988, 1995b; Fitzpatrick, 1993; Scheeres, 2014a; Scheeres et al., 2013b, Scheeres et al., 2014b) (Figure 1). Although some previous studies include the Czech Republic and northern Italy in the core, they are based on descriptions from Greek and Roman authors using second-hand information derived from political propaganda (Collis, 2003; Cunliffe 1997; Scheeres, 2014a). Hallstatt artefacts are also less frequent in these regions and often represent the HaD period specifically (Clive, 2010; Cunliffe, 1979, 1988; Fitzpatrick, 1993; Hauschild, 2010b, 2015; Kruta, 1991; Scheeres, 2014a; Scheeres et al., 2013b). Consequently, these areas were included in the expansion regions in this analysis.

This large area has been further divided into eastern and western sub-zones, based on differences in burial practices and artefacts. Daggers are specific to the eastern zone while axes are to the western; however, these differences often represent isolated finds (Collis, 2003; Cunliffe, 1997; Koch, 2006; Kruta, 1991). The eastern zone encompasses northern Croatia, eastern Slovenia, western Hungary, southwestern Slovakia, eastern Austria, the eastern Czech Republic, and northern Serbia (Collis, 2003; Cunliffe, 1997; Hodson, 1990; Koch, 2006; Kossack, 1959; Ljuština, 2009). The western zone includes Britain, northeastern France, northern Switzerland, southern Germany, western Austria, northern Italy and the western Czech Republic (Koch, 2006; Kossack, 1959; Warneke, 1999).

Little is known about the early periods, as it is not until the HaC period that there is evidence of significant building activities and fortifications (Cunliffe, 1997; Koch, 2006). However, diachronic changes in burial practice are evident. Cremation burials in urns with few grave goods, such as bowls, weapons, and jewellery are common during the early periods. Tumulus, or barrow, and inhumation burials become standard from the latter half of the HaB to HaD periods (Clive, 2010; Collis, 1984, 1986, 2003, 2004; Cunliffe, 1997; Hodson, 1990; Koch, 2006). During these periods, the quantity of grave goods increased. Burials of females were accompanied by a rich assortment of bronze ornaments, including anklets, bracelets, and brooches. Males were often buried with various weapons, such as daggers, swords, and spearheads or, in some regions, axes (Collis, 2004; Cowen, 1968, 1970; Gleirscher, 1996; Hodson, 1990; Pare, 1991; Rapin, 1991).

The later phases of this culture are presumed to be proto-Celtic, specifically the HaC and HaD periods, as those artefacts frequently associated with Celtic material culture, e.g. fibulae and torcs, are common (Collis, 2003; Cunliffe, 1997; James, 2005; Koch, 2007). However, these elements have also been associated with the Bronze Age Golasecca and Cagnate archaeological cultures in northern Italy (9th- 4th centuries BC and 1,200-450 BC, respectively) (Clive, 2010; Collis, 2003; Cunliffe, 1997; De Marinis, 1991; Gimbutas, 2011; James, 2005; Koch, 2006; Kristinsson, 2010; Mallory, 1992; Mallory and Adams, 1997; Stech, 2013; Weissenbacher, 2009). Burial practices similar to those during the HaA and HaB periods are also evident in the Urnfield culture, which dates from 1,300-750 BC (Collis, 2004; Gimbutas, 2011; Koch, 2006). Consequently, the initial phases of the Hallstatt culture (HaA and HaB) are often grouped under the Unrfield or Bronze Age cultural headings (Cunliffe, 1979, 1997; Gimbutas, 2011; Hodson, 1990; Meid, 2008; Sorensen et al., 2006).

Wealth began to increase during the HaC period in all regions in which this culture spread to, as indicated by imported prestige items that coincided with the presence of inhumation and barrow burials (Berresford-Ellis, 1990; Bofinger, 2006; Collis, 2003; Cunliffe, 1997; Hodson, 1990; Koch, 2006; Maier, 2003). The latter are accompanied by swords; richly decorated pottery; personal ornaments made of bronze; some possess a built-in wooden chamber (Cowen, 1968, 1970; Gleirscher, 1996; Hodson, 1990; Hopkins, 1957; Krausse, 2006; Pare, 1991). The accumulation of wealth facilitated social stratification. The differences between wealthy and poor became more pronounced, and an elite class emerged (Collis, 1986, 2003; Cunliffe, 1997; Hodson, 1990; Koch, 2006). Evidence of this stratification is suggested by grave goods. Elaborately designed objects of gold and silver as well as imported ivory, glass, and amber while rare, are only found in elite burials (Collis, 1986, 2003; Cunliffe, 1997; Hodson, 1990; Koch, 2006). Conversely, the majority of burials during this period contain objects with simple designs made of bronze or iron. The artefacts associated with the HaC period are markedly more complex than those of the preceding period (Collis, 1984, 2003; Cunliffe, 1984; Davies, 2000; Hodson, 1990). Some items, specifically jewellery and weapons, were procured from the surrounding regions, e.g., southern France and northern Italy, suggesting the aristocracy may have derived their wealth from trade (Buchsenschutz, 1995; Collis, 2003; Frey, 1995). Alternatively, the aristocracy may have been migrants from these regions.

The change in artefact quality and burial practices between the HaB and HaC periods may suggest migration. However, cultural diffusion and/or assimilation cannot be ruled out, as these periods have not been the focus of much research other than typological and chronological material inventories (Anctil, 2016; Collis, 2003; Cunliffe, 1997; Koch, 2006; Kruta, 1991). Nevertheless, it is evident that the groups possessing Hallstatt material culture during the above transition experienced a dramatic change in social stratification (Collis, 2003; Cunliffe, 1997; Hodson, 1990; Koch, 2006). A subsequent increase in prestige items such as Mediterranean imports including Attic pottery (pottery produced in the Attic Peninsula, encompassing the city of Athens, Greece), wine flagons and amphorae is evident during the HaD period (Collis, 1984; Heemstra, 2012; Gifford, 1960; Kossack, 1959; Nash, 1985; Wells, 1977; 1980). The aristocracy during this period was further distinguished by the presence of cart burials (Collis, 1986, 2003; Hodson, 1990; Poppi, 1991).

During this period, elite graves, those with carts and prestige items, are more concentrated in the western sub-zone of the Hallstatt culture than in previous periods (Collis, 2003; Gifford, 1960; Hodson, 1990; James, 2005; Poppi, 1991). This westward shift appears to be correlated with the establishment of a new Greek trading colony at Massalia (present-day Marseilles in southern France) located near the mouth of the Rhone River. The new chiefdoms lay in close proximity to major trade routes believed to have connected the Mediterranean, Rhine, Seine, Loire, and Upper Danube Rivers with the Rhone River corridor

(Buchsenschutz, 1995; Cunliffe, 1997; Collis, 1991, 2003; Diepeveen-Jansen, 2001; Gáti, 2014; Kruta, 1991; Wells, 1977). The distribution of artefacts and burial practices are diverse throughout the core regions associated with the HaD culture. Specifically, those regions, which have substantial published grave inventories, include Austria (Hallstatt, Dürrnberg, Pottenbrunn, and Franzhausen) and Germany (Hochdorf, southern Germany, Heuneburg, southern Germany, Hunsrück-Eifel, western Germany, and Baden-Württemberg, southwest Germany). These inventories suggest differential and interrelated patterns of intra-and-extra-regional contact (Collis, 2003; Cunliffe, 1997; Haffner, 1976; Hodson, 1964; 1990; Joachim, 1968; Koch, 2006; Knipper et al., 2017; Neugebauer, 1991; Schneifer, 2012; Wells, 1995a, b, c). Those in the expansion regions include France (Saint-Sulpice, Bobigny and the Marne region, northeastern France), Italy (Monte Bibele and Monte Vecchio, Bologna), Slovakia, (Bucany), the Czech Republic (Manětín-Hrádek) and Hungary (Herzogenburg and Pilismarot-Basaharc) (Almássy, 2009; Bondini et al., 2004; Brasili and Belcastro, 2003; Bujna, 1991; Bujna and Romsauer, 1983; Collis, 1991, 2003; Della et al., 2003; Horváth et al., 1990; Koch, 2006; Soudska, 1991, 1994; Schonfelder, 2010; Vitali and Lejars, 2010). Typical artefacts associated with this period include fibulae; rings; bracelets; torcs; silver and gold items; pottery and/or bronze vessels; gifts of meat (i.e., sheep); daggers; spears; and lances (Figures 2-4) (Bondini et al., 2004; Bujna and Romsauer, 1983; Collis, 1991, 2003; Koch, 2006; Rapin, 1991; Soudska, 1991, 1994; Vitali and Lejars, 2010). Gundlingen and Mindelheim swords (the dominant sword types during the HaC, HaD and subsequent periods) are also common (Figures 5 and 6) (Bretz-Mahler, 1971; Collis, 1991, 2003; Cowen, 1967, 1968, 1970; Cunliffe, 1997; De Navarro, 1972; Hodson, 1964, 1990; James, 2005; Koch, 2007; Kruta, 1991; Ramsl, 2002; Rapin, 1991; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Valentová and Sankot, 2012; Wendling and Wiltschke-Schrotta, 2015; Wendling et al., 2015). However, the above artefacts do not represent a comprehensive list of those recovered from the above sites and regions. Rather, they represent those described as characteristic of the HaD period that are commonly described in these regions. Although these regions have been more extensively documented comparatively, most of the artefact descriptions are still vague. The majority of artefacts are described as belonging to the Hallstatt period overall.

The numerous intra-and-extra-regional connections suggested by the distribution of the above artefacts are indicated in Table 1 (Bretz-Mahler, 1971; Bujna, 1991; Charpy, 1991; Cowen, 1968, 1970; Delabesse and Troadec, 1991; Haffner, 1976; Hellebrandt, 1999; Hellebrandt and Hellebrandt, 1990; Joachim, 1968; Koch, 2006; Kruta, 1991; Lejarst et al., 2004; Mandi et al., 2018; Marion et al., 2005a, b; Marion, 2008; Novinskzi-Groma, 2017; Rabsiler et al., 2017; Ramsl, 2002, 2012a, b, 2014a, b; Soudska, 1991; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Valentová and Sankot, 2012; Vitali, 1987, 1988, 1991; Vitali et al., 2002; Wendling et al., 2015; Wendling and Wiltschke-Schrotta, 2015).

Figure 2. Fibulae common in Hungary and Austria from the Hallstatt B-D periods (Modified from Alexander, 1965, Figure 3. Original scale not provided)

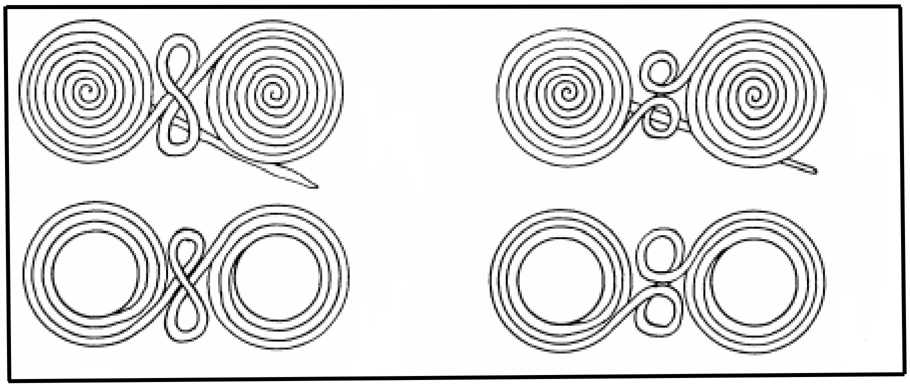


Figure 3. Bracelet type and design common in Switzerland and Austria during the Hallstatt D-La Tène periods (modified from Hodson, 1964, Figure 53. Original scale not provided).

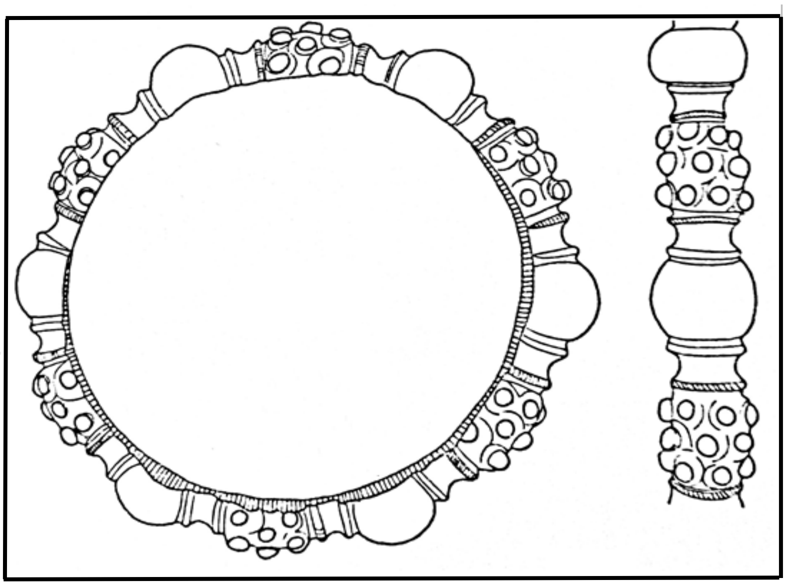


Figure 4. Torc type and design common in Switzerland, Austria and southern Germany during the Hallstatt D-La Tène periods (modified from Hodson, 1964, Figure 1. Original scale not provided).

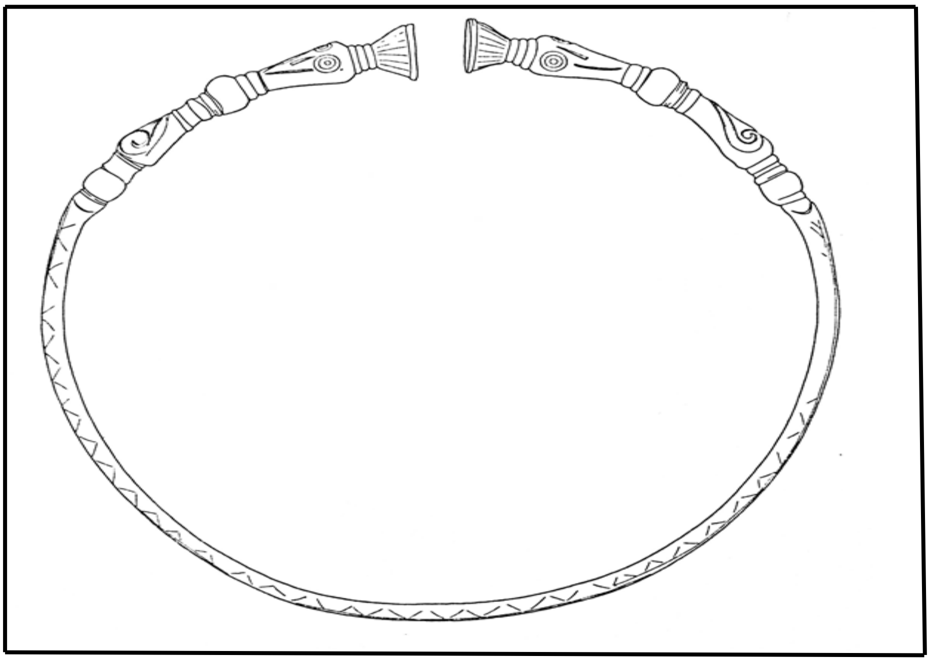


Figure 5. Gundlingen swords (Cowen, 1967, Figure 2. Original scale not provided).

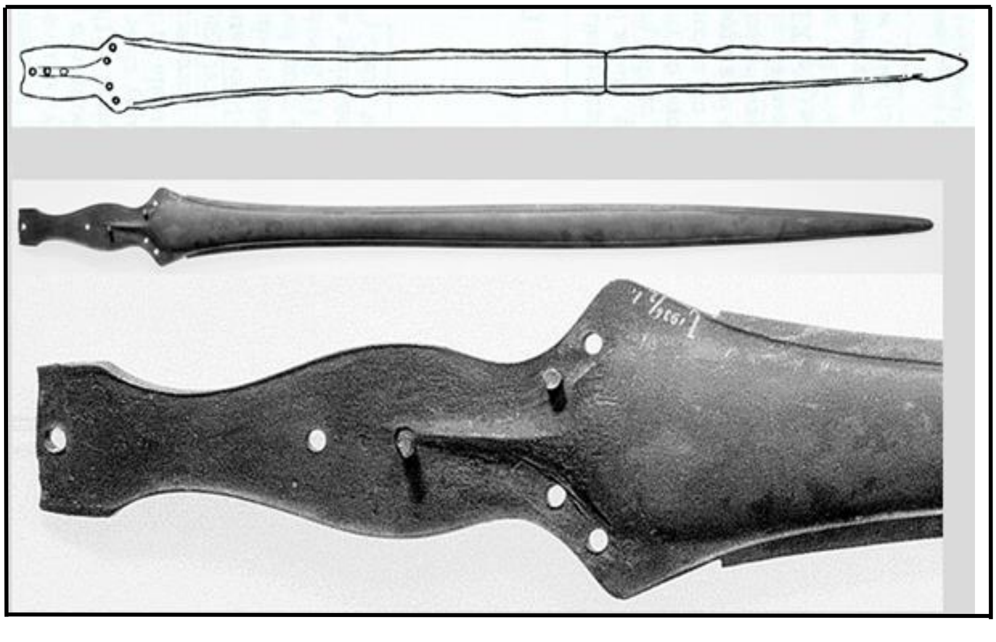
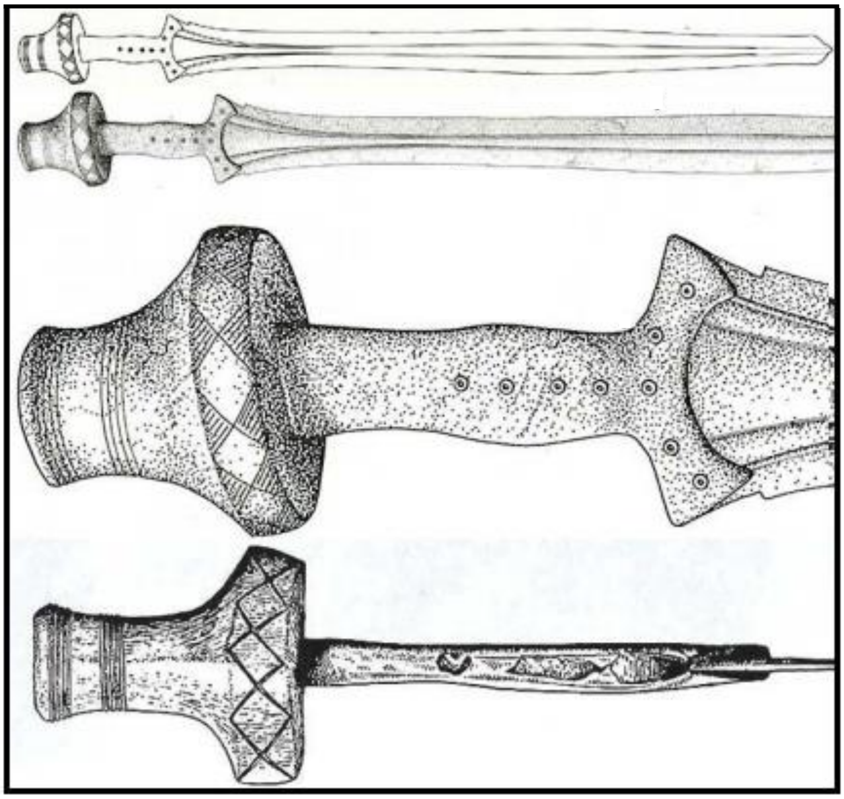


Figure 6. Mindelheim swords from Hallstatt grave 607 (Cowen, 1967, Figure 3. Original scale not provided).



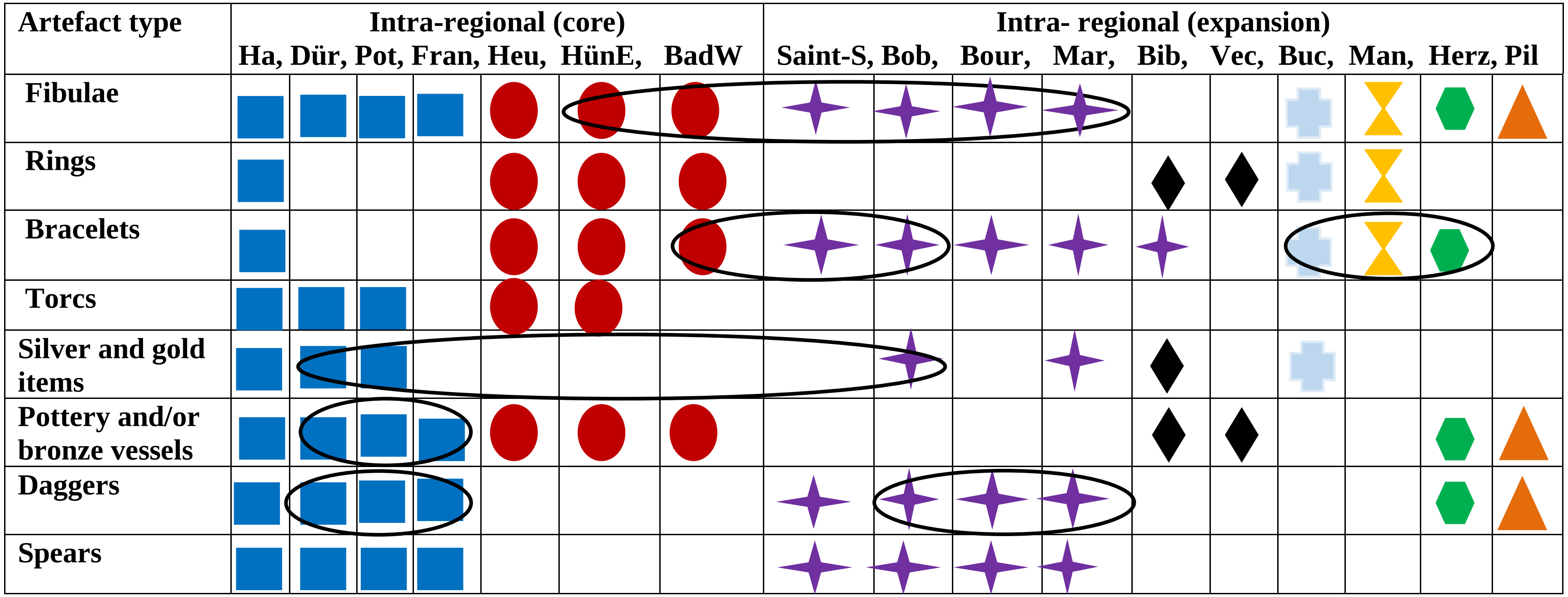
Although similar artefacts are common within several regions, there are subtle variations in art style and manufacturing technique (Collis, 2003; Kruta, 1991; Koch, 2006; Megaw, 1972). The artefacts in Table 1 represent those specific to the HaD period and represent those most commonly described and documented among and within the regions listed. As such their distributions facilitate broad regional comparisons and they have been used in several previous studies to link diverse regions (Bunja, 1991; Hellebrandt, 1999; Hellebrandt and Hellebrandt, 1990; Joachim, 1968; Koch, 2006; Kruta, 1991; Mandi et al., 2018; Neugebauer, 1991; Rabsiler et al., 2017; Ramsl, 2002, 2012a, b, 2014a, b; Soudska, 1991, 1994; Vitali et al., 2002; Wendling et al., 2015). However, these comparisons are often only based on a limited number, or one type of artefact and are site specific (Hellebrandt, 1999; Hellebrandt and Hellebrandt, 1990; Joachim, 1968; Koch, 2006; Kruta, 1991; Mandi et al., 2018; Rabsiler et al., 2017). Therefore, their distributions may not adequately or comprehensively represent the cultural connections during this period. The following abbreviations in Table 1 designate those regions, with substantial grave inventories within the core: Hallstatt (Ha), Dürrnberg (Dür), Pottenbrunn (Pott), Franzhausen (Fran), Heuneburg

(Heu), Hünsruck-Eifel (HünE) and Baden-Württemberg (BadW). Those for the expansion regions include: Saint-Sulpice (Saint-S), Bobigny (Bob), Marne (Mar), Monte Bibele (Bib), Monte Vecchio (Vec), Bucany (Buc), Manětín-Hrádek (Man), Herzogenburg (Herz) and Pilismarot-Basaharc (Pil).

In spite of the above limitations, the associations indicated by Table 1 suggest that populations possessing Hallstatt material culture had developed far-reaching contacts, either biological or cultural (Collis, 2003; James, 2005; Kruta, 1991). However, regional differences have not been the focus of much research (Bretz-Mahler, 1971; Harding, 2007; Laing and Laing, 1992; Laing, 2006; Megaw and Megaw, 2001). Locally produced artefacts copied the function, shape and decorative elements of imports but adapted and transformed them into an entirely new object or design (Bretz-Mahler, 1971; Duncan, 2008; Green, 1996; Harding, 2007). The art styles characteristic of the HaD period include geometric and curvilinear designs as well as a less common naturalistic style portraying humans and animals (Figure 7) (Harding, 2007; Laing and Laing, 1992; Megaw, 1972; Megaw and Megaw, 2001). As their distribution is comparable with the artefacts, the same abbreviations are used in Table 2.

Additional connections are suggested by similarities in burial practices throughout those regions with published cemetery descriptions (Collis, 2003; Gimbutas, 2011; Koch, 2006; Kristinsson, 2010). Extended and supine inhumations under a tumulus are common, however, variations in burial position, and orientation (e.g., north-south versus south-north) are evident and may suggest individual identity expression. Additionally, they may represent differences based on status, ascribed or earned, non-local individuals or age and sex (Collis, 2003; Jones, 1996; Koch 2006; Kruta, 1991; Wells, 1990, 1993, 2014). Although these differences are not often elaborated or comprehensively documented. However, the vehicle burials during this period have been described in more detail (Collis, 2003; Cunliffe, 1997, 2009; Halkon, 2013). Four-wheeled carts are common during the HaC period and continue in some regions into the HaD period where two-wheeled chariots predominate (Collis, 2003; Harbison, 1969; Koch, 2006; Kruta, 1991). These vehicles have been commonly described as carts or chariots, however, note that scholars use the terms interchangeably (Collis, 2003; Cunliffe, 1991, 1997; Furger-Gunti, 1991; Koch, 2006). Those regions which have notable documented variations in vehicle burial practices include Austria (Dürrnberg and Saltzwelten Hallein), Germany (Hochdorf), France (Saint Germain-en-Laye, Attichy and Vix) (Biel, 1981, 1982, 1991, 2012; Berthelier-Ajot, 1991; Claude, 2003; Collis, 2003; Cunliffe, 1997; James, 2005; Joffroy, 1954, 1960, 1962; Kruta, 1991; Tiefengraber and Wiltschke-Schrotta, 2014, 2015; Wendling et al., 2015).

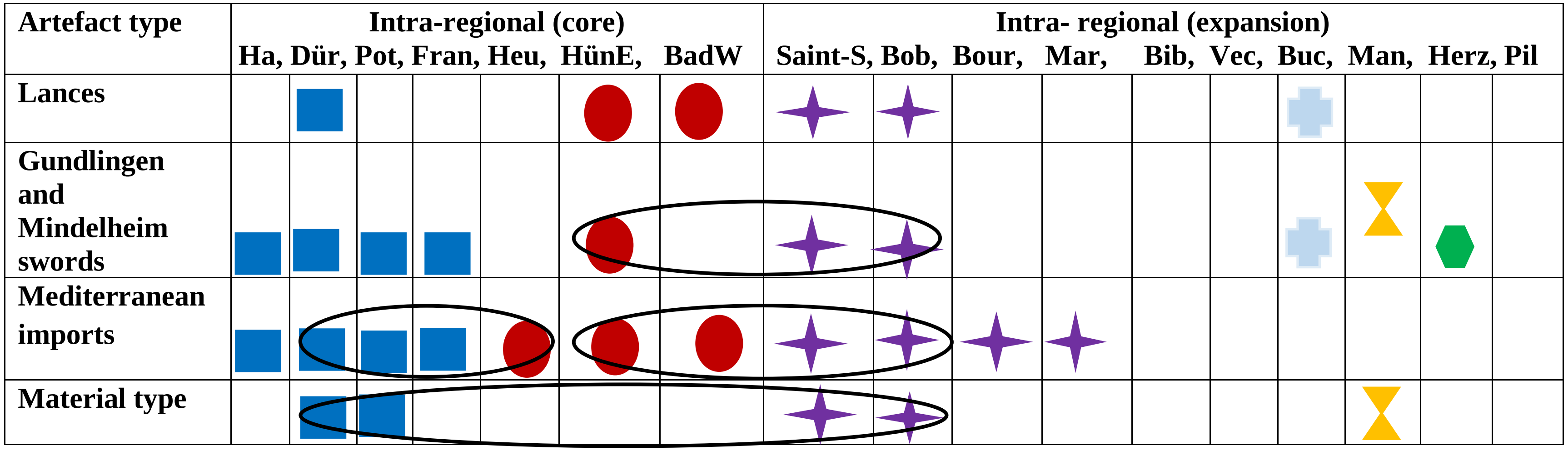
Table 1. Intra-and-extra-regional distribution of artefact types during the HaD period.



Artefact type	Intra-regional (core)							Intra- regional (expansion)									
	Ha,	Dür,	Pot,	Fran,	Heu,	HünE,	BadW	Saint-S,	Bob,	Bour,	Mar,	Bib,	Vec,	Buc,	Man,	Herz,	Pil
Fibulae	■	■	■	■	●	●	●	✦	✦	✦	✦			✚	⧗	⬢	▲
Rings	■				●	●	●					◆	◆	✚	⧗		
Bracelets	■				●	●	●	✦	✦	✦	✦	✦		✚	⧗	⬢	
Torcs	■	■	■		●	●											
Silver and gold items	■	■	■						✦		✦	◆		✚			
Pottery and/or bronze vessels	■	■	■	■	●	●	●					◆	◆			⬢	▲
Daggers	■	■	■	■				✦	✦	✦	✦					⬢	▲
Spears	■	■	■	■				✦	✦	✦	✦						

The differently coloured shapes indicate intra-regional connections within the core and expansion regions. Each geographic region is represented by 1 shape. The black circles indicate possible extra-regional connections. Core regions: Hallstatt (Ha), Dürrnberg (Dür), Pottenbrunn (Pott), Franzhausen (Fran), Heuneburg (Heu), Hünsruck-Eifel (HünE) and Baden-Württemberg (BadW). Expansion regions: Saint-Sulpice (Saint-S), Bobigny (Bob), Marne (Mar), Monte Bibele (Bib), Monte Vecchio (Vec), Bucany (Buc), Manětín-Hrádek (Man), Herzogenburg (Herz) and Pilismarot-Basaharc (Pil).

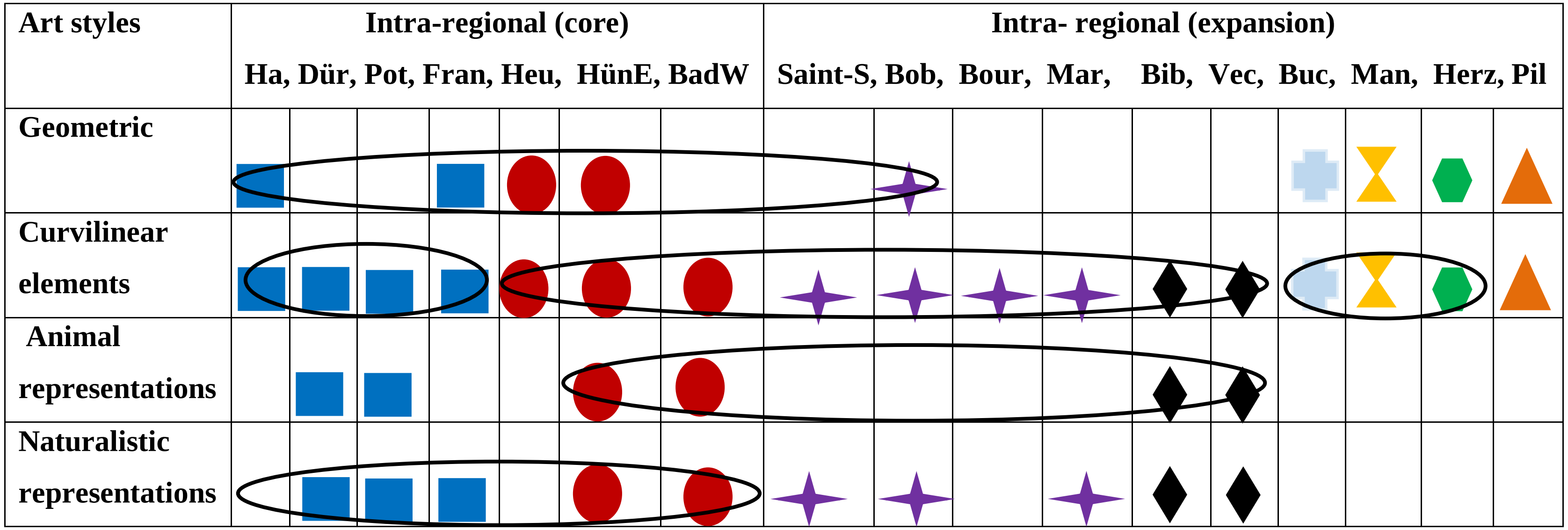
Table 1 continued. Intra-and-extra-regional distribution of artefact types during the HaD period.



Artefact type	**Intra-regional (core)**							**Intra- regional (expansion)**									
	Ha,	**Dür,**	**Pot,**	**Fran,**	**Heu,**	**HünE,**	**BadW**	**Saint-S,**	**Bob,**	**Bour,**	**Mar,**	**Bib,**	**Vec,**	**Buc,**	**Man,**	**Herz,**	**Pil**
Lances		■				●	●	✦	✦					✚			
Gundlingen and Mindelheim swords	■	■	■	■		●		✦	✦					✚	⧗	⬢	
Mediterranean imports	■	■	■	■	●	●	●	✦	✦	✦	✦						
Material type		■	■					✦	✦						⧗		

The differently coloured shapes indicate intra-regional connections within the core and expansion regions. Each geographic region is represented by 1 shape. The black circles indicate possible extra-regional connections. Core regions: Hallstatt (Ha), Dürrnberg (Dür), Pottenbrunn (Pott), Franzhausen (Fran), Heuneburg (Heu), Hünsruck-Eifel (HünE) and Baden-Württemberg (BadW). Expansion regions: Saint-Sulpice (Saint-S), Bobigny (Bob), Marne (Mar), Monte Bibele (Bib), Monte Vecchio (Vec), Bucany (Buc), Manětín-Hrádek (Man), Herzogenburg (Herz) and Pilismarot-Basaharc (Pil).

Table 2. Intra-and-extra-regional distribution of art styles during the HaD period.

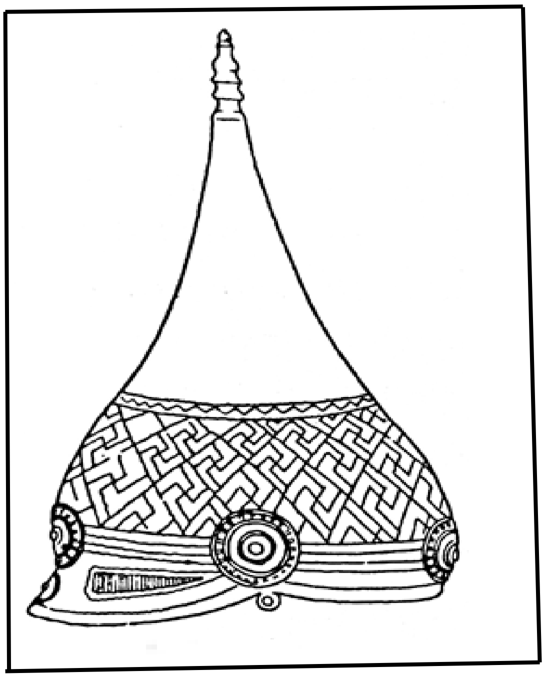


Art styles	**Intra-regional (core)**							**Intra- regional (expansion)**									
	Ha,	**Dür,**	**Pot,**	**Fran,**	**Heu,**	**HünE,**	**BadW**	**Saint-S,**	**Bob,**	**Bour,**	**Mar,**	**Bib,**	**Vec,**	**Buc,**	**Man,**	**Herz,**	**Pil**
Geometric	■			■	●	●			✦					✚	⧗	⬢	▲
Curvilinear elements	■	■	■	■	●	●	●	✦	✦	✦	✦	◆	◆	✚	⧗	⬢	▲
Animal representations		■	■			●	●					◆	◆				
Naturalistic representations		■	■	■		●	●	✦	✦		✦	◆	◆				

The different coloured shapes indicate intra-regional connections within the core and expansion regions. Each geographic region is represented by 1 shape. The black circles indicate possible extra-regional connections. Core regions: Hallstatt (Ha), Dürrnberg (Dür), Pottenbrunn (Pott), Franzhausen (Fran), Heuneburg (Heu), Hünsruck-Eifel (HünE) and Baden-Württemberg (BadW). Expansion regions: Saint-Sulpice (Saint-S), Bobigny (Bob), Marne (Mar), Monte Bibele (Bib), Monte Vecchio (Vec), Bucany (Buc), Manětín-Hrádek (Man), Herzogenburg (Herz) and Pilismarot-Basaharc (Pil).

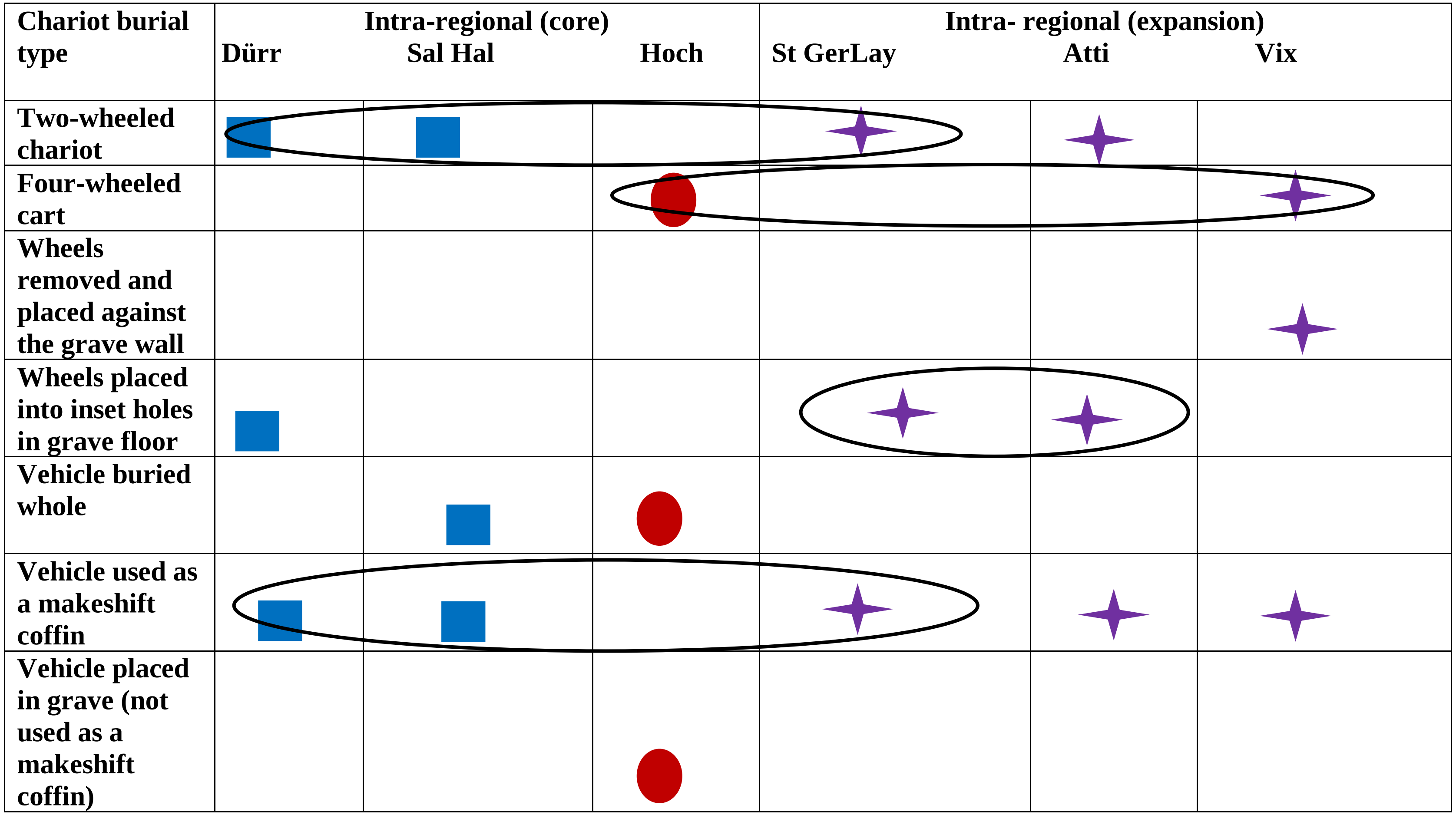
Regional variations suggested by the chariot and/or cart burial practices in the HaD period are designated in Table 3. The following abbreviations in Table 3 designate the above regions in the core: Dürrnberg (Dürr), Saltzwelten Hallein (Sal Hal), Hochdorf (Hoch). Those in the expansion regions include Saint Germain-en-Laye (St GerLay), Attichy (Atti) and Vix (Vix).

Figure 7. Geometric designs (Dechlete, 1914, Figure 4. Original scale not provided).



The documented differences in vehicle burials have been interpreted as indications of status and/or expressions of individual identity among the burial community, rather than representative of population or cultural differences (Collis, 2003; Cunliffe, 1997; James, 2005; Kruta, 1991; Wells, 1998). However, they may also reflect temporal differences, as they are commonly dated by the type of associated artefacts, e.g., fibulae and torcs (Collis, 2003; Cunliffe, 1997; James, 2005; Kruta, 1991; Wells, 1998). Thus, the observed differences in vehicle burials may indicate diachronic rather than social and/or cultural differences. However, these burials have been used to link diverse regions and populations (Collis, 2003; Cunliffe, 1997; James, 2005; Maier, 2003). The archaeological evidence suggests that the populations possessing Hallstatt material culture were not isolated within the core regions. Instead, they had far-reaching contacts with different communities in the expansion regions (Collis, 2003; James, 2005; Kruta, 1991).

Table 3. Intra-and-extra-regional distribution of chariot and/or cart burials during the HaD period.



Chariot burial type	Intra-regional (core)			Intra- regional (expansion)		
	Dürr	Sal Hal	Hoch	St GerLay	Atti	Vix
Two-wheeled chariot	■	■		✦	✦	
Four-wheeled cart			●			✦
Wheels removed and placed against the grave wall						✦
Wheels placed into inset holes in grave floor	■			✦	✦	
Vehicle buried whole		■	●			
Vehicle used as a makeshift coffin	■	■		✦	✦	✦
Vehicle placed in grave (not used as a makeshift coffin)			●			

The differently coloured shapes indicate intra-regional connections within the core and expansion regions. Each geographic region is represented by 1 shape. The black circles indicate possible extra-regional connections. Core regions: Dürrnberg (Dürr), Saltzwelten Hallein (Sal Hal), Hochdorf (Hoch). Expansion regions: Saint Germain-en-Laye (St GerLay), Attichy (Atti) and Vix (Vix).

La Tène archaeological background, location, and spread

The La Tène culture is also named after its type site, La Tène, on the northern side of Lake Neuchâtel in Switzerland which is dated to 450-50/15 BC (Collis, 2003; Cunliffe, 1997; James, 2005; Karl, 2006a; Koch, 2007). Excavations began in 1857 by Hansli Kopp after a prolonged drought lowered the lake level by approximately 2 metres. Eventually, 2,500 objects, mostly weapons, were uncovered (Collis, 2003; Cunliffe, 1997; James, 2005; Koch, 2007). Overall, 166 swords, most without traces of wear, 2,700 lance heads, 22 shield bosses, 385 brooches and chariot parts were found; some animal and human bones were found as well (Cunliffe, 1997; De Navarro, 1972). Interpretations of the site vary. Previous studies have suggested it was destroyed by high water or was a ritual deposition site (Collis, 2003; Cunliffe, 1997; De Navarro, 1972; Frey, 1991; James, 2005; Koch, 2007). This culture has a similar geographic distribution to the preceding Hallstatt, sometimes without a definitive break such that elements specific to each culture appear contemporaneously (Caulfield, 1981; Collis, 2003; Davies, 2000; James, 2005; Poppi, 1991). Consequently, the development of this culture has been interpreted as a consequence of the actual physical movement of Hallstatt populations subsequent to an avalanche that destroyed the salt mine located at the type site during the HaD period (Barth, 1991; Collis, 2003; Frey, 1991; Koch, 2007). This culture has also been intrinsically linked with the Celts based on the La Tène=Celtic paradigm.

The initial division of the Iron Age into the Hallstatt and later La Tène periods by Desor (1873) was purely chronological; no ethnic interpretations concerning the populations associated with the archaeological material were made. However, from the mid 19th century, ethnic definitions were applied to characteristic cultural elements such as art styles, weapons and personal ornaments (Collis, 1997; James, 2005). The early chronological divisions of the La Tène period into early, middle and late were based primarily on differences in artefact style and shape, such as brooch and scabbard shapes (Collis, 2003; Cunliffe, 1997; James, 2005; Koch, 2007). The later chronology of Reinecke (1965), in which the Iron Age was divided into Hallstatt A-D and La Tène A-D, is still used. However, this chronology is problematic because it was devised exclusively from material from southern Germany (Collis, 2003; Evans, 1981). In contrast, Dechelette assigned objects decorated in the Celtic style to the La Tène period, following the prevalent paradigm (Collis, 2003; Cunliffe, 1997; Dechelette, 1910; James, 2005; Koch, 2007). The known distribution of these objects was concentrated in an east-west zone encompassing southern Bohemia, Bavaria, Baden-Württemberg, southwest Germany, and northeastern France; which largely corresponded to the area he assigned to the Celts (Dechelette, 1910). Another system, developed by Müller (1999), that is widely used includes the following subdivisions: La Tène A (LTA, 450-400BC); La Tène B (LTB, 400/390-260/250 BC); La Tène C (LTC, 260/250-150 BC), and La Tène D (LTD, 100-50/15BC) (Collis, 2003; Cunliffe, 1997; Müller et al., 1999). This chronological system is based on temporal differences in artefact types, such as fibulae (Müller et al., 1999).

The above system will be used in this thesis as it is the most common and Celtic populations are predominantly dated following this chronology. However, as in the Hallstatt period, these systems did not account for all the regional variation and distribution of artefacts. Moreover, the distribution of La Tène culture may also have been region-specific, and may not have arrived in all the areas in which it is found at a similar date (Müller et al., 1999). Consequently, the above periods represent the earliest possible chronological divisions for this culture (Müller et al., 1999). As chronological systems based on artefact distribution and diachronic differences are used to categorise Hallstatt and La Tène artefacts, it is difficult to determine whether they represent cultures in their own right with specific origins followed by diffusion and/or assimilation. It is also problematic to assess whether they are overarching terms like "western-Neolithic", within which separate cultures can be identified (Koch, 2006; Kruta, 1991). Although the former is generally more accepted, the specific origins of these cultures are neither easily defined, nor reflective of a general evolution of archaeological cultures, as Reinecke's (1965) terminology implies.

At the beginning of the 5th century BC, the rich chiefdoms of the HaD period, such as Mont Lassois and Heuneburg (eastern France and southern Germany, respectively), were abandoned and the associated rich burials ceased (Caulfield, 1981; Collis, 2003; Cunliffe, 1994; 1997; James, 2005; Koch, 2006; Müller-Scheeßel, 2007). Around the same time, wealthy warrior societies began to appear to the north of these settlement centres (Buchsenschutz, 1995; Burmeister and Müller-Scheeßel, 2007; Caulfield, 1981; Collis, 2003; Cunliffe, 1994; 1997; James, 2005; Koch, 2007). However, not all settlements were abandoned (e.g., Dürrnberg, Austria) and there is no evidence that regions became significantly deserted. This suggests that some populations were able to weather the collapse of the salt mine during the HaD period, e.g., Pottenbrunn, Austria (Collis, 2003; Cunliffe, 1997; James, 2005; Koch, 2007; Maier, 2003; Smith, 2012). Coincident with shifts in settlement location, was an alteration in trading patterns. During the HaD/LTA transition archaeological evidence suggests that trade with Massalia via the Rhone halted, and was reoriented over the Alps to the new Greek towns of Spina and Adria, located near the Italian Adriatic coast, and to Etruscan settlements in the Po Valley (Cunliffe, 1991, 2018; Kruta, 1991; Maier, 2003; Meid, 2008; Stöllner, 2014; Verger, 1987; Wolf, 1993). However, the La Tène culture is not present in all phases throughout the areas to which it spread. During the LTA/LTB transition in some parts of eastern Belgium, Luxembourg, the Hunsrück-Eifel (western Germany) and Baden-Württemberg (southwest Germany) regions the former phase is absent (Barford, 1991; Barrett, 1994; Harding, 2004, 2007; Haffner, 1976; Joachim, 1968, 1991; James, 1993; Koch, 2006). It is unknown whether cultural change was coeval during these transitions or whether they represent different regional manifestations of contemporary cultures (Frey, 1972; Harding, 2007; Pauli, 1978). By the 1900s, the division between the Hallstatt and La Tène periods was defined largely by the presence of specific artefacts. These include fibulae, Gundlingen and Mindelheim swords, Pottery and/or bronze vessels, Mediterranean imports (e.g., Attic pottery, wine flagons, and amphorae) and material type (Harding, 2004, 2007; Haffner, 1976; Heemstra, 2012; Joachim, 1968, 1991; James, 1993; Rapin, 1991; Rigby, 2004).

Those regions for which cultural continuity is evident include Dürrnberg (Austria); Pottenbrunn (Austria); Heuneburg (southern Germany); eastern Belgium, Luxembourg, the Hunsrück-Eifel (western Germany), and Baden-Württemberg (southwest Germany) regions; Bobigny (France); the Marne region (northeastern France); Bucany (Slovakia); Manětín-Hrádek (Czech Republic); Herzogenburg (Hungary), and Pilismarot-Basaharc (Hungary) (Figure 1) (Bujna, 1991; Cowen, 1968, 1970; Haffner, 1976; Joachim, 1968, 1991; James, 1993; Koch, 2006; Kruta, 1991; Neugebauer, 1991; Rabsiler et al., 2017; Ramsl, 2002; Soudska, 1991, 1994; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015). Distributions in artefact type within the above regions are indicated in Table 4. As in the Hallstatt period, while similar artefacts are commonly found within several regions, there are subtle variations in art style and manufacturing technique (Bujna, 1991; Collis, 2003; Koch, 2006; Kruta, 1991; Ramsl, 2002; Soudska, 1991, 1994; Tiefengraber and Wiltschke-Schrotta, 2014, 2015). The following abbreviations are used to designate the above regions in Table 4: Dürrnberg (Dür); Pottenbrunn (Pott); Heuneburg (Heu); Hünsruck-Eifel (HünE); Baden-Württemberg (BadW); Saint-Sulpice (Saint-S); Bobigny (Bob); Marne (Marne); Monte Bibele (Bib); Monte Vecchio

(Vec); Bucany (Buc); Manětín-Hrádek (Man); Herzogenburg (Herz) and Pilismarot-Basaharc (Pil).

These regions may also be linked based on similarities in burial practices. Flat inhumations are common although burials under a tumulus occur contemporaneously (Koch, 2006; Kruta, 1991). Extended supine inhumations, oriented north-south were also common although subtle differences in orientation are evident (Collis, 2003; Cunliffe, 1997; Haffner, 1976; Joachim, 1968; Koch, 2006; Kruta, 1991). Although this transition has been the focus of previous research, the descriptions of artefacts and burial practices are limited and often reported as a site specific chronology. The extent of the documented variation within and between regions is not elaborated on (Collis, 2003; Cunliffe, 1997; Haffner, 1976; Joachim, 1968; Koch, 2006; Kruta, 1991). Therefore, it is difficult to determine the arrival and the incorporation of the La Tène culture into the above regions. It may have developed *in-situ* within some regions, however, there is also evidence of migration being a mechanism for its dispersal. In some regions such as Dürrnberg (Austria), Pottenbrunn (Austria), and the Champagne region (northeast France), the majority of HaD graves were cut into by those from the La Tène period (Charpy, 1996, 2009; Collis, 2003; Koch, 2006; Kruta, 1991; Neugebauer, 1991; Tiefengraber and Wiltschke-Schrotta, 2014, 2015).

Though the La Tène period overall has been the focus of several previous studies, their focus has been primarily on the geographic distribution of artefacts that are often reported on a case-by-case basis (Cunliffe, 1994, 1997; Jerem 1995; Joachim, 1991; Kaenel, 1991; Koch, 2006; Kruta, 1991; Sankot, 1991). This distribution has been documented primarily in a typological and/or descriptive manner (Cunliffe, 1997; Koch, 2006; Kruta, 1991). Bioarchaeological research and population history within the diverse regions possessing La Tène material culture has not been the focus of much research (Cunliffe, 1997; Koch, 2006; Kruta, 1991). Although some regions have been comparatively more extensively documented, most of the descriptions are still vague.

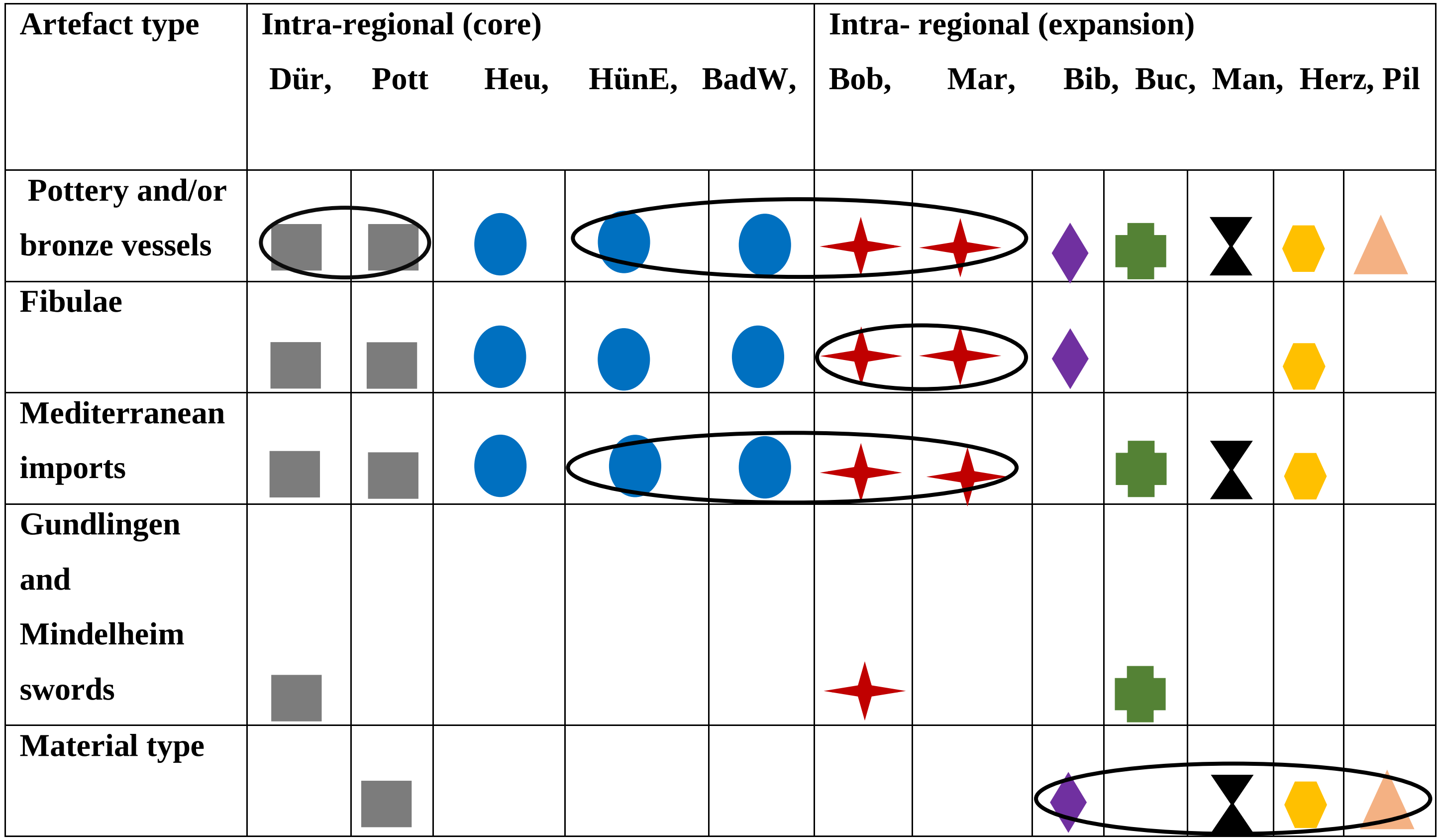
These regions include Austria (Dürrnberg, Pottenbrunn, Mannersdorf and Oberndorf); Switzerland (Münsingen-Rain and Basel-Gasfabrik); Germany (Hunsrück-Eifel, western Germany and Baden-Württemberg, southwest Germany); Czech Republic (Radovesice I and II, Kutná-Hora-Karlov and Manětín-Hrádek); east Yorkshire (Britain) (Rudston Makeshift and Wetwang Slack); France (Bobigny, the Champagne and Marne regions, northeastern France); Spain (the Alpanseque region, Soria, Spain); Romania (Ciumesti and Pişcolt); Italy (Monte Bibele and Monte Vecchio, Bologna); Slovakia (Bucany) and Hungary (Pilismarot-

Basaharc) (Biel, 1991; Bretz-Mahler, 1971; Bondini et al., 2004; Brasili and Belcastro, 2003; Bujna, 1991; Bujna and Romsauer, 1983; Della et al., 2003; Dent, 1982, 1984, 1995; Haffner, 1976; Hellebrandt, 1999; Jerem, 1981; Joachim, 1968; Krämer, 1964; Kruta, 1991; Marion, 2008, 2009; Németi, 1991; Neugebauer, 1991; Ramsl, 2002, 2003, 2011a, 2015; Ramsl et al., 2011b; Raftery, 1991; Soudska, 1991, 1994; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Valentová, 1991; Venclová et al., 2013a, b; Vitali and Lejars, 2010; Waldhauser, 1978, 1993; Wendling and Wiltschke-Schrotta, 2015; Wilde, 1995).

Typical artefacts associated with this period include some forms common to the preceding period, although with more embellishments and elaborate designs (Collis, 2003; De Marinis, 1977; Koch, 2006; Kruta, 1991). Gold and silver objects (e.g., beads, torcs, jewellery, brooches, and belt buckles) are more abundant. Fibulae; rings; bracelets (e.g., glass); torcs; wheel turned pottery; bronze vessels and gifts of meat such as sheep or pig, are common (Figures 8-11). Gundlingen and Mindelheim swords while common decrease in frequency (Bouzek, 2009; Champion, 1995; De Navarro, 1972; Gibson, 1995; Hellebrandt, 1999; Kaenel and Müller, 1989; Maini and Curci, 2013; Piggott, 1950; Pleiner, 1993; Potrebica et al., 2014). Antenna daggers and/or swords (with a characteristic set of paired curled projections at the hilt or top) are more prevalent (Figure 12). Mediterranean imports (e.g., Attic pottery, wine flagons, and amphorae) also increase in frequency. False filigree (ornamental openwork of delicate and intricate design) decorated brooches become common (Marion, 2008, 2009; Rapin, 1991; Soudska, 1994; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Vitali, 2003; Vitali, 2008; Wells, 2008; Wendling and Wiltschke-Schrotta, 2015). Distributions of the above artefacts are indicated in Table 5. Since the majority of previous studies have not consistently dated these artefacts to a specific period, i.e., LTA, those included in Table 5 represent those specific to the La Tène overall.

The above artefacts represent, as in the Hallstatt period, those which have been constantly and comprehensively documented. Consequently, they have been used in numerous previous studies to link diverse regions (Bretz-Mahler, 1971; Bondini et al., 2004; Brasili and Belcastro, 2003; Bujna and Romsauer, 1983; Della et al., 2003; Dent, 1982, 1984, 1995; Haffner, 1976; Hellebrandt, 1999; Marion, 2008, 2009; Soudska, 1994; Thorsten et al., 2017; Vitali, 2003; Vitali, 2008; Vitali and Lejars, 2010). These comparisons, as in the Hallstatt period, are often only based on a limited number of artefacts, are site specific and may therefore not sufficiently document the cultural connections during this period.

Table 4. Intra-and-extra-regional distribution of artefact types during the HaD/LTA transition



Artefact type	**Intra-regional (core)**					**Intra- regional (expansion)**						
	Dür,	**Pott**	**Heu,**	**HünE,**	**BadW,**	**Bob,**	**Mar,**	**Bib,**	**Buc,**	**Man,**	**Herz,**	**Pil**
Pottery and/or bronze vessels	■	■	●	●	●	✦	✦	◆	✚	⧗	⬢	▲
Fibulae	■	■	●	●	●	✦	✦	◆			⬢	
Mediterranean imports	■	■	●	●	●	✦	✦		✚	⧗	⬢	
Gundlingen and Mindelheim swords	■					✦			✚			
Material type		■						◆		⧗	⬢	▲

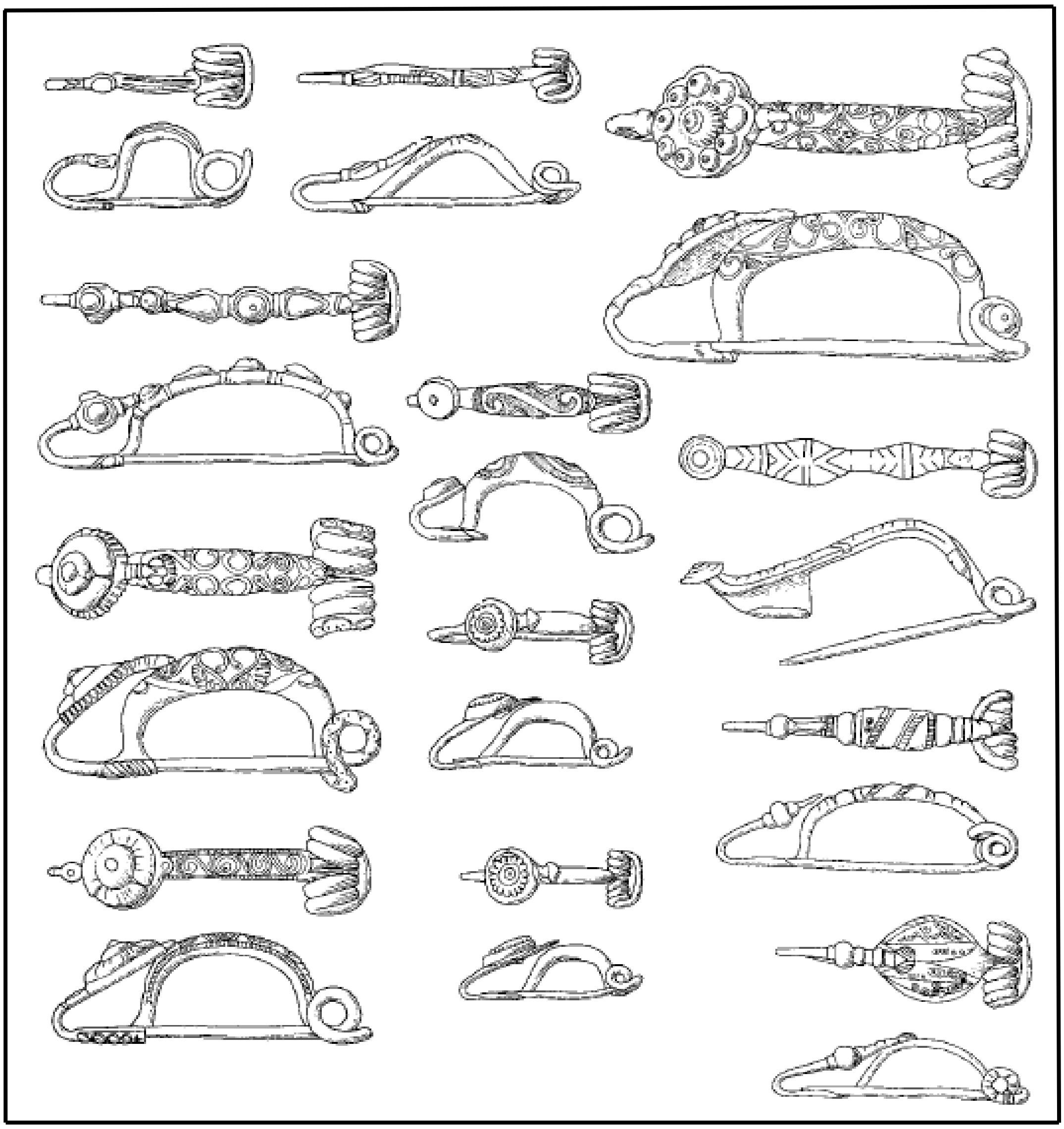
The differently coloured shapes indicate intra-regional connections within the core and expansion regions. Each geographic region is represented by 1 shape. The black circles indicate possible extra-regional connections. Core regions: Dürrnberg (Dür); Pottenbrunn (Pott); Heuneburg (Heu); Hünsruck-Eifel (HünE); Baden-Württemberg (BadW). Expansion region: Saint-Sulpice (Saint-S); Bobigny (Bob); Marne (Marne); Monte Bibele (Bib); Monte Vecchio (Vec); Bucany (Buc); Manětín-Hrádek (Man); Herzogenburg (Herz) and Pilismarot-Basaharc (Pil).

Additionally, as in the Hallstatt period, these artefacts represent those characteristic of the La Tène period in the above regions, as opposed to a comprehensive list (See page 19). Although the above artefacts have been used to characterize this period, they are not specific to this culture. Fibulae are also commonly associated with other cultures, including the Italic groups (Collis, 2003; D’Agostino, 1974, 1988; D'Agostino and Gastaldi, 1988; De Natale, 1992; Fredericksen, 1974; Koch, 2006; Serritella, 1995).

The intrinsic link between these objects and Celtic groups is related to the application of the La Tène=Celtic paradigm to diverse populations possessing specific artefacts. This association is accepted but not elaborated on in the field of Celtic studies (Collis, 2003; Cunliffe, 1997, 2009; Giles, 2012; Koch, 2006). The artefacts themselves may not be linked to one specific population, but their design and manufacture may be. Therefore, their association with Celtic groups is tenuous. However, in spite of this limitation, various connections are indicated by the distributions of artefacts, burial practices and art styles during this period (Biel, 1991, 2012; Bondini et al., 2004; Bujna, 1991; Budinský and Waldhauser, 2001, 2004; Charpy, 1991; Good, 2005; Haffner, 1976; Hellebrandt and Hellebrandt, 1999; Horváth, 1987; Joachim, 1968; Koch, 2006; Megaw, 1972; Németi, 1991; Marion et al., 2005a, b; Ramsl, 2002, 2011a, 2015; Ramsl et al., 2011b; Roulet, 1991; Rustoiu, 2008, 2011a, b, 2012, 2014; Rustoiu and Egri, 2014; Salac, 2011; Soudska, 1991, 1994; Stead, 1979, 1991; Tiefengraber and Wiltschke-Schrotta, 2012, 2014, 2015; Tanko, 2015; Vitali, 2003, 2008; Vitali and Lejars, 2010; Vitali, 2008; Valentová, 1991, 1993; Valentová and Sankot, 2012; Waldhauser, 1993).

The following abbreviations are used to designate the above regions in Table 5: Dürrnberg (Dür); Pottenbrunn (Pott); Mannersdorf (Mann); Oberndorf (Obe); Münsingen-Rain (MR); Basel-Gasfabrik (BG); Hunsrück-Eifel (HünE); Baden-Württemberg (BadW); Radovesice (Rad); Kutná-Hora-Karlov (KHK); Manětín-Hrádek (Man); Rudston Makeshift (Rud); Wetwang Slack (WWS); Bobigny (Bob); Champagne (Ch); Marne (Mar); Alpanseque (Alp); Pişcolt (Pi); Monte Bibele (Bib); Monte Vecchio (Vec); Bucany (Buc) and Pilismarot-Basaharc (Pil).

Figure 8. Diverse La Tène fibulae from Münsingen-Rain, Switzerland. The designs are also common in Austria (Hodson, 1964, Figure 22. Original scale not provided).



In spite of the above issues, the dispersals suggested by Table 5 indicate that the intra-and-extra-regional contacts developed during the La Tène period (1,200-475 BC) may have expanded and diversified compared to those during the Hallstatt period (450-50/15 BC) (Table 8) (Collis, 2003; De Marinis, 1977; James, 2005; Kruta, 1991; Wells, 2008). However, the nature of this dispersal has not been the focus of much research. The artefact distributions indicated by Table 5 suggest that it was more complex than previously assumed (Collis, 2003; Cunliffe, 1997; Koch, 2006).

Figure 9. Bracelet type and design common in Switzerland and Austria during the Hallstatt D-La Tène periods (modified from Hodson, 1964, Figure 58. Original scale not provided).

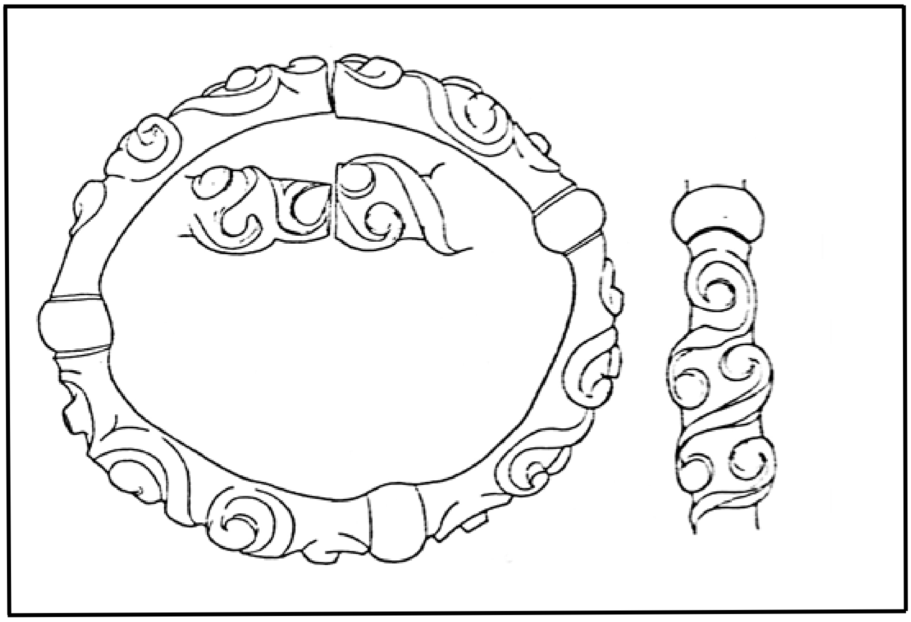


Figure 10. La Tène glass bracelet, design common in Switzerland and Austria (Hodson, 1964, Figure 73. Original scale not provided).

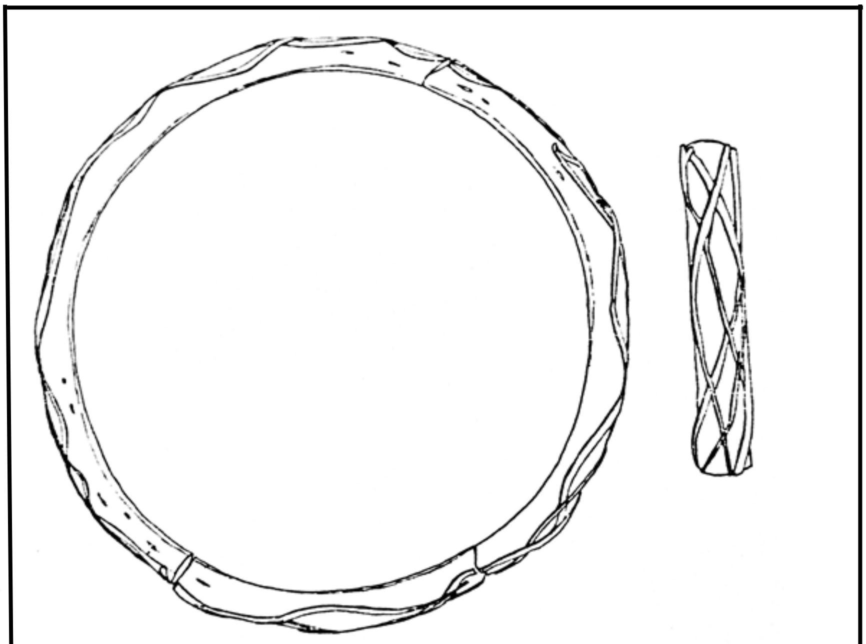


Figure 11. Torc Münsingen-Rain, Switzerland. The design is also common in Germany (Hodson, 1964, Figure 4. Original scale not provided).

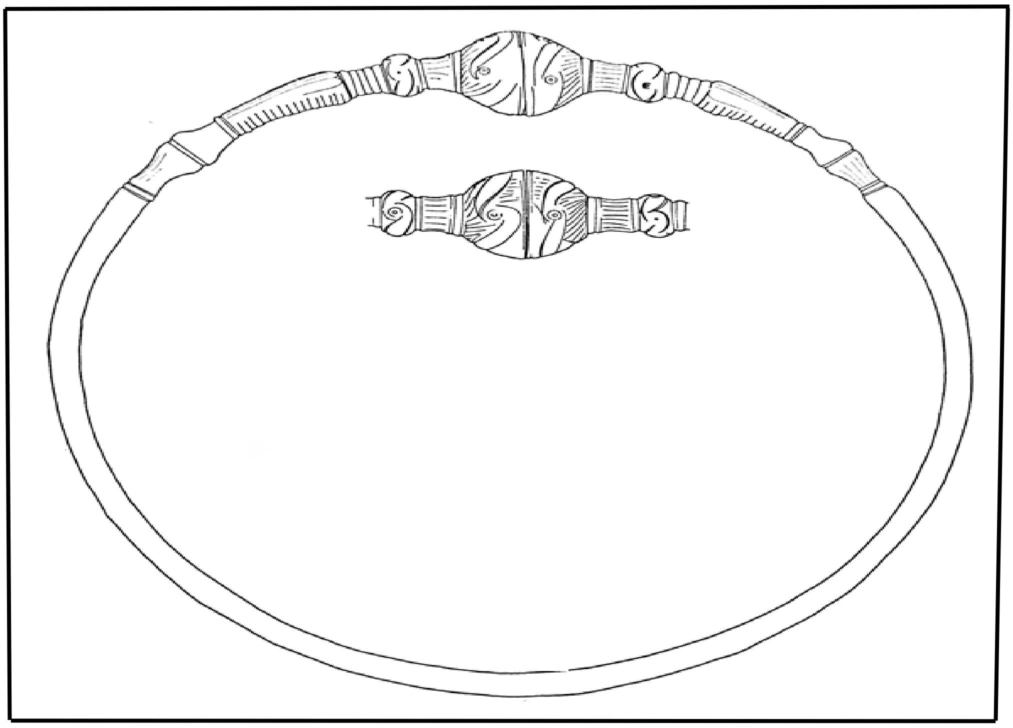
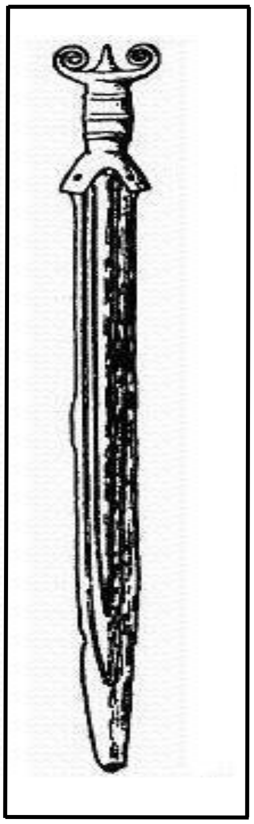


Figure 12. Antennae sword from La Tène, Switzerland (Child, 1930, Figure 2. Original scale not provided).

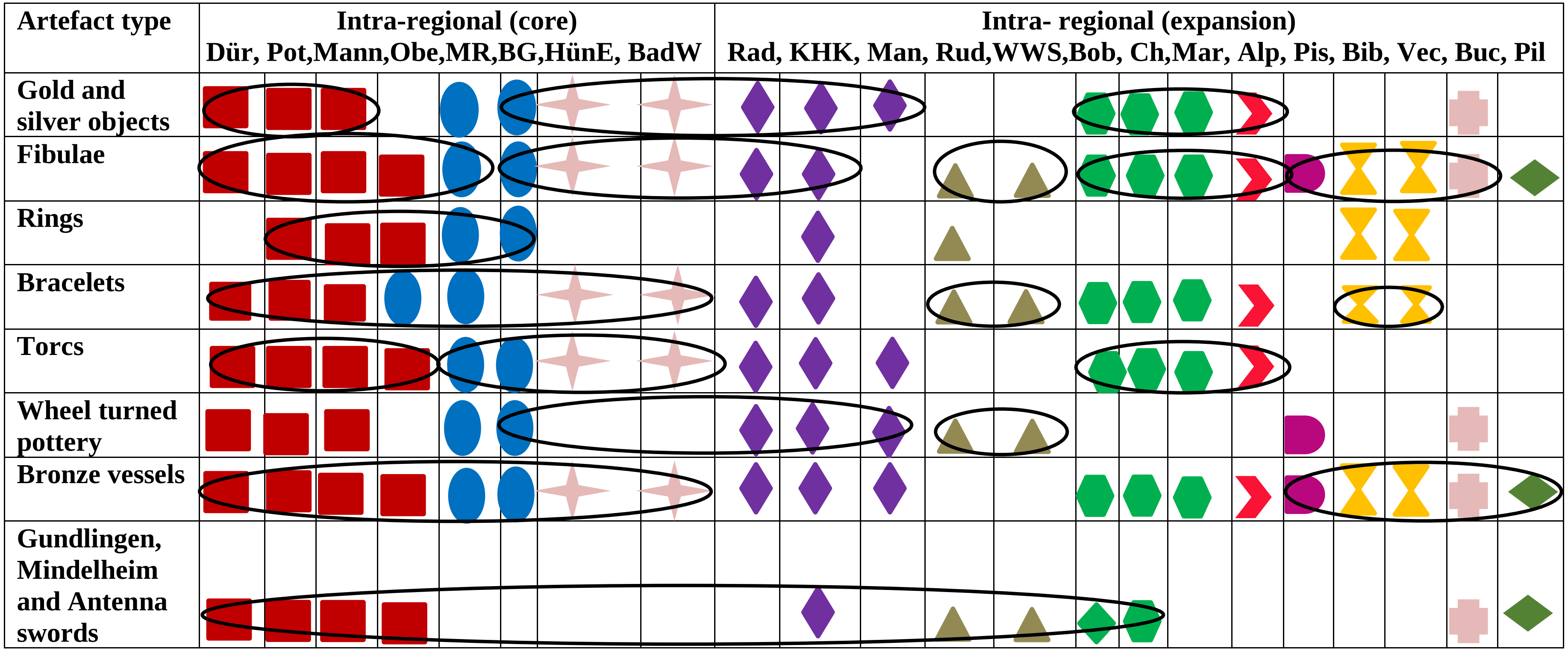


Regional variations in artefact manufacture and design are also common during this period. Local versions of La Tène artefacts (e.g., fibulae, torcs, and glass bracelets) copied the shape, design, and materials of the imports, creating new objects with varied local designs (Bouzek, 2009; Collis, 2003; Cunliffe, 1995b, 1997; Harding, 2007). Trans-Alpine contacts with Mediterranean regions introduced a range of classical plant motifs that influenced the subsequent development of La Tène art styles (Champion, 1976; Frey, 1972; Gosden et al., 2014; Harding, 2007; Megaw and Megaw, 1989, 2001; Pauli, 1978).

Two common motifs derived from imported natural designs are the palmette and the lotus (Figures 13 and 14) (Duval, 1991; Harding, 2007; Jope, 1995b; Laing and Laing, 1992; Laing, 2006). The incorporation of these elements was achieved in part by breaking up classical motifs into their component features, and subsequently re-assembling them in a new and unique composition (Harding, 2007; Laing and Laing, 1992; Harding, 2007; Szabó and Petres, 1992; Soudska, 1994; Waldhauser, 1978). This is evident in the composition of the palmette, which is commonly rendered as a simplified three-leaved motif in Mediterranean imports (Figure 14). In this period, the palmette is often split in half or further reduced to individual leaves (Harding, 2007; Laing and Laing, 1992; Megaw and Megaw, 1989, 2001). During subsequent periods La Tène art styles shifted towards movement-based forms, such as triskeles (a motif consisting of three interlocking spirals), S shapes and/or scroll motifs, animal and plant forms (Figure 16) (Duval, 1991; Harding, 2007; Laing and Laing, 1992; Megaw and Megaw, 2001; Verger, 1987). Metalwork in bronze, iron, and gold is characterized by inscribed and inlaid intricate spirals, enamelled designs and dragon pairs on scabbards (Figure 17) (Collis, 2003; Cunliffe, 1997; De Marinis, 1977; Eglof, 1991; Haseloff, 1991; Harding, 2007; Laing and Laing, 1992; Laing, 2006; Manning, 1995; Northover, 1984, 1995).

Dragon pairs comprise what has sometimes been regarded as a zoomorphic lyre, or a pair of opposed S-shapes with zoomorphic dragon like heads facing inwards and is common throughout Central Europe. This style may indicate the presence of a far-reaching trade network(s) due to its broad distribution (Green, 1996; Harding, 2007; Laing and Laing, 1992; Stead, 1984a, b; Szabó, 1974; Szabó and Petres, 1992). Regional variations are also common, as evident in the enamelled designs common in east Yorkshire (Britain) (Harding, 2007; Laing and Laing, 1992; Laing, 2006). Most of the metal objects in this region are decorated with brightly coloured (usually red and blue) enamelled designs (Harding 2007; Laing and Laing, 1992; Laing, 2006).

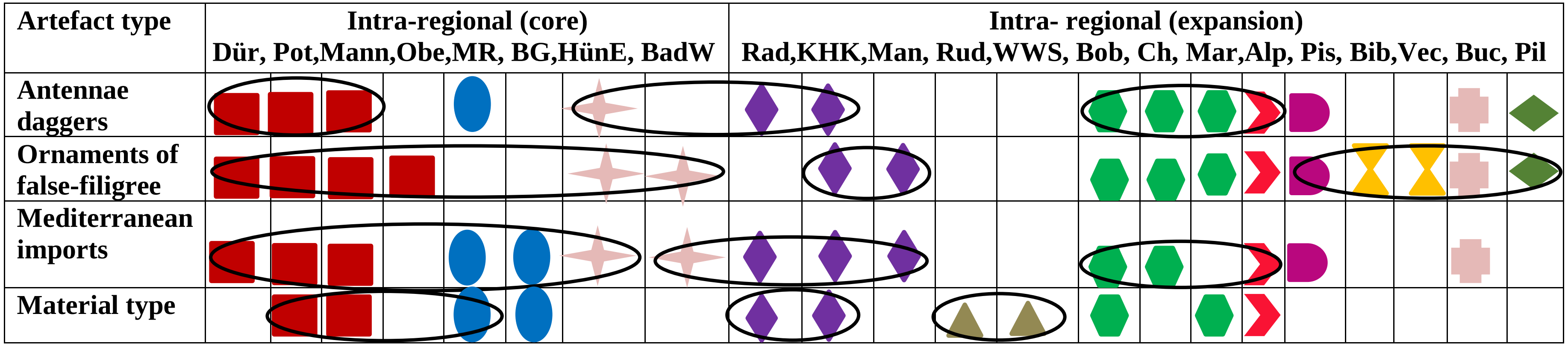
Table 5. Intra-and-extra-regional distribution of artefact types during the La Tène period.



Artefact type	Intra-regional (core)								Intra- regional (expansion)													
	Dür	Pot	Mann	Obe	MR	BG	HünE	BadW	Rad	KHK	Man	Rud	WWS	Bob	Ch	Mar	Alp	Pis	Bib	Vec	Buc	Pil
Gold and silver objects	■	■	■		●	●	✦	✦	◆	◆	◆			⬢	⬢	⬢	❯				✚	
Fibulae	■	■	■	■	●	●	✦	✦	◆	◆		▲	▲	⬢	⬢	⬢	❯	◗	⧗	⧗	✚	◆
Rings		■	■	■	●	●				◆		▲							⧗	⧗		
Bracelets	■	■	■	●	●		✦	✦	◆	◆		▲	▲	⬢	⬢	⬢	❯		⧗	⧗		
Torcs	■	■	■	■	●	●	✦	✦	◆	◆	◆			⬢	⬢	⬢	❯					
Wheel turned pottery	■	■	■		●	●			◆	◆	◆	▲	▲					◗			✚	
Bronze vessels	■	■	■	■	●	●	✦	✦	◆	◆	◆			⬢	⬢	⬢	❯	◗	⧗	⧗	✚	◆
Gundlingen, Mindelheim and Antenna swords	■	■	■	■						◆		▲	▲	◆	⬢						✚	◆

The differently coloured shapes indicate intra-regional connections within the core and expansion regions. Each geographic region is represented by 1 shape. The black circles indicate possible extra-regional connections. Core region: Dürrnberg (Dür); Pottenbrunn (Pott); Mannersdorf (Mann); Oberndorf (Obe); Münsingen-Rain (MR); Basel-Gasfabrik (BG); Hunsrück-Eifel (HünE); Baden-Württemberg (BadW). Expansion region: Radovesice (Rad); Kutná-Hora-Karlov (KHK); Manětín-Hrádek (Man); Rudston Makeshift (Rud); Wetwang Slack (WWS); Bobigny (Bob); Champagne (Ch); Marne (Mar); Alpanseque (Alp); Pişcolt (Pi); Monte Bibele (Bib); Monte Vecchio (Vec); Bucany (Buc) and Pilismarot-Basaharc (Pil).

Table 5 continued. Intra-and-extra-regional distribution of artefact types during the La Tène period.



The differently coloured shapes indicate intra-regional connections within the core and expansion regions. Each geographic region is represented by 1 shape. The black circles indicate possible extra-regional connections. Core region: Dürrnberg (Dür); Pottenbrunn (Pott); Mannersdorf (Mann); Oberndorf (Obe); Münsingen-Rain (MR); Basel-Gasfabrik (BG); Hunsrück-Eifel (HünE); Baden-Württemberg (BadW). Expansion region: Radovesice (Rad); Kutná-Hora-Karlov (KHK); Manětín-Hrádek (Man); Rudston Makeshift (Rud); Wetwang Slack (WWS); Bobigny (Bob); Champagne (Ch); Marne (Mar); Alpanseque (Alp); Pişcolt (Pi); Monte Bibele (Bib); Monte Vecchio (Vec); Bucany (Buc) and Pilismarot-Basaharc (Pil).

This technique involved carving designs into the surface of an object, filling them with powdered material, such as glass or coral, and firing until this material melted into a cohesive enamel structure (Champion, 1976; Giles, 2007; Harding, 2004, 2007; Laing and Laing, 1992; Stead, 1991a). The distributions of the above art styles throughout the La Tène period overall are indicated in Table 6. Although some variations and dispersals in style and technique have been typologically described, the majority have not been comprehensive.

Those that have been described are common in several regions including Austria (Dürrnberg, Pottenbrunn, Mannersdorf, and Oberndorf); Switzerland (Münsingen-Rain and Basel-Gasfabrik); Germany (Hunsrück-Eifel, western Germany, and Baden-Württemberg, southwest Germany); the Czech Republic (Radovesice I and II, Kutná-Hora-Karlov and Manětín-Hrádek); east Yorkshire (Britain) (Rudston Makeshift and Wetwang Slack); France (Bobigny, the Champagne and Marne regions, northeastern France); Italy (Monte Bibele and Monte Vecchio, Bologna); Slovakia (Bucany) and Hungary (Pilismarot-Basaharc) (Bataille et al., 2014; Biel, 1991; Bergmann, 2015; Bujan, 1991; Bujna and Romsauer, 1983; Champion, 1976; Charpy, 1991; Cunliffe, 1991, 2009; Duval, 1991; Harding, 2007; Hellebrandt and Hellebrandt, 1999; Kimmig, 1991; Laing and Laing 1992; Moosleitner et al., 1974; Németi, 1988, 1992, 1993; Neugebauer, 1991; Pauli, 1978; Penninger, 1972; Ramsl, 2011a, 2015; Ramsl et al., 2011b; Soudska, 1991, 1994; Stead, 1965b, 1991a; Venclová et al., 2013a, b). The following abbreviations are used to designate the above regions in Table 6: Dürrnberg (Dür); Pottenbrunn (Pott); Mannersdorf (Mann); Oberndorf (Obe); Münsingen-Rain (MR); Basel-Gasfabrik (BG); Hunsrück-Eifel (HünE); Baden-Württemberg (BadW); Radovesice (Rad); Kutná-Hora-Karlov (KHK); Manětín-Hrádek (Man); Rudston Makeshift (Rud); Wetwang Slack (WWS); Bobigny (Bob); Champagne (Ch); Marne (Mar); Monte Bibele (Bib); Bucany (Buc); Alpanseque (Alp); and Pilismarot-Basaharc (Pil).

Figure 13. Lotus motif. Arrows indicate sequential changes of the design (Adapted from Walters, 1893, Figure 2. Original scale not provided).

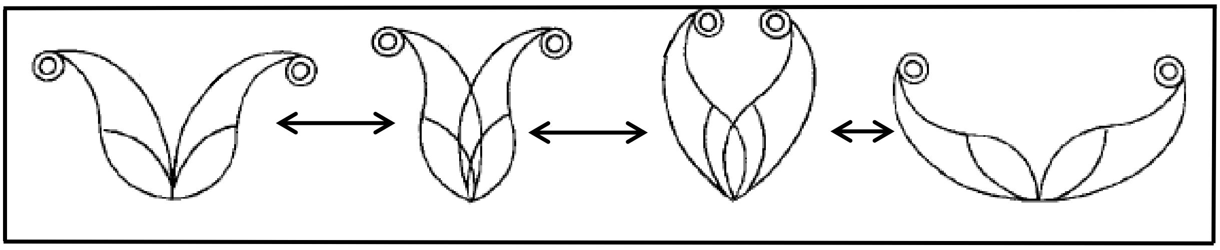


Figure 14. Palmette (Adapted from Walters, 1893, Figure 4. Original scale not provided).

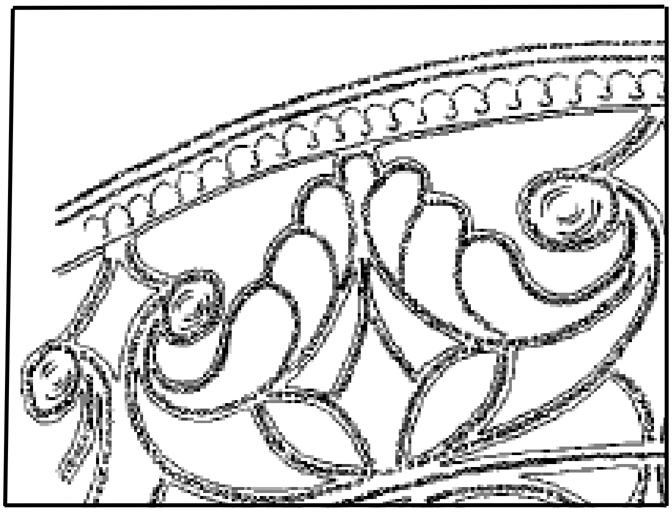


Figure 15. Triskeles (Jacobsthal, 1944, Figure 5. Original scale not provided).

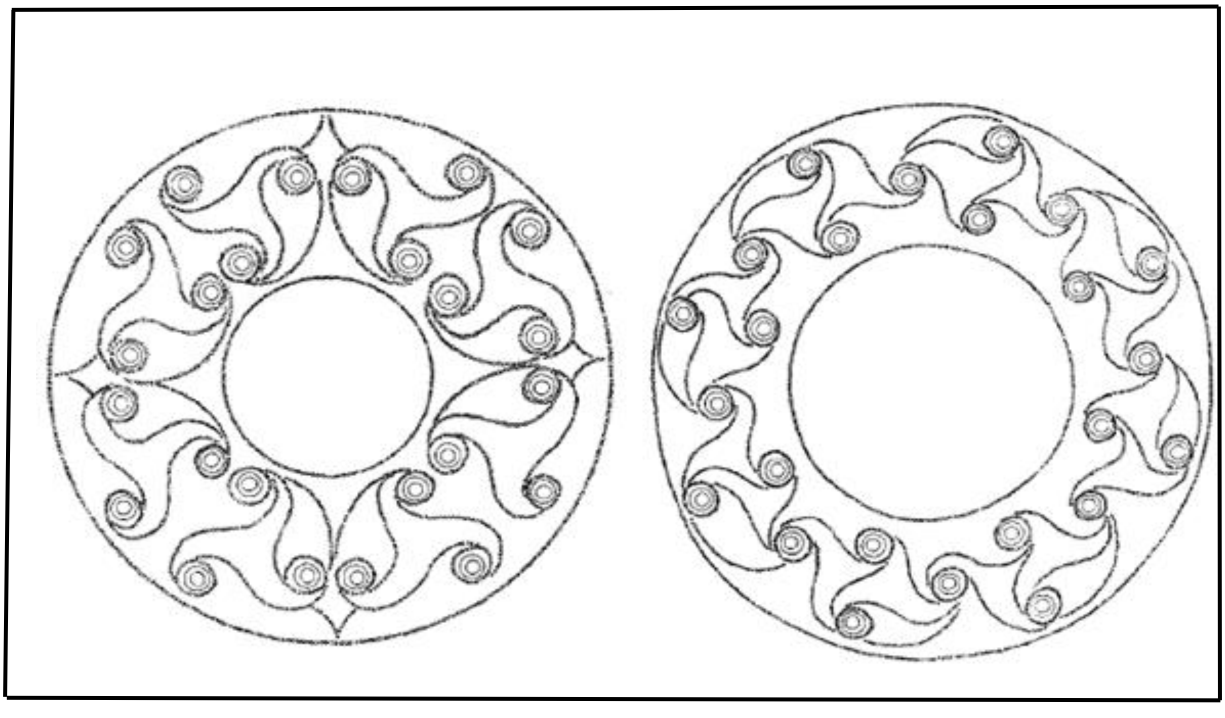


Figure 16. S shapes and/or scroll motifs (Jacobsthal, 1944, Figure 6. Original scale not provided).

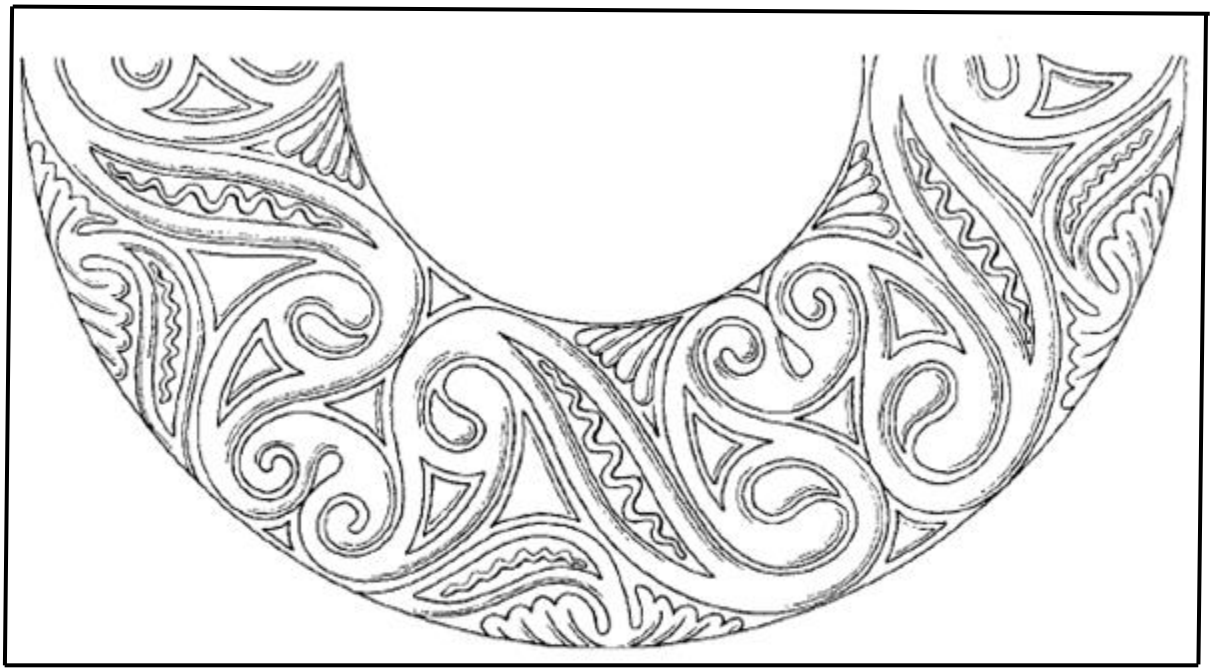
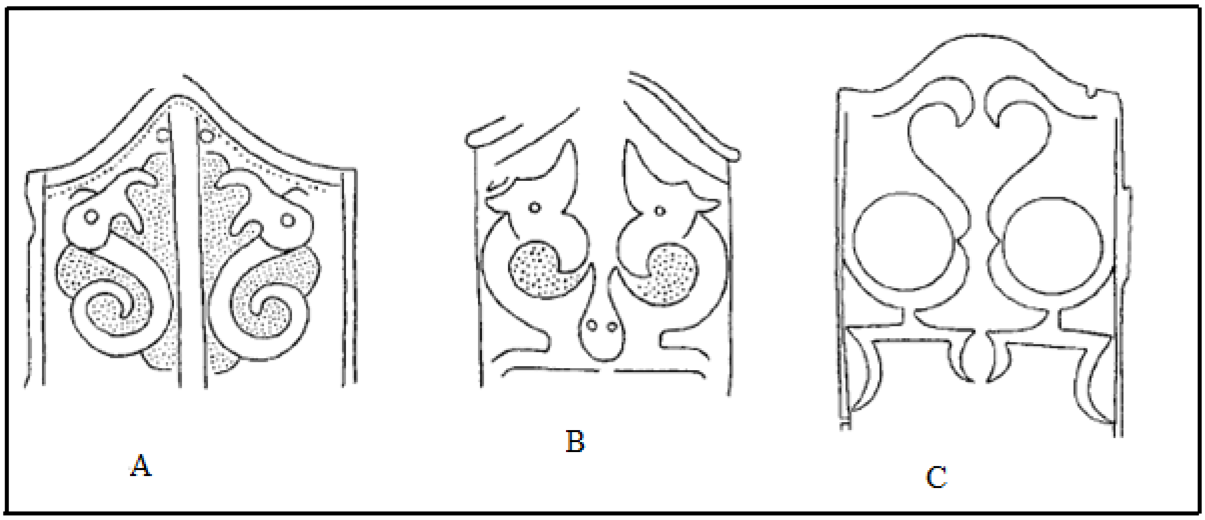


Figure 17. Dragon pairs on scabbards. Type A, Taliándörögd, Hungary; B, Type II, Münsingen, Switzerland; C, Type III, La Tène, Switzerland (Adapted from de Navarro, 1972; Stead 1984, Figure 5. Original scales not provided).



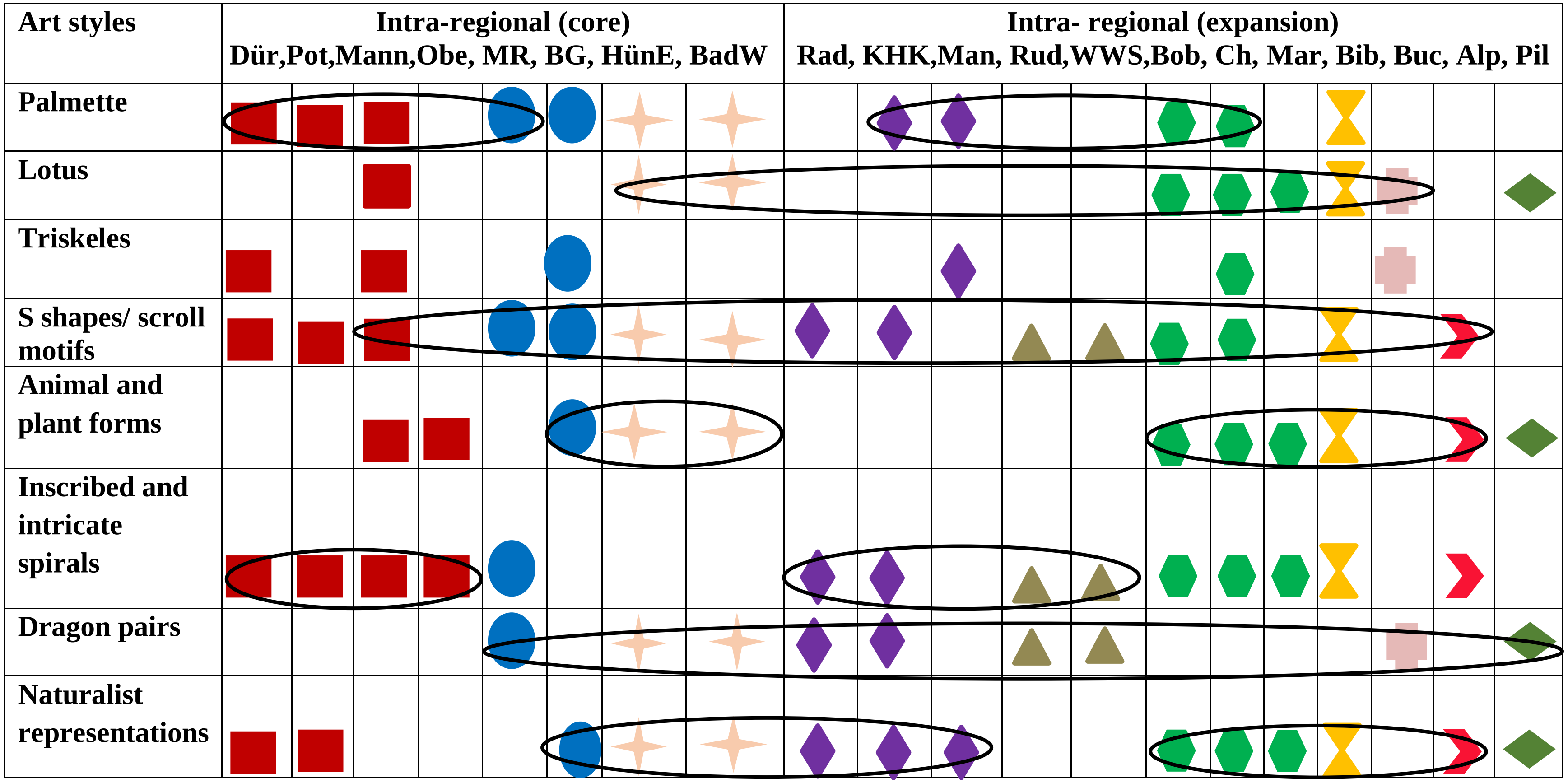
Additional connections are indicated by the documented burial practices throughout the above regions. Diachronic changes are evident during some transition periods. During the LTB/LTC transition, wealthy burials with tumuli decrease in frequency and flat inhumation graves increase (Cunliffe, 1997; Collis, 2003; Stead, 1979, 1991a; Thomas, 2003). In the LTC/LTD transition, cremation and flat inhumation burials occur contemporaneously (Cunliffe, 1991, 1997; Collis, 2003). During the La Tène period overall, burial practices are similar but subtle differences in position and orientation (e.g., north-south versus east-west and extended versus flexed) are observed (Cunliffe, 1984, 1991, 1997; Collis, 2003; Jones, 1996; Koch, 2006; Stead, 1991a; Smith, 2012; Wells, 1998). However, a greater degree of variation, similar to those in the Hallstatt period, is evident in the vehicle burials (Hawkes, 1960; Jay et al., 2012, 2013; Stead, 1965b, 1979, 1986; 1991; Stead and Rigby, 1999; Tiefengraber and Wiltschke-Schrotta, 2012; Van Endert, 1987; Wells, 1995a, b, c). The symbolic interpretation of these burials is still debated. Previous studies have suggested these burials are indications of status or represent a specific social class, e.g., warriors (Anthoons, 2011; Jay et al., 2012, 2013; Jay and Montgomery, 2020; Tiefengraber and Wiltschke-Schrotta, 2012).

The distributions of vehicle burials during the La Tène period are indicated in Table 7 (Biel, 1981; Berthelier-Ajot, 1991; Briggs, 2014; Claude, 2003; Diepeveen-Jansen, 2007; Furger-Gunti, 1991; Giles, 2012; Joffroy, 1954, 1961, 1962). Like in the Hallstatt period, these differences may also be temporal as the above burials are dated by the type and/or design of associated artefacts (Collis, 2003; Cunliffe, 1979, 1997; James, 2005; Kruta, 1991; Wells, 1998). Those regions which have notable documented variations in vehicle burials include Austria (Dürrnberg and Saltzwelten Hallein), Germany (Hochdorf, southern Germany), east Yorkshire (Britain) (Wetwang Slack, Kirkburn and Garton Station) and France (Somme-Bionne, Vix, Attichy, Saint Germain-en-Laye, and the Champagne and Marne regions) (Figures 18 and 19) (Biel, 1981; Berthelier-Ajot, 1991; Briggs, 2014; Claude, 2003; Collis, 1975, 1991, 2003, 2004; Diepeveen-Jansen, 2007; Dupuis, 1940; Furger-Gunti, 1991; Giles, 2012; Joffroy, 1954, 1961, 1962; Stead, 1991a; Stillingfleet, 1846). The following abbreviations will be used to designate those regions in Table 7. Dürrnberg (Dür); Saltzwelten Hallein (SH); Hochdorf (Hoch); Wetwang Slack (WWS); Kirkburn (Kir); Garton Station (GS); Somme-Bionne (SB); Champagne (Ch); Marne (Mar); Saint Germain-en-Laye (SGL); Attichy (At) and Vix (Vix). The vehicle burials from the HaD/LTA transition are also included in Table 7 as it is unknown which period they are dated (Bergmann, 2015; Brewster, 1971, 1980; Biel, 1981; Briggs, 2014; Claude, 2003; Chadwick, 1970; Dent, 1984, 1985; Fitzpatrick, 1984, 2007; Stead, 1991a; Stead and Rigby, 1999; Thorsten et al., 2017; Van Endert, 1987; Wells, 1995a, b, c).

Although the differences and dispersals of artefacts, art style, and burial practices have been documented during the Hallstatt and La Tène periods, their descriptions are vague, distributions are not often elaborated upon and they are regularly described as belonging to the period overall (Collis, 2003; Koch, 2006; Kruta, 1991). Some studies have attempted to provide comprehensive descriptions and dates to a specific period, e.g., LTA, although they are not common (Bondini et al., 2004; Bujna and Romsauer, 1983; Haffner, 1976; Hellebrandt, 1999; Joachim, 1968). In numerous previous studies, the observed differences are often reported on a case-by-case basis with little attempt at regional comparison (Bondini et al., 2004; Bujna and Romsauer, 1983; Cunliffe, 2009; Haffner, 1976; Hellebrandt, 1999; Joachim, 1968). Those that have attempted regional comparisons often only describe overall similarities which have been used to link broad geographic regions (Almássy, 2009; Bretz-Mahler, 1971; Bondini et al., 2004; Brasili and Belcastro, 2003; Bujna and Romsauer, 1983; Della et al., 2003; Dent, 1982, 1984, 1995; Haffner, 1976; Hellebrandt, 1999; Marion, 2008, 2009; Soudska, 1994; Thorsten et al., 2017; Vitali, 2003; Vitali, 2008; Vitali and Lejars, 2010).

Therefore, it is difficult to determine whether the observed diversity represents regional copies of trade and/or prestige items, *in-situ* change through time or migration events. Further, as these comparisons are often based on one, or a limited number of artefacts, it is difficult to determine if these broad comparisons adequately represent actual regional similarities in material culture (Bondini et al., 2004; Brasili and Belcastro, 2003; Bujna and Romsauer, 1983; Cunliffe, 2018; Della et al., 2003; Dent, 1982, 1984; Haffner, 1976; Hellebrandt, 1999; Hellebrandt and Hellebrandt, 1990; Joachim, 1968; Marion, 2008, 2009; Möllers et al., 2007; Soudska, 1994; Thorsten et al., 2017; Vitali, 2003; Vitali, 2008; Vitali and Lejars, 2010). It is also difficult to assess whether they are the result of the vague artefact descriptions or are based on presumed cultural similarities. Although the archaeological evidence suggests diverse intra-and-extra-regional contact, the nature of the associated descriptions make comprehensive comparisons difficult based on this evidence alone. However, despite this limitation, the observed diversity in artefacts, burial practice, and art styles indicates that connections during this period were likely more complex than previously presumed. Therefore, trade, migration, cultural diffusion and/or assimilation cannot be ruled out as possible mechanisms for the spread of the Hallstatt and La Tène material cultures.

Table 6. Intra-and-extra-regional distribution of art styles during the La Tène period.



Art styles	**Intra-regional (core)** **Dür,Pot,Mann,Obe, MR, BG, HünE, BadW**								**Intra- regional (expansion)** **Rad, KHK,Man, Rud,WWS,Bob, Ch, Mar, Bib, Buc, Alp, Pil**											
Palmette	■	■	■		●	●	✦	✦		◆	◆			⬢	⬢		⧗			
Lotus			■				✦	✦						⬢	⬢	⬢	⧗	✚		◆
Triskeles	■		■			●					◆				⬢			✚		
S shapes/ scroll motifs	■	■	■		●	●	✦	✦	◆	◆		▲	▲	⬢	⬢		⧗		❯	
Animal and plant forms			■	■		●	✦	✦						⬢	⬢	⬢	⧗		❯	◆
Inscribed and intricate spirals	■	■	■	■	●				◆	◆		▲	▲	⬢	⬢	⬢	⧗		❯	
Dragon pairs					●		✦	✦	◆	◆		▲	▲					✚		◆
Naturalist representations	■	■				●	✦	✦	◆	◆	◆			⬢	⬢	⬢	⧗		❯	◆

The differently coloured shapes indicate intra-regional connections within the core and expansion regions. Each geographic region is represented by 1 shape. The black circles indicate possible extra-regional connections. Core regions: Dürrnberg (Dür); Pottenbrunn (Pott); Mannersdorf (Mann); Oberndorf (Obe); Münsingen-Rain (MR); Basel-Gasfabrik (BG); Hunsrück-Eifel (HünE); Baden-Württemberg (BadW). Expansion region: Radovesice (Rad); Kutná-Hora-Karlov (KHK); Manětín-Hrádek (Man); Rudston Makeshift (Rud); Wetwang Slack (WWS); Bobigny (Bob); Champagne (Ch); Marne (Mar); Monte Bibele (Bib); Bucany (Buc); Alpanseque (Alp); and Pilismarot-Basaharc (Pil).

Figure 18. Somme-Bionne chariot burial. (colloque d'archéologie, 1897. Original scale not provided).

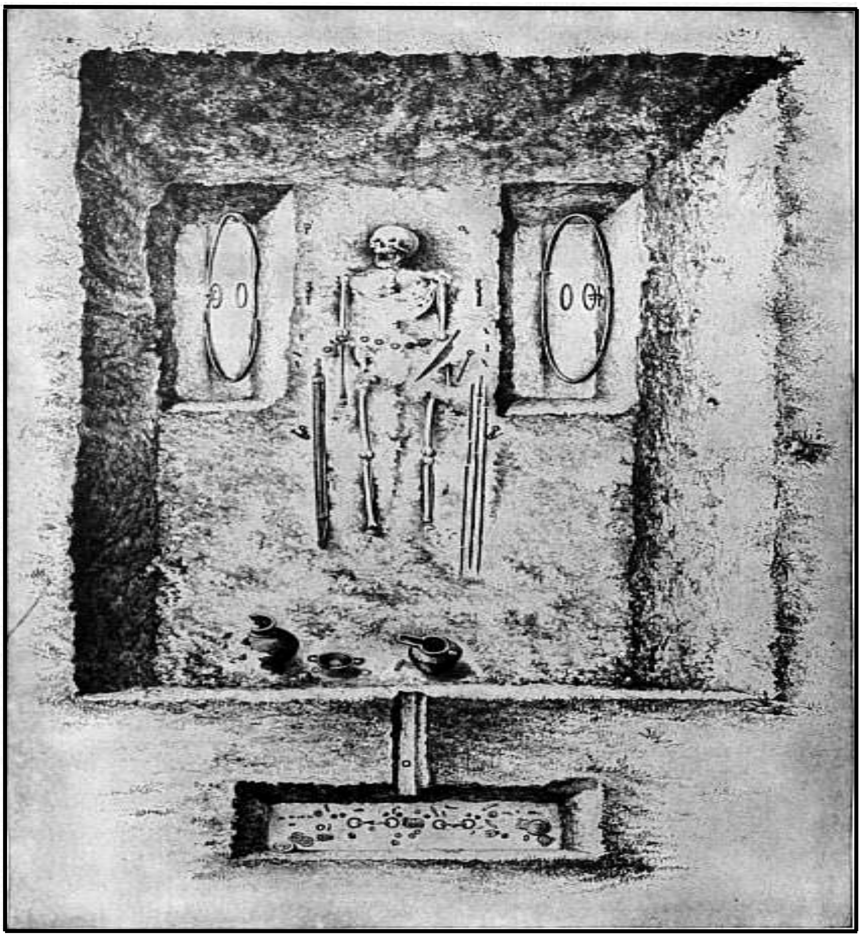


Figure 19. Saint Germain-en-Laye chariot burial (Gastebois & Fourdrignier, 1877. Original scale not provided).

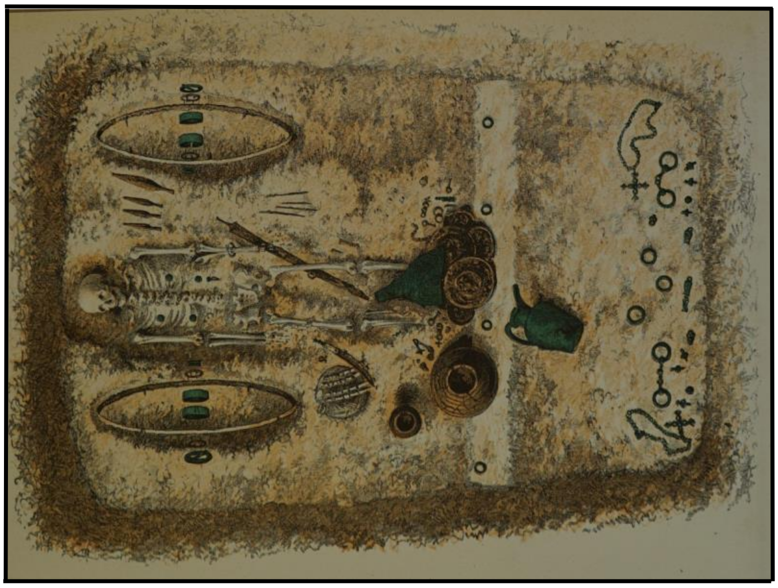
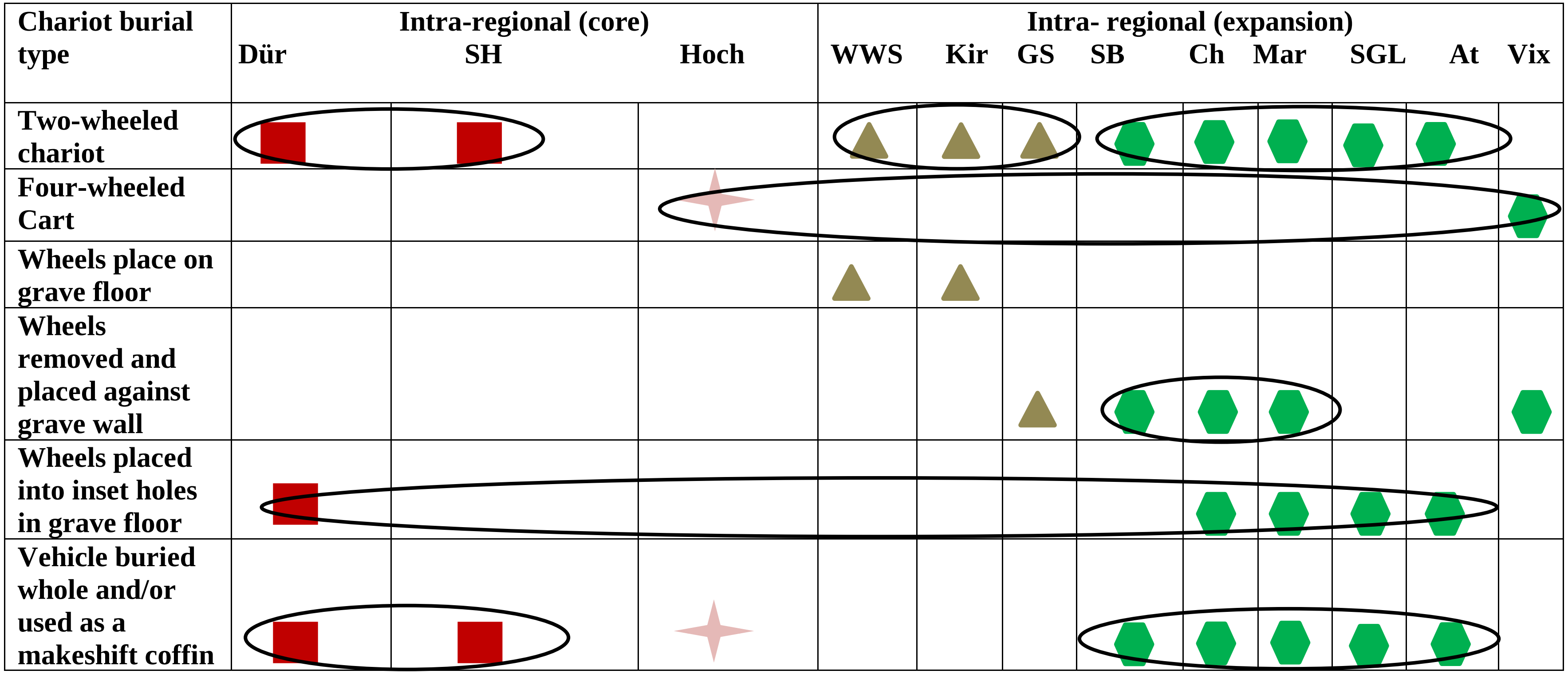


Table 7. Intra-and-extra-regional distribution of chariot and/or cart burials during the La Tène period.



Chariot burial type	**Intra-regional (core)**			**Intra- regional (expansion)**								
	Dür	**SH**	**Hoch**	**WWS**	**Kir**	**GS**	**SB**	**Ch**	**Mar**	**SGL**	**At**	**Vix**
Two-wheeled chariot	🟥	🟥		▲	▲	▲	⬢	⬢	⬢	⬢	⬢	
Four-wheeled Cart			✦									⬢
Wheels place on grave floor				▲	▲							
Wheels removed and placed against grave wall						▲	⬢	⬢	⬢			⬢
Wheels placed into inset holes in grave floor	🟥							⬢	⬢	⬢	⬢	
Vehicle buried whole and/or used as a makeshift coffin	🟥	🟥	✦				⬢	⬢	⬢	⬢	⬢	

The differently coloured shapes indicate intra-regional connections within the core and expansion regions. Each geographic region is represented by 1 shape. The black circles indicate possible extra-regional connections. Core regions: Dürrnberg (Dür); Saltzwelten Hallein (SH); Hochdorf (Hoch). Expansion regions: Wetwang Slack (WWS); Kirkburn (Kir); Garton Station (GS); Somme-Bionne (SB); Champagne (Ch); Marne (Mar); Saint Germain-en-Laye (SGL); Attichy (At) and Vix (Vix).

Table 7 continued. Intra-and-extra-regional distribution of chariot and/or cart burials during the La Tène period.

Chariot burial type	**Intra-regional (core)**			**Intra- regional (expansion)**								
	Dür	**SH**	**Hoch**	**WWS**	**Kir**	**GS**	**SB**	**Ch**	**Mar**	**SGL**	**At**	**Vix**
Vehicle dismantled and used as a makeshift coffin				▲	▲	▲		⬢	⬢			
Vehicle placed in grave (not used as a makeshift coffin)			✦									

The differently coloured shapes indicate intra-regional connections within the core and expansion regions. Each geographic region is represented by 1shape. The black circles indicate possible extra-regional connections. Core regions: Dürrnberg (Dür); Saltzwelten Hallein (SH); Hochdorf (Hoch). Expansion regions: Wetwang Slack (WWS); Kirkburn (Kir); Garton Station (GS); Somme-Bionne (SB); Champagne (Ch); Marne (Mar); Saint Germain-en-Laye (SGL); Attichy (At) and Vix (Vix).

However, trade has not been the focus of much research and is frequently only described in relation to Mediterranean imports. Consequently, the presence of diverse and inter-connected trade routes may have been more common and intricate than previously believed. Thus, trade and differential access to trade items as a mechanism for the spread of these cultures cannot be ruled out.

Associations between archaeological culture and ethnicity

The archaeological study of ethnicity became a focus of research with the advent of settlement archaeology, a theory of culture developed by Gustaf Kossinna (Bandović, 2012; Daniel, 1950, 1978; Knapp, 2001; Renfrew, 1993, 1994a, b; Trigger, 2006). The basis of settlement archaeology is that material culture could be grouped together by style and location in order to trace past cultures, ethnicities and population groups (Barth, 1969, 1998, 2010; Jones, 1997; Renfrew, 1993, 1994a, b; Trigger, 2006). The resulting material culture groups could be used to distinguish one population from another and tell when and where they came from (Jones, 1997; Knapp, 2001; Renfrew, 1993, 1994a, b). Settlement archaeology has been used to create a link between current populations and those in the past (Knapp, 2001; Jones, 1997). With the advent of the culture history paradigm, popularized by V Gordon Childe, in the late 19th and early 20th centuries, a systematic framework for the classification of cultures in space and time was established (Jones, 1997; Trigger, 2006). This approach provided the dominant framework for archaeological analysis throughout most of the 20th century (Barth, 1969, 1998, 2010; Childe, 1956; Jones, 1997; Trigger, 2006). Childe adopted Kossinna’s notion that artefacts if analysed by spatial context within a temporal framework could enable the classification of past cultures and ethnicities; as well as facilitating the creation of archaeological cultures (Bandović, 2012; Childe, 1956; Jones, 1997; Renfrew, 1993, 1994a, b; Trigger, 1980). These cultures have been interpreted to be related in some way to ethnicity and kinship ties (Barth, 1969, 1998, 2010; Fowler, 2004; Jones, 1997; Knapp, 2001; Renfrew, 1993, 1994a, b; Trigger, 2006).

One of the main assumptions underlying the culture history approach is that bounded cultural entities, derived from the archaeological record, correlate with specific populations or ethnic groups (Chapman, 1993; Derks and Roymans, 2009; Francis, 1947; Jones, 1997; Renfrew, 1994a, b). Thus, the existence of a group is, in turn, predicted based on the existence of a particular archaeological culture. Their presence and distribution subsequently became the main criteria used to delineate and map past cultures, populations, and ethnic groups and, to create links between these groups to the modern era (Fowler, 2004; Jones, 1997; Renfrew, 1994a, b). These typologies have been created by modern scholars and not by the people to which they are ascribed. Therefore, perceptions of relationships in the past may reflect our modern perceptions of ethnicity and may represent an ascribed modern construct (Fowler, 2004; Jones, 1997; Renfrew, 1994a, b). Under this approach, artefact style was interpreted as a marker for chronological stages however, this could also indicate cultural and ethnic changes within a region (Eriksen, 1992, 1993; Francis, 1947; Jones, 1997; Knapp, 2001; Renfrew, 1993; Trigger, 2006). Thus, the study of material culture, when studied by artefact style was interpreted to create and define populations and is linked to ethnicities in the past (Barth, 1969; Fowler, 2004; Jones, 1997; Renfrew, 1993, 1994a, b; Trigger, 2006).

With the advent of processual and post-processual archaeology, the interpretations of culture shifted and it came to be viewed as fluid (Jones, 1997; Renfrew, 1993, 1994a, b; Trigger, 2006). Under these schools of thought, it was viewed following the so-called aquatic view of culture. This approach was put forward by Binford (1962), under which culture was interpreted as undergoing minor changes and variations through time (Barth, 1969, 1998, 2010; Jones, 1997; Trigger, 2006). Ethnicity was perceived as an active part of the social identity of a population, and cultural boundaries had to be constantly maintained in order to distinguish one group from another. Although these approaches rejected culture history interpretations of past populations as nothing more than an end-product in themselves, they are still largely dependent upon material evidence that has been described and classified on the basis of what is an essentially a culture-historical epistemology (Barth, 1998, 2010; Jones, 1997; Knapp, 2001; Renfrew, 1993, 1994a, b; Trigger, 2006). An archaeological culture can have diverse origins and unifying features that give it apparent coherence, as archaeologically recognized and acknowledged, and may be the result of an array of broad processes, such as exchange networks, symbolic change, marriage practices (e.g., exogamy) or adoption of farming by hunter-gatherer groups (Cohen, 1978; Francis, 1947; Fowler, 2004; Renfrew, 1993, 1994a, b; Trigger, 2006). All of the above combine to create interlocking patterns of variation subsequently resulting in gradual rather than discrete spatial patterns and distribution of artefacts. Thus, archaeological cultures are difficult to correlate with ethnic groups as the spatial variation in archaeological material often is produced through interactions among diverse social processes (Cohen, 1978; Francis, 1947; Fowler, 2004; Renfrew, 1993, 1994a, b; Trigger, 2006). Artefacts often produce overlapping rather than discrete patterns of geographic distribution; ethnic and tribal entities may themselves be historical products of cultural contacts and interaction (Barth, 1998, 2010; Derks and Roymans, 2009; Eriksen, 1993; Jones, 1997; Knapp, 2001; Shennan, 1989).

Widespread and simultaneous changes in artefacts are therefore often interpreted as evidence for the spread of new populations with specific cultural traditions (Hodder, 1982; Jones, 1997; Knapp, 2001; Renfrew, 1993, 1994a, b). A high degree of homogeneity in material culture is regarded as the product of regular contact and interaction, whereas discontinuities in its distribution are assumed to be the result of social and/or physical distance. Gradual change has been attributed to internal drift in the prescribed cultural norms of particular groups, whereas more rapid change may be related to external influences, such as diffusion resulting from cultural contact, or the succession of one cultural group by another as a result of migration and/or conquest (Barth, 1969, 1998, 2010; Jones, 1997; Trigger, 2006; Wells, 2014). However, ethnic groups may also possess social and cultural commonalities across physical, genetic and/or linguistic boundaries and exhibit considerable variation within their respective populations (Eisenmann et al., 2018; Kossina et al., 2018; Jones, 1997; Renfrew, 1993; Riede et al., 2019).

The extent of contact along these boundaries depends on the cultural transformations brought about through interaction and the nature of relations between groups (Bourdieu, 1977; Comaroff and Comaroff, 1992; Jones, 1997; Renfrew, 1993, 1994a, b). Thus, manifestations of ethnicity are the product of an ongoing process involving multiple objectifications of cultural differences and the subsequent internalization of those differences within the shared dispositions of the habitus. This is defined as the way in which individuals perceive the social world around them and react to it, which is shared by people with similar backgrounds (i.e., ethnicity) (Jones, 1997; Renfrew, 1993, 1994a, b; Trigger, 2006). Such processes may lead to variations in associations between constructions of ethnic identity, in terms of broader idioms of cultural differences, objectified cultural difference, and the overall cultural practices and historical experiences generated in any given social context (Jones, 1997; Renfrew, 1993, 1994a, b; Trigger, 2006). The extent to which ethnicity is embedded in pre-existing cultural entities represented by a shared habitus is highly variable. Consequently, the cultural content of ethnicity may vary fundamentally and qualitatively in different contexts (Barth, 1969, 2010; Eriksen, 1992, 1993; Jones, 1997; Renfrew, 1993, 1994a, b). Therefore, there is unlikely to be a one to one relationship between expressions of a particular ethnic identity and the language and cultural practices associated with a particular group.

However, as there is no working definition of ethnicity, it difficult to differentiate the cultural and ethnic variations within and among groups.

Ethnicity can be loosely defined as a set of psychological and social phenomena which form under specific circumstances in order to create a group which is distinct from other surrounding groups (Barth, 1969; De Vos and Romanucci-Ross, 1975; Jones, 1997; Renfrew, 1994a, b; Trigger, 2006). These phenomena will manifest themselves in several ways, including burial practices and material culture. An ethnic group must internally recognize itself as distinct and must be externally recognized as a distinct group by others (Barth, 1969, 1998, 2010; Jones, 1997; Trigger, 2006). Thus, ethnic groups are fluid self-defining systems which are not regionally bounded. Ethnicity must be distinguished from mere spatial continuity and discontinuity in that it refers to self-conscious identification with a particular group of people (De Vos and Romanucci-Ross, 1975; Jones, 1997; Shennan, 1989). Yet in the process of social interaction, both real and assumed, cultural differences are articulated in the maintenance of ethnic boundaries (Barth 1998, 2010; Jones, 1997; Renfrew, 1993, 1994a, b). The concept of ethnicity results in numerous transient realizations of social differences within diverse contexts and involves the repeated production of distinctive material culture(s) (Cohen, 1978; Jones, 1997; Renfrew, 1993, 1994a, b; Shennan, 1989). The artefacts involved in constructing ethnic identity may vary in different social contexts and in relation to different forms and scales of social interaction (Jones, 1997; Shennan, 1989). Further, patterns in the production of material culture associated with the same ethnic identity may vary qualitatively as well as quantitatively in different contexts. Thus, a complex pattern of overlapping distributions of artefacts resulting from the transformation of ethnicity in different social contexts, rather than discrete uniform cultural entities may be visible archaeologically (Barth, 1969, 1998, 2010; Jones, 1997; Patterson, 1975; Renfrew, 1993, 1994a, b; Shennan, 1989; Trigger, 2006).

Ethnic identity has been constructed based on socio-structural relations and shared cultural practices that exist independently of the perceptions of the populations concerned. This identity can also be created through the subjective processes of perception and derived social organization of individuals themselves (See page 1) (Bentley, 1987; Eriksen, 1992; Jones, 1997; Renfrew, 1993, 1994a, b; Shennan, 1989). Through the process of social interaction, both real and assumed cultural differences are articulated in the maintenance of cultural boundaries (Barth, 1998, 2010; Jones, 1997; Patterson 1975; Renfrew, 1993, 1994a, b). Although it is still presumed that there is a relationship between culture and ethnicity, it is generally accepted that there is rarely a straightforward correlation (Blu, 1982; Jones, 1997; Renfrew, 1993, 1994a, b). The assumption that bounded cultural entities, and archaeological cultures, correlate with specific ethnic groups has been critiqued based on their correlation with archaeological cultures (Jones, 1997; Shennan, 1989; Trigger, 2006).

We cannot rely on artefacts as markers of identity, as they can pass from one culture to another. One group may copy those of another, but such copies are produced in terms of different conceptions of cultural relevance which express themselves as different technical approaches, or Chaîne opératoire (Barth, 1969, 1998, 2010; Clark, 1978; Fernández-Götz, 2014a, b, 2015; Jones, 1997; Renfrew, 1993, 1994a, b; Van Esterick, 1985). What may appear on the surface to be a widespread cultural identity in relation to a ubiquitous artefact form may represent more complex tribal relationships if how the artefact is situated within the Chaîne opératoire of different groups or populations is considered (Barth, 1969, 1998; Fernández-Götz, 2014a; Jones, 1997; Renfrew, 1993, 1994a, b; Trigger, 2006). Moreover, an archaeological culture can be regionally diverse due to intra-and/or-extra-regional contact or differential expressions of individual identity within a larger ascribed ethnicity. As ethnicity has been used prolifically to refer to diverse socio-cultural phenomena, and has no universally accepted definition, its application to archaeologically derived ethnic groups, such as the Celts, is problematic.

The modern concept of the Celts was constructed in the 18th and 19th centuries AD and is intrinsically linked with the externally imposed ethnonyms, ‘Kelto’, and ‘Galli’. The disputed origin and meaning of these terms calls into question their utility as ethnic identifiers (See page 1) (Collis, 2003; Cunliffe, 1997; Dietler, 1994; Fitzpatrick, 1996; James, 2005). Their origin, in Greek and Latin respectively, or whether they were Celtic terms is uncertain (Collis, 2003; Cunliffe, 1997; Dietler, 1994). Keltoi is believed to be either of Celtic or Greek origin, possibly meaning the “tall ones” (Koch, 2003, 2006; Mountain, 1998; Rankin, 1998; Sjögren, 1938). The etymology of the Roman term Galli is also ambiguous, possibly meaning “to be able to”, “to gain control of”, “stranger”, “enemy” or even “enemy of the state”, and has alternatively been described as an ethnic or tribal name (Koch, 2003, 2006, 2009a, b, 2013; Helmut et al., 2001; Stempel, 2008). The pejorative and descriptive nature of these terms suggests that they were applied as exonyms (externally derived ethnic identities) rather than as self-identifying ethnic terms (Collis, 2003; Cunliffe, 1997; Dietler, 1994; Fernández-Götz, 2014a, b, 2015). Further, they were used by the Greeks and Romans interchangeably for people who spoke Celtic languages and possessed similar material culture, as the terms are used today (Megaw and Megaw, 1995b, 1996; Moore, 2012). The inclusion of all groups possessing the Hallstatt and La Tène cultures under the term Celtic, without any knowledge of their underlying biological relationships, is derived from archaeological, linguistic, artistic and classical lines of evidence (Collis, 2003; Cunliffe, 1997; Dietler, 1994; James, 2005; Koch, 2006; Megaw and Megaw, 1995b, 1996). Therefore, their associations are superficial at best. The Celts are not believed to represent a cohesive population; rather, they are viewed as a loose association of tribes (Collis, 2003; Cunliffe, 1997; Dietler, 1994; Fernández-Götz, 2014a, b, 2015; Koch, 2003, 2006; Megaw and Megaw, 1995b, 1996). However, these disparate tribes are still referred to as Celtic based on the above lines of evidence. This stereotype while simplified, still captures popular imagination.

Modern Celtic scholarship regards the inhabitants of Central Europe as if they were, to some degree, representative of a single population and/or ethnicity. However, the archaeological evidence is at odds with this perspective (Cunliffe, 1997, 2018; Dietler, 1994; Fitzpatrick, 1996; Karl, 2002, 2004, 2010; Koch, 2003, 2006). Although similar artefacts are present throughout the areas that Celtic groups are believed to have inhabited, the presence of regional diversity renders their description as an ethnic group difficult. Further, previous studies have indicated the presence of biologically distinct populations within groups possessing Hallstatt and La Tène artefacts, e.g., specifically the Hallstatt D (Austria) and Münsingen-Rain (Switzerland) populations (Anctil, 2016; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). However, the presence of diverse ethnic groups within the regions possessing these artefacts has not been the focus of much research (Anctil, 2016; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). Therefore, the Hallstatt and La Tène material cultures may not necessarily represent a historical Celtic ethnicity. What they do represent are physical phenomena that existed in time and space and have been interpreted to represent this ethnicity. Consequently, the groups inhabiting Central Europe cannot be reliably described as Celtic, as it cannot be determined whether they possessed all the cultural traits that originally defined the Celts, nor can these traits be defined.

There could also be fluctuations in how this ethnicity was expressed throughout the diverse regions to which it spread (Dietler, 1994; Knapp, 2001; Megaw and Megaw, 1995b, 1996). The groups living in different regions of Gaul, a region encompassing France, Belgium, Luxembourg, Switzerland, the Netherlands, some parts of northern Italy, and Germany on the west bank of the Rhine, may have called themselves Celtic, but this does not mean they expressed their ethnic identity exactly the same (Arnold, 2006; Arnold and

Murray, 2003; Collis, 2003; Cunliffe, 2018; Dietler, 1994; Haselgrove, 1982, 1987; Knapp, 2001; Megaw and Megaw, 1995b, 1996; Roymans, 2009). Groups in different regions would likely have been influenced by differing internal and external stimuli, and small changes in how their ethnicities were expressed would likely be evident (Arnold, 1990, 1995, 2006; Arnold and Murray, 2003; Dietler, 1994; Drinkwater, 2014; Jones, 1997; Megaw and Megaw, 1995b, 1996). Further, ethnic identity is difficult to correlate with any specific artefact or material culture (Jones, 1997; Knapp, 2001; Renfrew, 1993, 1994a, b; Trigger, 2006). Certain artefacts and burial practices are assumed to be Celtic (e.g., torcs, fibulae and square barrows) and their presence alone has been used to describe a population as Celtic, with no logical justification as to why one artefact type is ethnically significant and another is not (Arnold, 1990, 1995, 2006; Arnold and Murray, 2003; Collis, 2003; Cunliffe, 2018; Dietler, 1994; Hodson, 1964; Koch, 2003, 2006; Ruiz Zapatero 1990, 1993, 1996; Shennan, 1989). For example, the presence of a La Tène fibulae in a burial does not necessarily designate the individual as a Celt. The design and manufacturing technique may represent a specific ethnicity or population, but it cannot be determined whether the object was in fact Celtic (Arnold, 1990, 1995, 2006; Arnold and Murray, 2003; Collis, 2003; Dietler, 1994; Megaw and Megaw, 1995b, 1996). It is evident, then, that the notion of a Celtic Iron Age Europe has developed in an almost ad hoc manner (Cunliffe, 1979, 1988; Dietler, 1994; Fitzpatrick, 1993; Megaw and Megaw, 1995b,1996; Wells, 1980, 1984; Woolf, 1993). The Celtic ethnic designation is geographical as much as it is cultural, and it does not necessarily indicate that these people spoke similar languages or called themselves Celtic. The theoretical basis of a Celtic Iron Age Europe is weak. However, the correlation between the Celts and the Iron Age is still prevalent within the field of Celtic studies. As is the La Tène=Celtic paradigm despite the regional diversity indicated by the archaeological evidence which does not support the application of this paradigm to diverse populations possessing Celtic artefacts or a presumed Celtic ethnicity.

Chapter 3: Celtic migration

Migration and mobility among and within populations facilitate cultural change, which may be visible in the archaeological record (Anthony, 1990, 1992, 1997; Baker et al., 2015). However, as these mechanisms represent different social processes, they will affect cultures differently. Consequently, it is necessary to distinguish between them. Migration is commonly defined as the dispersal of communities, groups or individuals that involves a change of geographic location over small or large distances with the intention of permanently relocating (Arnold, 2005; Arnold and Murray, 2003; Baker and Tsuda, 2015; Brumeister, 2000; Härke, 1998). Conversely, mobility is defined as the movement of groups or individuals with the intent of returning to their place of departure (Arnold, 2005; Brumeister, 2000; Ramsl, 2003). However, these processes are not mutually exclusive. Archaeological evidence of migration has been the focus of numerous studies and has been determined through examinations of artefacts and their temporal distributions (Anthony, 1990, 1997; Arnold, 2005; Arnold and Murray, 2003; Baker and Tsuda, 2015; Brumeister, 2000; Chapman, 1997; Fernández-Götz, 2020; Hakenbeck, 2008; Karl, 2005; Knipper et al., 2014, 2017; Ramsl, 2003). Migration of groups or individuals may have an observable impact on the material culture of the population into which they move. However, the transfer of artefacts through trade, cultural diffusion and/or assimilation may also result in observable differences, which may be differentially expressed (Anthony, 1990; Arnold, 2005; Chapman, 1997; Cunliffe, 1991; Fernández-Götz, 2020; Shennan, 1974). Some cultural elements, such as burial practices, may be more susceptible to change as they communicate specific symbolic meanings which may be more prone to internal and external influence (See pages 19, 32 and 54) (Anthony, 1990; Anthoons, 2007; Arnold, 2005; Chapman, 1997; Fernández-Götz, 2013, 2014a, b, 2015, 2020; Härke, 1998; Prien, 2005).

Changes in art styles, artefact manufacture and burial practices may indicate the immigration of a different cultural group into an indigenous community. However, population movements have often been seen as a main driving force of cultural change. Consequently, simplistic models for diachronic changes in material culture were common during the late 19th and early 20th centuries (Anthony, 1990; Anthoons, 2007; Arnold, 2005; Fernández-Götz, 2020; Härke, 1998; Prien, 2005; Trigger, 2006). Criticisms of previous migrationist models have focused on the oversimplification of numerous traditional interpretations of cultural change. These critiques have indicated the need to include a theoretical understanding of the complexity of the migratory process, its mechanisms and alternatives, such as trade, *in-situ* change, external influence, cultural assimilation, the presence of out of group slaves and/or captives, and how these factors contribute to the spread and diversification of material culture and the development of new designs or ways of thinking (Cameron, 2008, 2011, 2013, 2016; Larsson, 1994; Lenski, 2008, 2014; Osborn, 1994; Rothman, 2015). Further, migrations may not have been unidirectional, rather they may have been accompanied by waves of return migration, or migrants to and from their respective homelands (Anthony, 1990; Burmeister, 2000). It is also necessary to consider the relationship between migrants and the inhabitants of a specific region; as well as whether there is evidence of cultural hybridisation, assimilation, interaction, or the formation of new separate communities and/or ethnicities (see pages 1 and 54).

Current approaches to mobility and migration analyses are often accompanied by a theoretical understanding of the above processes and their interrelationships and complexity (e.g., Jay and Montgomery, 2020; Jay et al., 2012; Jay et al., 2013; Jay et al., 2019; Montgomery, 2002; Montgomery et al., 2007; Montgomery, 2017; Scheeres, 2014a; Scheeres et al., 2014b; Scheeres et al., 2013b; Moghaddam et al., 2014). These approaches have also attempted to move beyond the associations between ethnicity, ancestry, identity and material culture. Thus, representing a fundamental shift compared to the essentialist views that had characterized the earlier archaeological conceptualisations of culture and mobility studies (e.g., Fernández-Götz, 2020; Jay and Montgomery, 2020; Jay et al., 2012; Jay et al., 2013; Jay et al., 2019; Moghaddam et al., 2014; Montgomery, 2002; Montgomery et al., 2007; Montgomery, 2017; Scheeres, 2014a; Scheeres et al., 2014b; Scheeres et al., 2013b; Trigger, 2006). While recent archaeological approaches to mobility have surpassed the oversimplification and essentialist views common to past studies (Jay and Montgomery, 2020; Jay et al., 2012; Jay et al., 2013; Jay et al., 2019; Montgomery, 2002; Montgomery et al., 2007; Montgomery, 2017; Scheeres, 2014a; Scheeres et al., 2014b; Scheeres et al., 2013b; Moghaddam et al., 2014), ethnographic descriptions and written sources are still commonly used to reconstruct mobility among past populations and to provide additional evidence for the presence of migrants. Although Greek and Roman written sources may provide additional evidence for migration, mobility, and ethnic identity in Iron Age societies, some of these sources were written by outsiders that described the “foreign” populations of Iron Age Europe and Britain (Arnold, 2005; Dietler, 1994; Hanford, 1982; Hauschild, 2010b, 2015; Kruta, 1991; Schönfelder, 2002, 2010; Tomaschitz, 2002; Tütken et al., 2008; Wells, 2002).

The availability of these accounts are also unevenly distributed chronologically and geographically (Arnold, 2005; Dietler, 1994; Fernández-Götz, 2020; Hanford, 1982; Hauschild, 2010b, 2015; Kruta, 1991; Schönfelder, 2002, 2010; Tomaschitz, 2002; Tütken et al., 2008; Wells, 2002). Consequently, their descriptions are more likely to reflect political propaganda rather than accurate descriptions of diverse populations and their movements. Several classical authors (e.g., Pliny, Livy and Julius Caesar) describe several reasons for the migration of Celtic groups during the 4th and 3rd centuries BC (Arnold, 2005; Dietler, 1994; Hanford, 1982; Hauschild, 2010b, 2015; Kruta, 1991; Schönfelder, 2002, 2010; Tomaschitz, 2002; Tütken et al., 2008; Wells, 2002).

Though the classical sources are consistent in that these migrations involved large populations, the proposed explanations are diverse and ambiguous (Collis, 2010; Dietler, 1994; Stöckli, 1991; Tomaschitz, 2002; Wells, 1998, 2002). The Greeks and Romans frequently described the Celts as wandering tribes and/or highly mobile mercenaries or warriors who participated in virtually all military conflicts during the above period (Collis, 2003, 2010; Dobesch, 1996; Hauschild, 2015; Kruta, 1991; Pauli, 1991; Tomaschitz, 2002). However, whether the mercenaries were operating in their own interest or in that of other communities is not specified. Thus, migration during this period is associated with large-scale movement and/or invasion (See pages 19 and 32) (Burmeister et al., 2000; Collis, 2003; Prien, 2005; Schonfelder, 2010; Tomaschitz, 2002). Although it is unknown whether large-scale migration or increased individual mobility facilitated the spread of La Tène culture throughout much of Central Europe, the old model that it was spread through mass migration of homogenous Celtic tribes is still prevalent in the field of Celtic studies (Anthoons, 2007; Charpy, 2009; Collis, 2003; Fernández-Götz, 2016; Kaenel, 2007; Tomaschitz, 2002).

Although the migrations of several Celtic populations have been described by the Greeks and Romans, they are often incomplete, contradictory and predominantly influenced by political propaganda (Collis, 2003; Handford, 1982; Pauli, 1991; Polybius, 2012; Walbank and Scott-Kilvert, 1979). The earliest mentioned describe the invasions, approximately 390-360 BC, of northern Italy, Rome, southern Germany, and a contemporaneous migration into Pannonia (modern-day Hungary) (Collis, 2003; Hanford, 1976; Kruta, 1991; Pauli, 1991; Walbank and Scott-Kilvert, 1979). Julius Caesar described movements of several presumed Celtic tribes including the Helvetii, Tulingi, Rauraci, and Latobringi who are believed to have inhabited Switzerland although their homelands are unknown (Collis, 2003; Hanford, 1976). The failed migration in 58 BC of these groups into southwestern Gaul was the catalyst for his subsequent conquest of the region (Hanford, 1982). Caesar also described the migration of the Boii, who inhabited northern Italy, into this region. However, the intentions behind these proposed events are not described.

Moreover, the archaeological evidence does not support Caesar's claim, as there is no evidence of significant settlement abandonment. Further, the reported population sizes are not consistent and are not in line with the proposed population density in continental Europe for the Iron Age (Collis, 2003; Hanford, 1982). A census of the total numbers associated with these groups adds up to a total of 263,000 Helvetii, 36,000 Tulingi, 14,000 Latobringi, 23,000 Rauraci, and 32,000 Boii, in total 368,000 individuals of whom 92,000 were described as warriors (Collis, 2003; Hanford, 1982). It has been suggested that the actual numbers were around 40,000 warriors out of 160,000 total individuals or 100,000 individuals and 16,000 warriors. However, these numbers are also high for the time period (Delbrück, 1900; Furger-Gunti, 1984). The population density for this period has been estimated to be around 50 individuals per hectare, or 100 acres, or 50-80 individuals per km^2, urban and rural, respectively (Danielisova, 2014; Fernández-Götz, 2017; Fletcher, 2009; Zimmerman et al., 2009). As Caesar’s account of the above migrations is heavily influenced by his political agenda, it is difficult to determine whether they occurred at all (Arnold, 2005; Knipper et al., 2014, 2017; Tomaschitz, 2002; Welch et al., 1998). Further proposed migration or conquest events include the conquest of Delphi (279 BC) and the migration of the Belgae into southeastern England (a Celtic group inhabiting northern Gaul, on the west bank of the Rhine and north of the Seine River). The latter migration has been alternatively dated to the end of the 4th to beginning of the 3rd century BC or 150-100 BC, although the exact date for this migration is uncertain (Anthoons, 2007; Collis, 2003; Cunliffe, 1979, 1997; Szabó, 1991; Stead, 1991b). Migrations into other areas including, Turkey, Asia Minor, the Balkans, the Danube, and Carpathian regions, during the 4th and 3rd centuries BC have been reported (Arnold, 2005; Arnold and Murray, 2003; Collis, 2003; Cunliffe, 1997; Selinksy, 2015). Further, incursions into northern Italy and the Po Valley during the 3rd and 2nd centuries BC have also been described (Collis, 2003; Cunliffe, 1997; Szabó, 1991). The migration of Celtic groups from Gaul into the Iberian Peninsula has been recounted, though, no approximate date is provided (Almagro-Gorbea, 1991; Collis, 2003; Cunliffe, 1984, 1997). Numerous migrations have also been described through the lower Rhine region, southern Germany to the Netherlands (Almagro-Gorbea, 1991; Collis, 2003; Cunliffe, 1997; Fernández-Götz, 2020). However, evidence of these proposed events is fragmentary (Arnold, 2005; Arnold and Murray, 2003; Collis, 2003; Tomaschitz, 2002).

Additional military raids throughout the Balkans and the territory of the Scythians, populations inhabiting modern-day northern Serbia and Steppe regions north of the Black sea, have also been mentioned; however, none are described in detail (e.g., Pliny and Livy). (Arnold, 2005; Collis, 2003; Popović, 1996; Szabó, 1991; Wells, 2001). However, the presence of Celtic artefacts in the above regions may be the result of a combination of various processes, such as small-scale migration, individual mobility, trade, intensification of interregional exchange and local production of material culture in the La Tène style (Collis, 2003; Cunliffe, 1997; Fernández-Götz, 2020; Kock, 2006; Roymans, 2009). Further evidence of population movement and/or demographic decline is suggested by the decrease in the number of cemeteries that were in use during the LTB period in some areas. Their number decreases from approximately 162 to 36 within the Champagne region in northeast France (Collis, 2003; Demoule, 1999; Diepeveen-Jansen, 2001; Fernández-Götz, 2020; Kaenel, 2007; Müller-Scheeßel, 2007; Szabó, 1991; Verger, 1994). However, it has been suggested that this decrease is related to the loss of cemeteries through natural taphonomic processes and/or later construction (Collis, 2003; Demoule, 1999; Diepeveen-Jansen, 2001). Further, as the above numbers are estimates, the significance of their decrease may be overstated. This decrease has also been linked with the migration of Trans-Alpine populations into the Italian Peninsula, based on similarities in material culture (Charpy, 2009; Dörfler et al., 2000; Fernández-Götz, 2014a, 2016; Krausse and Nakoinz, 2000). However, this region was never completely deserted and continuity is evident in some areas (i.e., Beine-Suippes, northeastern France) (Charpy, 2009; Dörfler et al., 2000; Fernández-Götz, 2014a, 2016). This decline has alternatively been suggested to represent a migration into east Yorkshire (Britain) subsequently resulting in the presence of the Arras culture, an archaeological culture from the middle Iron Age in this region which is presumed to represent the Celts (See page 32) (Anthoons, 2007, 2011; Halkon, 2013, 2017; Schonfelder, 2010; Stead, 1991a, c).

Similar demographic decline is evident in the Hunsrück-Eifel region (western Germany), eastern Belgium and Luxembourg, where the number of settlements decreases during the LTB/LTC transition, although the numerical estimates are not provided. During the 6th and 5th centuries BC in the middle Rhine-Moselle region (western Germany and Luxembourg) there is evidence of increasing centralization and hierarchisation, represented in the archaeological record by the emergence of luxurious graves and hillforts (Collis, 2003, 2011; Fernández-Götz, 2014a; Hornung, 2008; Koch, 2006). However, this process came to an end during the 4th century BC, when the archaeological evidence indicates a period of discontinuity. Differences in the rich burials of the HaD period in Baden-Württemberg (southwest Germany) and those during the LTA period in the middle Rhine-Moselle region (western Germany and Luxembourg) have also been described; and have been argued to represent population movement due to demographic decline (see pages 19 and 32, Table 8) (Collis, 2003, 2011; Fernández-Götz, 2014a, 2020; Hornung, 2008; Koch, 2006). However, these differences are not specified, but rather brief descriptions of variations in burial practices and the quantity and type of prestige grave goods (Collis, 2003, 2011; Fernández-Götz, 2014a, 2020; Hornung, 2008; Koch, 2006). A decrease in the number of settlements is described, but the precise number of settlements before and during this period are not provided (Collis, 2003; Fernández-Götz, 2014a; Hornung, 2008; Koch, 2006). Consequently, comparison between these periods is not possible. The distribution of fortified settlements, or hillforts, have also been suggested to indicate population movement due to demographic decline.

The distribution of fortified settlements within the Scheldt River region (northern France, western Belgium, and southwestern Netherlands) have been compared to those in the middle Rhine-Moselle region (western Germany and Luxembourg). During the HaD period the majority of these settlements are found within the middle Rhine-Moselle region (western Germany and Luxembourg); whereas during the LTA period they are primarily found in the Aisne-Marne region (northern France). This shift has been argued to be linked to large-scale population movement during the HaD/LTA transition and, demographic decline (Collis, 2003; Cunliffe, 1997; Fernández-Götz, 2020; Koch, 2006; Mata, 2019). However, these comparisons are vague, and only similarities and possible connections are described in the literature (Collis, 2003; Cunliffe, 1997; Fernández-Götz, 2020; Koch, 2006; Mata, 2019). This demographic decline is also believed to be supported by a similar change in the distribution of trade items, such as, Etruscan Bronze artefacts, and Italian wine amphorae (Collis, 2003; Cunliffe, 1997; Fernández-Götz, 2020; Koch, 2006; Mata, 2019). The presence and distribution of La Tène material culture may be the result of migration of Celtic groups into the above regions. Though, a combination of several processes including small-scale or individual migration, intensification of extra-regional trade, local production of artefacts in the La Tène style either by indigenous groups or out of group slaves and/or captives cannot be ruled out as mechanisms for the spread of Celtic artefacts into these regions (Fernández-

Götz, 2020; Roymans, 2009). Changes in burial practices, including widespread adoption of cremation and the decline of the tumuli rite, are also evident within the above regions (See page 32) (Arnold, 2005; Arnold and Murray, 2003; Collis, 2003; Fernández-Götz, 2016; Hornung, 2008).

However, population decline in Central Europe may be linked with environmental conditions. Pollen records indicate a decrease in farming intensity and an increase in arboreal pollen during the 4th and 3rd centuries BC (Dörfler et al., 2000; Maise, 1998; Sirocko, 2009). The above records from this period indicate a decrease in farming intensity through examination and comparison of arboreal and crop pollen (Dörfler et al., 2000; Maise, 1998; Sirocko, 2009). During the above period a decrease in farming intensity is indicated as the former is comparatively more abundant, suggesting a corresponding decrease in the latter (Dörfler et al., 2000; Maise, 1998; Sirocko, 2009). However, the nature of this decrease is not quantified, nor is the type of pollen, arboreal or crop, indicated (Dörfler et al., 2000; Maise, 1998; Sirocko, 2009). Deteriorating climatic conditions also resulted in a colder and more humid environment during this period (Fischer et al., 2006; Grove, 1979; Kromer and Friedrich, 2007; Magny et al., 2009). An estimated drop in temperature of approximately 2°C and an increase in precipitation of ±10-20% compared to modern-day values occurred (Büntgen et al., 2011; Gutiérrez-Elorza and Peña-Monné, 1998; Lamb, 1977). Although the average temperature following this drop and the corresponding values for the preceding period are not provided (Büntgen et al., 2011; Gutiérrez-Elorza and Peña-Monné, 1998; Lamb, 1977). Consequently, comparisons between the 4th and 3rd centuries BC and other time periods are not possible.

Additionally the archaeological evidence suggests that populations were able to adapt to lower substance levels, as not all large settlements were abandoned, e.g., Münsingen-Rain (Switzerland) and Dürrnberg (Austria), and there is evidence for settlement continuity throughout this region (Hald, 2009; Kromer and Friedrich, 2007; Maise, 1998; Nortmann and Schönfelder, 2009; Rageot et al., 2019; Tinner et al., 2003). Further, in some regions, such as Münsingen-Rain (Switzerland) there is evidence of a shift in agricultural practices during this period (See page 145). Stable isotope evidence suggests an increase in δ^{13} carbon values, a stable isotopic measure that is commonly used to reconstruct the plant proportion of the diet, which suggests an increase in millet, a C^4 plant, consumption (Hunt el at., 2008; Le Huray and Schutkowski, 2005; Moghaddam et al., 2014; Motuzaite-Matuzeviciute et al., 2013; Schmidl et al., 2007). The presence of millet and its consumption has been evident since the

3rd millennium BC and is found in other Celtic regions including Heuneburg (southern Germany), Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) (Hunt et al., 2008; Motuzaite-Matuzevicitue et al., 2013; Le Huray and Schutkowski, 2005; Rageot et al., 2019). However, an increase in the above values may also indicate an increase in the consumption of fruit, seeds, roots or subsistence on domesticated animal resources (Cernusak et al., 2009; Lightfoot et al., 2014). Several food items, e.g., millet or domesticated animal sources, are also high in δ^{13} carbon. Consequently, an increase in their consumption will also result in an increase in the corresponding stable isotope values, i.e., δ^{13} carbon, recovered from archaeological human skeletal material (Hunt et al., 2008; Le Huray and Schutkowski, 2005; Moghaddam et al., 2014; Motuzaite-Matuzeviciute et al., 2013; Schmidl et al., 2007).

This dietary shift may have enabled the population at Münsingen-Rain (Switzerland), to weather the climate change. Although, other regions within the core and expansion areas, such as east Yorkshire (Britain), Basel-Gasfabrik (Switzerland), Magdalenenberg (southwest Germany), Heuneburg (southern Germany), Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic), were also able to adapt to the fluctuations in climate (See pages 145, 164, 168, 172 and 177) (Jay and Richards, 2006, 2007; Jay et al., 2008; Knipper et al., 2016; Le Huray et al., 2006; Le Huray and Schutkowski, 2005; Oelze et al., 2012; Rageot et al., 2019). However, there is no comparable evidence, e.g., pollen records, for variations in subsistence in these regions (Jay and Richards, 2006, 2007; Jay et al., 2008; Jay and Montgomery, 2020; Le Huray et al., 2006; Le Huray and Schutkowski, 2005; Oelze et al., 2012). This may suggest that dietary changes were not necessary in order to adapt to the deteriorating climate conditions. Alternatively, corresponding evidence for this variation may not have been recovered from the above regions.

Although a small part of the observed mobility may have been caused by climate change, it does not appear to have been the primary mechanism for diachronic cultural differences during this period (Evans, 2004; Fernández-Götz, 2016; Hauschild, 2010a; Müller et al., 2003; Müller, 2004; Pétrequin et al., 2010; Schönfelder, 2010; Tinner et al, 2003). Changes in burial practices are also evident during this period. Wealthy equipped tumuli decrease and flat inhumation graves increase (See page 32) (Collis, 2003, 2010; Dobesch, 1996; Waldhauser, 1999; Wells, 2002). Although diachronic changes in material culture are evident in some regions, using artefacts to determine individual and/or group mobility is problematic as these objects are frequently distributed (Brather, 2004; Eggl, 2003; Krämer,1985; Pollex et al., 2005; Tomaschitz, 2002). Further, these differences may have been facilitated by trade. However, trade networks and migration routes may not follow the same geographical pattern or distribution (Bofinger, 2006; Collis, 2003; Cunliffe, 1991, 1997, 2018; Fowler, 2004; Hodson, 1990; James, 2005; Koch, 2007; Maier, 2003; Tomaschitz, 2002). Thus, instead of one-way large-scale migration, movement during this period likely involved increased mobility of individuals and small groups (Collis, 2003, Cunliffe, 1997; Hodson, 1968; James, 2005; Koch, 2007; Stöckli, 1991).

The numerous regional connections indicated by the archaeological evidence may suggest migration, increased individual mobility and/or the presence of trade routes (Berecki, 2008; Collis, 2003; Cunliffe, 1997, 2018; Crişan 1978; Koch, 2007; Möllers et al., 2007; Zirra 1971, 1975, 1981). The Celts inhabited regions in close proximity to the Scythians, Dacians, Thracians, and Illyrians, populations in the Balkans, during the La Tène period. Trade networks are believed to have developed based on the presence of similar artefacts (e.g., bronze vessels, jewellery, and weapons) (See page 32) (Almássy, 2009; Collis, 2003; Cunliffe, 1997; Koch, 2006, 2007; Tomaschitz, 2002; Wells, 2001). Numerous previous studies have interpreted the presence of trade items only as indications of migration (Cunliffe, 1997; Eckardt et al., 2014; Möllers et al., 2007; Müller, 1998; Németi, 1988, 1989, 1992, 1993; Zirra, 1998). Yet, mobility and migration are difficult to verify based on archaeological evidence alone. It has been suggested that migrants are often buried according to the traditions of the culture into which they moved rather than retaining those of their homeland (See page 54) (Collis, 2003; Cunliffe, 1997; Eckardt et al., 2014; Giles, 2000; Kruta, 2004; Koch, 2003; Scheeres, 2014a; Scheeres et al., 2013b, 2014b; Tomaschitz, 2002). However, the reverse has also been suggested (Collis, 2003; Cunliffe, 1997; Giles, 2012; Kruta, 2004; Koch, 2003; Tomaschitz, 2002).

This evidence suggests that the old model of mass migration of homogenous Celtic groups based on archaeological evidence alone is questionable. Strontium and oxygen, $^{87}Sr/^{86}Sr$ and $\delta\ ^{18}O$, stable isotope analyses have been used to reevaluate questions of residential changes and inter-and-extra-regional contacts among these groups (Arnold, 2005; Hauschild, 2010b, 2015; Scheeres, 2014a; Scheeres et al., 2013b, 2014b; Schonfelder, 2010; Tutken et al., 2008). Stable isotope evidence of movement supports the archaeological evidence for extra-regional contact among the Radovesice I, II (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) populations (Scheeres, 2014a; Scheeres et al., 2013b, 2014b). A significant proportion of which were found to have migrated from surrounding areas in the Czech Republic, 74.3% (26 out of 35 individuals) and 76% (19 out of 25 individuals), respectively (Scheeres et al., 2013b, 2014b). In both regions the majority of males analysed were found to have moved into the area later in life, 81.25% and 70%, 13 out of 16 and 7 out of 10 individuals, correspondingly. The same goes for all of the analysed weapon burials from Radovesice I and II (Czech Republic) (See pages 103, 107, 164 and 168) (Scheeres, 2014a; Scheeres et al., 2013b, 2014b). However, male burials without weapons were also found to be non-local, 2 and 3 burials, respectively. At Radovesice I and II (Czech Republic) approximately 22.2%, 2 out of 9, of male burials with weapons, were local, while 77.7%, 7 out of 9 individuals, were non-local (Scheeres et al., 2013b, 2014b). Correspondingly, at Kutná-Hora-Karlov (Czech Republic) 33.3% were local and 66.6%, 3 out of 9 and 6 out of 9 individuals, respectively were non-local. This suggests that mobility among males was not restricted to warriors or mercenaries. Mobility in these regions was not restricted to males; females were found to have moved before adulthood was reached (Scheeres, 2014a; Scheeres et al., 2013b, 2014b). Patrilocality may explain migration among females into the region (See pages 103, 105 and 107) (Arnold, 2005; Karl, 2005; Knipper et al., 2014, 2017; Scheeres, 2014a; Scheeres et al., 2014b).

A similar pattern has been documented at Basel-Gasfabrik (Switzerland) where 37%, 20 out of 54 individuals, of the analysed sample was found to have migrated from surrounding areas, including those in the majority of male burials with weapons (3 out of 5 were of non-local individuals) (Knipper et al., 2017). However, the migrants were from farther away, such as the Black Forest, a region in southwestern Germany near the French border, and the Mediterranean area (Knipper et al., 2017). Migrants from further locations have also been documented at Magdalenenberg (southwest Germany) (See pages 103, 105 and 107) (Oelze et al., 2012). In this region 17.1%, 13 out of 76 individuals, were found to be non-local, including some of the weapon burials, 2 out of the 5 weapon burials changed residency before adulthood was reached (Oelze et al., 2012). However, the proportion of these burials that were local was not quantified (Oelze et al., 2012). The migrants were from diverse locations including Austria, France, northern Italy, the Alps, the Swiss Plateau, the Iberian Peninsula, and Heuneburg (southern Germany) (Oelze et al., 2012). Some of the above connections were also supported by the archaeological evidence; as 1 female was found with a bronze pendant specific to the north Italian Golasecca culture (Oelze et al., 2012). Trade between these regions may not adequately describe the presence of Gloaseccan material culture in Magdalenenberg (southwest Germany), as no other Gloaseccan artefacts were found (See pages 103, 105 and 107) (Oelze et al., 2012). Although patrilocality may explain the movement patterns observed in other regions, it may not have been a primary factor for migration to Magdalenenberg (southwest Germany) as the majority of migrants were males, 8 males and 5 females, respectively (Oelze et al., 2012). Further, most of the individuals were found to have moved during adulthood rather than before adulthood was reached (Oelze et al., 2012). This suggests that individual mobility may have been a factor for migration into this region (See pages 103, 105, 107 and 149). However, other processes including, patrilocality and small-scale or family migration cannot be ruled out.

Stable isotope evidence also supports limited extra-regional contact as evident in Nebringen (Stuttgart, Germany) where a significant proportion of the population, 88% (15 out of 17 individuals), was local (See pages 103, 105, 107 and 149) (Scheeres, 2014a; Scheeres et al., 2013b). However, identification of non-local individuals may have been impacted by the heterogeneous geological conditions of the region (Scheeres, 2014a; Scheeres et al., 2013b). A significant proportion of local individuals are also evident in the chariot burials at Kirkburn, Garton Station and Wetwang Slack (east Yorkshire, Britain), where all but 1 individual, out of 7, were found to be local (Jay et al., 2013). The Kirkburn chariot burial and 2 individuals from Wetwang Slack (east Yorkshire, Britain) were found to have moved into the region from elsewhere in Britain before adulthood was reached (See page 172) (Jay et al., 2013). The theory that the Arras culture was brought into east Yorkshire (Britain) by high status migrants from the Paris Basin (northern France) who utilized this burial practice appears to not be supported by the stable isotope evidence, as the majority of the individuals analysed were found to be local. However, individual mobility, such as, to and from the Paris Basin (northern France), may have resulted in the presence of similar cultural elements, e.g., burial practices, between the above regions (Collis, 2003; Cunliffe, 1997; Halkon, 2013, 2017; Stead, 1991a, c). Further, as the geology of these regions is similar, the stable isotope ratios may not differ significantly enough for the regions to be clearly separated (Jay et al., 2013; Jay and Montgomery, 2020). Consequently, the identification of non-local individuals, or regional mobility during life, may be skewed within these environments. Recent analysis and re-consideration of previously published data of the human skeletal material from Wetwang Slack (east Yorkshire, Britain) and Kirkburn (east Yorkshire, Britain) by Jay and Montgomery (2020), has indicated that the above non-local individuals may have actually been local, but were mobile regionally within Britain during their life-time rather than originating elsewhere before migrating into east Yorkshire (Britain). Stable isotope values that are consistent with an individual’s burial location do not necessarily indicate that they were local, or that they had not previously been mobile. They may have originated from a region where the bioavailable stable isotopes, strontium and oxygen, were very similar to those of the burial region (Jay and Montgomery, 2020). They might have moved away from the region before adulthood was reached, lived elsewhere for most of their lives and then returned to their homeland before death, or were brought back to be buried (Jay and Montgomery, 2020).

However, comparison of stable isotope ratios in teeth that form in successive stages, such as the first and third molars, can also be used to evaluate whether an individual obtained their diet from a similar, or single, geographical location throughout life or if they migrated into a region before adulthood was reached (Katzenberg and Waters-Rist, 2019). The speed of growth of various tissues can have an effect on the obtained stable isotope values from human and animal skeletal remains and teeth (Burton and Katzenberg, 2019; Katzenberg and Waters-Rist, 2019). Intra-tooth stable isotope analysis, and analysis of multiple teeth from the same individual, also provides a means to test the temporal relationship between residential changes before skeletal maturity was reached (Antoine et al., 2019; Katzenberg and Waters-Rist, 2019). First molars and third molars are commonly used for intra-tooth and intra-individual stable isotope analysis as the first molars are the first permanent teeth to develop, they begin forming around birth and are believed to mineralize (the incorporation of minerals into the tissue matrices) between 9 and 10 years of age (Hillson, 1996). The third molars are the most variable, they are the last teeth to erupt and are believed to mineralize between 9 and 13 years of age (Hillson, 1996). However, the exact timing of the mineralization process of individual teeth is debated (Hillson 1996; Montgomery 2002). Premolars are also used to construct intra-tooth stable isotope analyses, as they mineralize between 3 and 6 years of age, and can also be used to comparatively examine residential changes before maturity is reached (Evans and Chenery, 2006; Hillson, 1996). Thus, teeth that form at successive stages can provide a snapshot of the average intake of stable isotopes, such as $^{87}Sr/^{86}Sr$ and $\delta\ ^{18}O$, during the mineralization of each tooth (Burton and Katzenberg, 2019; Hillson 1996; Katzenberg and Waters-Rist, 2019; Montgomery 2002). Differences in the stable isotope values obtained from the first and third molars may appear to suggest a change in environment between the formation of these teeth. However, this variation may indicate intra-regional mobility, regular, or seasonal, movements throughout life (Evans and Chenery, 2006; Katzenberg and Waters-Rist, 2019). The relationship between the measured stable isotope value obtained from an individual and the value expected based on the region of recovery is not straightforward. The obtained values recovered from a local population, or individual, may be more or less consistent with those predicted (Burton and Katzenberg, 2019; Katzenberg and Waters-Rist, 2019; Pellegrini et al., 2016). Some individuals may have higher stable isotope values than expected due to short-term climate conditions and changes, such as colder, warmer, wetter and drier periods, that occurred during the formation of the teeth analysed (Pellegrini et al., 2016). Further, the distribution of ^{87}Sr/^{86}Sr and δ ^{18}O stable isotopes may vary within a single region, or show a marked difference between northern and southern locations (Pellegrini et al., 2016). Consequently, individuals that appear to be, or have been previously identified as non-local may actually have been intra-regionally mobile rather than migrants. Therefore, it is necessary to interpret the presence of non-local individuals within the wider context of their burial location and neighbouring regions.

The majority of the analysed individuals from Wetwang Slack (east Yorkshire, Britain) fall within the stable isotope range expected for the Yorkshire chalk (Jay and Montgomery, 2020). Although the majority of these individuals were local (3 out of 7 individuals), 4 were found to have high ^{87}Sr/^{86}Sr stable isotope values which are not consistent with the local chalk environment. However, these values are not unusual in the wider context of the Yorkshire Wolds (Jay and Montgomery, 2020). These individuals may have been conducting regular, or seasonal, movements between the chalk environment of the Wolds and other neighbouring locations, such as to and from water sources including, the east Yorkshire coast and the Humber estuary located on the east coast of northern England, and the freshwater spring sources local to the Wolds (See page 61) (Jay and Montgomery, 2020). The adult male from the Kirkburn chariot burial was found to have a comparably higher ^{87}Sr/^{86}Sr stable isotope ratio; however, this value falls within the range obtainable from the local environment, specifically the coarse grained sandstone bedrock, to the west of the burial site (Jay and Montgomery, 2020). This suggests the individual may have been mobile regionally within a relatively short distance of where he was buried (Jay and Montgomery, 2020).

Further indications of regional mobility are indicated by the nitrogen (δ ^{15}N) and sulphur (δ ^{34}S) stable isotope values from the remains of herbivorous animals (1 horse and 1 sheep) from Wetwang Slack (east Yorkshire, Britain). Nitrogen (δ ^{15}N) and sulphur (δ ^{34}S) are stable isotopic measures that are commonly used to reconstruct the terrestrial animal proportion of the diet, and to determine whether the principal foods consumed were from terrestrial or freshwater ecosystems (Drucker et al., 2016; Gilbert et al., 2019; Makarewicz and Sealy, 2015). At Wetwang Slack (east Yorkshire, Britain) these values were found to be similar to those obtained from the sampled human skeletal remains (Jay and Montgomery, 2020). However, the high $\delta^{15}N$ values were correlated with lower $\delta^{34}S$ values in both the human and animal bones analysed. Most of the values obtained from archaeological human skeletal material from the chalk environments in east Yorkshire and southern Britain are high, although this value is not specifically defined, nor is that of the local environment, so a direct comparison is not possible (Gron et al., 2018; Jay et al., 2019; Jay and Montgomery, 2020). Consequently, the individuals from which high values are obtained are not identified as local when compared to the British Geological Survey domain mapping stable isotope values (NERC Isotope Geoscience Laboratories (NIGL), 2018). Rather these values appear to be consistent with coastal locations rather than marine-derived limestone chalk environments such as those in east Yorkshire (Britain) (Jay and Montgomery, 2020). That said, this biosphere mapping is based on values obtained from modern plants. Thus, it is unknown whether these plants have been affected by atmospheric pollution. The Rothamsted project conducted an analysis of the 19th and 20th centuries British herbage (Poulton, 2006). This analysis indicated that during the 1860’s the δ^{34}sulphur stable isotope values were higher than they are today, and were comparable to prehistoric values. Though the exact nature of the difference in the stable isotope values from modern, prehistoric and those obtained during the beginning of the project were not quantified. Thus, a direct comparison of the stable isotope values from these periods is not possible (Poulton, 2006). The plants used to create the biosphere maps may not reflect the δ^{34}sulphur stable isotope values in prehistory (Jay and Montgomery, 2020; Poulton, 2006). Further, the plants used to construct these maps are limited in dispersal, as there is only one site where they are found which is located in the Yorkshire Wolds (Jay and Montgomery, 2020).

It is evident that identification of non-local individuals through comparison with these biosphere maps should be used with caution. However, in spite of the above caveat, the Iron Age population at Wetwang Slack (east Yorkshire, Britain) appears to be a settled community with no long-distance mobility currently evident (See pages 61 and 172) (Jay and Montgomery, 2020). Those individuals (3 out of 7 individuals) that have been identified as having higher $^{87}Sr/^{86}Sr$ stable isotope values were likely to have been mobile to some degree. The recent stable isotope analysis indicates that these individuals were moving around the regional landscape rather than being long-distance migrants (See page 61) (Jay and Montgomery, 2020). Additional connections between east Yorkshire (Britain) and continental

Europe (i.e., the adoption and/or import of La Téne culture in to east Yorkshire, Britain) are suggested by portable material culture, burial practices, art styles, trade items, the presence of captives and/or slaves and house structure.

Contact between Britain and continental Europe is believed to have been relatively limited until the end of the Iron Age (e.g., Carver, 2001; Cunliffe, 1988a, 1997; Daire, 2002; Fitzpatrick, 1989, 2001, 2003; Haselgrove, 1995; Macready and Thompson, 1984; Megaw, 1963; Morris, 2010; Stead, 1996; Trott and Tomalin, 2003). The Iron Age was not a time of isolation for Britain, as has been speculated in previous studies, nor were contacts limited to elite levels of society, as trade items have been found in non-elite graves and other contexts (See pages 19 and 32) (Collis, 2003; Cunliffe, 1988a, 1997, 2005, 2009; Davis and Gwilt, 2008; Fitzpatrick, 1989; James, 1999; Koch, 2006; Webley, 2015). However, the impression of limited cross-Channel contact throughout most of the Iron Age is derived, in part, from a narrow focus on the presence and distribution of portable material culture, (e.g., decorated metalwork and fibulae) and so-called high-status artefacts. This focus may have skewed the perspective of cross-Channel contact towards specific types of interactions, such as those between elite individuals at the expense of others (Collis, 2011; Fitzpatrick, 1993, 2001; Giles, 2012; Joy, 2015; Webley, 2015). The new genomic and stable isotope work on mobility and origin is also serving to further challenge these perceptions. Traditionally, invasions or migrations of people from continental Europe have been argued to have been the primary mechanism for indigenous cultural change and the appearance of continental La Tène artefacts (e.g., Collis, 2003, 2011; Cunliffe 1997, 2005; Fitzpatrick, 1993, 2001; Giles, 2012; Hingley, 2011; James, 1999; Koch, 2006; Webley, 2015). Such movements were invoked to explain the spread of new artefacts, technologies, art styles, and burial practices, as well as the spread of the Celtic languages. The presence, or presumed presence, of Celtic languages have also been argued to indicate the migration of Celtic groups into diverse regions (see page 91). However, the presence of Celtic languages and/or material culture do not necessarily indicate the presence of an ethnically Celtic population (see pages 54 and 91). For example, there were populations in the Central-western Iberian Peninsula that are believed to have spoken a Celtic language but for which there is no evidence of La Tène material culture (Ruiz Zapatero 1990, 1993, 1996).

Migration of continental groups has also been argued to have resulted in the appearance of the geographically restricted Arras culture in east Yorkshire (Britain) (e.g., Collis, 1997, 2011, 2018; Giles, 2012; Hill, 1995; Jope, 2000; Webley, 2015; Stead, 1991a, b, d). Identifying imports has been a focus of previous research, rather than locally made artefacts that mimic continental styles (e.g., Carver, 2001; Collis, 2003, 2005; Cunliffe, 1988a, 1997, 2005; Daire, 2002; Fitzpatrick, 1989, 2001, 2003; Harding 2007; Haselgrove, 1995; James, 1999; Koch, 2006; Laing and Laing, 1992; Laing, 2006; Macready and Thompson, 1984; Megaw, 1963; Morris, 2010; Stead, 1996; Trott and Tomalin, 2003; Webley, 2015). A small number of continental imports dating to the 6th and 5th centuries BC has been recovered particularly in and around the River Thames (a river that flows through lowland Britain) (e.g., Collis, 2003; Cunliffe, 1997, 2009; Harding 2007; James, 1999; Jope, 2000; Koch, 2006; Laing and Laing, 1992; Laing, 2006; Macdonald, 2007; Meyers, 1985). These include possible imports (e.g., fibulae) from the Mediterranean and Central Europe. However, it is debated whether these objects were deposited in the River Thames during the Iron Age or if they were washed out of burial and settlement contexts (see https://finds.org.uk/database for information about Iron Age artefacts from Putney recovered from the Thames) (e.g., Collis, 2003; Cunliffe, 1997, 2009; Harding 2007; James, 1999; Koch, 2006; Laing and Laing, 1992; Laing, 2006; Macdonald, 2007; Meyers, 1985). Early examples of La Tène artefacts have been found in Britain dating from after 400 BC, however, these objects are rare (Collis, 2003; Cunliffe, 1997, 2009; Garrow and Gosden 2012; Harding 2007; Jope 2000; Koch, 2006; Laing and Laing, 1992; Laing, 2006; Megaw and Megaw, 2001; Meyers, 1985).

Metalwork from Britain shows evidence for contact, specifically with the introduction of La Tène styles during the 5th and 4th century BC. Though these imported styles subsequently followed their own insular path of development in style and manufacture after 300 BC (Harding 2007; Karl, 2011; Laing and Laing, 1992; Laing, 2006; Macdonald, 2007; Megaw and Megaw, 2001; Webley, 2015). Prestige items have often been explained as diplomatic gifts, exchange or emulation among elite individuals on either side of the Channel (Collis, 2011; Cunliffe, 2005; Harding 2007; Joy, 2015; Laing and Laing, 1992; Laing, 2006; Macdonald, 2007). Other mechanisms for the arrival of continental Celtic artefacts in Britain include personal objects, gifts or trophies (e.g., the Gallic helmet recovered from Kent, Britain) (see https://canterburymuseums.co.uk/romanmuseum/explore/iron-age-helmet/ for a 3D reconstruction) (Farley et al., 2014). Although these diverse mechanisms imply the movement of individuals, ideas or beliefs; similarities in artefact design and manufacture may also be the result of parallel development among these diverse communities (Bradley and Smith, 2007; Collis, 2003, 2011; Cunliffe, 1997, 2009; Harding 2007; Hingley, 2011; Hunter, 2006; Joy, 2015; Koch, 2006; Laing and Laing, 1992; Laing, 2006; Morris, 2010; Stead, 1984). However, the observed similarities in artefact design and manufacture between Britain and continental Europe suggests some form of contact between communities within these regions; again, the genomic and isotope analysis of human remains from across Britain is supporting this hypothesis (Fernández-Götz, 2020; Millard, 2014; Madgwick et al., 2013; Montgomery et al., 2007; Schiffels et al., 2015; Webley, 2015).

Several artefacts and materials found in Britain have been argued to show evidence of cross-Channel contact, including metalwork, pottery, coral and coins (Collis, 2003; 2011; Cunliffe, 1997, 2009; Harding 2007; Joy, 2015; Stead, 1984; Karl, 2011; Koch, 2006; Laing and Laing, 1992; Laing, 2006; Macdonald, 2007; Megaw and Megaw, 2001; Webley, 2015). Artefacts have also been described as ‘imports’ based solely on the material from which they were manufactured, such as, silver, which was rarely used to manufacture objects in Britain during this time (Collis, 2011; Cunliffe, 1997, 2009; Joy, 2015; Stead, 1984; Karl, 2011; Koch, 2006; Laing and Laing, 1992; Laing, 2006; Macdonald, 2007; Megaw and Megaw, 2001; Webley, 2015). The coral inlays in metalwork (e.g., chariot equipment) are believed to derive from the Mediterranean (Harding 2007; Joy, 2015; Laing and Laing, 1992; Laing, 2006; Megaw and Megaw, 2001; Webley, 2015). Similarities in pottery styles between southeast England and neighbouring areas of northern France during the 6th and 4th centuries BC have also been described (Harding 2007; Collis, 2003; Cunliffe, 1997, 2009; Koch, 2006). The specific nature of these similarities are not often detailed, rather they are simply identified as complete import items. However, few actual metalwork imports, travelling in either direction, from Britain to continental Europe or the reverse, can be confidently identified (Collis, 2003; Cunliffe 2005; Harding 2007; James, 1999; Joy, 2015; Koch, 2006; Laing and Laing, 1992; Laing, 2006; Megaw and Megaw, 2001; Webley, 2015). Further, the number of imports found in Britain are modest (Fitzpatrick 2001; Harding 2007; Laing and Laing, 1992; Laing, 2006; Megaw and Megaw, 2001; Webley, 2015). Recognisable imports brought into southern Britain via western trade networks between northwest France, and southwest England, included Italian wine amphorae, Armorican pottery and coins (the region of Gaul located in northwestern France) (Collis, 2003; Cunliffe, 1990; Cunliffe and de Jersey, 1997; Fitzpatrick 2001; Harding 2007; Megaw and Megaw, 2001; Webley, 2015). The evidence for movement of British artefacts such as, pottery, coinage and shale exported as jewellery blanks into continental Europe is much more limited (Collis, 2003; Cunliffe 2005;

Cunliffe and de Jersey 1997; Harding 2007; Joy, 2015; James, 1999; Koch, 2006; Laing and Laing, 1992; Laing, 2006; Megaw and Megaw, 2001).

The presence of continental artefacts (e.g., from the Mediterranean) does not necessarily imply that direct contact existed between these regions, objects could have passed through several locations and contexts before reaching their final destination (Collis, 2003, 2011; Cunliffe, 2009, 2018; Joy, 2015; Karl, 2011; Koch, 2006; Sharples, 2010; van Noort, 2012; Webley, 2015). Consequently, the social significance of these items may have changed during the transmission process and/or when incorporated into a local indigenous culture (Collis, 2003, 2011; Hingley, 2011; Joy, 2015; Karl, 2011; Sharples, 2010). Celtic artefacts in Britain are debated to have initially followed the designs of those from continental Europe, such as the Palmette and dragon pairs, however, insular styles are more common from around 300 BC (See page 42, Figures 14 and 17) (Harding 2007; Joy, 2015; Koch, 2006; Laing and Laing, 1992; Laing, 2006; Macdonald, 2007; Megaw and Megaw, 2001; Stead 1996). However, art styles are not fixed, as new styles are added to the decorative repertoire over time. Older styles or motifs may be drawn from and included or referenced in later works (Garrow and Gosden, 2012; Harding 2007; Hunter, 2006, Joy, 2015; Koch, 2006; Laing and Laing, 1992; Laing, 2006; Megaw and Megaw, 2001; Webley, 2015). Consequently, designs cannot be considered in isolation. The shift towards insular art styles and the decrease in continental imports may indicate a breakdown or rerouting of trade routes, or that contact and/or the relationship(s) with communities in continental Europe had declined around 300 BC (e.g., changes in social and/or political structures of these communities) (Collis, 2003, 2011; Cunliffe, 1997, 2009, 2018; Hill and Hill, 2003; Joy, 2015; Koch, 2006; Stead, 1996). Further, very few discernible imports are described within Britain during this period (Collis, 2003; Cunliffe, 1997, 2009, 2018; Fitzpatrick, 1993; Hill and Willis, 2013; Joy, 2015; Koch, 2006).

It has also been suggested that imports and exports during this period may have been archaeologically invisible items including, grain; cattle; gold; silver; iron; hunting dogs; slaves and/or captives (Cunliffe, 2005; Fitzpatrick, 1993; Hill and Willis, 2013; Joy, 2015; Larsson, 1994; Lenski, 2008, 2014; Mata, 2019; Nash Briggs, 2003). However, these changes may also indicate an *in-situ* diachronic change in individual or community preference, or a decrease in the number of individuals moving to and from continental Europe (Collis, 2003, 2011; Cunliffe, 2009, 2018; Hunter, 2006; Joy, 2015; Webley, 2005; Stead, 1996). Additionally, the social reason for continuing stylistic links to continental Europe may have become less important culturally (Collis, 2011; Fernández-Götz, 2020; Harding 2007; Joy, 2015; Karl, 2011; Laing and Laing, 1992; Laing, 2006; Megaw and Megaw, 2001; Webley, 2015). Objects from continental Europe serve to physically manifest connections among these communities and social relations, however, the nature and importance of these connections changes over time (Collis, 2003, 2011; Harding 2007; Joy, 2015; Megaw and Megaw, 2001; Webley, 2015). The development of insular styles from 300 BC may also suggest that there was no longer a social need to maintain links to continental Europe through Celtic art, or that these linkages became less important (Collis, 2003, 2011; Fernández-Götz, 2020; Harding 2007; Joy, 2015; Megaw and Megaw, 2001; Webley, 2015). However, some artefacts can be stylistically linked with those from continental Europe, such as fibulae. This implies that some form of contact between Britain and continental Europe was still maintained, whether through artefact exchange and/or the movement of people to and from these regions (Collis, 2011; Fernández-Götz, 2020; Joy, 2015; Karl, 2011; Laing and Laing, 1992; Laing, 2006; Megaw and Megaw, 2001; Webley, 2015). Overall, the presence of La Tène material culture including fine metalwork and other decorated artefacts such as sword handles and scabbards (a sheath for holding a sword), suggests that contacts did exist and were maintained between Britain and continental Europe throughout the Iron Age. However, it is debated whether these contacts were intensive and/or sustained (Collis, 2003, 2011; Fernández-Götz, 2020; Harding 2007; Hingley, 2011; Joy, 2015; Karl, 2011; Laing and Laing, 1992; Laing, 2006; Megaw and Megaw, 2001; Webley, 2015).

It is often implied that only elite men would have been involved in cross-Channel relationships, even when female items, such as brooches or arm rings are imported. However, these items may have been imported for females as prestige items or were brought into Britain by females arriving in order to sustain or create alliances through marriage. Stable isotopic analyses have identified female migrants from continental Europe, supporting this notion (Colls, 2003; Cunliffe 1997, 2009, 2018; Harding 2007; Jay et al., 2012, 2013; Jay and Montgomery, 2020; Koch, 2006; Laing, 2006). Insular British artefacts found in continental Europe include, arm rings made from Kimmeridge shale from Dorset (southwest Britain) have been identified in graves dating from the 6th and 5th century BC in Switzerland, and at Manching (Bavaria) from the 3rd century BC, and in northwest France from the late 2nd to early 1st century BC (Colls, 2003; Cunliffe 1997, 2009; Koch, 2006; Teichmüller, 1992). Yet, the distributions of trade items may reflect regional differences in practices of their deposition, such as whether they were used as grave goods rather than their actual pattern of circulation within a community (Collis, 2003, 2011; Cunliffe 1997, 2009; Fernández-Götz, 2020; Hingley, 2011; Koch, 2006; Joy, 2015; Sharples, 2010; Webley, 2015). Control over trade items or prestige goods may have provided communities, or individuals, with the capacity to develop more social trade contacts with communities on either side of the Channel and North Sea (Collis, 2011; Hingley, 2011; Joy, 2015; Karl, 2011; Sharples, 2010). This social convergence may have facilitated the creation of multiethnic communities through the exchange of migrants and individual movement to and from neighbouring communities (see page 1) (Collis, 2011; Hingley, 2011; Joy, 2015; Karl, 2011; Sharples, 2010; Webley, 2015). Subsequently, a restructuring of the existing social structure within these communities may have resulted in a change or shift in ethnicity among migrants and out of group captives and/or slaves. Consequently, membership in an ethnic group may not have been based exclusively on kinship ties and was also likely based on place of residence (Cameron, 2008, 2011, 2013, 2016; Collis, 2011; Hingley, 2011; Karl, 2011; Larsson, 1994; Lenski, 2008, 2014; Mata, 2019; Webley, 2015). Therefore, the complexities in material culture should be used to examine the social networks among diverse groups rather than relying on their ethnic or cultural affiliations (see page 54) (Hingley, 2011; Jones, 1997; Renfrew, 1994a, b; Karl, 2011; Trigger, 2006). Other elements such as, house structure and burial practices, provide further evidence of connections, e.g., trade routes, social and/or ethnic, between communities in Britain and continental Europe (Karl, 2011; Webley, 2015).

Roundhouses have been identified at numerous sites in northern France and northwest Iberia dating from the end of the Iron Age (e.g. Albessard-Ball, 2011; Castro and Fernández, 1995; Cunliffe, 1990, 2009; Dechezleprêtre and Ginoux 2005; Harding, 1973, 2009). Similarities in roundhouses in the above regions include entrances facing east or southeast (Albessard-Ball, 2011; Castro and Fernández, 1995; Cunliffe, 1990, 2009; Harding, 1973, 2009; Joy, 2015; Karl, 2011; Pope, 2007, 2008; Webley, 2015). Although comparable trends in settlement dynamics on either side of the Channel and North Sea may represent parallel development within these communities; the possibility that they represent shared ideas that were exchanged among these groups cannot be ruled out (Collis, 2003, 2011; Cunliffe, 1990, 2009; Joy, 2015; Karl, 2011; Koch, 2006; Webley, 2015). Cultural similarities may be evident within societies with diverse origins that have similar developmental trajectories, such as burial practices and settlement structure (Collis, 2003, 2011; Cunliffe, 1990, 1997; Hingley, 2011; Karl, 2011; Sharples, 2010; Webley, 2015). However, as societies are in a continuous state of flux, these similarities should be interpreted in their respective cultural contexts.

Burial traditions during the middle and late Iron Age within Britain have also been argued to indicate connections with communities from continental Europe. These include a group of inhumation burials within stone cists (a small stone like coffin box or ossuary used to hold the bodies of the dead) in south Devon (England), Cornwall (Wales), and Scilly (Italy), that are believed to be dated to between the 4th and 3rd centuries BC and 1st century AD (e.g., Collis, 2003; Cunliffe, 1997, 2009; Koch, 2006; Webley, 2015). These burials have also been compared to contemporary cist cemeteries from Guernsey (a UK island territory off the coast of Normandy) and Brittany (a cultural region in northwestern France), however, the latter are unreliably dated, as they have been primarily dated by associated artefacts (e.g., Burns et al., 1996; Collis, 2003; Cunliffe, 1997, 2009; Henderson 2007; Koch, 2006). Though the similarities among these burials beyond the use of stone lined graves are not apparent or discussed in depth (Burns et al., 1996; Collis, 2003; Cunliffe, 1997, 2009; Henderson 2007; Koch, 2006). The inhumation burials of the Arras cultures from east Yorkshire (Britain) dating to around the 4th and 2nd centuries BC have also been linked to similar burials in northeastern France (e.g., Collis, 2003; Cunliffe, 1997, 2009; Good, 2005; Joy, 2015; Stead, 1991a, b, d; Webley, 2015). These burials share several similarities with those in northeastern France including, the use of barrows surrounded by square ditched enclosures and the presence of chariots within some of the graves. However, the use of chariots in these burials indicates an indigenous development rather than an exact replica of those from continental Europe, specifically those from the Champagne region (northern France) (See pages 19, 32, Table 7) (Anthoons, 2011; Hawkes, 1960; Jay et al., 2012, 2013; Stead, 1965b, 1979, 1986; 1991a, b, d; Stead and Rigby, 1999; Tiefengraber and Wiltschke-Schrotta, 2012; Van Endert, 1987; Wells, 1995a, b, c). Although the burial rite is similar though not identical to contemporary practices in the Champagne region (northern France) and the Belgian Ardennes (a region in southeast Belgium that extends into Luxembourg, northeastern France and northeastern Germany), the chariot itself was likely locally manufactured (Anthoons, 2011; Carter et al., 2010; Hawkes, 1960; Jay et al., 2012, 2013; Stead, 1965b, 1979, 1986; 1991a, b, d; Stead and Rigby, 1999; Tiefengraber and Wiltschke-Schrotta, 2012; Van Endert, 1987; Wells, 1995a, b, c).

Differences in these burials include the placement of the wheels in the grave, and whether the chariot was buried whole or dismantled and used as a makeshift coffin (Table 7)

(Anthoons, 2011; Carter et al., 2010; Hawkes, 1960; Jay et al., 2012, 2013; Stead, 1965b, 1979, 1986; 1991a, b, d; Stead and Rigby, 1999; Tiefengraber and Wiltschke-Schrotta, 2012; Van Endert, 1987; Wells, 1995a, b, c). However, in spite of these differences the presence of chariots in the above regions suggests some form of contact among populations in Britain and continental Europe. Large-scale migration from northern France has been invoked to explain the introduction and presence of this burial practice, but the consensus in recent studies is that if mobility occurred between regions it is likely to have been small-scale or individual movement (e.g., Collis, 2003, 2011; Cunliffe, 1997, 2009, 2018; Fernández-Götz, 2020; Jay and Montgomery, 2020; Joy, 2015; Knipper et al., 2014, 2016, 2017; Moghaddam et al., 2014; Oelze et al., 2012; Webley, 2015). Further, evidence for the incorporation of continental burial practices into the local culture in Britain is indicated by the difference in burial position and orientation, e.g., north-south verses south-north (See pages 19 and 32) (Anthoons 2007; Collis, 2003; Cunliffe, 1997, 2009, 2018; Giles, 2012; Koch, 2006; Stead, 1991a, b, d). Additionally, radiocarbon (^{14}C) dates from the Arras culture chariot burials suggests that this practice was in use during a short period around 200 BC (Jay et al., 2012), during which these burials were not common and were decreasing in frequency in continental Europe (Webley, 2015). The cremation rite of southeast England during the 1st century BC and 1st century AD, which shows close similarities to contemporary practices in northern France has also been argued to indicate connections among communities on either side of the Channel and North Sea (e.g., Collis, 2003; Cunliffe, 1997, 2009, 2018; Desenne et al., 2009a, b; Fitzpatrick 1997; Joy, 2015; Koch, 2006; Webley, 2015).

In both regions small groups of flat burials were common, sometimes associated with square enclosures (Collis, 2003; Cunliffe, 1997, 2009; Desenne et al., 2009a; 2009b; Fitzpatrick 1997; Joy, 2015; Koch, 2006; Webley, 2015). The adoption of new cultural elements, such as burial practices, may also be the result of a deliberate emulation by migrants of the dominant group (See page 54) (e.g., Collis, 2003, 2011; Cunliffe, 1997, 2018; Joy 215; Karl, 2011; Hingley, 2011). Some of the above similarities, between communities in Britain and continental Europe may not have been part of the original cultural package carried by individuals moving during their lifetimes or migrants, but were introduced later, transmitted along already existing channels or trade routes (Collis, 2003, 2011; Cunliffe, 2018; Joy, 2015; Koch, 2006). However, it is not possible to determine whether the above cultural phenomena represent primary elements, present within either communities in Britain and continental Europe, or secondary, diffused by migrants or individuals moving during their lifetimes (Collis, 2003, 2011; Cunliffe, 1997, Joy, 2015; Karl, 2011; Koch, 2006). Consequently, it is necessary to examine these societies both synchronically and diachronically. Synchronic models provide an understanding about how a particular society functioned; while diachronic models provide information about how societies change over time (e.g., varying settlement patterns, burial practices, presence and diversity in trade items) (Collis, 2003; 2011; Cunliffe, 1997; Hingley, 2011; Joy, 2015; Webley, 2015). Overall, it is evident that communities either side of the Channel and North Sea shared artefacts, technologies, ideas and practices throughout the Iron Age, with innovations travelling in both directions (Joy, 2015; Webley, 2015). The imports from continental Europe into Britain, also indicate that the trade and emulation of non-local material culture, design and customs was both a creative and selective process (Hingley, 2011; Joy, 2015; Karl, 2011; Webley, 2015).

Although the presence of continental imports in Britain indicates some form of contact between these communities, ethnographic and anthropological evidence suggests that slaves and/or captives could have influenced similarities in artefact design and manufacture (Cameron, 2008, 2011, 2013, 2016; Larsson, 1994; Lenski, 2008, 2014; Mata, 2019). However, these groups may not be identified archaeologically as they likely went through a transformative process, e.g., cultural assimilation or rejection/masking of their cultural autonomy, in response to a persistent external threat. Thus, these groups may have assimilated to the local indigenous culture of the region they moved into (Mata, 2012, 2019). The presence of slaves and/or captives is a multifaceted phenomenon with complex interconnected material, behavioural and ideological dimensions (Dal Lago and Katsari, 2008; Gronenborn, 2001; Marshall, 2015; Mata, 2019). The development of insular styles around 300 BC combined with the decreasing evidence of continental imports, may suggest a shift to an exchange of predominantly archaeologically invisible items (Cameron, 2008, 2011, 2013, 2016; Larsson, 1994; Lenski, 2008, 2014; Mata, 2019). Although it is likely that the skeletal remains of captives and/or slaves have already been encountered in the archaeological record but have not been recognised as such, as the specific cultural elements, such as restraints, that constitute material evidence of the presence of captives and/or slaves is not agreed on for prehistoric Europe (Arnold, 1988; Cameron, 2008, 2011, 2013, 2016; Larsson, 1994; Lenski, 2008, 2014; Mata, 2019; Thompson, 1993). The presence of these groups may also have a transformative impact on the developmental trajectory of a society. Thus, *in-situ* demographic and cultural changes may have resulted from the practice of taking captives and exchanging slaves. Consequently, the influence of these groups in relation to changes in material culture and the presence of local reproductions of trade items cannot be ruled out (Cameron, 2008 page 133). Overall, diverse lines of evidence including, artefact distribution, Celtic languages, settlement structure and burial practices, suggest that the adoption and import of La Tène culture in east Yorkshire (Britain) was a complex process and was not exclusively linked to the migration of continental groups into the region. Further, the stable isotopic evidence for the limited presence of non-local individuals in east Yorkshire (Britain) supports the notion that diverse mechanisms such as, small-scale migration, individual mobility, breakdown and rerouting of trade routes, were all involved in the transmission of La Tène material culture within this region.

A similar pattern is evident at Münsingen-Rain (Switzerland); only 14.7%, 5 out of 34 individuals, migrated into the region from other areas in the Swiss Plateau (Moghaddam et al., 2014; Scheeres, 2014a). The 6 weapon burials in this area were all within the range of the heterogeneous geological environment, suggesting that they were locals (See pages 103, 105, 107 and 145) (Moghaddam et al., 2014; Scheeres, 2014a). However, one individual buried with fibulae with characteristic northern Italian designs also had stable isotope values suggesting an origin somewhere warmer; but with similar geologic conditions as the Swiss Plateau, such as Italy or the Spanish coast (Bowen and Ravenaugh, 2003; Longinelli and Selmo, 2003; Scheeres, 2014a). A similar pattern is also evident in 2 other individuals with local grave goods who are also believed to have migrated from similar areas (Scheeres, 2014a).

Comparable levels of intra-regional homogeneity have been found in Monte Bibele (Bologna, Italy) and Manching (southern Germany) where 81%, 17 out of 21 individuals, and 77%, 14 out of 18 individuals, respectively, of the analysed samples, were local (See pages 103, 105 and 107) (Oelze et al., 2012; Scheeres et al., 2013b; Schweissing, 2013; Waneke, 1999). However, the homogeneous geological conditions might have complicated the identification of non-local individuals at Monte Bibele (Bologna, Italy) (Scheeres et al., 2013b). The weapon burials in the above regions were also predominantly local (Scheeres et al., 2013b; Schweissing, 2013; Waneke, 1999). At Monte Bibele (Bologna, Italy) 2 out of 6 weapon burials changed residency before adulthood was reached, however, these individuals came from other intra-regional locations (Scheeres et al., 2013b). Based on the above stable isotope analyses mobility among the so-called warriors may vary by region (See pages 103, 105 and 107). However, further samples are necessary to determine whether this pattern is also observed in other areas. This suggests that the description of highly mobile Celtic warriors by the Greeks and Romans is only partially supported.

Although the application of strontium stable isotopes, $^{87}Sr/^{86}Sr$, to mobility studies has indicated diverse migration patterns among populations, recent research has indicated that the commonly used strontium, $^{87}Sr/^{86}Sr$, reference maps may be incorrect (Thomsen and Andreasen, 2019). These maps are often based on modern-day surface water. Use of agricultural lime may substantially change the stable isotopic compositions of surface waters in low to non-calcareous soils (soil not containing lime or chalk and mostly composed of calcium carbonate). Recent research has suggested that the strontium stable isotope, $^{87}Sr/^{86}Sr$, compositions in water from farmland unaffected by agriculture compared to that from previously established reference maps are diverse (Thomsen and Andreasen, 2019). The average stable isotope ratios decreased from 0.7131 to 0.7099, suggesting that stable isotope ratios obtained from similar environments may need to be re-evaluated (Thomsen and Andreasen, 2019). This decrease suggests that the number of non-local individuals identified, or sample distributions in archaeologically derived samples from regions with this specific soil composition may have been artificially inflated.

That said, this analysis was conducted on surface water from western Denmark, so further samples are necessary to determine whether this pattern is evident in different regions (Thomsen and Andreasen, 2019). Further, the above decrease in stable isotope ratios is only evident in regions with a specific type of soil. Consequently, it is unknown whether the use of agricultural lime may affect the stable isotopic composition in those with other soil compositions. Stable isotope analysis in regions with low to non-calcareous soils, where strontium data are scarce, may not be affected by the use of agricultural lime. Additionally, a potential increase in $^{87}Sr/^{86}Sr$ stable isotope values in archaeological human skeletal material may have occurred due to the unintentional consumption of rock grit, from millstones, stones used to grind grain (Johnson et al., 2019). However, this unintentional consumption has not been found to result in a significant change, in spite of producing bioaccessible $^{87}Sr/^{86}Sr$ stable isotope values (Johnson et al., 2019). The unintentional ingestion of rock grit has been found to unlikely constitute more than 1% of the diet, by mass, consequently the potential increase in $^{87}Sr/^{86}Sr$ stable isotope values measured from British human archaeological skeletal material is not significant and is also unlikely to be greater than .001 (Johnson et al., 2019). Therefore, the use of millstones, either locally derived or imported, and the potential regular consumption of rock grit produced from their use will likely have a negligible effect on $^{87}Sr/^{86}Sr$ stable isotope values obtained from human archaeological skeletal material. Moreover, this ingestion is also unlikely to produce anomalously high $^{87}Sr/^{86}Sr$ stable isotope values or identify false migrants (Johnson et al., 2019). However, it is unknown whether this pattern is also evident in other areas, as the above correlation was conducted only using British archaeological material (Johnson et al., 2019). Furthermore, stable isotope analyses also often include evidence about the ratios of biologically available strontium from studies on other materials including, rocks, soils, archaeological human and animal samples from regions with similar geologic conditions (Knipper et al., 2017; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). Therefore, as the strontium ratios, $^{87}Sr/^{86}Sr$, are compared among these categories, the identification of local and non-local individuals may not be impacted significantly. However, due to sample size limitations and the potential for a discrepancy in ratios obtained from regions where agricultural lime was used, the results of stable isotope analyses should be interpreted with a degree of caution.

Although some stable isotope ranges used to reconstruct mobility among past populations may be affected by agricultural processes, those associated with Celtic populations are also supported by the archaeological evidence (See pages 19, 32 and 54) (Jay et al., 2013; Knipper et al., 2014, 2016, 2017; Scheeres, 2014a; Scheeres et al., 2013b). This suggests that the identification of non-local individuals may not have been impacted by agricultural processes. However, further analyses of Celtic populations in regions affected by the above mechanisms are necessary in order to determine whether the identification of non-local individuals has been affected. Some individuals buried with non-local artefacts have also been found to be migrants, as at Monte Bibele (Bologna, Italy), Münsingen-Rain (Switzerland) and Magdalenenberg (southwest Germany) (Oelze et al., 2012; Scheeres, 2014a; Scheeres et al., 2013b). However, the correlations between archaeological and stable isotope evidence are not always straightforward. Many individuals buried with trade items, e.g., wine flagons, are local (See pages 19, 32, 54 and 145) (Knipper et al., 2017; Oelze et al., 2012; Scheeres, 2014a; Scheeres et al., 2013b). Thus, the correlations between mobility and Celtic warriors may be tenuous.

There is evidence for a high level of mobility among the so-called Celtic warrior burials, but this association is not found throughout all of the regions they presumably inhabited. Thus, the highly mobile mercenaries described by the Greeks and Romans may have been restricted to specific locations (i.e., regionally) (Hauschild, 2015; Scheeres et al., 2014b; Tomaschitz, 2002). The spread of Celtic weaponry throughout Europe alternatively supports the mobility of mercenaries or the presence of trade routes through which the weapons and other materials were exchanged (See pages 19, 32 and 54) (Arnold, 2005, 2016a, b; Arnold and Hagmann, 2015; Georganas, 2018; Fernández-Götz and Arnold, 2017, 2018; Hauschild, 2010a, b, 2015; Scheeres, 2014a; Scheeres et al., 2013b, 2014b; Webster, 1996). However, burial with a weapon does not always correlate with individual mobility (Scheeres et al., 2013b). This is evident at Nerbringen (Stuttgart, Germany), Monte Bibele (Bologna, Italy), and Magdalenenberg (southwest Germany), where the majority of burials with weapons were local individuals (Oelze et al., 2012; Scheeres et al., 2013b, 2014b; Schweissing, 2013; Waneke, 1999).

Burials of adult males with peri-and ante-mortem weapon injuries accompanied by weapons have been interpreted as warriors in numerous previous studies, but this association is contested, as not all human remains buried with weaponry have injuries (Anderson et al., 2018; Arnold, 2005, 2016a, b; Arnold and Hagmann, 2015; Bertaud, 2017; D'Onofrio, 2011; Fernández-Götz and Arnold, 2017, 2018; Georganas, 2018; Harrison, 2015; Härke,1990; Jordan, 2016; Kurila, 2007; Pitman, and Doonan, 2018; Rustoiu and Berecki, 2015; Rustoiu, 2013; Thorpe, 2013; Ucko,1969; Webster, 1996; Whitley, 2002). Further, injuries presumed to be associated with combat have been found in burials without weapons (See page 229) (Anderson et al., 2018; Arnold, 2005, 2016a, b; Arnold and Hagmann, 2015; Bertaud, 2017; D'Onofrio, 2011; Fernández-Götz and Arnold, 2017, 2018; Georganas, 2018; Harrison, 2015; Härke,1990; Jordan, 2016; Kurila, 2007; Pitman, and Doonan, 2018; Rustoiu and Berecki, 2015; Rustoiu, 2013; Thorpe, 2013; Ucko,1969; Webster, 1996; Whitley, 2002). Age estimates of the individual human remains and comprehensive weapon descriptions are also not often presented (Oelze et al., 2012; Scheeres et al., 2013b). Consequently, these burials are often only described as possessing a weapon as those in the above regions. Some of the weapons recovered from weapon burials have been interpreted to represent prestige items or family keepsakes, as some have been repaired repeatedly (Arnold, 2005, 2016a, b; Arnold and Hagmann, 2015; Bertaud, 2017; Fernández-Götz and Arnold, 2017, 2018; Harrison, 2015; Jordan, 2016; Oelze et al., 2012; Rustoiu, 2013; Scheeres et al., 2013b, 2014b; Schweissing, 2013; Waneke, 1999; Whitley, 2002). However, evidence of repair is also not frequently described. Therefore, the presence of a weapon alone may not designate the individual as a warrior. Although some of these burials may represent warriors, their individual mobility as indicated isotopically does not support that described by the Greeks and Romans (Oelze et al., 2012; Scheeres et al., 2013b, 2014b; Schweissing, 2013;

Tomaschitz, 2002; Waneke, 1999). The stable isotope evidence does not support Scheeres's et al (2013b, c) conclusions that the degree of mobility indicated among the burials with weapons, and thus mercenaries, is in line with that proposed by the Greeks and Romans. The stable isotope evidence suggests that movement among these groups was predominantly intra-regional. Opposed to the extra-regional movement throughout Central Europe and into Britain, Asia Minor and Turkey described by the Greeks and Romans (See pages 103, 105 and 107) (Arnold, 2005, 2016a, b; Arnold and Hagmann, 2015; Fernández-Götz and Arnold, 2017, 2018; Oelze et al., 2012; Scheeres, 2014a; Scheeres et al., 2013b, c, 2014b; Schweissing, 2013; Selinsky, 2015; Tomaschitz, 2002; Waneke, 1999). Further, the majority of these burials were of local individuals. Therefore, the presumed degree of mobility among the so-called Celtic warriors is tenuous. However, a significant degree of mobility before adulthood was reached is evident within these regions (Knipper et al., 2014; Scheeres, 2014a; Scheeres et al., 2014b).

Evidence for mobility before adulthood was reached has been found at some Central European Iron Age sites associated with the Celts, including Basel-Gasfabrik (Switzerland), Glauberg (Hesse, Germany), Radovesice I and II (Czech Republic), and Kutná-Hora-Karlov (Czech Republic) (Knipper et al., 2014; Scheeres, 2014a; Scheeres et al., 2014b). At Basel-Gasfabrik (Switzerland) a significant proportion of females, 85.7%, 6 out of 7 individuals, compared to 17.3%, 4 out of 23 males, had migrated into the region before adulthood was reached (See pages 103, 105 and 107) (Knipper et al., 2017). A similar pattern is evident at Glauberg (Hesse, Germany) and Radovesice I and II (Czech Republic), 66.7% and 66.6% of females, 4 out of 6 and 6 out of 9 individuals, respectively, compared to 33.3% and 81.2% of males, 2 out of 6 and 13 out of 16 individuals, respectively moved into the region before adulthood was reached (Knipper et al., 2014; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). At Kutná-Hora-Karlov (Czech Republic), 61.5% of females, 8 out of 13 individuals, and 70% of males, 7 out of 10 individuals, migrated to the region before adulthood was reached (See pages 103, 105 and 107) (Knipper et al., 2013, 2014, 2017; Müller-Scheeßel et al., 2015; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). This suggests that the females in these regions may have followed a patrilocal residence pattern (Knipper et al., 2017). However, it is not mentioned whether individuals from Radovesice (Czech Republic), moved before adulthood was reached. Consequently, a direct comparison of mobility during these periods between the sexes and to other regions is not possible. Furthermore, the social and biological differences in the definitions of the terms sub-adult, adolescence and adulthood are not described in the original site reports. Consequently, at the time of writing, because none of the populations have been subject to life course analyses, and there are no indigenously authored primary sources for these communities, it is not known how these regions created their life courses, and the extent to which these changed over time. The application of the above terms reflects our modern understanding of these age-categories, rather than those of past cultures, as for the most part, these remain unknown. These categories are also not necessarily applicable to biological age, (the physical ageing of the body), or social age, (a culturally constructed category of age appropriate behaviour and attitudes), and we must always be mindful that a cemetery population is likely to contain different generational cohorts (Halcrow and Tayes, 2011; Inglis and Halcrow, 2018; Mays et al., 2017; Sofaer 2006a, b, 2011).

Moreover, it is difficult to correlate the applications of these terms in past and modern societies, as the specific cultural milieu in which individuals are situated is not static, and may not be correlated with biological age (Inglis and Halcrow, 2018; Mays et al., 2017; Sofaer 2006a, b, 2011). Funerary studies across Europe suggest that although Iron Age society was structured according to age and gender (e.g., Arnold, 2016) even within one country, there was considerable variation between communities, as seen in the life course analyses of Dorset and east Yorkshire, in England (Hamlin, 2007; Giles, 2012). The evidence for considerable regional heterogeneity across Iron Age Europe, suggests that there was no one single life course (Pope and Ralston, 2011). Since the above terms were likely to have varied intra-and-extra-regionally it is difficult to determine which age category or term is best suited to encompass the differences inherent in their application. Further, it is unknown whether modern application of the terms ‘infant’, ‘childhood’, ‘children’ or ‘adolescence’ are an adequate representation of those used in the past. Consequently, it is necessary to document the specific age-at-death categories used by osteologists to categorize infants, children (sub-adults) and adults, and to recognize that these categories were not static, are socially constructed, varied culturally and likely do not adequately represent an individuals social age (Halcrow and Tayles, 2011; Inglis and Halcrow, 2018; Mays et al., 2017).

Additionally, as the entire sample in the above regions was not analysed, the identification of non-local individuals may have been impacted. Furthermore, similar geologic conditions in different regions might result in some population movements being invisible, and while stable isotope analysis can identify first generation immigrants their descendants may not be, as their $^{87}Sr/^{86}Sr$ and $\delta\ ^{18}O$ stable isotope values will reflect those of the regions they immigrated to rather than those of their homelands (Jay and Montgomery, 2020; Jay et al., 2012; Müller-Scheeßel et al., 2015; Scheeres, 2014a; Scheeres et al., 2013b, 2014b; Tomaschitz, 2002). However, in spite of the sample size limitations, individual and small-scale migration appears to have been common (Collis, 2003; Müller-Scheeßel et al., 2015; Scheeres, 2014a; Scheeres et al., 2013b, 2014b; Tomaschitz, 2002). Although individual and movement before adulthood was reached is indicated within the above regions, evidence of family mobility has been suggested at Radovesice II (Czech Republic) (Scheeres et al., 2013b, 2014a, b). A group of 3 associated adult burials believed to represent a family group, based on similar artefacts and burial location (i.e., clustered together), were found to have stable isotope ranges indicating migration from a similar extra-regional location, although this region could not be determined (See pages 103, 105 and 107) (Scheeres, 2014a; Scheeres et al., 2013b, 2014b). However, the presumption that these burials represent a family group is uncertain, as it is based only on archaeological evidence. A high rate of individual mobility has also been found at Glauberg (Hesse, Germany) where 31.6%, 6 out of 19 individuals, from elite burials, migrated from surrounding regions during childhood or before adulthood was reached (See pages 103, 105 and 107) (Knipper et al., 2014).

However, the number of males and females comprising this sample is not described (Knipper et al., 2014). Therefore, it is difficult to determine which sex was more frequently moving into this region. This finding suggests that entire families, as well as individuals, were mobile during the Iron Age (Arnold, 2005; Collis, 2003; Cunliffe, 1997; Karl, 2005; Müller-Scheeßel et al., 2015; Parkes, 2006; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). However, the majority of individuals who migrated before adulthood was reached within Glauberg (Hesse, Germany) and Basel-Gasfabrik (Switzerland) were female, which indicates a patrilocal residence pattern among these regions (Knipper et al., 2014, 2017; Müller-Scheeßel et al., 2015; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). The relatively high mobility rates among sub-adults, as evident in the above regions, may be explained by the social structure of La Tène communities, in which hierarchy is presumed to have played a significant role (Collis, 2003; Knipper et al., 2013, 2014, 2017; Long, 2005; Müller-Scheeßel et al., 2015; Scheeres, 2014a; Scheeres et al., 2013b, 2014b).

The Greeks and Romans, as well as some medieval sources, describe a system of allegiance fosterage occurring during the Iron Age. This system consisted of a child being educated by one foster family or successive families that lasted from infancy or later childhood until marriage (Arnold, 2005; Karl, 2005; Müller-Scheeßel et al., 2015; Parkes, 2006). However, this system in Iron Age Europe has not yet been fully supported, as the main literary descriptions are derived from Irish, Welsh and Scottish texts which date to the Medieval Period (See page 91). Consequently, it should be applied to Iron Age populations with caution. However, this system could explain the observed stable isotope variation, which suggests that a significant proportion of sub-adults had grown up in different communities to those in which they were born (Arnold, 2005; Karl, 2005). Fosterage, in medieval literature, is more often described as involving boys, evidence for mobility before adulthood was reached among girls is more likely specifically related to patrilocal residence patterns or exogamy (Arnold, 2005; Karl, 2005; Knipper et al., 2014, 2017).

Although the spread of the La Tène culture has been linked with the movement of populations and individuals, these events may not have occurred frequently. As evident by the significant proportion of local individuals in some regions (e.g., Nebringen, Stuttgart, Germany). The stable isotope data suggests varying levels of mobility and intra-and-extra-regional contact. This is in-line with previous nonmetric dental analyses indicating the presence of regionally diverse populations in Central Europe during this period (See pages 103, 105 and 107) (Anctil, 2016; Maxová et al., 2011). Individuals appear to have been moving irrespective of being in the core or expansion regions; thus, these geographic designations may be nominal.

Linguistic evidence for the presence of the Celts

The association between the Celts and the Hallstatt and La Tène cultures is also derived from the linguistic work of Edward Lhuyd (1707) and Paul-Yves Pezron (1703) (Campanile, 1976; Collis, 2003; Cunliffe, 1994, 1997). They described the languages spoken in the regions associated with these cultures as Celtic, based on Caesar's description of a population in Gaul referring to themselves as Celts. Subsequently, when these cultures were encountered in the 19th century, they were described as Celtic following the convention that similarities in spoken languages and artefacts can be used to define a culture or population (Collis, 2003; Cunliffe, 1997; James, 2005; Koch, 2006; Trigger, 2006). Thus, if the populations inhabiting these regions were linguistically Celtic, they were culturally as well. Consequently, the modern concept of the Celts is also derived from a language association, although there is not much evidence for linguistic differences within the above groups.

Further, the continental Celtic languages, those spoken in continental Europe, are extinct and the majority of the inscriptions are fragmentary. Therefore, it is difficult to determine the degree of variation among these languages and their approximate boundaries. Consequently, these languages have been partially reconstructed from place names, inscriptions, words borrowed from Germanic or Italic languages, and references in Latin texts (Charles-Edwards, 1995; Collis, 1999; Evans, 1983; Gohil, 2005, 2006; Joseph, 2010; Lane, 1933; Renfrew, 1987). They likely had a range of dialects, although how many and their relationships are not known (Evans, 1979; Fleuriot, 1988; Prokić and Nerbonne, 2013; Rickford and Rickford, 1995; Salmons, 1992; Schmidt, 1986c). Continental Celtic languages appear to have died out around 500 AD. By contrast, in the British Isles the Celtic languages have survived (Charles-Edwards, 1995; Evans, 1983, 1986; Schmidt, 1986; Renfrew, 1987).

The Celtic languages are classified as a branch of the Indo-European (IE), family of languages (Campanile, 1976; Collis, 2003; Evans, 1983; Fortson, 2004; Mallory, 1992; Renfrew, 1987). The IE language family has around 445 languages and dialects and includes most of the major extant languages of Europe as well as parts of western, Central, and south Asia (Kortlandt, 1989; Forster and Toth, 2003; Fortson, 2004; Mallory, 1989, 1992; Mallory and Adams, 1997). Although Celtic is accepted as an IE language, its place within this language family is still debated (Britain and Trudgill 1999; Charles-Edwards, 1995; Dyen et al., 1992; Evans, 1983; Fortson, 2004; Kortlandt, 1990, 2007, 2018; Mallory, 1992; Mallory and Adams, 1997). The earliest records of Celtic language(s) are the Leptonic inscriptions of northern Italy a region presumedly inhabited by the Celts. The oldest are associated with the Golasecca, Canegrate and Hallstatt cultures (Ball and Fife, 1993; Ball and Muller, 2012; Eska, 1998; Evans, 1995; Isaac, 2010; Joseph, 2010; Renfrew, 2013). However, it is difficult to determine with which culture they are associated with as there is a lack of absolute chronology associated with the inscriptions in these regions (Charles-Edwards, 1995; Cowgill, 1975; Ellis, 1995, Korolec, 1995; Prosdocimi, 1991). The Celtic languages represented by these inscriptions are distinguished by the difference in the expression of the kw and p sounds.

The division between these languages has been established based on two primary criteria. The first division is based on the development of an IE kw sound (a k +u sound), which is expressed differently in the P and Q Celtic languages (Cowgill, 1975; Campanile, 1976; De Hoz, 1992; Forester and Toth, 2003). P Celtic languages include Gaulish, spoken in Gaul, and Brittonic (the ancestor of modern Welsh, Cornish, and Breton) (Collis, 2003;

Cowgill, 1975; Schmidt, 1988; Koch, 1992, 2006; Renfrew, 2013). Q Celtic languages include Goidelic (the ancestor of Manx, modern Irish and Scottish Gaelic) (Ball and Fife, 1993; Collis, 2003; Cowgill, 1975; Koch, 1992, 2006; Nicholson, 1904; Renfrew, 2013; Schmidt, 1988). These languages were subsequently adopted into the continental Celtiberian languages (a combination of Iberian and Celtic languages) by the inhabitants of the Iberian Peninsula (Ball and Fife, 1993; Collis, 2003; Cowgill, 1975; De Hoz, 1992; Fleuriot, 1988; McCone, 1991; Nicholson, 1904; Oppenheimer 2007; Wodtko, 2010, 2013). The kw sound appears as either a ku or K sound in Celtiberian and arguably in some Gaelic dialects such as Scottish Gaelic and Manx (Cowgill, 1975; De Hoz, 1992; Fleuriot, 1988; McCone, 1991, 1996; Nicholson, 1904). However, the above pronunciations have been transliterated as a q sound as these languages were initially translated through Latin, hence the term Q Celtic for these languages (Ball and Fife, 1993; Renfrew, 2013; Wodtko, 2010, 2013). The IE kw sound appears as a P sound in the Gaulish and Brittonic languages (Collis, 1999; Collis, 2003; Delamarre, 2003; Sims-Williams, 1998a; Oppenheimer, 2007, Waddell, 1969; Wodtko, 2010, 2013).

It is believed that these changes occurred after the split between the P and Q languages (Eska, 1998; Fleuriot, 1988; Nicholson, 1904; Renfrew, 1987; Schmidt, 1986). The second division, is based on geographic location and includes the insular and continental languages, spoken in the British Isles continental Europe, respectively. The insular languages include Goidelic and Brittonic (Cowgill, 1975; De Hoz, 1992; Fleuriot, 1988; Isaac, 2010; Mallory, 2016; McCone, 1991; Nicholson, 1904). The continental languages include Leptonic, Gaulish, and the Celtiberian languages (Collis, 2003; Cowgill, 1975; Eska and Evans, 1993; Eska, 1998; Koch, 1992, 2006; Renfrew, 2013; Schmidt, 1988). Other languages that have been argued to be part of this language family include, Galatian, spoken in the Galatian area of Turkey, and Noric, spoken in Central and eastern Europe (Delamarre, 2003; Falileyev, 2007; Freeman, 2001). However, as these languages are only known from exceedingly limited and highly fragmentary inscriptions, so their place within the above language family is uncertain (Cowgill, 1975; Eska and Evans, 1993; Eska, 1998; Schmidt, 1988; Koch, 1992, 2006; Renfrew, 2013). Further, several languages are presumed to have been Celtic based on where they were spoken, or believed to have been spoken (Collis, 2003; Cowgill, 1975; Eska and Evans, 1993; Eska, 1998; Schmidt, 1988; Koch, 1992, 2006; Renfrew, 2013). These include Camunic, Ligurian, Lusitanian, and Raetian. These languages were spoken in the Alps, southeastern France, northern Italy, the Iberian Peninsula, Switzerland, and northern Italy respectively (Collis, 2003; Cowgill, 1975; Eska and Evans, 1993; Eska, 1998; Schmidt, 1988; Koch, 1992, 2006; Renfrew, 2013). However, these languages have not been the focus of much research as they are also known from extremely limited and highly fragmentary short inscriptions. Consequently, the relationships among Celtic languages have been predominantly established based on the Gaulish, Brittonic Goidelic, Celtiberian and Leptonic languages.

Although the P and Q division is still used, the insular and continental division is more common; as it is unknown whether the above sound changes were present in all insular and continental languages (Collis, 2003; Cowgill, 1975; Eska and Evans, 1993; Eska, 1998; McCone, 1991, 1996; Schmidt, 1988; Schrijver, 1995; Koch, 1992, 2006; Renfrew, 2013). Consequently, the sound changes may not adequately reflect the range of variation between these languages. Therefore, the presence of shared cognates, words having a common linguistic origin (e.g., English: father, German: Vater), are frequently used to reconstruct relationships among the insular and continental languages (Ball and Fife, 1993; Carroll, 1992; Cowgill, 1975; Falileyev, 2007; Gohil, 2005, 2006; McCone, 1996; Renfrew, 2013). Specifically, cognates are used, as they are believed to represent root words that can be traced back to a shared ancestral language, i.e. the IE languages (Carroll, 1992; Kondrak, 2001; Krishnamurti et al., 1983; Pagel, 2016; Rama et al., 2018). Lower percentages of shared cognates may suggest a longer temporal separation and subsequent differentiation (Carroll, 1992; Kondrak, 2001; Krishnamurti et al., 1983; Pagel, 2016; Rama et al., 2018).

The insular languages are believed to be more similar to one another than to the continental (Cowgill, 1975; Falileyev, 2007; Gohil, 2005, 2006; McCone, 1996). Since these languages share less than 20% of cognates with other IE languages, this suggests an early separation between these languages (Novotna and Blazek, 2006; Oppenheimer, 2007; Parsons and Williams, 2000; Parsons, 2012). Brythonic, Goidelic, and Gaelic share 30% of cognates, indicating a later split. However, as Goidelic shares more cognates with the insular languages its classification as a continental language is questionable (McCone, 1996; Oppenheimer, 2006). Based on the differences in shared cognates, the split between insular and continental Celtic may have happened as early as 3,200-2,500 BC. Therefore, this split may have occurred after the IE languages spread throughout continental Europe, approximately 4,000-3,000 BC (Atkinson and Gray, 2017; Forester et al., 2004; Forester and Toth 2003; Gray and Atkinson, 2003). Alternatively, it has been suggested that Gaulish may have been separated from the other insular languages by 5,200 kya. Goidelic and Brittonic may have split around

1,100 BC (Atkinson and Gray, 2017; Forester et al., 2004; Forester and Toth 2003; Gray and Atkinson, 2003; Novotna and Blazek, 2006). The above dates are constant with a Neolithic and/or Bronze Age migration suggesting that the insular Celtic languages may have arrived in the British Isles earlier than presumed. Though, the date of 5,200 kya represents the oldest possible movement into the region (Byrne et al., 2018; Forester et al., 2004; Forester and Toth 2003; Gray and Atkinson, 2003; Novotna and Blazek, 2006). A date of 3,200 ± 1,500 kya, has been proposed for the split between Gaulish, Goidelic, and Brythonic. However, this date should be regarded as tentative, as it is based on only three descendant branches (Forester and Toth 2003; Gray and Atkinson, 2003; Nicholson, 1904; Novotna and Blazek, 2006).

Though the linguistic dates suggest an early introduction of the insular languages in this region, the archaeological evidence is at odds with this perspective (Cunliffe, 2009; Charles-Edwards, 1995; Evans, 1986, 1995; Forester et al., 2004; Green and Piggott, 1983; Green, 1998; Greenwell, 1906; Halkon, 2013; Hodson, 1964; James, 1999; Jackson, 1948). If these languages moved into the British Isles during the Neolithic/Bronze Age, then their movement is not likely connected to the movement of La Tène artefacts during the Iron Age. Further, there is some evidence of cultural continuity from the Bronze Age into the Iron Age, i.e., settlement patterns and house structure (Collis, 2003; Cunliffe, 1997; Dent, 1982, 1984; James, 2005; Koch, 2006; Stead, 1991a). Given the lack of evidence for a large-scale migration into this region during the Iron Age and the estimated arrival of the insular languages, it has been suggested that these languages were already established in the British Isles prior to the arrival of people bearing the La Tène material culture (See pages 19, 32 and 61) (Charles-Edwards, 1995; Collis, 2003; Cunliffe, 2009; Charles-Edwards, 1995; Evans, 1986, 1995; Forester et al., 2004; Halkon, 2013; Hodson, 1964; James, 1999). Therefore, the association between the insular languages and this culture within the British Isles is questionable. If these languages were spoken prior to the arrival of the above culture, the application of the term Celt to this region may be nominal or strictly linguistic. However, the influence of small-scale migration and/or population movement along Atlantic trade routes cannot be ruled out.

The distribution of Celtic place names including briga (hill), dunum (fort) and magnus (market), is in line with the above mechanisms (Cunliffe, 1997; Falileyev, 2007; Heine, 2008; Jackson, 1948). The distribution of these place names extends throughout most of Central Europe including northern Gaul, southern Germany, northern Italy, Hungary, and into Britain and Ireland (Collis, 2003; Gohil, 2005, 2006; Parsons, 2012; Sims-Williams, 2006). Although there is a record of these inscriptions from Cornwall, Wales, Ireland, and Scotland before and after the Roman invasions, around 55-54 AD, their relative frequencies are low (Collis, 2003; Gohil, 2005, 2006; Parsons, 2012; Sims-Williams, 2006). Place names only represent 27% of the linguistic inscriptions found throughout England, indicating a limited presence or distribution of the insular languages (Fortson, 2004; Forester and Toth, 2003; Sims-Williams, 2006). However, the total number of inscriptions is not quantified (Fortson, 2004; Forester and Toth, 2003; Sims-Williams, 2006). Their distribution throughout the above regions may indicate interactions among populations (i.e., trade or gene flow), or their application by the Romans to regions possessing similar material culture and/or languages. Since these similarities are not described in detail and are derived from Roman political propaganda, it is difficult to determine if they are representative of actual linguistic similarity.

In spite of their low-frequencies in distribution, place name evidence has been used to link the insular languages to those in historic Gaul and the Iberian Peninsula (Collis, 2003; Forester and Toth, 2003; Sims-Williams, 2006). Place names have been interpreted to indicate the presence of Celtic languages and people; however, this may not be the case (Falileyev, 2007; Falileyev et al., 2010; Sims-Williams 1998, 2006; Joseph, 2010; Parsons, 2012). In Albania and Kosovo, both Pannonian (a proto-Slavic language spoken in present-day Hungary and the Slavic regions) and Celtic inscriptions have been found (Joseph, 2010; Sims-Williams 1998, 2006). Though, the majority of the tribal and place names are Pannonian in origin (Falileyev, 2007; Falileyev et al., 2010; Sims-Williams, 1998a). Therefore, the presence of these inscriptions does not necessarily designate an area as inhabited by Celtic people or languages. However, due to the nature of the continental language inscriptions (e.g., fragmentary), it is difficult to determine their geographic distribution.

The majority of the continental inscriptions are found in the Iberian Peninsula and northern Italy; relatively few are from Central Europe. Therefore, their geographic distribution and diversity is unknown. Further, as the continental languages are based, in part, on the transliteration of the q sound through Latin, their resulting relationships with the insular languages are questionable (Ball and Fife, 1993; Charles-Edwards, 1995; Collis, 2003; Eska, 1998; Evans, 1995; Koch, 2006). It is also difficult to determine the extent of this influence has had on the reconstruction of the continental languages, as it is unknown whether the resulting relationships are representative of differences between these languages or between the continental languages and Latin (Borsley and Roberts, 1996; Collis, 2003; Cunliffe, 1997; Novotna and Blazek, 2006). Consequently, it is difficult to determine the extent of the diversity among these languages, i.e., whether they represent different dialects (a particular form of a language that is specific to a geographic region and/or ethnic group) or different languages (Ball and Fife, 1993; Prokić and Nerbonne, 2013; Salmons, 1992). Furthermore, the phylogenetic reconstruction of the continental languages is questionable as it is primarily based on the Celtiberian and Leptonic inscriptions (Forester and Toth 2003; Gray and Atkinson, 2003; Nicholson, 1904; Novotna and Blazek, 2006). Moreover, it is unknown whether the initial divisions between the insular and continental languages are valid distinctions, as they were based on the differential expression of the IE kw sounds and geographic location (Ball and Fife, 1993; Collis, 2003; Renfrew, 1992, 2013; Wodtko, 2010, 2013).

It is also uncertain whether these divisions are only a convenient way to describe these languages or are a valid way of dividing them (Heine, 2008; McCone, 1996, Oppenheimer, 2007; Trask, 1996). Further divisions have been postulated among the continental languages, including the establishment of the Italo-Celtic language branch. This proposed division is based on the presumption of shared features (i.e., cognates) and the presence of La Tène artefacts in northern Italy. However, the presence of these features does not necessarily facilitate the formation of a new language branch (Forester and Toth, 2003; Schmidt, 1991; Warnow, 1997; Watkins, 1966). Therefore, this division is not believed to represent a specific language or language family (Cowgill, 1970; Forester and Toth, 2003; Isaac, 2004, 2010; Kortlandt, 1981, 2007; Russell, 1995; Schmidt, 1991; Warnow, 1997; Watkins, 1966; Weiss, 2012; Winfred, 1997). Rather this branch is believed to represent a nominal division between the Italic and continental languages based on the suspected existence of an ancestral Italo-Celtic language (Forester and Toth, 2003; Schmidt, 1991; Warnow, 1997; Watkins, 1966). However, as the diversity among the continental languages, their relationships to one another and their subsequent diffusion throughout Europe are unknown; their relationships to other IE languages are hypothetical and may have resulted in the formation of new language branches and/or families (De Hoz, 1992; Forester and Toth, 2003; Isaac, 2004, 2010; Kortlandt, 1981, 2007; Watkins, 1966; Winfred, 1997). Therefore, it is difficult to determine whether the presence of linguistic similarities, such as shared cognates, indicate similar languages or different processes including word borrowing; the exchange of words among population across linguistic boundaries with or without gene flow

Carroll, 992; De Hoz, 1992; Forester and Toth, 2003; Isaac, 2004, 2010; Kortlandt, 1981, 2007; Schmidt, 1991; Warnow, 1997; Watkins, 1966; Winfred, 1997).

Shared cognates between the Italic and Celtic languages may have derived from word borrowing across linguistic boundaries. Alternatively, the presumption of shared features may simply be that, a presumption (Carroll, 992; De Hoz, 1992; Forester and Toth, 2003; Isaac, 2004, 2010; Kortlandt, 1981, 2007; Schmidt, 1991; Warnow, 1997; Watkins, 1966; Winfred, 1997). This presumption is based on similarities between the Leptonic, Celtiberian and Italic branches. Although the Italic and Leptonic languages are believed to have been spoken in close proximity, there is no evidence that they were spoken farther south than present-day Milan, whereas the Celtiberian languages (i.e., Tartessian) were spoken predominantly in the Iberian Peninsula (Forester and Toth, 2003; Isaac, 2004, 2010; Kortlandt, 1981, 2007). Tartessian, a language spoken in southern Portugal and southwestern Spain prior to Roman invasion, has been classified as Celtiberian and/or Celtic (Koch, 2009b, 2010, 2012, 2013; Rodriguez, 2002a, b). However, it has also been classified as a language isolate, with no demonstratable relationship to other languages, as there are no significant connections with the other IE languages (Correa, 1989; de Hoz, 2010; Isaac, 2004, 2010; Kortlandt, 1981, 2007). Tartessian has also been suggested to be related to the Iberian or Basque languages, thus the Celtic elements may represent word borrowing (Correa, 1989; de Hoz, 2010; Hunley and Long, 2005; Koch, 2009b, c, 2010, 2013; Rodriguez, 2002a, b; Untermann, 1997). The process of word borrowing make it difficult to estimate the formation of new languages or dialects and their subsequent splits.

Estimating the time since the continental, insular, Italic and Leptonic languages split from a common proto-language is difficult as the duration of their period of common ancestry and underlying relationships are unknown (Forester and Toth, 2003; Isaac, 2004, 2010; Kortlandt, 1981, 2007). However, the length of time since one or more languages diverged from an earlier proto-language may be estimated through the application of lexicostatistics and glottochronology. Lexicostatistics, the quantitative comparison of cognates and glottochronology, the attempt to use these methods to estimate the length of time since one or more languages diverged from an earlier proto-language, have been used to estimate the approximate dates of this divergence and subsequent diffusion. However, there are several inherent problems with each method (Bergsland and Vogt, 1962; Campbell, 1988; Gray and Atkinson, 2003; Haarmann, 1990; Sankoff, 1970). Glottochronology examines the chronological relationships between languages, following two assumptions. First, that there is a relatively stable basic vocabulary, cognates, shared by all languages. Second, that any linguistic replacements occur analogical to radioactive decay, by assuming a constant rate of cognate replacement which is summarized into percentage scores (Bergsland and Vogt, 1962; Campbell, 1988; Carroll, 1992; Gray and Atkinson, 2003; Haarmann, 1990; Holm, 2003; Kirk et al., 1985; Swadesh, 1952; Thomason and Kaufman, 1992).

However, the assumption of strict cognate replacement rarely holds, making discrete estimates unreliable (Atkinson and Gray, 2017; Bergsland and Vogt, 1962; Campbell, 1988; Gray and Atkinson, 2003; Kirk et al., 1985). Glottochronology has been found to account for a significant proportion of the variance among IE languages, but the accuracy of the timing of language divergence using this method is inherently controversial (Bergsland and Vogt, 1962; Campanile, 1976; Dyen, 1962b, 1963; Gray and Atkinson, 2003; Haarmann, 1990; Hoijer, 1956; Holm, 2003; Sjøberg and Sjøberg, 1956). Due to the inclusion of borrowed words among descendant language branches, the resulting divergence estimates can be distorted; as word borrowing across linguistic boundaries does not necessarily indicate a substantial change (Atkinson and Gray, 2017; Brainerd, 1970; Campbell, 1988; Dyen, 1962b, 1963; Gray and Atkinson, 2003; Holm, 2003; Sankoff, 1970; Thomason and Kaufman, 1992). Moreover, by summarizing cognate changes into percentage scores, much of the discrete character data, terms and/or elements specific to one language, is lost. Consequently, the ability of this method to reconstruct linguistic history accurately is reduced. A further problem involves the notion of a dialect continuum, which complicates language mapping and diffusion estimates (Bergsland and Vogt, 1962; Gray and Atkinson, 2003; Heeringa and Nerbonne, 2001; Holm, 2003; Kirk et al., 1985; Thomason and Kaufman, 1992). A dialect continuum refers to the process by which languages accumulate differences geographically. Languages can be spatially dispersed, due to migrations or incursions by other populations, and in the absence of integrative mechanisms (e.g., word borrowing) they will eventually diverge from one another to form dialects (Brainerd, 1970; Bickel, 2019; Campbell, 1988; Chambers and Trudgill, 1998; Dyen, 1962b, 1963). Subsequently, they can become unintelligible over time and appear to represent distinct languages (Gray and Atkinson, 2003; Haarmann, 1990; Herringa and Nerbonne, 2001; Holm, 2003; Prokić and Nerbonne, 2013; Salmons, 1992; Sankoff, 1970; Williamson, 2000).

However, in spite of a linguistic gradient, there is no significant boundary between groups speaking different dialects, as the change is gradual (Campbell, 1988; Gray and Atkinson, 2003; Prokić and Nerbonne, 2013; Salmons, 1992; Sankoff, 1970). Grouping such languages or dialects together as a single coherent family erroneously conveys the impression that the populations speaking them composed a single community (Campbell, 1988; Dyen, 1962b, 1963; Gray and Atkinson, 2003; Haarmann, 1990; Holm, 2003; Kirk et al., 1985; Sankoff, 1970). However, as there is no universally accepted definition of what constitutes a dialect verses a separate language, it is difficult to determine whether dialect or language boundaries are more accurate in regards to population separation (Gray and Atkinson, 2003; Haarmann, 1990; Holm, 2003).

A further issue with glottochronology and lexicostatistics is how new languages emerge (Campbell, 1988; Dyen, 1962b, 1963; Gray and Atkinson, 2003; Haarmann, 1990; Holm, 2003). New languages can emerge based on descent from a common proto-language, as well as from changes in language structure and word borrowing (Kirk et al., 1985; Sankoff, 1970; Starostin, 2013; Thomason and Kaufman, 1992). However, these processes do not necessarily indicate a change in language boundaries; rather, they may indicate interaction between individuals or populations with or without substantial gene flow (Campbell, 1988; Dyen, 1962b, 1963; Gray and Atkinson, 2003; Haarmann, 1990; Holm, 2003; Kirk et al., 1985; Sankoff, 1970; Starostin, 2013). Further, substantial borrowing of words and/or phrases makes phylogenetic tree-based methods, such as lexicostatistics and glottochronology, inappropriate. Moreover, the clustering methods used tend to produce inaccurate trees when languages evolve slowly rather than among languages that share a recent common ancestor (Gray and Atkinson, 2003; Haarmann, 1990; Holm, 2003; Kirk et al., 1985; Sankoff, 1970; Starostin, 2013; Thomason and Kaufman, 1992).

Additionally, the presumed rate of change used in these analyses is based on modern languages, which undergo more rapid change (Campbell, 1988; Dyen, 1962b, 1963; Gray and Atkinson, 2003; Haarmann, 1990). This is at odds with the underlying assumption of a uniform rate of change these methods rely on (Campbell, 1988; Dyen, 1962b, 1963; Gray and Atkinson, 2003; Haarmann, 1990; Ono, 2019). Words do not disappear from a language, instead new lexical forms, words or phrases, constantly compete with old forms, rendering them obsolete and eliminating them from a languages lexical repertoire, the spoken language (Campbell, 1988; Dyen, 1962b, 1963; Gray and Atkinson, 2003; Haarmann, 1990; Holm, 2003; Kirk et al., 1985; Sankoff, 1970; Thomason and Kaufman, 1992). Languages have been found to differ appreciably in regards to the rate of lexical change as the rate of word replacement is likely to be different for each word or phrase in a given language (Campbell, 1988; Dyen, 1962b, 1963; Gray and Atkinson, 2003; Haarmann, 1990; Holm, 2003; Kirk et al., 1985; Sankoff, 1970; Thomason and Kaufman, 1992).

These changes are likely to have derived from events that are unpredictable and, therefore, cannot be computed uniformly. The results of linguistic dating and divergence are sometimes at odds with known and archaeologically derived data, and difficulties in determining equivalent terms across languages (Bergsland and Vogt, 1962; Dyen, 1962b, 1963; Gray and Atkinson, 2003; Haarmann, 1990; Holm, 2003; Starostin, 2013; Thomason and Kaufman, 1992). Moreover, brief periods of common ancestry among language families may not be evident through lexicostatistical dating (Forester and Toth, 2003; Isaac, 2004, 2010; Kortlandt, 1981, 2007; Schmidt, 1991; Winfred, 1997). Since the timing of linguistic diffusion derived from lexicostatistics and glottochronology are often at odds with known archaeological data, the application of these methods to unknown language systems, such as the Celtic languages, is highly suspect (Fortson, 2004; Forester and Toth, 2003; Gray and Atkinson, 2003; Sims-Williams, 2006). However, in spite of the issues outlined above lexicostatistics and glottochronology are still utilized in order to determine the relationships among languages, although their application has decreased in favor of new methods (Atkinson et al., 2005; Dellert and Buch, 2016; Gapur et al., 2018; Kaplan, 2017; Novotna and Blazek, 2006; Ono, 2019; Starostin, 2013; Zhang and Gong, 2016).

Recent methods including character state and Bayesian phylogenetic methods are more widely used. These methods facilitate cognate evolution analyses in single or multiple dimensions and produce phylogenetic trees from standard wordlists of basic vocabulary with branch lengths that reflect differential degrees of independent evolution (Currie et al., 2013; Huff and Lonsdale 2011; Levinson and Gray, 2012). The above methods can be mapped onto geographical space in order to assess the likely pathway of expansion and facilitate testing of dispersal scenarios (Currie et al., 2013; Huff and Lonsdale 2011; Levinson and Gray, 2012; Pompei et al., 2011; Robbeets and Bouckaert, 2018; Wichmann et al., 2010). These analyses have indicated the split between the Celtic and IE languages likely occurred sometime after their spread into continental Europe, during the Neolithic/Bronze Age. The split between the insular and continental languages likely happened around 1,000-500 BC (Bouckaert et al., 2012; Forester et al., 2004). The above date for the split between IE and Celtic languages is the same as that estimated form the percentage of shared cognates (Forester and Toth 2003; Gray and Atkinson, 2003; Kortlandt, 2018). However, the date for the split between the insular and continental languages is vastly different, 1,000-500 BC versus 3,200-2,500 BC.

This difference is likely related to the fact that estimating a split between languages or families, through shared cognates represents the earliest possible date (Bouckaert et al., 2012; Forester et al., 2004; Forester and Toth 2003; Gray and Atkinson, 2003; Kortlandt, 2018).

The Celtic languages have been used to link diverse populations together without knowledge of their underlying biological relationships (See pages 19 and 32) (Cunliffe, 1997; Evans, 1979; Forester and Toth, 2003). Although the presence of a common or related language may indicate a common biological origin, the genetic and linguistic assimilation of diverse migrants within a larger population may increase their genetic heterogeneity (Bickel, 2019; Creanza et al., 2015; Longobardi et al., 2015; Sokal, 1988; Sokal et al., 1988). The immigrant groups may have been initially homogeneous, but they subsequently become genetically incorporated into the local population. The resulting mixed population may adopt the languages of either the immigrants or the local population, or a mixture of both (Bickel, 2019; Creanza, et al., 2015; Longobardi, et al., 2015). Previous studies have indicated a connection between linguistic and genetic differentiation among populations (Bickel, 2019; Cavelli-Sforza et al., 1988; Cavelli-Sforza et al., 1992; Chen et al., 1995; Creanza et al., 2015; Excoffier et al., 1991, 1987; Greenberg et al., 1986; Greenhill et al., 2017; Longobardi, et al., 2015; Sokal, 1988; Sokal et al., 1988, 1989, 1990). These studies have also shown that the rate of change in the frequency of some alleles, pairs or series of genes that determine hereditary characteristics, across boundaries between language families in Europe is higher than across comparable lines drawn at random (Excoffier et al., 1987; Greenberg et al., 1986; Longobardi et al., 2015; Sokal, 1988; Sokal et al., 1988, 1989, 1990). Regions of genetic change have been found to correlate with genetic, linguistic and physical boundaries as well as geographic distance (See pages 103, 105 and 107) (Barbujani et al., 1990; Bickel, 2019; Chen et al., 1995; Creanza et al., 2015; Greenhill et al., 2017; Longobardi et al., 2015; Sokal, 1988; Sokal et al., 1988, 1989, 1990).

These findings suggest that the processes leading to linguistic diversity may also have brought about genetic variation. Linguistic boundaries may also act as reproductive barriers, resulting in a difference in gene frequencies among spatially close populations (Coia et al., 2013; Greenberg et al., 1986; Greenhill et al., 2017; Longobardi, et al., 2015; Sokal, 1988; Sokal et al., 1988, 1989, 1990). The allocation of these boundaries with increased genetic differentiation may be the result of their active attribution in preventing gene flow between groups. Alternatively, the geographical differentiation of linguistic groups that came into contact created a zone of cultural and linguistic variation (See pages 103, 105 and 107)

(Bickel, 2019; Chen et al., 1995; Creanza et al., 2015; Greenhill et al., 2017; Longobardi, et al., 2015). Overall, populations have been found to differ more among language families than within, with regard to their respective rates of gene flow (Bickel, 2019; Chen et al., 1995; Creanza et al., 2015; Georgi et al., 2010; Greenhill et al., 2017; Longobardi et al., 2015; Sokal, 1988; Sokal et al., 1989). Among the major linguistic families within Europe including, Albanian; Baltic; Basque; Balto-Slavic; Celtic; Finnic; Germanic; Greek; Romance; Semitic; Slavic; Turkic and Ugric, the majority of the observed genetic variation was found to correlate with the observed linguistic boundaries (Bickel, 2019; Creanza et al., 2015; Georgi et al., 2010; Greenhill et al., 2017; Longobardi et al., 2015; Sokal, 1988; Sokal et al., 1989). However, some variation has been observed within language families in relation to geographic distance (i.e., north and south Germanic). This variation may suggest that relatively homogenous populations associated with the above language families moved into Europe and expanded and differentiated geographically (See pages 103, 105 and 107) (Bickel, 2019; Creanza et al., 2015; Greenhill et al., 2017; Longobardi et al., 2015; Sokal, 1988; Sokal et al., 1989, 1990).

The genetic diversity observed among populations located on different sides of a linguistic boundary could be attributed to reduced gene flow across the boundary (Greenhill, et al., 2017; Longobardi, et al., 2015; Sokal, 1988; Sokal et al., 1989, 1990). Although some linguistic boundaries have been found to correlate with physical boundaries, several are not associated with any known physical barriers (Barbujani and Sokal, 1990; Creanza et al., 2015; Greenhill et al., 2017; Longobardi, et al., 2015). Therefore, languages themselves may act as barriers to gene flow and enhance the genetic variation observed among populations (Barbujani and Sokal, 1990; Creanza et al., 2015; Greenhill et al., 2017). Thus, the presence of genetic boundaries among populations within the core and expansion regions may also indicate linguistic boundaries.

Intra-and-extra-regional genetic variation among Celtic populations

Genome-wide SNP (Single Nucleotide Polymorphisms) data indicate that modern Europeans, in varying proportions, descended from 3 ancestral populations: northern Palaeolithic Eurasians, western European hunter-gatherers and early near eastern Neolithic farmers (Bramanti et al., 2009; Haak et al., 2015; Lazaridis et al., 2014; Skoglund et al., 2012). However, while the distribution of Y-chromosome, a genealogical test used to examine the patrilineal ancestry of an individual, and mtDNA, a similar test to determine the maternal lineage, throughout continental Europe have been the focus of numerous previous studies; few have linked specific haplogroups, a combination of specific genes that are closely linked and are inherited together, or sub-clades, a sub-group of a particular haplogroup e.g., R1b-S28/U152, to the Celts (Bramanti et al., 2009; Haak et al., 2015; Lazaridis et al., 2014; Skoglund et al., 2012). The majority of these studies depend on DNA, a molecule that contains an individuals genetic code, from the modern Celtic fringe (i.e., the six Celtic "nations", Scotland, Ireland, the Isle of Man, Cornwall, Brittany, and Wales) and Central Europe to constitute a baseline for Celtic DNA (Allentoft et al., 2015; Busby et al., 2012; Capelli et al., 2003; Cassidy et al., 2015; Haak et al., 2015; Richards, et al., 2002; Rosser et al., 2000; Semino et al., 2004; Sykes, 2006; Torroni et al., 1998, 2001; Wilson et al., 2001; Winney and Walter, 2016). However, most previous studies use the term Celtic in a purely nominal way, relying on a combination of associations from linguistics and archaeology (See pages 19, 32 and 91) (Hill et al., 2000; Lell and Wallace, 2000; McEvoy et al., 2004; Oppenheimer, 2012). It is unknown how much movement occurred within each sample or population analysed; as a result, the actual population history may not be adequately represented. The observed variation is presumed to represent the HaD or La Tène period overall, as such these samples are also not often temporally specific (Busby et al., 2012; Cassidy et al., 2015; De Beule, 2009, 2010). Further, the majority of previous studies have focused on Y-chromosome variation, specifically the R1b haplogroup, the most common paternal Y-chromosome lineage in Western Europe, while limited previous research, comparatively, has focused on mtDNA variation (Haak et al., 2015; Lucotte, 2015; McEvoy et al., 2004; Myres et al., 2007; Myres et al., 2011; Oppenheimer, 2007, 2012; Sjodin and Francois, 2011; Sykes 2006).

The Y-chromosome haplogroup R1b and various sub-clades, those that have been the focus of research, have been intrinsically linked with the Celts as they occur in high frequencies where Celtic languages were spoken and the Hallstatt and La Tène material cultures were present (See pages 19, 32 and 91) (Busby et al., 2012; Cassidy et al., 2015; De Beule, 2009, 2010; Haak et al., 2015; Lucotte, 2015; McEvoy et al., 2004; Oppenheimer, 2007, 2012; Rootsi et al., 2011; Sjodin and Francois, 2011; Sykes 2006). However, as R1b is the most commonly occurring paternal lineage in Central Europe, its distribution may not be intrinsically linked with Celtic groups. High frequencies of Y-chromosome haplogroup and sub-clades are observed within the core including R1b-S28/U152, R1b-S28/Z36 R1b-

S21/U106, and I-L38/S154 and I-L38/M223, whereas those in the expansion regions include R1b-L21/S145, R1b-M153/M167, R1a/L260, R1a-M458, R1a-Z280 (Cassidy et al., 2015; De Beule, 2009, 2010; Lucotte, 2015; Oppenheimer, 2007, 2012; Sykes 2006; Underhill et al., 2015). However, the relative percentages of the above Y-chromosome haplogroups and sub-clades, as identified in modern populations, discussed in the following sections have not been quantified (e.g. they are not described based on the number of individuals found to have the above haplogroups and/or sub-clades. Rather they are documented as generalized regional percentages such as, 15-20%).

Evidence for genetic diversity within the core regions

The R1b-S28 haplogroup, specifically the U152 sub-clade, has been dubbed the southern European R1b haplogroup or the Alpine haplotype (Busby et al., 2012; Cruciani et al., 2011; McEvoy et al., 2004). It is found in high frequencies, 25-40%, in northern Italy and southwestern France, whereas low frequencies occur in Switzerland, the Czech Republic, Belgium, Slovakia, Austria, Luxembourg, the Netherlands and southern Germany (Busby et al., 2012; Cruciani et al., 2011) (See Figure 1 in Myres et al., 2010 for a map showing the R1b haplogroup distributions listed in this and the following section). This subclade has been associated with the Gauls, the Belgae and the Celts (Busby et al., 2012; Cruciani et al., 2011; McEvoy et al., 2004). The Z36 sub-clade has also been associated with Celtic populations; as it occurs in moderately high frequencies, approximately 30-40%, in Italy including, Liguria and Lombardy, France, southwestern Germany (specifically Baden-Württemberg), and western Switzerland (See page 61) (De Beule, 2009; Klyosov, 2012b, Klyosov and Tomezzoli, 2013; Lucotte, 2015; Myres et al., 2010) (See Figure 1 in Myres et al., 2010 for a map showing the R1b haplogroup distributions listed in this and the following section). Lower frequencies, 20-30%, are found in southern Germany, Switzerland, the Czech Republic, and Slovakia (Klyosov, 2012b, Klyosov and Tomezzoli, 2013; Lucotte, 2015; Myres et al., 2010; Oppenheimer, 2007; Simoni et al., 2000). However, this sub-clade has been argued to be a marker of Italic ancestry, as it is common in Italy (Busby et al., 2012; Cruciani et al., 2011; De Beule, 2009). Alternatively, it may reflect migrations of Celtic groups into northern Italy, which subsequently diversified or integrated into the local populations (Cruciani et al., 2011; Lucotte, 2015; Manco, 2015; Myres et al., 2010; Richards et al., 2002; Rosser et al., 2000; Torroni et al., 1998, 2001).

The R1b-S21 haplogroup, specifically the U106 sub-clade is common around the western core of the Urnfield and Hallstatt areas, along the Rhine to the Netherlands and along the Danube to Bulgaria (De Beule, 2009, 2010**;** McEvoy et al., 2004; Roosti et al., 2011). Subsequently, this haplogroup has been dubbed the northwestern R1b haplogroup or the Germanic haplogroup (Cruciani et al., 2011; De Beule, 2009, 2010; Lucotte, 2015; McEvoy et al., 2004; Roosti et al., 2011). The spread of this sub-clade has been linked to both Germanic and Celtic migrations throughout the regions associated with Hallstatt culture (See pages 19 and 61) (Cruciani et al., 2011; De Beule, 2009, 2010; Lucotte, 2015; McEvoy et al., 2004). The highest frequencies, 18-37%, occur in Austria, Germany, Denmark, England, and the Netherlands (Busby et al., 2012; Cruciani et al., 2011; Myres et al., 2010) (See Figure 1 in Myres et al., 2010 for a map showing the R1b haplogroup distributions listed in this and the following section). The modern distributions of the U152 and U106 sub-clades correlate with mtDNA lineages including H5, J and K (Arnason et al., 2000; Cruciani et al., 2007; Di Giacomo et al., 2004; Helgason et al., 2001; Hill et al., 2000; Lell and Wallace, 2000; Richards et al., 2002; Torroni et al., 2000). MtDNA haplogroup H5 occurs in similar frequencies, 5-8%, in Slovenia, Belgium, Romania, Germany, Slovakia, and Switzerland (Finnila et al., 2001; Richards et al., 2002; Torroni, 2000). Haplogroup K is common in slightly higher frequencies, 10-15%, in Belgium, France, Austria, and the Netherlands. It is also found in low frequencies in Britain, 8%, which has been suggested to represent migrations into Britain from continental Europe (See page 61) (Simoni et al., 2000; Torroni et al., 2000) (See Figure 1 in Myres et al., 2010 for a map showing the R1b haplogroup distributions listed in this and the following section). However, the relative percentages of the mtDNA haplogroups and sub-clades, as documented in modern populations believed to be associated with the Celts, have also not been quantified and are described simply as generalized regional percentages.

The I-L38 haplogroup, including the S154 and M223 sub-clades, have also been associated with the spread of the La Tène culture as their distributions are similar to that of the R1b-U152 haplogroup north of the Alps (De Beule, 2009, 2010). The S145 sub-clade occurs in high frequencies, 10-25%, in Switzerland, Belgium, Luxembourg, northern and Central Germany, the Harz mountains, northeastern France, the Iberian Peninsula, and the British Isles (where the insular languages were spoken) (See pages 61 and 91) (Capelli et al., 2003; De Beule, 2009, 2010) (See Figure 1 in Myres et al., 2010 for a map showing the R1b haplogroup distributions listed in this and the following section). This sub-clade is believed to have spread from Germany into England through Belgium in tandem with the La Tène culture (De Beule, 2009, 2010). Alternatively, it has been suggested that it was autochthonous to the region between the Alps, Central Germany, and Belgium and was subsequently assimilated into the Celtic gene pool during the Hallstatt or La Tène periods (See page 61) (Capelli et al., 2003; De Beule, 2010; Lucotte, 2015). The m223 sub-clade has been specifically associated with historic Gaul as it occurs in high frequencies, 10-20%, in France and Luxemburg (Capelli et al., 2003; De Beule, 2010; Lucotte, 2015) (See Figure 1 in Myres et al., 2010 for a map showing the R1b haplogroup distributions listed in this and the following section).

Evidence for genetic diversity within the expansion regions

The Y-chromosome haplogroup R1b-L21, specifically the S145 sub-clade has been dubbed the insular, or Atlantic, Celtic haplotype (Busby et al., 2012; Capelli, 2003; Cassidy et al., 2015; Lucotte, 2015; Weale et al., 2002; Wilson et al., 2001). High frequencies, 20-40%, occur in southern Britain, northern Portugal and along the Atlantic façade (the Atlantic coastline of continental Europe) (Busby et al., 2012; Capelli, 2003; Cassidy et al., 2015; Lucotte, 2015; Weale et al., 2002; Wilson et al., 2001) (See Figure 1 in Myres et al., 2010 for a map showing the R1b haplogroup distributions listed in this section). However, the highest frequencies, in modern populations, of the above sub-clade occur in the historical region of Brittany, France is 62%. However, this frequency may be related to the immigration of insular Britons during the 5th century AD due to expansion of the Anglo-Saxons within this region (See page 61) (Cassidy et al., 2015; Lucotte, 2015). The high frequency in Britain may be related to populations moving along the Atlantic trade routes (Cruciani et al., 2011; Lucotte, 2015; Manco, 2015). Subsequently, it has been associated with the insular La Tène culture, as it is found in regions where insular Celtic languages are still spoken today (Busby et al., 2012; Cassidy et al., 2015; Lucotte, 2015; Weale et al., 2002; Wilson et al., 2001). The R1b-M153 haplogroup, particularly the M167 sub-clade has been associated with Celtic groups in the Iberian Peninsula (See page 61) (Cruciani et al., 2011; Lucotte, 2015). This sub-clade is common, 15-25%, in regions of Spain and Portugal which have a Celtic-Basque-Iberian heritage, such as Minho, Galicia, Asturias, Cantiberia, Euskara, and Catalonia

(Cassidy et al., 2015; Cruciani et al., 2011; Lucotte, 2015; Manco, 2015) (See Figure 1 in Myres et al., 2010 for a map showing the R1b haplogroup distributions listed in this section).

The R1a haplogroup including the M458, L260, and Z280 sub-clades have been associated with populations within the expansion regions. These sub-clades have been alternatively associated with Slavic, Baltic and Celtic populations as high frequencies, 30-57%, are common in Slovakia, Slovenia, Hungary, Romania, Poland, and the Czech Republic (See page 61) (Kushniarevich et al., 2013; Pamjav et al., 2012; Pliss et al., 2015; Rozhanskii and Klyosov 2012; Underhill et al., 2015; Woźniak et al., 2010). Intra-regional diversity within the expansion regions is suggested by the distributions of the R1b-Z280 and M458 sub-clades. The R1b-Z280 sub-clade is common, 20-35%, in Slovakia, Slovenia, and Hungary and is not found in the Czech Republic, whereas the reverse is evident in the distribution of the M458 sub-clade (See page 61) (Rozhanskii and Klyosov 2012; Underhill et al., 2015) (See Figure 1 in Myres et al., 2010 for a map showing the R1b haplogroup distributions listed in this section).

Several maternal lineages correlate with these sub-clades including H1; H5; H6; H7; H11; K; U4; U5; I; J and V (Malyarchuk et al., 2003, 2006; Manco, 2015; Richards et al., 2002; Torroni et al., 2000). MtDNA haplogroup H1is common in the Iberian Peninsula, northwestern Serbia, and southern France at similarly low frequencies, 5-10% (See page 61) (Achille et al., 2004; Loogvali et al., 2004; Malyarchuk et al., 2003; Richards et al., 2002; Torroni et al., 2000). However, as haplogroup H5 is associated with both the core and expansion regions, it is difficult to determine which areas it was originally associated and those into which it subsequently moved. Haplogroups H6 and H7 are common at similar frequencies, 10-15%, in Slovakia and the Iberian Peninsula respectively (Alvarez-Iglesias et al., 2009; Malyarchuk et al., 2003) (See Figure 1 in Myres et al., 2010 for a map showing the R1b haplogroup distributions listed in this section). H11 is common throughout Central Europe at similarly low frequencies 10-15%, whereas Haplogroup K, is common in northwest Europe at similar frequencies 5-15% (See page 61) (Malyarchuk et al., 2003, 2006; Richards et al., 2002; Simoni et al., 2000; Torroni et al., 2000).

U4 occurs at low frequencies across Europe, 2-8.5%, although slightly higher frequencies are observed in the Baltic and Slavic regions, 8-10% (Malyarchuk et al., 2003; Richards et al., 2002; Torroni et al., 2000). Thought mtDNA haplogroup U5 is common throughout northeastern Europe, 5-12%, it occurs at higher frequencies, 10-20%, in northern Spain, Slovakia, Croatia, the Czech Republic, southern Germany and southern France (See page 61) (Knipper et al., 2014; Malyarchuk et al., 2003, 2006; Olade et al., 2014; Richards et al., 2002; Torroni et al., 2000; Vidrová et al., 2008) (See Figure 1 in Myres et al., 2010 for a map showing the R1b haplogroup distributions listed in this section). MtDNA haplogroups I, J and V are relatively evenly distributed in low frequencies across Europe, 8-10.4%, and occur at slightly high frequencies, 10-14%, in southwestern France, Gaul and the Iberian Peninsula (See page 61) (Maca-Meyre et al., 2003; Soarea et al., 2009; Richards et al., 2002; Sykes, 2001; Torroni et al., 2000) (See Figure 1 in Myres et al., 2010 for a map showing the R1b haplogroup distributions listed in this section).

Further evidence for genetic diversity within the expansion regions is suggested by the modern European genetic composition of the British Isles. Sykes (2006) and Oppenheimer (2007, 2012) examined the distribution of the Y-chromosome R1b and mtDNA haplogroups among the modern populations in the British Isles compared to those in continental Europe. However, the underlying microsatellite markers and sub-clads were not described (Oppenheimer, 2007, 2012; Sykes, 2006). The frequency of the R1b haplogroup varies throughout Britain, 73- 98%, whereas in Scotland it accounts for 60% of the Y-chromosome DNA (Oppenheimer, 2007, 2012; Sykes, 2006). The remaining 40%, in this region, belongs to the I, R1a, and J haplogroups (See page 61) (Oppenheimer, 2007, 2012; Sykes, 2006). Throughout these regions, the highest proportion of the R1b haplogroup is associated with men with Gaelic surnames. The mtDNA distribution throughout Britain predominantly involves haplogroups U5, H, T, V, and J (Oppenheimer, 2007, 2012; Sykes, 2006). Although haplogroup U5 is found in higher frequencies in western and northern Europe, it only occurs in low frequencies, 8-10% in the British Isles (Oppenheimer, 2007; Sykes, 2006; Torroni et al., 2000; Winney and Walter, 2016). Consequently, it has been argued that this haplogroup moved into Britain from continental Europe (Oppenheimer, 2007; Sykes, 2006). Although mtDNA haplogroup H is common throughout continental Europe, it also occurs at high frequencies in Britain, 50-60%. Haplogroup T is also found in both regions, however, at lower frequencies, 3-12%, and 3-8% respectively. A similar pattern is evident in the distribution of haplogroup V, 3-8% and 3-5% correspondingly (See page 61) (Oppenheimer, 2007; Roostalu et al., 2007; Sykes, 2006; Winney and Walter, 2016).

MtDNA haplogroup J contains two sub-clades, J-16192 and J-16193, that have been argued to have some linguistic associations, particularly in the British Isles (Arnason et al., 2000; Forester et al., 2004; Hill et al., 2000; Simoni et al., 2000; Wilson et al., 2001). The J-16192 sub-clade has only been found high concentrations in areas speaking Celtic languages including Cornwall, Wales, Scotland, and Northern Ireland (Arnason et al., 2000; Cruciani et al., 2007; Di Giacomo et al., 2004; Forester et al., 2004; Helgason et al., 2001; Hill et al., 2000; Lell and Wallace, 2000). The J-16193 sub-clade is present in high frequencies in the Goidelic speaking areas of Britain and Ireland (Arnason et al., 2000; Cruciani et al., 2007; Di Giacomo et al., 2004; Forester et al., 2004; Helgason et al., 2001; Hill et al., 2000; Lell and Wallace, 2000). Consequently, the above sub-clades are believed to represent British Celtic mtDNA (See pages 61 and 91) (Arnason et al., 2000; Cruciani et al., 2007; Di Giacomo et al., 2004; Forester et al., 2004; Helgason et al., 2001; Hill et al., 2000; Lell and Wallace, 2000).

The Y-chromosome haplogroups I, R1a, and J are likely intrusive to the British Isles and are believed to have arrived during the Neolithic, as their distributions are limited and similar to those in continental Europe during this period. However, the nature of their similarity and subsequent distribution in Britain is not described in detail or quantified (Cruciani et al., 2004, 2007; Di Giacomo et al., 2004; Hill et al., 2000; McEvoy et al., 2004; Richards et al., 2000; Richards et al., 2002; Rosser et al., 2000; Rootsi et al., 2004; Semino et al., 2004; Scozzari et al., 2001; Torroni, 1998, 2001b; Weal et al, 2002). Thus, while these haplogroups may be present in regions associated with Celtic material culture and/or language in the British Isles, their arrival during the Neolithic is not consistent with the arrival of the Hallstatt and La Tène cultures during the Iron Age (See pages 61 and 91) (Collis, 2003; Cunliffe, 1997; Oppenheimer, 2007; 2012; Richards et al., 2002; Semino et al., 2004; Sykes, 2006).

Modern European genetic diversity within the Y-chromosome and mtDNA haplogroups within England has also been suggested to be clinal. Leslie et al (2015) examined the modern European genetic differentiation within England to determine whether there was evidence for a cohesive Celtic population in the non-Saxon regions. However, in this analysis, the term Celt was applied to modern populations in a strictly nominal way. The modern European genetic profiles of 2,039 individuals from the "People of the British Isles" collection were analysed (Leslie et al., 2015). Specifically, it included individuals for whom all 4 grandparents were born within 80 km of each other and for whom the average birth year was 1885 (Leslie et al., 2015). While the sample distribution attempted to control for geographic region, the potential for migration into the British Isles in preceding generations was not addressed. The potential for movement within the region prior to the generation analysed was also not assessed. Genetic differentiation throughout this region was found to correspond to natural geographical boundaries, i.e., Orkney, Cornwall and Devon. Most of the modern European genetic clusters observed were highly localized with many occurring in non-overlapping regions (See page 61) (Leslie et al., 2015). Distinctive clusters have also been documented throughout England, Scotland and Wales, specifically, north and south Wales, northern England, Scotland, Northern Ireland, and Central and southern England (Leslie et al., 2015).

The above clusters suggest relative genetic isolation within the regions. Some modern European genetic lineages that are believed to have substantially contributed to the observed genetic differentiation, include Belgium, western Germany and northwestern France (Leslie et al., 2015). The distributions of these lineages most likely represent older migrations as the haplogroups had time to spread and become differentiated from those in continental Europe. Those lineages that contributed minimally include Denmark, northern Germany, northern France, and northern Spain. The dispersal of the above lineages most likely represent recent migration events, as the haplogroups are more similar to those in continental Europe. Additionally, they have not diversified as much as would be expected for an early migration event (See page 61) (Leslie et al., 2015). However, no absolute or approximate dates are provided for the above migrations. Nor is the estimated similarity, or dissimilarity, to the corresponding haplogroups in continental Europe quantified. Further, the underlying microsatellite markers were not described, so a direct comparison with other European populations is not possible. As the contribution of the above lineages were not quantified, beyond substantial or minimal and they were not described as either Y-chromosome or mtDNA it is difficult to determine the extent of movement between regions (See page 61). Although in spite of these shortcomings, the presence of clinal modern European genetic variation and differential regional admixture from continental European populations within Britain suggests differential rates of intra-and extra-regional gene flow. The haplogroups and sub-clades associated with the Celts throughout the core and expansion regions are diverse and varied; which suggests that they were predominately differentiated through sub-clades of the major European Y-chromosome and mtDNA haplogroups (Arnason et al., 2000; Cruciani et al., 2007; Di Giacomo et al., 2004; Helgason et al., 2001; Hill et al., 2000; Lell and Wallace, 2000). There is some evidence of overlapping haplogroup distributions within these regions, suggesting differential rates of small-scale migration, gene flow, captivity and/or enslavement, and movement along trade routes (See page 61) (Aldhouse-Green, 2002; Arnold, 1988; Lenski, 2008, 2014).

This all indicates that there is more regional genetic variation among populations associated with the Celts than previously assumed. However, as previous studies have relied on the Y-chromosome and mtDNA haplogroup distributions of modern populations, they might not adequately reflect the amount of diversity in the Iron Age. Further, these studies have attempted to document this distribution in broad geographic regions where linguistic and archaeological evidence indicates the presence of Celtic populations; rather than documenting regional variation in haplogroup distribution among these diverse groups. However, the genetic evidence indicating the presence of distinct Y-chromosome and mtDNA haplogroups throughout the regions associated with the Celts is in line with the archaeological and linguistic evidence suggesting small-scale migration, demic diffusion and/or assimilation.

Chapter 4: Methodological background

Dental anthropology

Dental anthropology, a subfield of biological anthropology, is defined as the study of humans and their closest relatives through analyses of their teeth. It is associated with bioarchaeological analysis and incorporates techniques from the fields of genetics, anatomy, paleontology, and dentistry. The anthropological study of teeth focuses on the subtleties and variation in morphology and tooth size. Dental morphology is an effective method for assessing interpopulation variation and relationships. This method also provides insight into the degree of variation at the microevolutionary, within and among populations, and macro-evolutionary, between and among species, levels (Bernal et al., 2010; Bunimovitz, 1990; Buikstra et al., 1990; Campbell, 1925; Dahlberg, 1956, 1963, 1971; Edgar, 2004; Hillson, 1996; Irish, 2005, 2010; Scott and Irish, 2017; Scott and Turner, 1997; Turner, 1969). The bioarchaeological analyses of microevolutionary patterns falls into two types of study: dental metric (size) and nonmetric (morphological). Nonmetric dental traits are discrete anatomical units that occur in varying degrees of expression within, between, and among populations, thus making them ideal for numerous analyses including, bioarchaeological, biodistance, population history and structure analyses (Campbell, 1925; Garn et al., 1966, 1979; Harris, 1977, 2008; Nichol, 1990; Richards and Telfer, 1979; Scott and Turner, 1988; Townsend and Brown, 1978a, b). Dental morphological study involves the examination of specific nonmetric crown and root traits.

Differences in dental morphology observed between populations, defined as communities of interbreeding individuals, can be explained as resulting from one or more evolutionary forces. Populations that share several attributes such as specific morphological traits or adapted to similar environments, are more closely related than populations in which differences are observed (Irish and Turner, 1989; Scott and Irish, 2017; Turner, 1989). Crown and root morphological traits show patterns of distinct geographic variation. Significant differences in these traits between populations suggests influence from genetic drift, mutation, gene flow, and consequently affinity among populations (Bedrick et al., 2000; Harris and Sjøvold, 2004; Hanihara, 2008, 2010; Hillson, 1996; Irish, 1993, 1998a, b, c, 2000, 2005, 2010; Irish and Guatelli-Steinberg, 2003; Sjøvold, 1973). Through documentation of their frequency of occurrence and expression and subsequent statistical comparison, it is possible to infer degrees of biological relationships between, among and within populations (Berry, 1978; Campbell, 1925; Nichol, 1990; Shaw, 1931; Scott and Turner, 1988; Townsend and Brown, 1978a, b). Early studies investigating nonmetric traits revealed and documented this variation between populations (Hellman, 1928; Hrdlička, 1920; Kraus et al., 1959). Hrdlička, (1920) was the first to describe and classify the degree of shovel shaped incisors (which have marginal ridges causing the tooth to appear scooped or shovel shaped) among human and non-human populations. The distribution of this trait also indicated similarity between the dentition of Asians and Native Americans (Hrdlička, 1920). Observations and descriptions of cusp number, groove pattern, and variation in root structure were documented by TD Campbell (1925), M Hellman (1928), and JCM Shaw, (1931) who also urged physical anthropologists to place more emphasis on the study and analysis of dental variation. Several traits are characteristic of certain macroregional populations, such as incisor shovelling in Mongoloid populations and Carabelli's cusp (a small accessory cusp predominantly found on the upper first molars) in Caucasian populations (Hrdlička, 1920; Kraus et al., 1959).

In 1956, Dahlberg created a series of reference plaques in an attempt to standardize the observations and descriptions of nonmetric traits. Hanihara (1963) also developed a series of reference plaques similar to Dahlberg’s for deciduous teeth, after which it became apparent that broad-scale standardization was essential to enhance comparability in the growing field of dental morphometrics (Dahlberg, 1956; Hanihara, 1963). Subsequently, a comprehensive series of dental plaques and scoring forms for permanent teeth were developed by Christy Turner II and colleagues (Turner et al., 1991). The series of plaques used to score variation in the expression of dental morphological traits, known as the Arizona State University Dental Anthropological System, ASUDAS, became the standard and most widely recommended method used to identify nonmetric dental traits (Hillson, 1996; Scott and Turner, 1988; Turner et al., 1991). The ASUDAS system consists of 24 rank-scale plaques, with detailed descriptions of each trait and the various forms of expression, for scoring crown and root traits of the adult permanent dentition.

Although over 100 nonmetric traits have been observed and described, 36 of these, based on the work of Irish (1993), have been used in numerous studies and have proven particularly successful in characterizing and comparing the biological affinity among and within populations (See page 181) (Anctil, 2016; Coppa et al., 1998, 2000, 2007; Cucina et al., 1999; Hanihara, 2008, 2010; Irish, 1993, 1997, 1998b, c, 2000, 2005, 2006, 2008, 2010, 2016; Irish et al., 2014, 2018; Irish and Guatelli-Steinberg, 2003; Matsumura et al., 2009; Turner, 1967, 1969, 1971, 1976, 1984, 1985a, b, 1990). These include discrete crown traits, such as Carabelli's trait and incisor shovelling, as well as root variants such as lower molar root number (Figures 51-54, Appendix 1) (Irish, 1993; Turner et al., 1991). For a detailed description of the dental morphological variation among and between populations, see Scott and Turner (1997) and Scott and Irish (2017).

There are several benefits associated with this system. First, the traits themselves are evolutionarily stable, e.g., dental morphological traits in the ASUDAS system are stable in form and are present in human populations, modern and extinct, regardless of the genetic correlations among these groups. Second, they can be observed through mild levels of dental wear if the antimere (a pair of opposite corresponding bilaterally symmetrical parts) is available in extreme cases, or are unaffected by wear in the case of root and osseous traits (Figure 35). Third, they are easy to locate and identify. Fourth, they have minimal rates of inter-and-intra observer error in recording. Fifth, they are independent of one another. Sixth, sexual dimorphism does not affect their expression. Seventh, they represent all dental morphological fields, or tooth type (e.g., incisor). Eighth, they are independent of tooth size. Ninth, there is a substantial amount of comparable data. Tenth, they have a high genetic component in expression, 40-80%. (Dempsey and Townsend, 2001; Hanihara, 2008, 2010; Hughes and Townsend, 2013; Irish, 1993, 2005, 2006, 2016; Irish and Nelson, 2008; Irish et al., 2018, 2020; Larsen, 2015; Martion-Torres et al., 2007; Rightmire, 1999; Scott, 1973, 1980; Scott and Turner, 1997; Turner et al., 1991). However, as the exact modes of inheritance for dental morphological traits are unknown, discussed further in the following sections, the specific genetic component for each trait is also unestablished. Consequently, the genetic component in expression for these traits is reported as a range, i.e., 40-80% (Dempsey and Townsend, 2001; Hanihara, 2008, 2010; Hughes and Townsend, 2013; Irish, 1993, 2005, 2006, 2016; Irish and Nelson, 2008; Irish et al., 2018; Larsen, 2015; Martion-Torres et al., 2007; Rightmire, 1999; Scott, 1973, 1980; Scott and Turner, 1997; Turner et al., 1991).

The ASUDAS system has also facilitated the identification of specific dental complexes, a collection of nonmetric traits shared in specific macroregional populations at high, intermediate and low frequencies that differentiate them from other populations (See page 181). These complexes are predominantly based on nonmetric traits as observed on permanent teeth, although several have been conducted using deciduous teeth (Aguirre et al., 2006; Hillson and Antoine, 2003; Kieser, 1984). In addition to the standards for recording dental morphological data, specific types of statistical analyses are standard as well. Early analyses relied on analytical models such as the coefficient of racial likeness (CRL), a generalized distance measure which estimates the divergence between populations means (Pearson, 1926). However, this method came under criticism as clear standards for interpretation of the CRL value have not been identified, it does not work well with small samples, only a single standard deviation is used for all groups analysed, and correlation among variables is not considered (Fisher, 1936; Penrose, 1954; Seltzer, 1937). Although subsequently different distance statistics were developed, such as Penrose distance and Sanghvi's measure of dissimilarity, these methods were also criticized as the differences among groups were difficult to interpret, correlation and covariance were not accounted for and were not representative of actual biological similarities among or within populations (Berry, 1978; Penrose, 1954; Rolf and Sokal, 1965; Sanchvi, 1953). These early statistical methods were subsequently supplanted by two prominent multivariate, univariate and/or descriptive statistical analyses, the MMD distance statistic and a modification of Mahalanobis' generalized distance for metric traits (such as tooth size) often referred to as pseudo-D^2 (Grewal, 1962; Harris, 2008; Hanihara and Ishida, 2005; Harris and Sjøvold, 2004; Konigsberg, 1990; Irish, 2010; Mahalanobis, 1936; Mahalanobis et al., 1949; Manly, 1986, 2005; Sjøvold, 1977). Other statistics commonly used for nonmetric trait analyses, in order to identify relationships between and among populations, include PCA, discriminant function analysis, and multidimensional scaling (Hillson, 1996; Hanihara 2008; Harris and Sjøvold, 2004; Irish, 1993, 1998a, b, c, 2000, 2005, 2006, 2010, 2016, Irish et al., 2014, 2018; Sjøvold, 1973).

Models for calculating these relationships and assessing population structure using phenotypic traits are also common (Harpending and Jenkin, 1973; Relethford and Blangero, 1990). However, the model introduced by Relethford and Blangero (1990) for assessing biological affinity from genetic frequencies is the most frequently used. This model was adapted from previous models, those of Harpending and Jenkins (1973) and Harpending and Ward (1982), used for examining the distribution of allele frequencies for use with phenotypic (the observable characteristics of an individual resulting from the interaction between genetics and environment) qualitative data (Harpending and Jenkins, 1973; Harpending and Ward, 1982; Relethford and Blangero, 1990). This model predicts when the rate of extra-regional gene flow into populations is equal, a linear relationship between the average within-group variation and approximate genetic distance to the regional centroid (i.e., mean) should be observed (Blangero 1990; Relethford and Blangero, 1990; Relethford and Harpending, 1994). Conversely, when rates of extra-regional gene flow are disproportionate, populations will not follow this model because those that have higher rates of extra-regional gene flow should be more heterogeneous (i.e., have higher within-group variation) than those that have little or no external gene flow (See page 135) (Blangero 1990; Relethford and Blangero, 1990; Relethford, 1994, 2004; Relethford et al., 1997). Further, estimates of heterozygosity, genetic diversity, among populations can be plotted against that which is observed, to indicate those that exhibit high levels of extra-regional gene flow in comparison to those in which it is limited (Blangero 1990; Relethford, 1994, 2001; Relethford et al., 1997; Relethford and Harpending, 1994). This model assumes that the traits or genes being compared are selectively neutral (those that have neither negative nor positive effects) and that rates of mutation are potentially equal across populations (Blangero 1990; Relethford and Blangero, 1990; Relethford and Harpending, 1994; Relethford, 1994, 2004, 2007; Relethford et al., 1997).

Variation in the phenotype of the dentition expressed as variation in trait frequencies can result from genetics, environment, diet, dental ontogeny, development or developmental history, and maternal health. Even though teeth can be influenced by and directly interact with the environment, the size, form, and morphology, excluding pathological conditions, are predominantly influenced by genetics and environmental adaptions and interactions (Berry, 1976; Biggerstaff, 1975; Larsen, 2015; Scott, 1973; Scott and Turner, 1997; Turner, 1967). Although no studies have been conducted to determine whether any of these traits are under selection and/or are adaptations to different environments. Consequently, the effect of this evolutionary force on nonmetric traits and subsequent dental morphological analyses are unknown. Therefore, the results of these analyses should be interpreted in light of this caveat (Berry, 1976; Biggerstaff, 1975; Larsen, 2015; Scott, 1973; Scott and Turner, 1997; Turner, 1967). Variations in trait frequencies and underlying phenetic relationships among and within populations can be determined through an analysis of population history, structure and biodistance.

Population history and structure

A fundamental goal of bioarchaeological analyses is to reconstruct population history and structure with the intention of gaining an improved understanding of the social and biological connections among populations or groups (Relethford, 1996). Population history can be defined as a record of events experienced by a population that impact their biological histories, such as migration and demographic expansion or collapse (Relethford, 1996). Population structure can be defined as a method to explore and describe patterns in this variation and its distribution (Relethford, 1996). Biodistance analysis, a measurement of the similarity and diversity among and within populations or groups and, is often calculated using the mean difference in phenotypic expression, is a commonly employed method for examining variation within and between populations resulting from such events (Buikstra et al., 1990; Hefner et al., 2016; Pietrusewsky, 2014; Pilloud et al., 2016; Relethford and Blangero, 1990; Relethford, 1996). Therefore, population history, structure, and biodistance are inextricably linked concepts and are shaped by biological processes such as genetic drift and gene flow; which are themselves impacted by human behaviours like preferential mating and migration (Konigsberg, 2006; Relethford and Blangero, 1990; Relethford, 1996). Although population structure and biodistance analyses cannot directly test for particular human behaviours, they can be indirectly evaluated by examining biological variation in morphological and/or genetic data (Konigsberg, 2006; Long, 1966; Mielke, 2006; Relethford and Blangero, 1990; Relethford, 1996).

Population structure measures forces such as gene flow and involves the identification of shared genetic variants among individuals and accordingly facilitates the categorizing of groups into sub-populations (Hubisz et al., 2009; Konigsberg, 2006; Konigsberg and Buikstra, 2006; Pritchard et al., 2000; Relethford and Blangero, 1990; Relethford, 1996; Relethford and Lees, 1982). This analysis can be conducted at the sub-population to population level or at the individual sub-population level (Crow and Aoki, 1984; Exoffier et al., 1992; Greenbaum et al., 2016; Pritchard et al., 2000; Pickrell and Pritchard, 2012; Saitou and Nei, 1987). Consequently, it is assumed that populations were able to interbreed and were thus contemporaneous in time and space. Comparing populations or groups that are vastly spatially or temporally disparate violates this assumption (Exoffier et al., 1992; Konigsberg, 200; Konigsberg and Buikstra, 2006; Pritchard et al., 2000; Relethford and Blangero, 1990; Relethford and Lees, 1982). As some archaeologically derived populations are dated by associated artefacts, the resulting analysis should be interpreted in light of this caveat. A population is defined by three primary criteria in population genetics (Dow and Cheverud, 1985; Gillespie, 2004; Hartl, 2000; Hartl and Clark, 2006; John, 2004; Lowe et al., 2017; Pritchard et al., 2000; Winsor et al., 2017). The first of these criteria is individuals occupying a defined area. The second is the potential for all individuals and populations to interbreed and have, presumed, equal access to partners. The third is that populations are from the same species (Gillespie, 2004; Hartl, 2000; Hartl and Clark, 2006; Hunley, 2002; John, 2004; Pritchard et al., 2000). Criterion one may be an issue in archaeological contexts, as archaeologists determine what constitutes a population's defined area (Blangero, 1990; Relethford, 1996). Further, these definitions may vary. One population may be defined using geographic boundaries, while another may be defined based on presumed social boundaries based on differences in material culture.

Condition two is often complicated due to limited sample sizes and poor preservation, which necessitates the combination of samples from multiple sites and/or imprecise chronological dates (Blangero, 1990; Konigsberg, 2006; Relethford and Blangero, 1990; Relethford, 1996). Consequently, when possible, it is advised to restrict archaeological samples to specific individual populations, or to those within a realistic geographic distance of one another so that interaction and possibly mating can be reasonably assumed (Knudson and Stojanowski, 2008). Requirement three is easily met as only one species exists among modern human populations.

Biodistance

Biodistance analyses use phenotypic data to estimate genetic similarity and to reconstruct patterns of population origins, gene flow and long-distance migration (Buikstra et al., 1990; Larsen, 2015; Stojanowski and Schillaci, 2006). The goals of these analyses are diverse and include broad geographic and regional investigations of population affinity; tracing biological relationships temporally and spatially; reconstructing past population history and structure; investigating microevolutionary processes (e.g., gene flow, genetic drift, and selection); assessing past exchange networks; mechanisms of population integration (i.e., colonisation and assimilation); patterns of mobility and kinship level analyses and investigating the influence of geography and other isolating mechanisms on the observed biological variation

(Alt and Vach, 1998; Bermudez de Castro et al., 2010; Buikstra et al., 1990; Konigsberg and Buikstra, 1995; Knudson and Stojanowski, 2008; Irish and Guatelli-Steinberg, 2003; Martinón-Torres et al., 2007; Pilloud and Larsen, 2011; Stojanowski, 2003; Tishkoff and Gonder, 2007). Further, these analyses may provide an alternative to the establishment of archaeologically derived population boundaries than analyses of the material culture alone (See page 54) (Hefner et al., 2016; Konigsberg and Buikstra, 1995; Pilloud, 2009). However, the majority focus on the assessment of biological affinity among and within populations and attempt to determine those traits driving the observed variation (Adams, 1968; Adams et al., 1978; Anthony, 1990; Burmeister et al., 2000; Cabana, 2002; Godde, 2009; Hubbard et al., 2015; Irish, 1993, 2005, 2016; Irish et al., 2014; Konigsberg, 2006; Relethford and Blangero, 1990; Slatkin, 1995).

Early studies during the late 1800s and early 1900s into dental and skeletal variation formed the basis for subsequent biodistance analyses. However, these studies were predominantly descriptive and typological. Further, these investigations were concerned with attempting to describe and identify racial types rather than assessing the underlying biological relationships among populations (Blumenbach, 1865; Hrdlička, 1920, 1921, 1927; Kitson, 1931; Morton, 1839; Shaw, 1931). Although contemporary analyses are not concerned with racial classification, it has been argued that they have not moved beyond the descriptive and typological approaches characteristic of these early studies (Armelagos and van Gerven, 2003). However, biodistance analysis is still commonly used for examination of past populations and their underlying social and biological relationships.

The basic premise of these analyses is that biological similarities between populations are based on phenotypic and/or genetic similarities that reflect biological affinity, as indicated by either skeletal or genetic variation. These similarities can be an indication of shared ancestry, genetic drift, and/or gene flow (Buikstra et al., 1990; Irish, 2010; Konigsberg and Buikstra, 1995; Mackay, 2014). As such, the nature of contemporary analyses does not facilitate the assignment of populations into arbitrary categories. However, the complex relationship among human behaviour and these mechanisms does not often result in a parsimonious explanation (Leslie, 1985; Reed, 2006; Relethford, 1996, 2016; Relethford and Crawford, 1995). The significance of increasing or decreasing biological interaction from a social perspective in addition to how these relationships change through time is also taken into account (Knudson and Stojanowski, 2008). When the biological variants being investigated have similar rates of mutation or are evolving by genetic drift, so that they reflect interactions between populations rather than adaptions to specific environments, the similarities between groups likely reflect the outcome of both long-term or short-term processes (e.g., multigenerational gene flow and recent migrations, respectively) (Konigsberg and Buikstra, 1985; Knudson and Stojanowski, 2008; Stojanowski and Schillaci, 2006). Correspondingly, through examination of genetic or phenotypic variants, the genetic or historical interactions between and among populations can be assessed. Subsequently, the use of phenotypic variants in place of genetic to reconstruct population structure and biological affinity among and within populations has become common (Brookfield, 2016; Buikstra et al., 1990; Konigsberg and Buikstra, 1985; Knudson and Stojanowski, 2008).

However, several issues have been critiqued related to the underlying assumption that phenotypic and genetic reconstructions of biological affinity based on biodistance estimates will be comparable (Stojanowski and Schillaci, 2006). These critiques focus on several aspects of biodistance analyses including the type of traits used and the correlation between allele frequencies and phenotypes (Stojanowski and Schillaci, 2006). First, as only surface traits are the focus of analysis, their entire range is not considered. Second, this approach assumes changes in allele frequencies result in measurable changes in phenotypes, which can be determined analytically. Third, that biodistance measures reflect biological processes that can be used to interpret behaviours such as migration. Fourth, there is a relationship between phenotypic and genetic frequencies. Fifth, archaeological samples are representative of past populations which are temporally specific (Stojanowski and Schillaci, 2006).

Regarding the first issue, it has been suggested that contemporary methods for evaluating nonmetric trait variation only consider surface traits, those visible on the crown surface. Consequently, the entire range of trait expression may not be evaluated, which may result in erroneous biodistance estimates. Some traits have been argued to be expressed within the enamel (the tissue which covers the outer surface of the tooth) as opposed to on the outer surface (Skinner et al., 2008, 2009). These traits are only evident deep within the enamel-dentine junction, the boundary between the enamel and the underlying dentine (the calcified tissue underlying the enamel) (Skinner et al., 2008, 2009). However, the presence and effect of this variation among modern human populations is unknown, as these traits have only been documented within extinct hominin species (Skinner et al., 2008, 2009). Furthermore, it is unknown whether these traits are influenced by genetics or the environment. The biological variants being examined in a biodistance analysis must reflect genetic variation and not environmental influence; therefore, their inclusion in a biodistance analysis may not reflect phenotypic variation (Skinner et al., 2008, 2009). In relation to the second issue, changes in allele frequency over time can be caused by microevolutionary processes including natural selection, mutation, gene flow, and genetic drift (Blangero and Konigsberg, 1991; Brookfield, 2016; Daubert et al., 2016; Irish, 1993, 2005, 2016; Irish et al., 2018; Konigsberg, 2006; Relethford and Blangero, 1990). Biodistance analyses based on variation in dental nonmetric traits has facilitated the assessment of these processes within and among populations in numerous previous studies. The results of these studies have been found to be in line with known genetic and/or phenotypic variation (Hubbard et al., 2015; Irish, 1993, 2005, 2016, Irish et al., 2014, 2018, 2020; Konigsberg, 2006; Relethford and Blangero, 1990). This suggests that biodistance analysis is an effective method for examining the above processes within and among populations.

Concerning the third caveat, it has been suggested that previous studies have relied too much on a single type of data to calculate biodistance (Corruccini, 1974; Smith, 1972). The different types of data may provide different interpretations of behaviours, such as migration, within each population being analysed (Corruccini, 1974; Smith, 1972). Interpretations of biodistance and population structure commonly include analysis of these behaviours consequently, it should be taken into consideration that they cannot be directly tested through analytical approaches (Buikstra et al., 1990; Konigsberg and Buikstra, 1985; Knudson and Stojanowski, 2008). Instead, subsequent interpretations should also rely on additional data from ethnographic, historical and archaeological sources in order to establish reliable interpretations of the observed patterns (See pages 32 and 54) (Knudson and Stojanowski, 2008; Stojanowski and Schillaci, 2006).

With respect to the fourth concern, the relationship between phenotypic and genetic variation is complex. Previous studies have attempted to assess the concordance between biodistance estimates using nonmetric cranial, post-cranial and genetic data. However, few studies have examined this relationship using nonmetric dental data (Bernardo et al., 2011; Brewer-Carias et al., 1976; Corruccini et al., 1982; Harris, 1977; Hubbard, 2012; Hubbard et al., 2015; Irish et al., 2020; Sofaer et al., 1972b; Wijsman and Neves, 1986). Additionally, they have relied on pooled and previously published data, as well as a limited number of nonmetric traits, consequently not enough traits, have been used for a viable comparison (Harris, 1977; Sanghvi, 1953; Sofaer et al., 1986). Further, it has been suggested that the results of these early studies were likely influenced by the polygenic, influenced by more than one gene, nature of dental traits. In other words, a potentially large number of genes are controlling dental traits. Discrepancies among the results of these studies may also have been related to the time period in which they were conducted, i.e., the 1970-1980's, as they utilized genetic markers that were commonly used in this time period and are not in contemporary studies, such as blood group and serum protein variant frequencies (Brewer-Carias et al., 1976; Corruccini et al., 1982; Harris, 1977; Sofaer et al., 1972b; Wijsman and Neves, 1986). Most recent studies involving variation in nuclear DNA utilize either SNP or Short Tandem Repeat (STR) Polymorphism frequencies due to their polymorphic nature (Alveres-Sandoval, et al., 2015; Busby et al., 2012; Cruciani et al., 2011; Hoffecker et al., 2016; Oppenheimer, 2012; Rubicz et al., 2010). Microsatellite markers, a short segment of repeated DNA sequences which vary among individuals and populations, are also frequently used in studies of population differentiation (De Beule, 2011; Oppenheimer, 2007, 2012; Sykes, 2006). However, the above methods were not widely used at the time when these studies were published (Busby et al., 2012; Butler, 2006 and Schanfield, 2007; De Beule, 2011; Lucotte, 2015; Oppenheimer, 2012). Furthermore, there was no established collection standards for dental nonmetric variation available at this time, as the ASUDAS system had not been established (Sofaer et al., 1972b). This lack of standardization contributed to issues with reliable scoring of nonmetric traits and higher potential intra-observer error (Sofaer et al., 1972b; Stojanowski and Johnson, 2015).

Concerning the fifth issue, that selective preservation often influences archaeologically derived samples, as a result, it is necessary to presume that these samples accurately reflect the overall composition of past populations (Buikstra et al., 1990; Stojanowski and Schollaci, 2006). As burial practices and environmental conditions affect the preservation of skeletal material, it is often necessary to utilize selective sampling strategies to ensure adequate representation of the variation present in a given population is analysed (Buikstra et al., 1990; Stojanowski and Schollaci, 2006). Consequently, it is not possible to assess the total range of variation that was initially present in archaeologically derived samples. Subsequently, the conclusions as to population history and structure derived from biodistance estimates based on such samples may be limited. In order to address this issue, it is necessary to interpret archaeologically derived samples as a subset of the actual population (Buikstra et al., 1990; Stojanowski and Schollaci, 2006). However, as small samples often necessitate the pooling of multiple archaeological sites, or cemeteries, for a viable statistical analysis, it is necessary to interpret the results of analyses based on such samples with caution.

Model-free and model-bound approaches

Biodistance, population history, and structure analysis have significantly benefitted from innovations in multivariate statistics and the development of diverse methodological approaches. Due to these innovations and developments, biodistance studies are classified as either model-free or model bound. Model-free often precede model-bound analyses, as they explore the morphological affinities among and within populations, or the patterns observed in this variation (Irish, 2010; Relethford and Lees, 1982). However, the majority of biodistance analyses are model-free as they assess population differentiation without directly investigating its causes (Irish, 2010; Relethford and Lees, 1982). Further, this approach does not require the assessment of study parameters or rely on *a priori* assumptions.

Rather, they analyse differences in the morphological affinity and phenotypic similarity among populations in order to summarize the observed diversity through calculation of a biodistance matrix (Irish, 2010; Relethford and Lees, 1982). The overall patterns are subsequently interpreted in light of population history and structure, and compared to data from archaeological, linguistic and cultural contexts to determine which samples, or sample pairs, are most phenetically similar (Irish, 1993, 1997; Knudson and Stojanowski, 2008). No inherent assumptions about populations must be made prior to model-free analyses. Such as, that the populations analysed are contemporaneous before population history, structure and biodistance can be calculated (See page 119) (Irish, 2010; Konigsberg, 1990; Relethford and Lees, 1982). Model-bound approaches incorporate population history and structure models to analyze phenotypic and quantitative data, with complex polygenic, developmental, and environmental influences that show continuous or semi-continuous variation in any given population (Irish, 2010; Relethford and Harpending, 1994; Relethford and Lees, 1982). These approaches are used to determine the evolutionary forces, such as genetic drift, gene flow or natural selection, that contribute to the underlying biological relationships and morphological differentiation within or among populations (See page 119) (Konigsberg, 2006; Relethford and Blangero, 1990; Williams-Blangero et al., 1990; Von Cramon-Taubadel and Weaver, 2009). These approaches also attempt to explain the causes for the observed relationships (Conner 1990; Irish, 2010; Konigsberg 1988; Konigsberg and Buikstra 1995; Powell and Neves 1999). As such, they require that certain assumptions are met and that samples are characterized through statistical examination of population parameters (Relethford and Blangero, 1990; Relethford and Harpending, 1994;

Relethford and Lees, 1982). Further model-bound approaches test hypotheses while model-free approaches are descriptive (Knudson and Stojanowski, 2008; Stojanowski and Buikstra, 2004).

Although model-free approaches are still used, model-bound approaches for assessing population structure are becoming more common (Irish, 2010; Konigsberg, 2006; Relethford and Blangero, 1990). The application of these approaches enables contemporary biodistance analyses to surpass the previously mentioned criticism that they are still predominantly descriptive and typological (Armelagos and van Gerven, 2003). Previous distance statistics were based on the mean frequencies of morphological traits and genes. However, the application of multivariate statistical methods facilitates the evaluation of their diversity within and among populations (Kundson and Stojanowski, 2008; Relethford and Blangero, 1990; Stojanowski and Buikstra, 2004). Further, contemporary biodistance analyses are not concerned with classifying or analyzing populations according to typological assessments of racial differences. Instead, populations are examined according to their underlying genetic relationships as indicated through diversity in morphological and genetic traits (See page 119) (Coppa et al., 1998, 2000, 2007; Hanihara, 2008, 2010; Irish, 2010, 2015; Irish et al., 2014, 2018; Pacelli and Márquez-Grant, 2010; Scott et al., 2013a, c). Therefore, modern biodistance analyses do not facilitate the documentation, or categorization, of populations based on the typological and descriptive frameworks of the 19th and early 20th centuries.

Heritability of nonmetric traits

Heritability is a statistical estimate of the probability that a trait will be passed from parent to offspring and is separated into two types, broad and narrow (Hartl, 2000; Mackay, 2014). In a broad sense, heritability measures the extent to which phenotypic variation is determined by genotypic variation including dominant, additive and epistatic traits, multi-gene interactions that affect phenotypes (Hartl, 2000; Mackay, 2014). In a narrow sense only the proportion of phenotypic variance that is determined by additive traits is measured (Hartl, 2000; Mackay, 2014). Although both types of heritability analysis are commonly used, those examining nonmetric trait variation frequently rely on narrow sense. Biodistance analyses use selectively neutral traits, those with high heritabilities (Hartl, 2000; Mackay, 2014). However, it is necessary that such traits are not rare within or among populations, as these variants typically indicate familial rather than population level relationships (Alt and Vach, 1998; Berry and Berry, 1967; Berry, 1978; Scott and Turner, 1997; Sjøvold, 1973).

Modern understanding of the modes of inheritance of nonmetric traits is based in part on the work of Hans Grüneburg (1952), that established a framework for modern understanding of quasi-continuous variation, phenotypes that vary continuously (Grüneburg, 1952). It was discovered, through analyses of mice, that the inheritance of some morphological variants did not conform to the pattern expected based on Mendelian inheritance. Subsequent analysis into the absence of the third molar demonstrated that tooth germ size was the principal controlling factor in the absence of that tooth (Grüneburg, 1952). When a tooth germ did not reach its developmental threshold or its particular size, the dental hard tissues, e.g., enamel, did not form (Grüneburg, 1952). These analyses enabled the development of a quasi-continuous variation model, which presumes that there is an underlying continuous genetic variation that determines the threshold for presence or absence of a particular morphological trait (Grüneburg, 1952; Scott and Turner, 1997; Scott and Irish, 2017). If the degree of trait expression exceeds the threshold, it will be present and the phenotype will vary based on how much it is surpassed; whereas if trait expression falls below the threshold, it will not be present (Grüneburg, 1952; Scott and Turner, 1997). Consequently, a quasi-continuous trait can be defined as a continuous variable whose expression has a visible and a nonvisible range (Sofaer, 1970). The visible range is the phenotypic variation that is observed if the threshold is exceeded, while the nonvisible range referrers to the underlying genetic variation (Grüneburg, 1952; Scott and Turner, 1997; Sofaer, 1970; Scott and Irish, 2017). Individuals have their own probability of meeting and/or exceeding the threshold of expression for each trait and it can vary depending on environmental influences (Tyrrell, 2006).

Nichol (1989) conducted the first in-depth assessment of the inheritance of multiple nonmetric traits, 17 crown traits, based on observations from dental casts from 83 nuclear families were recorded. The data was subsequently submitted to a complex segregation analysis (CSA) (Nichol, 1989). CSA determines whether the observed patterns follow those expected based on Mendelian ratios for dominance, codominance, and recessive inheritance (Morton et al., 1971). Although two-allele, single locus models of inheritance were the focus of early CSA, mixed models accounting for polygenetic and random environmental components are currently common (Cheverud, 1984, 1988; Lalouel et al., 1983; Morton et al., 1971; Morton and MacLean, 1974). It was subsequently determined that the majority of nonmetric traits have a polygenic model of inheritance through a CSA using both a single locus and an additive polygenic model (Lalouel et al., 1983; Morton et al., 1971; Morton and MacLean, 1974; Nichol, 1989; Nei, 1972; Nei and Roychoudhury,1974; Zhao et al., 2000). Therefore, trait development is regulated by the action of genes at many loci, each with a small and additive effect, in addition to environmental effects (Scott and Turner, 1997; Scott and Irish, 2017). Although this mode of inheritance is generally accepted, the contributions of various genes to this variation has not been determined (Berry and Berry, 1967; Berry, 1978; Harris, 1977; Hughes and Townsend, 2011, 2013; Irish, 2015, 2016; Nichol, 1989; Scott, 1973; Scott and Irish, 2017). However, it is agreed that variation in the phenotype of the dentition, expressed as variation in trait frequencies, can result from genetics, environment, diet, dental ontogeny and maternal health (Hughes and Townsend, 2011, 2013; Scott and Irish, 2017; Scott and Turner, 1997).

Assessing the heritability of tooth size and shape is complicated, as it varies within and among populations and through time (Harris and Rathbun, 1991; Scott and Irish, 2017; Scott and Turner, 1997). It has been hypothesized that at least 10 genetic loci are involved in the expression of each dental morphological trait. Overall, nonmetric traits are believed to represent roughly 100 genetic loci (Berry, 1979). However, it has also been suggested that different quantities of loci are associated with the different dental developmental stages (Nanci, 2017; Tooth and Craniofacial Development Group, 2005; Townsend et al., 2003). It has been estimated that approximately 20 different genes are associated with the cap stage, in which cells are arranged into a developing tooth, of dental development. It has also been estimated that 21 genes are associated with the bell stage, in which the differentiation of dental hard tissues including enamel and dentine takes place. A further 14 genes are associated with the differentiation stage (in which the developing teeth are differentiated into tooth classes such as incisors) and 11 genes are associated with the secretory phase in which enamel formation and secretion begins (Nanci, 2017; Tooth and Craniofacial Development Group, 2005). These stages represent the various developmental stages during which teeth begin to develop and subsequently determine the placement and spacing of dental cusps and initiate and control amelogenesis, the formation of enamel on teeth (Nanci, 2017). Additional genes, including several Homeobox variants (a large group of genes that direct the formation of several structures during human embryonic development, which are involved in morphogenesis, anatomic development) have also been documented (Mitchell et al., 2006; Suryadeva and Mohammadi, 2015). Recent studies have suggested that up to 100 genes may be involved in the entire embryonic phase of tooth development (Abu-Hussein, et al., 2015; Doshi et al., 2016; Duboule, 1994; Han et al., 2018; Puthiyaveetil et al., 2016; Rinky et al., 2013; Sharpe, 1995, 2000; Suryadeva and Mohammadi, 2015). However, the exact number of genes controlling for each dental trait has yet to be determined.

Previous studies have focused on the heritability of and underlying mechanisms controlling tooth size and shape (Alvesalo and Tigerstedt, 1974; Berry, 1978; Biggerstaff, 1975; Hughes and Townsend, 2011, 2013; Irish, 2015, 2016; Menezes et al., 1974; Osborne, 1963; Osborne et al., 1958; Portin and Alvesalo, 1974; Potter et al., 1976; Scott, 1973; Staley and Green, 1974; Sofaer et al., 1972a; Townsend and Brown 1978a, b). To estimate the heritability of tooth dimensions and nonmetric traits twin and familial studies have been conducted (Alvesalo and Tigerstedt, 1974; Berry, 1978; Biggerstaff, 1975; Hughes and Townsend, 2011, 2013; Irish, 2015; Menezes et al., 1974; Osborne, 1963; Osborne et a., 1958; Portin and Alvesalo, 1974; Potter et al., 1976; Scott, 1973; Sofaer et al., 1972a; Staley and Green, 1974; Townsend and Brown 1978a, b). The degree to which variability in traits is controlled by heredity opposed to environmental influences is also a focus of these studies. The concordance between the two is often compared between identical and fraternal twins (Hughes and Townsend, 2011, 2013; Kaul et al., 1985; Kieser, 1990; Scott and Porter, 1984; Scott and Turner, 1997; Skrinjaric et al., 1985; Townsend et al., 1988; Townsend et al., 1992; Townsend et al., 2008). Identical twins share both a genotype and an environment, whereas fraternal twins share an environment and less similar genotypes. Consequently, the range of heritability for morphological traits, 40-80%, and size, 60-80% has been well established (See pages 113, 119 and 125). However, as with dental nonmetric traits the exact modes of inheritance and the specific degree of genetic influence on tooth size are unknown. Therefore, the influence is also reported as a range, i.e., 60-80% (Hughes and Townsend, 2013; Jordan and Abrams, 1992; Mizoguchi, 1978; Scott and Irish, 2013a, c; Scott and Irish, 2017; Scott and Turner, 1997; Townsend et al., 2008; Willermet et al., 2013). The exact proportion of genetic control for each trait is unknown, as no large-scale comprehensive study examining this control on multiple traits has been conducted. However, due to the moderate to the high genetic component, analysing variability in tooth size and morphology provides insight into the degree of variation at the macro-evolutionary and micro-evolutionary levels (See page 113) (Dempsey and Townsend, 2001; Hawkey, 1998; Larsen, 2015; Mizoguchi, 1978; Nichol, 1990; Schnutenhaus and Rösing, 1998; Scott and Turner, 1997; Scott and Irish, 2017; Turner, 1969).

Twin studies also demonstrate that dental crown traits exhibit a range of morphological variation both between and within individuals as well as populations (Biggerstaff, 1969; Bockmann et al., 2010; Hughes and Townsend, 2011, 2013; Irish, 2015, 2016; Kaul et al., 1985; Kieser, 1990; Martinón-Torres et al., 2007; Mihailidis et al., 2013; Scott and Potter, 1984; Scott and Irish, 2017; Scott and Turner, 1997; Skrinjaric et al., 1985; Townsend et al., 1988; Townsend et al., 1992). This variation can involve the whole tooth or be limited to particular aspects of the crown (Hughes and Townsend, 2013; Hughes et al., 2007; Larsen, 2015; Lundstrom, 1967; Rightmire, 1999; Scott, 1973; Scott and Irish, 2017; Townsend and Martin, 1992; Townsend et al., 2009; Woodroffe et al., 2010). Many traits show significant covariation, which is a likely result of their shared developmental trajectory (Hughes and Townsend, 2013). There is an allometric relationship, i.e., the study of size in relation to shape, among teeth. This relationship includes dimensional variables such as size, area, volume, and those that may be influenced by these thresholds, including tooth number and molar cusp number, which are likely to be highly correlated phenotypically (Hughes and Townsend, 2013; Scott and Irish, 2017; Scott and Turner, 1997). Numerous previous studies have focused on the heritability of nonmetric traits; however, little research has been undertaken to document the genes affecting them (Garn et al., 1959; Garn et al., 1963, 1966; Hershkovitz, 1971; Hunter et al., 2010; Jernvall, 2000; Jernvall and Jung, 2000; Potter et al., 1976; Salazar- Hershkovitz Ciudad and Jervall, 2005, 2010; Sofaer et al., 1972a; Scott, 1973; Staley and Green, 1974; Townsend and Brown, 1978a, b).

The contributions of genotype and development to the size and distribution of molar cusps, determined through application of a patterning cascade model of cusp development, has been the focus of some research (Astorino et al., 2015; Duner, 2011; Jernvall, 2000; Jernvall and Jung, 2000; Moormann, 2011; Moormann et al., 2013; Salazar-Ciudad and Jernvall, 2005, 2010; Skinner at al., 2008, 2009; Thesleff et al., 2001; Tonge, 1971). This model provides an evolutionary developmental framework which facilitates analysing the diversity in tooth crown morphology and size; as influenced by the developmental limitations of the tooth and the genetic activation of particular genes (Duner, 2011; Jernvall and Jung, 2000; Jernvall et al., 1994; Moormann, 2011; Moormann et al., 2013). The enamel knots (the growth site of a cusp) which dictate crown morphology (i.e., cusp number) and tooth germ size track the underlying developmental processes (Jernvall, 2000; Jernvall and Jung, 2000; Paul et al., 2017; Salazar-Ciudad and Jernvall, 2010). Enamel knots develop an inhibitory zone which controls the size and spacing of cusps within each molar, while the activation of particular genes control their growth rates and initiation (Jernvall and Jung, 2000; Paul et al., 2017). Based on the observed intercusp distances compared to overall tooth size, the width and height of cusps could be reliably predicted (Jernvall, 2000; Jernvall and Jung, 2000; Paul et al., 2017). Though this model was initially based on seal teeth, it has been adapted for analysis of human teeth (Hunter et al., 2010; Moormann, 2011; Paul et al., 2017). Previous research has shown this model to successfully predict variation in Carabelli's cusp expression, such as size, in relation to other cusps on the first molar (Duner, 2011; Morita et al., 2014; Paul et al., 2017).

Several lines of evidence, including familial correlations, population variation, and twin studies, indicate that genetic variability is a major factor in crown and root trait development (Hunter et al., 2010; Hughes and Townsend, 2011, 2013; Irish, 2016; Jernvall, 2000; Jernvall and Jung, 2000; Jernvall and Thesleff, 2000; Paul et al., 2017; Potter et al., 1976; Scott and Turner, 1997; Salazar-Ciudad and Jernvall, 2010; Skinner at al., 2008; Tonge, 1971; Townsend et al., 1992). However, trait expression is also influenced to some degree by environmental factors, as observed in the differential expression of morphological traits on alternate sides of the dentition, also known as fluctuating asymmetry (Garn et al., 1996; Scott and Irish, 2017; Scott and Potter, 1984; Scott and Turner, 1997). This is evident in studies of individuals and identical twins, where a trait may be expressed to a greater degree on a given tooth for one individual and less so on the antimere (Scott and Potter 1984). Bilateral asymmetry has also been frequently observed in populations experiencing greater environmental stress (See page 113) (Bailit et al., 1970; Bollini et al., 2009; Riga et al., 2014; Townsend et al., 2016; Van Dongen et al., 1999). As bilateral trait development is controlled by the underlying genome, fluctuating asymmetry is believed to reflect the inability of development to occur against random perturbations, known as developmental instability. Therefore, it can be said to represent the level of stress to which individuals are exposed (Moller and Swaddle, 1997; Polak, 2003). Consequently, fluctuating asymmetry is believed to be related to environmental factors such as lack of nutrients, high viral loads, and other internal or external influences impacting development (Coster et al., 2013; DeLeon, 2007; Klingenberg and Nijhout, 1999; Luís and Silva, 2016; Riga et al., 2014). Consequently, the effects of several diverse phenomena may represent environmental influences on the underlying genotype (Biggerstaff, 1973; Luís and Silva, 2016; Mayhall and Saunders, 1986; Nichol, 1990).

Differential trait expression has been the focus of several previous studies. Specific traits such as Carabelli's cusp, an additional cusp on the tongue side of the upper first molars, have been examined in relation to asymmetrical expression in several of these studies (Alvesalo et al., 1975; Baume and Crawford, 1980; Biggerstaff, 1973; Garn et al., 1966; Graham and Ozener, 2016; Goose and Lee, 1971; Guatelli-Steinberg et al., 2013; Kieser et al., 1986; Marado, et al., 2017; Sciulli, 2002; Townsend and Martin, 1992). Symmetrical expression on this trait has been observed in few individuals, i.e., 12 out of 423 individuals, and when asymmetry was observed, it was random and there was no evidence of trait expression varying consistently (Biggerstaff, 1973; Nichol, 1990; Townsend and Martin, 1992). Asymmetry in this trait is high and is observed up to 45% for the permanent first molars (Biggerstaff, 1973; Saunders and Mayhall, 1982; Townsend and Martin, 1992). This suggests that the high degree of asymmetry observed in Carabelli cusp expression may be the result of environmental influences on the formation of enamel knots and the subsequent folding of the enamel epithelium (tissue) (Biggerstaff, 1973; Hunter et al., 2010; Nichol, 1990; Townsend and Martin, 1992). Different degrees of expression of this trait have also been documented between teeth of the same individual, and monozygotic and dizygotic twins. However, this difference in not often quantified in relation to trait grades, degree of trait expression (See Appendix I) (Biggerstaff, 1973; Marado et al., 2017; Nichol, 1990; Townsend and Martin, 1992). Further, it has been suggested that fluctuating asymmetry may also be related to sample size and dental wear affecting trait scoring in archaeological samples (Marado et al., 2017; Nichol, 1990; Townsend and Brown, 1980; Townsend and Martin, 1992). Though, the level of plasticity of nonmetric traits under different environmental contexts has not been the focus of much systematic research. However, the tendency towards bilateral expression is consistent with the notion that there is a strong genetic component involved in dental trait expression (Irish, 2010, 2016; Irish et al., 2018; Scott and Irish, 2013, 2017; Turner et al., 1991).

Correlations between genetic and dental morphological data sets and reconstructions of biological affinity, population history and structure

Numerous studies support the concept that nonmetric traits are determined by genetic factors acting during dental morphogenesis. Therefore, their analysis can be used as a proxy for inferring biological affinity among populations and/or groups (See pages 113 and 119) (Bowcock et al., 1994; Hubbard et al., 2015; Hughes and Townsend, 2013; Irish, 2010, 2016; Irish et al., 2018, 2020; Scott and Irish, 2013, 2017; Scott and Turner, 2007; Stojanowski et al., 2013). These traits have been used in numerous studies to assess population genetic affinities and microevolutionary trends among populations (Cadien et al., 1974; Delgado-Burbano et al., 2010; Hubbard et al., 2015; Hughes and Townsend, 2013; Irish, 2010, 2016; Irish et al., 2014, 2018, 2020; Scott and Irish, 2013, 2017; Scott and Turner, 2007; Stojanowski et al., 2013). It has been suggested that nonmetric traits can be used to determine population history, and structure, with greater accuracy than other skeletal structures (See pages 113, 118, 119 and 125) (Hubbard et al., 2015; Hughes and Townsend, 2013; Irish, 2010, 2016; Irish et al., 2018, 2020; Scott and Irish, 2013, 2017; Scott and Turner, 1997). A significant correlation has been found between nonmetric and nuclear microsatellite data used to distinguish global and regional populations. This supports the assumption that morphological traits provide similar information about biological affinity and population structure and history as genetic data (Hubbard, 2012; Hubbard et al., 2015; Irish et al., 2020; Ricaut et al., 2010; Scott and Turner 1997).

Several studies have compared distance matrices calculated using nonmetric traits to those determined using genetic data (Brewer-Carias et al., 1976; Hubbard, 2012; Irish et al., 2020; Ricaut et al., 2010; Sofaer et al., 1972b; Wijsman and Never, 1986). The results of these studies support a strong correlation in reconstructions of biological affinity based on these data (Cavalli-Sforza et al., 1994; Hubbard, 2012; Irish et al., 2020; Ricaut et al., 2010; Scott and Irish, 2017; Scott and Turner, 1997). Further analyses have supported the notion that the biodistance data obtained from dental traits will be concordant with that from genetic based studies (Hubbard 2012, et al., 2015; Irish et al., 2020; Rathmann et al., 2017; Ricaut et al., 2010). These studies have examined the efficiency of genetic versus nonmetric data for detecting familial groupings and whether biodistance data constitute an alternative to genetic markers. The dental data have been compared to genetic markers including mtDNA, nuclear microsatellites, a section of repeated DNA, SNPs and Y-chromosome microsatellites (Hubbard 2012; Hubbard et al., 2015; Irish et al., 2020; Rathman et al., 2017; Ricaut et al., 2010). The notion that nonmetric traits represent an alternative to genetic markers has been supported when examining affinity at the individual and population level (Hubbard 2012; Hubbard et al., 2015; Irish et al., 2020; Rathmann et al., 2017; Ricaut et al., 2010). However, the genetic data has been found to be slightly more reliable when assessing close genetic proximities between individuals, such as kinship. Since dental traits evolve slowly, they may provide a population history more in line with a deeper time scale than genetic data (Hubbard 2012; Irish et al., 2020; Rathmann et al., 2017; Ricaut et al., 2010). Thus, while there is a significant concordance between genetic, dental and skeletal nonmetric data, the dental data specifically, may be better suited for population level rather than individual level analysis (See pages 113 and 119) (Rathmann et al., 2017; Ricaut et al., 2010). Therefore, nonmetric traits are most likely to accurately estimate kinship when the degree of relationship among individuals is close (i.e., parent and child and the traits used are specific to familial inheritance, or are rare familial variants) (Ricaut et al., 2010).

Hubbard (2012) provided further support for a significant concordance between genetic and dental nonmetric data. Specifically, Hubbard (2012) examined whether the variants in dental morphology and nuclear DNA produced similar patterns of intergroup biological affinity among regional populations. Paired genetic and dental data were compared among four modern Kenyan (African) populations. A positive but not significant correlation (r=0.500, p=.021) was found between the two data sets. However, the sample size for dental traits was small (9 nonmetric traits) and may have impacted the results (Hubbard, 2012). Previous studies indicate that biodistance analyses should be based on as many traits as possible. Furthermore, the 4 populations analysed occupied the same region in Kenya (Africa) and it is believed that they originated from the same group of Bantu farmers that migrated out of Central Africa (Hubbard, 2012; Merritt, 1975; Nurse and Spear, 1985). Thus, it is possible that there might not have been enough variation to distinguish differences between the groups. However, both datasets provided a similar overall picture of the relationships among the populations (Hubbard, 2012). As the initial genetic dataset was larger than the dental, 2 additional analyses were conducted using 30 and 15 loci, respectively (Hubbard, 2012). The results of the 30 loci analysis indicated an overall increase in the distance values with no change in the relationships among the population pairs. However, in the 15 loci analysis, the distances were significantly reduced so that few distinctions were observed among the 4 samples (Hubbard, 2012). These preliminary analyses are in line with previous studies indicating that the number rather than the combination of traits may have more of an influence on biodistance estimates (See page 119) (Hanihara, 2008, 2010; Irish, 2010, 2015; Irish, 1993, 1998a, b, c, 2000, 2005, 2010; Irish et al., 2014, 2018; Pacelli Márquez-Grant, 2010; Scott et al., 2013a, c).

A similar correlation has been documented between nonmetric dental and neutral genetic data (Rathmann et al., 2017). However, this correlation was based on composite trait and genetic distributions from broad geographic regions (e.g., Europe and Italy). The nonmetric traits used in this analysis represent those characteristic of broad geographic dental complexes rather than those which comprise specific regional European populations. SNP and dental data, 12 nonmetric traits, from previously published sources representing 13 populations were matched and subsequently compared by region (Rathmann et al., 2017). Though a strong and positive correlation (r=0.574, p< 0.001) was found between the data sets, the range of variation may not be adequately represented (Rathmann et al., 2017). Further, the range of trait variation within these broad complexes is not completely documented (e.g., Europe) (Adler, 2005; Anctil, 2016; Coppa et al., 1998, 1999, 2000, 2007; Hallgrímsson et al., 2004; Henneberg, 1998; Hsu et al., 1999; Khudaverdyan, 2013; Maxová et al., 2011; Mcilvaine et al., 2014; Pacelli and Márquez-Grant, 2010; Rathmann et al., 2016, 2019; Scott et al., 2013b; Vargiu et al., 2009; Zubova, 2014). Although in spite of this limitation, the above correlation supports the notion that dental data can be used in place of genetic and suggests that the variation in nonmetric traits in these broad groups is enough to distinguish between them. Comparing unpaired data at a global scale may be common practice, however, it may result in a sampling bias, as the genetic variation between modern populations may be low compared to within-group variation (Barbujani et al., 1997; Deka et al., 1995b; Edwards, 2003; Jorde et al., 2000; Li, 1991; Witherspoon et al., 2007). Therefore, the correlation between the neutral genetic and dental data above may represent minimum values rather than exact correlations. Paired data from individuals or populations may provide a more accurate estimate of these phenotype correlations (Rathmann et al., 2017). However, the strong concordance indicates that both these datasets provided a similar overall picture of the biological affinity among populations. These findings further emphasize the notion that genetic data are not always better than dental for evaluating biological affinity, population history, and structure (See pages 113, 118 and 119) (Hubbard, 2012; Hubbard et al., 2015; Irish et al., 2020; Rathmann et al., 2017).

Differential levels of aDNA, ancient DNA, preservation often limit the sample size as well as which regions of the DNA that can be analyzed in order to understand variation among and within populations (Brown and Brown, 2011; Burger et al., 1999; Eisenmann et al., 2018; Mulligan, 2006). Conversely, the use of nonmetric data, though also inexorably limited in some cases, can often provide larger datasets than aDNA in cases of poor preservation. Although genetic data can provide information about the biological affinity among and within populations, it should not be considered a standard by which other estimates of biodistance are measured. Specifically, if genetic and dental datasets do not produce comparable biodistance estimates, this does not mean that genetic data are better suited to such analyses. Instead, the different types of phenotypic and genetic data that contribute to reconstructions of past behaviours and relationships among and within populations and why these differences exist should be evaluated (Hubbard, 2012; Irish et al., 2020; Rathmann et al., 2017). Although more research is necessary to fully understand the modes of nonmetric trait heritability; a complete understanding of these processes is not essential to perform affinity analyses. Numerous previous studies have indicated a significant concordance between dental, genetic, archaeological, linguistic and historical data among and within populations with known and unknown history and affinity (e.g., Berry and Berry 1967; Berry, 1978, 1979; Biggerstaff, 1973; Coppa et al., 2007; Dahlberg, 1951, 1971; Hillson, 1996; Hughes et al., 2007; Irish, 1993; 2005, 2010; Kimura et al., 2009; Sadier et al., 2014; Scott and Turner, 1997; Scott and Irish, 2017; Turner, 1967; Willermet et al., 2013).

Assessing interpopulation variation and relationships: correlations between genetic and geographic isolation by distance (IBD)

Isolation by distance (IBD) is a situation in which biological difference increases with geographic distance and will occur when populations are relatively non-mobile and inter-population gene flow is restricted (Kimura and Weiss, 1964; Konigsberg, 1990; Relethford, 2004; Slatkin, 1993; Wright, 1943). IBD is commonly used to examine inter-population variation and genetic relationships among geographically dispersed populations, through comparison of dental nonmetric traits (Cucina, 2015; Dicke-Toupin, 2012; Edgar, 2004; Horwath, 2012; Hubbard, 2012, Hubbard et al., 2015; Huffman, 2014; Irish et al., 2018. 2020; Marando and Silva, 2016; Relethford, 2004; Scherer, 2004, 2007). Patterns of genetic variation among geographically disperse populations can be characterized in two ways. Either increasing genetic differentiation and inter-population geographic separation, or up to a distance beyond which no biological correlation is detectable (Kimura and Weiss, 1964; Konigsberg, 1990; Relethford, 2004; Slatkin, 1993; Wright, 1943). Therefore, in situations where populations are relatively isolated from one another, genetic drift, as opposed to gene flow, will dominate the population structure (Konigsberg, 1990; Relethford, 2004; Slatkin, 1993). Regions with high levels of gene flow among groups will exhibit low levels of genetic variation. In contrast, regions with low levels of gene flow will be more genetically diverse (See page 113) (Konigsberg, 1990; Relethford, 2004; Slatkin, 1993). Limited dispersal results in genetic differences between populations proportional to the geographic distance which separates them (Kimura and Weiss, 1964; Konigsberg, 1990; Relethford, 2004; Slatkin, 1993; Wright, 1943). Thus, isolation by distance is used to help corroborate the genetic and ethnic affiliations among populations (Konigsberg, 1990; Relethford, 2004; Wright, 1943).

Wright (1943) introduced two different models of IBD; the first does not account for short-distance dispersal while in the second this dispersal is incorporated (Corre and Kremer, 1998; Kimura and Weiss, 1964; Konigsberg, 1990; Relethford, 2004; Wright, 1943). The former model is somewhat artificial and proposes that a meta-population (a group of spatially separated populations that interact through gene flow) is divided into two geographically, unique sub-populations between which gene flow occurs at random. Except for a proportion of migrants drawn at random from the meta-population (Kimura and Weiss, 1964; Konigsberg, 1990; Lalouel, 1977; Relethford, 2004; Wright, 1922, 1943, 1951). As this situation is most likely to occur within a group of islands, it is referred to as the island model. Though, this model is not likely to be exactly observed among other groups as gene flow from other neighbouring populations is not accounted for (Kimura and Weiss, 1964; Konigsberg, 1990; Relethford, 2004; Wright, 1943, 968, 1969). However, the dispersal of individuals is limited and short distance movements are usually predominant (Corre and Kremer, 1998; Kimura and Weiss, 1964; Konigsberg, 1990; Wright, 1943). Further, migrants entering populations are more likely to come from some neighbouring regions, or groups, than to be drawn at random from the entire meta-population, as is assumed in the island model (Kimura and Weiss, 1964; Konigsberg, 1990; Slatkin, 1993; Wright, 1943, 1978).

The latter model is more accurate, as a population is composed of continuously distributed individuals (Corre and Kremer, 1998; Konigsberg, 1990; Relethford, 2004). In absence of selection, genetic differentiation among sub-populations results from an equilibrium between genetic drift and gene flow (Boileau et al., 1992; Konigsberg, 1990; Malécot, 1973; Morton, 1973, 1977; Relethford, 2004; Slatkin and Maddison, 1990; Slatkin, 1993). Therefore, the degree of biological variation among these populations is related to gene flow, as it decreases the number of migrants per generation also decreases (Boileau et al., 1992; Konigsberg, 1990; Relethford, 2004; Slatkin and Maddison, 1990; Slatkin, 1993). Under this model, populations in remote locations may become genetically distinct simply due to geographic isolation, thus restricting the probability of genetic exchange with one another (Kimura and Weiss, 1964; Konigsberg, 1990; Morton, 1973). More distant populations will remain phenetically distinct for a longer period of time, and thus exhibit a weaker relationship between gene flow and distance (Kimura and Weiss, 1964; Konigsberg, 1990; Mantel, 1967; Schillaci et al., 2009). Local sub-populations are small in comparison to the meta-population and gene flow occurs exclusively within them (Kimura and Weiss, 1964; Konigsberg, 1990; Relethford, 2004). These groups subsequently experience differential rates of gene flow and inbreeding (See page 113) (Kimura and Weiss, 1964; Konigsberg, 1990; Malécot, 1973; Morton, 1973, 1977; Relethford, 2004; Slatkin and Maddison, 1990; Slatkin, 1993).

Chapter 5: Materials and methods

The core region is represented by the proto-Celtic Hallstatt D skeletal collection from Hallstatt (Austria) which comprises 44 recorded individuals (sample locations are presented in Figure 20). A group of isolated burials from the Stuttgart region in Germany that represents 43 documented individuals. The skeletal material was pooled to obtain an adequate sample size for statistical analysis. The burials represented by this collection are all temporally contemporaneous with the others and have similar burial features and customs. The cemetery population from Münsingen-Rain (Switzerland), which comprises a total of 77 individuals. The skeletal material from Nebringen (Stuttgart, Germany), that consists of 26 recorded and collected burials. The cemetery population from Pottenbrunn (Traisen valley, Austria), and includes 46 documented individuals and the skeletal collection from Dürrnberg (Austria), and comprises 128 individuals total (n=48 and 80 for the Hallstatt and La Tène phases, respectively). The expansion regions are represented by the skeletal collection from Radovesice I and II (Teplice, Czech Republic), which combined includes 57 recorded individuals. These collections were pooled to obtain an adequate sample size for statistical analysis. The cemetery population from Kutná-Hora-Karlov (Prague, Czech Republic), which consists of 48 documented individuals. The skeletal material from Wetwang Slack (east Yorkshire, Britain), which consists of a total of 180 individuals. The skeletal material from Rudston Makeshift (east Yorkshire, Britain), which comprises a total of 175 individuals, of which a sub-sample of 45 randomly chosen individuals were selected for analysis.

The comparative skeletal material is represented by the Pontecagnano collection from Campania (southern Italy). The entire skeletal collection from this site comprises 700 individuals, of which a sub-sample of 45 randomly chosen individuals dating to 650-260 BC were selected for analysis. The above cemetery populations will be discussed in detail in the following sections. The total number of individuals used in this analysis, adults and sub-adults, with permanent dentitions, for which dental nonmetric traits could be scored are presented in Table 8 (See page 181 for more information about the inclusion of adults and sub-adults in dental nonmetric trait analysis). Further only those individuals without severely worn dentitions were included in this analysis (the choice of dentitions that were used in this analysis is further discussed in the subsequent data collection section, page 181).

For all the samples, the previously established age-at-death-determinations and sex estimations published in the individual site reports were used. The specific age-at-death categories and sex estimations published in the individual site reports for the samples are provided in Appendix VIII (See page 181, Appendix VIII). These estimates were determined through analyses of tooth eruption, dental wear, epiphyseal and cranial suture closure, and examination of secondary sex characteristics of the skull as well as examination of the pelvis (Budinský and Waldhauser, 2004; Dent, 1983, 1984; D'Agostino, 1974; Fredericksen, 1974; Hodson, 1968, 1990; Krämer, 1964; Rabsiler et al., 2017; Stead, 1991a; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Valentová, 1991; Valentová and Sankot, 2012; Waldhauser, 1993, 1999; Wendling and Wiltschke-Schrotta, 2015; Wendling et al., 2015).

Table 8. The 12 samples used in this thesis and the number of individuals scored.

Samples	**Region**	**Date**	**Number of individuals scored**	**Total number of individuals recovered**
German (GER)[a]	Stuttgart, Germany	400-260 BC LTA-B/C	35	43
Nebringen (NEB)[a]	Stuttgart, Germany	400-250 BC LTA-B/C	22	26
Pottenbrunn (POTT)[a]	Traisen valley Austria	400-200 BC LTA-B/C	41	46
Hallstatt D (HalD)[a]	Hallstatt, Austria	650-350 BC HaD	42	44
Münsingen-Rain (MunRain)[a]	Münsingen Switzerland	420-240 BC LTA-C	42	77
Dürrnberg Hallstatt (DURH)[a]	Hallein, Austria	650/620-450 BC HaD	35	48

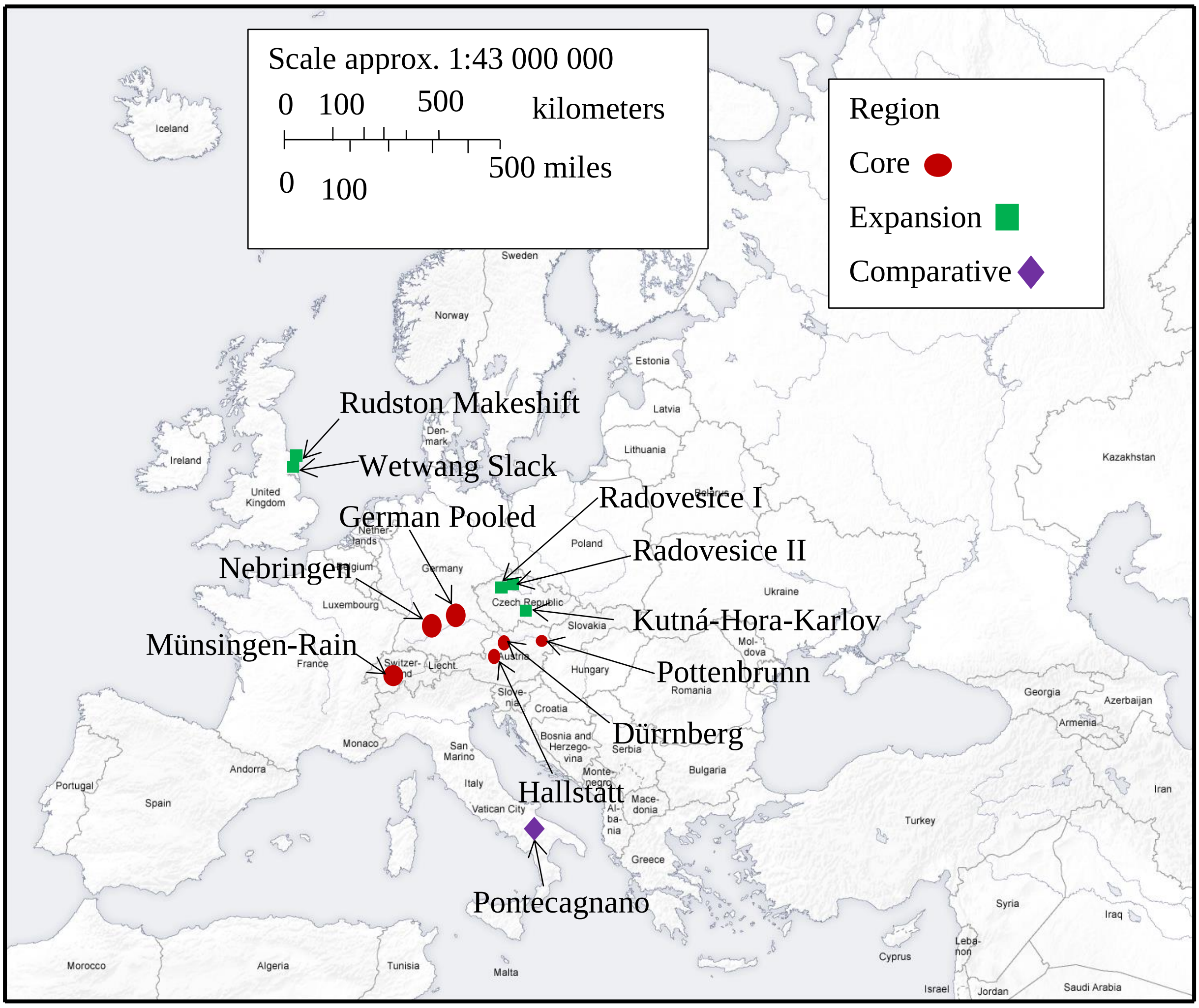
[a] Sample abbreviations used in subsequent Tables and Figures. German (GER); Nebringen (NEB); Pottenbrunn (POTT); Hallstatt D (HalD); Münsingen-Rain (MunRain); Dürrnberg Hallstatt (DURH); Dürrnberg La Tène (DURL); Kutná-Hora-Karlov (KHK); Rudston Makeshift (RUD); Wetwang Slack (WWS); Pontecagnano (PON).

Table 8 continued. The 12 samples used in this thesis and the number of individuals scored.

Samples	**Region**	**Date**	**Number of individuals scored**	**Total number of individuals recovered**
Dürrnberg La Tène (DURL)[a]	Hallein, Austria	450-150 BC LTA-C	67	80
Radovesice (RAD)[a]	Teplice, Czech Republic	380-250 BC LTB-C	40	57
Kutná-Hora-Karlov (KHK)[a]	Prague, Czech Republic	380-250 BC LTB-C	37	48
Rudston Makeshift (RUD)[a]	east Yorkshire, Britain	400-100 BC LTB-D	40	45
Wetwang Slack (WWS)[a]	east Yorkshire, Britain	400-100 BC LTB-D	150	180
Pontecagnano (PON)[a]	Campania, Italy	650-260 BC HaD-LT B/C	35	700

[a] Sample abbreviations used in subsequent Tables and Figures. German (GER); Nebringen (NEB); Pottenbrunn (POTT); Hallstatt D (HalD); Münsingen-Rain (MunRain); Dürrnberg Hallstatt (DURH); Dürrnberg La Tène (DURL); Kutná-Hora-Karlov (KHK); Rudston Makeshift (RUD); Wetwang Slack (WWS); Pontecagnano (PON).

Figure 20. Map of Europe with sample locations designated (Figure modified from generic mapping tools).



Core region samples

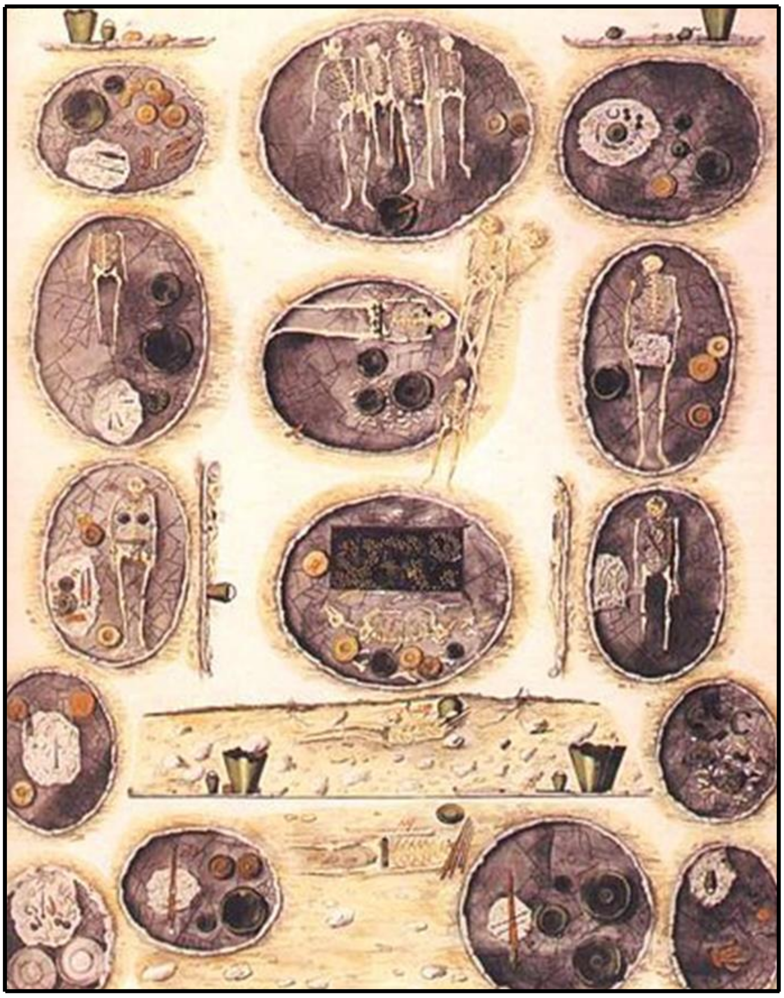
Hallstatt D, Austria

The Hallstatt cemetery is located in the Salzkammergut region of Austria, where the majority of the material evidence associated with the Hallstatt culture was first identified (Figures 1, 20 and 21) (Hodson, 1990). Initial excavations from 1846-1863, led by Johann Georg Ramsauer, revealed 980 graves. Subsequent excavations continued off and on until 1899, and again from 1937-1939 yielding a total of 1,045 burials (Hodson, 1990). The majority of the recovered skeletal material from this cemetery is fragmentary, therefore it is difficult to adequately determine the age-at-death and estimate sex of the recovered individuals (See Table 8 and Appendix VIII for the age-at-death estimates, the methods used by the recording archaeologist to estimate sex and the number of individuals included in this analysis). Further, the majority of the burials dating to the earlier periods, specifically the HaA-C periods, were cremations (Hodson, 1990). Thus, it is not possible to determine the above categories for the majority of the recovered skeletal material (Hodson, 1990). However, age-at-death could be determined for most of the individuals recovered from the HaD section of this cemetery, as inhumations are common during this period (Appendix VIII) (Hodson, 1990).

Those analysed in this thesis represent a group of 44 burials excavated by Frederick Morton in 1937-1939 and date to 650-350 BC, representing the HaD period specifically (Table 8, page 19) (Hodson, 1990). The majority of the burials were supine and extended, aligned north-south and facing north. However, flexed burials facing east or west have also been found (Hodson, 1990). Artefacts are comparatively numerous and include fibulae; rings; bracelets; torcs; gold and silver items; pottery; bronze vessels; swords; daggers; spears; and Mediterranean imports, including wine flagons and jugs (See page 19) (Hodson, 1990). Although the above artefacts have been documented, they have not been described in detail and have only been described as being characteristic of the Hallstatt period (Hodson, 1990). Regional comparisons to those from other Hallstatt and La Tène period cemeteries have not been conducted (Hodson, 1990). The cemetery population has been the subject of limited previous research (Anctil, 2016; Collis, 1986; Hodson, 1990; Hopkins, 1957). However, the majority of these studies have focused on general descriptions of the artefacts and cemetery (Collis, 1986; Hodson, 1990; Hopkins, 1957).

The cemetery population has been the subject of a previous biodistance analysis, as previously mentioned (Anctil, 2016). However, this analysis utilized a randomly selected sub-sample from the HaD period, n=30 (>17 years old), due to time constraints. Since the author’s first study the remaining 12 individuals, with dentitions (>17 years old) were included in this analysis (Table 8). Enabling all the available dentitions from the site to be included in this research (See page 138). It has been suggested that the population was of high status, and therefore wealthy, due to the presence of prestige items and the nearby salt mine that enabled the population to have control of a viable commodity (Adshead, 1992; Barth, 1991; Cavruc and Harding, 2012; Hodson, 1990; Nenquin, 1961).

Figure 21. Drawing commissioned by Johann Ramsauer documenting the cemetery at Hallstatt, Austria, watercolour painting done by a local artist (Johann Georg Ramsauer, 1874. Original scale not provided, original figure number unknown).



German pooled sample, Stuttgart, Germany

This sample dates from the LTA-B/C period, based on associated artefacts, and consists of 43 geographically isolated burials that are dispersed throughout Stuttgart, southern Germany (Figures 1 and 20) (Table 8, Appendix VIII). These burials were excavated during the early to mid to late 1900s (Balkwill, 1976; Burmeister et al., 2000; Dehn, 2013; Ebrecht et al., 2014; Gleirscher, 2006; Miron, 2012; Müller-Scheeßel, 2007; Paret, 1924, 1938; Stuck, 1985). However, the initial excavation reports for these burials have been lost. Therefore, the exact excavation dates, the specific burial locations, age-at death determinations and methods used to estimate the sex of these individuals are not available (Appendix VIII) (Burmeister, 2000; Gleirscher, 2006; Müller-Scheeßel, 2007). Consequently, these burials are described as being located within a broad geographic region, i.e., Stuttgart, Germany, rather than according to specific individual locations (Burmeister, 2000; Gleirscher, 2006; Müller-Scheeßel, 2007). Further, the age-at-death categories and sex estimations for these individuals are described on a case-by-case, or individual, basis e.g., adult male (Appendix VIII) (Burmeister, 2000; Dehn, 2013; Ebrecht et al., 2014; Gleirscher, 2006; Miron, 2012; Müller-Scheeßel, 2007; Stuck, 1985). It is unknown whether they initially formed part of a larger cemetery that was lost through taphonomic processes, such as erosion, construction, agricultural processes or; whether they represent isolated burials relating to deaths that occurred during the course of migration through the region (Balkwill, 1976; Burmeister et al., 2000; Dehn, 2013; Ebrecht et al., 2014; Gleirscher, 2006; Miron, 2012; Müller-Scheeßel, 2007; Paret, 1924, 1938; Stuck, 1985).

The burials comprising this sample include; Inringen (n=6); Gundlingen (n=6); Mullheim-Dattingen (n=3); Stuttgart Zuffenhausen (n=3); Birkenfeld (n=5); Tubingen Drendingen (n=3); Stuttgart Zuf Rotwegsiedlu (n=3); Korntal Leonb (n=3); Kircheim (n=3); Waiblingen Flur Wasserst (n=3); Korntal Seewaldberg (n=4) and Cannstatt (n=1) (See page 138) (Table 8, Appendix VIII) (Ebrecht, 2014; Müller-Scheeßel, 2007; Paret, 1924; Struck, 1985; Werner, 1938). Some of the above burials, e.g., Inringen, Gundlingen and Birkenfeld have been suggested to represent the remnants of larger cemeteries (Burmeister, 2000; Ebrecht et al., 2014; Miron, 2012; Stuck, 1985). However, these burials are dispersed and construction within these regions did not uncover any further burials (Burmeister, 2000; Dehn, 2013; Ebrecht et al., 2014; Miron, 2012; Stuck, 1985). Consequently, these burials were regarded as isolated burials in this analysis.

The majority of the above burials are oriented north-south, either flexed or extended and facing east (Balkwill, 1976; Burmeister et al., 2000; Dehn, 2013; Ebrecht et al., 2014; Gleirscher, 2006; Miron, 2012; Müller-Scheeßel, 2007; Paret, 1924, 1938; Stuck, 1985). These burials have not been the focus of much research since their initial discovery, other than general grave and artefact descriptions (Balkwill, 1976; Burmeister et al., 2000; Dehn, 2013; Ebrecht et al., 2014; Gleirscher, 2006; Miron, 2012; Müller-Scheeßel, 2007; Paret, 1924, 1938; Stuck, 1985). This sample was included in subsequent analyses in order to explore the population history in the region.

Münsingen-Rain, Switzerland

Münsingen-Rain is one of the largest La Tène period cemeteries in Switzerland and is located south-east of the small town of Münsingen, which is situated in the Aar Valley between the regions of Thun and Bern and dates to 420-240/150 BC (Figures 1, 20 and 22) (Hodson, 1968, 1998; Hung, 1962; Jud, 1998; Müller et al., 2008; Stockli, 1975; Wiedmer-Stern, 1908). The cemetery was discovered in 1906 on a small plateau of a river terrace during gravel quarrying (Hodson, 1968; Hung, 1962; Jud, 1998; Müller et al., 2008; Wiedmer-Stern, 1908). Subsequent excavations in 1906 led by Jakob Wiedmer-Stern uncovered 220 graves, of which skulls of 77 individuals total, those that were determined to have "superior" preservation, were recovered and collected (Figure 22, Table 8, Appendix VIII) (Hodson, 1968; Hung, 1962; Jud, 1998). However, the remaining skeletal material was documented but not removed and was subsequently reburied (Hodson, 1968; Jud, 1998; Wiedmer-Stern, 1908).

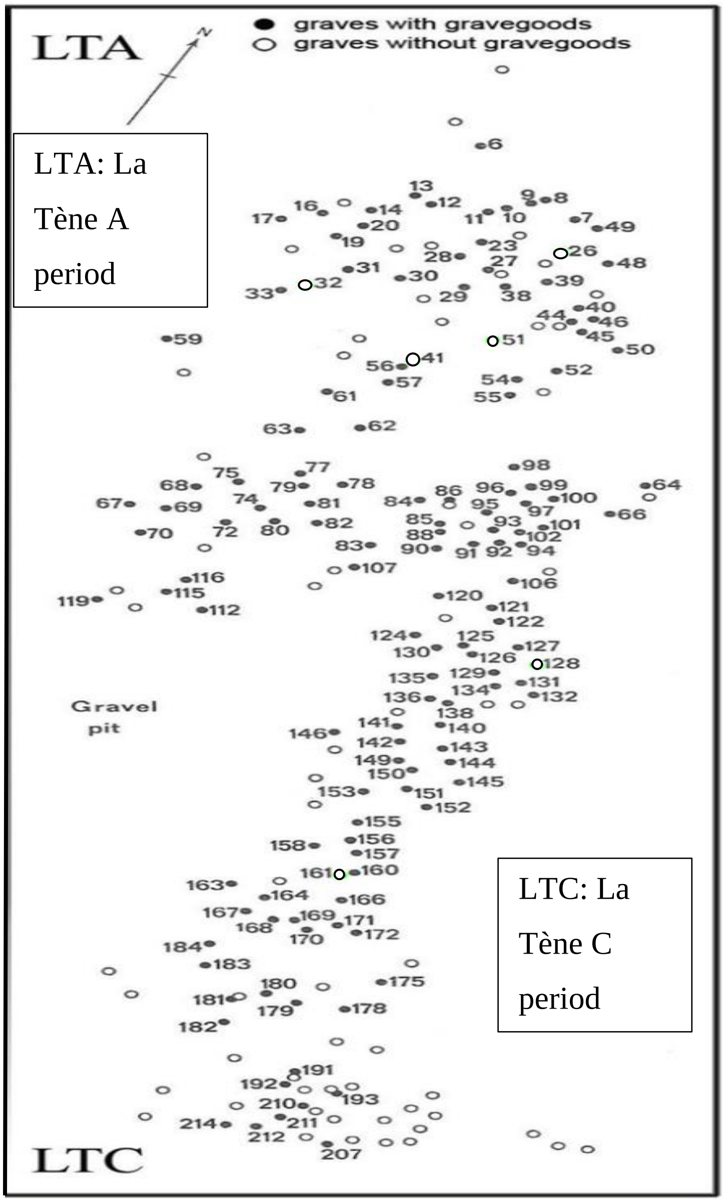
The majority of the burials were supine and extended, aligned north-south facing north. However, there are instances of flexed burial positions facing east or west sometimes with evidence of a wooden or makeshift stone coffin (Hinton, 1986; Hodson, 1968; Müller, 1998; Müller et al., 2008; Wiedmer-Stern, 1908). There does not appear to be any segregation based on sex or age (Hodson, 1968). The northern part of the cemetery dates to the LTA period, while the burials at the southern end of the cemetery date to the LTC period (Table 8). An abundance of artefacts have been recovered from this cemetery; such as fibulae; bracelets; torcs, bronze vessels; wheel-turned pottery; glass beads; gold and silver items (See page 32) (Figures 8-11) (Hodson, 1968; Kaenel, 1990). Some of the sub-adult burials (e.g., >17 years of age) were accompanied by artefacts typically found with adult females, such as jewellery, while some burials contained no artefacts at all (Hodson, 1964; Hung, 1962; Jud, 1998). Weapons and lances also have been recovered from male graves. The abundance of prestige grave goods, such as Mediterranean imports, gold and silver items, have been argued to indicate the cemetery was used by the inhabitants of a small settlement community composed of high-status individuals (Alt et al., 2005; Hinton, 1986; Martin-Kilcher, 1973).

The artefacts also suggest a degree of mobility within the burial community (Moghaddam et al., 2014, 2016; Scheeres, 2014a). Some of the fibulae, bracelets, and materials, such as amber, have connections to eastern Belgium, Luxembourg, the Hunsrück-Eifel (western Germany), and Baden-Württemberg (southwest Germany) regions (See page

32) (Hodson, 1964; Müller, 1998; Müller et al., 2008). However, these items are predominately associated with the LTA and LTC period graves, suggesting differential access to trade items through time (Table 8) (Hodson, 1964; Müller et al., 2008). Although the skeletal material recovered from Münsingen-Rain (Switzerland) has been the focus of a wide range of previous research; these analyses have been limited due to the condition of the collection, i.e., only skulls are available (Hinton, 1986; Hodson, 1968; Kutterer and Alt, 2008; Martin-Kilcher, 1973; Moghaddam et al., 2014, 2016; Müller, 1998; Müller et al., 2008). Previous research includes skeletal inventories, morphological kinship analyses based on epigenetic characteristics of the skull, stable isotope analysis, craniometric, and aDNA analyses (See page 61) (Hinton, 1986; Hodson, 1968; Kutterer and Alt, 2008; Martin-Kilcher, 1973; Moghaddam et al., 2014, 2016; Müller, 1998; Müller et al., 2008; Uerpmann, 2005). Typological and chronological artefact inventories have also been conducted. However, they have not been compared to those from other regions across continental Europe (Hinton, 1986; Hodson, 1968). A biodistance analysis has also been performed, to determine whether the population shared any biological affinity to those from the previous proto-Celtic period, specifically Hallstatt D (Austria) (Anctil, 2016).

The subsequent statistical analysis supported phenetic divergence among the proto-Celtic Hallstatt D (Austria) and La Tène Münsingen-Rain (Switzerland) samples (Anctil, 2016). Although these initial results indicated phenetic heterogeneity, biological diversity, between the above samples, the extent of this variation throughout the regions associated with Celtic material culture is still unknown. Therefore, the skeletal material from this cemetery was included in the present analysis. The previous analysis was conducted on a sub-sample of the available skeletal material, n=33, (>17 years old). However, since the author’s first study, additional skeletal material was available, n=9 (>17 years old), and was subsequently incorporated into this analysis. Enabling all the available dentitions from the site to be included in this research (See page 138).

Figure 22. Distribution of graves within the La Tène cemetery of Münsingen-Rain (Switzerland) (Modified from Hodson, 1968, Figure 2. Original scale not provided).



Morphological kinship analyses have been argued to indicate a high degree of homogeneity among the burial community, based on retention of the metopic suture (a cranial suture between the two halves of the frontal bone) (Hauschild, 2010a, b; Kutterer and Alt, 2008). Although the retention of this suture may appear to support the initial interpretation of a small closely related settlement community, it is only present in 4 adults (aged 20-50) who are not spatially restricted within the cemetery (Appendix VIII) (Alt et al., 2005; Barnes, 1994, 2012; Hauschild, 2010a, b; Kutterer and Alt, 2008). This interpretation is also supported by the stable isotope evidence, as only 14.7%, 5 out of 34 individuals were found to be non-local (See page 61) (Moghaddam et al., 2014; Scheeres, 2014a). The third molars and human ribs, or rib fragments were predominantly used in the above stable isotopic analyses (Moghaddam et al., 2014; Scheeres, 2014a; Scheeres et al., 2014b). Although in 3 cases the first or second molar was used in order to obtain the $^{87}Sr/^{86}Sr$ and O^{18} values, as the third molar was not available for analysis or due to severe dental wear (Moghaddam et al., 2014; Scheeres, 2014a; Scheeres et al., 2014b). In these cases the level of wear on the teeth selected for analysis was severe and no nonmetric traits could be observed. Therefore, these teeth were also too worn for inclusion any subsequent dental nonmetric trait analysis (Moghaddam et al., 2014; Scheeres, 2014a; Scheeres et al., 2014b) (See page 181 for a discussion of dental wear and nonmetric traits, Figure 34 for an example of severe dental wear and Appendix III). However, the majority of the individuals identified as non-local were not specifically from the LTA period; only 18 out of 34 individuals were from this period (See page 61) (Moghaddam et al., 2014; Scheeres, 2014a). As such it is difficult to determine whether the above migration rate is consistent with this period or cemetery overall. The low frequency of non-local individuals also supports the notion that extra-regional contacts and migration into the region may have been limited to trade, small-scale migration or individual movement (Alt et al., 2005; Moghaddam et al., 2014; Scheeres, 2014a).

Cranial deformations and possible deformations have also been identified within the burial community, 10 and 28 respectively, and are present in all chronological phases (Alt et al., 2005; Kutterer and Alt, 2008; Müller et al., 2008). These deformations were initially argued to have been intentional and to represent an elite group within the cemetery (Alt et al., 2005; Müller et al., 2008). However, subsequent CT scans have indicated that some of the deformations, n=10, were the result of abnormal suture closure (Kutterer and Alt, 2008). Probable deformations, n=28, were determined to be the result of taphonomic processes during burial (Kutterer and Alt, 2008). Further, those individuals with either of the above deformations were not restricted to a specific area of the cemetery (Kutterer and Alt, 2008). Therefore, these deformations as an indicator for genetic relationships among the burial community remains questionable. Although aDNA analyses have been conducted, the samples contained insufficient traces of aDNA (Uerpmann, 2005).

Nebringen, Stuttgart, Germany

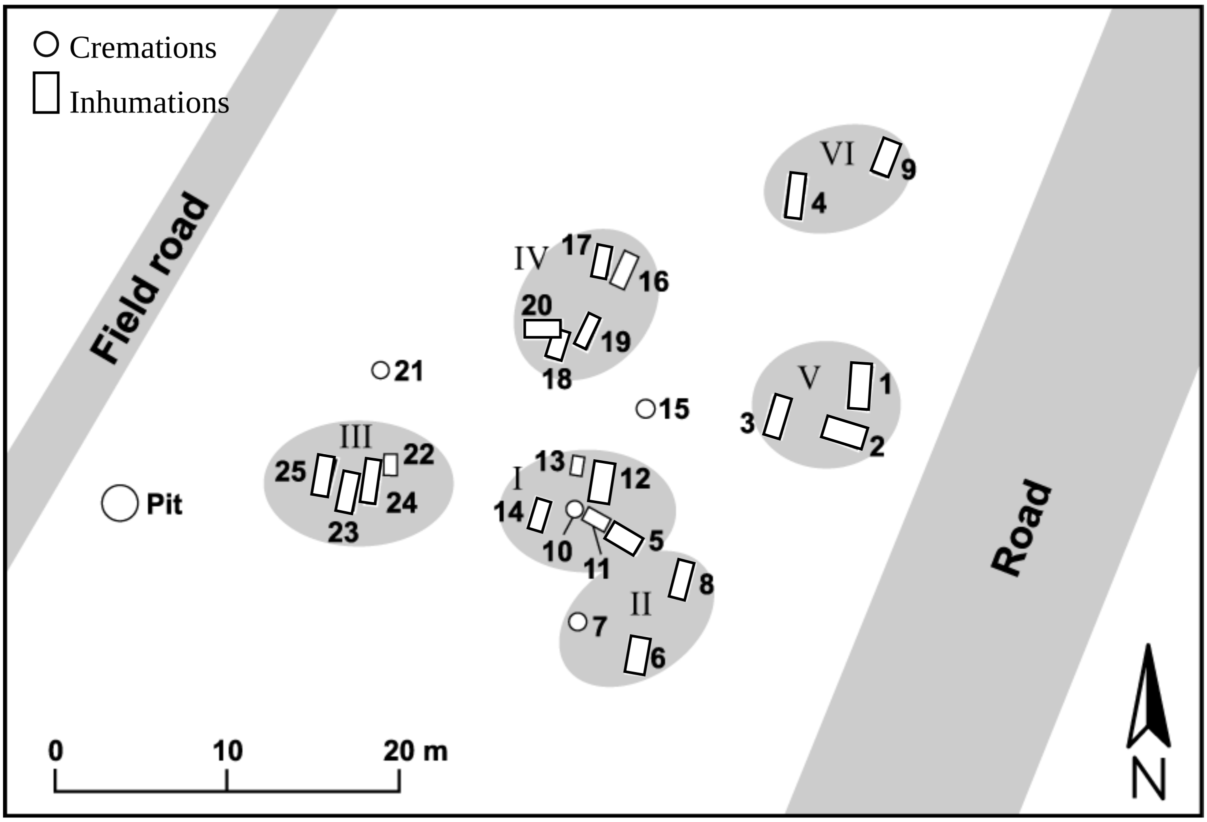
The cemetery of Nebringen “Baumsacker” is located about 35 km southwest of Stuttgart and dates to 400-250 BC (Figures 1, 20 and 23) (Krämer, 1964). During road construction in 1959, 6 graves were discovered (Krämer, 1964). Subsequent rescue excavation in 1959 uncovered 26 burials, 21 inhumations, 4 cremations and a few isolated skeletal fragments from an additional unidentified grave (See page 138) (Table 8, Appendix VIII) (Krämer, 1964). Some burials are believed to have been lost due to construction, agricultural or taphonomic processes, such as erosion. Consequently, the number of burials is believed to have been as high as 35 (Krämer, 1964, 1966; Scholz et al., 1999). Further, in spite of rescue attempts, during the 1959 excavations, several burials and associated artefacts were destroyed, notably the so-called chief’s burial, grave number 11 (Krämer, 1964, 1966). Thus, limited skeletal and archaeological material remains for analysis (Krämer, 1964, 1966; Scheeres, 2014a; Scholz et al., 1999). Limited previous analyses have been conducted on the recovered skeletal material and artefacts (Krämer, 1964; Maraz, 1977; Scheeres, 2014a; Scholz et al., 1999).

The majority of these analyses have focused on chronological descriptions (Krämer, 1964; Maraz, 1977), although a stable isotopic analysis examining mobility among the burial community has been conducted (See page 61) (Scheeres, 2014a). The burials form approximately 6 groups the majority of which were extended and supine, oriented approximately northeast to southwest and facing west. However, flexed burials oriented east-west facing east, sometimes with evidence of a coffin, and one prone burial have also been found (Krämer, 1964, 1966; Scheeres, 2014a). Though, the material from which the documented coffins were constructed is not reported. These included the so-called warrior burials and 1 sub-adult burial (Krämer, 1964, 1966; Scholz et al., 1999). As most burial groups contained the burials of both sexes as well as sub-adults and both high and low-quality artefacts, the groupings may be arranged according to family association rather than social status (Appendix VIII) (Krämer, 1964, 1966; Scheeres, 2014a).

No temporal variation in burial practices is evident during the use of the cemetery. The cremation burials, rather than representing a shift in burial practices, are believed to have occurred at or around the same time as the inhumations, since they are found within the same stratigraphic level (Scheeres, 2014a; Scholz et al., 1999). As the burials are shallow it has been suggested that others, inhumations and/or cremations, may have been lost (Krämer, 1964, 1966). However, the approximate grave depth is not provided (Krämer, 1964, 1966). The cemetery was used for approximately 150 years (Scheeres, 2014a). This relatively short duration may suggest that the cemetery was abandoned after a settlement collapse. This notion is also supported by the continuous cemetery use throughout the LTB and C periods in the southern Bavarian Alpine foothills (southern Germany) and the Danube Valley (Austria, Slovakia, Hungary, Croatia, Serbia, Romania, Bulgaria, Moldova, and Ukraine) (Krämer, 1964; Maraz, 1977). The apparent settlement abandonment in the Württemberg region (southwest Germany bordering Switzerland and France), during this period also supports this presumption (Kimmig, 1983; Krämer, 1964; Scholz et al., 1999). This has been argued to provide further evidence of migration into the surrounding regions during this period (Scheeres, 2014a). Although, it has also been suggested that Nebringen (Stuttgart, Germany) was populated by a small community of farmers and was subsequently abandoned as a result of deteriorating climate conditions (See page 61) (Krämer, 1964, 1966). However, there is no evidence of these conditions affecting the population at Nebringen (Stuttgart, Germany) or those in the above regions (Kimmig, 1983; Krämer, 1964; Scholz et al., 1999). Therefore, abandonment during the LTB/LTC period may have been the result of a breakdown or rerouting of trade routes. However, as the cemetery was destroyed during construction and has not been the focus of much research, it is possible that this evidence was lost. Consequently, climate change cannot be ruled out as a cause for settlement abandonment. The notion of access to trade items, or routes, as an underlying cause for abandonment and subsequent migration is partly supported by the recovered artefacts.

The majority of the artefacts include fibulae; bracelets; torcs; bronze items; swords and some prestige items, such as a gold torc (Krämer, 1964, 1966; Maraz, 1977). A helmet and gold torc have also been recovered from the so-called chief’s burial. The presence of these prestige items resulted in this designation; however, this individual may also have been a warrior (See pages 32 and 61) (Krämer, 1964; Maraz, 1977; Scholz et al., 1999). However, as this grave was almost entirely destroyed by construction, it is unknown whether other prestige items, or weapons were lost (Krämer, 1964, 1966; Scholz et al., 1999). Further, the presence of a gold torc in this burial distinguishes it from the other warrior burials, which only have swords, or remnants of, preserved (Krämer, 1964, 1966). Consequently, it is difficult to determine whether the above proposed designations are accurate.

Figure 23. The cemetery of Nebringen-Baumsäcker. The grave groups I to VI represent the assumed familial groups. Circles represent child burials while rectangles represent adult burials (Modified from Krämer, 1964, Figure 2).



Although the above artefacts have not been the focus of much research, and have only been vaguely described, there is some evidence of extra-regional contact (Krämer, 1964, 1966; Maraz, 1977; Scholz et al., 1999). A fibula similar in construction to those recovered from Hungary and Romania suggest some form of contact between these regions (Krämer, 1964; Maraz, 1977; Scheeres, 2014a). However, as there is limited archaeological evidence of extra-regional contact, the population at Nebringen (Stuttgart, Germany) is believed to have had limited access to trade items and/or routes (Krämer, 1964, 1966; Maraz, 1977; Scheeres, 2014a). This notion is supported by stable isotope analyses as 88%, 15 out of 17 individuals selected based on archaeological criteria, of the population was found to be local (See page 61) (Scheeres, 2014a). The same dental and human skeletal elements used at Münsingen-Rain (Switzerland) were primarily used for the above stable isotopic analyses (Scheeres, 2014a; Scheeres et al., 2014b). Consequently, the ability to observe and record dental nonmetric traits was not affected. However, in a few cases, 2 individuals, the first or second molar was used in place of the third, because the third molar was not available for analysis or due to severe dental wear (Scheeres, 2014a; Scheeres et al., 2014b). The first or second molars that were selected for stable isotopic analysis were also severely worn, therefore they could not be included in any subsequent dental nonmetric trait analysis (Scheeres, 2014a; Scheeres et al., 2014b) (See page 181 for a discussion of dental wear and nonmetric traits, Figure 34, for an example of severe dental wear and Appendix III).

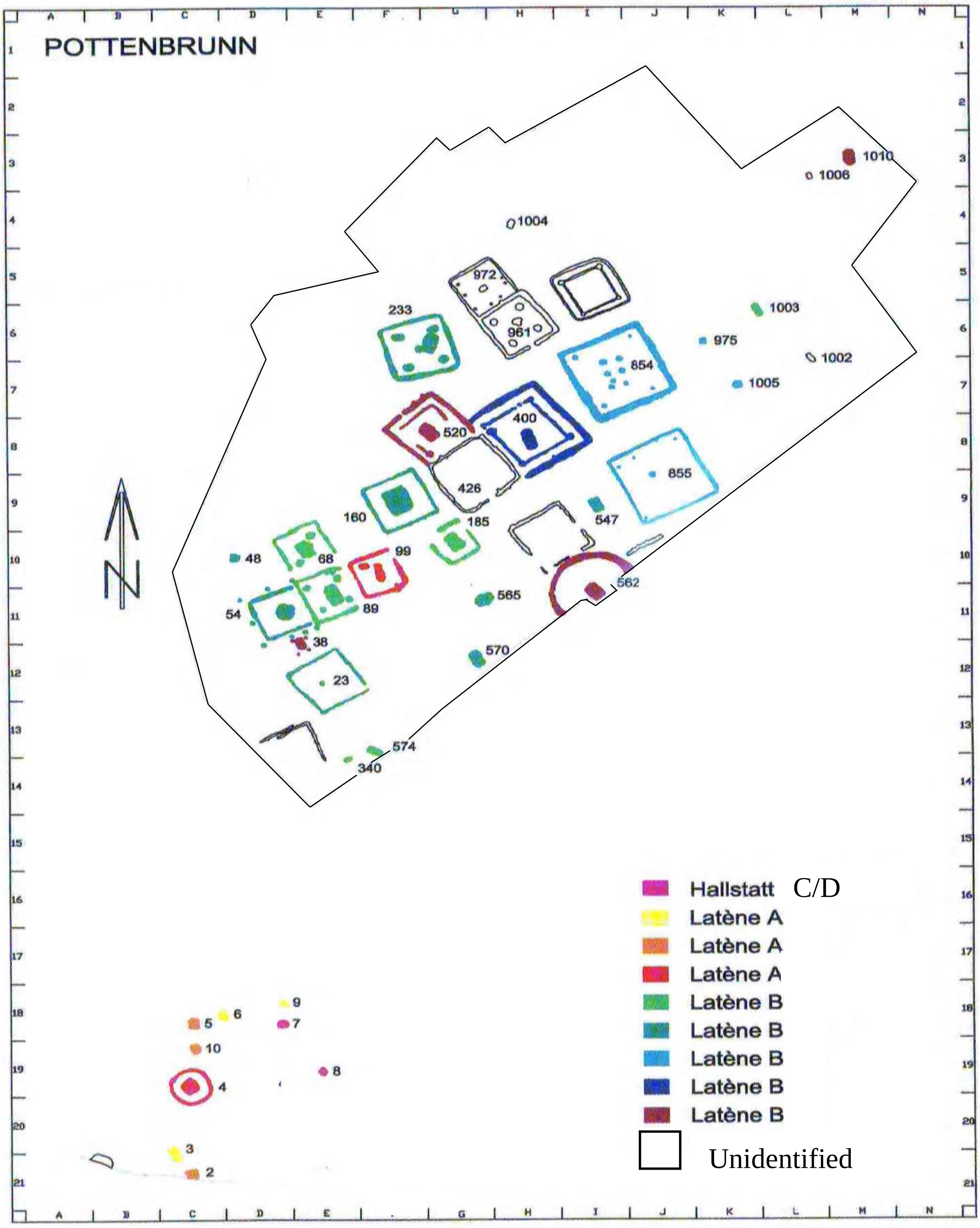
Pottenbrunn, Austria

Pottenbrunn is located in northeast Austria, on the southwestern edge of the district of St Pölten (northeast, Austria) and dates from the HaC/D-LTA-B/C periods (Figures 1, 20 and 24) (Table 8) (Neugebauer, 1991; Ramsl, 2002). This cemetery was discovered in the 1930s during the rebuilding of the old federal road between Pottenbrunn and Ratzersdorf (Ramsl, 2002). Subsequent excavations led by J Bayer uncovered 2 burials dating to the HaC/D period and 12 graves dating to the La Tène period 4 additional burials dating to the Bronze Age were also discovered nearby (Bayer, 1930; Neugebauer, 1991; Ramsl, 2002). However, the proximity of these burials to the Pottenbrunn (Austria) cemetery is not described. It is also unknown whether these burials were part of a larger nearby cemetery or were part of Pottenbrunn (Austria) (Neugebauer, 1991; Ramsl, 2002). Rescue excavations continued off and on until 1982 under JW Neugebauer and P Scherrer (Neugebauer, 1991, 1992; Ramsl, 2002). In total, 46 inhumations, including several double burials, and 11 cremations were uncovered, most of which were surrounded by enclosure ditches (Figure 24, page 138 and Appendix VIII) (Ramsl, 2002). Numerous additional burials without preserved skeletal material were also uncovered throughout the course of the above excavations (Ramsl, 2002). However, the burials were not provided with a specific numerical sequence and are therefore not sequential (Ramsl, 2002). All of the site features, such as enclosure ditches and post holes, were catalogued using the same numerical scheme.

Most of the individuals buried at Pottenbrunn (Austria) were buried in a supine and extended position aligned northeast-southeast and facing north often with evidence of a coffin (Ramsl, 2002). However, the material used to construct the coffins is not reported. Additional burial positions including, flexed burials, facing east or west have also been documented. The cemetery population from Pottenbrunn (Austria) has been the focus of some research over the years (Ramsl, 2002, 2003, 2012a, b, 2018). However, these studies have focused on chronological descriptions of the artefacts and general descriptions of the cemetery (Ramsl, 2002). Some attempts at regional comparisons have been conducted, however, in regard to specific artefacts or burials (Ramsl, 2002, 2012a, b). The majority of the single inhumations are rectangular or circular in shape, whereas both are evident in the cremation and double burials (Ramsl, 2002). There is no evidence for a diachronic change in burial practices, as both appear to have occurred simultaneously (Ramsl, 2002). The cremation burials are believed to have been interred in pottery vessels, as pottery sherds have been found associated with the majority of these burials (Ramsl, 2002). Several burials have post holes nearby or surrounding them, although the exact number is not quantified. The purpose of these post holes is debated (Ramsl, 2002). Although they are believed to represent mortuary houses, it has also been suggested that they were used to designate specific burials, e.g., elites (Ramsl, 2002, 2012a, b). Alternatively, it has been suggested that their presence represented some element of the burial practices in Pottenbrunn (Austria), such as temporarily distinguishing the burial (Ramsl, 2002, 2012a, b). However, the construction of mortuary houses is the more commonly accepted interpretation (Ramsl, 2002, 2012a, b).

An abundance of artefacts have also been recovered, including fibulae; rings; bracelets; gold and silver items; pottery and/or bronze vessels; swords; daggers; knives; spears; lances; Mediterranean imports (including wine flagons and jugs); gifts of meat (e.g., sheep); and decorated iron rods (See page 32) (Ramsl, 2002, 2012a, b). These rods have been described as scepters although their exact purpose is unknown (Ramsl, 2002, 2012a, b). Other prestige items include a sword scabbard decorated with gold foil and a hollow bronze pendant that had been silver coated (Ramsl, 2002). Several intra-and-extra regional connections have been suggested based on the above artefacts (Charpy, 1991; Penninger, 1975; Ramsl, 2002, 2012a, b). Similarities in fibulae to those from Dürrnberg (Austria) have been documented (Table 5) (Ramsl, 2002, 2012a, b). Extra-regional connections have also been described based on fibulae, bracelets and Ornaments of false-filigree, to northwestern Switzerland, the Rhineland (west Germany), and the Champagne region (northeast France), respectively (See page 32) (Charpy, 1996, 2009; Furger-Gunti, 1982; Penninger, 1975; Ramsl, 2002, 2012a, b).

Figure 24. The cemetery of Pottenbrunn (Austria) (Modified from Ramsl, 2002, Figure 3. Original scale not provided).



Further connections have also been suggested based on an ornamental pin which is described as being similar to those from the Balkan regions (Southeast Europe) (Ramsl, 2002, 2012a, b; Stoianovich, 2015). However, the exact nature of these connections has not been described in detail, only their possible presence has been mentioned (See page 32) (Charpy, 1991; Penninger, 1975; Ramsl, 2002). Therefore, it is not clear if the above connections are based on artefacts, art styles and/or mechanical construction. Evidence of both diverse and far reaching regional connections suggests that the burial community at Pottenbrunn (Austria) had access to a trade route(s) that enabled them to obtain prestige items (Charpy, 1991; Penninger, 1975; Ramsl, 2002).

Dürrnberg, Austria

This cemetery is located in the region of Dürrnberg and was excavated in an ad hoc manner. Various burial grounds, or grave fields, were discovered through the course of construction and subsequent excavation during the 19th century (Figures 1, 20 and 26) (Lavelle et al., 2019; Moosleitner, 1991; Rabsiler et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2012, 2014, 2015; Wendling et al., 2015). Consequently, the material excavated from the cemetery was published initially as a series of different connected grave fields, including Friedhof, Lettenbuhl, Romersteig and Eislfeld. Although Friedhof and Lettenbuhl were initially believed to be two separate grave fields, subsequent excavations revealed they were connected (Tiefengraber and Wiltschke-Schrotta, 2014). However, they are still described according to their initial separate designations. Further, these different grave fields, overall, are believed to represent one burial community, as they possess similar material culture, burial practices, are in close geographic proximity and were inhabited at the same time (Stöllner, 1998; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015). Subsequent publications have followed this initial format for the sake of continuity, therefore, the cemetery information presented in this thesis will also follow this format.

Dürrnberg is located in the Hallein region of Salzburg, Austria. The cemetery, overall, was used from the HaD-LTC period (Table 8) (Moosleitner, 1991; Rabsiler et al., 2017; Stöllner, 1998; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015; Wendling et al., 2015). Excavations in the Eislfeld, Friedhof and Lettenbuhl areas began in 1928-1932 led by O Klose and E Penninger after construction uncovered 6 burials (Klose, 1932; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015). There are some descriptions from these early excavations, but no drawings from this excavation phase exist. Subsequent excavations were conducted from 1979-1982 in

Romersteig, from 1983-1984, briefly in 1987, and from 1996-1997 in Friedhof and Lettenbuhl, led by F Moosleitner, JW Neugebauer and K Zeller, respectively (Neugebauer, 1983, 1984; Tiefengraber and Wiltschke-Schrotta, 2015; Zeller, 1997, 2001). During the 1983-1984 excavations, a settlement area near the Friedhof and Lettenbuhl grave fields was uncovered (Tiefengraber and Wiltschke-Schrotta, 2015). Although Friedhof, Lettenbuhl and Romersteig were excavated in response to construction, during the above periods, Eislfeld was excavated continuously from 1963-1997 (Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015).

The above excavations were accompanied by a significant improvement in documentation, which allowed for a re-assessment of the initial excavations (Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015). Consequently, it was determined that the 1928-1932 excavations only recorded the richer graves (Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015). Subsequently, throughout the course of the above excavations, these burials were re-examined on-site and the poorer burials were recorded (Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015). The recovered skeletal material has been the focus of a wide range of previous research, and is one of the most important reference sites for the chronology of the Hallstatt and the La Tène periods in the region (Lavelle and Stöllner, 2018; Neugebauer, 1983, 1984; Rabsiler et al., 2017; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015; Zeller, 1997, 2001). These previous studies have focused on chronological descriptions of the artefacts, general descriptions of the cemetery, dental and skeletal inventories and pathological and trauma documentation. However, these analyses were largely site specific with little attempt at regional comparisons (Lavelle and Stöllner, 2018; Neugebauer, 1983, 1984; Zeller, 1997, 2001).

Although previous analyses have been conducted on the skeletal material, they have been limited due to the condition of the collection. The majority of the skeletal remains from Dürrnberg (Austria) are very poorly preserved and some are fragmented (Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015). Several graves, up to 36%, 40 burials, in most of the grave fields contained no skeletal remains, which is likely due to the unsystematic initial excavations (Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015). There are several instances of multiple burials and grave reuse, as 17 individuals have been recovered from one grave, e.g., Romersteig (Tiefengraber and Wiltschke-Schrotta, 2015;

Wendling and Wiltschke-Schrotta, 2015). Numerous burials also have evidence of secondary and/or reburial, grave robbery and evidence of later period graves cutting into those from the preceding period (Rabsiler et al., 2017; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015; Wendling et al., 2015). Therefore, it is unknown whether the different temporal phases also correspond to a concomitant biological change. Consequently, for this analysis, the cemetery was divided into two phases, Dürrnberg Hallstatt and Dürrnberg La Tène, in order to determine whether a biological change was evident between these phases. The total number of individuals, adults and sub-adults with permanent dentitions (>17 years old) assigned to either the Hallstatt D or La Tène periods were used to construct the above temporal periods used in this analysis (Appendix VIII). Overall, 307 individuals have been recovered from the Friedhof, Lettenbuhl, Romersteig and Eislfeld grave fields within the Dürrnberg (Austria) cemetery (See Table 8 for the number of individuals included in this analysis, page 138 and Appendix VIII).

Friedhof and Lettenbuhl grave fields

To date, 22 inhumation burials have been recovered from Lettenbuhl, whereas 26 have been uncovered from Friedhof (Tiefengraber and Wiltschke-Schrotta, 2015). Approximately 50% of burials in both regions contained more than one individual, 11 and 13 burials, respectively (Tiefengraber and Wiltschke-Schrotta, 2015). Males, females, and sub-adults are represented (Table 8, Appendix VIII). In both grave fields, approximately two-thirds, 66.67%, of the burials were inhumations and one third, 33.3%, were cremations buried in urns (Tiefengraber and Wiltschke-Schrotta, 2015). This high proportion of cremations is significantly different from the other Dürrnberg (Austria) grave fields where these burials are less common (Tiefengraber and Wiltschke-Schrotta, 2015). Both the initial and the intensive phases of funeral activity at both cemeteries date to the beginning of the HaD period (Tiefengraber and Wiltschke-Schrotta, 2015). The majority of the burials from Friedhof, 46.2%, predominantly date to the HaD period, while only 15.4% date to the LTA period (Table 8). A similar pattern is evident at Lettenbühel (Tiefengraber and Wiltschke-Schrotta, 2015). During the early LTA period, burials decreased and considerable parts of both grave fields were converted into settlement areas (Tiefengraber and Wiltschke-Schrotta, 2015). At the end of the LTA period, the Friedhof settlement was abandoned and the entire area was reused as a burial ground again during the LTB period (Table 8) (Tiefengraber and Wiltschke-Schrotta, 2015). The latest burials in both grave fields date to the LTC period (Table 8) (Tiefengraber and Wiltschke-Schrotta, 2015). Evidence of grave reuse is only evident in burials from this period (Tiefengraber and Wiltschke-Schrotta, 2015).

The majority of individuals were buried in an extended and supine or flexed position, oriented north-south and facing north (Tiefengraber and Wiltschke-Schrotta, 2015). However, crouched burials oriented east-west and facing east, have been found (Tiefengraber and Wiltschke-Schrotta, 2015). The inhumations were predominantly placed in enclosed wooden grave-chambers, occasionally covered by stones and barrows (Tiefengraber and Wiltschke-Schrotta, 2015). In some cases, latter period grave chambers were built directly above earlier ones, resulting in a vertical sequence (Tiefengraber and Wiltschke-Schrotta, 2015). The artefacts recovered are comparatively numerous and include, fibulae; rings; bracelets; torcs; pottery; bronze chain belts; swords; knives; antenna-hilt daggers; spears; gifts of meat (e.g., sheep); ornaments of false-filigree; Mediterranean imports; gold and silver items (wine flagons and jugs) (See page 32) (Tiefengraber and Wiltschke-Schrotta, 2015). Ceramic vessels containing liquid have also been recovered, although the type of liquid is not specified (Tiefengraber and Wiltschke-Schrotta, 2015). Most of the sub-adult burials were accompanied by items typically found with adult females, including jewellery and pottery (Appendix VIII) (Tiefengraber and Wiltschke-Schrotta, 2015).

Romersteig grave field

The Romersteig grave field is oriented north-west, and is located to the south of the region of Dürrnberg (Austria) and was in use from the HaD-LTC periods (Table 8) (Wendling and Wiltschke-Schrotta, 2015). The burials in this area are oriented in an irregular sequence and are topographically separated into a western and an eastern group (Wendling and Wiltschke-Schrotta, 2015). Multiple burials are common in this grave field, 98 burials comprising 66 inhumations from 27 grave chambers, 18 cremations and 14 graves with no preserved skeletal remains, the majority of which date to the LTA-C periods, have been recovered (Table 8, Appendix VIII) (Wendling and Wiltschke-Schrotta, 2015). In addition to single burials, a considerable number of multiple burials within one single chamber are common, including several burials containing between 7-17 individuals (Wendling and

Wiltschke-Schrotta, 2015). In spite of the frequency of multiple burials, their social and ideological implications are debated (Wendling and Wiltschke-Schrotta, 2015). It has been suggested that close social bonds, such as kinship, connected those individuals buried in the same chamber (Wendling and Wiltschke-Schrotta, 2015). However, it has also been suggested that these burials indicate reuse of the burial chambers (Wendling and Wiltschke-Schrotta, 2015).

Construction of the grave chambers is similar to those from Friedhof and Lettenbühel. Additionally, there is evidence of one probable cremation located near the site of a possible funeral pyre (Wendling and Wiltschke-Schrotta, 2015). This interpretation is based on the presence of significant burning activity in this area. Settlement structures have also been found which are believed to date to the HaD period, based on similarities to those from Friedhof and Lettenbühel which were occupied during this period (Wendling and Wiltschke-Schrotta, 2015). Barrows have been found in both regions of Romersteig, although they are more common in the western area (Wendling and Wiltschke-Schrotta, 2015). During the LTB period, funeral activity declines in the eastern region and ceases overall for a short period. However, the duration of this period is not described (Wendling and Wiltschke-Schrotta, 2015). Funeral activity increases again briefly during the beginning of the LTC period, after which the entire area was reconverted into a settlement area (Table 8) (Wendling and Wiltschke-Schrotta, 2015).

The majority of the individuals were buried in a supine and extended position (Wendling and Wiltschke-Schrotta, 2015). However, burial orientation does not follow any particular pattern, north-south, east-west, and south-north orientations are common (Wendling and Wiltschke-Schrotta, 2015). These different orientations are believed to have been used simultaneously, as they are not specific to any temporal phase (Wendling and Wiltschke-Schrotta, 2015). Numerous artefacts similar to those from Friedhof and Lettenbühel have been recovered (See pages 32 and 157) (Wendling and Wiltschke-Schrotta, 2015). However, amber and glass bead necklaces have also been found (Wendling and Wiltschke-Schrotta, 2015).

Eislfeld grave field

Eislfeld dates to the HaD-LTB period and is the largest grave field in the region, both in terms of surface area and the number of burials (Figure 26, Table 8) (Thorsten et al., 2017). The majority of the burials date to the HaD period, 45% (88 individuals), and only 32% (63 individuals) date to the LTA period (Thorsten et al., 2017). Overall, 11 individuals have been dated to the HaD/LTA transition, while 2 graves dating to the LTB period suggest a decline in funeral activity during this period (Thorsten et al., 2017). The remaining 29 individuals could not be assigned to a specific phase (Table 8, Appendix VIII) (Thorsten et al., 2017). Inhumations in grave chambers similar to those in the other grave fields are common. However, some burials appear to have been dug directly into the ground surface (Thorsten et al., 2017). Their relative size varies throughout the grave field (Thorsten et al., 2017). Barrows were also common in this region, although due to taphonomic processes and intensive agricultural activity few have been identified on the ground surface (Thorsten et al., 2017). A vertical sequence in burial chamber construction is also common, which may suggest a biological or social relationship among these individuals (Thorsten et al., 2017). Secondary and cremation burials dug into existing barrows have also been recovered. Some possible cremation sites, 2, with significant evidence of burning, have been identified, 1 that is associated with a specific grave complex (K124) in the eastern part of the grave field, whereas the other is located at the centre of the burial area (Thorsten et al., 2017).

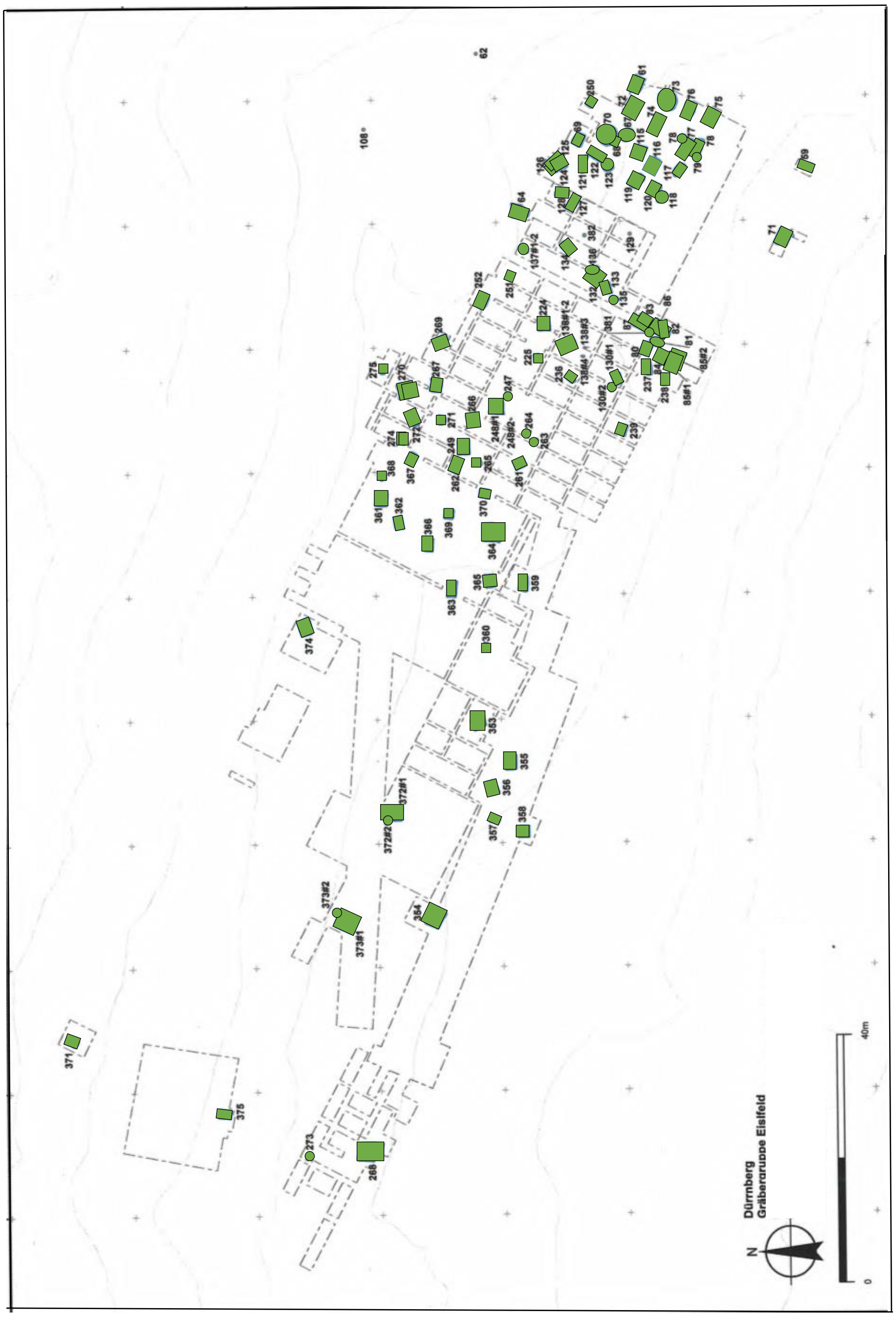
The burials are concentrated in the eastern section and of the grave field and decrease in the west (Thorsten et al., 2017). The majority of burials, 121, are within a chamber, in an extended and supine position. However, secondary burial and grave reuse resulted in the dislocation of skeletal material and artefacts. Therefore, it is difficult to determine the extent of deviations from the above burial position (Thorsten et al., 2017). Of the total 194 excavated graves, 1 in which no skeletal remains had survived to be excavated, 151 were inhumations (Thorsten et al., 2017) (Appendix VIII). The chambers were often used for multiple burials, and are believed to have been used by family groups (Thorsten et al., 2017). The number of individuals buried in collective graves varies between 5 and 7 individuals. Cremations and subsequent burial in grave chambers were also common (Thorsten et al., 2017). Out of the 38 identified cremations, only 16 were buried in separate individual graves (Thorsten et al., 2017). One chariot burial has also been recovered, in which the wheels were placed in separate holes dug into the grave floor and the body of the chariot was used as a makeshift coffin (Table 7) (Thorsten et al., 2017). However, the material used to construct the documented coffins is not reported (Thorsten et al., 2017).

The recovered artefacts are numerous and similar to those from the Romersteig, Friedhof, and Lettenbühel grave fields within the Dürrnberg (Austria), Pottenbrunn (Austria), and Mannersdorf (Austria) cemeteries (See pages 152, 155 and 158) (Thorsten et al., 2017). Similarities to other extra-regional locations have also been described including, Münsingen-Rain (Switzerland), Basel-Gasfabrik (Switzerland), eastern Belgium, Luxembourg, the Hunsrück-Eifel (western Germany), and Baden-Württemberg (southwest Germany) regions (See pages 61 and 145) (Thorsten et al., 2017). Although some differences are evident such as, lances; spears; earrings; full size and miniature axes; wine flagons and jugs; elaborately decorated pins; bronze belt plates; and a set of gold hollow circular beads believed to be hair clips or accessories (Figure 25). Decorated iron rods believed to be scepters and a range of gold objects, including fibulae decorated with gold foil have also been recovered (Thorsten et al., 2017). The abundance and range of artefacts suggests that the population had far-reaching trade connections and access to numerous prestige and high-status items (Thorsten et al., 2017). Both extra-and-intra-regional connections have been indicated by the artefacts throughout the Dürrnberg (Austria) cemetery, which may suggest a degree of mobility within the burial community (See page 61, Table 5) (Thorsten et al., 2017). Similarities in several artefacts such as, bracelets; fibulae; sceptres; necklaces; and material type (amber and glass) to those from Pottenbrunn (Austria), Mannersdorf (southern Germany), Münsingen-Rain (Switzerland), Basel-Gasfabrik (Switzerland), eastern Belgium, Luxembourg, the Hunsrück-Eifel (western Germany), and Baden-Württemberg (southwest Germany) regions have been described (See pages 32, 145, Table 5) (Neugebauer, 1991; Ramsl et al., 2011b; Thorsten et al., 2017). As at the Hallstatt type site, it has been suggested that the population was of high status, and therefore wealthy, based on the abundant presence of trade and high-quality artefacts. Additionally, the nearby salt mine would have provided the population with control of a viable commodity (See page 19) (Adshead, 1992; Banffy, 2013; Harding, 2013a, b; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015). Access to trade routes also supports the notion that the population was of comparably high status, and wealthy, due to the copious presence of the above artefacts combined with the active nearby salt mine. However, Dürrnberg (Austria) may also have been a trading centre (Lavelle et al., 2019; Rabsiler et al., 2017; Swidrak, 1999; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015). Population expansion and decline have been suggested during the overall use of the Dürrnberg (Austria) cemetery, as evident in the changes from settlement to funerary areas and the reverse (Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015).

This may support the notion that Dürrnberg (Austria) was a trading centre, however, as no stable isotope analyses have been conducted the frequency of non-local individuals is unknown. Alternatively, the apparent population increase and decline may have been the result of salt mining activities or deteriorating climate conditions (Adshead, 1992; Banffy, 2013; Swidrak, 1999; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015). However, there is no corresponding evidence for a change in subsistence to adapt to changes in climate (See page 61) (Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015). Therefore, the above mechanisms and the possibility that Dürrnberg (Austria) was a trading centre cannot be ruled out.

Figure 25. Potential reconstruction of gold hair clips recovered from Eislfeld. (Modified from Thorsten et al., 2017, Figure 217. Original scale not provided).

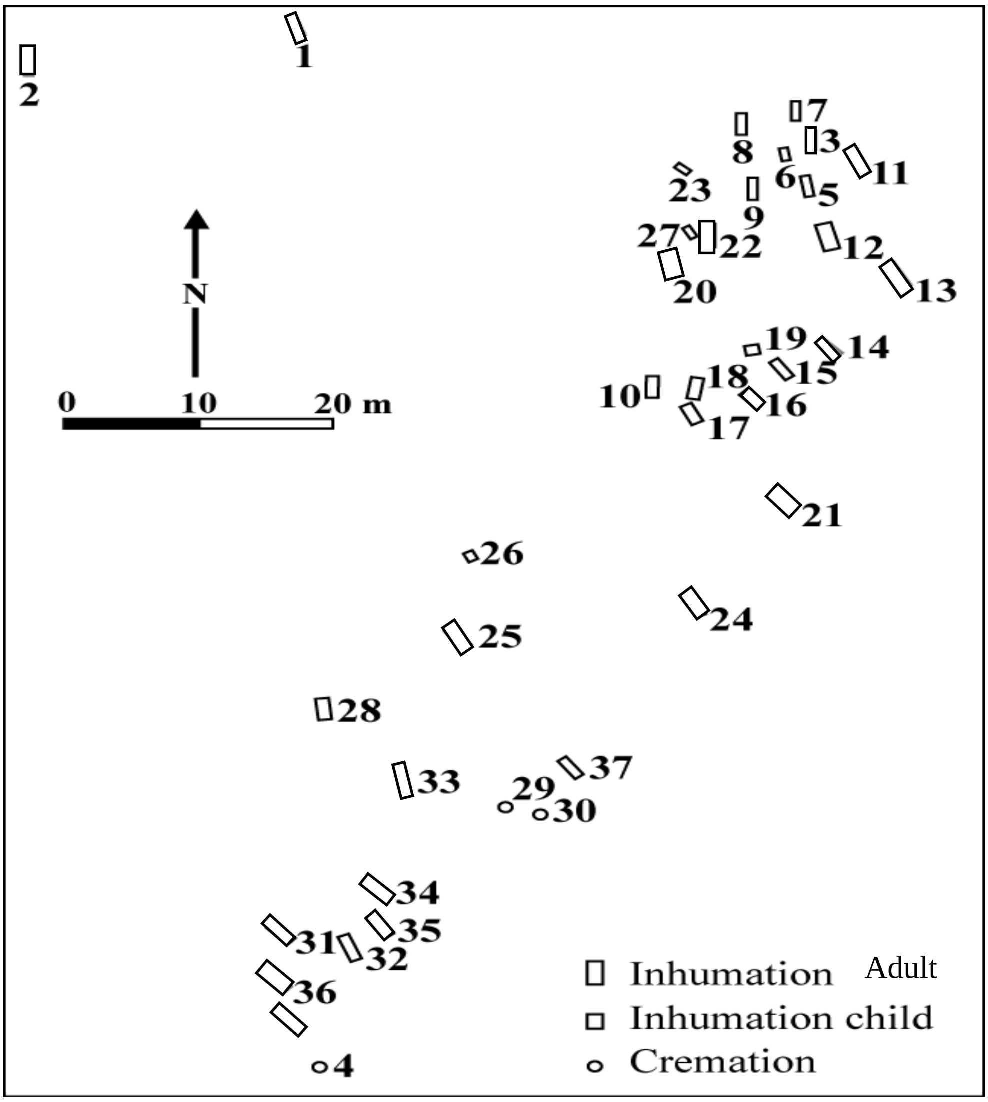
Figure 26. Distribution of graves within the Eislfeld grave field of the Dürrnberg (Austria) cemetery (Modified from Rabsiler et al., 2017, Figure 3).



Expansion region samples

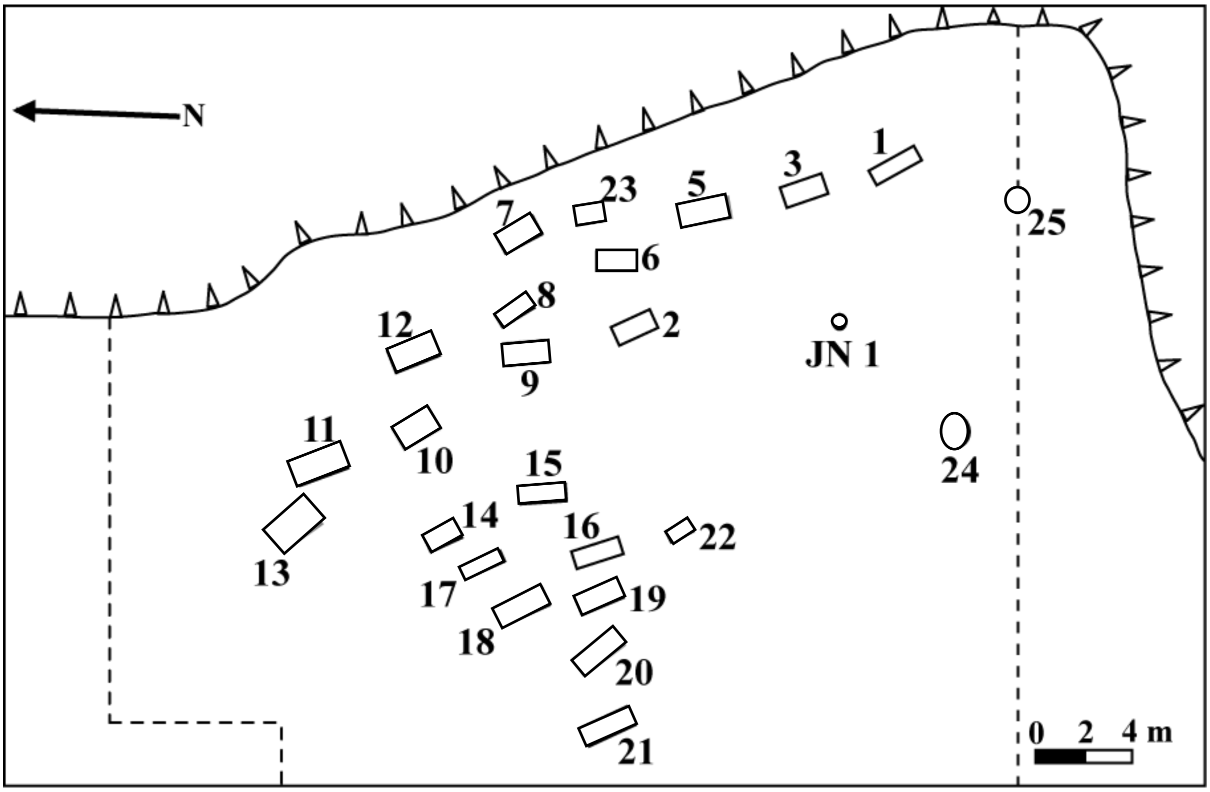
Radovesice I and II, Czech Republic

Figure 27. The cemetery of Radovesice I (Czech Republic) "Vápenka" (Modified from Waldhauser, 1987, Figure 1).



The cemeteries of Radovesice I and II (La Tène B-C, 380-250 BC) are located in north-west Bohemia (Czech Republic) only 950 metres from each other, and 6 km south of Teplice in the foreland of the Ore Mountains (Figures 1, 20 and 27-28) (von Arburg, 2007). Although the cemeteries are close to one another, it is unclear whether they represent a single or two distinct populations (Waldhauser, 1999). In 1974 rescue excavations commenced after coal mining revealed a settlement northwest of the Radovesice I (Czech Republic) cemetery, which is believed to have been intensively occupied from the HaC-LTD periods (Table 8) (Budinský and Waldhauser, 2004; Waldhauser, 1987, 1993, 1999).

Figure 28. The cemetery of Radovesice (Czech Republic) II "Na Vyhlidce". The dotted and solid lines, black triangles and the JN1 designation are not defined. (Modified from Budinský and Waldhauser, 2004, Figure 2).



The settlement associated with the Radovesice II (Czech Republic) cemetery has not been discovered and is believed to have been destroyed by subsequent building work since the Middle Ages (Budinský and Waldhauser, 2004). Subsequent excavations at Radovesice I (Czech Republic) in 1976 uncovered 34 inhumations and 3 cremation burials (Waldhauser, 1987, 1993). Excavations at Radovesice II (Czech Republic), which is located to the northeast, began in 1981 and uncovered 23 inhumations (Budinský and Waldhauser, 2004) (Table 8, Appendix VIII). However, the recovered skeletal material is highly fragmented (Budinský and Waldhauser, 2004; Waldhauser, 1993). Although 21 adults, 2 sub-adults, 8 mature individuals, and 2 infants have been described (Budinský and Waldhauser, 2004; Waldhauser, 1993; Herrmann et al., 1990; Scheeres, 2014a; Scheeres et al., 2014b) (Table 8, Appendix VIII). Burials dating to the LTD period have not been found, and are believed to have been destroyed by construction, agricultural or taphonomic processes (Budinský and Waldhauser, 2004). The majority of the burials are extended and supine and oriented north-south, facing north. Both cemeteries were in use at the same time (Budinský and Waldhauser, 2004; Waldhauser, 1993).

Beginning in the LTB period prestige items and La Tène artefacts become less common, while Bohemian style objects, with more naturalistic and curvilinear designs, including, fibulae and bracelets, become more common (Budinský and Waldhauser, 2004; Cižmář, 1995; Drda and Rybova, 1994; Waldhauser, 1999). However, La Tène artefacts including torcs; wheel turned pottery; swords; daggers; bronze vessels and ornaments of false-filigree are still common (See page 32) (Budinský and Waldhauser, 2004; Kuželka et al., 2004; Valentová and Sankot, 2012). Connections to the Danube, Moravia (eastern Czech Republic), a historical region in the Czech Republic, and southern Bavarian regions (southeastern Germany), a federal state, a union of partially self-governing provinces or states under a central federal government, of southeastern Germany, are evident in design and manufacture (Budinský and Waldhauser, 2004; Drda and Rybova, 1994; Grinin et al., 2004; Hanakpva, 2004; Macháček, 2012; Minahan, 2000; ; Rowley, 2011; Sheehan, 1993; Štefan, 2011; Waldhauser, 1999). The above regions represent geographic areas that historically had either a cultural, ethnic, linguistic or political basis regardless of their modern-day borders (Grinin et al., 2004; Hasil, 2015; Macháček, 2012; Minahan, 2000; Rowley, 2011; Sheehan, 1993; Štefan, 2011). Moravia and Bavaria remain in use as names of municipalities and geographic regions, the distinction between these areas is also evident culturally, ethnically and linguistically within the Czech Republic and Germany (Grinin et al., 2004; Hasil, 2015; Macháček, 2012; Minahan, 2000; Rowley, 2011; Sheehan, 1993; Štefan, 2011).

However, the connections indicated by the above La Tène artefacts are not elaborated on by previous researchers (Budinský and Waldhauser, 2004; Drda and Rybova, 1994; Hanakpva, 2004; Waldhauser, 1999). Although the type and design of artefacts are similar between Radovesice I and II (Czech Republic), there are some subtle differences, such as jewellery type, as sapropelite (coal) bracelets are only common at Radovesice I (Czech Republic) (Waldhauser, 1999; Valentová and Sankot, 2012). Though, as this difference is not quantified, it is difficult to determine whether this represents an actual division between these sites (Valentová and Sankot, 2012).

During the end of the LTB, or beginning of the LTC, period the settlement at Radovesice I (Czech Republic) was abandoned and burials ceased in both cemeteries

(Budinský and Waldhauser, 2004; Valentová and Sankot, 2012). This has been linked with either population growth and/or decline and subsequent migration into other neighbouring intra-and-extra-regional locations (Dobesch, 1996; Stöllner, 1998; Valentová and Sankot, 2012). Burial practices also changed during this period, as flat graves become more common and the use of tumuli decline (Budinský and Waldhauser, 2004; Valentová and Sankot, 2012). The use of flat graves has also been linked to the presumed population decline during the LTB/LTC period (Table 8). The archaeological visibility, and recovery, of cemeteries and their associated settlements, may have been affected by subsequent agriculture and building activities (Budinský and Waldhauser, 2004; Dobesch, 1996; Stöllner, 1998; Valentová and Sankot, 2012; Waldhauser, 1999).

The Radovesice (Czech Republic) cemeteries have been the focus of some previous research. Although, this research has primarily been chronological, typological and descriptive, a stable isotopic analysis has been conducted (See page 61) (Budinský and Waldhauser, 2004; Dobesch, 1996; Stöllner, 1998; Scheeres, 2014a; Scheeres et al., 2014b; Valentová and Sankot, 2012; Waldhauser, 1987, 1993, 1999). The stable isotopic analyses were primarily conducted on the third molars and human ribs, or rib fragments and therefore, did not affect the subsequent ability to observe and record dental nonmetric traits (Scheeres, 2014a; Scheeres et al., 2014b). However, in the few cases, 2 individuals from Radovesice I and 1 from Radovesice II (Czech Republic), the first or second molars were used because the third molars were not available for analysis or due to severe dental wear. However, the level of wear on these teeth was severe, e.g., no nonmetric traits could be observed. Consequently, they were too worn for inclusion in dental nonmetric trait analysis (Scheeres, 2014a; Scheeres et al., 2014b) (See page 181 for a discussion of dental wear and nonmetric traits, Figure 34, for an example of severe dental wear and Appendix III). The extra-regional connections that have been indicated through artefact distribution are not fully supported by the stable isotope evidence (Scheeres, 2014a; Scheeres et al., 2014b) (See page 61, Tables 5 and 6). The majority of individuals 74.3% , 26 out of 35 individuals, from Radovesice I and II (Czech Republic) migrated into the region from the surrounding areas in the Czech Republic (Scheeres, 2014a; Scheeres et al., 2014b). The high mobility rate during this period may appear to support population growth and subsequent frequent migration from neighbouring areas (Scheeres et al., 2014b). However, other processes, such as exogamy, allegiance fosterage, climate change, enslavement and/or capture may have also resulted in the high frequency of non-local individuals (See page 61). Although allegiance fosterage may have resulted in an increase in individual mobility during this period, it is unknown to what extent this practice was common in Iron Age Europe (Scheeres, 2014a; Scheeres et al., 2014b). Further, it is unknown whether individuals from Radovesice (Czech Republic) moved during childhood or before adulthood was reached (Scheeres, 2014a; Scheeres et al., 2014b). Therefore, allegiance fosterage may not have been a primary mechanism for migration into the region. Although there is evidence for deteriorating climate conditions during this period, not all settlements in the region were abandoned (Valentová and Sankot, 2012). Further, evidence of agricultural misfortune resulting from these conditions was not present at those settlements that were also abandoned (See page 61) (Budinský and Waldhauser, 2004; Dobesch, 1996; Valentová and Sankot, 2012; Waldhauser, 1999). Nor is this evident at Radovesice I and II (Czech Republic).

Therefore, settlement abandonment during the LTB/LTC period may have been the result of social processes such as the breakdown or rerouting of trade routes (Fischer, 2006; Grove, 1979; Kromer and Friedrich, 2007; Magny et al., 2009). Further, the suggestion that Radovesice I and II (Czech Republic) were trading centres based on the presence of prestige items, including Mediterranean imports and gold and silver objects, and the high mobility rate supports the above processes as mechanisms for settlement abandonment (See pages 32 and 61) (Budinský and Waldhauser, 2004; Valentová and Sankot, 2012; Waldhauser, 1999). However, as the underlying biological relationship between these groups is unknown; it is difficult to determine whether they represented a comprehensive trading centre, or if the similarity in material culture is the result of access to similar prestige items and trade routes. The differences in jewellery distribution between the sites may support the latter. Although this diversity may also be related to individual preference among the burial communities, designation of social status or artefact loss due to construction prior to excavation. Further, as the presence of sapropelite bracelets at Radovesice I (Czech Republic) is not quantified, this distinction may be arbitrary.

Kutná-Hora-Karlov, Czech Republic

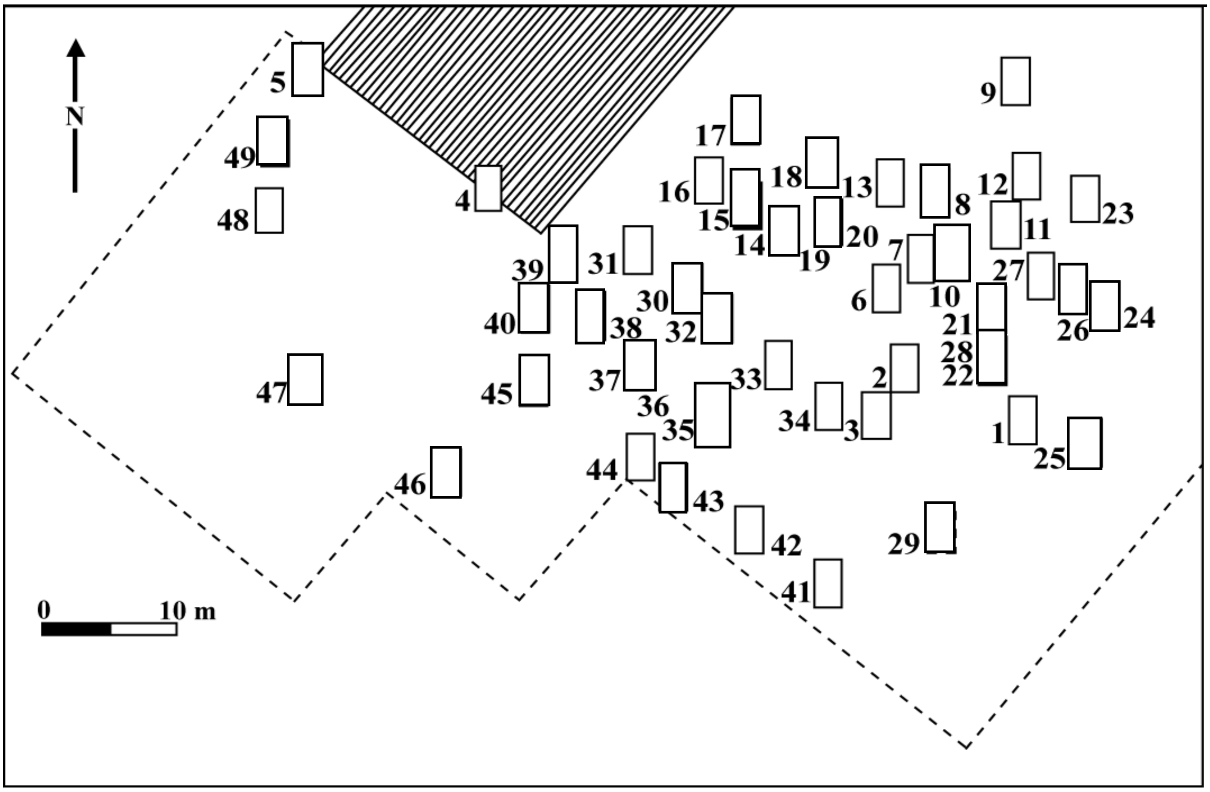
The Kutná-Hora-Karlov cemetery is located on the south-eastern edge of the Elbe valley, approximately 65 km east of Prague and is dated to 380-250 BC (Figures 1, 20 and 29). The cemetery dates to the LTB period and is believed to have been abandoned during the LTC period (Table 8) (Salac, 2011; Venclová, 2008; Valentová and Sankot, 2012). However, there is evidence for continued settlement use in the nearby Elbe Valley into the late LTD period. Although these sites are not believed to be connected to the Kutná-Hora-Karlov (Czech Republic) cemetery, as there is no archaeological evidence for a large-scale migration into the region during this period (See page 61) (Valentová and Sankot, 2012; Valentová, 2002, 2003). A total of 6 graves were significantly disturbed during construction of a farm and sewage system; subsequent rescue excavations were conducted from 1988-1989 (Valentová, 1991, 1993; Valentová and Sankot, 2012). As a result, some of the recovered skeletal material is highly fragmented (Valentová and Sankot, 2012; Valentová, 2002, 2003). A total of 48 inhumation burials and 1 cremation were recovered (Valentová, 1991; Valentová and Sankot, 2012) (Table 8, Appendix VIII). Although it is believed that the total number of burials may have been as high as 55 or more, due to the shallow grave depth, some graves are believed to have either eroded away or to have been destroyed by construction (Valentová, 1991; Valentová and Sankot, 2012).

The majority of the burials are concentrated within the northeastern part of the cemetery and are primarily extended and supine, oriented north-south and facing north (Valentová, 1991; Valentová and Sankot, 2012). Prior to excavation of the Kutná-Hora-Karlov (Czech Republic) cemetery, only a minimal representation of La Tène burials and material culture had been recovered and documented in the region (Lorenz, 1978; Velemínský, 1999; Velemínský et al., 2004; Waldhauser, 2001). Consequently, the spread of this culture throughout this region was previously known only from older and poorly documented finds (Valentová and Sankot, 2012).

Most individuals are adults, with both sexes represented, although some sub-adults have been recovered (Valentová and Sankot, 2012). However, sub-adults and infants are underrepresented, which may be the result of the shallow grave depth and subsequent loss of these burials (Table 8, Appendix VIII) (Valentová and Sankot, 2012). Settlement structures have been found within the region however, none have been associated with the Kutná-Hora-Karlov (Czech Republic) cemetery due to its relative geographic isolation from these structures (Budinský and Waldhauser, 2004; Cižmář and Valentová, 1977; Valentová, 1996, 2002, 2003). However, the degree of this isolation is not described in detail, nor is it measured. Artefacts are comparatively numerous, and include bracelets; belts; paired foot and finger rings; arm rings; necklaces; torcs; fibula; swords; daggers; shields; lances; wooden boxes; gold and silver items; ornaments of false-filigree; wheel turned pottery; and Mediterranean imports (See page 32) (Budinský and Waldhauser, 2004; Holodnák and

Waldhauser, 1984; Cižmář and Valentová, 1977; Valentová, 1996, 2002, 2003; Valentová and Sankot, 2012). The presence of both neck and arm rings in a single burial has been suggested to indicate population or individual movement from the Marne and Moselle regions (northern and eastern France), and/or the Upper Rhine Valley, Basel (Switzerland) and Nebringen (Stuttgart, Germany) where similar graves have been found (See pages 32 and 61) (Lorenzo, 1980; Kruta, 1979). However, these associations are not elaborated on and are simply mentioned as possible (Kruta, 1979; Valentová, 2002, 2003; Valentová and Sankot, 2012).

Figure 29. The cemetery of Kutná Hora "Karlov". The dotted lines and the shaded area are not defined. (Modified from Valentová, 1993, Figure 2).



Fibula forms, identical in construction and design, have also been identified in the Jenišův Újezd cemetery (Czech Republic, LTB-D), suggesting an inter-regional connection (Table 5) (Cižmář, 1995; Kruta, 1979; Valentová and Sankot, 2012; Waldhauser, 1977). The burials with weapons form a homogenous concentration within the cemetery and occur more intensively during the LTB period (Valentová and Sankot, 2012). These burials and rich female graves are believed to indicate that the population was of high social status, as they account for more than half the total number of graves (Sankot, 2010; Valentová and Sankot, 2012). Alternatively, Kutná-Hora-Karlov (Czech Republic) may have been a trading centre, due to the high proportion of prestige items, such as gold and silver objects, fibulae, jewellery and Mediterranean imports (See pages 32 and 61) (Valentová and Sankot, 2012). The cemetery has been the focus of limited typological, chronological and descriptive research, although some stable isotope, bioarchaeological and dental analyses have been conducted.

Stable isotopic analysis was conducted on 27 of the 48 inhumations from Kutná-Hora-Karlov, these individuals were also selected according to archaeological criteria (See page 61) (Scheeres, 2014a; Scheeres et al., 2014b). The same skeletal elements and teeth were used in the stable isotopic analysis of these individuals as at Radovesice I and II (Czech Republic), e.g., third molars and human ribs, or rib fragments (Scheeres, 2014a; Scheeres et al., 2014b). However, in some cases, 3 individuals from Kutná-Hora-Karlov (Czech Republic) the first or second molars were used in place of the third for similar reason as at Radovesice (Czech Republic). In these cases the tooth used, either the first or second molar, also had severe dental wear (Scheeres, 2014a; Scheeres et al., 2014b). Therefore, these teeth could not be included in any subsequent dental nonmetric trait analysis (Scheeres, 2014a; Scheeres et al., 2014b) (See page 181 for a discussion of dental wear and nonmetric traits, Figure 34, for an example of severe dental wear and Appendix III).

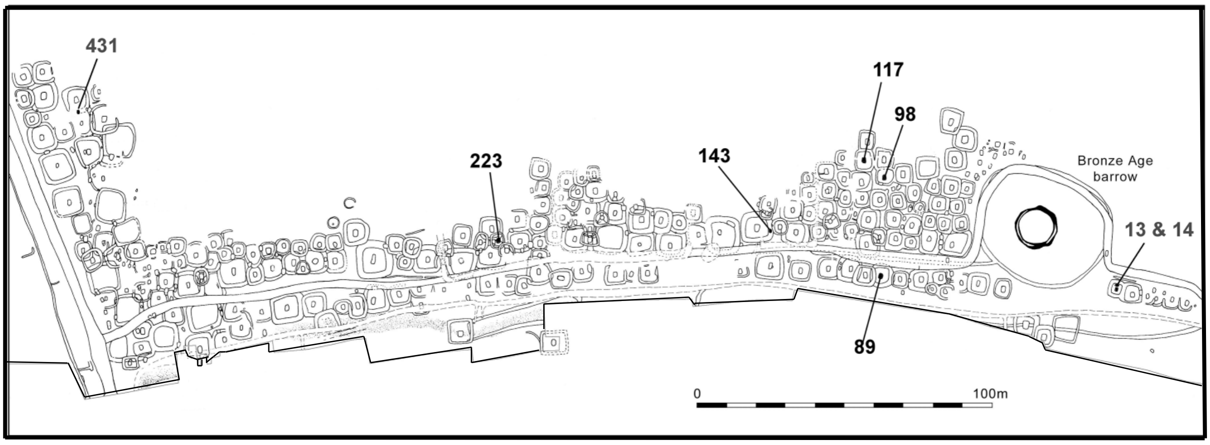
Though extra-regional connections have been suggested based on artefact distribution, like at Radovesice I and II (Czech Republic), they are not fully supported by the stable isotope evidence (Scheeres, 2014a; Scheeres et al., 2014b) (Tables 5 and 6). The majority of individuals, 76%, 19 out of 25 individuals, were found to have migrated into the region from other areas in the Czech Republic (See page 61) (Scheeres, 2014a; Scheeres et al., 2014b). This high mobility rate is comparable to that at Radovesice I and II (Czech Republic) and also appears to represent population growth and subsequent large-scale migration from neighbouring areas (Scheeres, 2014a; Scheeres et al., 2014b). The high mobility rate and abundance of prestige items may support the notion that Kutná-Hora-Karlov (Czech Republic) was a trading centre. However, similar mechanisms as at Radovesice (Czech Republic) may have been responsible for the high degree of mobility (See pages 61, 164 and 168) (Budinský and Waldhauser, 2004; Fischer, 2006; Grove, 1979; Kromer and Friedrich, 2007; Magny et al., 2009; Sankot, 2010; Valentová, 1996, 2002, 2003; Valentová and Sankot, 2012). Although, as the settlement associated with Kutná-Hora-Karlov (Czech Republic) has not been found, it is not possible to determine whether evidence of adaptions to deteriorating climate conditions were present (Sankot, 2010; Valentová and Sankot, 2012). Therefore, the notion that climate change was not a primary reason for settlement abandonment at Kutná-Hora-Karlov (Czech Republic) may be supported by the lack of corresponding evidence elsewhere in the Czech Republic (See pages 164 and 168). However, deteriorating climate conditions and similar social processes leading to abandonment as at Radovesice I and II (Czech Republic) cannot be ruled out.

It has been suggested that the condition of the skeletal material from this cemetery does not facilitate bioarcheological analysis (Zvara, 1999). However, as only a proportion of the skeletal material is fragmented, the overall condition of the collection does not preclude this analysis. Consequently, Maxová and colleagues (2011) conducted a biodistance analysis to determine whether this population shared any biological affinity to temporally contemporaneous populations in Central and southern Italy (Maxová et al., 2011). However, it is not designated whether specific or composite Italian populations were examined and compared (Maxová et al., 2011). Further, previously published dental data was used and no corresponding description as to the compatibility of the data sets is provided. The MMD distance statistic is mentioned as well, although no corresponding results are listed (Maxová et al., 2011). However, results from Chi-square tests and the Yates correlation are provided (Maxová et al., 2011). Although this analysis did support phenetic divergence among the Kutná-Hora-Karlov (Czech Republic) and Italian samples, this divergence was based on the difference in expression in a limited number of morphological traits, e.g. Tuberculum Dentali and Groove Pattern (Appendix I) (Maxová et al., 2011). Moreover, it is not described whether only these traits were used in the statistical analyses or if these were the only traits that showed and difference among the samples. Further, it is not described whether the above divergence was between the Kutná-Hora-Karlov (Czech Republic) and the Central or southern Italian samples. Consequently, it is difficult to determine whether the results of this analysis adequately reflect the phenetic variation among these populations (Maxová et al., 2011).

Wetwang Slack, east Yorkshire, Britain

Wetwang Slack, 300-100 BC, is the largest Iron Age inhumation cemetery excavated in Britain, and one of the largest known in western Europe (Dent, 1982, 1984; Jay et al., 2012; Jay and Richards, 2007; Stead, 1991a). The cemetery lies on the south side of a chalk dry valley, or Slack, near the modern village of Wetwang in the district of the east Riding of Yorkshire (Britain) (Figures 1, 20 and 31). The cemetery extends for 1.8 km along the valley floor (Figure 30) (Brewster, 1980; Dent, 1979, 1982, 1984). Several cemeteries sharing similar material culture, e.g., square barrows, chariot burials and the presence of La Tène artefacts, have been documented in east Yorkshire (Britain) and have been grouped together under the broad Arras Culture heading (Figure 31) (Brewster, 1980; Collis, 2003; Cunliffe, 1997; Dent, 1982; Greenwell, 1906; Stead, 1979, 1991a). Although the underlying biological relationships among these groups are unknown, the documented similarities, such as square barrows, suggest significant biological or cultural interaction.

Figure 30. Wetwang Slack (east Yorkshire, Britain) cemetery during the 1965 excavation (Modified from Dent, 1984, Figure 8).



Square barrows with surrounding ditches are predominantly found in the Arras culture cemeteries and are considered characteristic of this culture (Collis, 2003; Cunliffe, 1997; Dent, 1982; Mizoguchi, 1992; Stead, 1979, 1991a, c). Those at Wetwang Slack (east Yorkshire, Britain) are arranged linearly along earlier barrow ditches for a distance of approximately 400 metres, an arrangement common to several of the Arras culture cemeteries (Stead, 1979, 1991a, c). The earliest graves are grouped in the south-western section of the cemetery and subsequently extended to the east and north (Dent, 1982, 1984). Although the cemetery has been the focus of numerous studies, very little has been published other than the chariot burials (See page 32) (Cunliffe, 2004, 2005; Dennison, 2001; Dent, 1982, 1984, 1985a, b; Giles, 2012; Good, 2005; Hill, 2001, 2002; Selkirk, 1984; Stead, 1991a; Whimster, 1981). Moreover, there has been a lack of absolute chronology, as the majority of the dating has been ascertained through stratigraphy, artefact and time period associations (Dent, 1982, 1984, 1995; Stead, 1979, 1991a). The cemetery is believed to have been in use for approximately 350-400 years and has been broadly dated to 400-100 BC (Dent, 1982, 1984). It has also been suggested that the majority of the burials occurred during the 3rd to 2nd centuries BC (Jay et al., 2012). These dates are in line with those from a chronological analysis of 43 La Tène fibulae types, which suggest that La Tène D period fibulae arrived in the region during the 2nd century BC (Jay et al., 2012).

However, there are several issues with this chronology, few graves contain associated artefacts, regional diversity within east Yorkshire (Britain) was not accounted for as only brooches from Wetwang Slack (east Yorkshire, Britain) were used, and the dates represent the earliest possible and are thus broad approximations. Additionally, the majority are distinctly British without parallel in continental Europe, as such only some could be compared directly and are not quantified (Jay et al., 2012). Consequently, the broad dates ascribed to this cemetery, 400-100 BC, will be used in this thesis. In spite of these issues, this chronology has been applied to other Arras culture cemeteries in east Yorkshire (Britain), based on the presumption that they represent one biological population (Jay et al., 2012). Further, recent ^{14}C dates from 14 of the burials indicate that the cemetery was in use from 300-140 BC (Jay et al., 2012). However, these dates should be viewed with a degree of caution as they were derived from a subset of the total burials. In spite of the lack of absolute dates, the chariot burials have been dated more directly (Jay et al., 2012). Three chariot burials have been recovered, all of which date to a short time span around 200 BC (Jay et al., 2012).

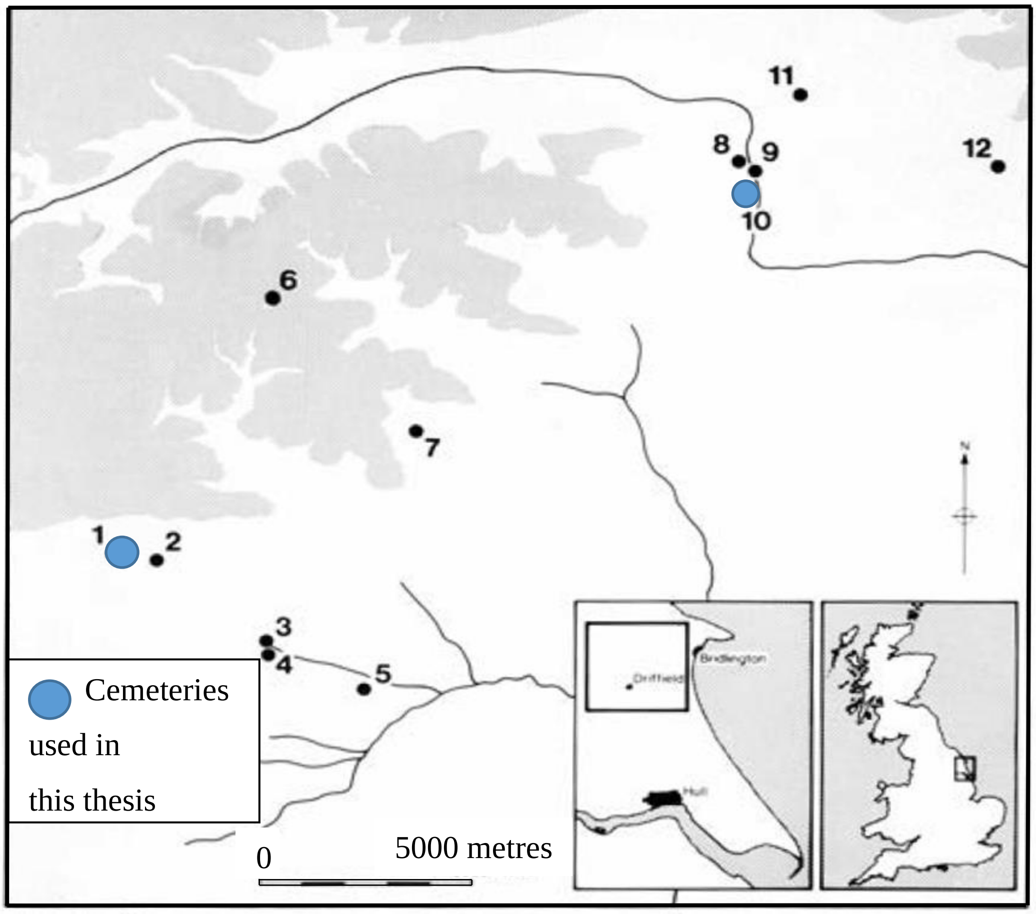
The reopening of the W Clifford Watts gravel quarry in the nearby region of Garton Slack in 1963 led to the discovery of the Wetwang Slack (east Yorkshire, Britain) cemetery. Excavations led by JR and R Mortimer, began in 1965-1975 and again from 1975-1981, led by J Dent (Dent, 1982, 1984). Several Bronze Age barrows are associated with the cemetery, the largest of which is located on the east side of the cemetery (Dent, 1982, 1984). In total, 448 burials were identified, 21 of which were graves in which no skeletal remains had survived to be excavated. A further 37 skeletal remains were recovered from disturbed contexts, such as trench burials. In total the skeletal collection comprises 427 recorded individuals (Table 8, Appendix VIII). A total of 238 barrows that spread along the southern edge of the cemetery have been documented, all but 18 of which contained a central grave (Dent, 1982, 1984, 1995b). Of these, 220 have the typical Arras culture square enclosure with a central burial mound (Dent, 1979, 1982, 1984, 1995). The remaining barrows have been described as round; however, it is believed that the edges were eroded away due to taphonomic or agricultural processes (Dent, 1984, 1995). Although the majority of the recorded burials were within barrows, 170 were identified as satellite burials (Dent, 1982, 1984, 1995).

There are also several isolated burials away from the main cemetery, including a chariot burial (Dent, 1982, 1985). In total, 3 chariot burials have been uncovered, all of which were aligned along the north-south axis of the cemetery. One contained the remains of a young woman, which represents an unusual association in the Arras culture (Stead, 1991a, c). The young woman was interred on her right side, with her arms extended and legs bent, as were the other 2 male chariot burials (Dent, 1984, 1995; Stead, 1991a). Two types of graves have been described within the cemetery; primary graves, which are central to a ditched enclosure, and secondary graves which are cut into or around the burial platform or ditch. Secondary burials were commonly found interred in the top fill of either the gravel pit, under the barrow mound, or in the surrounding enclosure ditch (Dent, 1984, 1995; Giles, 2012). This type of burial rite is commonly associated with sub-adults or infants. In total, 127 graves were found along the enclosures, although not all contained skeletal remains (Appendix VIII) (Giles, 2012; Stead, 1991a).

Familial use of the barrows has been suggested as the majority of infant burials have been recovered from secondary burials located within burial mounds (Dent, 1984, 1995). The deposition of infants in this manner may be related to the low number of infants and sub-adults recovered, as the burials may have been destroyed by agricultural or taphonomic processes (Appendix VIII) (Stead, 1979, 1991a; Tibbetts, 2006, 2008). Most of the individuals buried at Wetwang Slack (east Yorkshire, Britain) were buried laying on the left side in a crouched or flexed position, aligned north-south and facing north. However, some individuals are laid out on an east-west axis and facing east (Dent, 1982, 1984). There are also some extended and arched backwards burials, sometimes with evidence of a wooden coffin or timber lining (Dent, 1982, 1984; Stead, 1979, 1991a). Although diachronic changes in burial practices have been documented at other Arras culture cemeteries, no similar changes are apparent at Wetwang Slack (east Yorkshire, Britain), where the various burial practices appear to have been in use contemporaneously (Dent, 1984, 1995; Stead, 1979, 1991a, c). However, there is evidence of a diachronic change in barrow construction through time, as the later period graves are smaller and deeper (Dent, 1984, 1995; Stead, 1991a).

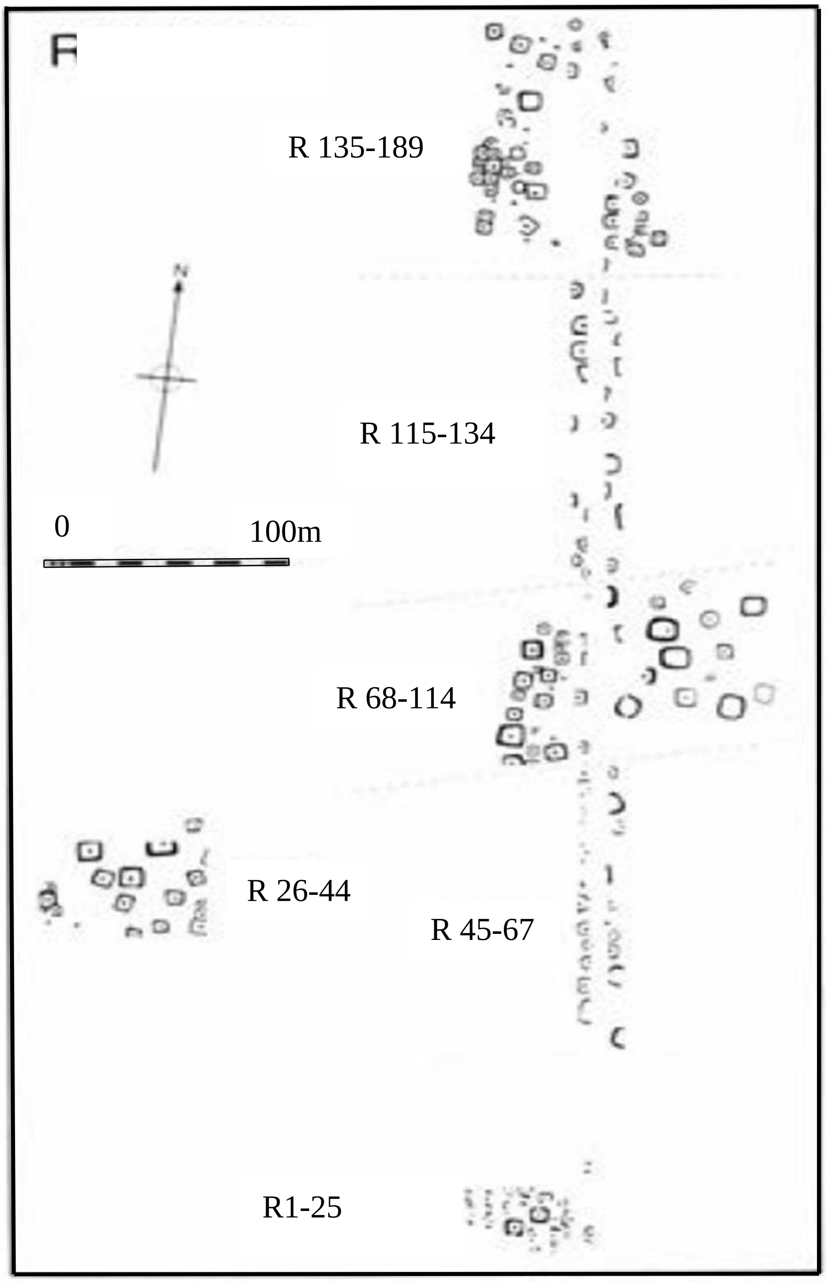
Though, the nature of this change is not quantified, thus, a direct comparison of the grave and barrow construction is not possible (Dent, 1984, 1995; Stead, 1991a). Artefacts have only been recovered from a few graves, only 21.5% and include pottery; fibulae; animal bones; jewellery; brooches; metalwork and few weapons (See page 32) (Dent, 1984, Good, 2005). Prestige items are more commonly associated with the earlier graves and include fibulae, brooches and jewellery (Dent, 1984, 1985; Stead, 1991a, c). A diachronic change in artefact distribution has also been documented, as the later period graves have fewer associated grave goods (Dent, 1982, 1984, 1985; Stead, 1991a, c).

Figure 31. East Yorkshire, showing the sites of excavated Iron Age burials; **1**. Wetwang Slack (east Yorkshire, Britain); 2. Garton Slack; 3. Garton Station; 4. Kirkburn; 5. Eastburn; 6. Cowlan; 7. Danes Graves; 8. Burton Fleming (BF1-22), 9. Rudston (R190-208); **10**. Rudston Makeshift (east Yorkshire, Britain); (R1-189); 11. Burton Fleming (Bell Slack, BF 23-64); 12. Grindale (Huntow) (Modified from Stead, 1991a, Figure 3). Bold numbers indicate those samples used in this thesis.



Rudston Makeshift, east Yorkshire, Britain

Figure 32. Rudston Makeshift Cemetery (east Yorkshire, Britain) and the relative positions of R1-189 (Modified from Stead, 1991a, Figure 5).



Similar Arras material culture such as fibulae, jewellery, and weapons are also associated with the Rudston Makeshift cemetery (east Yorkshire, Britain) which dates to 400-100 BC (Figures 1, 20, and 31-32) (Collis, 2003; Cunliffe, 1997; Stead, 1979, 1991a). The cemetery extends for 600 metres east-to-west and 750 metres north-to-south. Burials R1-R189 are arranged in a reverse L pattern with the southern branch and the eastern branch spreading alongside the Gypsey Race River Valley (Figures 31 and 32) (Giles, 2012; Stead, 1991a). The cemetery is bounded on the southern side by a pair of ditches and regimented barrows that follow the alignment of the Valley (Giles, 2012; Stead, 1991a). Although Rudston Makeshift (east Yorkshire, Britain) has been the focus of some previous research it has been predominantly descriptive, the skeletal collection has not been the focus of much analysis (Anctil, 2016; Giles, 2012, Stead, 1991a). Excavations were conducted from 1967-1971 and uncovered burials R68-114. Further excavations in 1973 and 1975 revealed burials R135-189, which were recovered from a ditch in the west section of the cemetery (Giles, 2012; Stead, 1991a). Several secondary burials, as well as some pottery sherds, were also recovered from these ditches. However, none of these burials contained any associated artefacts (Stead, 1991a). Artefacts have only been recovered from some graves, are less common in later period burials, and are similar to those recovered from Wetwang Slack (east Yorkshire, Britain) (See pages 32 and 172) (Giles, 2012; Stead, 1991a). Similar prestige items are also commonly associated with the earlier period graves (Giles, 2012; Stead, 1991a).

A total of 154 barrows were excavated, 11 of which yielded no central grave and 16 of which were not excavated completely (Stead, 1991a). In total, 189 burials and 180 individuals were identified (Table 8, Appendix VIII). Most of the individuals were buried lying on their left side in a flexed or crouched position, aligned north-south with and facing east. Though, some were aligned east-west and facing west (Stead, 1991a). However, as at Wetwang Slack (east Yorkshire, Britain), there are some extended and contracted burials, sometimes with evidence of a wooden coffin (Stead, 1979, 1991a). As at Wetwang Slack (east Yorkshire, Britain), there is also no evidence for diachronic changes in burial practices (Stead, 1979, 1991a). Central graves were found in less than half of the barrows throughout the cemetery, particularly in those that are smaller than 7 metres across (Giles, 2012; Stead, 1991a). The barrows have been described as square although most are not truly square, several have well rounded corners (Giles, 2012; Stead, 1991a). However, this difference has been attributed to erosion through either natural taphonomic processes or ploughing (Stead, 1991a). Further barrows are believed to have been lost completely, as some flat graves have only a slight trace of their surrounding ditches (Giles, 2012; Stead, 1991a). There is no evidence of an overall linear barrow arrangement, nor does there appear to be any significance to the burial groupings (Giles, 2012; Stead, 1991a). However, it has been suggested that the barrows in the northeastern section of the cemetery may have had a linear arrangement as they are roughly parallel with the Gypsey Race River (Giles, 2012; Stead, 1991a). The western area is markedly different, the barrows are distributed at random, rectangular and oval barrows without central graves and secondary burials in the associated ditches are common (Giles, 2012; Stead, 1991a). In the south-east corner of the site, the remains of an earlier domestic settlement and traces of a roundhouse and 5 post holes have been located (Stead, 1991a).

Comparative sample: Pontecagnano, Campania, Italy

This cemetery is located in the town of Pontecagnano in Campania (southern Italy) and dates from the 9th-3rd centuries BC (Figures 1 and 20). Pontecagnano was first settled in the Late Bronze Age and subsequently became an independent city populated by a mix of native Italic people from the internal highlands known as, Samnites, Etruscan colonists, and Greek settlers (D'Agostino, 1974; D'Agostino and Gastaldi, 1988; Fredericksen, 1974). Excavations began in the 1960s as a result of highway construction which uncovered several graves (D'Agostino, 1974; Fredericksen, 1974). However, the initial excavations were unsystematic and the exact boundaries of the cemetery are unknown (D’Agostino, 1974; Fredericksen, 1974). It has been estimated that as many as 6,000 burials may have originally represented the cemetery (D’Agostino, 1974, 1988; Fredericksen, 1974). Though, only the skeletal remains of 700 individuals have been recovered, due to the unsystematic nature of the initial excavations and construction without prior archaeological analyses in the region (D’Agostino and Gastaldi, 1988; De Natale, 1992; Serritella, 1995) (Table 8, Appendix VIII). Although, subsequent excavations, from 1973-1990, during which the Iron Age material was recovered, were more systematic in nature. Consequently, more precise age and date categories were provided for the cemetery overall and the recovered individuals from this period (D’Agostino and Gastaldi, 1988; De Natale, 1992; Serritella, 1995) (Appendix VIII).

Most of the individuals during the early phases of the Iron Age were buried in a supine and extended or flexed position, aligned north-south and facing north (D'Agostino, 1974; D'Agostino and Gastaldi, 1988; De Natale, 1992; Robb, 2019; Serritella, 1995). Burial positions and orientations changed throughout the use of the cemetery; however, these differences are not described in detail, only the presence of diversity is mentioned (D'Agostino, 1974, 1988; De Natale, 1992; Robb, 2019; Serritella, 1995). However, there are some flexed and crouched burials, aligned east-west and facing east or west (D'Agostino, 1974; De Natale, 1992; Serritella, 1995). Numerous artefacts have been recovered including fibulae; rings; bracelets; gold and silver items; pottery; bronze vessels; wine flagons and jugs; swords; daggers and spears (See page 32) (Cencetti, 1989; D'Agostino and Gastaldi, 1988; De Natale, 1992; Robb, 2019; Serritella, 1995). Some sub-adult burials were accompanied by jewellery, pottery or bronze vessels, while several burials contained no grave goods at all (Cencetti, 1989; D'Agostino and Gastaldi, 1988; De Natale, 1992; Serritella, 1995). Although burial position and orientation changed markedly from the 9th- 3rd centuries BC, they do not appear to be sex or age specific (D'Agostino, 1974; D'Agostino and Gastaldi, 1988; Fredericksen, 1974). Consequently, these changes are believed to be the result of migrants into the region, designation of status or temporal changes in individual preferences (D'Agostino, 1974; D'Agostino and Gastaldi, 1988; Fredericksen, 1974).

The skeletal material has been the subject of many anthropological studies (Becker, 1993; Cencetti, 1989; D'Agostino, 1974; D'Agostino and Gastaldi, 1988; De Natale, 1992; Fredericksen, 1974; Fornaciari et al., 1984, 1986; Germana and Fornaciari, 1992; Lombardi et al., 1984, 1992; Mallegni et al., 1984; Pardini et al., 1983; Petrone, 1995; Robb, 1994, 1997, 1998, 2019; Robb et al., 2001; Scarsini and Bigazzi, 1995; Serritella, 1995; Sonego, 1991). These previous studies have focused on chronological descriptions of the artefacts; dental and skeletal inventories; pathological analyses, general descriptions of the cemetery; and cultural comparisons to other Italian cemeteries dating to the same period (Becker, 1993; Cencetti, 1989; D'Agostino, 1974; D'Agostino and Gastaldi, 1988; De Natale, 1992; Fredericksen, 1974; Fornaciari et al., 1986; Germana and Fornaciari, 1992; Petrone, 1995; Robb, 1994, 1997, 1998; Scarsini and Bigazzi, 1995; Serritella, 1995). A previous biodistance analysis by the author (2016) has also been conducted on a sub-sample, n=31 (>17 years old), due to time constraints, and also dating to 650-260 BC, from this cemetery (Anctil, 2016). This analysis was conducted to determine whether there was evidence for phenetic divergence among Pontecagnano (southern Italy) and other European Iron Age cemetery populations associated with the Celts (Anctil, 2016). Subsequent statistical analysis indicated phenetic diversity among the analysed Iron Age groups (Anctil, 2016). However, regional variation among European Iron Age populations, including those associated with the Celts, is still unknown.

For the purposes of this thesis, it was considered appropriate to limit the analysed individuals, including adults and sub-adults with permanent dentitions (>17 years old), to burials from a discrete and roughly contemporaneous period, 650-260 BC. Since the author's first study (2016) additional skeletal material was available and was subsequently incorporated into this analysis (Anctil, 2016). Consequently, a sub-sample of 14 randomly chosen individuals, due to time constraints, dating to the above period were included in this analysis (Table 8, Appendix VIII). Consequently, in total 45 randomly chosen individuals were analysed from the Pontecagnano (southern Italy) cemetery population (Table 8, Appendix VIII). Although several previous analyses have been conducted, this skeletal material was included for purely comparative purposes. Pontecagnano (southern Italy) was chosen as the location of the cemetery lies outside the known area of maximum Celtic expansion, the population has not been associated with Celtic material culture, languages or ethnicity, it is contemporaneous with the other samples and to help establish the range of phenetic diversity among European populations during the Iron Age irrespective of the La Tène=Celtic paradigm.

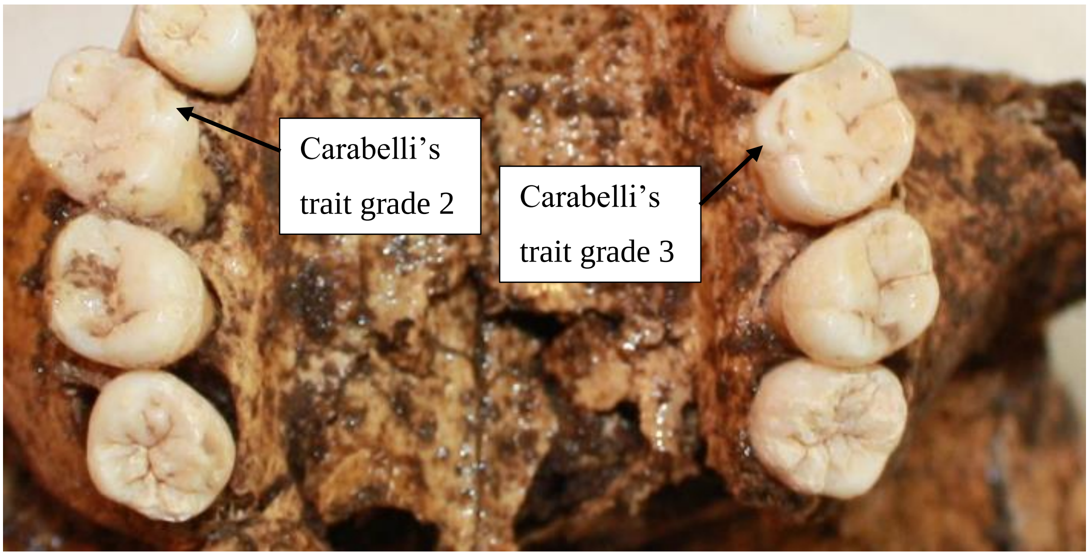
Data collection

Each sample listed above was examined for observable dental morphological crown and root traits (See Table 8 for the total individuals scored for dental nonmetric traits for each sample). Data were collected using the standardized ASUDAS system that is well established for determining inter-trait variations (See page 114 for more detail about the ASUDAS system) (Coppa et al., 2007; Cucina et al., 1998; Irish, 1993; 2010, 2016; Irish et al., 2014, 2018; Scott and Irish, 2017). Although the ASUDAS system consists of >100 nonmetric traits, a subset of 36 traits, based on the work of Irish (1993), were used for this analysis (Figures 51-53) (See page 114, Table 9 for a list of the 36 traits used in this thesis and Appendix I descriptions of these specific dental traits). These traits have been used in numerous previous studies and have proven successful in characterizing and comparing biological affinity among and within populations (Coppa et al., 1998, 2000, 2007; Cucina et al., 1999; Hanihara, 2008, 2010; Irish, 1993, 1997, 1998b, c, 2000, 2005, 2006, 2008, 2010, 2016; Irish et al., 2014, 2018; Irish and Guatelli-Steinberg, 2003; Matsumura et al., 2009; Turner, 1969; 1984, 1985). Some traits such as, maxillary and mandibular tori (bony outgrowths on the interior surface of the maxilla or mandible) have multifactorial origins, and have a polygenic mode of inheritance in which several genes and environmental factors interact to produce these traits. Additionally, other traits are also influenced by skull dimensions and growth patterns. For example, rocker jaw, a mandible with a continuous convex curve along the inferior surface of the mandibular corpus which causes it to rock back-and-forth when placed on a flat surface (Irish, 1993, 2006, 2008; Scott and Irish, 2017). Nonmetric traits were scored following the ASUDAS scoring procedures, and corresponding trait breakpoints, outlined in Turner et al (1991) (Appendix I). Frequencies of occurrence for each dental crown and root nonmetric trait were recorded for each sample on ASUDAS scoring sheets (Appendix 1).

The total sample sizes used in this analysis are presented in Table 8. Information about the individuals excavated, number of individuals included or excluded from this analysis, the methods used by the recording osteologist to determine age-at-death and estimate sex for adults are presented in Appendix VIII. As the traits used in this analysis have not been found to be sexually dimorphic the sexes were pooled following standard procedure (Irish, 1993, 2016; Irish et al., 2014, 2018; Scott and Irish, 2017; Turner et al., 1991). The ASUDAS system, and the corresponding trait breakpoints, outlined in Turner et al (1991) are based on permanent dentition; only adults and sub-adults with permanent dentitions (>17 years old) were included in this analysis (See page 114, Appendix VIII). However, the samples were not composed entirely of individuals, within the above age categories, with complete dentition (e.g., 32 teeth). Consequently, those traits that could be scored, based on the available dentition per sample, were scored and recorded.

Those few individuals with limited teeth available for analysis, e.g., <15, were included as the number of traits able to be observed and recorded were similar to those individuals with more teeth preserved, due to differential tooth preservation, wear and pathologies. In cases of bilateral expression, both antimeres were recorded. In order to allow for asymmetry, the side with the greatest degree of trait expression was counted in an effort to establish the maximum genetic potential for each trait (Figure 33) (Irish, 1993; Irish et al., 2014, 2018; Turner, 1985; Turner et al., 1991; Scott and Irish, 2017). To maximize sample size in cases where only one side was present that side was scored and presumed to represent the highest degree of expression (See pages 113 and 119) (Irish, 1993, 2016; Irish et al., 2014, 2018; Scott and Turner, 1997; Turner, 1985; Turner et al., 1991; Scott and Irish, 2017). Traits were scored twice under the same conditions, e.g., lighting, on non-adjacent days, to assess intra-observer error (intra-observer error will be discussed further in chapter 6).

Figure 33. Example of dentition with bilateral trait expression, superior occlusal view of the maxilla. Carabelli's trait is visible on both sides of the dentition, however, the degree of trait expression is not equal. In these cases, the highest degree of trait expression was counted and presumed to represent the greatest genetic potential for the trait. Rudston Makeshift (east Yorkshire, Britain) burial 99, adult male.



Major differences in wear among samples, when encountered, was documented and acknowledged to help account for the missing completely at random, MCAR, assumption (Scott and Irish, 2017). A sampling bias may occur when teeth that are subjectively considered too worn are not included in subsequent analyses. Consequently, the missing data are assumed to be missing completely at random (Burnett, 2016) (See Appendix III for a description of MCAR and its effect on dental nonmetric trait analysis). In some cases a tooth that exhibits heavy dental wear is excluded from any subsequent analyses, due to the assumption that any nonmetric traits were worn away. Dental nonmetric traits for heavily worn teeth are subsequently scored as no data. However, in some cases, some traits were, in fact, absent as should have been scored as a grade 0 (Appendix III) (Burnett, 2016). Documenting the differences in dental wear among the samples helps to account for the MCAR assumption by acknowledging the fact that a potential sampling bias has occurred in the scoring of nonmetric traits as no data instead of a grade 0 (Appendix III) (Burnett, 2016).

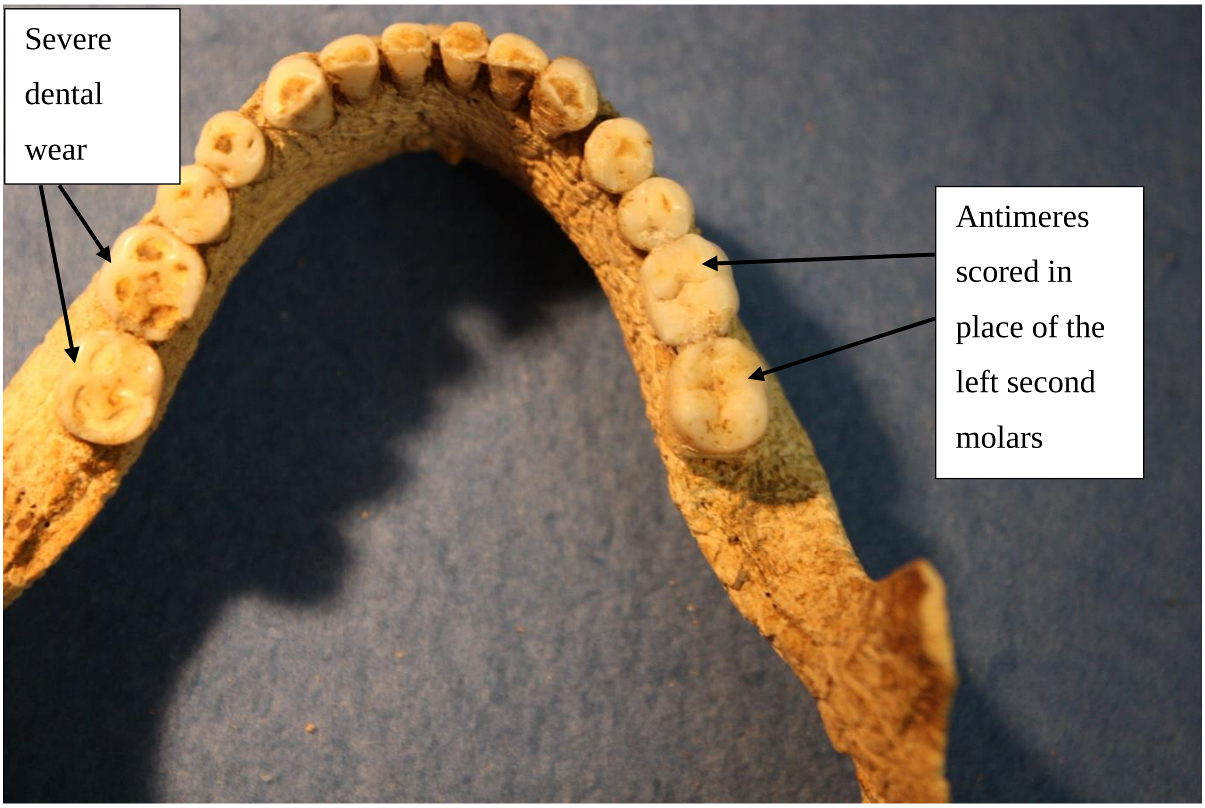
Trait grades were not downgraded or upgraded, instead, the level of wear was recorded per tooth (Irish, 1993, 2006; Irish et al., 2014, 2018). Although the above methods enable moderately worn dentitions to be recorded and subsequently included in analyses and maximizes sample size, the majority of the samples in this thesis only had mild to moderate dental wear (Burnett, 1986, 2016; Burnett et al., 2013). When observed severe wear was predominantly encountered over the majority of the dentition, therefore, these individuals were removed from subsequent analysis (Figure 34). Thus, it was subsequently determined whether the level of dental wear facilitated trait scoring or whether the amount of wear was too great for any traits to be scored. Those few dentitions which had moderate to severe dental wear on specific teeth, such as the molars, the antimere, when available, was scored (Figure 35). However, when the antimere was not available and the level of wear was too great (i.e., the enamel was completely gone) the tooth was not scored for any trait.

Quantitative analysis

The 36 traits were subsequently entered into Statistical Package for Social Sciences, SPSS, version 25.0. Differences in the frequencies of these traits provide the basis for comparing and describing the samples (Tables 8 and 9). These traits were dichotomized into categories of present or absent based on each trait's appraised morphological thresholds, according to standard protocol as described by Scott (1973), Nichol (1990), Turner et al (1991) and Irish (1993). Trait dichotomization is necessary to calculate inter-sample phenetic distances with the MMD distance statistic (See pages 188 and 206) (Haeussler et al., 1988; Sjøvold, 1977). Dichotomization facilitates tabulation of trait frequencies and is required before the data are compared using the MMD (Green and Suchey, 1976; Harris and Sjøvold, 2004; Irish, 1993, 1997, 2010, 2016; Irish et al., 2014, 2018; Sjøvold, 1973, 1977). The number of individuals per sample expressing a particular trait will be determined, along with the total number of individuals for whom the trait could be scored (Table 9). From these data, the percentage of each trait's occurrence by sample will be calculated (Table 9). From an examination of the resulting data, a characterization of each sample based on the suite of traits and a rudimentary phenetic comparison among samples can be obtained.

Figure 34. Example of severe dental wear excluded from data collection. Superior occlusal view of the mandible. Dürrnberg (Austria), La Tène Eislfeld burial 309 individual number 1, adult female.

Figure 35. Example of dentition for which the antimere had to be scored because of severe wear. Superior occlusal view of the mandible. Münsingen-Rain (Switzerland), burial 53, adult female.



Principal components analysis (PCA)

PCA is used to edit and remove problematic traits prior to MMD analysis (Green et al., 1979; Green and Suchey, 1976; Harris and Sjøvold, 2004; Irish, 2008, 2010, 2016; Irish et al., 2014, 2018). Fixed or largely invariant traits, those traits having minimal or no discriminatory value, were removed, including those that occurred at 0% and 100% across all samples; as these traits contribute no relevant information for identifying differences among samples. Further, their inclusion in any subsequent analysis can result in negative MMD values. These values can result in spurious results, or relationships, as they have no “biological meaning” (Harris and Sjøvold, 2004, p 91). Traits with observations of <10%

across all samples were also removed as the analysis is not intended to correct for trait observations of less than 10 (Green et al., 1979; Green and Suchey, 1976). The remaining traits were submitted to PCA to identify those that are most likely to drive inter-sample variation, those that are minimally discriminatory and additional non-contributory traits (Harris and Sjøvold, 2004; Irish, 2010). In this thesis, any variable not receiving a PCA loading of at least |0.500| on any component was eliminated from subsequent analysis (See page 202) (Irish, 2008, 2010, 2016; Irish et al., 2014, 2018).

In PCA, the original correlated variables are linearly transformed into a smaller set of uncorrelated compound variables (Abdi and Williams, 2010; Irish, 2010; Jakson, 2005; Jolliffe, 2002; Jolliffe and Cadima, 2016; Lever et al., 2017; Pearson, 1901; Rasmus and Smilde, 2014). This reduction in dimensionality, or variance, produces fewer linearly uncorrelated variables, or principal components (Harris and Sjøvold, 2004; Irish, 2010; Jakson, 2005; Jolliffe, 2002; Jolliffe and Cadima, 2016; Lever et al., 2017; Rasmus and Smilde, 2014). The first component explains the greatest amount of variance, followed by the second and third, and so on (Harris and Sjøvold, 2004; Irish, 2010; Jakson, 2005; Jolliffe, 2002; Jolliffe and Cadima, 2016; Lever et al., 2017; Rasmus and Smilde, 2014). These principal components retain most of the information from the original variables while remaining mutually uncorrelated and orthogonal (Harris and Sjøvold, 2004; Irish, 2010; Jakson, 2005; Jolliffe, 2002; Jolliffe and Cadima, 2016; Lever et al., 2017; Rasmus and Smilde, 2014). Correlations, or loadings, are computed between the original variables and the principal components (Irish, 2010; Jakson, 2005; Jolliffe, 2002; Jolliffe and Cadima, 2016; Lever et al., 2017; Rasmus and Smilde, 2014). Samples can then be plotted facilitating a visual comparison of the similarities and differences and to determine whether they can be grouped (Abdi and Williams, 2010; Irish, 2010; Jakson, 2005; Jolliffe, 2002; Jolliffe and Cadima, 2016; Lever et al., 2017; Rasmus and Smilde, 2014). PCA was chosen for this analysis as the specific dental traits that are accountable for the observed inter-sample variation are identified. Varimax rotation of the PCA coordinates was also chosen for this analysis because the difference between large and small component loadings can be maximized (Irish, 2010, 2016; Jakson, 2005; Jolliffe, 2002; Jolliffe and Cadima, 2016; Lever et al., 2017; Rasmus and Smilde, 2014).This method is used to support the identification of any additional non-contributory traits from PCA. Varimax rotation is a change of coordinates used in PCA which maximizes the sum of the variances of the squared component loadings

(Irish, 2010, 2016; Jakson, 2005; Jolliffe, 2002; Jolliffe and Cadima, 2016; Lever et al., 2017; Rasmus and Smilde, 2014).

It is recommended that the inter-sample distances be based on as many traits as possible; however, these traits should not be highly correlated with one another as this may lead to erroneous distances or spurious relationships (Irish, 2010, 2016; Jakson, 2005; Jolliffe, 2002; Jolliffe and Cadima, 2016; Lever et al., 2017; Rasmus and Smilde, 2014; Sjøvold, 1977). The undichotomized rank-scale ASUDAS data was submitted to the Kendall's tau-b correlation coefficient in order to evaluate the inter-trait correlation. This method was chosen over others, such as a chi-square test of proportions, as this approach is the most conservative (Irish, 2010). Further, rank grades are more likely to indicate inter-trait correlations and more traits may be removed from subsequent analysis (Irish, 2010). Consequently, those traits remaining are more likely to provide an accurate representation of the inter-sample phenetic distances (Irish, 2010). Those traits that were found to be correlated, with a Kendall's tau-b (t_b) value of ≥ 0.5, comparatively low PCA component loadings and low sample sizes were, removed from subsequent analysis (See page 202, Appendix II). Those traits excluded from subsequent analysis include, labial curve UI1 and cusp 5 UM1 (See page 196, Table 10). In total 20 traits were used in this analysis (See Table 9 for a list of these traits).

Mean measure of divergence (MMD)

The MMD distance statistic has been used in numerous biological affinity studies (e.g., Berry and Berry, 1967, 1972; Berry, 1974; Hubbard, 2012; Irish, 1993, 1997, 1998a, b, c, 2005, 2006, 2008, 2010, 2016; Irish and Guatelli-Steinberg, 2003; Irish and Turner, 1990; Irish et al., 2014, 2018; Larsen, 2015; Sjøvold, 1973, 1977). It is a dissimilarity measure, high values are indicative of greater phenetic distance between samples while low values indicate greater affinity (Irish, 2010, 2016; Irish et al., 2018). MMD values have been shown to correlate strongly with geographic distances, making the statistic applicable to affinity studies (Hanihara, 1989; Hubbard, 2012; Huffman, 2014; Irish, 2010, 2016, Irish et al., 2018, 2020; Nikita, 2015; Vargiu et al., 2009). The MMD formula with the Freeman and Tukey (1950) angular transformation incorporated is as follows:

Equation 1. MMD formula with the Freeman and Tukey angular transformation incorporated (Freeman and Tukey, 1950, Figure 1).

$$\mathrm{MMD} = \frac{\sum_{i=1}^{r} (\theta_{1i} - \theta_{2i})^2 - (1/(n_{1i} + 1/2) + 1/(n_{2i} + 1/2))}{r} \qquad (1)$$

Where:

r = number of uncorrelated traits

θ = angular transformation, where the observed proportion, p, is an unbiased estimator of the population proportion, P, that here θ= [1/2] $\sin^{-1}$ (1-(2k)/ (n+1)) 1 [1/2] $\sin^{-1}$ (1-2 (k+1)/ (n+1))

k = count of positive observations of trait “i"

n = number of individuals examined for trait “i”

Following the assumption that phenetic similarity approximates genetic affinity among samples, CAB Smith’s MMD distance statistic, paired with the Freeman and Tukey angular transformation, which corrects for low (<0.05) or high (>0.95) trait frequencies and small sample sizes (n>10), was used to test the hypotheses in this thesis (See pages 13 and 14) (Freeman and Tukey, 1950; Green and Suchey, 1976; Irish, 2010; Sjøvold, 1973, 1977). This distance statistic provides a quantitative estimate of inter-sample biological distance and phenetic similarities based on the similarities among nonmetric traits (Green and Suchey, 1976; Irish 2010, 2016; Irish et al., 2014, 2018; Sjøvold, 1973, 1977). The MMD distance statistic can also be used on summary data, such as occurrence proportions for each trait in compared data sets. Therefore, the MMD can be used on incomplete data sets, such as those derived from archaeological material (Irish, 2010).

In order to determine whether the samples differ significantly, and therefore are phenetically distinct, each MMD value is compared to its standard deviation (SD) (See page 206) (Green and Suchey, 1976; Irish, 2010; Sjøvold, 1973, 1977). If the MMD value is greater than two times its SD then the null hypothesis that the samples represent the same biological population is rejected at the 0.025 alpha level (Irish, 2010, 2016; Irish et al., 2014, 2018; Sjøvold, 1973, 1977). Conversely, an insignificant MMD value that is less than two times its SD, means it is impossible to distinguish between two samples because they are phenetically indistinguishable, or the size of one or both is small, which can result in an excessively large standard deviation (Sjøvold, 1977). This distance statistic was chosen because it has several advantages over other distance measures, including the way missing data is handled. Those traits that have substantial missing data, e.g., a value of 0, can be included without adversely affecting the statistical calculations as in other distance measures, such as Mahalanobis D^2 (Schillaci et al., 2009). Further, traits that have little or non-contributory information, those that do not drive variation between or among samples, can be removed from subsequent analysis without biasing the MMD distance values (Harris and Sjøvold, 2004, p 91).

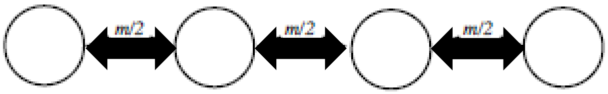
Multidimensional scaling (MDS)

Multidimensional scaling (MDS) was chosen to graphically illustrate the relationships among the samples as identified by the MMD distance statistic. MDS was chosen because it is an effective and largely unbiased method to illustrate affinities between samples (Cox and Cox, 2001; Irish, 2010, 2016; Irish et al., 2014, 2018; Kruskal and Wish, 1978). This method produces two and three-dimensional representations of the proximity data, as a geometric configuration of points (Cox and Cox, 2001; Irish, 2010; Kruskal and Wish, 1978). Although MDS graphs can be produced in a number of dimensions, two-dimensional scaling was chosen for this analysis. Shorter distances among the samples indicate similarity while larger distances indicate dissimilarity (See page 211) (Irish, 2010, 2016; Irish et al., 2014, 2018). A spatial representation of the sample distribution was produced by SPSS version 25.0 procedure Proxscal.

Isolation by distance (IBD)

Isolation by distance is commonly used to substantiate the genetic and ethnic relationships within and among populations (Kimura and Weiss, 1964; Konigsberg, 1990; Relethford, 2004; Slatkin, 1993; Wright, 1943). Limited dispersal, i.e., movement or migration, will result in genetic differences among populations which is proportional to the geographic distance between them, under the assumption that genetic affinity is inverse to spatial distance (See page 135) (Kimura and Weiss, 1964; Konigsberg, 1990; Relethford, 2004; Slatkin, 1993; Wright, 1943). In populations with relatively low effective rates of dispersal, most exchange will occur between neighbouring populations. The migration rate is also the highest between adjacent populations and declines linearly as a function of distance (Konigsberg, 1990; Morton, 1973; Relethford, 2004; Slatkin, 1993). This pattern is common for populations distributed in linear habitats (Relethford, 2004; Slatkin, 1993). The correlation in gene frequencies between populations decreases exponentially as a function of the number of geographic steps between them (Kimura and Weiss, 1964). Therefore, this model is referred to as the stepping-stone model (See page 135) (Kimura and Weiss, 1964; Malécot 1955; Wright 1943). The phenetic correlation between populations is therefore correlated with the rate of migration (Figure 36) (Kimura and Weiss, 1964; Relethford, 2004; Malécot 1955; Wright 1943).

Figure 36. Linear stepping stone model as illustrated between neighbouring populations. The m/2 designates the proportion of individuals exchanged during each generation between adjacent populations (Modified from Kimura and Weiss, 1964, Figure 2).



The stepping stone model can be modified to and apply to between one and three-dimensions (Konigsberg, 1990; Malécot, 1969; Morton, 1977; Slatkin and Maddison, 1990; Slatkin, 1993). In the one-dimensional model gene flow changes systematically by linear processes such as mutation and migration. Under this model, in each generation an individual can migrate at most 1 step in either direction between neighbouring populations (Konigsberg, 1990; Relethford, 2004; Slatkin and Maddison, 1990; Slatkin, 1993). In other words, migration is restricted to be between adjacent populations. Under the two-dimensional model, in each generation, a population exchanges migrants with four surrounding populations but the effective total population number in each remains the same (Hardy and Vekemans, 1999;

Konigsberg, 1990; Malécot, 1969; Morton, 1977; Slatkin and Maddison, 1990; Slatkin, 1993). However, the rate of migration may vary directionally. In the three-dimensional model, a cubic array of populations extends to infinity in all directions (Konigsberg, 1990; Malécot, 1969; Morton, 1977; Slatkin and Maddison, 1993; Slatkin, 1993). Each population has 6 adjacent sub-populations which exchange migrants during each generation. However, the rate of migration under the above models will be directionally dissimilar (Konigsberg, 1990; Malécot, 1969). Genetic correlation falls off more quickly with increasing geographic distance in the three-dimensional model compared to the one and two-dimensional models (Konigsberg, 1990; Slatkin and Maddison, 1990; Slatkin, 1993).

When gene flow occurs predominantly between immediately adjacent populations the number of migrants may be determined by the spatial distribution of the populations (Austerlitz et al., 1997; Baker and Moeed, 1987; Konigsberg, 1990; Relethford, 2004; Slatkin and Maddison, 1990; Slatkin, 1993). However, gene flow should not be viewed in relation to the actual number of migrants moving between populations or groups during each generation. Instead, it should be viewed as equivalent to the number of migrants required to account for the observed phenetic variation if they could move directly between populations (Konigsberg, 1990; Slatkin and Maddison, 1990; Slatkin, 1993). A linear relationship between the average within-group phenetic variation and approximate geographic distance should be observed when the rate of extra-regional gene flow into populations is equal (Blangero, 1990; Konigsberg, 1990). However, when this rate is uneven populations which have higher migration rates will likely be more heterogeneous, compared to those that have limited external gene flow (See page 135) (Blangero 1990; Ibrahim et al., 1996; Kimura and Weiss, 1964; Konigsberg, 1990).

Under the uni-dimensional stepping stone model, a linear correlation between biological affinity and geographic distance is expected as populations move in linear directions along a continuum of neighbouring populations (Konigsberg, 1990; Relethford, 2004; Slatkin, 1993). Therefore, coefficients of determination can be calculated via linear regression in order to determine the percent of phenetic variation that is explained by the geographic distances between populations (Konigsberg, 1990; Relethford, 2004; Slatkin, 1993). Genetic variation can be plotted against geographic distance in order to determine which populations are more or less phenetically distinct from one another than expected based on geographic distance (Konigsberg, 1990; Relethford, 2004; Slatkin, 1993). Although as the migration and/or transportation routes between geographically diverse populations are not generally known, inter-population straight-line distances are commonly used (Irish et al., 2018; Konigsberg, 1990; Relethford, 2004). Consequently, these distances are approximations and do not reflect reality on the landscape, as would be any potential migrations routes throughout the core and expansion regions (Irish et al., 2018; Konigsberg, 1990; Relethford, 2004). Thus, although potentially underestimates, linear distances between samples were used as they should be less biased for analytical purposes (Irish et al., 2018; Konigsberg, 1990; Relethford, 2004). As the spatial distances used in this analysis are approximations, the simplest, linear uni-dimensional stepping stone variant of the model was used (Konigsberg, 1990). The Geographic Distance Matrix Generator (vers, 1.2.3) was employed to calculate inter-sample straight-line distances (Ersts, 2014).

Mantel Test

The significance of the relationship between phenetic, and by proxy genetic, and geographic distances can be determined with a Mantel's permutation test (Smouse et al., 1986; Wright, 1943). A Mantel test was performed to contrast the symmetric MMD and geographic distance matrices, to test for correlations among samples and to determine whether the observed differences are the result of isolation by distance (Huffman, 2014; Smouse et al., 1986; Smouse and Long, 1992). This method calculates the correlation between matrices using the Pearson’s product-moment correlation coefficient (Pearson’s r) (Mantel, 1967; Mantel and Valand, 1970). Significance values are derived from random permutations of the data within these matrices, by row or column, to examine changes in the correlation coefficients. Correlation between the geographic and symmetric MMD matrices was performed using the R program and the Mantel test from the ade4 library package (Dray et al., 2018; R Core Team, 2017). The standard Mantel test formula is as follows:

Equation 2. Standard Mantel test (Diniz-Filno et al., 2013, Figure 3).

$$Z_N = \frac{\sum_{i=1}^{n}\sum_{j=1}^{n}(g_{ij}-\overline{\mathbf{G}})\times(d_{ij}\times\overline{\mathbf{D}})}{\mathrm{var}(\mathbf{G})^{1/2}\times\mathrm{var}(\mathbf{D})\ ^{1/2}}$$

Where:
i: population 1
j: population 2
g_{ij}: genetic distances between populations
d_{ij}: geographic distances between populations
G: means of the genetic distances between populations
D: mean of the geographic distances between populations
var(G): variance of the genetic matrix
var (D): variance of geographic matrix

Because the Mantel test is derived from the sum products of distances its value depends on how many populations are studied, as well as the magnitude of their distances (Guillot and Rousset, 2013; Manly, 1985; Mantel, 1967; Smouse et al., 1986). Here, values close to 1 indicate that an increase in geographic distance between populations is related to an increase in their genetic distance. Values close to 0 indicate there is no relationship between the two matrices (Diniz-Filno et al., 2013).

Hierarchical cluster analysis

Cluster analysis using between group linkage and Wards method was used to provide a further illustration of the among sample affinities based on the MMD distance values. Cluster analysis is a method for the identification of homogenous subgroups (Blei and Lafferty, 2009; Everitt et al., 2011; Hair et al., 2009; Yim and Ramdeen, 2015). This analysis combines samples into homogeneous clusters by merging them into a series of sequential steps (Blei and Lafferty, 2009; Everitt et al., 2011; Yim and Ramdeen, 2015). Therefore, increasing within group homogeneity and among group heterogeneity within and among the resulting clusters. Average linkage and Ward's method were chosen to provide an additional graphical representation of the variation among the samples. The average linkage procedure defines the distance between groups as the average distance between each of the members. This method provides a more accurate evaluation of the distances between clusters than those derived from single and complete linkage (Blei and Lafferty, 2009; Everitt et al., 2011; Yim and Ramdeen, 2015). In this method, the distance between two clusters is defined as the average distance between all cases in one cluster compared those in another cluster (See page 215) (Blei and Lafferty, 2009; Everitt et al., 2011; Yim and Ramdeen, 2015). Rather than deriving clusters based on the minimum or furthest distances between pairs or cases, as outliers may have an impact on the resulting clusters derived from single and complete linkage (Blei and Lafferty, 2009; Everitt et al., 2011; Yim and Ramdeen, 2015).

Ward’s method creates clusters that minimize the within and between group variance (Blei and Lafferty, 2009; Everitt et al., 2011; Murtagh 2014). As the joining of clusters increases variability, in this method clusters are created in a way that least increases the within group variance. Cluster linkage in Ward's method is based on the sum of squares (See page 215) (Everitt et al., 2011; Murtagh 2014; Szekely, 2005; Yim and Ramdeen, 2015). The clusters provided by these methods are presented as dendrograms, with each branch representing a separate cluster. Although dendrograms can be used for identifying similarities among populations, they are not direct reconstructions of population history.

PCA, MMD, MDS, IBD and Cluster analysis were chosen as the best methods available for this analysis because of their respective abilities to determine the specific dental nonmetric traits that are accountable for the inter-sample variation; as well as providing an estimate of inter-sample phenetic affinity based on similarities and differences in these traits. Therefore, the combined results of these methods can be used to identify key traits driving inter-sample variation, to identify inter-sample dental phenetic affinities, graphically illustrate those affinities, and to determine whether phenetic differentiation increases with geographic distance among samples. Detailed examination of the results and interpretations are provided in Chapter 7.

Chapter 6: Results

The dental trait percentages and frequencies for each sample are presented in Table 9. As mentioned, 1 of the samples is geographically and descriptively associated with the proto-Celts (Hallstatt D, Austria), 6 are associated with the core (Münsingen-Rain, Switzerland, Dürrnberg Hallstatt, Austria, Dürrnberg La Tène, Austria, Pottenbrunn, Austria, Nebringen, Stuttgart, Germany, and a pooled German sample, Stuttgart, Germany), and 4 are associated with the expansion regions (Wetwang Slack, east Yorkshire, Britain, Rudston Makeshift, east Yorkshire, Britain, Kutná-Hora-Karlov, Czech Republic, and Radovesice I and II, Czech Republic). The remaining sample is not associated with the Celts, Pontecagnano (southern Italy), and was included for comparative purposes. Although some differences in ASUDAS scores occurred, these differences never occurred across a trait breakpoint (e.g., on the order of a grade, the degree of trait expression, 1 versus a grade 2) (Appendix I). Intra-observer scoring error was calculated using a Wilcoxon signed-rank test, the results of which fell into the acceptable range. Since the p-value was greater than 0.05, 0.089, the null hypothesis that there is no difference between the first and second set of trait observations was not rejected. This test indicates that there is a high degree of intra-observer repeatability and concordance.

The pooled German sample has high frequencies, relative to the other samples, of Lingual cusp LP2 (range of 32.30%- 75% across samples), Hypocone UM2 (1.66%-10.71%) and C7 LM1 (0%-5.71%) (Table 9). The latter are also observed in similar frequencies in the Nebringen (Stuttgart, Germany), Münsingen-Rain (Switzerland), Radovesice (Czech Republic), Kutná-Hora-Karlov (Czech Republic), Pontecagnano (southern Italy) and Hallstatt D (Austria) samples. High frequencies of Root Number UM2 (2.17%-11.11%) are observed in the Nebringen (Stuttgart, Germany) sample. Similar frequencies are also found in the Pottenbrunn (Austria), Münsingen-Rain (Switzerland), Hallstatt D (Austria), Dürrnberg Hallstatt (Austria), and Rudston Makeshift (east Yorkshire, Britain) samples. Those traits observed at high frequencies in the Pottenbrunn (Austria) sample include; Interruption Groove UI2 (8.57%- 21.87%) and Root number UP1 (0%-12.19%) (Table 9). These traits are also found at similar frequencies in the Nebringen (Stuttgart, Germany), Hallstatt D (Austria), Radovesice (Czech Republic), Dürrnberg Hallstatt (Austria), and Rudston Makeshift (east Yorkshire, Britain) samples. The Münsingen-Rain (Switzerland), sample has high frequencies of Tuberculum Dentale UI2 (0%-14.25%) and Groove Pattern LM2 (27.17%-38.23%) (Table 9). The former is also found in high frequencies in the Nebringen (Stuttgart, Germany), Pottenbrunn (Austria), Dürrnberg (Austria), Hallstatt D (Austria) and Dürrnberg La Tène (Austria). The latter is found in similar frequencies among all the samples. High frequencies of Anterior Fovea LM1 (33.33%-80.55%) are found in the Hallstatt D (Austria) sample, whereas the remaining traits occur at similar frequencies to the other samples (Table 9).

A similar pattern is evident in the Dürrnberg Hallstatt (Austria) and Dürrnberg La Tène (Austria) samples. As only high frequencies of C1–C2 Crest LM1 (6.45%-16.66%), Cusp number LM1 (9.67%-23.88%), and Deflecting wrinkle LM (6.89%-16.66%) are observed in the above samples, respectively (Table 9). The former also occurs in similar frequencies in the Hallstatt D (Austria), Münsingen-Rain (Switzerland) and German (Stuttgart, Germany), samples. The latter is also found in the Nebringen (Stuttgart, Germany), Pontecagnano (southern Italy), Pottenbrunn (Austria). Wetwang Slack (east Yorkshire, Britain) and Hallstatt D (Austria) samples at similar frequencies. Carabelli's Trait UM1 (30%-75%) and Groove Pattern LM2 are found in high frequencies in the Radovesice (Czech Republic) sample (Table 9). Similar frequencies of the former are also observed in the Pontecagnano (southern Italy), Rudston Makeshift (east Yorkshire, Britain), Münsingen-Rain (Switzerland) and Hallstatt D (Austria) samples (Table 9). The Kutná-Hora-Karlov (Czech Republic) and Hallstatt D (Austria) samples have high frequencies of Anterior Fovea LM1 (80%). The Rudston Makeshift (east Yorkshire, Britain) sample has high frequencies of Labial Curvature UI1 (0%-21.42%) and Distal Accessory Ridge UC (30.76%-75%) (Table 9). These traits are also found in similar frequencies in the Hallstatt D (Austria), Radovesice (Czech Republic), Kutna-Hora-Karlov (Czech Republic), Pottenbrunn (Austria) and German (Stuttgart, Germany) samples, respectively. High frequencies of Cusp 5 UM1 (3.33%-16.66%); Parastyle UM3 (3.57%-12.50%); Enamel Extension UM1 (5.40%-14.90%), Rocker Jaw (8.33%-33.33%); Tome's Root LP1 (5.26%-26.1%); Root Number LM1 (5%-27.77%); Root Number LM2 (26.63%-32.50%); Protostylid LM1 (5.26%-32.14%); Torsomolar Angle LM3 (5.55%-31.42%) and Groove Pattern LM2 are found in the Pontecagnano (southern Italy) sample (Table 9). The Wetwang Slack (east Yorkshire, Britain) sample has high frequencies of Cusp number LM2 (5.71%-31.91%), and Root Number LC (4.76%-30%).

Table 9. Dental trait percentages (%) and number of individuals scored (n) for the core and expansion region samples.

		Core and expansion region samples											
Trait [1]		**GER**	**NEB**	**POTT**	**MunRain**	**HALD**	**DURH**	**DURL**	**RAD**	**KHK**	**RUD**	**PON**	**WWS**
Winging UI1	%	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
(+ = ASU 1)	n	0	0	0	0	0	0	0	0	0	0	0	0
Labial Curvature UI1	%	21.42	10.52	12.12	12.50	23.33	11.11	20.00	15.62	21.87	26.66	0.00	18.69
(+ = ASU 2-4)	n	28	19	33	32	30	27	65	32	32	30	28	107
Palatine torus	%	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
(+=ASU 2-3)	n	0	0	0	0	0	0	0	0	0	0	0	0
Shovelling UI1	%	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
(+=ASU 2-6)	n	0	0	0	0	0	0	0	0	0	0	0	0
Double Shovelling UI1	%	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
(+=ASU 2-6)	n	0	0	0	0	0	0	0	0	0	0	0	0
Interruption Groove	%	0.0	18.18	21.87	8.57	8.88	12.50	10.76	9.37	9.67	9.37	10.00	10.09
UI2(+=ASU+)	n	32	22	32	35	34	32	65	32	31	32	30	109
Tuberculum Dentale	%	6.25	13.63	12.50	14.28	5.88	12.50	12.30	9.37	3.22	12.50	0.0	9.17
UI2 (+=ASU2-6)	n	32	22	32	35	34	32	65	32	31	32	30	109
Bushman canine UC	%	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
(+=ASU1-3)	n	0	0	0	0	0	0	0	0	0	0	0	0
Distal accessory ridge	%	75.00	65.00	75.00	69.23	75.00	69.23	60.00	72.00	79.16	80.00	60.00	59.85
UC (+=ASU2-5)	n	24	20	24	26	24	26	60	25	24	25	25	142
Hypocone UM2	%	10.71	5.88	3.57	3.03	3.12	3.57	1.66	6.66	6.45	3.12	6.89	5.63
(+=ASU3-6)	n	28	17	28	33	32	28	60	30	31	32	29	142
Cusp 5 UM1	%	6.66	5.88	3.33	3.33	3.87	6.89	4.68	3.87	10.00	10.00	16.66	3.42
(+=ASU2-5)	n	30	17	30	30	31	29	64	31	30	30	30	146

[1] ASU rank-scale trait breakpoints from Irish (1993, 1997, 1998 a, b, 2005, 2006, 2014, 2016; Irish et al., 2018), Scott and Irish (2017) and Scott and Turner (1997). German (GER); NEB (Nebringen); Pottenbrunn (POTT); MunRain (Münsingen-Rain); HALD (Hallstatt D); Dürrnberg Hallstatt (DURH); Dürrnberg La Tène (DURL); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

Table 9 continued. Dental trait percentages (%) and number of individuals scored (n) for the core and expansion region samples.

		Core and expansion region samples											
Trait[1]		**GER**	**NEB**	**POTT**	**MunRain**	**HALD**	**DURH**	**DURL**	**RAD**	**KHK**	**RUD**	**PON**	**WWS**
Carabelli's trait UM1 (+=ASU2-7)	%	56.66	52.94	58.06	61.29	64.51	60.00	73.84	75.00	46.66	66.66	66.66	64.66
	n	30	17	31	31	31	30	65	32	30	30	30	150
Parastyle UM3 (+=ASU1-5)	%	6.45	5.26	6.25	6.45	6.06	3.22	4.83	6.45	6.06	6.25	12.50	3.57
	n	31	19	32	31	33	31	62	31	33	32	30	140
Enamel extension UM1 (+=ASU1-3)	%	6.25	10.52	6.45	6.45	6.45	6.45	6.25	6.25	5.40	6.25	14.90	6.66
	n	32	19	31	31	31	31	64	32	33	32	30	150
Root number UP1 (+=ASU2+)	%	7.14	10.00	12.19	9.52	10.25	10.71	0.0	10.25	3.33	10.25	0.0	0.0
	n	15	20	41	42	39	28	26	39	30	39	35	48
Root number UM2 (+=ASU3+)	%	7.14	11.11	10.52	10.00	10.25	10.00	2.63	7.50	5.40	10.52	0.00	2.17
	n	14	18	38	40	39	20	38	40	37	38	35	46
Peg-reduced UI2 (+=ASU P or R)	%	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	n	0	0	0	0	0	0	0	0	0	0	0	0
Odontome P1–P2 (+=ASU +)	%	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	n	0	0	0	0	0	0	0	0	0	0	0	0
Congenital absence UM3(+=ASU -)	%	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	n	0	0	0	0	0	0	0	0	0	0	0	0
Midline diastema UI1 (+≥0.5mm)	%	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	n	0	0	0	0	0	0	0	0	0	0	0	0
Lingual cusp LP2 (+=ASU 2-9)	%	75.00	68.42	61.53	71.42	70.37	67.85	60.00	70.37	67.78	66.66	60.71	63.84
	n	28	19	26	28	27	28	65	27	28	27	28	130

[1] ASU rank-scale trait breakpoints from Irish (1993, 1997, 1998 a, b, 2005, 2006, 2014, 2016; Irish et al., 2018), Scott and Irish (2017) and Scott and Turner (1997). German (GER); NEB (Nebringen); Pottenbrunn (POTT); MunRain (Münsingen-Rain); HALD (Hallstatt D); Dürrnberg Hallstatt (DURH); Dürrnberg La Tène (DURL); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

Table 9 continued. Dental trait percentages (%) and number of individuals scored (n) for the core and expansion region samples.

		Core and expansion region samples											
Trait[1]		**GER**	**NEB**	**POTT**	**MunRain**	**HALD**	**DURH**	**DURL**	**RAD**	**KHK**	**RUD**	**PON**	**WWS**
Anterior fovea LM1	%	76.66	80.0	68.57	79.41	80.0	64.51	60.00	78.12	80.0	79.41	78.57	62.18
(+=ASU2-4)	n	30	20	35	34	35	31	65	32	35	34	28	119
Mandibular torus	%	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
(+=ASU2-3)	n	0	0	0	0	0	0	0	0	0	0	0	0
Groove pattern LM2	%	33.33	27.77	35.29	38.23	37.14	35.29	36.36	38.23	34.28	35.29	38.23	32.41
(+=ASU Y)	n	30	18	34	34	35	34	66	34	35	34	34	145
Rocker jaw	%	8.33	11.76	11.76	11.76	12.50	11.76	12.50	6.25	6.25	7.69	33.33	20.0
(+=ASU 1-2)	n	12	17	17	17	16	17	16	16	16	13	15	130
Cusp number LM1	%	17.14	21.05	19.44	18.18	19.44	15.15	23.88	12.50	14.64	9.67	20.00	16.36
(+=ASU6+)	n	33	19	36	34	36	33	67	33	36	36	30	135
Cusp number LM2	%	5.71	22.22	20.00	21.21	18.75	18.75	29.68	18.75	17.64	16.66	16.66	16.31
(+=ASU5+)	n	35	18	34	33	32	32	64	32	34	31	30	141
Deflecting wrinkle	%	10.00	15.78	12.50	12.12	12.90	10.00	16.66	10.33	6.89	9.37	13.33	13.86
LM(+=ASU 2-3)	n	30	19	30	33	31	30	60	30	29	32	30	137
C1–C2 crest	%	16.66	10.52	13.33	15.15	16.12	16.66	8.19	13.33	10.00	9.67	6.45	7.85
LM1(+=ASU+)	n	30	19	30	33	31	30	61	30	30	31	30	60
Protostylid LM1	%	10.71	5.26	10.0	10.00	10.34	9.37	48.33	9.09	10.0	8.82	32.14	9.33
(+=ASU1-6)	n	28	19	30	30	29	32	60	31	30	34	28	135
Cusp 7 LM1	%	5.71	5.55	0.0	0.00	2.77	0.0	0.0	0.00	0.00	0.0	0.0	0.0
(+=ASU2-4)	n	35	18	34	34	36	33	66	34	33	35	34	140

[1] ASU rank-scale trait breakpoints from Irish (1993, 1997, 1998 a, b, 2005, 2006, 2014, 2016; Irish et al., 2018), Scott and Irish (2017) and Scott and Turner (1997). German (GER); NEB (Nebringen); Pottenbrunn (POTT); MunRain (Münsingen-Rain); HALD (Hallstatt D); Dürrnberg Hallstatt (DURH); Dürrnberg La Tène (DURL); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

Table 9 continued. Dental trait percentages (%) and number of individuals scored (n) for the core and expansion region samples.

		Core and expansion region samples											
Trait[1]		**GER**	**NEB**	**POTT**	**MunRain**	**HALD**	**DURH**	**DURL**	**RAD**	**KHK**	**RUD**	**PON**	**WWS**
Tome's root LP1(+=ASU3-5)	%	10.00	11.76	10.52	9.09	11.1	5.55	12.00	16.66	9.52	5.26	26.31	11.11
	n	10	17	19	22	18	18	50	18	21	19	19	45
Root number LC (+=ASU2+)	%	10.00	5.00	8.33	8.33	11.41	5.71	22.38	5.55	4.76	5.71	6.06	30.00
	n	10	20	36	36	35	35	67	36	21	35	27	50
Root number LM1(+=ASU3+)	%	5.60	5.00	5.60	5.50	5.60	5.60	10.63	5.55	5.26	5.55	27.77	11.10
	n	19	20	18	18	20	18	47	18	19	18	18	50
Root number LM2(+=ASU2+)	%	10.00	10.00	15.00	15.38	11.90	7.69	2.63	10.25	10.00	12.50	32.50	4.34
	n	10	20	40	39	42	20	38	39	20	40	30	46
Torsomolar angleLM3(+=ASU+)	%	5.55	5.26	5.88	5.88	5.55	5.88	17.64	5.71	4.16	5.88	31.42	17.64
	n	18	19	34	34	36	34	49	35	24	35	33	58

[1] ASU rank-scale trait breakpoints from Irish (1993, 1997, 1998 a, b, 2005, 2006, 2014, 2016; Irish et al., 2018), Scott and Irish (2017) and Scott and Turner (1997). German (GER); NEB (Nebringen); Pottenbrunn (POTT); MunRain (Münsingen-Rain); HALD (Hallstatt D); Dürrnberg Hallstatt (DURH); Dürrnberg La Tène (DURL); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

The dental nonmetric traits observed at high frequencies are characteristic of morphologically simple, fewer morphological traits, mass-reduced dentitions, low frequencies of traits that add size such as, additional cusps, often associated with European populations, in spite of high frequencies of a few mass-additive traits, those that add size, (such as Carabelli's trait UM1) (See page 215, Appendix III) (Hanihara, 2008; Hillson, 1996; Mayhall et al., 1982; Scott and Irish, 2017).

Principal components analysis (PCA)

Several non-contributory traits, those that occur at 0% or 100% across all samples, were removed from further analysis (See page 186). These included Winging UI1, Palatine torus, Shovelling UI1, Double Shovelling UI1, Bushman Canine UC, Odontome P1-P2, Congenital Absence UM3, Midline Diastema UI1, Mandibular torus, and Peg-Reduced UI2. This initial round of trait editing reduced the number of traits to 26. After the remaining trait frequencies were calculated, the data were submitted to PCA to identify the specific traits most responsible for the observed inter-sample variation. As sample size must be larger than 10 in any subgroup for the Freeman-Tukey transformation for unequal sample variances to work, Cusp 7 LM1 was removed from further analysis, reducing the number of traits to 25 (See page 186). These percent data, the trait frequencies among the samples, were then submitted to PCA to identify additional largely non-contributory traits across all samples. Ten components with eigenvalues >2.0 were obtained that accounted for 100% of the total variance. However, examination of the accompanying scree plot suggests that the first two components, which account for 82.12% of the variance, are the most important (Figure 37). A Two-dimensional scatterplot of the component scores is presented in Figure 38. Separation among the samples is evident. Unrotated loadings for these components are listed in Table 10. The PCA component loadings, eigenvalues and variance explained for the first 3 components, the rotated component matrix and a three-dimensional scatterplot of the component scores are presented in appendix VI for comparison (Tables 17 and 18 and Figure 63, respectively).

Traits with strong positive and negative values (>|0.500|) are responsible for driving most of the inter-sample variation (Irish, 2010, 2016; Irish et al., 2014, 2018). Very strong (>0.7) positive loadings for component 1, x-axis, include Root number UP1, Root number UM2, Lingual cusp LP2, Anterior fovea LM1, Deflecting wrinkle LM and C1–C2 crest LM1, and are most responsible for pushing the samples with high percentages of these traits towards the positive end of the x-axis. Conversely, very strong negative loadings (< -0.7) include Carabelli’s UM1, Protostylid LM1, Tome’s root LP1, Root number LM1, Root number LM2, and Torsomolar angle LM3, and are responsible for pushing samples with high percentages of these traits towards the negative end of the x-axis. Very strong positive loadings for component 2, y-axis, include Groove pattern LM2, Cusp number LM1, and Root number LC. Similarly, very strong negative loadings for component 2, y-axis, include Tuberculum Dentale UI2, Distal accessory ridge UC, Cusp number LM2, and Parastyle UM3. Hypocone UM2, Interruption groove UI2, and Rocker jaw were dropped from further analysis as they are mostly non-contributory (loadings < |0.500| on all axes).

Figure 37. Scree plot indicating that the first two components which account for 82.12% of the variance are the most important.

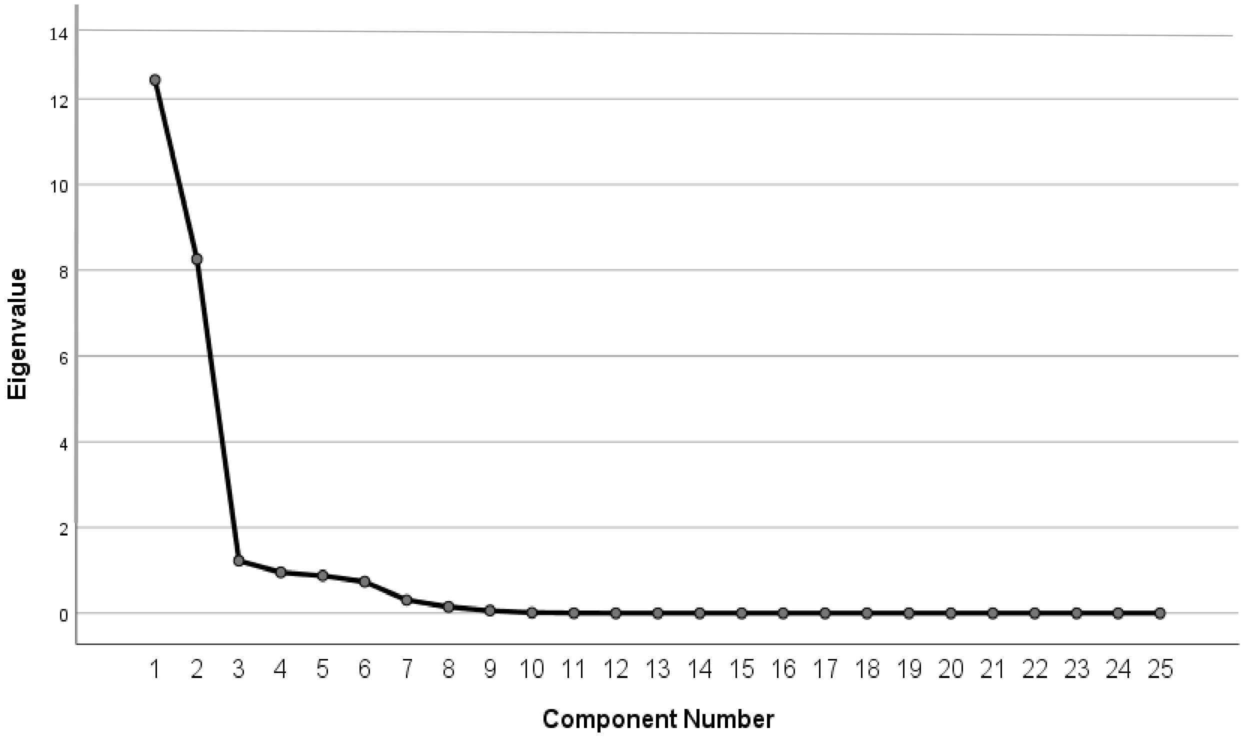


Figure 38. Two-dimensional scatterplot of the first two components among the samples for 25 dental traits. The first two components account for 82.12% of the total variance (47.85% on the x-axis and 34.27% on the y-axis) (See Table 8 for sample abbreviations). Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná -Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

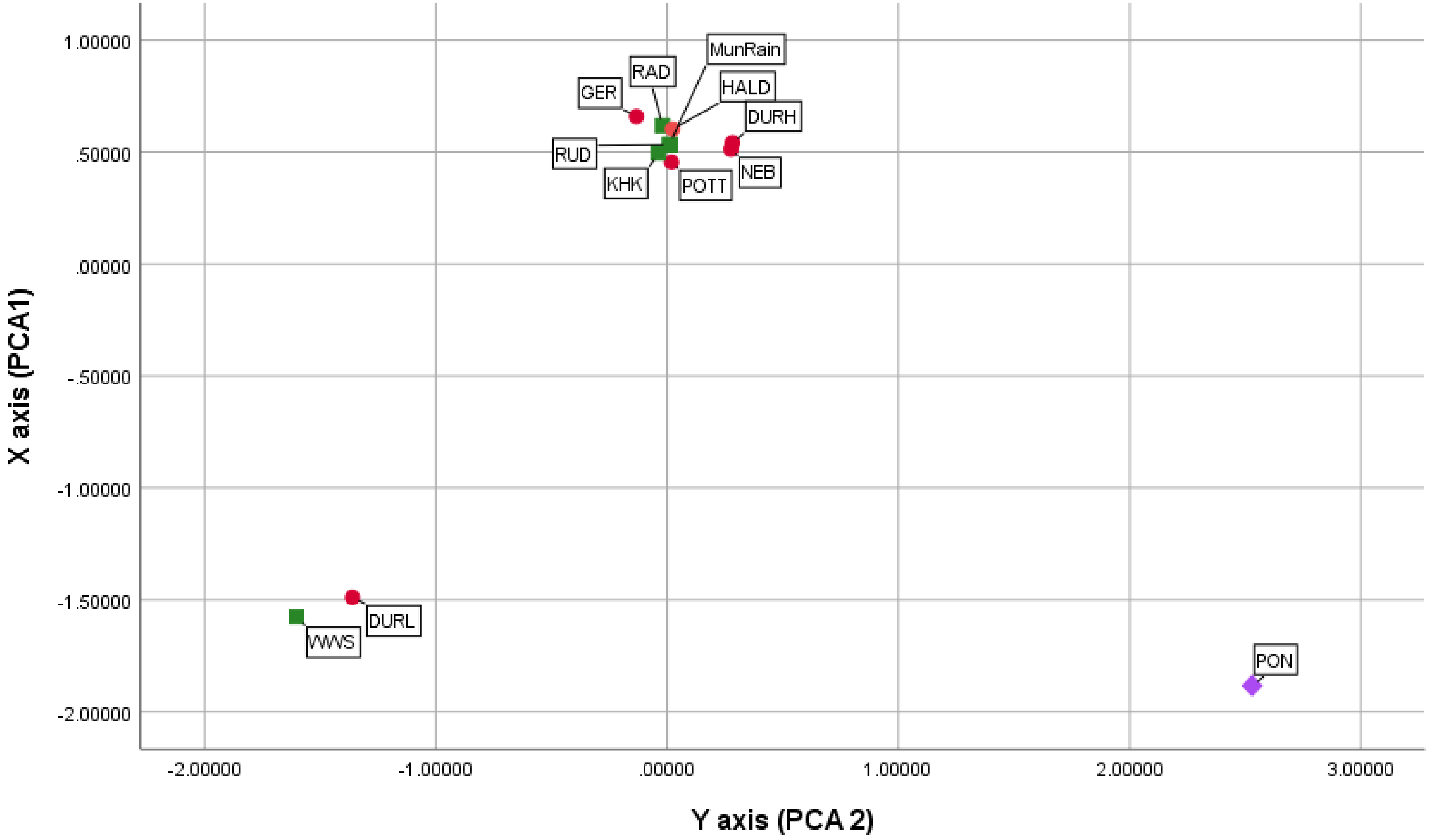


Table 10. Component loadings, eigenvalues and variance explained for the samples.

Trait*	Component PCA 1	PCA 2
Eigenvalue	12.440	8.261
Variance	47.855	34.277
Total Variance	47.855	82.133
Labial Curvature UI1	.362	**-.556**
Interruption groove UI2	-.156	.416
Tuberculum Dentale UI2*	.487	**-.866**
Distal accessory ridge UC*	.321	**-.832**
Hypocone UM2	-.215	-.427
Cusp 5 UM1	**-.511**	.464
Carabelli's trait UM1*	**-.851**	.319
Parastyle UM3*	**-.524**	**-.803**
Enamel extension UM1*	.022	**.669**
Root number UP1*	**.797**	-.056
Root number UM2*	**.790**	**.607**
Lingual cusp LP2*	**.994**	.090
Anterior fovea LM1*	**.895**	.035
Groove pattern LM2*	**.648**	**.754**
Rocker jaw	-.432	.353
Cusp number LM1*	.406	**.703**
Cusp number LM2*	-.416	**-.802**
Deflecting wrinkle LM*	**.864**	.259
C1–C2 crest LM1*	**.752**	-.302
Protostylid LM1*	**-.729**	-.364
Tome's root LP1*	**-.882**	.164
Root number LC*	-.202	**.866**
Root number LM1*	**-.782**	.162
Root number LM2*	**-.735**	-.130
Torsomolar angle LM3*	**-.835**	.342

*Denotes the 20 final traits used for MMD analysis after editing (Table 9). Boldface numbers indicate "strong" loadings (i.e., > |0.500|).

Although it is recommended that inter-sample distances be based on as many traits as possible, these traits should not be highly correlated, as this may lead to erroneous distances or spurious relationships (See pages 113 and 119) (Irish et al., 2014; Irish, 2010, 2015, 2016; Irish and Guatelli-Steinberg, 2003; Sjøvold, 1977). Inter-trait correlation was assessed by submitting the rank-scale ASUDAS data to the Kendall's tau-b correlation coefficient. A further 2 further trait pairs were found to be highly correlated (i.e. tb ≥ 0.5), labial curve UI1 and Tuberculum Dentale UI2 (tb=.751) and cusp 5 UM1 and Carabelli’s UM1 (tb=.518) (Appendix II). A Bonferroni correction was also performed on this percent data, the trait frequencies, however, no further trait pairs were found to be significantly correlated and no further traits were identified as non-contributory. In conjunction with their relatively low loadings and small sample sizes, labial curve UI1 and cusp 5 UM1 were removed from further analysis. In the end, 20 traits, denoted by asterisks in Table 10, were used for the final MMD comparison.

Mean measure of divergence (MMD)

This multivariate statistic provides a quantitative estimate of divergence between samples based on the degree of phenetic similarity for the suite of dental and osseous traits analysed (See page 188). All samples were compared using the initial 25 and final 20 traits. The resulting distance matrix for the 25-trait comparison among all 12 samples is presented in Table 11. Intra-and-extra-regional diversity among the samples is indicated by the 25-trait MMD analysis, as 46 of the 66 sample pairs are significantly different from one another at the .025 alpha level. Separation among the samples by the core and expansion regions is not evident, as the majority of the samples are biologically distinct from one another. Although some traits such as Groove Pattern LM2, occur at similar frequencies across several samples including, Münsingen-Rain (Switzerland), Radovesice (Czech Republic), and Pontecagnano (southern Italy) sample uniformity within these regions is not indicated by the distance matrix. However, the patterns indicated by the 25-trait distance matrix include invariant and other non-contributory traits indicated by PCA and the Kendall's tau-b correlation coefficient. Consequently, these patterns represent initial inter-sample affinities. A 20 trait comparison, with Hypocone UM2, Interruption groove UI2, Rocker jaw, Labial curve UI1, and Cusp 5 UM1 removed, was conducted to determine the subsequent inter-sample affinities. The final 20 traits included in MMD analyses include; Tuberculum Dentale UI2; Distal accessory ridge

UC; Carabelli’s trait UM1; Parastyle UM3; Enamel extension UM1; Root number UP1; Root number UM2; Lingual cusp LP2; Anterior fovea LM1; Groove pattern LM2; Cusp number LM1; Cusp number LM2; Deflecting wrinkle LM; C1–C2 crest LM1; Protostylid LM1; Tome’s root LP1; Root number LC; Root number LM1; Root number LM2; Torsomolar angle LM3 (Table 10).

The resulting distance matrix for all 12 samples is presented in Table 12. Although phenetic diversity is indicated, there is a greater emphasis on among sample divergence, after removing the above traits, the number sample pairs that are significantly different increased from 46 to 64 out of 66. After removing highly correlated and other largely non-contributory traits the majority of the sample pairs are slightly more distinct from one another than in the preceding 25 trait comparison. All but 2 sample pairs, Dürrnberg Hallstatt (Austria), Dürrnberg La Tène (Austria), and Kutná-Hora-Karlov (Czech Republic) and Radovesice (Czech Republic), are significantly different from one another at the .025 alpha level. Although the Dürrnberg (Austria) sample is not significantly different temporally, the MMD distances decrease during the La Tène period.

The 20 trait MMD analysis indicates that the Dürrnberg Hallstatt (Austria) and Dürrnberg La Tène (Austria) samples represent the same biological population. Therefore, a final 20 trait MMD analysis with these samples combined was conducted; in order to gain an impression of the inter-sample affinities and to determine whether the phenetic relationships indicated by the preceding 20 trait analysis are supported. The resulting distance matrix for all 11 samples is presented in Table 13. Overall heterogeneity is again indicated as 54 out of the 55 sample pairs are significantly different from one another at the .025 alpha level. The samples are not separated by geographic region as in the previous comparison. Similar frequencies are also observed in some traits including, Groove Pattern LM2 and Carabelli's Trait UM1, among some sample pairs such as Münsingen-Rain (Switzerland), and Hallstatt D (Austria). However, sample and region uniformity are not indicated by the distance matrix (Table 13). The MMD analyses also suggest that there is greater diversity among the Iron Age populations associated with Celtic material culture and/or language than previously established. Further, the comparative sample, Pontecagnano (southern Italy) is also significantly different from the remaining samples. This suggests that there is also more phenetic diversity among Iron Age European populations than previously documented.

Table 11. MMD distance matrix for 25 traits among all samples. The values above the diagonal are the standard deviations, and the values below are the MMD values.

Samples	**GER**	**NEB**	**POTT**	**RAD**	**KHK**	**MunRain**	**HALD**	**RUD**	**PON**	**DURH**	**DURL**	**WWS**
GER	0	0.029	0.024	0.026	0.025	0.024	0.024	0.025	0.025	0.026	0.021	0.020
NEB	0.035	0	0.024	0.025	0.026	0.025	0.025	0.025	0.024	0.026	0.021	0.018
POTT	0.032	0.066	0	0.020	0.022	0.020	0.020	0.022	0.020	0.020	0.021	0.016
RAD	0.051	0.049	0.044	0	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.016
KHK	0.058	0.044	0.042	0.049	0	0.020	0.020	0.020	0.021	0.021	0.022	0.015
MunRain	0.051	0.064	0.055	0.055	0.046	0	0.020	0.020	0.020	0.020	0.020	0.015
HALD	0.058	0.047	0.050	0.056	0.053	0.058	0	0.020	0.020	0.020	0.021	0.016
RUD	0.047	0.036	0.042	0.054	0.050	0.048	0.052	0	0.020	0.021	0.020	0.016
PON	0.072	0.050	0.077	0.070	0.070	0.066	0.074	0.087	0	0.021	0.028	0.022
DURH	0.047	0.068	0.061	0.053	0.049	0.059	0.052	0.050	0.077	0	0.021	0.016
DURL	0.040	0.040	0.030	0.030	0.041	0.028	0.024	0.041	0.074	0.024	0	0.016
WWS	0.048	0.056	0.048	0.050	0.051	0.043	0.040	0.062	0.079	0.041	0.021	0

Underlined MMD distances indicate significant differences at the 0.025 level. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná - Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

Table 12. MMD distance matrix for 20 traits among all samples. The values above the diagonal are the standard deviations, and the values below are the MMD values.

Samples	**GER**	**NEB**	**POTT**	**RAD**	**KHK**	**MunRain**	**HALD**	**RUD**	**PON**	**DURH**	**DURL**	**WWS**
GER	0	0.033	0.027	0.027	0.028	0.026	0.027	0.027	0.026	0.028	0.016	0.021
NEB	0.070	0	0.027	0.027	0.028	0.026	0.027	0.026	0.027	0.028	0.022	0.020
POTT	0.061	0.071	0	0.021	0.022	0.021	0.021	0.021	0.022	0.022	0.022	0.017
RAD	0.059	0.061	0.049	0	0.022	0.021	0.021	0.022	0.022	0.023	0.022	0.017
KHK	0.063	0.058	0.045	0.040	0	0.021	0.022	0.021	0.021	0.022	0.021	0.017
MunRain	0.062	0.073	0.057	0.053	0.045	0	0.021	0.021	0.022	0.022	0.022	0.017
HALD	0.069	0.067	0.055	0.056	0.049	0.058	0	0.021	0.022	0.022	0.021	0.017
RUD	0.058	0.060	0.052	0.053	0.047	0.053	0.051	0	0.022	0.022	0.022	0.017
PON	0.066	0.058	0.065	0.055	0.050	0.062	0.057	0.079	0	0.023	0.022	0.017
DURH	0.062	0.070	0.060	0.059	0.060	0.058	0.053	0.064	0.084	0	0.022	0.017
DURL	0.046	0.046	0.045	0.048	0.045	0.047	0.045	0.054	0.057	0.041	0	0.012
WWS	0.054	0.061	0.060	0.066	0.062	0.062	0.057	0.077	0.065	0.057	0.028	0

Underlined MMD distances indicate significant differences at the 0.025 level. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

Table 13. MMD distance matrix for 20 traits among all samples, with the Dürrnberg (Austria) sample combined. The values above the diagonal are the standard deviations, and the values below are the MMD values.

Samples	**GER**	**NEB**	**POTT**	**RAD**	**KHK**	**MunRain**	**HALD**	**RUD**	**PON**	**DUR**	**WWS**
GER	0	0.029	0.026	0.026	0.026	0.026	0.026	0.026	0.026	0.020	0.017
NEB	0.082	0	0.029	0.029	0.028	0.029	0.029	0.029	0.029	0.023	0.020
POTT	0.078	0.082	0	0.026	0.026	0.026	0.026	0.026	0.027	0.020	0.017
RAD	0.078	0.083	0.078	0	0.027	0.026	0.027	0.026	0.027	0.019	0.017
KHK	0.056	0.058	0.056	0.053	0	0.026	0.026	0.026	0.026	0.020	0.017
MunRain	0.078	0.082	0.078	0.078	0.056	0	0.026	0.026	0.026	0.020	0.017
HALD	0.078	0.082	0.079	0.078	0.056	0.078	0	0.026	0.027	0.020	0.017
RUD	0.078	0.082	0.079	0.078	0.057	0.078	0.079	0	0.026	0.020	0.017
PON	0.064	0.059	0.063	0.072	0.085	0.063	0.063	0.063	0	0.020	0.017
DUR	0.043	0.045	0.042	0.041	0.057	0.043	0.043	0.043	0.065	0	0.012
WWS	0.079	0.083	0.078	0.077	0.083	0.078	0.079	0.078	0.076	0.025	0

Underlined MMD distances indicate significant differences at the 0.025 level. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

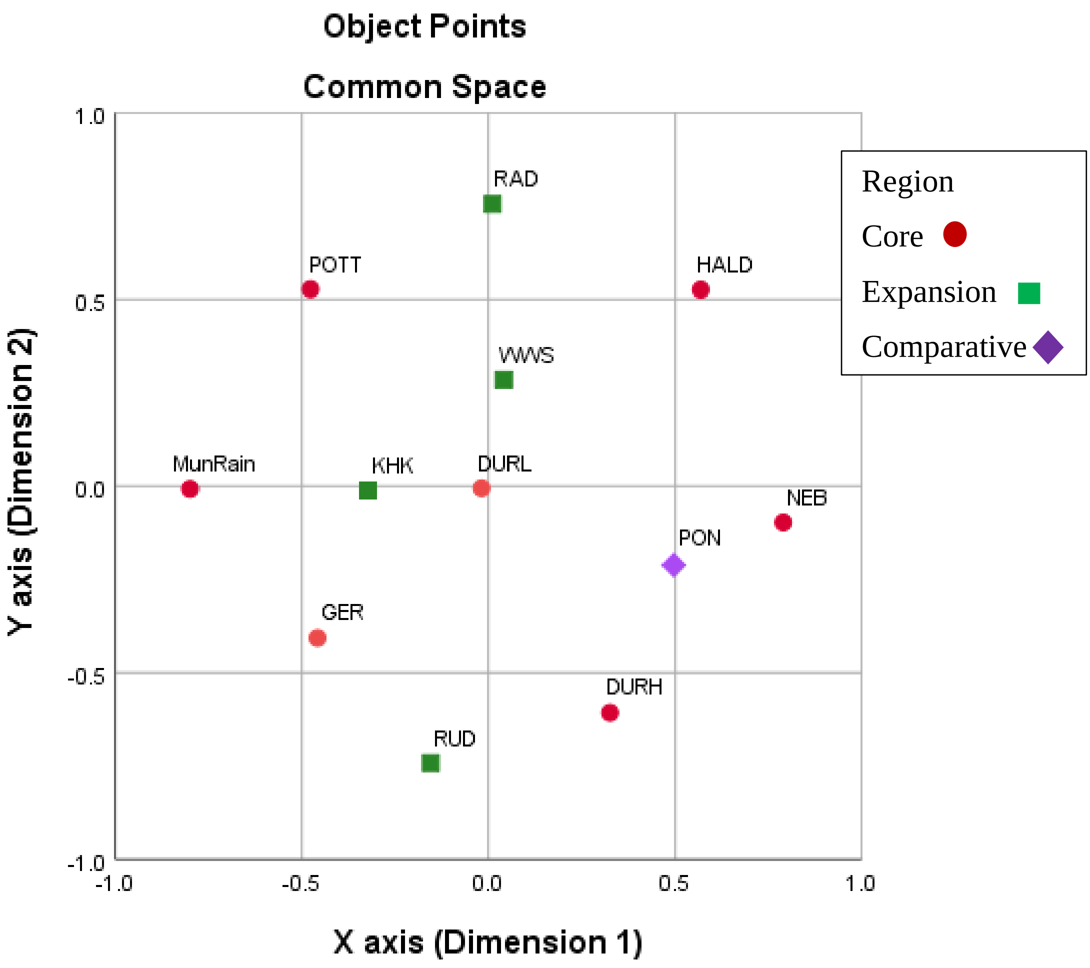
Both of the 20 trait MMD matrices support the notion of limited if any, gene flow between and within the regions analysed. However, small scale migration not influencing gene flow significantly cannot be ruled out.

Multidimensional scaling (MDS)

The MDS Proxscal procedure was used to produce a graphical representation of the MMD values. MDS treats each of the MMD values as Euclidean distances. Samples in close proximity in the MDS configuration have lower MMD scores than those that are farther apart (See page 190). Two-dimensional MDS Proxscal graphs based on the 25 and 20 trait MMD matrices are presented in Figures 39, 40, and 41. Three-dimensional MDS ALASCAL graphs based on the above matrices are presented in appendix VII for comparison (Figures 64-66). The MDS stress value is a measure of the goodness of fit, or representations, of the scaled compared to the unscaled data in reduced space. The lower the stress value the better the fit or correlation between the scaled and unscaled data (Kruskal and Wish, 1978). The stress value between the MMD and MDS datasets was determined through a Kruskal's stress formula (Kruskal and Wish, 1978).

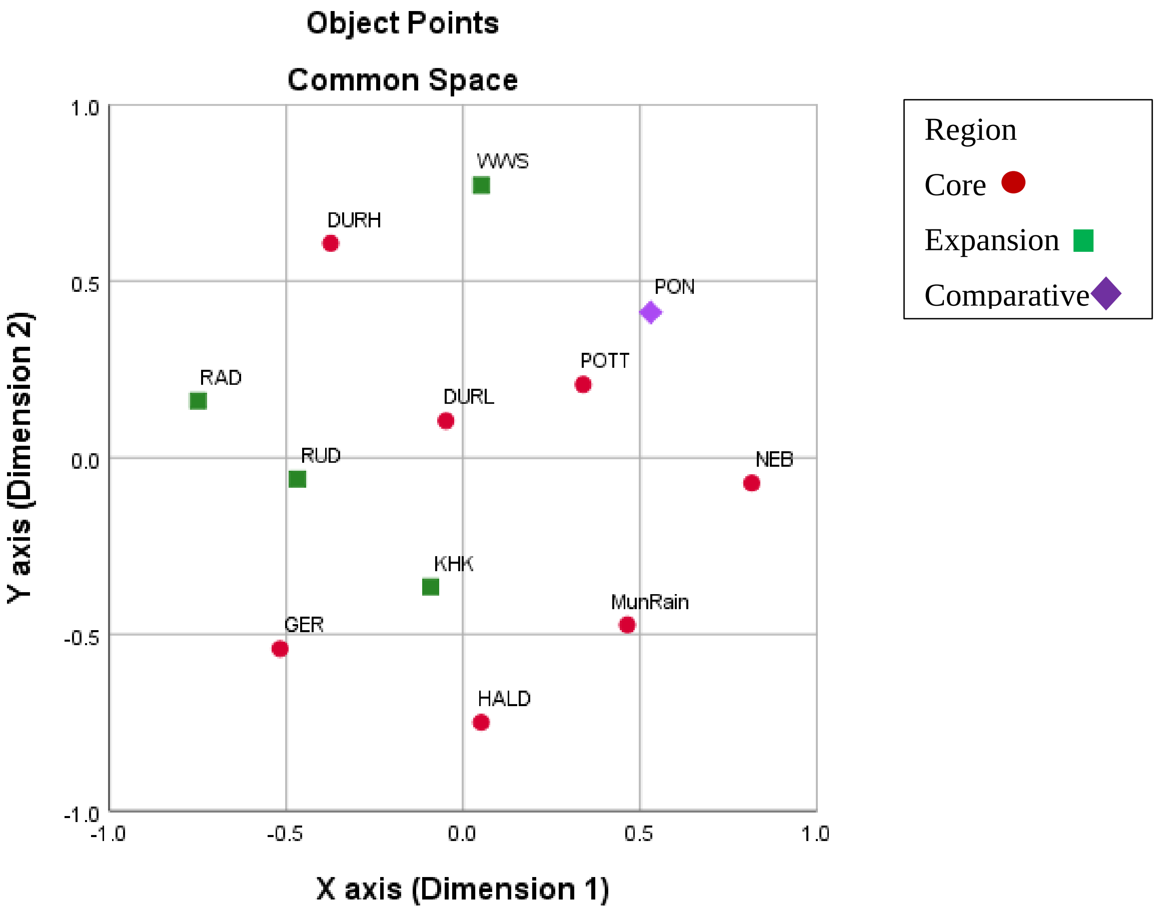
Values less than 0.10 indicate low stress and a good fit between the data sets whereas, values greater than 0.15 represent the opposite (See page 190) (Borgatti, 1997). The Kruskal's stress formula value is 0.056 in this analysis. This value indicates that the two data sets, MMD and MDS, have low stress, and the MDS graphs provide an excellent representation of the MMD derived relationships (Borgatti, 1997; Kruskal and Wish, 1978). The r^2 value is a measure of the variance of the scaled values that is accounted for by their corresponding MMDs; in this analysis, r^2 is 0.945. The correlation coefficient, r, between the MDS and MMD distances is produced by taking the square root of r^2 (Kruskal and Wish, 1978). Therefore, in this analysis, the two matrices are highly correlated, r =0.972. This indicates that 97.2% of the variance is explained by these distance values. In this case, the two-dimensional solution is an accurate representation of the MMD derived phenetic relationships.

Figure 39. Two-dimensional MDS graph of the 25 trait MMD distances among the samples. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).



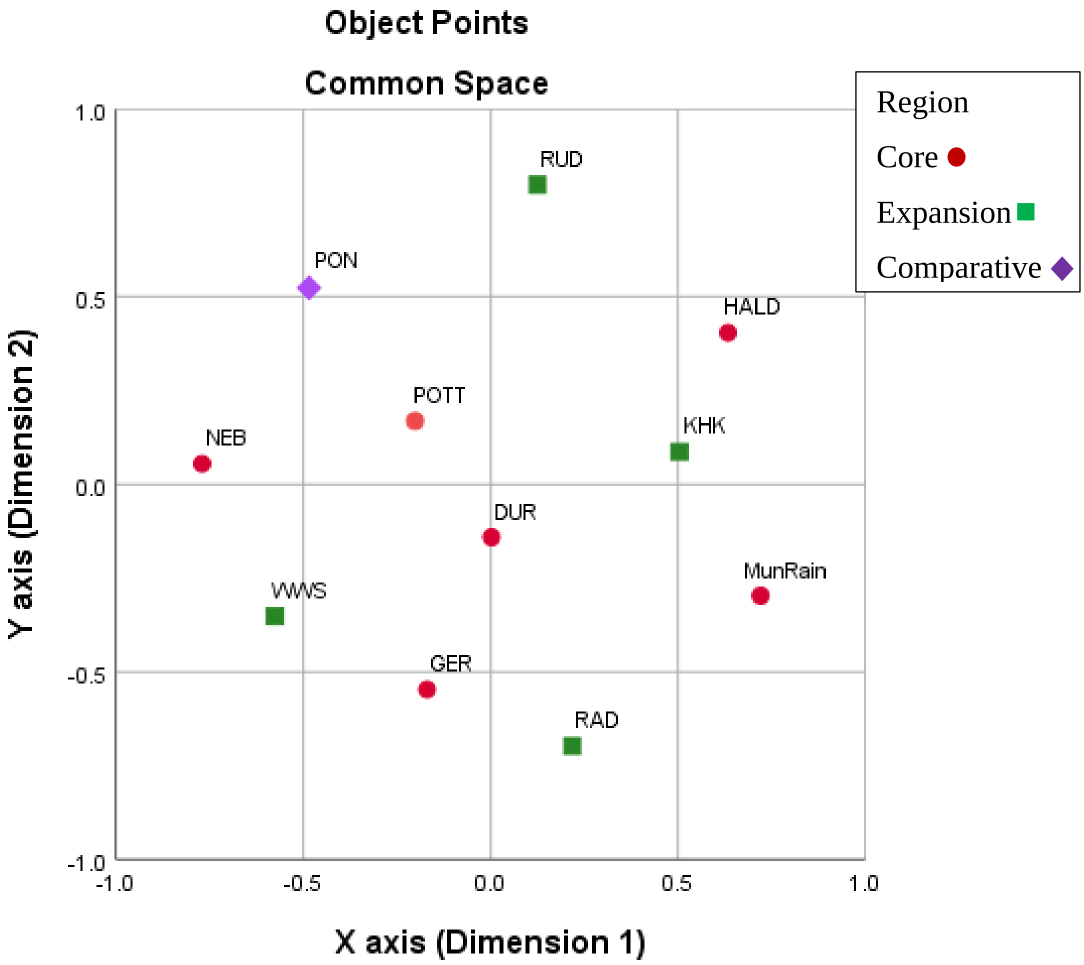
The configurations of the 25, and 20 trait MDS graphs share some patterning with the PCA graph including the relative positions of the Dürrnberg La Tène (Austria), Dürrnberg pooled (Austria), Pottenbrunn (Austria) and Rudston Makeshift (east Yorkshire, Britain) samples. However, the phenetic divergence among the samples is evident (Figures 38 and 39-41, respectively).

Figure 40. Two-dimensional MDS graph of the 20 trait MMD distances among all the samples. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).



Inspection of Figures 39, 40 and 41 reveals a clear separation among the samples. Although the relative positions of some of the samples in the 25 and both 20 trait MDS graphs are switched, due to differential trait weighting, the distances between the samples remains comparatively the same. Greater separation among the samples is evident, through both the 20 trait comparisons, otherwise, the patterning between the MDS graphs is similar in the association of samples by geographic region. Although some traits occur at similar frequencies among the majority of the samples such as Groove pattern LM2, this uniformity is not reflected in the MDS or PCA graphs (Figures 38 and 39-41, respectively).

Figure 41. Two-dimensional MDS graph of the 20 trait MMD distances among the samples, with the Dürrnberg (Austria) sample combined. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).



This suggests that the observed trait similarity may not be related to frequent gene flow among the samples. Rather, it may reflect similarities present in the parent population(s) and subsequent diversification. Consequently, the samples analysed may have become genetically distinct due to other processes such as isolation by distance, limited external gene flow from the regions analysed, and increased gene flow from other neighbouring regions not analysed.

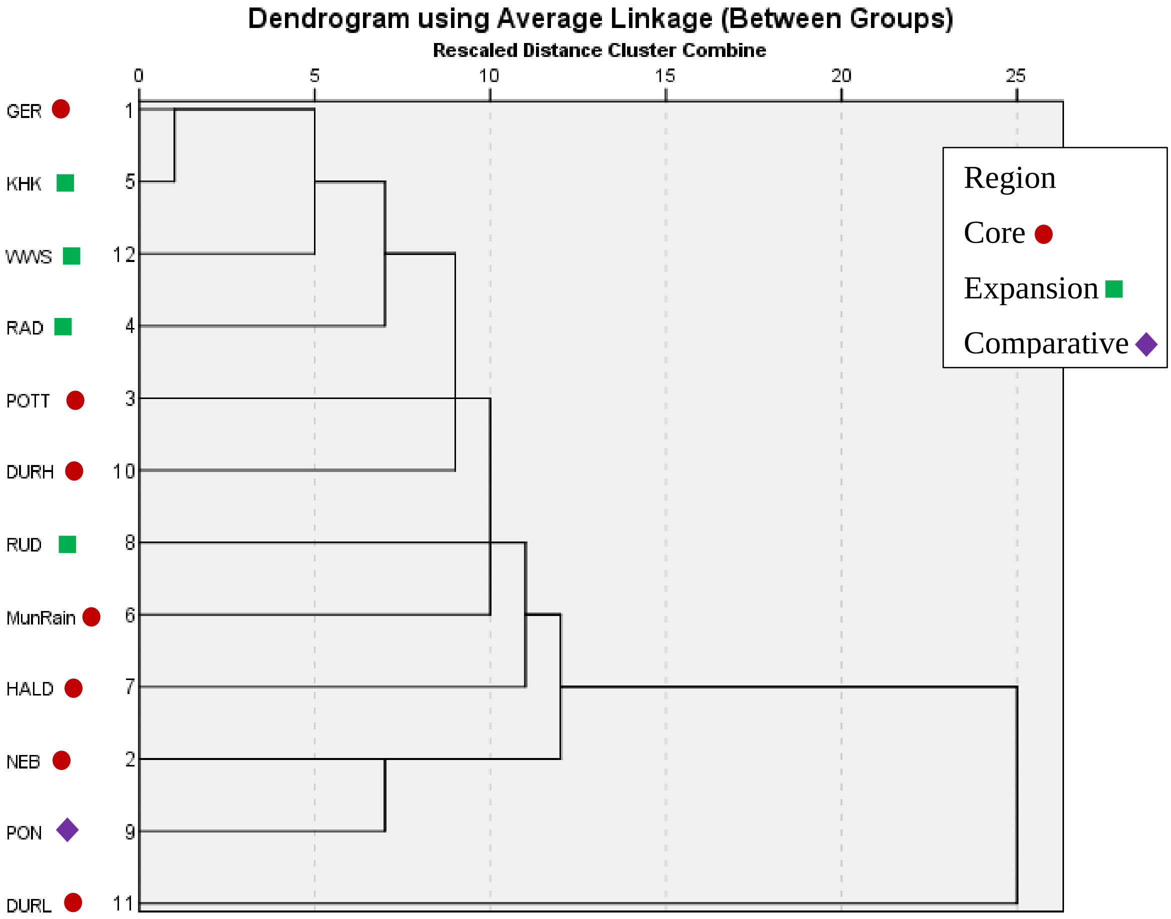
Hierarchal cluster analysis

Hierarchical cluster analysis with between group linkage and Wards method were used to provide a further illustration of among-sample affinities and sample distributions, based upon the symmetric MMD distance values for the 25 and both 20 trait comparisons, with the Dürrnberg (Austria) sample temporally separated and combined, and are presented in Figures 42-47, respectively (See page 194). Inspection of the 25 and both 20 trait dendrograms supports the clear separation among the samples as indicated by the MDS and PCA graphs (Figures 38 and 39-41, respectively). There is also no evidence for separation among the samples into the core and expansion regions.

Further, as in the preceding MDS and PCA graphs, there is also no association by known linguistic or genetic relationships, with the exception of the Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) samples (Figures 38 and 39-41, respectively). These samples are clustered together in both the 20 trait dendrograms with the Dürrnberg sample pooled and temporally separated (Figures 44-47). Although the Dürrnberg (Austria) period samples also represent the same biological population they are not clustered together. The La Tène period sample is more distinct from the remaining samples in both the 25 and 20 trait pooled dendrograms. This may be related to the decreasing MMD values during this period (Table 13).

The configurations of the 25 and both 20 trait dendrograms indicate similar regional sample distributions and separation among the samples as in the PCA and MDS graphs (Figures 38 and 39-41, respectively). However, in the 20 trait pooled dendrograms the Dürrnberg La Tène (Austria) and Wetwang Slack (east Yorkshire, Britain) samples are comparatively more distinct (Figures 46 and 47). The Dürrnberg La Tène (Austria) and Dürrnberg Hallstatt (Austria) samples are also clustered together, although not closely.

Figure 42. Between Group Linkage 25 traits among all samples. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).



This further supports the notion that while these samples may be phenetically indistinct the decreasing MMD distances indicate differential social processes, such as fluctuating migration rates and marriage practices during these periods. The difference in the separation among the samples indicated by comparison of the 25 and both 20 trait dendrograms may be related to the different methods used, average and minimal variance, respectively (Figures 42-47).

Figure 43. Wards Method 25 traits among all samples. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

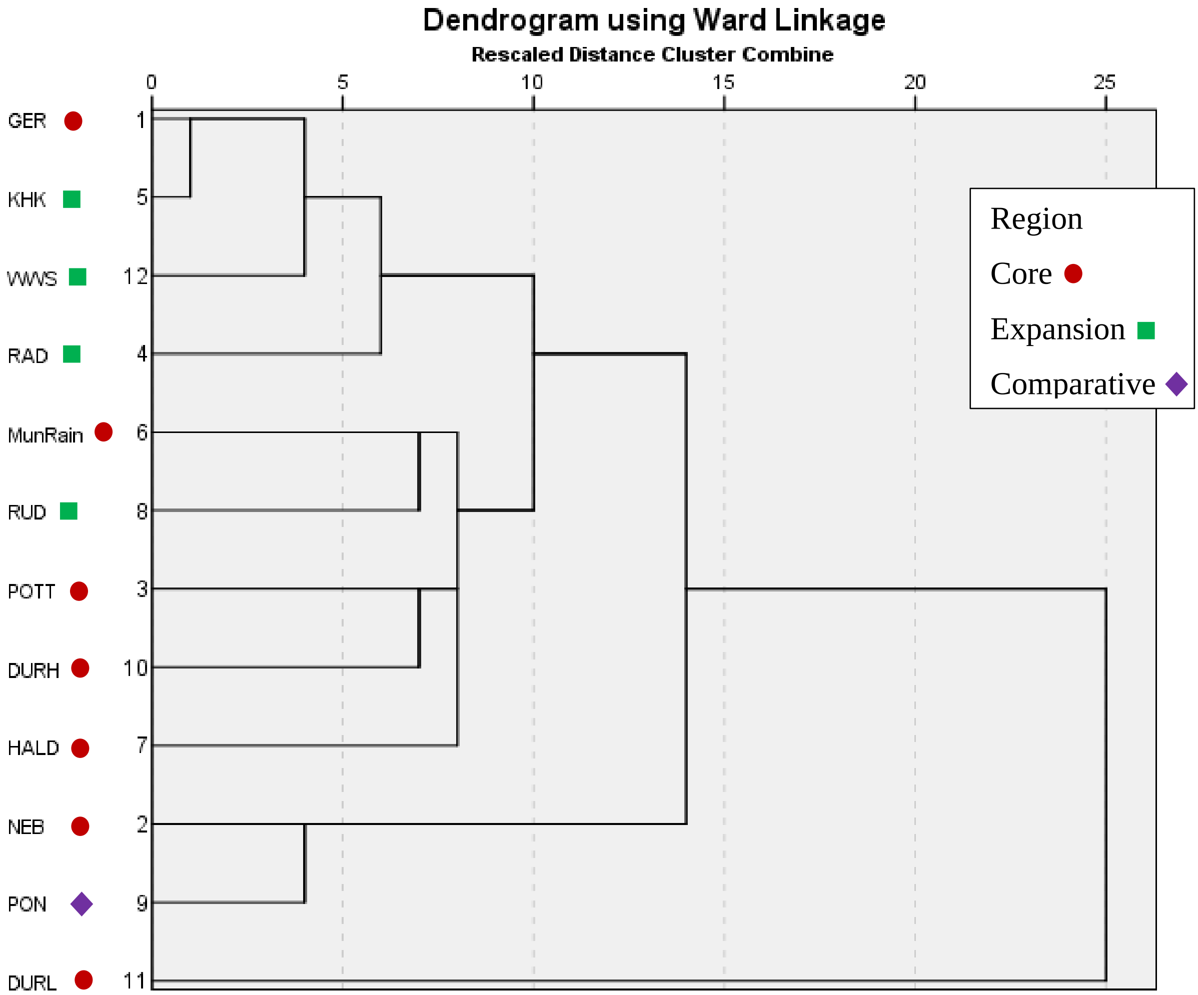
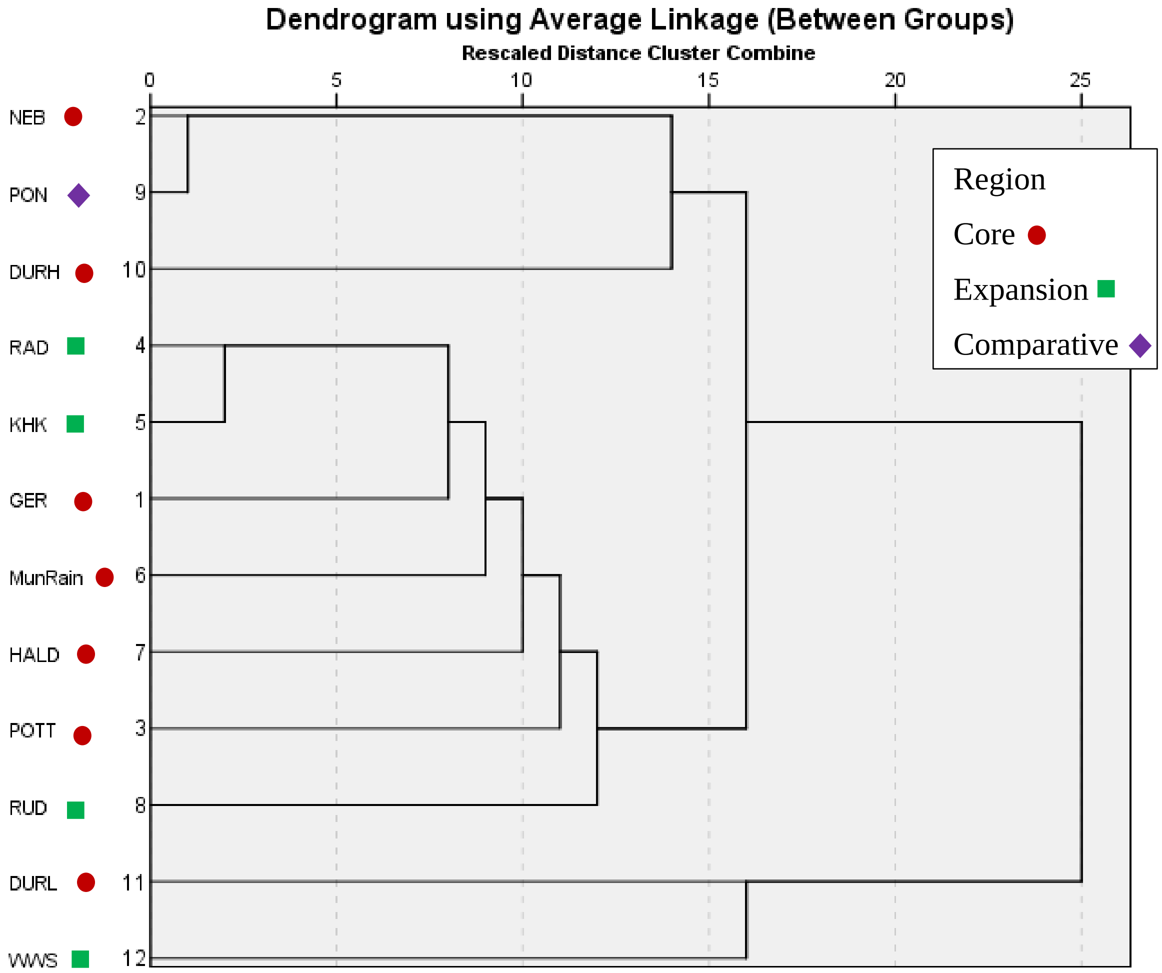
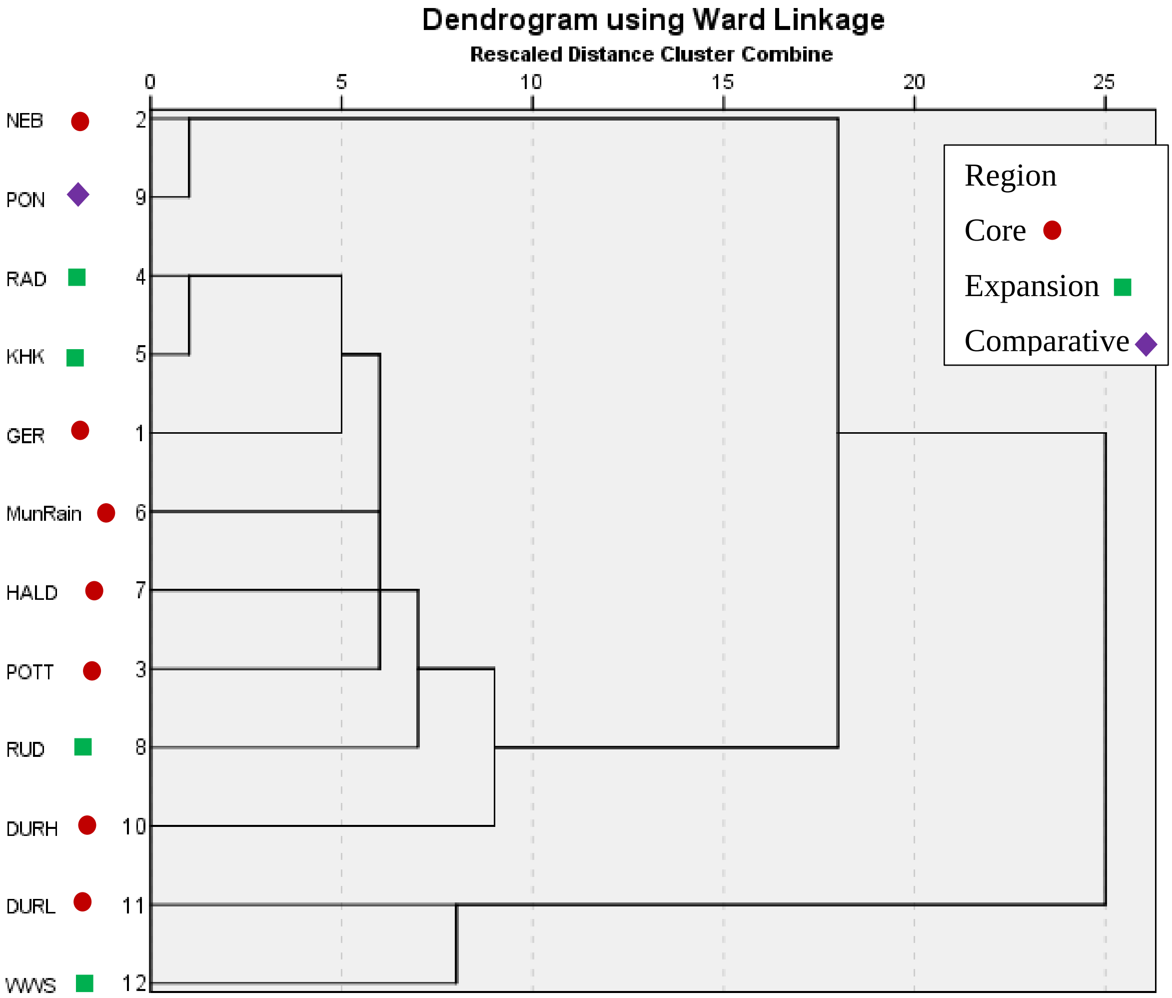


Figure 44. Between Group Linkage 20 traits among all samples. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).



Alternatively, the slight difference in the clusters may be related to differential gene flow, genetic drift, isolation, captives and/or enslavement among the samples. However, the composition of the German (Stuttgart, Germany), Rudston Makeshift (east Yorkshire, Britain) and Pontecagnano (southern Italy) samples may be related to the slight differences in clusters and the relative positions of these samples in the MDS and PCA graphs (Figures 38 and 39-41, respectively). Due to the fact that these samples represent pooled or sub-samples, they may not adequately represent the range of variation present within these samples during the Iron Age. In spite of this limitation, the sample distribution indicated by both 20 trait dendrograms supports those indicated by the MDS graphs (Figures 39-41 and 44-47).

Figure 45. Wards Method 20 traits among all samples. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).



The sample distribution indicated by the 20 trait dendrograms with the Dürrnberg (Austria) sample combined are similar to those from the preceding 20 trait comparison (Figures 46-47 and 44-45, respectively). The Dürrnberg (Austria) and Wetwang Slack (east

Yorkshire, Britain) samples are also comparatively distinct, and the remaining clusters are similar. As discussed throughout this chapter, there is significant intra-and-extra regional heterogeneity among the samples analysed. Although the remaining sample distributions may not indicate any known linguistic or genetic relationships, the inadequacy of the supporting evidence makes interpretations based on these lines of evidence alone difficult, and therefore tenuous.

Figure 46. Between Groups Linkage 20 traits among all samples, with the Dürrnberg (Austria) sample combined. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

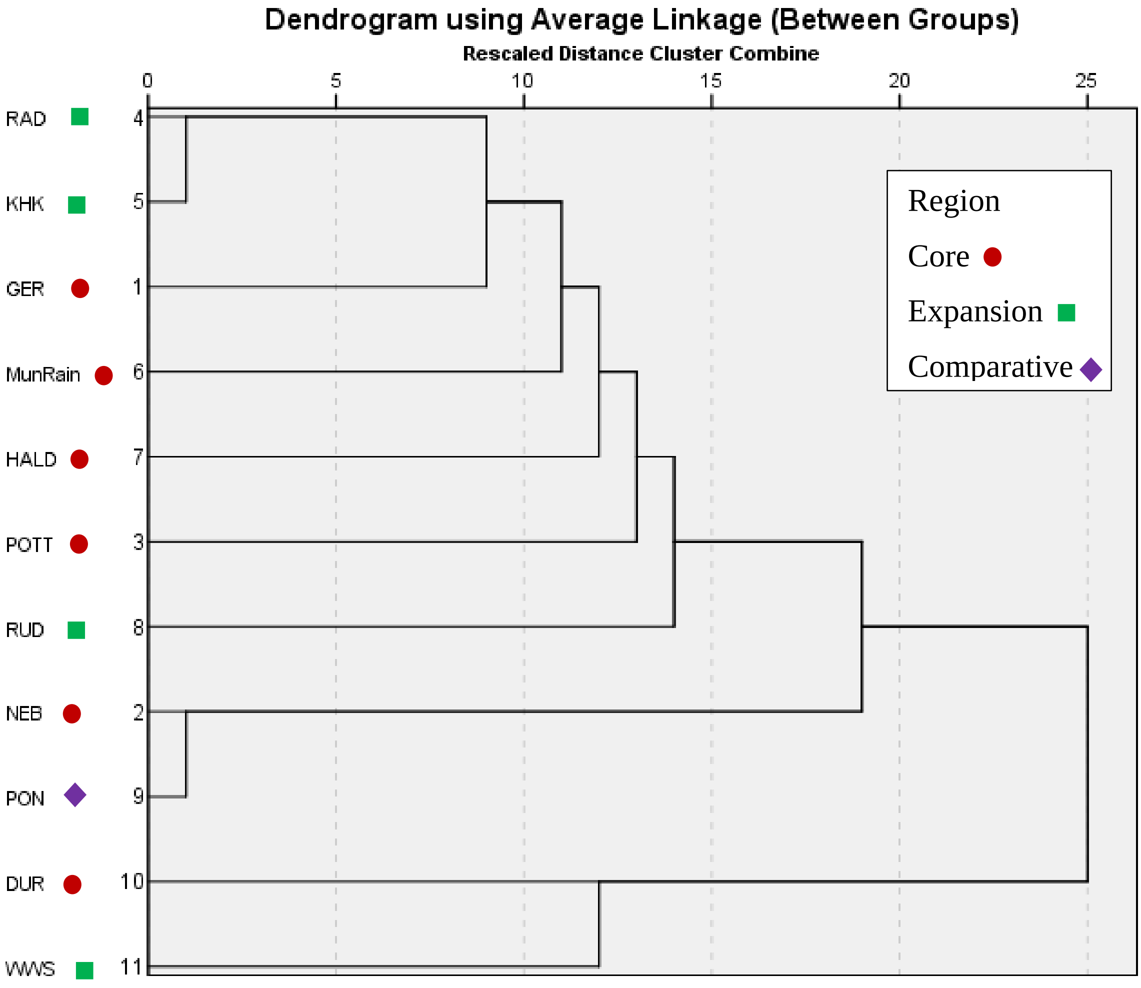
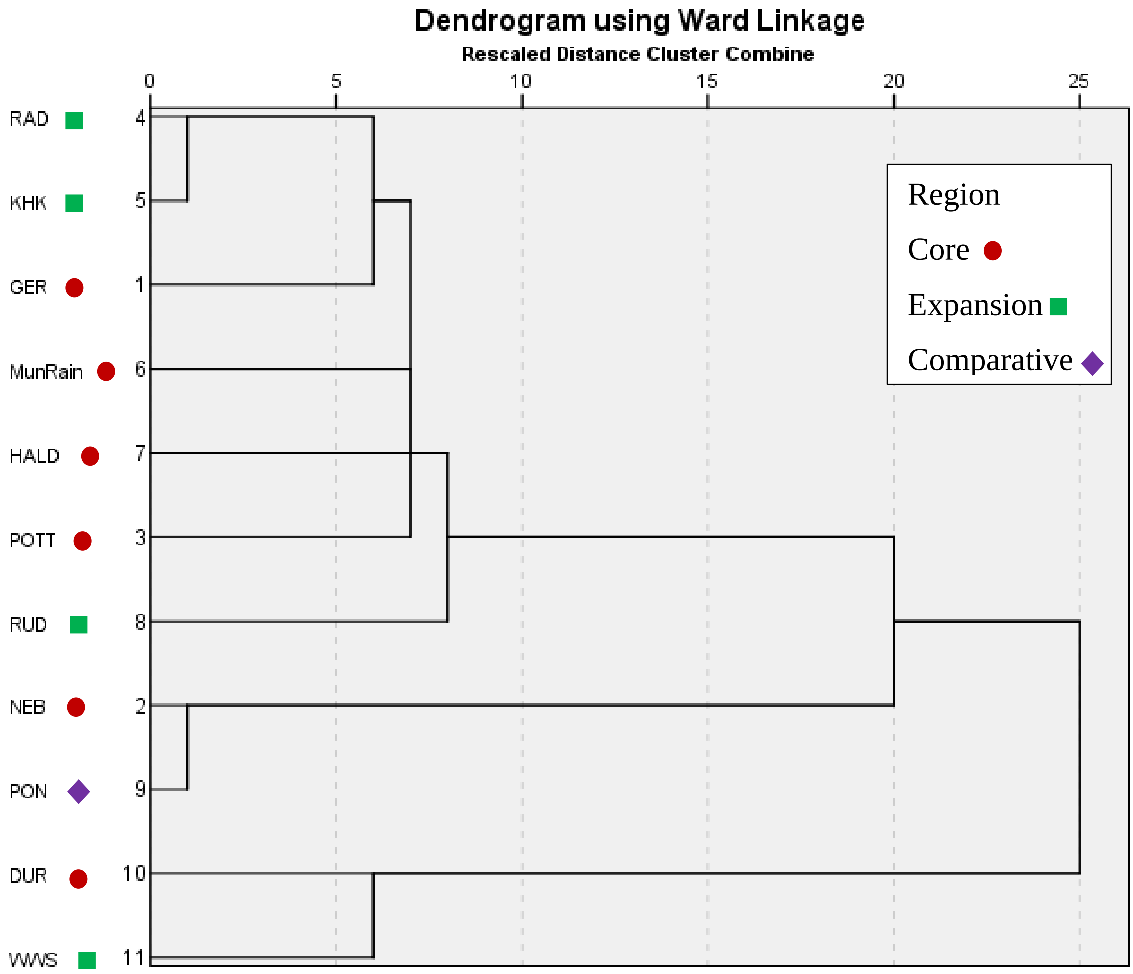


Figure 47. Wards Method 20 traits among all samples, with the Dürrnberg (Austria) sample combined. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).



Isolation by distance (IBD)

To quantify the apparent correspondence between phenetic distance and spatial proximity, the 20 trait MMD distances with the Dürrnberg (Austria) sample combined were compared with the geographic distances among sites or regions (Table 14). However, the geographic distances listed in Table 14 are straight-line distances, which can be problematic because the topographical landscape determines how people move and the resulting biocultural isolation among populations (See pages 190 and 193). The Mantel correlation between matrices, r=0.195 (p=.102), is positive though weak and is not significant (Cohen, 1988). However, after the Pontecagnano (southern Italy) sample was removed from analysis r increases to .276 (p=0.097), and when the German pooled (Stuttgart, Germany) and Rudston Makeshift (east Yorkshire, Britain) samples were also removed r further increases to .309 (p=0.049) a moderate positive correlation (See pages 193 and 221) (Cohen, 1988; Irish, et al., 2018). Here, an r value >0.3 indicates a moderate positive correlation, following previous research (Cohen, 1988; Irish et al., 2018). These samples were removed as they are either pooled, German (Stuttgart, Germany) or sub-samples, Pontecagnano (southern Italy) and Rudston Makeshift (east Yorkshire, Britain). Consequently, the inclusion of these samples may have resulted in a spurious correlation between the two matrices and/or among the samples. Lastly, each sample was plotted individually compared to the rest using the geographic and symmetric MMD distances, using the phenetic and geographic distances from Tables 13 and 14 as coordinates on the x-and-y-axes. One sample comparison per region, as well as the comparative sample scatterplots, are presented in Figures 48-50. The remaining sample scatterplots are presented in Appendix IV (Figures 55-62). In each scatterplot, a solid black linear equation reference line with a slope (b) of 1 and a y-intercept (a) of 0 is also provided (e.g., y=0+1x, where y=a+bx). This line illustrates the sample distribution if a 1:1 correspondence between spatial and phenetic distances existed among the samples. The actual sample locations indicate those which are closer phenetically to the respective sample than anticipated, those below the reference line, and those that are more phenetically distinct, those above the line, relative to their geographic separation. The values presented in Table 15, indicating the correlation between phenetic and geographic distances, are provided for comparative purposes because the abovementioned data points are not independent due to the underlying population structure (Roseman and Auerbach, 2015).

The values indicate that isolation by distance alone does not explain the observed population structure in the samples (Table 15). These results further imply that some of the samples were not plotted where they ought to be, following the assumption that phenetic affinity is directly related to spatial variation. Focusing on intra-regional comparisons within the core, Hallstatt D (Austria), German (Stuttgart, Germany), Pottenbrunn (Austria), and Nebringen (Stuttgart, Germany) (except when compared to Dürrnberg, Austria) are plotted above the black reference line. This indicates that they are more divergent phenetically from the remaining core samples than anticipated based on geographic location. The opposite is true for those samples below this line, Dürrnberg (Austria) (when compared to Nebringen (Stuttgart, Germany) (Figures 48 and 55-59).

Table 14. Symmetrical geographic straight-line distance matrix (km) among the samples (using actual or approximated center of each site or geographic region).

Samples	**GER**	**NEB**	**POTT**	**RAD**	**KHK**	**MunRain**	**HALD**	**RUD**	**PON**	**DUR**	**WWS**
GER	0	176.23	481.47	394.15	406.96	243.80	358.01	852.02	1012.66	315.14	834.50
NEB	176.23	0	643.40	488.43	523.92	310.49	530.80	681.42	1172.15	488.60	664.22
POTT	481.47	643.40	0	316.22	241.22	619.16	156.16	1259.10	828.69	192.77	1240.94
RAD	394.15	488.43	316.22	0	76.44	622.49	343.39	993.29	1118.52	336.06	975.30
KHK	406.96	523.92	241.19	76.44	0	619.58	285.68	1061.50	1052.81	285.85	1043.44
MunRain	243.80	310.49	619.16	622.49	619.58	0	466.40	951.81	910.53	426.69	936.03
HALD	358.1	530.80	156.16	343.39	285.68	466.40	0	1182.57	778.68	43.39	1164.56
RUD	852.02	681.42	1259.10	993.29	1061.50	951.81	1182.57	0	1850.31	1144.20	18.17
PON	1012.66	1172.15	828.69	1118.52	1052.81	910.53	778.68	1850.31	0	796.76	1833.60
DUR	315.14	488.60	192.77	336.06	285.85	426.69	43.39	1144.20	796.76	0	1126.22
WWS	834.50	664.22	1240.94	975.30	1043.44	936.03	1164.56	18.17	1833.60	1126.22	0

Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutna-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

Figure 48. Two-dimensional scatterplot of the German (Stuttgart, Germany) (GER) sample relative to the other samples based on geographic (x-axis) versus. phenetic (y-axis) distances. Solid black linear equation reference line with slope (b) of 1 and y-intercept (a) of 0 provided (i.e., y=0+1x, where y=a+bx) to illustrate where the other sample would be if a 1:1 correspondence existed between the distances. DUR (Dürrnberg); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); POTT (Pottenbrunn); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack); Pon (Pontecagnano).

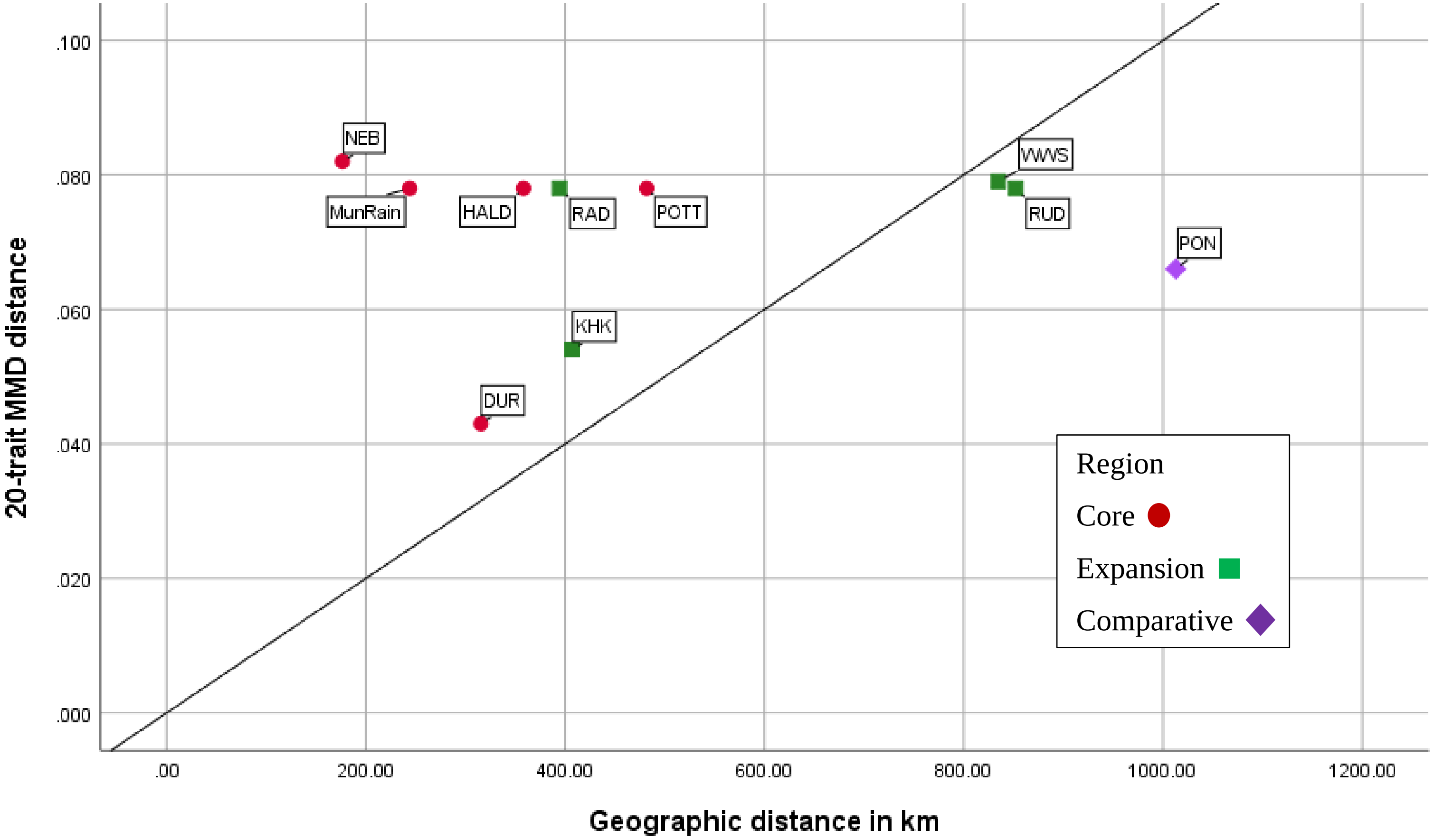


Figure 49. Two-dimensional scatterplot of the Radovesice (Czech Republic) (RAD) sample relative to the other samples based on geographic (x-axis) versus phenetic (y-axis) distances. Solid black linear equation reference line with slope (b) of 1 and y-intercept (a) of 0 provided (i.e., y=0+1x, where y=a+bx) to illustrate where the other sample would be if a 1:1 correspondence existed between the distances. DUR (Dürrnberg); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); POTT (Pottenbrunn); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack); Pon (Pontecagnano).

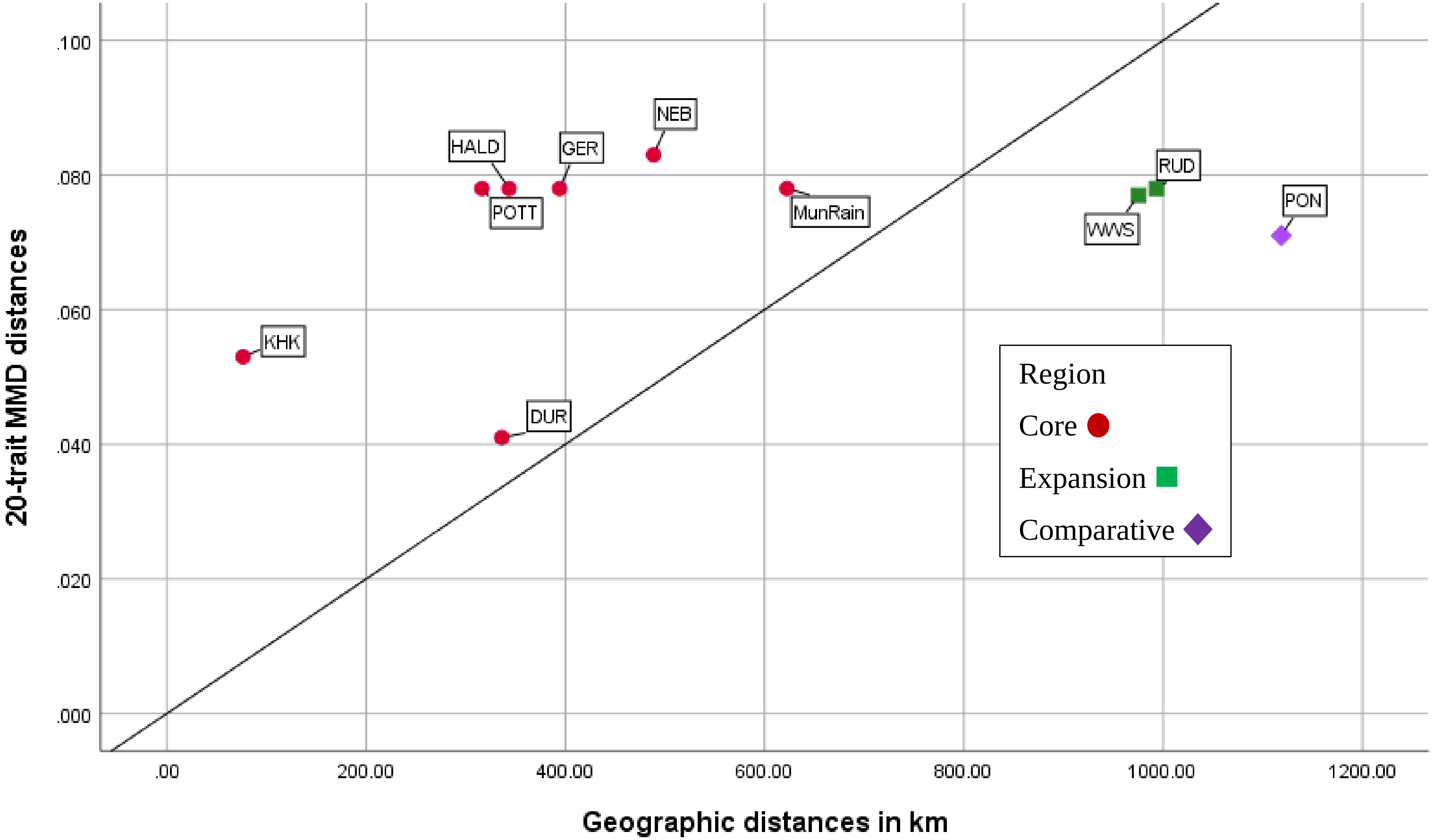


Figure 50. Two-dimensional scatterplot of the Pontecagnano (southern, Italy) (PON) sample relative to the other samples based on geographic (x-axis) versus phenetic (y-axis) distances. Solid black linear equation reference line with slope (b) of 1 and y-intercept (a) of 0 provided (i.e., y=0+1x, where y=a+bx) to illustrate where the other sample would be if a 1:1 correspondence existed between the distances. DUR (Dürrnberg); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); POTT (Pottenbrunn); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

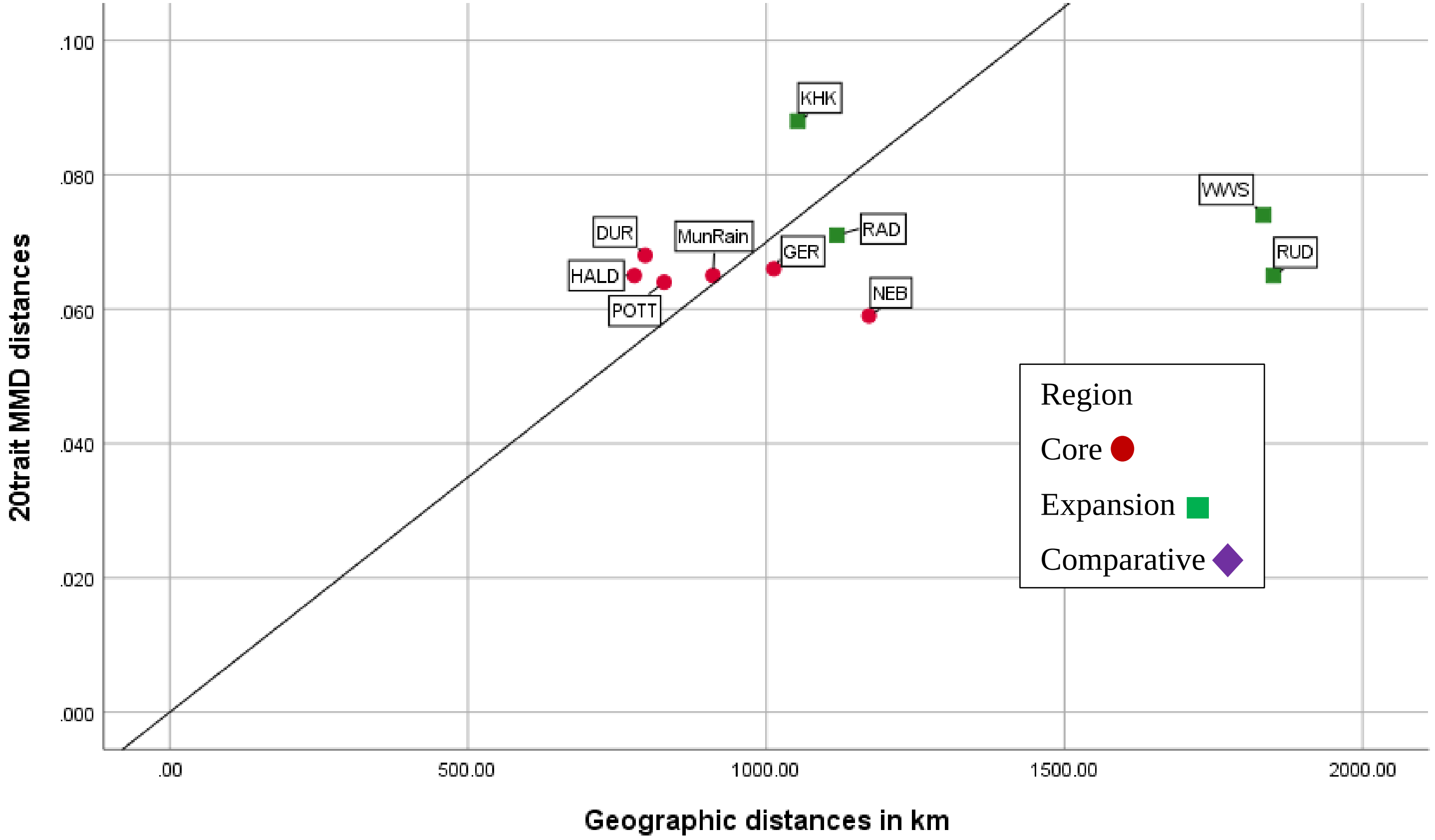


Table 15. Coefficients of determination calculated via linear regression for all the samples.

Sample	**r**	**p**
GER	.434	.247
NEB	.361	.276
POTT	.457	.157
RAD	.500	.105
KHK	.470	.120
MunRain	.465	.150
HALD	.444	.171
RUD	.681	.020
PON	.573	.065
DUR	.352	.287
WWS	.663	.022

Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

Focusing on intra-regional comparisons in the expansion regions, Kutná-Hora-Karlov (Czech, Republic) (except when compared to Rudston Makeshift, east Yorkshire, Britain), Radovesice (Czech Republic), Wetwang Slack (east Yorkshire, Britain) (when compared to Rudston Makeshift, east Yorkshire, Britain) and Rudston Makeshift (east Yorkshire, Britain) (when compared to Wetwang Slack, east Yorkshire, Britain) are plotted above the black reference line. Pontecagnano (southern Italy), Wetwang Slack (east Yorkshire, Britain) and Rudston Makeshift (east Yorkshire, Britain) (except in the Rudston Makeshift, east Yorkshire, Britain, and Wetwang Slack, east Yorkshire, Britain comparisons) are plotted below the line (Figures 49, 50 and 60-62).

Emphasising extra-regional comparisons (core to expansion regions), those samples above the line include Kutná-Hora-Karlov (Czech, Republic) (except when compared to the Münsingen-Rain, Switzerland, Rudston Makeshift, east Yorkshire, Britain, and Wetwang Slack, east Yorkshire, Britain samples), Radovesice (Czech Republic) (except when compared to Pontecagnano, southern Italy), Wetwang Slack (east Yorkshire, Britain) and

Rudston Makeshift (east Yorkshire, Britain) (when compared to Nebringen, (Stuttgart, Germany) (Figures 48-50 and 55-62). Those below the line include, Nebringen (Stuttgart, Germany) and German (Stuttgart, Germany) (when compared to Pontecagnano, southern Italy), Dürrnberg (Austria) (when compared to Nebringen, Stuttgart, Germany, Rudston Makeshift, east Yorkshire, Britain, and Wetwang Slack, east Yorkshire, Britain), Nebringen (Stuttgart, Germany) (when compared to Dürrnberg, Austria), Münsingen-Rain (Switzerland) (except when compared to Kutná-Hora-Karlov, Czech Republic), Hallstatt D (Austria) (when compared to Rudston, east Yorkshire, Britain, and Wetwang Slack, east Yorkshire, Britain), Pottenbrunn (Austria) (when compared to Rudston Makeshift, east Yorkshire, Britain, and Wetwang Slack, east Yorkshire, Britain) (Figures 48-50 and 55-62). Overall, those samples above and below the black reference line vary depending on specific sample comparisons. This indicates a separation among the samples rather than a grouping by region. However, some core and expansion samples are almost consistently plotted above and below the black reference line (e.g., Hallstatt D, Austria, Nebringen, Stuttgart, Germany, and Rudston, east Yorkshire, Britain). Although the above Mantel correlation indicates a moderate positive association between geographic and phenetic distance; there does not appear to be a relationship among the samples and IBD based on the corresponding r values (Table 15). This suggests that although IBD may partly explain the population structure in the regions analysed, it was not the primary mechanism driving the observed intra-and-extra-regional variation. Other mechanisms influencing this variation including differential migration into each region before or during the Hallstatt and La Tène periods, small-scale migration, cultural assimilation, marriage practices (exogamy), and captives and/or enslavement cannot be ruled out as underlying causes or contributing to the observed population structure.

Chapter 7: Discussion, conclusion and future research

Discussion

Diverse populations within the core and expansion regions have been intrinsically linked based on perceived similarities in burial practice, art styles, and material culture. Subsequently, these associations have resulted in the creation of the so-called La Tène=Celtic paradigm (See page 1) (Collis, 2003; Cunliffe, 1984, 1991, 1997, 2009, 2018; Giles, 2012; Koch, 2006, 2007). The complex nature and scale of the interactions, population history, development trajectories, trade, exchange and the underlying biological relationships among presumed Celtic populations have not been the focus of much previous research (See page 1) (Anctil, 2016; Maxová et al., 2011; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). Rather, the majority of previous research examining the spread of Hallstatt and La Tène artefacts has been chronological and typological. Additionally, this research has focused primarily on documentation and descriptions of diachronic change throughout the regions in which the above artefacts are found (Anthoons, 2007, 2011; Collis 1973, 1996, 2003; Cunliffe, 1997, 2018; Giles, 2012; James, 2005; Koch, 2006). However, in spite of these limitations the notion of geographically distinct core and expansion regions are still commonly held within the field of Celtic studies (See page 1) (Collis, 2003; Cunliffe, 1997, 2018; Koch, 2006).

Very few studies, e.g., aDNA, stable isotope, bioarchaeological and dental anthropological, have examined the biological relationships among populations possessing Celtic material culture (Anctil, 2016; Maxová et al., 2011; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). Although variation in dental nonmetric traits among Iron Age European populations has been indicated by previous research, these analyses have focused on modern populations and those traits characteristic of the broad European geographic dental complex (See page 1) (Coppa et al., 1998, 2000, 2007; Hallgrímsson et al., 2004; Hsu et al., 1999; Khudaverdyan, 2013; Maxová et al., 2011; Pacelli and Márquez-Grant, 2010; Scott et al., 2013b; Vargiu et al., 2009; Weets, 2004; Zubova, 2014). Prior research has indicated that the underlying biological relationships among the above groups is more complex than previously assumed (See pages 1, 141 and 145) (Anctil, 2016; Maxová et al., 2011; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). The morphological traits that comprise specific regional populations within Europe and their variation among and within archaeological samples, from any period, have not been the focus of much research (Adler, 2005; Anctil, 2016; Coppa et al., 1998, 1999, 2000, 2007; Cucini et al., 1999; Hallgrímsson et al., 2004; Henneberg, 1998; Hsu et al., 1999; Khudaverdyan, 2013; Maxová et al., 2011; Mcilvaine et al., 2014; Pacelli and Márquez-Grant, 2010; Rathmann et al., 2016, 2019; Scott et al., 2013b; Thorson, 2018; Vargiu et al., 2009; Zubova, 2014). Consequently, the range of dental nonmetric trait variation and phenetic diversity among and within diverse European populations, whether archaeological or modern, is unknown (See pages 1 and 113). Although, previous work by the author has examined the distribution of nonmetric traits among the proto-Celtic and Celtic groups during the Iron Age, in Britain and continental Europe; the biological affinity among these diverse groups has largely been ignored by Celtic scholars (Anctil, 2016). So, archaeological and modern European populations have been broadly characterized and described as having morphologically simple mass reduced dentitions (See page 202, Appendix III) (Anctil, 2016).

The archaeological evidence suggests the presence of diverse intra-and-extra-regional contact; however, the associated artefact descriptions are primarily typological and limited in scope (Arnold, 1988; Brewster, 1980; Dent, 1979, 1982, 1984; Hodson, 1990; Lenski, 2008, 2014; Cameron, 2008, 2011, 2013, 2016; Nash Briggs, 2003; Ramsl, 2002, 2003; Stead, 1979, 1991a; Wendling et al., 2015; Scheidel, 1997). Although some regional variation in artefact design and manufacture has been documented, only the presence of these differences has been mentioned. The exact nature of these connections is not described in detail (See pages 19 and 32) (Budinský and Waldhauser, 2004; Hodson, 1990; Müller, 1998; Müller et al., 2008; Velemínský, 1999; Velemínský et al., 2004; Waldhauser, 1987, 1993). Further, the influence of migrants, captives and/or slaves and how they contribute to the spread of material culture, particularly in relation to the development of new designs or ways of thinking, is unknown (Cameron, 2008, 2011, 2013, 2016; Lenski, 2008, 2014).

Though Hallstatt and La Tène artefacts such as, gold and silver objects, and Mediterranean imports (e.g., Attic pottery, wine flagon, and amphorae), have been comparatively better documented in some regions, e.g., Dürrnberg (Austria), and Münsingen-Rain (Switzerland), the majority of descriptions are still vague (See pages 19, 32, 145 and 155) (Bouzek, 2009; Hellebrandt, 1999; Kaenel and Müller, 1998; Marion, 2009; Soudska, 1994; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Vitali, 2003; Vitali, 2008; Wendling and Wiltschke-Schrotta, 2015; Wells, 2008). Consequently, these artefacts in previous studies focused on the Celts have been used to link the diverse regions in which they are found (See pages 19, 32 and 54) (Brewster, 1980; Budinský and Waldhauser, 2004; Dent, 1979, 1982, 1984; Müller, 1998; Müller et al., 2008; Stead, 1979, 1991a; Waldhauser, 1987, 1993). However, the majority of regional comparisons involve broad geographic areas that are often based on a limited number of artefacts or are site specific (See page 54). These artefacts are also predominantly described as belonging to the Hallstatt or La Tène periods overall, rather than to a specific division, e.g., LTA (Hodson, 1990; Müller, 1999; Tiefengraber and Wiltschke-Schrotta, 2012, 2014, 2015). Thus, the temporal and cultural associations among Celtic artefacts and populations may be uncertain (See page 54). Moreover, their distribution alone may not adequately document the extent and diversity of the cultural connections among the populations in which Hallstatt and La Tène material culture is found (See pages 19, 32 and 54). Therefore, the intrinsic link between these material cultures and Celtic populations is primarily derived from modern interpretations of their ethnicity and the application of the La Tène=Celtic paradigm to the diverse groups possessing the above artefacts (see page 54). However, in spite of these limitations, the archaeological evidence indicates the presence of varied and far-reaching connections during these periods, which are likely more complex than previously presumed.

Trade as a mechanism for the spread of Celtic material culture and throughout the regions in which it is found has not been the focus of much research (see pages 1, 19 and 32) (Anthoons, 2007, 2011; Collis 1973, 1996, 2003; Cunliffe, 1997, 2018; Giles, 2012; James, 2005; Koch, 2006). Documentations and descriptions of trade have predominantly focused on the distribution of Mediterranean imports along the Atlantic trade route (See page 32) (Collis, 2003; Cunliffe, 1997, 2018; Koch, 2006). Although, local productions of trade items, i.e., fibulae, have been documented, regional diversity in design, manufacture, and the presence of local reproductions have not been described in detail (Collis, 2003; Cunliffe, 1997, 2018; Koch, 2006). As such, trade and differential access to trade routes as a mechanism for the spread of the Hallstatt and La Tène material cultures throughout the regions to which they spread cannot be ruled out. Further, the presence of captives and/or slaves producing artefacts and designs, similar to those from their homelands may also be a cause for regional variation within the above archaeological cultures (See page 54) (Arnold, 1988; Lenski, 2008; 2014). Artefacts such as fibulae and weapons may represent trade and/or regional variants, but to determine the possible extent and influence of trade, captives and/or slaves throughout the regions containing Celtic artefacts, it is necessary to move beyond the La Tène=Celtic paradigm.

The presence of these artefacts has been used to identify populations as Celtic, regardless of their number and evidence of other cultural associations. The distribution of isolated find supports the differential incorporation of the above cultures into diverse populations within the broad regions described as Celtic (See pages 32 and 54) (Collis, 2003; Koch, 2006; Kruta, 1991; Selinsky, 2015). Thus, Celtic ethnicity, ancestry and culture have been frequently ascribed based on the presence of a single or limited number of artefacts and similarities in burial practices (See page 54) (Collis, 2003; Koch, 2006; Kruta, 1991). Specific artefacts and burial practices are presumed to be Celtic, such as torcs, fibulae, and square barrows, and their presence alone has been used to designate a population as Celtic. However, no logical justification is provided as to why one artefact or burial practice is ethnically significant and another is not (See page 54) (Collis, 2003; Dietler, 1994; Hodson, 1964; Koch, 2003, 2006; Ruiz Zapatero 1990, 1993, 1996; Shennan, 1994). Further, as artefacts, are produced and integrated into different conceptions of cultural relevance, move and are copied between cultures it is difficult to rely on them as markers of identity (Halkon, 2017).

Intra-and-extra regional contact can also result in regional diversity within an archaeological culture, as evident in the Hallstatt and La Tène cultures (See page 61) (Collis, 2003; Dietler, 1994; Hodson, 1964; Koch, 2003, 2006; Ruiz Zapatero 1990, 1993, 1996; Shennan, 1994). Therefore, what may appear to be a ubiquitous artefact may represent more complex tribal, group and population relationships. The association between the Iron Age and a Celtic ethnicity and ancestry have been derived in part, from modern interpretation and associations between archaeological culture and identity. Thus, the ascribed Celtic identity to diverse populations throughout Iron Age Europe is as much geographical as it is cultural (See pages 1 and 54). The potential presence of multiethnic communities, multiple ancestral lineages, and the maintenance of multiple ethnic identities within one community is often ignored by Celtic scholars (Frangipane, 2015; Hill, 1994; Lightfoot, 2015; Manzanilla, 2015; Rothman, 2015). Moreover, ascribed, externally constructed and perceived ethnic identities have also played a role in the discourse of the application of a Celtic identity to numerous diverse populations (See page 1) (Blanton, 2015; Bonacchi et al., 2016, 2018; Frangipane, 2015; Goldstein, 2015; Grufludd et al., 1999; Hingley, 2018; Hingley et al., 2018; Lightfoot, 2015; Manzanilla, 2015; Rothman, 2015). The application of Celtic ethnicity and/or ancestral heritage within and among populations in Iron Age Europe and Britain is still primarily reliant on the association between archaeological culture and identity. Consequently, the application of ethnicity, or ancestry, to an archaeologically derived population such as the Celts is problematic. Although linguistic evidence has been used to ascribe a Celtic identity to numerous groups, this association is problematic as well. The intrinsic link between the presumption of a spoken Celtic language and population is based in part on their geographic distribution (See pages 19, 32 and 91) (Ball and Fife, 1993; Ball and Muller, 2012; Collis, 2003; Forester et al., 2004; Forester and Toth 2003; Gray and Atkinson, 2003). However, due to the nature of the available linguistic evidence, fragmentary, it is difficult to reconstruct the underlying relationships among groups presumed to have spoken Celtic languages. Therefore, it is difficult to determine the degree of variation among languages identified as Celtic and their approximate boundaries (See page 91) (Barbujani and Sokal, 1990; Creanza et al., 2015; Greenhill et al., 2017; Longobardi, et al., 2015). In spite of the above limitation, the spread or presence of these languages is often linked with the spread of Celtic material culture, large-scale migration and settlement collapse (Ball and Fife, 1993; Collis, 2003; Cunliffe, 1997, 2009; Forester et al., 2004; Forester and Toth 2003; Gray and Atkinson, 2003).

Settlement abandonment has been suggested to have occurred during the Hallstatt and La Tène periods and is believed to have accompanied the diachronic changes in burial practices and the quality and quantity of artefacts during the HaD/LTA and LTC/LTD transitions (See page 61, Table 8) (Collis, 2003; Cunliffe, 1997; James, 2005; Koch, 2007; Maier, 2003). However, there is no evidence, e.g., deteriorating climate conditions, that regions become significantly deserted (Collis, 2003; Cunliffe, 1997; James, 2005; Koch, 2007; Maier, 2003; Smith, 2012). Thus, it is unlikely that large-scale migration events occurred frequently within or from these regions. Instead, mobility likely involved smaller groups or single individuals and was related to exogamy, trade, warfare or allegiance fosterage (See page 61) (Anctil, 2016; Collis, 2003; Cunliffe, 1997, 2010, 2018; James, 2005; Koch, 2007; Scheeres, 2014a; Scheeres et al., 2013b, 2014b;Waldhauser, 1999). Further, as cultural continuity is evident in some regions during the HaD/LTA and LTC/LTD transitions, the similarities and regional differences in material culture throughout these regions may indicate increased individual mobility or small-scale migration (See page 61) (Anctil, 2016; Collis, 2003, Cunliffe, 1997; Hodson, 1968; James, 2005; Koch, 2007; Stöckli, 1991).

Stable isotope analyses also support varying levels of individual mobility and intra-and-extra-regional contact (Knipper et al., 2013, 2014, 2017; Müller-Scheeßel et al., 2015; Scheeres, 2014a; Scheeres et al., 2013b, 2014b). These analyses may appear to support the notion that Celtic warriors were highly mobile, as described by the Greek and Roman primary sources (Nash Briggs, 1984, 1985, 2003). However, stable isotope research has shown that the mobility associated with the so-called warriors was predominantly intra-regional (See page 61) (Knipper et al., 2013, 2014, 2017; Müller-Scheeßel et al., 2015; Scheeres, 2014a; Scheeres et al., 2013b, 2014b).

The frequency of non-local weapon burials has been found to vary by region. Although in some regions such as Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) the majority of males were found to have moved into the region later in life (Scheeres, 2014a; Scheeres et al., 2013b, 2014b). At Radovesice (Czech Republic) 22.2%, 2 out of 9, of male burials with weapons, were local, while 77.7%, 7 out of 9 individuals, were non-local (Scheeres, 2014a; Scheeres et al., 2014b). A similar pattern is evident at Kutná-Hora-Karlov (Czech Republic) 33.3%, 3 out of 9 individuals were local and 66.6%, 6 out of 9 individuals were non-local (Scheeres, 2014a; Scheeres et al., 2014b). The presence of weapons in the burials of local individuals suggests that mobility among males in these regions was not limited to the so-called warriors (See page 61). Further, the above regions also had a significant proportion of non-local individuals overall, 74.3%, 26 out of 35 individuals, and 76%, 19 out of 25 individuals, respectively (Scheeres, 2014a; Scheeres et al., 2013b, 2014b). Trade items in these regions have also been found in burials associated with both local and non-local individuals (Knipper et al., 2017; Oelze et al., 2012; Scheeres, 2014a; Scheeres et al., 2013b). The archaeological evidence suggests a high level of mobility among the alleged Celtic warriors, but this association is not found in all the regions in which these burials have been found (See pages 61, 164 and 168) (Knipper et al., 2017; Oelze et al., 2012; Scheeres, 2014a; Scheeres et al., 2013b). Therefore, the classical Greek and Roman descriptions of the highly mobile Celtic warriors and/or mercenaries may have been restricted to specific regions (Hauschild, 2015; Scheeres et al., 2014b; Tomaschitz, 2002). Moreover, the presence of Celtic weapons throughout Europe has been argued to support the high level of mobility among warriors. However, the distribution of these items may also indicate the presence of diverse trade routes through which Celtic weapons and other materials and items were exchanged (See pages 32 and 61) (Arnold, 2005, 2015, 2016a, b; Arnold and Hagmann, 2015; Georganas, 2018; Fernández-Götz and Arnold, 2017, 2018; Hauschild, 2010a, b, 2015; Scheeres et al., 2013b, 2014b; Webster, 1996). Although burial with a weapon, may not always correlate with or indicate individual mobility (Scheeres et al., 2013b). This is evident in several regions including, Nerbringen (Stuttgart, Germany), Monte Bibele (Bologna, Italy), and Magdalenenberg (southwest Germany), in which the majority of the burials with weapons were of local individuals (See pages 61 and 149) (Oelze et al., 2012; Scheeres et al., 2013b, 2014b; Schweissing, 2013; Waneke, 1999).

In several previous studies, weapon burials associated with evidence of injuries derived from combat have been correlated with warriors, however, this association is disputed as not all individuals given a weapon burial have injuries derived from combat present (Anderson et al., 2018; Arnold, 2005, 2015, 2016a, b; Arnold and Hagmann, 2015; Bertaud, 2017; D'Onofrio, 2011; Fernández-Götz and Arnold, 2017, 2018; Georganas, 2018; Harrison, 2015; Härke,1990; Jordan, 2016; Kurila, 2007; Pitman, and Doonan, 2018; Rustoiu and Berecki, 2015; Rustoiu, 2013; Thorpe, 2013; Ucko,1969; Webster, 1996;Whitley, 2002). Furthermore, injuries derived from, or associated with, combat have been found in burials without weapons (See page 61) (Anderson et al., 2018; Arnold, 2005, 2016a, b; Arnold and Hagmann, 2015; Bertaud, 2017; D'Onofrio, 2011; Fernández-Götz and Arnold, 2017, 2018; Georganas, 2018; Harrison, 2015; Härke,1990; Jordan, 2016; Kurila, 2007; Pitman, and Doonan, 2018; Rustoiu and Berecki, 2015; Rustoiu, 2013; Thorpe, 2013; Ucko,1969; Webster, 1996; Whitley, 2002).

Moreover, these burials are often only described as possessing a weapon, with age estimates of the individual human skeletal remains and comprehensive weapon descriptions often not provided (Oelze et al., 2012; Scheeres et al., 2013b). Several of the weapons recovered from these burials have been repaired repeatedly, and have been interpreted to represent prestige items or family keepsakes; although any evidence of repair, the location(s) and estimated frequency is not often described (See page 61) (Arnold, 2005, 2016a, b; Arnold and Hagmann, 2015; Bertaud, 2017; Fernández-Götz and Arnold, 2017, 2018; Harrison, 2015; Jordan, 2016; Oelze et al., 2012; Rustoiu, 2013; Scheeres et al., 2013b, 2014b; Schweissing, 2013; Waneke, 1999; Whitley, 2002). Consequently, the presence of a weapon alone may not designate the individual as a warrior. Thus, the correlation between the presence of weapon burials throughout the regions possessing Celtic artefacts and the presumption of highly mobile mercenaries may be tenuous.

Although, some of these burials may represent warriors, their mobility as indicated by stable isotope analysis does not support that described by the Greeks and Romans (Arnold, 2005, 2016a, b; Arnold and Hagmann, 2015; Fernández-Götz and Arnold, 2017, 2018; Oelze et al., 2012; Scheeres, 2014a; Scheeres et al., 2013b, 2014b; Schweissing, 2013; Tomaschitz, 2002; Waneke, 1999). This evidence also does not support the notion that the degree of mobility indicated among burials with weapons, and thus mercenaries, is in line with that reported by the Greeks and Romans (See page 61) (Knipper et al., 2014; Oelze et al., 2012; Scheeres, 2014a; Scheeres et al., 2014b). This evidence suggests that mobility among the so-called warriors was predominantly intra-regional (Knipper et al., 2014; Oelze et al., 2012; Scheeres, 2014a; Scheeres et al., 2014b). Furthermore, analysis of mobility within several regions has shown that both males and females were mobile before reaching adulthood, including Kutná-Hora-Karlov (Czech Republic), Radovesice I and II (Czech Republic), Basel-Gasfabrik (Switzerland), Glauberg (Hesse, Germany) (See pages 61, 164 and 168) (Knipper et al., 2014; Scheeres, 2014a; Scheeres et al., 2014b). These findings are in line with the previous nonmetric dental analyses indicating the presence of biologically distinct populations within the regions associated with the Celts (See pages 1, 141 and 145) (Anctil, 2016; Maxová et al., 2011). Residential changes and individual mobility do not appear to be confined to the core or expansion regions; individuals appear to have been moving within regions irrespective of these designations. Consequently, the stable isotope evidence does not support frequent large-scale migrations within these regions. Therefore, the large numbers of Celtic tribes migrating throughout Central Europe and into Britain, documented by the Romans, could be considered as pure propaganda (See page 61) (Collis, 2003; Delbrück, 1900; Furger-Gunti, 1984; Handford, 1982). Instead, mechanisms including isolation, small-scale or individual migration, fosterage, exogamy, limited extra-regional mobility, and gene flow, may have influenced the population history and/or structure within the above regions (Konigsberg, 2006; Relethford, 1996; Relethford and Blangero, 1990). Thus, the old model of mass migration during the 4th and 3rd centuries BC of homogeneous Celtic populations that abandoned their homelands in the core, and migrated into the expansion regions may not explain the range of biological and ethnic variation among these groups (See page 61). The available modern European genetic evidence further supports the notion of a greater degree of biological variation among these groups than previously indicated.

Different Y-chromosome and mtDNA haplogroups and sub-clades are evident within and among the regions associated with Celtic material culture and language(s) (Busby et al., 2012; Capelli, 2003; Cassidy et al., 2015; Cruciani et al., 2011; Lucotte, 2015; Weale et al., 2002; Wilson et al., 2001). The presence of overlapping haplogroups and sub-clades, within these regions suggests that a combination of different mechanisms including small-scale migration and genetic drift may have resulted in the observed diversity (See pages 103, 105 and 107) (Busby et al., 2012; Capelli, 2003; Cassidy et al., 2015; Cruciani et al., 2011; Lucotte, 2015; Weale et al., 2002; Wilson et al., 2001). However, previous studies have relied on the Y-chromosome and mtDNA haplogroup and sub-clade distributions indicated by modern populations (Busby et al., 2012; Cruciani et al., 2011; Lucotte, 2015; Weale et al., 2002; Wilson et al., 2001). Consequently, they might not adequately reflect the amount of diversity within or among populations during the Iron Age (See pages 103, 105 and 107). Further, these studies have attempted to document the above distribution in broad geographic regions associated with Celtic populations (Busby et al., 2012; Cruciani et al., 2011; Lucotte, 2015; Weale et al., 2002; Wilson et al., 2001). Therefore, the range of variation among the diverse region-specific groups is unknown. However, despite these limitations, the modern European genetic evidence is in line with the archaeological, linguistic and stable isotope evidence indicating small-scale migration, demic diffusion and/or assimilation (See pages 61, 103, 105 and 107).

Although the above lines of evidence suggest the presence of diverse regional populations, they alone have not been sufficient to determine the underlying biological relationships, population history, and structure within the core and expansion regions. Therefore, the degree of phenotypic variation within and among populations in these regions is unknown. However, biodistance analyses provide a measure of diversity within and among populations or groups through examination of phenotypic expression (See page 119) (Buikstra et al., 1990). This analytical method facilitates comparisons among populations based on genetic and/or phenotypic characters including dental morphological traits (Buikstra et al., 1990). These traits are discrete anatomical units that show patterns of distinct geographic variation, as well as within, between, and among populations (See pages 113, 119, 124, 125 and 131). Significant differences in the frequency of trait expression between populations suggest influence from mechanisms such as gene flow, genetic drift, and mutation. Differences in dental nonmetric trait expression can therefore be used to determine affinity between and among populations (Bedrick et al., 2000; Buikstra et al., 1990; Harris and Sjøvold, 2004; Hanihara, 2008, 2010; Hillson, 1996; Irish, 1993, 1998a, b, c, 2000, 2005, 2010; Irish and Guatelli-Steinberg, 2003; Sjøvold, 1973). Further, the establishment of the ASUDAS system, which is the standard and most widely used method for identifying nonmetric traits, has facilitated comparisons of broad geographic and region-specific populations (See pages 113 and 119) (Hillson, 1996; Scott and Turner, 1988; Turner et al., 1991). The ASUDAS system, specifically 36 of these traits, based on the work of Irish (1993) has been used in numerous previous studies and have been established as successful in describing and comparing the biological affinity among and within populations (Anctil, 2016;

Coppa et al., 1998, 2000, 2007; Cucina et al., 1999; Hanihara, 2008, 2010; Irish, 1993, 1997, 1998b, c, 2000, 2005, 2006, 2008, 2010, 2016; Irish et al., 2014, 2018; Irish and Guatelli-Steinberg, 2003; Matsumura et al., 2009; Turner, 1969; 1984, 1985).

Previous biodistance analyses, based on dental morphological data, have documented the presence of regional diversity and biologically distinct populations within the regions associated with the Celts (See pages 1, 141 and 145) (Anctil, 2016; Maxová et a., 2011). Although there are some differences between the results of dental and genetic analyses, the discrepancies are likely the result of the fact that dental traits evolve slowly. Therefore, they may provide a population history more in line with a deeper time scale than the genetic data (Hubbard, 2012; Irish et al., 2020; Ricaut et al., 2010). However, previous genomic analyses have found a significant and positive correlation ($r=0.574$, $p< 0.001$ and $r=0.500$, $p=.021$) between dental nonmetric and nuclear microsatellite data used to distinguish global and regional populations (See pages 1, 125 and 131) (Hubbard, 2012; Rathmann et al., 2017). This supports the notion that dental morphological traits provide similar information about biological affinity and population structure as genetic data (Hubbard, 2012; Hubbard et al., 2015; Irish et al., 2020; Ricaut et al., 2010; Scott and Turner 1997). The heritability of dental traits, 40%-80%, further supports the association between genetic and dental datasets (See pages 113, 125 and 131) (Jordan and Abrams, 1992; Mizoguchi, 1978; Scott, 1991; Scott and Irish, 2017; Scott and Turner, 1997; Willermet et al., 2013). Therefore, dental morphological data can be used to represent, by proxy, the genetic variation among and within populations. These data were used to address the following research questions:

1. Do Celtic populations within the expansion regions exhibit more phenetic diversity than those within the core?
2. Were populations in the expansion regions acculturated, genetically influenced by the arriving Celts, and/or replaced?
3. Are the observed morphological differences among the samples within the core and expansion regions explained by an isolation by distance model?

The following sections will explore each research question in relation to the biological variation among the samples analysed.

Do Celtic populations within the expansion regions exhibit more phenetic diversity than those within the core?

The biological affinity analysis indicates that the populations in the expansion regions exhibit less phenetic diversity than those within the core as 2 samples within these regions are biologically indistinguishable; whereas all the samples within the core are phenetically diverse. Although 2 samples in each region are not phenetically diverse, those within the core represent different temporal periods of one sample, Dürrnberg Hallstatt (Austria) and Dürrnberg La Tène (Austria), while those in the expansion regions represent 2 separate samples, Kutná-Hora-Karlov (Czech Republic) and Radovesice (Czech Republic). However, the sample composition is not evenly distributed within these regions, as there are more core than expansion samples, 6 and 4, respectively. Therefore, the core regions may appear to exhibit more phenetic diversity because there are more samples. In spite of the discrepancy in sample distribution, there is no evidence for population continuity based on the samples analysed, with the exception of those above. Some of the sample pairs have comparably low MMD values including, Dürrnberg La Tène (Austria), and Wetwang Slack (east Yorkshire, Britain) 0.028 and Dürrnberg (Austria), and Wetwang Slack (east Yorkshire, Britain), 0.025, respectively (See page 206). However, all of the remaining sample pairs have significant and moderate to high phenetic distances comparatively. Intra-and-extra regional diversity is indicated by the 25 trait MMD comparison (Table 11). Phenetic heterogeneity, among most of the samples, is indicated by both 20 trait MMD comparisons (Tables 12 and 13). However, there is a greater emphasis on divergence in the 20 trait analyses, with the Dürrnberg (Austria) sample combined (See page 206). Based on the above MMD analyses, the null hypothesis that there is no difference in dental nonmetric traits is rejected at the .025 alpha level for all samples, except the Dürrnberg (Austria), Kutná-Hora-Karlov (Czech Republic) and Radovesice (Czech Republic) samples. These samples have MMD values that are less than 2 times their SD, this indicates that they are phenetically indistinguishable and represent the same biological population (See page 206) (Irish, 2010, 2016; Irish et al., 2014, 2018; Sjøvold, 1973,1977). The remaining samples represent biologically distinct populations, as their MMD values are greater than 2 times their SD (See pages 188, 206, Tables 12 and 13) (Irish, 2010, 2016; Irish et al., 2014, 2018; Sjøvold, 1973,1977).

Although the Hallstatt and La Tène periods of the Dürrnberg (Austria) sample are not significantly different from one another, the MMD distances decrease during the La Tène period (20 trait MMD values 0.058-0.084 and 0.041-0.057, respectively) (See page 206). Mechanisms such as, rerouting of trade routes, a change in locations from which marriage partners or migrants were drawn, increased migration from neighbouring intra-and-extra-regional populations during the La Tène period, or migration into the region prior to the HaD period may have resulted in a decrease in phenetic differentiation within this sample (See pages 19, 61, 206 and 206, Table 8). Additionally, it has been suggested that Dürrnberg (Austria) may have been a trading centre, based on the abundant presence of trade and high-quality artefacts. The presence of an active nearby salt mine also supports this notion, as the population would have had control of a valuable commodity (See pages 61 and 155) (Adshead, 1992; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015).

Further support is provided by the apparent demographic expansion and decline during the La Tène period, evident in the conversion of burial to settlement areas and the subsequent reconversion into burial areas (Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015). Although, this apparent population increase and decline may also have been the result of deteriorating climate conditions or the declining productivity of the salt mine (See pages 155, 157, 158 and 159) (Adshead, 1992; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015). However, as no stable isotope analysis has been conducted on the skeletal material from Dürrnberg (Austria), the number of non-local individuals is unknown. Consequently, it is difficult to determine whether the decreasing MMD values indicate decreasing phenetic similarity during the Hallstatt and La Tène periods due to an increase in the number of migrants (See page 61). Alternatively, the decreasing phenetic similarity may be related to a prior migration into the region and subsequent phenetic diversification through gene flow or genetic drift. However, other processes such as small-scale migration, exogamy, and cultural assimilation cannot be ruled out. Similar processes may also have resulted in the phenetic similarity between the Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) samples.

The regions in the Czech Republic in which the Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) samples are located are in close geographic proximity, only 76.44 km apart. Therefore, they may have derived from the same original population, and it is possible the samples had not become phenetically distinct (See pages 164, 168 and 221). Alternatively, frequent gene flow between the samples may have occurred through processes such as exogamy and migration, to the extent that they became genetically indistinguishable from one another. However, the Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) samples were discovered through the course of construction, which destroyed several graves and fragmented much of the recovered skeletal material (Valentová, 1991; Valentová and Sankot, 2012). Further, the shallow grave depth at Kutná-Hora-Karlov (Czech Republic) may have resulted in the loss of several burials due to construction, taphonomic or agricultural processes such as erosion (Valentová, 1991; Valentová and Sankot, 2012). These processes and shallow grave depth are also believed to have reduced the number of burials recovered from Nebringen (Stuttgart, Germany) (See pages 149 and 168) (Krämer, 1964). Therefore, Radovesice (Czech Republic) Kutná-Hora-Karlov (Czech Republic) and Nebringen (Stuttgart, Germany) may represent sub-samples. Additionally, the Radovesice (Czech Republic) sample was pooled to obtain an adequate sample size for statistical analysis and comprises both the Radovesice I and II (Czech Republic) cemeteries. Since it is unknown whether these cemeteries represent a single or composite population, the pooled sample may not adequately represent the range of variation within the original population (See page 164).

The German (Stuttgart, Germany), Rudston Makeshift (east Yorkshire, Britain), and Pontecagnano (southern Italy) samples also represent pooled or sub-samples, and as such are also subject to the above caveat. The Münsingen-Rain (Switzerland) sample can also be said to be a sub-sample, as only the skulls of 77 out of 220 individuals were recovered (See page 145). Consequently, the above samples may represent a proportion of the variation present in the original populations. The results of the biodistance analysis may need to be interpreted with a degree of caution in regard to these samples. However, no additional skeletal material from the above samples is available for analysis. Thus, these samples do not need to be interpreted with the same degree of caution as the German (Stuttgart, Germany), Rudston Makeshift (east Yorkshire, Britain), and Pontecagnano (southern Italy) samples. Although no additional skeletal material is available from Radovesice (Czech Republic) this sample represents a composite sample and therefore should be interpreted with caution, as described above. Therefore, further samples are necessary to determine the biological affinity within those regions represented by either pooled or sub-samples.

However, an overall trend towards limited intra-regional and no extra-regional gene flow is suggested by the MMD distance values among the samples. Although increased intra-and-extra-regional gene flow within these broad geographic regions cannot be ruled out; as the samples reflect a proportion of the total possible phenetic and regional variability during this period. Both the 20 trait MMD distances (0.028-0.084 and 0.025-0.085, respectively) also support a significant degree of phenetic variation among the core and expansion regions, those represented by the samples, compared to that indicated by the other lines of evidence, i.e., archaeological (See pages 32, 206, Tables 12 and 13). These distances also support the phenetic divergence between the Celtic samples and the comparative sample, Pontecagnano (southern Italy). This divergence supports the presence of greater regional variation among European Iron Age populations than previously assumed. Further, the presence of biologically distinct populations associated with and without Celtic material culture suggests that the La Tène=Celtic paradigm may be nominal. The observed phenetic diversity also supports the potential issues with utilizing type artefacts, such as fibulae, to characterize a culture and its subsequent dispersals, as the presence of these artefacts alone cannot be reliably used to establish ethnic and biological relationships (See pages 32 and 206) (Collis, 2003; Cunliffe, 1997, 2009; Giles, 2012; Koch, 2006). The overall sample distributions indicated by the MMD distances, the nominal application of the La Tène=Celtic paradigm, and the issue with the associations of type artefacts are also indicated by the MDS graphs and cluster Dendrograms (See pages, 194, 199, 211 and 215, Figures 39-41 and 46-47, respectively) (Collis, 2003; Cunliffe, 1997, 2009; Giles, 2012; Koch, 2006).

The quantitatively identified inter-sample trends as indicated by the MMD matrices are also evident in the MDS graphs and hierarchical cluster dendrograms (See pages 206, 211 and 215, Figures 39-41 and 42-47, respectively). The sample distributions indicated by the MDS graphs share similar distributions. However, the relative positions of some samples, such as Pontecagnano (southern Italy), and Wetwang Slack (east Yorkshire, Britain) are switched due to differential trait weighting (See pages 211 and 215). The configurations of the 25 and both 20 trait MDS graphs also share some patterning with the PCA graph, including the relative positions of the Dürrnberg La Tène (Austria), Dürrnberg pooled (Austria), and Rudston Makeshift (east Yorkshire, Britain) samples (See page 202, 211, Figures 38 and 39-41, respectively). Although the core and expansion region samples are interspersed, in the PCA and all of the MDS graphs, clear separation among samples is evident (See pages 202 and 211, Figures 38 and 39-41, respectively). Further, in the above graphs, the samples are interspersed by region. Therefore, the separation of Celtic populations and material culture into the core and expansion regions may be nominal. The social and/or cultural changes within these regions are also not explained by the current application of the core and expansion model within the field of Celtic studies. The temporal and geographic designation of the above areas does not consider the diverse internal social dynamics and individual development trajectories of the societies involved (See page 1) (Cordell 1979; Martin and Plog 1973; Tainter and Gillio 1980). However, this model is still utilized in the field of Celtic studies to describe populations throughout Iron Age Europe possessing Celtic material culture and languages; regardless of the complex nature and interactions among populations within the above regions (Collis, 2003; Koch, 2006). The sample distributions indicated by the above graphs also suggest that the observed variation may also indicate the presence of region-specific rather than broad geographically distributed populations or groups. This pattern and the presence of diverse populations possessing Celtic material culture are also supported, in part, by the archaeological evidence.

The archaeological evidence indicates far-reaching and diverse intra-and-extra-regional connections during the Hallstatt and La Tène periods (See pages 19, 32, Table 8) (Almagro-Gorba, 1991; Budinský and Waldhauser, 2004; Haffner, 1976; Joachim, 1968; Krämer, 1964; Koch, 2006; Ramsl, 2002; Rustoiu, 2008, 2011a, b; Rustoiu and Egri, 2014; Salac, 2011; Soudska, 1994; Tiefengraber and Wiltschke-Schrotta, 2012, 2014; Valentová, 1991, 1993 Valentová and Sankot, 2012; Waldhauser, 1993). Dispersal of typical artefacts such as, fibulae; torcs; bracelets; Mediterranean imports (e.g., Attic pottery, wine flagons, and red-figure pottery); gold and silver items indicate the development and maintenance of the above connections during these periods (See pages 19, 32, Tables 1, 4 and 5) (Budinský and Waldhauser, 2004; Collis, 2003; Haffner, 1976; Joachim, 1968; Krämer, 1964; Koch, 2006; Ramsl, 2002; Rustoiu, 2008, 2011a, b; Rustoiu and Egri, 2014). However, the distributions of the above artefacts are still commonly interpreted under the La Tène=Celtic paradigm. Although the archaeological evidence does not support the notion of broad geographically distributed populations or groups; the presence of Celtic artefacts are still interpreted to indicate the presence of Celtic populations (See pages 32 and 54) (Cunliffe, 1997, 2009; Collis, 2003; Giles, 2012; Hauschild et al., 2013; Hellebrandt, 1999; Hellebrandt and Hellebrandt, 1990; James, 1999; Koch, 2003, 2006; Kruta, 1991; Marion et al., 2005a, b; Marion, 2008; Ramsl, 2002, 2012a, b, 2014a, b; Scheeres, 2014a; Scheeres et al., 2013b, 2014b; Stead, 1991a; Vitali, 1987, 1988, 1991; Vitali et al., 2002; Wendling et al., 2015). The presence of regional variation in artefact design, manufacture and distribution further support the presence of biologically distinct populations, as indicated by the MMD distances (See page 206). The above connections are also supported by the distribution of Celtic art styles, and burial practices during the Hallstatt and La Tène periods (See pages 19, 32, Tables 2, 6, 3 and 7, respectively). However, the patterns indicated by the dispersal of these artefacts are more diverse and indicative of a greater degree of regional connectivity than described by previous studies (See pages 32 and 206). The spread of Celtic material culture during the 4th and 3rd centuries BC has been predominantly interpreted to indicate large-scale migration. However, the above distributions are in line with small-scale migration, individual movement, limited intra-and-extra-regional movement, cultural diffusion and/or assimilation. The spread of Celtic artefacts through these mechanisms is also supported by the MMD values and the available stable isotope analyses (See page 61 and 206).

However, as the samples analysed only represent a proportion of the total populations within the core and expansion regions, they may be phenetically similar to other groups, not analysed, within these regions. The Dürrnberg (Austria) sample may be phenetically similar to other Austrian samples such as Mannersdorf (Austria), Oberndorf (Austria), and Ossarn (Austria). The Kutná-Hora-Karlov (Czech Republic) and Radovesice (Czech Republic) samples may have more affinity to others within the Czech Republic including Jenišův Újezd (Czech Republic) and Manětín-Hrádek (Czech Republic), a finding which is partly supported by the stable isotope evidence. Some regions had comparatively high numbers of non-local individuals such as Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) where 74.3% (26 out of 35 individuals) and 76% (19 out of 25 individuals) of the individuals were migrants, respectively (See page 61) (Scheeres, 2014a; Scheeres et al., 2014b). However, these individuals migrated into the region from the surrounding areas rather than from extra-regional locations (Scheeres, 2014a; Scheeres et al., 2014b). Limited intra-regional movement is also supported by the stable isotope evidence for non-local individuals from Münsingen-Rain, Switzerland (Moghaddam et al., 2014; Scheeres, 2014a). The majority of the population was local, only 14.7%, 5 out of 34 individuals, migrated from the neighbouring areas in the Swiss Plateau (Moghaddam et al., 2014; Scheeres, 2014a). A similar pattern is evident at Nebringen (Stuttgart, Germany), Manching (southern Germany), and Monte Bibele (Bologna, Italy), where 88%, 15 out of 17 individuals, 77%, 14 out of 18 individuals, 81%, 17 out of 21 individuals, respectively, of the populations, were found to be local (Scheeres, 2014a; Scheeres et al., 2013b; Scheeres et al., 2014b; Schweissing, 2013; Waneke, 1999). Limited mobility is also evident in Kirkburn (east Yorkshire, Britain), Garton Station (east Yorkshire, Britain) and Wetwang Slack (east Yorkshire, Britain) (Jay et al., 2013; Jay and Montgomery, 2020). Further, in the majority of the populations with comparatively high amounts of non-local individuals, e.g., Radovesice (Czech Republic), movement was primarily intra-regional (See page 61). However, there is also evidence for limited extra-regional movement. The majority of migrants from Magdalenenberg (southwest Germany) and Basel-Gasfabrik (Switzerland), 17.1%, 13 out of 76 individuals, and 37%, 20 out of 54 individuals, respectively, were from extra-regional locations (Knipper et al., 2017; Oelze et al., 2012).

Migrants identified in the above European studies were from diverse and geographically distant locations including, Austria, France, Heuneburg (southern Germany), northern Italy, the Alps, the Swiss Plateau, the Iberian Peninsula, the Black Forest, a region in southwestern Germany near the French border, and the Mediterranean (See page 61). (Knipper et al., 2017; Oelze et al., 2012). Further, the majority of the individuals that moved during adulthood and were males (Knipper et al., 2017; Oelze et al., 2012). This suggests that individual mobility was common within some regions associated with the Celts. Rather than the large-scale population-level migration reported by the Greeks and Romans. The above stable isotopic evidence also suggests that limited extra-regional migration and relatively high intra-regional movement may have characterized Celtic populations (See page 61). However, the degree and directionality of migration associated with these populations appear to be region-specific. Further samples are necessary to determine whether limited extra-regional movement is also evident in other regions associated with the Celts. The comparatively high degree of intra-regional mobility within the regions analysed, except for Nebringen (Stuttgart, Germany) may also reflect a rerouting or breakdown of trade routes (See page 61). Alternatively, changes in marriage partner procurement networks may have impacted mobility. However, patrilocality, small-scale and/or family migration cannot be ruled out as mechanisms driving migration throughout the above regions. The patterns indicated by the archaeological, stable isotope, and MMD values are also supported by the available modern European genetic and extinct linguistic evidence (See pages 61, 103, 105, 107 and 206).

The modern European distribution of Y-chromosome and mtDNA haplogroups and sub-clades (e.g., R1b-S28/U152 and H5) supports the presence of distinct populations within the diverse regions broadly defined as Celtic. However, as previous modern European genetic analyses have relied on the Y-chromosome and mtDNA distributions indicated by modern populations, they might not adequately reflect the amount of diversity in the Iron Age (See pages 103, 105 and 107) (Busby et al., 2012; Cassidy et al., 2015; Cruciani et al., 2011; Lucotte, 2015; McEvoy et al., 2004; Weale et al., 2002; Wilson et al., 2001). Although variations in regional patterns are indicated by the above lines of evidence, the available linguistic inscriptions are more limited. Despite the longstanding association between a spoken Celtic language and an ethnically or biologically Celtic population, there is not a considerable indication of linguistic differences throughout the regions these languages are believed to have spread (See page 91). Since the continental Celtic languages are extinct and the majority of the inscriptions are fragmentary; it is difficult to determine the degree of variation among populations based on the presence and distribution of these languages and their approximate linguistic boundaries (See page 91) (Arnold, 2005; Collis, 2003; Tomaschitz, 2002). However, based on the significant concordance between ancient and modern genetic and extinct linguistic data; the presence of genetic boundaries, as indicated by the distributions of haplogroups and the MMD distances, may be used as a proxy for linguistic boundaries among Celtic populations (See pages 105, 107 and 206) (Barbujani et al., 1990; Bickel, 2019; Creanza et al., 2015; Greenhill et al., 2017; Longobardi et al., 2015; Sokal, 1988; Sokal et al., 1988, 1989, 1990). Although the preceding biodistance analysis indicates the presence of phenetic heterogeneity among the samples, the results may need to be interpreted with a degree of caution.

As the samples have been predominately dated by associated artefacts, they may be pooled temporally. Consequently, temporal differences may not be adequately represented. However, as the populations associated with the Hallstatt and La Tène cultures are predominately dated by artefact association, except for a few studies, these dates often represent the only available dates in most cases (See pages 19 and 32) (Collis, 2003; Cunliffe, 1979, 1997; Hodson, 1990; James, 2005; Jay et al., 2013; Jay and Montgomery, 2020; Kruta, 1991; Müller, 1999; Tiefengraber and Wiltschke-Schrotta, 2012, 2014, 2015; Wells, 1998). Therefore, these dates may represent the earliest possible movement of the above cultures into specific regions. Although some populations, e.g., Dürrnberg (Austria), have been assigned to specific periods such as LTA, this association is still based on presumed artefact dates and distributions. Consequently, the majority of previous studies have ascribed populations associated with these cultures to the period overall (See pages 19 and 32). Additionally, those samples that can be broken down by period from the above region are too small for statistical analysis (i.e., a sample size of < 20 individuals) the results of which would likely be tenuous or represent spurious relationships (See pages 113 and 119) (Irish, 1993, 1997, 2008, 2010). Other potential issues with the samples include the assumptions of population history and structure analyses. The caveats associated with these analyses may appear to be violated by the geographic distribution of the samples. Under these analyses, it is assumed that populations were able to interbreed and therefore were contemporaneous in time and space (See page 118) (Alt et al., 2012; Exoffier et al., 1992; Konigsberg, 2006; Relethford and Blangero, 1990). Comparisons of populations that are vastly temporally and spatially disparate violates this caveat, e.g., sub-Saharan Africa and Turkey (Alt et al., 2012; Exoffier et al., 1992; Konigsberg, 2006; Relethford and Blangero, 1990).

Further, archaeological samples that are dated by associated artefacts may also violate this assumption, as it is unknown whether they are contemporaneous (See page 118). Although the samples used in this analysis have been dated in the above manner and are geographically separate; the stable isotope and archaeological evidence suggest that they were able to interbreed and were roughly contemporaneous (See page 61). Moreover, the Hallstatt D (Austria) and Dürrnberg Hallstatt (Austria) samples are not contemporaneous with the others; however, it is believed that populations during this period migrated into neighbouring regions after the collapse of the salt mine at the type site (Barth, 1991; Collis, 2003; Cunliffe, 1997). Consequently, these samples were included in this analysis as they may have interbred with those remaining. However, as the sample dates may represent the earliest possible, there may have been more intra-regional similarity than indicated by the MMD values (See page 206). Further, as these dates are the only available, and the above manner is still the predominant method for dating Celtic populations, it is unlikely that more temporally specific populations will become available for analysis. The stable isotope evidence indicates that diverse and geographically separate populations were able to interbreed such as those from Magdalenenberg (southwest Germany), northern Italy and the Iberian Peninsula (Knipper et al., 2017; Oelze et al., 2012). Although the number of migrants moving within the above regions indicates small-scale or individual migration; the presence of individuals from geographically dispersed areas suggests that these populations were able to interbreed to some extent (See pages 61, 206 and 221). The presence of diverse and far-reaching connections between the samples analysed, also supports the notion that these groups were able to interbreed. However, it is advised that, when possible, archaeological samples be restricted to populations within a realistic geographic distance so that interbreeding can occur (See pages 118 and 119) (Knudson and Stojanowski, 2008). The geographic distances of some samples such as Rudston Makeshift (east Yorkshire, Britain) and Wetwang Slack (east Yorkshire, Britain) may appear to violate this assumption. However, the above evidence for migration across vast distances indicates that interbreeding across similar distances did occur during the Iron Age. Further, the stable isotope analyses indicating movement into diverse and distant regions may only represent a proportion of the total sample available for analysis (See page 61). Dietary and mobility stable isotope information suggests that many Iron Age people spent their lives local to their burial place or within their tribal territory, such as the data observed for east Yorkshire (Britain) (Jay and Montgomery, 2020). The Iron Age population from Wetwang Slack (east Yorkshire, Britain) has been found to be a predominantly local community with currently no evidence for long-distance mobility (See pages 61 and 172) (Jay and Montgomery, 2020). Strontium stable isotope values indicate that a few individuals (3 out of 7 individuals) were mobile to some extent. However, these individuals were not likely long-distance migrants and were instead moving around the regional landscape (See pages 61 and 172) (Jay and Montgomery, 2020).

Additionally, there is evidence for long-distance movement of adults and sub-adults within Iron Age Britain and possibly a few individuals from Europe have been reported from Kent, Derbyshire, and west Yorkshire (Britain) (Millard, 2014; Montgomery et al., 2007). There is also stable isotope evidence from cattle and horses in this period, which shows that some animals were travelling over 100 km (Bendrey et al., 2008; Hamilton et al., 2019; Madgwick et al., 2013; Montgomery et al., 2007; Schulting et al., 2019; Stevens et al., 2013b). This suggests that if animals, e.g., cattle, were moving so were people. Therefore, movement into these regions may have been more common than indicated. Additionally, there is accumulating evidence for long-distance mobility of people and cattle within Iron Age Britain, such as from Ham Hill hillfort (Somerset) (Madgwick et al., 2013) and the A1M motorway in west Yorkshire (Montgomery et al., 2007) (see also, Chadwick, 2008; Hamilton et al., 2019; Schulting et al., 2019; Stevens et al., 2013b). At the site of Cliffs End Farm (Kent), movement throughout the Bronze and Iron Age is indicated (McKinley et al., 2014; Millard, 2014). Therefore, the MMD distances should be interpreted considering the above assumptions. As the samples represent archaeological populations, the regional comparisons, indicated by the MMD distances, may also need to be interpreted with a degree of caution due to the presence of heavy dental wear. Although methods such as trait downgrading and upgrading facilitate the scoring of moderately worn dentitions to increase sample sizes, these methods were not used (See page181, Appendix III) (Irish et al., 2014, 2018; Scott and Irish, 2017). Instead, the level of wear was recorded per tooth, major differences in wear were also documented when encountered to account for the MCAR assumption (Scott and Irish, 2017). Further, the majority of the samples had similar degrees of wear, mild to moderate. Severe dental wear, when observed, was encountered over the majority of an individual's dentition (See page 181, Appendix III). Consequently, these individuals were removed from the ensuing analysis. It was subsequently determined whether the degree of wear permitted trait scoring or not. Moderate to severe dental wear when encountered was restricted to specific teeth such as the molars. In these cases, the antimere was scored when available. Although when the antimere was not available or the level of wear was too great, the affected tooth was not scored for any trait (See page 181, Figure 34). Variation in sample sizes (among those used in this analysis) may also have minimized the extent of the biological diversity, or lack thereof among the samples as indicated by the MMD distances (See page 206, Table 8). Therefore, the samples may not document all the variation present in the original populations. Thus, the possibility of within-population variation cannot be ruled out. However, the overall pattern indicated by the MMD distances is also supported by the archaeological, stable isotope, extinct linguistic and modern European genetic evidence (See pages 19, 32, 61, 91, 103, 105, 107, 119, 124 and 206). This suggests that while there may have been more intra-regional phenetic similarity in the original populations than indicated by the biodistance analysis, limited extra-regional movement and genetic drift likely characterized the population structure of the samples. Further, as the results of the biodistance analysis are supported by the above lines of evidence and previous analyses; the underlying phenetic relationships are likely representative of those in the original populations.

In spite of the above limitations, the preceding biodistance analysis indicates that the majority of the samples represent biologically distinct populations. This suggests that limited intra-and-extra-regional gene flow, genetic drift, small-scale migration, cultural diffusion and/or assimilation likely characterized the population structure within the core and expansion regions. A finding that supports those of a previous biodistance analysis suggesting the presence of biologically distinct populations associated with the Hallstatt and La Tène cultures (See pages 141 and 145) (Anctil, 2016). These analyses further suggest that these processes were occurring among populations irrespective of their presence in the core or expansion regions. The notion that the spread of Celtic material culture occurred in tandem with a concomitant biological change is not supported. However, further samples, from the core and expansion regions, are necessary to determine whether the above patterns are also observed in other regional populations associated with the Celts.

Were populations in the expansion regions acculturated, genetically influenced by the arriving Celts, and/or replaced?

Both the 20 trait MMD distances, with the Dürrnberg (Austria) sample combined and temporally separated, suggest that the samples analysed within the expansion regions were likely acculturated through trade, cultural diffusion and/or assimilation (See page 206, Tables 12 and 13). The samples from the above regions are biologically distinct from those within the core, this suggests that they were not genetically influenced or replaced, through large-scale migration and gene flow by populations from these regions (See pages 188 and 206). The null hypothesis that there is no difference in nonmetric traits among these populations is rejected at the 0.025 alpha level for most of the sample pairs. The alternative hypothesis is supported in regard to the Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) samples. However, the regional distribution of the samples may have resulted in those in the core appearing more diverse. The overall phenetic diversity among the majority of the samples analysed indicates that genetic drift rather than gene flow is likely to have influenced the population structure. However, small-scale migration not significantly influencing gene flow, and isolation cannot be ruled out. Therefore, at this broad geographic level, population and/or ethnic diversity among the samples is suggested except for those mentioned above. This suggests that the notion that migration was a primary factor for the spread of Celtic material culture into the expansion regions may not be supported (See pages 19, 32, 61 and 206). Although there is some evidence of migration among the above samples and within the different temporal periods of the Dürrnberg (Austria) sample, it does not appear to have been common among the diverse regions represented by the samples. This notion is supported by the archaeological, stable isotope and modern European genetic evidence (See pages 61, 105 and 107).

The above lines of evidence indicate diverse and far-reaching intra-and-extra-regional variation during the Hallstatt and La Tène periods (Atkinson and Gray, 2017; Busby et al., 2012; Collis, 2003; Cruciani et al., 2011; Forester et al., 2004; Forester and Toth 2003; Gray and Atkinson, 2003; Haffner, 1976; Joachim, 1968; Koch, 2006; Krämer, 1964; Kruta, 1991, 2004; Ramsl, 2002, 2015; Ramsl et al., 2011b). However, the above patterns are more varied and suggest a higher degree of regional concordance than those indicated by the biodistance analyses (See pages 19 and 32). This discrepancy suggests that the samples were likely relatively isolated and had limited to no gene flow with one another. Consequently, processes such as trade, cultural diffusion and/or assimilation may have resulted in the similarities in material culture and presumably language more than previously believed. However, the presence and influence of captives and/or slaves on the diachronic changes in material culture cannot be ruled out. This notion is further supported by both the 20 trait MMD distances, which indicate limited intra-regional and no extra-regional gene flow (See page 206). The presence of biologically distinct populations, and by proxy ancient or modern genetic and linguistic boundaries, indicates that the spread of Celtic material culture into the expansion regions analysed was not accompanied by a concomitant biological change. Therefore, the La Tène=Celtic paradigm and the old mass migration model may not adequately explain the observed phenetic variation among presumed Celtic populations. The MMD values further support the tenuous association ascribed by the above paradigm and model to the diverse populations analysed (See page 206). However, this model does not explain the underlying biological relationships, aDNA, stable isotope and bioarchaeological studies, among the samples. Rather, migration among the diverse regions represented is suggested.

The period of Celtic migrations has been the focus of previous research. However, the longstanding question of whether the spread of La Tène material culture throughout the expansion regions, during the 4th and 3rd centuries BC, was related to increased individual mobility or large-scale migration is still prevalent within the field of Celtic studies (See page 61) (Anthoons, 2007; Arnold, 2005; Fernández-Götz, 2013, 2014a, b; Prien, 2005; Ramsl, 2003; Tomaschitz, 2002). Previous attempts to model migration scenarios from the core to expansion regions have primarily focused on the information provided by the Greek and Roman authors, as well as the presence of Celtic artefacts in any quantity, including isolated finds (See pages 19, 32 and 61) (Anthoons, 2007; Arnold, 2005; Chapman, 1997; Fernández-Götz, 2013, 2014a, b; Hakenbeck, 2008; Karl, 2005; Knipper et al., 2014, 2017; Prien, 2005; Ramsl, 2003; Tomaschitz, 2002).

However, the proposed migrations and processes driving the observed cultural expansion during the above period, as described by Greek and Roman authors, are ambiguous (Anthoons, 2007, 2011; Collis, 2003; Cunliffe, 1997; James, 2005; Tomaschitz, 2002). Movements of Celtic populations have been described primarily as massive large-scale events that involved entire populations which expanded from Central Europe and subsequently spread throughout the rest of Europe and into Asia Minor and Turkey (See page 61) (Anthoons, 2007, 2011; Collis, 2003; Cunliffe, 1997; James, 2005; Selinsky, 2015; Tomaschitz, 2002). However, the proposed scale of these migrations, described by the Greeks and Romans, is not supported by the archaeological, modern European genetic, and stable isotope evidence (See pages 19, 32, 61, 103, 105 and 107) (Collis, 2003; Delbrück, 1900; Furger-Gunti, 1984; Handford, 1982). Archaeological evidence of migration has been the focus of several studies (Anthony, 1990, 1992, 1997 Arnold, 2005; Brumeister, 2000; Härke, 1998). Several previous analyses have attempted to determine the presence of non-local individuals almost exclusively through examinations of the variance in material culture associated with diverse populations and their temporal and chronological distributions (Anthony, 1990, 1997; Arnold, 2005; Brumeister, 2000; Chapman, 1997; Hakenbeck, 2008; Karl, 2005; Knipper et al., 2014, 2017; Ramsl, 2003).

The diverse artefacts associated with the Hallstatt and La Tène cultures may not reflect a Celtic ethnicity or designate the diverse cultures to which they spread as Celtic. Consequently, the identity ascribed to these artefacts may be nominal or based in part on modern perceptions and interpretations of this identity (See page 54). Further, a Celtic or other ethnic identity was not likely transferred along with the objects themselves. Although the objects may be Celtic, they may not have been used and incorporated in the same, or similar ways, in different cultures. The spread of these artefacts also may represent trade routes or items, and therefore, far-reaching cultural rather than biological connections (Arnold, 1995, 2005; Collis, 2003; Cunliffe, 1997, 2018; Roberts and Vander Linden, 2011; Schillinger et al., 2017; Stark et al., 2008; Stead, 1979). Therefore, the presence of these artefacts may not denote the spread of a Celtic people, or ethnicity, as indicated in the preceding biodistance analysis (See pages 19 and 32) (Anthoons, 2007, 2011; Collis, 1973; Collis, 2003; Cunliffe, 1984, 1991, 1994, 1997, 2009; Dent, 1982, 1985, 1995; Giles, 2012; Hodson, 1964, 1968, 1990; Scheeres, 2014a; Scheeres et al., 2013b, 2014b; Stead, 1991a). Although migration is evident among some of the samples, Radovesice (Czech Republic), Kutná-Hora-Karlov (Czech Republic) and Dürrnberg (Austria) it may also have been a mechanism for the spread of Celtic material culture, but at a much smaller scale than previously believed (See page 61). Further samples from the core and expansion regions, are necessary to determine whether there is corresponding evidence for small-scale intra-regional migration among other Celtic populations. The 20 trait MMD distances among all samples also suggest that migration may partially explain the observed population structure with regards to the above samples (See page 206, Tables 12 and 13). Additionally, if the above samples represent trading centres, as supported by the archaeological and stable isotope evidence, they would likely have had ethnically diverse populations (Tiefengraber and

Wiltschke-Schrotta, 2012, 2014, 2015; Scheeres, 2014a; Scheeres et al., 2013b; Valentová, 1991, 1993; Valentová and Sankot, 2012; Wendling et al., 2015). Furthermore, based on the above MMD distances, there was no gene flow between the above samples and the neighbouring regions analysed. However, gene flow may have occurred between these groups and other intra-and-extra-regional populations not analysed (See page 206). Consequently, the possibility that they represent trading centres cannot be ruled out.

Further support for migration is indicated by settlement abandonment during the LTB/LTC period, at Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) (See pages 61, 164, 168, Table 8). The artefacts associated with these populations include several costly and exotic prestige items. However, these items are primarily associated with the LTB period (Table 8) (Salac, 2011; Rabsiler et al., 2017; Valentová, 1991, 1993; Valentová and Sankot, 2012). This finding, combined with the fact that they were abandoned during the LTC period, supports the notion that large-scale migration to another region occurred during this period (Table 8). However, due to the shallow grave depth, and the potential for burial loss due to construction or agricultural processes, it is unknown whether the regions were in fact abandoned (Valentová, 1991; Valentová and Sankot, 2012). Further, rerouting or breakdown of trade routes may have resulted in the decline in prestige items and migration during the beginning of the LTC period. Settlement abandonment is also believed to have occurred during the HaD/LTA and LTC/LTD transitions (Table 8). This process is also believed to have occurred in tandem with changes in burial practice and the spread of Celtic material culture (See pages 61, 164 and 168) (Collis, 2003; Cunliffe, 1997; James, 2005; Koch, 2007; Maier, 2003).

Settlement abandonment during the above periods has also been interpreted to support large-scale migration in the regions in which it is evident (Collis, 2003; Cunliffe, 1997; James, 2005; Koch, 2007; Maier, 2003). Although settlement abandonment has been documented in some areas such as Hallstatt D (Austria), during these transitions, there is no evidence that they become significantly deserted (Collis, 2003; Cunliffe, 1997; James, 2005; Koch, 2007; Maier, 2003; Smith, 2012). Further, there is evidence for settlement continuity during the above transitions in several regions including, Münsingen-Rain (Switzerland) and Dürrnberg (Austria) (See pages 145 and 155). This indicates that while migration may have facilitated the spread of Hallstatt and La Tène artefacts, the observed diachronic changes in material culture likely resulted from diverse social processes, including trade, exogamy, cultural diffusion and/or assimilation (Collis, 2003; Cunliffe, 1997, 2018; James, 2005; Koch, 2007; Maier, 2003; Smith, 2012). These processes as mechanisms for the spread of Celtic artefacts are also supported by the available stable isotope evidence.

Overall, the stable isotopic information indicates that some regions, such as Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) had comparatively high numbers of non-local individuals (Scheeres, 2014a; Scheeres et al., 2014b). However, the majority were not from extra-regional locations (See page 61) (Scheeres, 2014a; Scheeres et al., 2014b). The latter supports the notion that while some settlements may have been abandoned during the LTC period, a large-scale migration event from the core to expansion regions during this period is not likely (See page 61, Table 8). Deteriorating climate conditions during the 4th and 3rd centuries BC have also been argued to have been a cause for migrations of Celtic populations during this period (Büntgen et al., 2011; Fischer et al., 2006; Grove, 1979; Gutiérrez-Elorza and Kromer and Friedrich, 2007; Lamb, 1977; Magny et al., 2009; Guiterrez-Elorza and Peña-Monné, 1998). The average temperature has been estimated to have decreased by 2°C, while precipitation increased by approximately ±10-20% (Büntgen et al., 2011; Fischer, 2006; Grove, 1979; Gutiérrez-Elorza and Peña-Monné, 1998; Kromer and Friedrich, 2007; Lamb, 1977; Magny et al., 2009). Although since no corresponding temperature and precipitation values for the preceding period have been documented for comparison, it is not possible to determine the scale of these changes (See page 61) (Büntgen et al., 2011; Gutiérrez-Elorza and Peña-Monné, 1998; Lamb, 1977).

However, there is no evidence that climate changes were a primary driving force behind migration during this period. The archaeological evidence indicates that some populations, such as Münsingen-Rain (Switzerland) adapted to these changes through corresponding dietary changes, i.e., an increase in millet consumption (See pages 61 and 145) (Hunt el al., 2008; Moghaddam et al., 2014; Motuzaite-Matuzeviciute et al., 2013). Others such as, Dürrnberg (Austria), east Yorkshire (Britain), Basel-Gasfabrik (Switzerland), Magdalenenberg (southwest Germany), Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic), were able to adapt to lower subsistence levels without any significant dietary change, based on stable isotope and environmental studies (See pages 155, 164, 168, 172 and 177) (Jay and Richards, 2006, 2007; Jay et al., 2008; Jay and Montgomery, 2020; Le Huray et al., 2006; Le Huray and Schutkowski, 2005; Oelze et al., 2012). However, the absence of apparent dietary changes in the above regions may indicate that corresponding evidence has not been recovered (Jay and Richards, 2006, 2007; Jay et al., 2008; Jay and Montgomery, 2020; Le Huray et al., 2006; Le Huray and Schutkowski, 2005; Oelze et al., 2012). Alternatively, this may suggest that dietary changes were not necessary to adapt to the deteriorating climate conditions. Although climate change may have caused some of the observed mobility, it does not appear to have been the primary mechanism for the observed phenetic and cultural variation during the above period (See page 61) (Evans, 2004; Fernández-Götz, 2016; Hauschild, 2010a; Müller et al., 2003; Muller, 2004; Pétrequin et al., 2010; Schonfelder, 2010; Tinner et al., 2003). The overall pattern of limited intra-and-extra-regional migration indicated by the archaeological and stable isotope evidence is also supported by the available modern European genetic evidence (See pages 61, 105 and 107). Although there is evidence for different Y-chromosome and mtDNA haplogroups, and sub-clades, throughout the regions analysed, they are based on modern distributions.

Therefore, the degree of variation during the Iron Age may not be adequately represented. However, the presence of genetically distinct populations in these regions is supported by both the 20 trait MMD distances (See page 206, Tables 12 and 13). This suggests that while the degree of variation may be underrepresented, Celtic material culture was not restricted to phenetically similar groups, except for the Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) samples. The modern European genetic evidence further supports the notion that the expansion region samples were likely acculturated through trade, cultural diffusion and/or assimilation. Diverse lines of evidence support this notion such as archaeological, stable isotope, and modern European genetic. However, based on the nature of the available linguistic evidence, fragmentary and limited, support for the above notion is difficult to determine (See pages 61, 91, 103, 105 and 107). Consequently, as the phenetic relationships indicated by the MMD distances can be used as a proxy for linguistic boundaries, this evidence may support this notion. The evidence for some intra-regional and limited or no extra-regional movement, as indicated archaeologically and through the MMD derived phenetic relationships further supports this notion.

Previous studies have focused almost exclusively on the diachronic and presumed biological changes within the expansion regions (Anthoons, 2007, 2011; Collis, 1973; Collis, 2003; Cunliffe, 1984, 1991, 1994, 1997, 2009; Dent, 1982, 1985, 1995; Giles, 2012; Hodson, 1964, 1968, 1990; Scheeres, 2014a; Scheeres et al., 2013b, 2014b; Stead, 1965a, b, 1976, 1985b, 1984b, 1991a, b, c, 1999, 2006). However, the preceding biodistance analysis indicates that these changes were not restricted to these regions. Variation of a similar scale is also evident within the samples from the core, suggesting that the populations within these regions may have been acculturated rather than genetically influenced and/or replaced as well. Therefore, the old model of mass migration and the presumption that the spread of Celtic material culture into the expansion regions was the result of one-way movement from the core are not supported. Rather, the above lines of evidence and both the 20 trait MMD distances support the presence of far-reaching and diverse connections among populations in these regions (See page 206). Further, the assumption that migration was a primary factor for the spread of Celtic artefacts is not supported. The diverse populations possessing these artefacts may have subsequently lost their cultural autonomy and have been subsumed into a greater nominal Celtic identity. Therefore, the variation within the Hallstatt and La Tène artefacts found throughout these regions may represent diverse populations and/or different ethnicities (See page 54). Consequently, the above cultures may not be representative of Celtic populations, ethnicity or ancestry throughout the regions they extended.

Are the observed morphological differences among the samples within the core and expansion regions explained by an isolation by distance model?

The broad geographic variation and presence of biologically distinct populations within the core and expansion regions are further supported by the differences in dental trait frequencies among the samples. The core region samples have high frequencies of several traits including, Deflecting Wrinkle LM, C1–C2 Crest LM1, and Lingual Cusp LP2 (See page 196, Table 9). High frequencies of numerous traits including, Distal Accessory Ridge UC, Labial Curvature UI1, and Carabelli’s trait UM1 are observed in the expansion regions (See page 196, Table 9). Some traits such as Groove Pattern LM2 and Anterior Fovea LM1 are observed at similar frequencies among both regions (See page 196, Table 9). Although the expansion regions appear to have higher frequencies of most traits, comparatively, the majority of these are observed in the sub-samples, Rudston Makeshift (east Yorkshire, Britain) and Pontecagnano (southern Italy) (See page 196, Table 9). The variation in nonmetric traits among the samples is likely caused by numerous processes such as small-scale migration, limited intra-and-extra-regional gene flow, genetic drift, and isolation by distance. Geographic boundaries such as the Alps may have acted as barriers to gene flow among the samples. The intra-and-extra-regional patterns indicated in the comparative-sample scatterplots are comparable to those from the PCA and MDS graphs (See pages 202 and 211, Figures 48-50, 55-62, 38 and 39-41, respectively). Some variation is evident, due to differential trait weighting, but the general pattern is recurrent. The samples are interspersed and a clear separation evident. This pattern is also observed in the comparative sample dendrograms (See page 215, Figures 44-47). However, in these comparisons, the 2 samples that are phenetically indistinguishable, Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) are clustered together. This supports the notion that limited gene flow characterised the population structure among the samples analysed. The observed patterns further imply that the majority of the samples are more phenetically divergent than expected based on their geographic locations, based on the assumption that genetic affinity is inverse to spatial distance (See page 206).

Numerous intra-and-extra-regional comparisons are indicated by the comparative sample scatterplots (Figures 48-50 and 55-62, respectively). Those samples that are plotted above or below the black reference line are not consistent and vary depending on specific sample comparisons. (Figures 48, 55-59 for intra-regional comparisons, Figures 49, 60-62 for extra-regional, and Figure 50 for the comparative sample, respectively). Further, the samples are interspersed and no clear geographic separation is evident (See page 206). This suggests that the geographic division of Celtic populations into the core and expansion regions may be nominal. The complex relationships among and within these regions were likely influenced by trade and exchange more than is presumed or documented within the field of Celtic studies (Anthoons, 2011; Collis, 2003; Cunliffe, 1997, 2018; Giles, 2012; Halkon, 2013, 2017; Koch, 2006; Kruta, 1991). The extent of trade among these regions may have been of sufficient scale to create dependent relations of a centre and periphery nature among populations within the core and expansion regions; however, it is difficult to determine the extent, directionality and trajectory of any exchange as Celtic material culture within these areas is not consistently documented or described (See pages 1, 19 and 32) (Anthoons, 2011; Collis, 2003; Cunliffe, 1997, 2018; Giles, 2012; James, 2005; Koch, 2006; Kruta, 1991). Furthermore, the identification of the trade route(s) through which Hallstatt and La Tène artefacts were transported alone is not sufficient to support the notion of a direct centre and periphery relationship between these regions. Rather, the presence of these artefacts throughout Iron Age Europe, evidence of regional diversity in design and manufacture, and the presence of biologically distinct populations possessing these items suggest that populations in these regions had access to diverse and far-reaching trade routes.

The notion of a geographic division between populations in the core and expansion regions is likely also intrinsically linked with the old model of mass migration during the 4th and 3rd centuries BC. Consequently, isolation by distance may partly explain the observed population structure, but it was not likely the primary process driving the variation among the samples (See pages 61 and 206). The comparative sample scatterplots further support differential rates of several processes such as small-scale migration, genetic drift, gene flow, and prior migration into the regions analysed before or during the Hallstatt and La Tène periods as driving the observed phenetic variation among the samples, such as in the preceding Bronze Age (Figures 48-50 and 55-62) (Callaway, 2017; Cassidy et al., 2016; Hamilton et al., 2019; Madgwick et al., 2013; McKinley et al., 2014; Millard, 2014; Montgomery et al., 2007; Oppenheimer, 2007, 2012; Pearson et al., 2019; Schulting et al., 2019; Stevens et al., 2013b; Sykes, 2006). However, as Rudston Makeshift (east Yorkshire, Britain) represents a sub-sample these results should be interpreted with a degree of caution regarding this sample (See pages 177). Some of the other samples have the same composition, or are pooled, such as German (Stuttgart, Germany) and Pontecagnano (southern Italy) (See pages 143 and 179). Thus, caution should also be used in light of their associations with isolation by distance. However, prior migration(s) into some of the regions analysed cannot be ruled out (See page 206).

The modern European genetic evidence suggests that the Y-chromosome haplogroups R1a, I, and J are likely intrusive to the British Isles and may have arrived during the Neolithic, 4,000-2,500 BC (See page 107) (Cruciani et al., 2004, 2007; Di Giacomo et al., 2004; Hill et al., 2000) (See Figure 1 in Myres et al., 2010 for a map showing the R1b haplogroup distributions listed in this section). The distributions of these haplogroups are limited and similar to those in continental Europe during this period (See page 107) (McEvoy et al., 2004; Richards et al., 2000; Richards et al., 2002; Rosser et al., 2000; Rootsi et al., 2004; Semino et al., 2004; Scozzari et al., 2001; Torroni, 1998, 2001b; Weal et al., 2002). After individuals carrying these haplogroups moved into this region, they interacted biologically with the local populations and subsequently diversified (See page 107). However, the Rudston Makeshift (east Yorkshire, Britain) and Wetwang Slack (east Yorkshire, Britain) samples are almost consistently plotted below the black reference line. Indicating that they are less phenetically divergent than expected based on geographic location. The opposite is true when these samples are compared to one another (See page 206, Figures 61-62). This suggests that limited gene flow likely occurred between the Rudston Makeshift (east Yorkshire, Britain) and Wetwang Slack (east Yorkshire, Britain) samples and comparatively higher rates may have occurred with others in east Yorkshire, and neighbouring areas. This notion is supported by the geographic proximity of these samples to one another and others in this region (Figure 31). Wetwang Slack (east Yorkshire, Britain) is comparatively geographically closer to other cemeteries including, Garton Station (east Yorkshire, Britain), whereas Rudston Makeshift (east Yorkshire, Britain) is in closer proximity to Burton Fleming (east Yorkshire, Britain). Further, the grouping of the cemeteries in east Yorkshire (Britain) suggests that gene flow may have been restricted to between adjacent groups (Figure 31). Consequently, the populations in this region may have been more phenetically diverse than presumed. Therefore, the application of the broad Arras cultural heading to these diverse populations may be nominal. However, due to the composition of the Rudston Makeshift (east Yorkshire, Britain) sample, further samples are necessary to determine whether this pattern is supported.

Since these samples are frequently less divergent than expected based on location, prior migration into Britain during the Hallstatt or La Tène periods cannot be ruled out. However, based on the MMD distances extra-regional gene flow between Rudston Makeshift (east Yorkshire, Britain) and Wetwang Slack (east Yorkshire, Britain) and the remaining samples was likely not frequent (See page 206, Tables 12 and 13). This notion is also supported by the observed similarities in some traits such as, Groove Pattern LM2, among the samples (See page 206, Table 9). Although this similarity is not likely related to frequent gene flow or migration among the samples, as indicated by both the 20 trait MMD distances, it may represent those present in the parent population(s) (Tables 9, 12 and 13). Subsequent diversification, limited admixture, and isolation during the above periods likely resulted in the observed population structure within the Rudston Makeshift (east Yorkshire, Britain) and Wetwang Slack (east Yorkshire, Britain) samples. This notion is also supported by their respective MMD distances compared to the remaining samples during the above periods (0.047-0.077 and 0.028-0.077, respectively). However, a greater emphasis on divergence is evident in the MMD distances in the 20 trait MMD comparison with the Dürrnberg (Austria) sample combined (0.043-0.082 and 0.025-0.083, respectively) (See page 206, Tables 12 and 13). This suggests that those populations intermixing with the Dürrnberg (Austria) sample during the above periods may have also interbred with Rudston Makeshift (east Yorkshire, Britain) and Wetwang Slack (east Yorkshire, Britain). The higher MMD values with the latter 20 trait comparison support the notion that migration and/or inbreeding among these groups was not frequent. The relative positions of the remaining samples, above or below the black reference line, are similar, except for Kutná-Hora-Karlov (Czech Republic) (See page 206, Figures 54 and 55). This suggests that gene flow between the above samples and those remaining may have involved similar populations but to different extents. Further, the high MMD distances in these comparisons may also indicate the breakdown and/or rerouting of trade routes. The relative scarcity of Hallstatt or La Tène artefacts in east Yorkshire (Britain) and the abundant presence of distinctly British items also supports the above notions (See pages 19 and 32).

Prior migration during the Hallstatt or La Tène periods also cannot be ruled out among the remaining samples. Other sample pairs that are less phenetically distinct than expected based on geographic location include, Nebringen (Stuttgart, Germany), Dürrnberg (Austria), Münsingen-Rain (Switzerland) and Kutná-Hora-Karlov (Czech Republic) (See page 206, Figures 48, 50, 51 and 53, respectively). This suggests that similar processes likely resulted in the observed phenetic diversity among these samples. Further, as those samples above and below the reference line are interspersed the spread of Celtic artefacts was likely more complex than previously believed. Although due to the composition of some samples such as Pontecagnano (southern Italy), Rudston Makeshift (east Yorkshire, Britain), and the pooled German sample (Stuttgart, Germany), these results may need to be interpreted with a degree of caution. However, the overall patterning indicates clear separation and limited gene flow among the samples. This supports the notion that diverse and numerous mechanisms contributed to the observed population structure and variation, including those mentioned above.

The significance of the relationship between phenetic, by proxy genetic, and geographic distances was determined by the Mantel correlation (See pages 193 and 206) (Kimura and Weiss, 1964; Konigsberg, 1990; Wright, 1943). This correlation between the MMD and geographic distance matrices, r=.309 (p=0.049) is a moderate positive correlation (See page 221) (Cohen, 1988). The above Mantel correlation indicates that isolation by distance partly explains the phenetic differences among the samples analysed. Therefore, the null hypothesis that there is no significant difference in nonmetric traits and geographic distances is rejected at the 0.025 alpha level for most of the samples. However, there does not appear to be a relationship among the samples and Isolation by distance based on the corresponding r values (See pages 190, 193, 221, Table 15). Consequently, the results of the preceding analysis do not support isolation by distance as the primary mechanism behind the observed variation. Rather, diverse processes such as small-scale migration, and limited intra-and-extra regional gene flow were likely driving the phenetic variation among the samples analysed. Although, between the Radovesice (Czech Republic) and Kutná-Hora-Karlov

(Czech Republic) samples gene flow rather than isolation and genetic drift likely resulted in the observed phenetic similarity. However, within the remaining samples, genetic drift and isolation likely dominated the population structure. The above correlation between phenetic and geographic distances was determined using inter-population straight-line distances, as the migration and/or transportation routes between the geographically diverse core and expansion regions are not known with certainty. Although these distances do not reflect reality on the landscape and are therefore approximations (as are some sample locations used in this analysis), any potential migration routes throughout these regions would be approximations as well (See pages 135, 190 and 206). Further, some populations that are in close geographic proximity are phenetically distinct, such as Rudston Makeshift (east Yorkshire, Britain) and Wetwang Slack (east Yorkshire, Britain). This suggests that any potential migration routes among Celtic populations in close proximity may not represent those actually used. Although linear distances are potential underestimates, they should be less biased for analytical purposes (See pages 135 and 206) (Irish et al., 2018; Konigsberg, 1990; Relethford, 2004).

Therefore, gene flow among the samples did not likely occur frequently, with the exception of Kutná-Hora-Karlov (Czech Republic), and Radovesice (Czech Republic). Although gene flow between Kutná-Hora-Karlov (Czech Republic) and Dürrnberg (Austria) may have occurred more regularly with other intra-regional populations or other large trading centres, resulting in ethnically diverse populations. The stable isotope evidence also suggests that small-scale and individual migration was common among geographically diverse populations (See page 61). This suggests that migration associated with trading centres may have occurred more frequently among intra-regional locations. Consequently, individual movement among extra-regional locations may have been more common. However, gene flow with other extra-regional populations not analysed cannot be ruled out. Thus, additional samples are necessary in order to determine whether this pattern is supported in other regions.

Samples that are in close geographic proximity in the core such as, Hallstatt D (Austria) and Pottenbrunn (Austria) have mostly large and significant MMD distances, based on the 20 trait comparison with the Dürrnberg (Austria) sample combined (0.043-0.082 and 0.042-0.082, respectively). A similar pattern is also evident in the expansion region samples such as Rudston Makeshift (east Yorkshire, Britain) and Wetwang Slack (east Yorkshire, Britain) (0.043-0.082 and 0.025-0.083, respectively) (See page 206, Table 13). The MMD values for the above samples are similar, although slightly lower, in the 20 trait comparison among all the samples (Table 12). This indicates that the spread of Hallstatt and La Tène material culture throughout these regions was more complicated than simple one-way movement to the expansion regions. The results indicate that there is partial support for isolation by distance as a cause for the observed phenetic diversity among the samples. However, the observed underlying biological relationships are more complex than previously assumed under the La Tène=Celtic paradigm. Consequently, several processes including, migration prior to or during the Hallstatt and La Tène periods; small-scale migration and/or individual movement during these periods; gene flow; genetic drift; isolation; limited intra-and-extra-regional gene flow; cultural diffusion and/or assimilation likely characterised the population structure of the samples. This finding is in line with the archaeological, art style, modern European genetic, stable isotope, and linguist lines of evidence; that indicate diverse and far-reaching connections, regional diversity and limited extra-regional movement (See pages 19, 32, 61, 105 and 107). The historical descriptions of the spread of Celtic populations, languages and material culture as described by Greek and Roman authors may partly reflect the actual distributions. This is suggested by the presence of phenetically diverse populations compared to the Pontecagnano (southern Italy) sample, which is located outside the known area of maximum Celtic expansion (See pages 138 and 179). However, the above descriptions cannot be relied on exclusively as the descriptions and ascribed associations, ethnic, cultural and/or biological, have been inextricably linked and jumbled. Subsequently creating a situation in which the ensuing view of Celtic Iron Age Europe has been perceived as timeless and traditional, yet has little explanatory value.

Summary and conclusions

The primary goals of this thesis were to determine if populations within the expansion regions exhibited more phenetic diversity than those within the core; whether populations in these regions were acculturated, genetically influenced by the arriving Celts, and/or replaced. A further goal was to determine if the observed dental morphological differences among the samples within the above regions are the result of isolation by distance. The biological distance estimates suggest the following. First, populations in the expansion regions exhibit less biological diversity than those within the core. Specifically, two samples within these regions are biologically indistinguishable, the remaining two are biologically distinct, and all samples within the core are phenetically diverse. Thus, populations in the expansion regions are genetically distinct from those in the core and were likely acculturated, not genetically influenced by these groups. Limited intra-and-extra regional gene flow and genetic isolation explain the population structure within the above regions. Second, overall phenetic heterogeneity, biological diversity, and population discontinuity are indicated, as the majority of the samples within both regions are biologically distinct from one another. This diversity may also reflect genetic and linguistic boundaries among the samples. Third, waves of migration from the core during the 4th and 3rd centuries BC were not likely responsible for diachronic changes in material culture within the expansion regions. Fourth, the separation of populations and material culture into the core and expansion regions; and the application of Celtic ethnicity to diverse populations possessing artefacts and a spoken language(s) identified as Celtic may be a nominal association, i.e., in name only. Simply put, the comparative results suggest that these groups represent biologically distinct populations.

The null hypothesis that there is no difference in nonmetric traits among populations in the expansion regions is rejected at the 0.025 alpha level for most of the sample pairs. The alternative hypothesis is not supported for 2 samples, Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) in these regions as they are phenetically indistinguishable (See page 206, Tables 12 and 13). However, the regional distribution of the samples may have resulted in those in the core appearing more diverse. Therefore, more samples from the expansion regions are necessary to determine whether this pattern is also evident. The samples are characterized by an overall morphologically simple, mass-reduced dentition often associated with European populations, despite high frequencies of some mass-additive traits such as Carabelli's trait UM1 (See pages 196 and 202, Appendix III). Those samples in the expansion regions may appear to have higher frequencies of several traits, as well as a more diverse dental complex. However, the majority of these traits occur within the sub-samples, Rudston Makeshift (east Yorkshire, Britain) and the comparative sample, Pontecagnano (southern Italy). Therefore, the expansion region samples may not be characterized by comparatively higher frequencies of these traits. Notable differences are evident in individual trait frequencies among the samples, which influence the overall phenetic dissimilarity (See pages 196, 239 and 250). Although some traits occur at similar frequencies among most of the samples, such as Groove pattern LM2, this uniformity is not reflected in the 20-trait MMD distances, dendrograms, MDS or PCA graphs (See pages 196, 202, 206, 211, Tables 12 and 13, Figures 38, 39-41 and 44-47 respectively). This suggests that the observed trait similarity is not likely related to frequent gene flow among the samples. Instead, it may represent similarities that were present in the parent population(s) and subsequent diversification. The samples may have become genetically distinct due to other processes such as isolation, genetic drift, limited intra-and-extra regional gene flow from the regions analysed, and increased gene flow from other neighbouring regions not analysed. The presence of phenetic diversity among all but 2 of the samples, those mentioned above, suggests that the geographic division among populations possessing Celtic material culture, languages, burial practices, and art styles may be nominal. Further, the presence of genetically distinct populations within these regions suggests that the association between these populations, and the Hallstatt and La Tène cultures may be tenuous.

However, the samples may have been pooled temporally, as they are dated, primarily, based on associated artefacts. Further, as this dating method is still commonly used, most populations have been assigned to either the Hallstatt or La Tène period overall. As such, the temporal differences between and within the samples analysed may not be adequately represented. Consequently, as the majority of Celtic populations are dated in this manner, these dates often represent those only available (See pages 19, 32 and 54) (Collis, 2003; Cunliffe, 1979, 1997; James, 2005; Kruta, 1991; Müller, 1999; Wells, 1998). Therefore, the dates assigned to Celtic populations may actually represent the earliest possible movement of Hallstatt or La Tène artefacts into the diverse regions which they spread. Further, this manner is still commonly used to assign dates to Celtic populations. Few studies have attempted to assign more specific dates, e.g., LTA 450-400 BC, to specific populations such as Dürrnberg (Austria) (Hodson, 1990; Jay et al., 2013; Tiefengraber and Wiltschke-Schrotta, 2012, 2014, 2015). Additionally, these divisions are still based on chronological distributions of artefacts (See pages 19, 32 and 54). Further, those samples that can be sub divided into distinct temporal categories are often too small for statistical analyses. Consequently, these analyses would likely result in tenuous and/or spurious reconstructions of population affinity. The geographic separation of the samples may suggest that they were not likely to interbreed. However, the stable isotope evidence indicates that vastly geographically separated populations were able to interbreed (See page 61) (Jay et al., 2013; Knipper et al., 2017; Moghaddam et al., 2014; Oelze et al., 2012; Scheeres, 2014a; Scheeres et al., 2014b). Overall, the results of the preceding biodistance analysis suggest that Iron Age populations were more phenetically diverse than assumed. However, the results of this analysis should be interpreted with a degree of caution in relation to the geographic distribution of the samples and their ability to interbreed.

The effect of dental wear on nonmetric trait observation and recording should also be taken into consideration in light of the results of the preceding analysis. Other potential issues include the sample composition, pooled and sub-samples and the potential loss of burials due to shallow grave depth, construction, taphonomic or agricultural processes. Therefore, the degree of variation present in the original populations may not be represented by the samples (See pages 181, 239 and 250). Although the temporal and regional differences among the samples may be under represented, the presence of phenetic heterogeneity indicates the presence of biologically distinct populations associated with Hallstatt and La Tène cultures. Therefore, the presence of increased intra-regional similarity cannot be ruled out. Although the results should be interpreted in light of the above caveats, they are supported by other lines of evidence such as stable isotope, archaeological, modern European genetic and linguistic (See pages 61 and 91). This suggests that the phenetic relationships indicated by the MMD distances likely represent those during the Iron Age. Further, the presence of diverse populations within the broad regions described as Celtic, suggests that there is a greater degree of phenetic variation among populations during this period than previously assumed.

The available stable isotope evidence also supports limited-intra-and-extra-regional gene flow, small-scale and individual migration among the samples (Jay et al., 2013; Jay and Montgomery, 2020; Knipper et al., 2013, 2014, 2017; Moghaddam et al., 2014; Oelze et al., 2012; Scheeres, 2014a; Scheeres et al., 2014b). The Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) samples have comparatively high migration rates, 74.3% (26 of 35 individuals) and 76% (19 of 25 individuals), respectively (See pages 61, 229, 239, 250 and 256) (Scheeres, 2014a; Scheeres et al., 2013b, 2014b). However, the stable isotope evidence does not support large-scale migration, as the number of migrants in the majority of the regions analysed was comparatively low (See pages 61, 164 and 168) (Jay et al., 2013; Jay and Montgomery, 2020; Knipper et al., 2013, 2014, 2017; Moghaddam et al., 2014; Oelze et al., 2012; Scheeres, 2014a; Scheeres, 2014b). Further, in those regions above with higher numbers of non-local individuals, there was no evidence that these individuals were part of a single migration event. The stable isotope evidence further suggests that residential changes and individual mobility may not have been confined to the core or expansion regions (See pages 61, 229 and 250). Movement appears to have been occurring irrespective of the above regional designations. The far-reaching and diverse connections indicated by Tables 1, 4 and 5 also support the above notion. However, the archaeological evidence suggests that populations during the Iron Age, possessing Celtic artefacts, were more inter-connected (See pages 19 and 32) (Almagro-Gorba, 1991; Budinský and Waldhauser, 2004; Haffner, 1976; Joachim, 1968; Krämer, 1964; Koch, 2006; Ramsl, 2002; Rustoiu, 2008, 2011a, b; Salac, 2011; Soudska, 1994; Tiefengraber and Wiltschke-Schrotta, 2012, 2014; Valentová, 1991, 1993; Valentová and Sankot, 2012; Waldhauser, 1993). This discrepancy may indicate the presence of diverse and numerous trade routes throughout continental and non-continental Europe during this period. The presence of diverse haplogroups and sub-clades, genetic population markers, within the regions associated with the Celts further supports the above notion (See pages 103, 105 and 107) (Busby et al., 2012; Cassidy et al., 2015; Cruciani et al., 2011; Lucotte, 2015; McEvoy et al., 2004; Weale et al., 2002; Wilson et al., 2001).

However, this evidence is based on the distributions indicated by modern populations. Therefore, the diversity indicated by the modern European genetic evidence may not adequately reflect that in the Iron Age. The linguistic evidence suggests the presence of diverse insular and continental Celtic languages (See pages 91, 103, 105 and 107). However, due to the nature of the available inscriptions (e.g., fragmentary and geographically dispersed) it is difficult to determine whether the above notions are also supported (Ball and Fife, 1993; Ball and Muller, 2012; Cowgill, 1975; Campanile, 1976; De Hoz, 1992; Eska, 1998; Evans, 1995; Forester and Toth, 2003; Isaac, 2010; Joseph, 2010; Renfrew, 2013). However, the phenetic diversity indicated by the MMD distances may be used as a proxy for genetic and linguistic boundaries among the samples (See page 91) (Barbujani et al., 1990; Bickel, 2019; Creanza et al., 2015; Greenhill et al., 2017; Longobardi et al., 2015; Sokal, 1988; Sokal et al., 1988, 1989, 1990). Consequently, differential rates of several processes including, limited intra-and-extra-regional gene flow, genetic drift, small-scale and prior migrations, and isolation likely resulted in the population structure observed among the samples. Although the spread of Hallstatt and La Tène artefacts have been interpreted to represent migration, large-scale and/or frequent, this notion as the primary mechanism for their dispersal is not supported by the MMD distances (See page 206). However, evidence for migration is suggested by the 20 trait MMD distances for the Dürrnberg (Austria) Hallstatt and La Tène period samples. Although these temporal periods are phenetically indistinguishable, the MMD distances decrease during the La Tène period (See page 206). Diverse social processes including the breakdown and rerouting of trade routes, differential migration rates, change(s) in populations from which marriage partners were drawn, or migration into the region prior to the Hallstatt period may have resulted in the decreasing phenetic differentiation within this sample.

Migration and/or frequent gene flow may also have occurred between the Radovesice (Czech Republic) and Kutná-Hora-Karlov (Czech Republic) samples as they are also phenetically indistinguishable (See pages 206, 239, 250 and 256). These samples may have originated from the same parent population and therefore had not become phenetically distinct. Frequent gene flow through exogamy or migration between the above samples may also have resulted in the observed phenetic similarity. Although migration may have occurred among, and within, the above samples, it does not appear to have been common among those remaining. Further, the MMD distances do not support the large-scale migration throughout the regions possessing Celtic artefacts as described by the Greeks and Romans. Consequently, the old model of mass migration during the 4th and 3rd centuries BC, and the large numbers associated with migrating Celtic tribes described by the Greeks and Romans, is not supported and may be in part the result of Roman political propaganda (See page 61) (Collis, 2003; Delbrück, 1900; Furger-Gunti, 1984; Handford, 1982). Although as the samples are all phenetically distinct from the comparative sample, Pontecagnano (southern Italy) some of the cultural affiliations described by those above may represent actual cultural relationships (See pages 61, 206 and 256). However, additional samples are required to determine the extent of this association. These affiliations should be interpreted with caution as the Greeks and Romans habitually described Celtic populations using prerogative externally applied ethnonyms. Further, the terms the Greeks and Romans commonly used to describe the Celts, Keltoi/Celtae and Galli/Gallia respectively, were used interchangeably as they are today (Collis, 1996, 1997, 2003; Cunliffe, 1997; Karl, 2002, 2004, 2007, 2010; Moore, 2012). This suggests that while some descriptions may be relied on, the majority may represent political propaganda derived from second-hand information (See pages 54 and 61). This notion is also supported by the MMD distances (See page 206, Tables 12 and 13). The presence of biologically distinct populations associated with Celtic artefacts suggests that the association between these artefacts and a biologically Celtic population may be tenuous. The moderate positive correlation, r-.309, p=0.049, between the samples and geographic distance also supports this notion (See pages 206, 221 and 256). The results further indicate that isolation by distance was not likely the primary mechanism behind the observed variation among the samples. However, further samples are necessary to determine whether this pattern is also observed among other Celtic population within the core and expansion regions (see pages 206 and 256, Table 15). Thus, a combination of limited intra-and-extra-regional gene flow, genetic drift, isolation, small-scale, individual or prior temporal migration, trade, cultural diffusion and/or assimilation are likely responsible for the observed cultural, genetic and linguistic variation among the samples. Therefore, the ethnic affiliation assigned to the samples does not appear credible based on the preceding biodistance analysis. This suggests that the population history and structure among Celtic populations are more complex than previously assumed under the La Tène=Celtic paradigm.

In the field of Celtic studies, the presence of Hallstatt or La Tène artefacts, have been interpreted to indicate the presence of an ethnically, biologically, linguistically or culturally Celtic population. However, the dispersal of these artefacts is not likely only related to migration throughout the regions to which they spread. Therefore, other mechanisms for this dispersal, such as trade routes, the presence and influence of captives and/or slaves on the diachronic changes in material culture, particularly concerning the development of new designs or ways of thinking, cannot be ruled out (See page 54) (Arnold, 1988; Cameron, 2008, 2011, 2013, 2016; Lenski, 2008; 2014; Nash Briggs, 2003; Scheidel, 1997). Further, it is difficult to determine if the presence of these artefacts signifies the presence of a Celtic population. Although the presence of certain artefacts, such as fibulae, have been used to link diverse populations to the Celts; they are also associated with other cultures, e.g., Italic (See pages 32 and 54) (Collis, 2003; D’Agostino, 1974, 1988; D'Agostino and Gastaldi, 1988; De Natale, 1992; Fredericksen, 1974: Koch, 2006; Serritella, 1995). Thus, the description of the artefacts themselves as Celtic may be tenuous, or nominal. However, their design and subsequent variations may be characterized as such. Consequently, cultural assimilation and diffusion are equally viable hypotheses to explain the wide geographic distribution and incorporation of the Hallstatt and La Tène cultures, into diverse populations throughout continental and non-continental Europe. The vast interconnected trade network that likely existed in Iron Age Europe brought diverse populations and/or tribes into contact with one another and enabled these cultures, and the Celtic languages to spread throughout these regions. The differential incorporation of these cultures into these diverse groups further supports the notion of differential rates of processes such as cultural assimilation and diffusion throughout the regions associated with the Celts.

However, the spread of Celtic material culture throughout Iron Age Europe is still intrinsically linked with the La Tène=Celtic paradigm. This concept is still prevalent in the field of Celtic studies and is commonly used to designate populations as Celtic, regardless of documented regional differences. Consequently, the theoretical frameworks that surround modern Celtic research are predominantly derived from interpretations of ethnicity, ancestry, interpopulation connectivity, population history and the contextualization of archaeological cultures via a culture history approach. New theoretical and methodological frameworks, processual and post-processual approaches, have gradually attempted to replace this concept (See pages 1 and 54) (Clark, 2014; Jones, 2002; Johnson, 2011; Trigger, 2006). However, Celtic ethnicity and ancestral heritage, as applied to diverse populations, are still predominantly reliant on material evidence derived from a culture history epistemology. Although few previous studies have indicated the presence of phenetically diverse populations associated with Celtic artefacts; regional diversity has not been the focus of much dental anthropological, archaeological or stable isotopic research (See page 54) (Anctil, 2016; Maxová et al., 2011). Further, bioarcheological analyses on the populations associated with the Celts are limited. Therefore, the degree of variation among the diverse populations possessing Hallstatt and La Tène artefacts is largely unknown (Anctil, 2016; Maxová et al., 2011). Although this diversity is supported by other lines of evidence such as archaeological, stable isotope, linguistic and modern European genetic, these alone have not been sufficient to document its extent (See pages 19, 32, 61, 91, 103, 105 and 107). However, the results of the previous biodistance analyses indicate the complex nature of the underlying biological relationships among Celtic populations (Anctil, 2016; Maxová t al., 2011). These analyses further support the notion that to determine the extent of the phenetic variation among these populations it is necessary to rely on diverse lines of evidence and to move beyond those above and the La Tène=Celtic paradigm.

The presence of phenetically distinct populations, and/or ethnic groups, which have been intrinsically linked with the Celts suggests that the Hallstatt and La Tène material cultures do not necessarily represent a historical Celtic ethnicity. Rather, they represent physical phenomena that existed in time and space and have been interpreted to represent a Celtic ethnicity or ancestry. Consequently, these cultures may not be representative of any specific ethnic group. Further, it cannot be demonstrated that they specifically represent a Celtic ethnicity. They have been ascribed to this ethnicity and ancestry because they are commonly found in regions believed to have been inhabited by people presumed to be Celtic, linguistically, culturally or biologically. The correlations between the Greek and Roman descriptions of Celtic populations throughout these regions have also resulted in this ascribed ethnicity (See pages 1 and 54) (Collis 2003; Cunliffe, 1997, 2009, 2018; Koch, 2006, 2007). Previous studies have defined the Celts through perceived similarities in archaeological culture, linguistics, art styles and burial practices (Chadwick, 1970; Collis, 1997a, b, 1999;

Cunliffe, 1984, 1991, 1994, 1997, 2018; De Marinis, 1977; Dietler, 1994; Dunham, 1991; Giles, 2012; Karl, 2002, 2004, 2007, 2010; Koch, 2003, 2006, 2007, 2009b, 2013; Kruta, 2004; Maier, 2003; Meid, 2008; Oppenheimer, 2007; Poppi, 1991; Royrvik, 2012). Although these studies have attempted to establish the presence of the Celts throughout the core and expansion regions, they were operating under the premise that the term Celt is biological as well as cultural.

However, the pejorative definitions associated with the classical terms, the inherent linguistic nature of the modern term, and the inconsistent application of these terms make application to a specific population and/or group difficult (Collis, 2003; Cunliffe, 1997; James, 2005; Karl, 2010). The application of the term Celt as an ethnonym is further complicated by the consensus, in the field of Celtic studies, that there is some degree of shared identity among the diverse populations associated with Hallstatt and La Tène artefacts. However, the nature of this shared identity is not further elaborated (Collis, 2003; Cunliffe, 1997, 2018; James, 2005). The presence of phenetically distinct populations, as indicated by both the MMD comparisons, also supports the notion that the term Celt/Celtic may not have any biological meaning and may be purely a cultural phenomenon (See page 19, 32, 54 and 206). Consequently, the term Celtic cannot be reliably used as a pan-European ethnic label for populations inhabiting continental and non-continental Europe during the Iron Age.

It is more appropriate to contextualize groups associated with the above artefacts as a fluid network of autonomous societies speaking related languages linked by exchange networks, and shared certain artefacts and social practices that have been differentially incorporated into diverse regional cultures. If the ascribed Celtic ethnicity associated with these populations is ruled out as a constructed and artificial stereotype, derived in part from modern interpretations and associations, these regions instead can be described as interaction zones among different cultures. The presence of biologically distinct samples within these regions, suggests that these diverse populations may have lost their cultural autonomy and were subsumed into a greater Celtic identity. Further, the diverse lines of evidence suggest that the intrinsic link between Celtic ethnicity and material culture may be nominal. Thus, the modern concepts of the Celts can be said to be a contemporary construct that has hindered the understanding of the extent of regional diversity and cultural autonomy among diverse populations throughout Iron Age Europe.

Future Work

There are several prospects for future biodistance analyses notably to include more intra-and-extra-regional samples to address the extent of the biological affinity among these diverse populations; as well as establishing whether these groups are phenetically similar to those used in this analysis. There are several avenues for future work (See Armit et al., 2020, for information about the social and biological relationships between Iron Age Britons and populations in continental Europe). First, comparison of the Hallstatt D (Austria) sample in this analysis, to others from the same period, e.g., those within the Hünsruck-Eifel and Baden-Württemberg (southwest Germany) regions. Second, analysis of other regional Iron Age samples not associated with the Celts. Third, examination of the nonmetric traits within the different east Yorkshire (Britain) cemeteries. Fourth, examination and comparison of the diverse proto-Celtic and Celtic populations. Fifth, comparison of the La Tène populations in the Champagne (northeast France) region to those in Yorkshire. The above analyses will help to establish the level of biological diversity among populations possessing Celtic material culture and language(s) during the Iron Age, as well as further examining the extent to which Celtic ethnicity and cultural identity have been ascribed to these diverse groups. Consequently, the range of dental nonmetric variation within European populations during the Iron Age will also be improved. Further, the diverse cultural heritage and autonomy among populations throughout Iron Age Europe, previously associated with the Celts, will be documented. This will also illuminate possibilities for future analyses into the population history of these populations irrespective of the La Tène=Celtic paradigm.

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Appendix I

Morphological crown and root features

Maxillary traits

Winging U1I

Upper central incisors may be rotated mesiolingualward, giving a V-shaped appearance when viewed from the occlusal surface. No reference plaque. Four possible grades may occur:

1) Bilateral winging
2) Unilateral winging
3) No expression
4) Counter winging

Labial Curvature UI1

Labial surface of the tooth may display a notable convex curvature. Reference plaque ASU UI1 labial curvature grades scored as:

0) No expression
1) Trace curvature
2) Weak curvature
3) Moderate curvature
4) Strong curvature

Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

Palatine Torus

Linear bony exostosis that may develop along the palatine suture, in adults only. No reference plaque is available for this trait. Five possible ASU grades are:

1) No expression
2) Trace (1-2 mm elevation)
3) Medium (2-5 mm)
4) Marked (>5 mm)
5) Very marked (may be as high as 10 mm)

Shovel UI1

The possible presence of mesial and distal vertical ridges on lingual surfaces, giving the tooth a shovel-like appearance. Six grades can be scored with reference plaque ASU UI1 shovel:

0) No expression
1) Faint expression
2) Trace ridges
3) Semi-shovel shaped
4) Shovel shaped
5) Marked shovelling

Double shovel UI1

Both mesial and distal marginal ridges may be present on the labial surface. Six possible grades have been established on reference plaque ASU UI1 double-shovel:

0) No expression

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1) Trace ridges on one margin
2) Trace ridges on both margins
3) One moderate and one trace ridge
4) Two moderate ridges
5) One large and one moderate ridge
6) Two large ridges

Interruption Grove UI2

Grove on lingual borders of teeth. No reference plaque is available for this trait. Rather, this trait is graded as absent or present and location.

Tuberculum Dentale UI2

Ridging or cusp formation may occur on the mediolingual surface. There are eight possible grades using reference plaques ASU UC tuberculum dentale (grades 1-4), and ASU UC distal accessory ridge (grades 5-6):

0) No expression
1) Faint ridging
2) Trace ridging
3) Strong ridging
4) Pronounced ridging
5) A weakly developed cuspule
5) Weakly developed cuspule with free tip
6) Strong cusp with free tip

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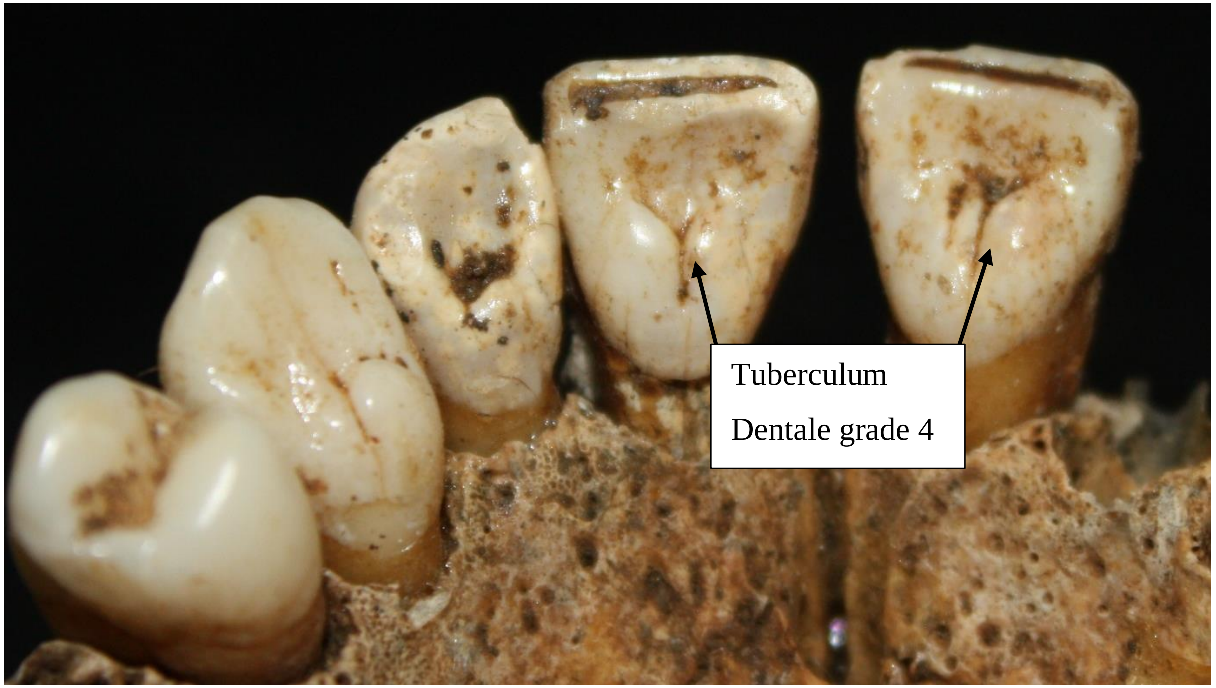
[393] Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

Figure 51. Example of Tuberculum Dentale grade 4. Superior occlusal view of the maxilla. Nebringen (Stuttgart, Germany) burial 7417, adult male.



Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

Mesial Ridge UC (Bushman Canine)

A mesiolingual ridge which may be notably larger than the distolingual ridge, may incorporate the tuberculum dentale. This trait is also called “Bushman Canine” after Morris (1975). Four Possible grades may be scored with reference plaque ASU UC mesial ridge:

0) No expression
1) ML ridge larger than DL, and weakly attached to the tuberculum dentale
2) ML ridge larger than DL, and moderately attached to the tuberculum dentale
3) ML ridge is much larger than the DL, and is fully incorporated into the tuberculum dentale

Distal Accessory Ridge UC

Anterior to upper canine distal marginal ridge, another distolingual ridge can be found. This feature can be very pronounced. The six possible ASU grades on reference plaque DAR UC are:

0) No expression
1) Ridge is very faint
2) Ridge is weakly developed
3) Ridge is moderately developed
4) Ridge is strongly developed
5) Ridge is very large

Hypocone UM

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[395] Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

Cusp 4 may range from absent to large and developed. Seven possible grades exist and can be scored with the ASU UM hypocone reference plaque:

0) No expression
1) Faint ridge present
2) Faint cuspule present
3) Small cusp present
3.5) Moderate-sized cusp present
4) Large cusp present
5) Very large cusp present

Cusp 5 (Metaconule) UM1

The possible presence of a fifth cusp between the third and fourth cusps. There are six possible grades that can be scored with the reference plaque ASU UM cusp 5:

0) No expression
1) Tiny round cusp
2) Tiny wedge-shaped cusp
3) Small cusp
4) Medium-sized cusp
5) Large cusp

Carabelli’s Trait UM1

If this trait is present, the Mesiolingual aspect of upper molars may show a range of variation from a furrow to a large free cusp. An eight-grade classification, originated by Dahlberg (1956), is used for this trait and can be scored with reference plaque Zoller Laboratory UM Carabelli cusp:

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[396] Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

0) No expression

1) Furrow

2) Pit

3) Double furrow

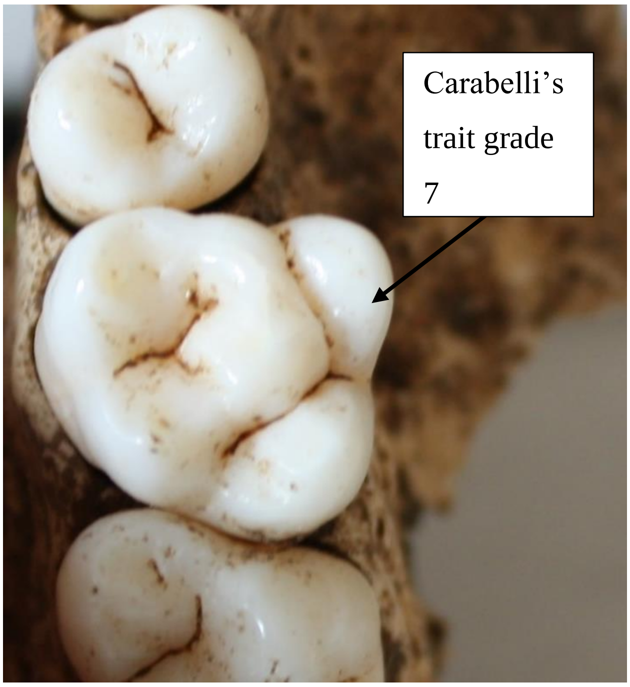
4) Small attached cusp

5) Large attached cusp

6) Small free cusp

7) Large free cusp

Figure 52. Example of Carabelli’s trait, grade 7. Superior occlusal view of the maxilla. Pontecagnano (southern Italy) burial 373, adult female.



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[397] Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

Parastyle UM3

If present, the buccal surface may display variation from a pit to a free cusp. There are six grades evident on the reference plaque ASU UM parastyle:

0) No expression
1) Pit
2) Small attached cusp
3) Small free cusp
4) Medium-sized free cusp
5) Large free cusp

Enamel extension UM1

An extension of the enamel border may be present which may extend toward the root apex. No reference plaque. Four possible ASU grades may be scored:

0) No expression
1) A short extension (up to 1 mm)
2) A medium extension (up to 2 mm)
3) A lengthy extension (up to 4 mm +)

Root Number UP1

The number of free roots. No reference plaque. This trait is scored according to number of roots present.

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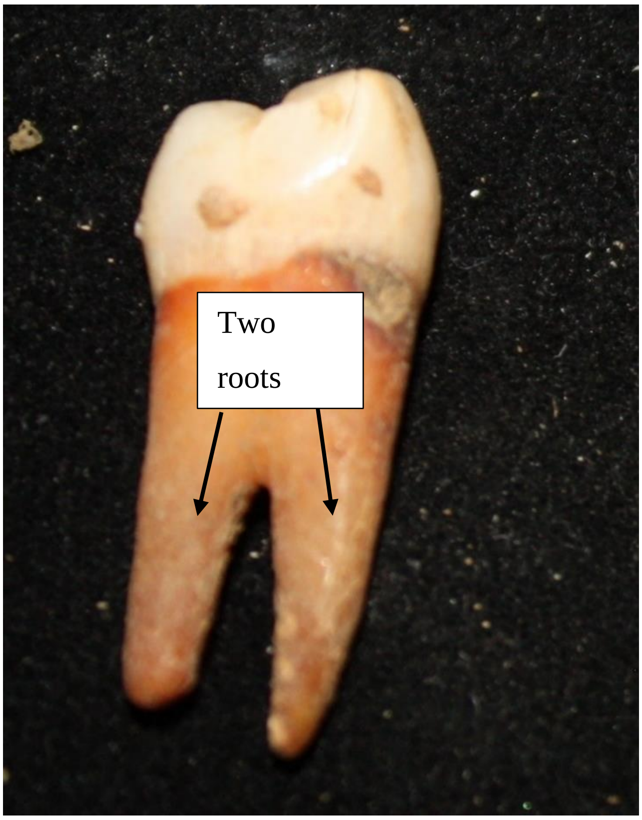
Figure 53. Example of Root Number UP1. Distal side view. Nebringen (Stuttgart, Germany) burial 7403, adult male.



Root number UM2

The upper second molar may be reduced in size and display very simple morphology. There is no reference plaque for this trait. Rather, it is scored as normal or peg-shaped.

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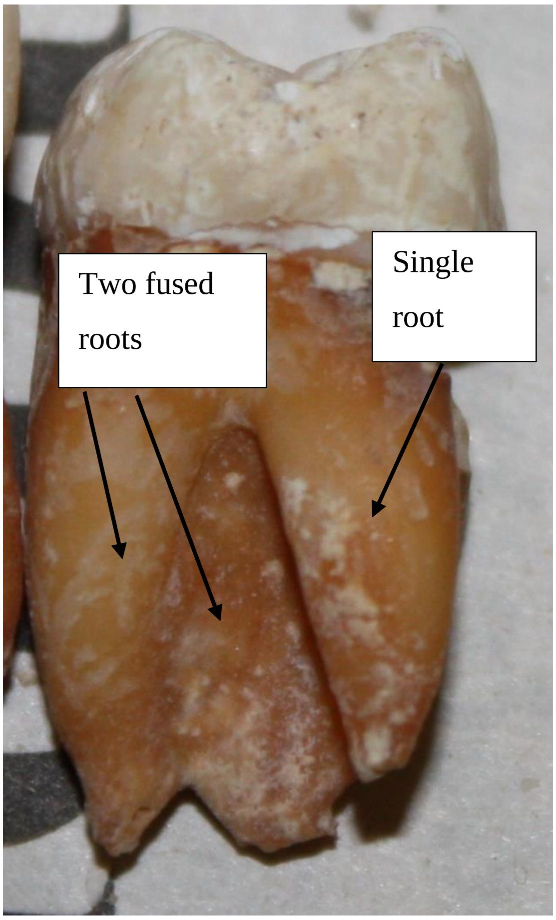
399 Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

Figure 54. Example of Root Number UM2. Two rooted UM2, one inter-radial projection separates one root from two fused roots. Buccal, cheek side, view. Kutná-Hora-Karlov (Czech Republic) Burial 15, individual 1, adult male.



Odontome P1-P2

This trait refers to any pin sized, spike-shaped enamel and dentine projection occurring on the occlusal surface of the premolars. No reference plaque is available for this trait. Instead it is scored as either present or absent.

Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

Congenital Absence UM3

The upper third molar may not be formed in adults. There is no ASU reference plaque for this trait. It is also scored as tooth present of absent.

Midline Diastema

In addition to the ASUDAS traits, the occurrence of the UI1 midline diastema has also been recorded. Previous research suggests that this trait can be recorded as a present/absent level of dichotomization (Irish, 1993, 1997, 1998 a, b, c, 2016; Irish et al., 2014; Irish and Turner, 1989, 1990). This trait is recorded based on a measurement between the upper central incisors:

0) No diastema (space < .5 mm)
1) Diastema (space ≥ .5 mm)

The midline diastema has been found to occur in high frequencies in many aboriginal African populations, however, it is not common in other populations (Dervall, 1949; Jacobson, 1982; Shaw, 1931; Sperber, 1958; Van Reenen, 1964). Thus, this feature may prove to be a useful African marker.

Mandibular traits

Lingual Cusp Number LP2

The number of lingual cusps observed on the lower premolars are recorded. Four possible grades can be scored with the ASU LP2 reference plaque: 0-3 cusps

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Anterior Fovea LM1

A depression that may occur anterior to cusps 1 and 2 on the lower first molar. This trait can range in expression from absent, to a large depression with a ridge connecting the mesial margins of the two first two cusps. There are five possible grades which are scored with the ASU LM1 anterior fovea reference plaque:

0) No expression
1) Faint depression anterior to cusps
2) Small depression
3) Medium depression
4) Large depression

Mandibular Torus

A nodular bony exostosis may develop on the lingual side of the mandible near the lower canine and premolars. No reference plaque is available for this trait. Rather, four possible ASU grades exist and are scored as follows:

0) No expression
1) Traces elevation
2) Elevation between 2 to 5 mm
3) Elevation greater than 5 mm

Groove Pattern LM2

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[402] Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

The pattern created by the connections among the cusps on the occlusal surface of the lower second molar. There is no reference plaque for this trait. The three possible grades are recorded as follows:

Y: Cusps 2 and 3 touch
X: Cusps 1 and 4 touch
+: Cusps 1 through 4 touch

Rocker Jaw

This trait is observed on the inferior surface curvature of the mandibles horizontal ramus. This trait is age-dependent and only occurs in adults. There is also no reference plaque for this trait. Instead it is recorded as three possible ASU grades:

0) No expression
1) Slight curvature of the Jaw
2) Extreme curvature, allowing the jaw to rock back and forth when placed on a flat surface

Cusp Number LM1

The number of cusps present on the lower first molar, excluding the metaconulid, cusp 7. No reference plaque is available for this trait. Three possible grades exist, 4-6 cusps, and are recorded as the number present.

Cusp Number LM2

[403] Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

The number of cusps present on the lower second molar, excluding the metaconulid. There is also no reference plaque for this trait. The three possible grades, 4-6 cusps, are scored as the number present.

Deflecting Wrinkle LM1

A medial ridge may be present on occlusal surface of the lower first molar, and be present on cusp 2. Expression of this ridge can range from absent, to a large which may connect with cusp 3. There are four possible grades observed on the reference plaque ASU LM deflecting wrinkle:

0) No expression
1) Ridge extends ½ way across the cusp
2) Ridge extends completely across the cusp
3) Ridge extends into the central groove

C1-C2 (Distal Trigonid) Crest LM1

A ridge may connect the distal borders of cusps 1 and 2 on the lower first molar. This trait is scored as present or absent with the aid of a reference plaque developed by Hanihara (1961) for deciduous teeth.

Protostylid LM1

A paramolar cusp that may occur on the mesiobuccal surface of cusp 1 on the lower first molar. The trait is often associated with the buccal groove, a groove on the cheek side of the lower first molar, and can range from a pit to a separate cusp. There are eight possible ASU grades which are scored using the Zoller Laboratory reference plaque LM protostylid:

[404] Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

0) No Expression
1) Buccal pit
2) Distal deviation of the buccal groove
3) Secondary mesial groove occurs
4) Secondary groove is larger than 3
5) Secondary groove is larger than 4
6) Small cusp
7) Large cusp

Cusp 7 (Metaconulid) LM1

An additional cusp may be present in the lingual groove between cusps 2 and 4 on the lower first molar. Six possible grades exist and can be scored with the ASU LM1 cusp 7 reference plaque:

0) No expression
1) Faint cusp
1A) Faint bulge on the lingual surface of cusp 2
2) Small cusp
3) Medium-sized cusp
4) Large cusp

Tome’s Root LP2

This trait is observed when a deep groove is observed on the mesial and distal root surfaces. There are six possible grades which are scored with the ASU LP Tome’s root reference plaque:

0) No expression

Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

1) Shallow groove is present
2) Moderate groove is present
3) Deep groove is present
4) Very deep groove is present
5) Two free roots are present

Root Number LC

The number of free roots observed on the lower canine. No reference plaque is available for this trait. Rather, it is scored according to number of free roots present.

Root Number LM1

The number of free roots that are evident on the lower first molar. There is also no reference plaque for this trait. It is also scored based on the number of free roots that are observed.

Root Number LM2

The number of free roots observed on the lower second molar. No reference plaque is available for this trait. It is also scored based on the number of roots which are observed.

Torsomolar Angle LM3

The lower third molar may be rotated and be oriented towards a line drawn through the middle of the lower first and second molars. There is also reference plaque for this trait.

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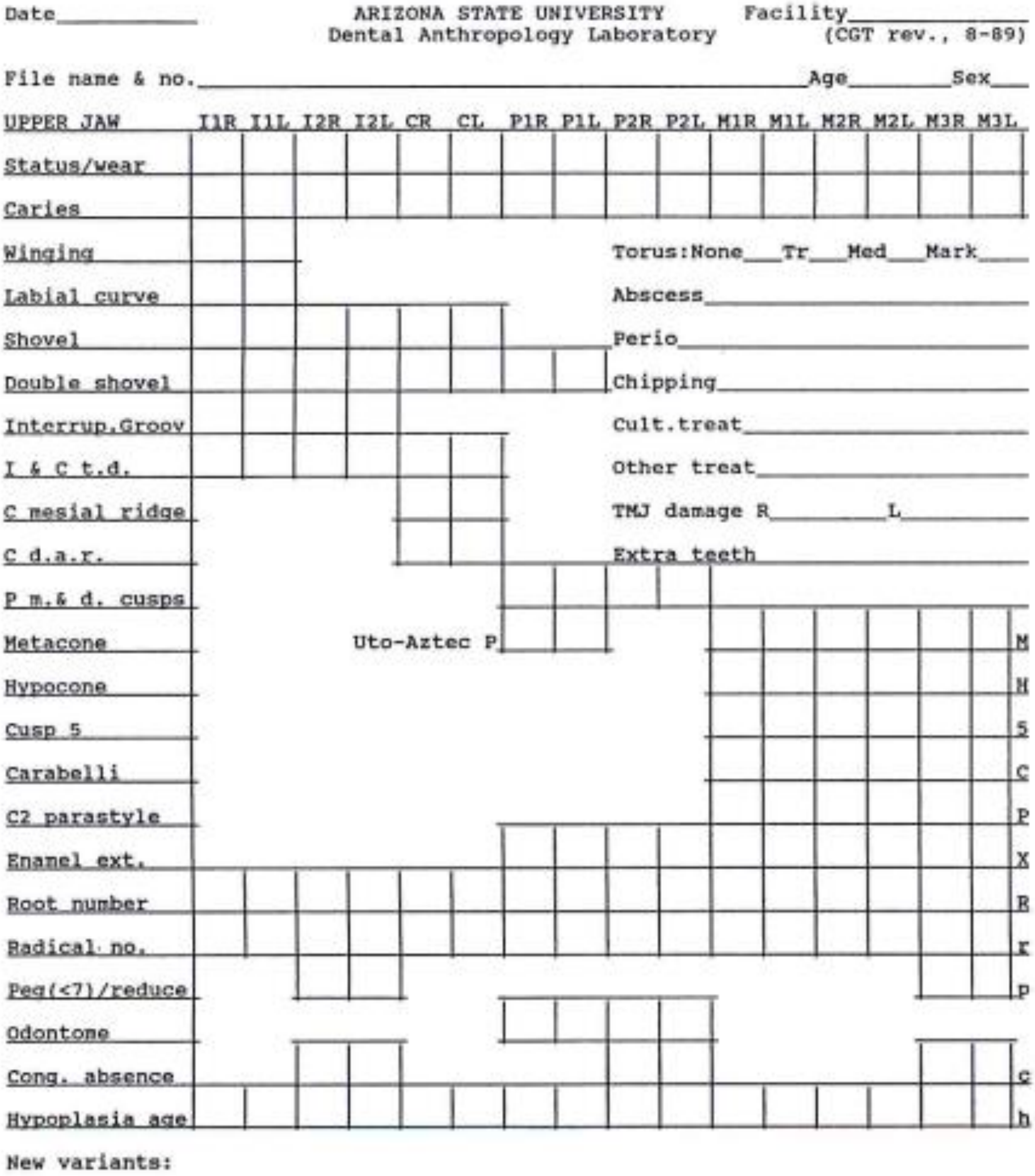
[406] Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

Three possible trait grades exist and include: straight, buccal rotation, and lingual rotation. This trait is recorded based on the degree of rotation.

ASUDAS scoring sheet for maxillary dentition (Turner et al., 1991).



Date___________

ARIZONA STATE UNIVERSITY
Dental Anthropology Laboratory

Facility_____________
(CGT rev., 8-89)

File name & no.____Age_______Sex___

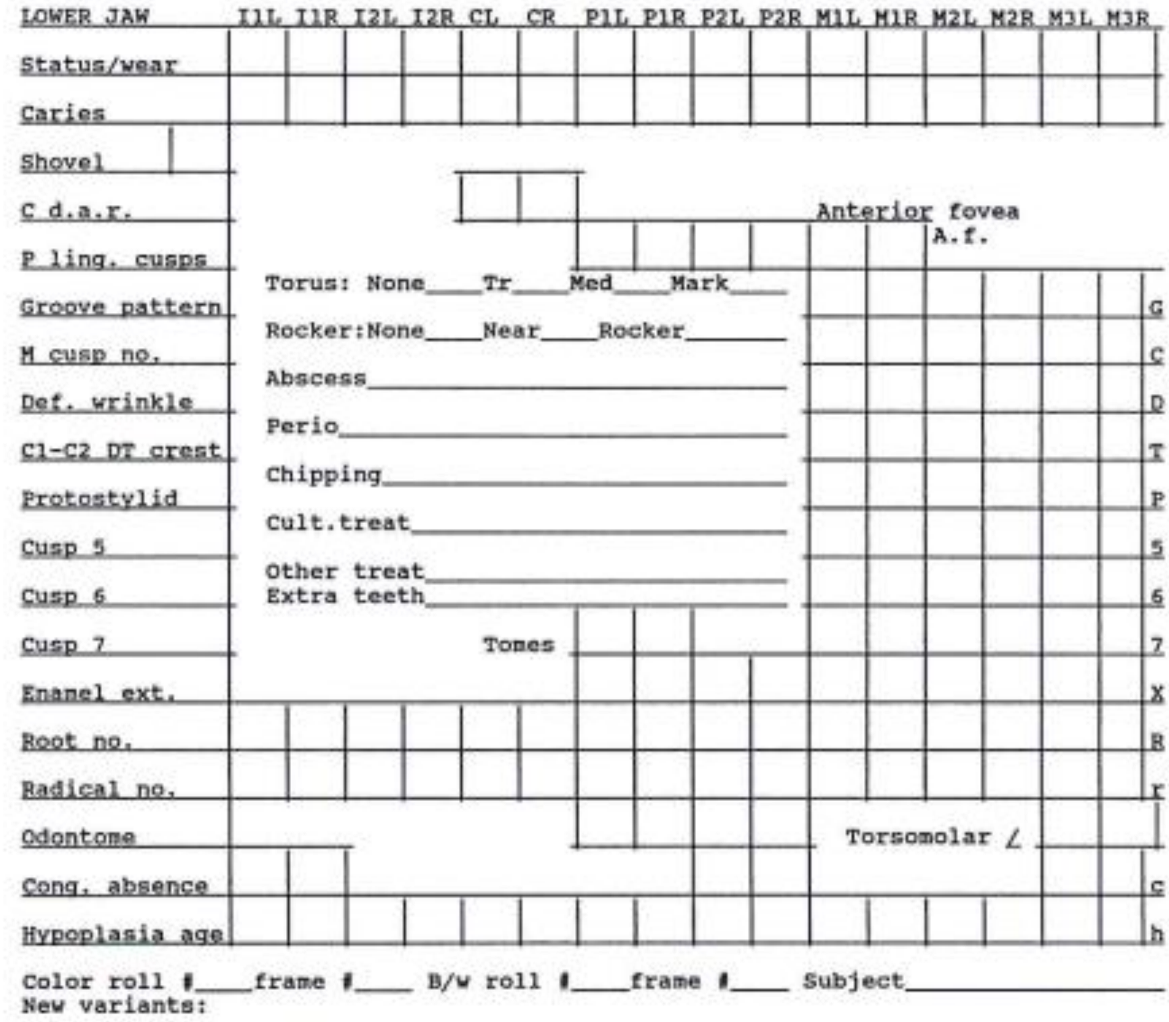
UPPER JAW	I1R	I1L	I2R	I2L	CR	CL	P1R	P1L	P2R	P2L	M1R	M1L	M2R	M2L	M3R	M3L	
Status/wear																	
Caries																	
Winging																	
Labial curve																	
Shovel																	
Double shovel																	
Interrup.Groov																	
I & C t.d.																	
C mesial ridge																	
C d.a.r.																	
P m.& d. cusps																	
Metacone						Uto-Aztec P											M
Hypocone																	H
Cusp 5																	5
Carabelli																	C
C2 parastyle																	P
Enamel ext.																	X
Root number																	R
Radical no.																	r
Peg(<7)/reduce																	p
Odontome																	
Cong. absence																	c
Hypoplasia age																	h

Torus:None___Tr___Med___Mark____
Abscess_______________________
Perio_________________________
Chipping______________________
Cult.treat____________________
Other treat___________________
TMJ damage R________L_________
Extra teeth___________________

New variants:

Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

ASUDAS scoring sheet for mandibular dentition (Turner et al., 1991).



LOWER JAW I1L I1R I2L I2R CL CR P1L P1R P2L P2R M1L M1R M2L M2R M3L M3R
Status/wear
Caries
Shovel
C d.a.r.
P ling. cusps
Groove pattern
M cusp no.
Def. wrinkle
C1-C2 DT crest
Protostylid
Cusp 5
Cusp 6
Cusp 7
Enamel ext.
Root no.
Radical no.
Odontome
Cong. absence
Hypoplasia age

Anterior fovea
A.f.

Torus: None____Tr____Med____Mark____
Rocker:None____Near____Rocker_______
Abscess____________________
Perio____________________
Chipping____________________
Cult.treat____________________
Other treat____________________
Extra teeth____________________

Tomes

Torsomolar ∠

G
C
D
T
P
5
6
7
X
R
r
c
h

Color roll #____frame #____ B/w roll #____frame #____ Subject__________________
New variants:

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[408] Turner C II, Nichol CR, Scott GR. 1991. Scoring procedures for key morphological traits of the permeant dentition: the Arizona State University Dental Anthropology System Advances in dental anthropology. New York: Wiley-Liss p 13-31.

Appendix II

Kendall’s Tau-b Table

Trait[a]	**Labial Curvature UI1**	**Tuberculum Dentale UI2**	**Distal accessory ridge UC**	**Hypocone UM2**	**Cusp 5 UM1**	**Carabelli’s trait UM1**	**Parastyle UM3**	**Enamel extension UM1**	**Root number UP1**
Labial Curvature UI1	tb=.209 α .590	**tb=.751** **α .018**	tb=.226 α .690	tb=.167 α .175	tb=.353 α .740	tb=.392 α .391	tb=.316 α .476	tb=.140 α .207	tb=.138 α .194
Tuberculum Dentale UI2	**tb=.751** **α .018**	tb=.258 α .292	tb=.348 α .156	tb=.408 α .459	tb=.157 α .692	tb=.118 α .473	tb=.175 α .276	tb=.255 α .364	tb=.330 α .282
Distal accessory ridge UC	tb=.382 α .745	tb=.364 α .218	tb=.256 α .239	tb=.210 α .390	tb=.110 α .580	tb=.425 α .540	tb=.405 α .285	tb=.156 α .191	tb=.104 α .178
Hypocone UM2	tb=.125 α .403	tb=.314 α .443	tb=.234 α .497	tb=.204 α .868	tb=.396 α .337	tb=.108 α .297	tb=.282 α .857	tb=.276 α .177	tb=.248 α .775
Cusp 5 UM1	tb=.252 α .757	tb=.233 α .695	tb=.330 α .528	tb=.191 α .433	tb=.088 α .197	**tb=.518** **α .011**	tb=.159 α .233	tb=.142 α .488	tb=.202 α .393
Carabelli’s trait UM1	tb=.405 α .438	tb=.218 α .177	tb=.376 α .132	tb=.402 α .294	**tb=.518** **α .011**	tb=.418 α .208	tb=.229 α .355	tb=.127 α .318	tb=.101 α .247
Parastyle UM3	tb=.435 α .220	tb=.419 α .683	tb=.094 α .589	tb=.191 α .396	tb=.377 α .170	tb=.289 α .296	tb=.291 α .300	tb=.073 α. 490	tb=.100 α. 132
Enamel extension UM1	tb=.366 α .726	tb=.146 α .463	tb=.131 α .813	tb=.314 α .959	tb=.178 α .152	tb=.270 α .815	tb=.055 α .728	tb=.141 α .433	tb=.399 α .296
Root number UP1	tb=.305 α .215	tb=.305 α .190	tb=.295 α .122	tb=.146 α .222	tb=.247 α .456	tb=.385 α .520	tb=.399 α .375	tb=.355 α .145	tb=.417 α .280

[a] Bold values indicate significant correlations, tb represents the test value and α represents the alpha value.

Kendall’s Tau-b Table cont.

Trait	**Labial Curvature UI1**	**Tuberculum Dentale UI2**	**Distal accessory ridge UC**	**Hypocone UM2**	**Cusp 5 UM1**	**Carabelli’s trait UM1**	**Parastyle UM3**	**Enamel extension UM1**	**Root number UP1**
Root number UM2	tb=.220 α .102	tb=.345 α .402	tb=.280 α .502	tb=.190 α .652	tb=.140 α .741	tb=.108 α .799	tb=.332 α .421	tb=.303 α .291	tb=.333 α .225
Lingual cusp LP2	tb=.199 α .636	tb=.357 α .343	tb=.247 α .556	tb=.242 α .564	tb=.154 α .715	tb=.173 α .531	tb=.201 α .633	tb=.201 α .633	tb=.247 α .556
Anterior fovea LM1	tb=.242 α .564	tb=.226 α .482	tb=.130 α .259	tb=.145 α .771	tb=.393 α .324	tb=.324 α .434	tb=.433 α .204	tb=.350 α .195	tb=.290 α .145
Groove pattern LM2	tb=.220 α .102	tb=.141 α .234	tb=.305 α .220	tb=.353 α .393	tb=.140 α .703	tb=.421 α .190	tb=.393 α .652	tb=.325 α .145	tb=.305 α .248
Rocker jaw	tb=.399 α .226	tb=.315 α .255	tb=.191 α .201	tb=.427 α .215	tb=.435 α .620	tb=.245 α .140	tb=.333 α .463	tb=.438 α .857	tb=.399 α .259
Cusp number LM1	tb=.403 α .827	tb=.259 α .150	tb=.314 α .102	tb=.177 α .842	tb=.190 α .421	tb=.108 α .799	tb=.226 α .318	tb=.131 α .366	tb=.338 α .277
Cusp number LM2	tb=.220 α .396	tb=.305 α. 217	tb=.190 α .525	tb=.199 α .458	tb=.226 α .590	tb=.443 α .318	tb=.167 α .345	tb=.396 α .253	tb=.440 α .210
Deflecting wrinkle LM	tb=.252 α .142	tb=.209 α .416	tb=.258 α .233	tb=.382 α .740	tb=.142 α .088	tb=.141 α .738	tb=.262 α .531	tb=.472 α .238	tb=.104 α .806
C1–C2 crest LM1	tb=.472 α .316	tb=.251 α .199	tb=.158 α .088	tb=.417 . .353	tb=.101 α .191	tb=.253 α .472	tb=.105 α .706	tb=.337 α .285	tb=.324 α .434

[a] Bold values indicate significant correlations, tb represents the test value and α represents the alpha value.

Kendall’s Tau-b Table cont.

Trait	**Root number UM2**	**Lingual cusp LP2**	**Anterior fovea LM1**	**Groove pattern LM2**	**Rocker jaw**	**Cusp number LM1**	**Cusp number LM2**	**Deflecting wrinkle LM**	**C1–C2 crest LM1**
Protostylid LM1	tb=.372 α. .238	tb=.112 α .792	tb=.102 α .811	tb=.332 α .421	tb=.353 α .392	tb=.280 α .502	tb=.141 α .377	tb=.226 α .591	tb=.373 α .363
Cusp 7 LM1	tb=.175 α. .208	tb=.305 α .055	tb=.372 α .840	tb=.226 α .482	tb=.130 α .190	tb=.154 α .337	tb=.353 α .417	tb=.102 α .140	tb=.208 α .300
Tome’s root LP1	tb=.155 α. .055	tb=.233 α .640	tb=.403 α .320	tb=.338 α .840	tb=.173 α .530	tb=.305 α .438	tb=.266 α .435	tb=.290 α .215	tb=.170 α .100
Root number LC	tb=.220 α. 080	tb=.402 α .500	tb=.234 α .427	tb=.320 α .154	tb=.102 α .220	tb=.205 α .324	tb=.146 α .366	tb=.397 α .247	tb=.285 α .475
Root number LM1	tb=.132 α .757	tb=.372 α .842	tb=.303 α .108	tb=.141 α .055	tb=.393 α .813	tb=.190 α .055	tb=.234 α .330	tb=.205 α .141	tb=.399 α .178
Root number LM2	tb=.314 α .305	tb=.220 α .757	tb=.190 α .102	tb=.324 α .102	tb=.201 α .556	tb=.318 α .633	tb=.304 α .443	tb=.177 α .842	tb=.372 α .250
Torsomolar angle LM3	tb=.293 α .683	tb=.178 α .088	tb=.226 α .459	tb=.259 α .771	tb=.318 α .226	tb=.130 α .141	tb=.438 α .771	tb=.377 α .202	tb=.280 α .345

[a] Bold values indicate significant correlations, tb represents the test value and α represents the alpha value.

Kendall’s Tau-b Table cont.

Trait	**Root number UM2**	**Lingual cusp LP2**	**Anterior fovea LM1**	**Groove pattern LM2**	**Rocker jaw**	**Cusp number LM1**	**Cusp number LM2**	**Deflecting wrinkle LM**	**C1–C2 crest LM1**
Root number UM2	tb=.305 α .450	tb=.255 α .253	tb=.465 α .339	tb=.305 α .255	tb=.305 α .252	tb=.467 α .287	tb=.305 α .575	tb=.256 α .353	tb=.350 α .396
Lingual cusp LP2	tb=.305 α .428	tb=.355 α .297	tb=.334 α .173	tb=.132 α .528	tb=.375 α .608	tb=.335 α .173	tb=.160 α .548	tb=.374 α .261	tb=.473 α .334
Anterior fovea LM1	tb=.297 α .256	tb=.322 α .463	tb=.148 α .226	tb=.393 α .237	tb=.132 α .580	tb=.297 α .160	tb=.243 α .564	tb=.399 α .208	tb=.440 α .160
Groove pattern LM2	tb=.334 α .564	tb=.460 α .337	tb=.138 α .088	tb=.256 α .532	tb=.261 α .173	tb=.399 α .208	tb=.328 α .498	tb=.367 α .877	tb=.372 α .238
Rocker jaw	tb=.160 α .374	tb=.131 α .322	tb=.173 α .261	tb=.265 α .626	tb=.233 α .663	tb=.148 α .580	tb=.261 α .248	tb=.441 α .548	tb=.364 α .440
Cusp number LM1	tb=.274 α .670	tb=.197 α .297	tb=.443 α .396	tb=.440 α .353	tb=.342 α .264	tb=.140 α .328	tb=.208 α .399	tb=.248 α .190	tb=.160 α .173
Cusp number LM2	tb=.248 α .297	tb=.476 α .131	tb=.350 α .132	tb=.131 α .757	tb=.440 α .397	tb=.197 α .320	tb=.160 α .675	tb=.372 α .640	tb=.380 α .132
Deflecting wrinkle LM	tb=.173 α .604	tb=.334 α .464	tb=.320 α .397	tb=.463 α .308	tb=.457 α .608	tb=.334 α .463	tb=.173 α .242	tb=.197 α .088	tb=.398 α .367
C1–C2 crest LM1	tb=.423 α .463	tb=.396 α .132	tb=.374 α .564	tb=.422 α .755	tb=.367 α .870	tb=.334 α .608	tb=.132 α .480	tb=.148 α .173	tb=.448 α .160

[a] Bold values indicate significant correlations, tb represents the test value and α represents the alpha value.

Kendall’s Tau-b Table cont.

Trait	**Labial Curvature UI1**	**Tuberculum Dentale UI2**	**Distal accessory ridge UC**	**Hypocone UM2**	**Cusp 5 UM1**	**Carabelli’s trait UM1**	**Parastyle UM3**	**Enamel extension UM1**	**Root number UP1**	**Labial Curvature UI1**
Protostylid LM1	tb=.385 α .687	tb=.346 α .385	tb=.308 α .414	tb=.172 α .535	tb=.242 α .469	tb=.228 α .587	tb=.165 α .695	tb=.373 α .366	tb=.251 α .460	tb=.423 α .297
Cusp 7 LM1	tb=.440 α .320	tb=.160 α .548	tb=.243 α .564	tb=.334 α .173	tb=.399 α .208	tb=.208 α .499	tb=.334 α .305	tb=.205 α .626	tb=.197 α .641	tb=.146 α .741
Tome’s root LP1	tb=.398 α .328	tb=.384 α .129	tb=.385 α .346	tb=.337 α .870	tb=.365 α .577	tb=.335 α. .080	tb=.254 α .898	tb=.372 α .238	tb=.205 α .315	tb=.335 α .417
Root number LC	tb=.280 α .580	tb=.240 α .190	tb=.274 α .088	tb=.402 α .393	tb=.354 α .250	tb=.334 α .173	tb=.242 α .564	tb=.374 α .261	tb=.245 α .676	tb=.197 α .641
Root number LM1	tb=.146 α .741	tb=.398 α .328	tb=.396 α .250	tb=.347 α .322	tb=.263 α .205	tb=.198 α .208	tb=.267 α .108	tb=.160 α .294	tb=.320 α .445	tb=.322 α .393
Root number LM2	tb=.360 α .578	tb=.205 α .875	tb=.335 α .215	tb=.366 α .482	tb=.141 α .377	tb=.234 α .345	tb=.153 α .455	tb=.353 α .208	tb=.332 α .102	tb=.190 α .055
Torsomolar angle LM3	tb=.399 α .177	tb=.314 α .175	tb=.417 α .141	tb=.153 α .090	tb=.241 α .140	tb=.372 α .804	tb=.238 α .112	tb=.226 α .102	tb=.373 α .591	tb=.305 α .190

[a]Bold values indicate significant correlations, tb represents the test value and α represents the alpha value.

Kendall’s Tau-b Table cont.

Trait	**Protostylid LM1**	**Cusp 7 LM1**	**Tome’s root LP1**	**Root number LC**	**Root number LM1**	**Root number LM2**	**Torsomolar angle LM3**
Protostylid LM1	tb=.305 α .353	tb=.191 α .215	tb=.234 α .377	tb=.230 α .417	tb=.131 α .073	tb=.324 α .482	tb=.302 α .393
Cusp 7 LM1	tb=.124 α .130	tb=.366 α .153	tb=.403 α .443	tb=.108 α .208	tb=.450 α .591	tb=.220 α .390	tb=.302 α .345
Tome’s root LP1	tb=.257 α .073	tb=366 α .145	tb=.314 α .131	tb=.357 α .490	tb=.283 α .150	tb=.397 α .240	tb=.403 α .146
Root number LC	tb=.438 α .131	tb=.366 α .153	tb=.438 α .205	tb=.245 α .280	tb=.377 α .427	tb=.262 α .102	tb=.208 α .132
Root number LM1	tb=.337 α .258	tb=.443 α .203	tb=.226 α .130	tb=.382 α .130	tb=.438 α .190	tb=.393 α .140	tb=.372 α .141
Root number LM2	tb=.353 α .202	tb=.417 α .366	tb=.333 α .757	tb=.373 α .591	tb=.393 α. 170	tb=.277 α .153	tb=.191 α .088
Torsomolar angle LM3	tb=.305 α .255	tb=.124 α .324	tb=.220 α .434	tb=.366 α .652	tb=.287 α .177	tb=.345 α .402	tb=.402 α .752

[a] Bold values indicate significant correlations, tb represents the test value and α represents the alpha value.

Appendix III

Disadvantages of using teeth as a research tool[1]

Although there are many advantages to using teeth as a research tool, there are also several disadvantages. Information can be lost through wear and pathology, related to individual age and post-depositional damage. Further, single-rooted teeth (i.e., incisors) are often lost during curation and excavation. In skeletal collections, it is common to have all the multi-rooted posterior teeth (i.e., molars) with no anterior teeth (i.e., incisors). Consequently, highly variable sample sizes for shovelling versus Carabelli's cusp are common. The global range of dental variation has not been completely documented, resulting in patterns of regional population affinity and variation that are not completely understood. Fluctuating asymmetry can have a negative effect on trait expression; however, this downside can be avoided. Although fluctuating asymmetry occurs throughout the dentition; the antimeres can be scored with confidence in relation to the level of trait expression (Irish, 1993; Scott and Turner, 1997). Most traits are present on both antimeres because teeth are mirror images of each other, albeit inexact.

As such, antimeres can be scored following two methods. One method involves counting only one side in all specimens (Haeussler et al., 1988; Scott and Turner, 1997). The second method is to score both antimeres and, allowing for asymmetry, count the side with the greatest expression (Scott and Turner, 1997). Because dental traits are continuous variants, they are difficult to score consistently into ordinal grades; differences in trait frequencies can exist between analyses that result in differential population affinity assessments. To avoid potentially biased data, proper scoring procedures should be exercised (Burnett et al., 2013; Nichol and Turner, 1986; Stojanowski and Johnson, 2015; Turner et al., 1991). Dental wear results from three primary sources, striation, abrasion and erosion, and can also contribute to differential trait scoring, as the near-occlusal traits are more affected at the early wear-stages (Burnett, 2016). Attrition is the result of occlusal contact and interproximal contact between adjacent teeth. Abrasion is the result of friction between teeth, items or substances introduced into the mouth (Burnett et al., 2013). Abrasion resulting from food items includes non-spatially specific wear, as well as localized wear, and is derived from

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1. Anctil M. 2016. Ancient Celts: Myth, invention or reality? Dental affinities among continental and non-continental Celtic groups. M.A. Thesis. UAF. p 54-60.

specific food processing (Burnett et al., 2013). Nondietary causes of abrasion include sand in the diet, toothbrushes, toothpicks and using teeth as tools (Burnett et al., 2013; Bergström and Lavstedt, 1979; Erdal, 2008; Frayer, 1991; Larsen, 1985; Turner and Anderson, 2003; Ungar et al., 2001). Erosion is the chemical destruction of the dental tissues, e.g., enamel and dentine, in the absence of plague and is a modern phenomenon (Burnett et al., 2013; Kaidonis, 2008). Causes include vomiting, consuming highly acidic foods or beverages (Burnett et al., 2013; Holbrook et al., 2003; Kaidonis, 2008; Pindborg, 1970). Attrition, abrasion, and erosion rarely occur in isolation. Attrition and abrasion likely occurred in tandem in nonindustrialized societies, whereas the soft foods consumed as part of the modern diet have moderated the effects of abrasion (Burnett et al., 2013; Khan and young, 2011). Further, its effects are complex as wear increases with age and may differ between the sexes and populations (Burnett et al., 2013; Molnar, 1971; Tomenchuk and Mayhall, 1979). As such wear is a potential source of frequency bias in dental morphological study and may result in the misinterpretation of morphological traits (Burnett et al., 2010, 2013; Burnett, 1998, 2016; Morris, 1970). Scoring of nonmetric traits can be biased in two ways. The first is designated as grade shift, which occurs when a trait is scored as having a lesser frequency, trait downgrading, or having a greater frequency than actually present, trait upgrading, expression than is actually present. Both trait downgrading and upgrading affect trait counts by reducing or increasing frequencies of occurrence, respectively (Burnett et al., 2010, 2013). Additionally, a sampling bias may occur when teeth that are subjectively considered too worn for inclusion in subsequent analyses, and the missing data are assumed to be missing completely at random (MCAR) (Burnett, 2016).

A particular trait even in the presence of heavy wear may be included for analysis, however, a trait which is absent on a similarly worn tooth is not (Burnett, 2016). Consequently, in the latter case, the tooth is excluded from analyses due to the assumption that the trait was worn away and is thus scored as no data. Although, in some cases, the trait was, in fact, absent as should have been scored as a grade 0 (Burnett, 2016). Thus, the frequency of a particular trait can be artificially increased when the missing completely at random, MCAR, assumption is violated (Burnett, 2016). One solution is to only score teeth with similar levels of wear. However, such similarity among samples, particularly archaeological samples, may not be readily available therefore significantly limiting sample sizes (Burnett et al., 2010; Burnett, 2016). Alternatively, acknowledgment of major

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differences in wear among samples may affect particular traits that will help account for the MCAR assumption. Selecting only specific traits that are minimally or not affected by wear (i.e., root traits) is another alternative. As traits near the surface (i.e., shovelling) are more affected at early stages of wear than traits located lower on the crown surface (i.e., groove pattern). Shifting the standard breakpoints (the level of expression at which each trait is scored as present) upwards is the simplest solution, which can reduce or eliminate wear biases (Irish, 1993, 2006; Irish et al., 2014). This solution enables moderately worn dentitions to be recorded and subsequently included in analyses, and maximizes sample size (Burnett, 1986, 2016; Burnett et al., 2013).

Wear-related biases can be determined through analysis of trait frequencies across wear grades, which can indicate systematic grade shifting. Frequency and wear biases have been identified in previous studies (Burnett et al., 2010, 2013; Burnett, 2016). Significant wear biases have been found in the frequency of incisor shovelling, maxillary premolar accessory ridges, and lower molar cusp number. Wear related biases have also been reported in UI1 shovelling, UI1 double shovelling, canine distal accessory ridge UC, UM1 enamel extension, LM2 cusp number, and LM1 deflecting wrinkle (See Appendix 1 for trait descriptions) (Burnett et al., 2013; Burnett, 2016; Stojanowski and Johnson, 2015). These biases can lead to both intra-and inter-observer error through differential scoring, although this effect can be minimized by examination of trait frequencies across wear grades. Frequency of occurrence can be compared to tooth-specific wear scores to determine the relationship between wear and morphology. Only comparing samples, or teeth, with similar degrees of wear can also mitigate the effects of these biases. However, finding such similarity among samples, particularly archaeological samples, may not always be possible (Burnett et al., 2013). As a result, this method can significantly limit the samples available for comparison and analysis (Burnett, 2016; Burnett et al., 2013). Another method is to only select and score those specific traits that are minimally or not affected by wear, such as root traits. Shifting the breakpoints upwards can reduce or abolish certain wear biases size (Burnett, 1986, 2016; Burnett et al., 2013). An alternative method of addressing these biases is to acknowledge that there is a difference in wear among the samples being compared. A cautionary description detailing that some trait frequencies may have been affected should also be included (Burnett, 1986, 2016; Burnett et al., 2013). This method is recommended as trait upgrading is often only necessary when sample sizes need to be increased, or where

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moderate to heavy wear is the norm; as it may lead to a spurious relationship among samples (Burnett, 1986, 2016; Burnett et al., 2013). Further, the underlying biological relationships, and variation, among samples may be obscured (Burnett et al., 2013). Patterns of missing data can also be examined to determine whether observer error accounts for differential trait recording (Stojanowski and Johnson, 2015).

The rank scale plaques comprising the ASUDAS system promote intra-and inter-observer recording repeatability, especially between observers (Stojanowski and Johnson, 2015). Strict adherence to the ASUDAS standards and the use of intra-observer error checks can minimize the effects of error (Hillson, 1996; Irish, 1993, 1997, 1998a, b, c, 20002; Scott and Turner, 1997; Turner et al., 1991). Observer error can be limited through multiple scoring events by the same and/or numerous individuals and statistical analysis of the results. Such as a paired samples t-tests and Wilcoxon signed-rank test can determine whether the discrepancies in the scores fall within an acceptable range. Additional measures, such as grade dichotomization, are used to address concordance issues between observers (Nichol and Turner, 1986; Turner et al., 1991; Scott and Turner, 1997; Stojanowski and Johnson, 2015).

Another potential disadvantage is the lack of knowledge of the exact modes of inheritance. However, previous nonmetric analyses have indicated population affinities in line with genetic and known linguistic evidence and distribution without a complete understanding of the modes of inheritance. Dental traits have been argued to be polygenetic with a quasi-continuous range of expression or the existence of a gene model for specific traits (Dahlberg, 1971; Hubbard, 2012; Jernvall, 2000; Jernvall and Jung, 2000; Nichol, 1990; Noss et al., 1983; Salazar-Ciudad and Jernvall, 2010; Scott, 1973; Skinner at al., 2008 Turner, 1969, 1969). However, because dental size and morphology have a substantial genetic component (40-80% and 60-80% respectively), understanding the exact modes of inheritance is not necessary for affinity studies (Hubbard, 2012; Hughes and Townsend, 2013; Jernvall, 2000; Jernvall and Jung, 2000; Nichol, 1990; Noss et al., 1983; Salazar-Ciudad and Jernvall, 2010; Scott, 1973; Skinner at al., 2008 Turner, 1969, 1969). The concordance between biodistance estimates obtained from dental and genetic data also supports the use of dental traits in these analyses. The lack of standardization, however, is not as easy to overcome.

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The lack of standardization in scoring procedures between studies results in errors when utilizing previously published data. Because dental traits are continuous variants and are thus difficult to score consistently along an ordinal scale, they may be evaluated based on individual training and/or personal opinion (Hillson, 1996; Scott and Turner, 1997; Turner et al., 1991). However, with the advent of the ASUDAS system, this issue has been somewhat reduced (Haeussler et al., 1988; Irish, 2010, 2015; Irish et al., 2014; Nichol and Turner, 1986; Scott and Turner, 1997). Adherence to the ASUDAS protocols and intra and inter-observer error trials combined with statistical analysis can minimize the effect of differential trait scoring. Asymmetry in the antimeres may also impact dental nonmetric trait analysis, as the morphology of one antimere is not necessarily matched by the opposite (Nichol and Turner, 1986; Scott and Turner, 1997). Some studies have indicated that fluctuating asymmetry of nonmetric traits increases from the mesial to distal (front to back) teeth (Saunders and Mayhall, 1982). However, a high degree of concordance has been found between the antimeres, and little evidence has subsequently been found for directional asymmetry (Garn et al., 1966; Mizoguchi, 1992).

Advantages of using teeth as a research tool[1]

Although there are disadvantages to the analysis of dental nonmetric traits, their effects can be minimized through careful adherence to the ASUDAS system and the use of inter-and-intra-observer checks. The loss of information through dental wear and/or post-mortem depositional damage can be minimized if the antimere is available for analysis (Irish, 1993, 2010, 2015; Irish et al., 2014; Scott and Turner, 1997). However, numerous previous studies have described the relationships among populations, and/or groups, which mirror, and are concordant, with those based on genetics, linguistics, documented population history and other skeletal morphological traits (Irish, 1993, 1998, 2010, 2015; Irish et al., 2014 Scott and Turner, 1997). This indicated that dental morphological analyses, with the ASUDAS system, are applicable to biodistance studies despite diverse levels of tooth wear.

Overall, the disadvantages of dental morphological analysis do not preclude its use. As analysis of dental morphological variation has been shown to determine broad and regional scale population differentiation and affinity, the results of which have been independently corroborated by genetic and linguistic analyses when the linguistic distribution

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is known in numerous previous studies (Coppa et al., 2000, 2007; Hanihara, 2008, 2010; Irish, 1993, 2010, 2015; Irish et al., 2014). However, when the linguistic distribution and relationships are unknown the link between languages and populations is tenuous, although dental phenetic relationships can be used to approximate the linguistic and genetic boundaries (Hanihara, 2008, 2010; Hubbard, 2012; Irish, 1993, 2010, 2015; Irish et al., 2014). Dental morphological analysis is, therefore, a useful tool for determining biological affinity among, between, and within populations.

Teeth have several attributes that make them especially suited to anthropological analysis. They are hard, primarily the enamel, which has the lowest porosity and highest density of all body tissues (Hillson, 1996; Kraus et al., 1969). The mineralized fluorhydroxyapatite (mineralized substance formed by the reactions between small amounts of fluoride and hydroxyapatite) enamel covers the crown, thus protecting the underlying dentine; making the teeth less susceptible to degradation after death (Hillson, 1996). Therefore, teeth are better able to survive in the archaeological record. Teeth act as an intermediary between individuals and their environment and their use as tools and everyday interaction with the environment can leave diagnostic scars. This relationship allows for interpretations about the interactions between individuals and their environments, resulting in discernible clues as to diet, health and the cultural use of teeth (Frayer et al., 1988; Larsen, 1985; Merbs, 1983; Molleson and Jones, 1991).

Teeth are also less affected by the environment than other living tissues such as bone. Once teeth are formed, they do not change, with the exception of attrition and pathological damage. Because environmental stressors do not affect teeth as much as other living tissues, they can be used for short-term affinity studies within and between populations (Hillson, 1996; Turner, 1969; Hillson, 1996). Teeth also evolve slowly, enabling long term diachronic studies through analysis of tooth morphology. However, dramatic changes in both dental morphology and tooth size are evident subsequent to the development of food production and ceramic technology. Samples of both living and dead individuals can be compared, thereby allowing for comparisons between extinct and extant populations. Moreover, teeth, while complex, display a largely consistent range in size within species and sex (Irish, 1993, 2010; Scott, 1973; Scott and Turner, 1997; Turner et al., 1991). Teeth are also evolutionally conservative (Irish, 1993, 2010; Scott and Turner, 1997; Turner et al., 1991). Therefore, teeth are well-suited to provide insight into numerous genetic, pathological, behavioural, cultural,

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and environmental relationships, making them a preferred subject of biological inquiry. Dental analysis has been employed in several fields, including, genetics, growth and development, pathology, forensics, and hominid origins, because of the attributes mentioned above.

On a global scale, morphological trait frequencies have been found to vary according to broad geographical categories. Nonmetric traits are discrete anatomical units that are expressed at differing frequencies within and among populations, thus allowing for interpretations at both micro-and macro-evolutionary levels (Hubbard, 2012; Irish, 1993, 2010, 2015; Irish et al., 2014). Morphological traits have a high genetic component, 40-80%, which facilitates their use in biodistance, population history and structure analyses. The results of which have been shown to corroborate those from other lines of evidence including, linguistic, genetic, historical and archaeological (Hubbard, 2012; Irish, 1993, 2010, 2015; Irish et al., 2014; Ricaut et al., 2010). Further, a concordance between biodistance estimates obtained from dental and genetic data suggests that dental data are suitable for providing estimates of biological affinity in line with genetic analyses (Hubbard, 2012; Ricaut et al., 2010). Regional and global relationships have been revealed through nonmetric trait analysis, the results of which are in line with genetic and linguistic evidence where known (Hubbard, 2012; Irish, 1993, 2010, 2015; Irish et al., 2014). Indicting the patterns of population affinity indicated through dental nonmetric analysis is not an artefact of the analysis, but actually represents a true affinity relationship. Several studies have indicated a strong correlation between genetic and dental reconstructions of biological affinity (Cavalli-Sforza et al., 1994; Cavalli-Sforza et al., 1988; Hubbard, 2012; Ricaut et al., 2010; Scott and Turner, 1997; Sofaer et al., 1972b; Wijsman and Never, 1986).

Further, previous studies have indicated that the biodistance data collected from dental traits will be significantly and positively concordant with that from genetic based studies (Hanihara, 2008; Hubbard, 2012; Ricaut et al., 2010; Turner, 1987, 1989). Although there are some differences between the results of nonmetric trait and genetic analysis, the discrepancies between the two are likely due to the fact that dental traits evolve slowly they may provide a population history more in line with a deeper time scale than the genetic data.

Because ASUDAS traits do not follow simple inheritance patterns, the phenetic differences and similarities between and within populations can be used to approximate levels of genetic affinity (Berry, 1968; Dahlberg, 1971; Garn et al., 1963; Grüneburg, 1965;

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Hubbard, 2012; Irish, 1993, 2010, 2015; Irish et al., 2014; Jackes et al., 2001; Kollar and Baird, 196; Scott and Turner, 1997; Sofaer, 1970). Thus, dental nonmetric traits can be used to determine the amount of gene flow between populations. During the early period of nonmetric trait analysis, researchers utilized these traits to describe and document population differences and general differences in trait expression. These comparative studies were used on both global and regional scales as well as the derivation of modern populations from a common ancestral population (Turner, 1984, 1985). On a regional scale, the frequency of trait expression between prehistoric populations from India was determined to be intermediate in relation to trait expression to Europeans and Asians (Lukacs and Walimbe, 1984). These analyses have also indicated the presence of region-specific rather than broad geographically distributed populations and/or groups, with a trend towards limited intra-and-extra-regional mobility (Hubbard, 2012; Irish, 1993, 2010, 2015; Irish et al., 2014; Scott and Turner, 1997). Specific dental complexes have been identified for the Mongoloid and Australian dentitions based on the frequencies of specific dental traits such as incisor shovelling, Carabelli's cusp, and Tomes root (Scott and Turner, 1997). Variations in the frequencies of nonmetric dental traits have enabled regional divisions based on population history. These variations among populations have been classified into broad geographical categories based on their specific combination of high, intermediate, and low morphological trait expression (Scott and Turner, 1997; Turner et al., 1991).

Western Eurasians are characterized by morphologically simple teeth overall (Mayhall et al., 1982). Sub-Saharan Africans have high frequencies of lower first molar cusp 7, Carabelli's cusp UM1, and cusps 5 and cusp 6 LM1. Sino-Americans exhibit higher frequencies of dental morphological variation and exhibit more morphological traits. The Sunda Pacific groups, in Polynesia and Micronesia, fall into the middle range for trait frequency. Finally, the Sahul-Pacific groups, Australia, New Guinea, and other Melanesian groups, exhibit high and intermediate frequencies, of several morphological traits (Townsend et al., 1990; Hanihara, 1968). Although there is evidence for global-scale variations in morphological trait frequencies there is also regional variation that can indicate variations within the broad dental complexes. The ASUDAS system is the most widely used and useful method for scoring and evaluating dental nonmetric traits. The use of this standardized system minimizes observer error and enables the use of common terminology. Only those

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traits that have been associated with genetic heritability are included in the system (Nichol and Turner, 1986; Scott and Turner, 1997).

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Appendix IV

Figure 55. Two-dimensional scatterplot of the Nebringen (NEB) sample relative to the other samples based on geographic (x-axis) versus phenetic (y-axis) distances. Solid black linear equation reference line with slope (b) of 1 and y-intercept (a) of 0 provided (i.e., y=0+1x, where y=a+bx) to illustrate where the other sample would be if a 1:1 correspondence existed between the distances. Ger (German); DUR (Dürrnberg); POTT (Pottenbrunn); HALD (Hallstatt D); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack); Pon (Pontecagnano).

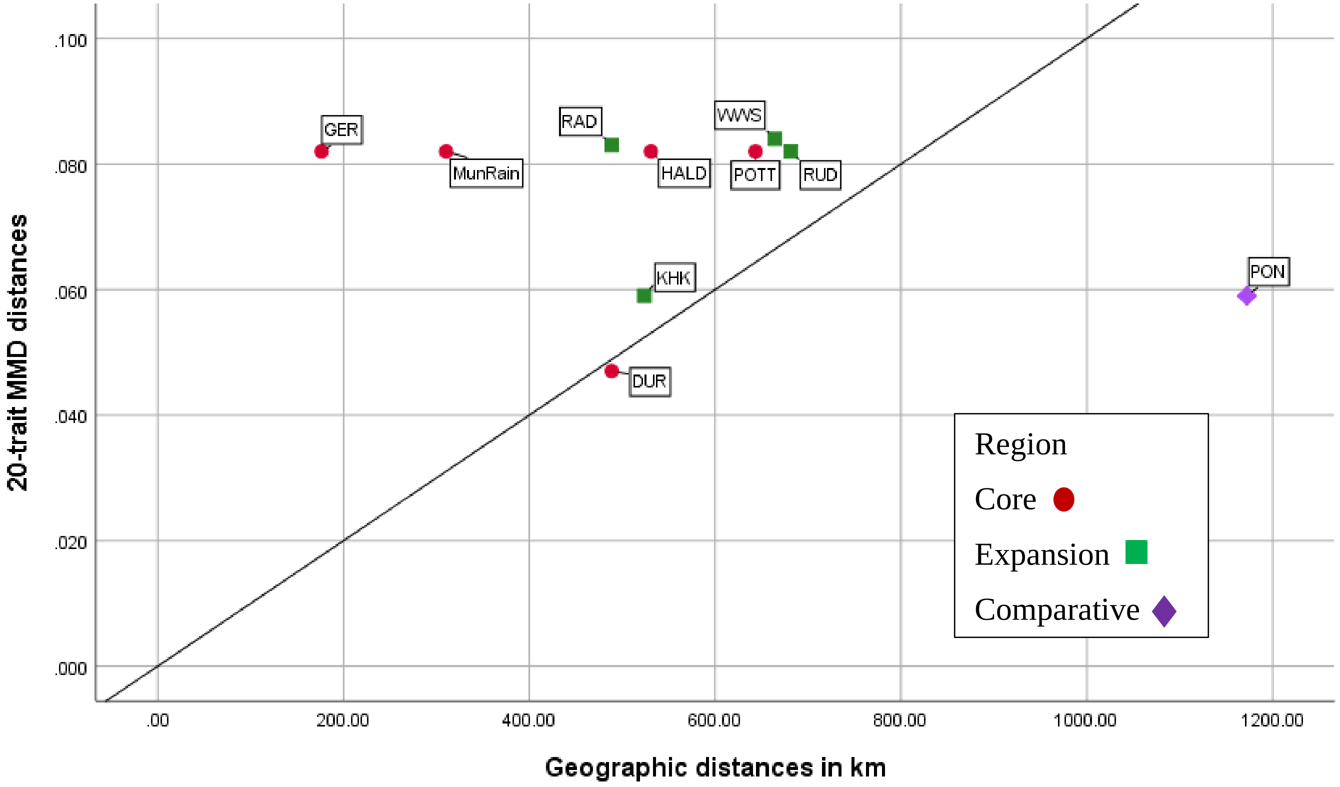


Figure 56. Two-dimensional scatterplot of the Pottenbrunn (POTT) sample relative to the other samples based on geographic (x-axis) versus phenetic (y-axis) distances. Solid black linear equation reference line with slope (b) of 1 and y-intercept (a) of 0 provided (i.e., y=0+1x, where y=a+bx) to illustrate where the other sample would be if a 1:1 correspondence existed between the distances. Ger (German); DUR (Dürrnberg); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack); Pon (Pontecagnano).

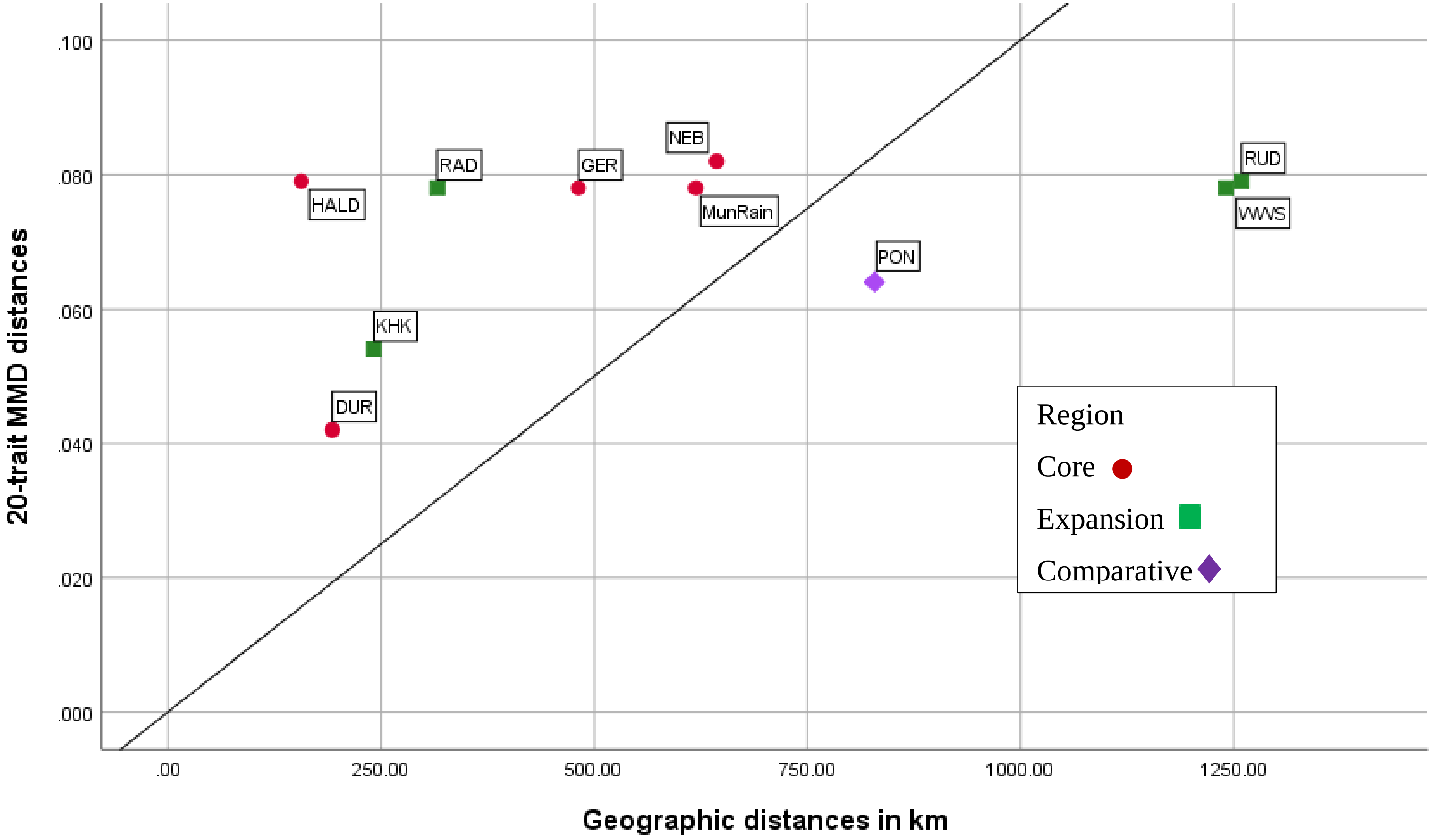


Figure 57. Two-dimensional scatterplot of the Dürrnberg (DUR) sample relative to the other samples based on geographic (x-axis) versus phenetic (y-axis) distances. Solid black linear equation reference line with slope (b) of 1 and y-intercept (a) of 0 provided (i.e., y=0+1x, where y=a+bx) to illustrate where the other sample would be if a 1:1 correspondence existed between the distances. HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); POTT (Pottenbrunn); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack); Pon (Pontecagnano).

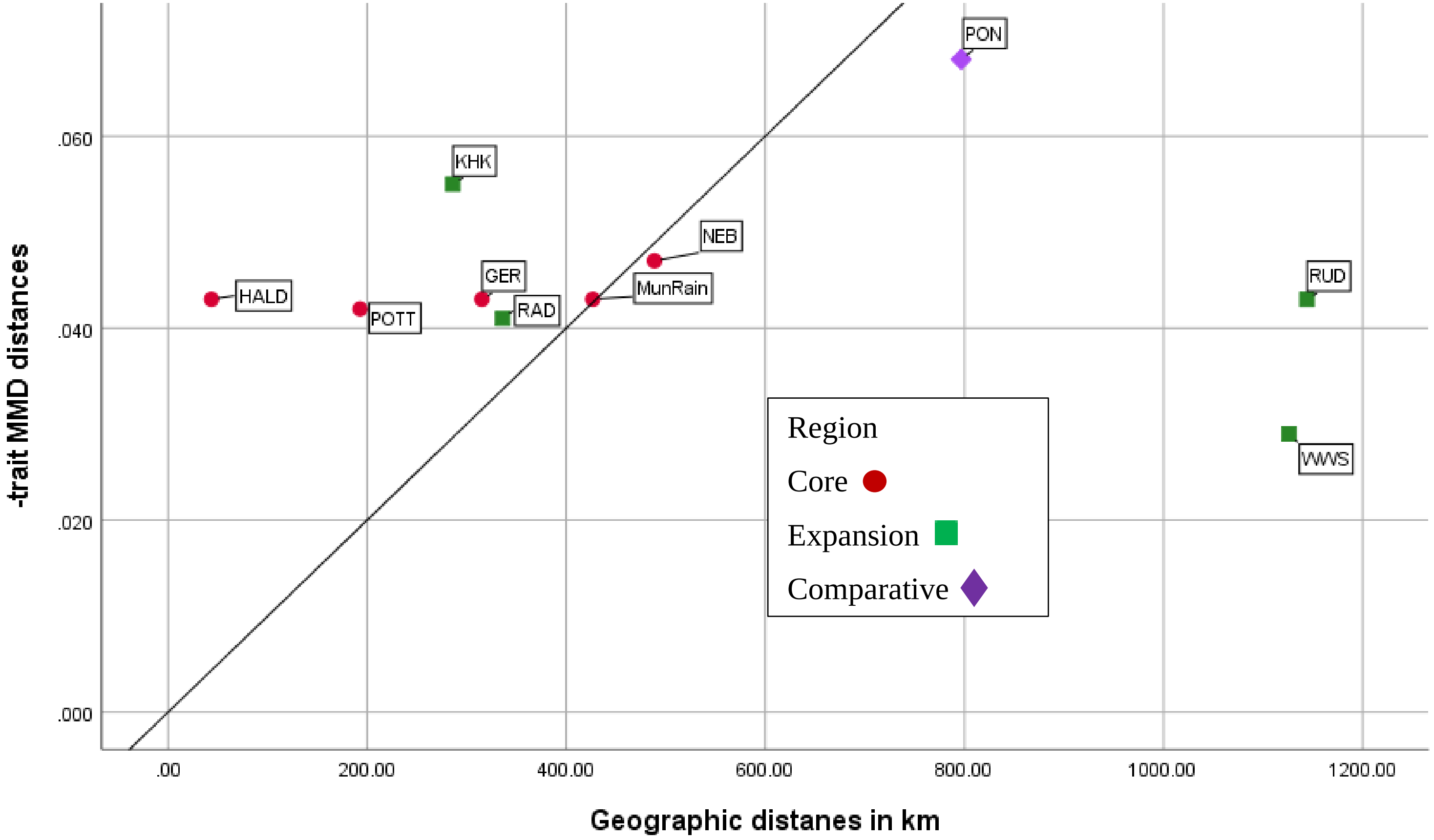


Figure 58. Two-dimensional scatterplot of the Münsingen-Rain (MunRain) sample relative to the other samples based on geographic (x-axis) versus phenetic (y-axis) distances. Solid black linear equation reference line with slope (b) of 1 and y-intercept (a) of 0 provided (i.e., y=0+1x, where y=a+bx) to illustrate where the other sample would be if a 1:1 correspondence existed between the distances. DUR (Dürrnberg); HALD (Hallstatt D); German (GER); NEB (Nebringen); POTT (Pottenbrunn); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack); Pon (Pontecagnano).

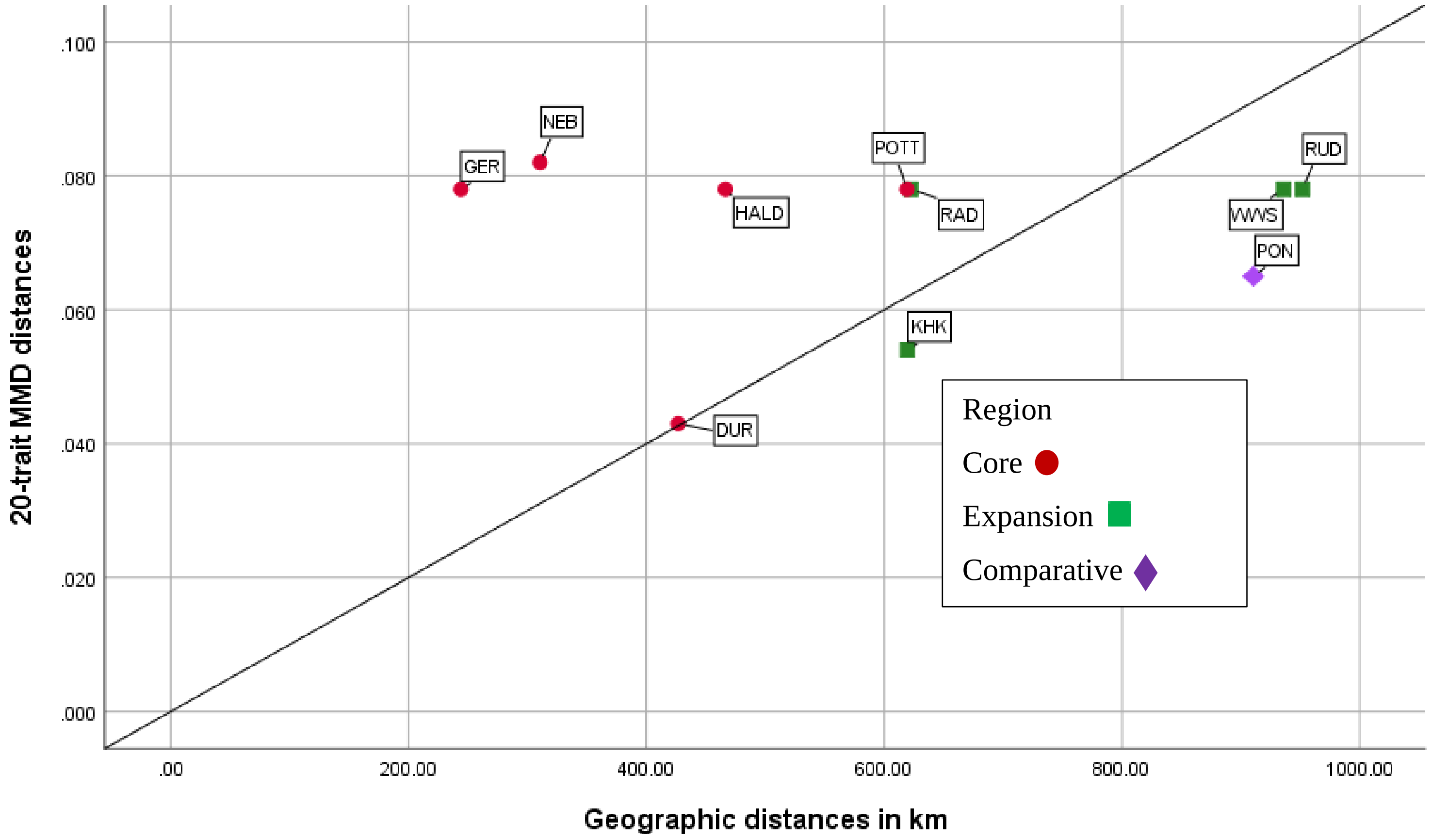


Figure 59. Two-dimensional scatterplot of the Hallstatt D (HALD) sample relative to the other samples based on geographic (x-axis) versus phenetic (y-axis) distances. Solid black linear equation reference line with slope (b) of 1 and y-intercept (a) of 0 provided (i.e., y=0+1x, where y=a+bx) to illustrate where the other sample would be if a 1:1 correspondence existed between the distances. DUR (Dürrnberg); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); POTT (Pottenbrunn); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack); Pon (Pontecagnano).

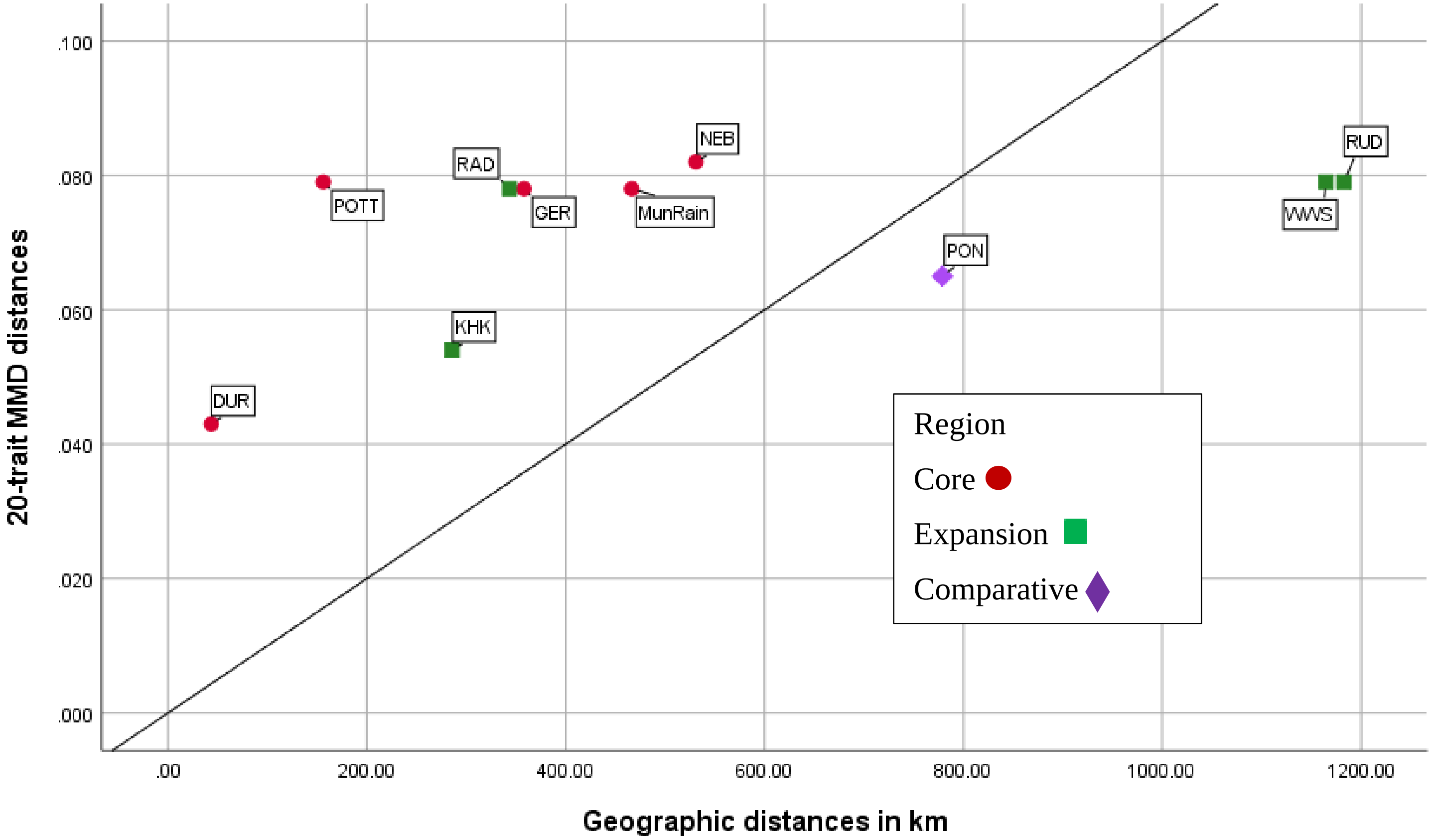


Figure 60. Two-dimensional scatterplot of the Kutná-Hora-Karlov (KHK) sample relative to the other samples based on geographic (x-axis) versus phenetic (y-axis) distances. Solid black linear equation reference line with slope (b) of 1 and y-intercept (a) of 0 provided (i.e., y=0+1x, where y=a+bx) to illustrate where the other sample would be if a 1:1 correspondence existed between the distances. DUR (Dürrnberg); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); POTT (Pottenbrunn); RAD (Radovesice); RUD (Rudston Makeshift); WWS (Wetwang Slack); Pon (Pontecagnano).

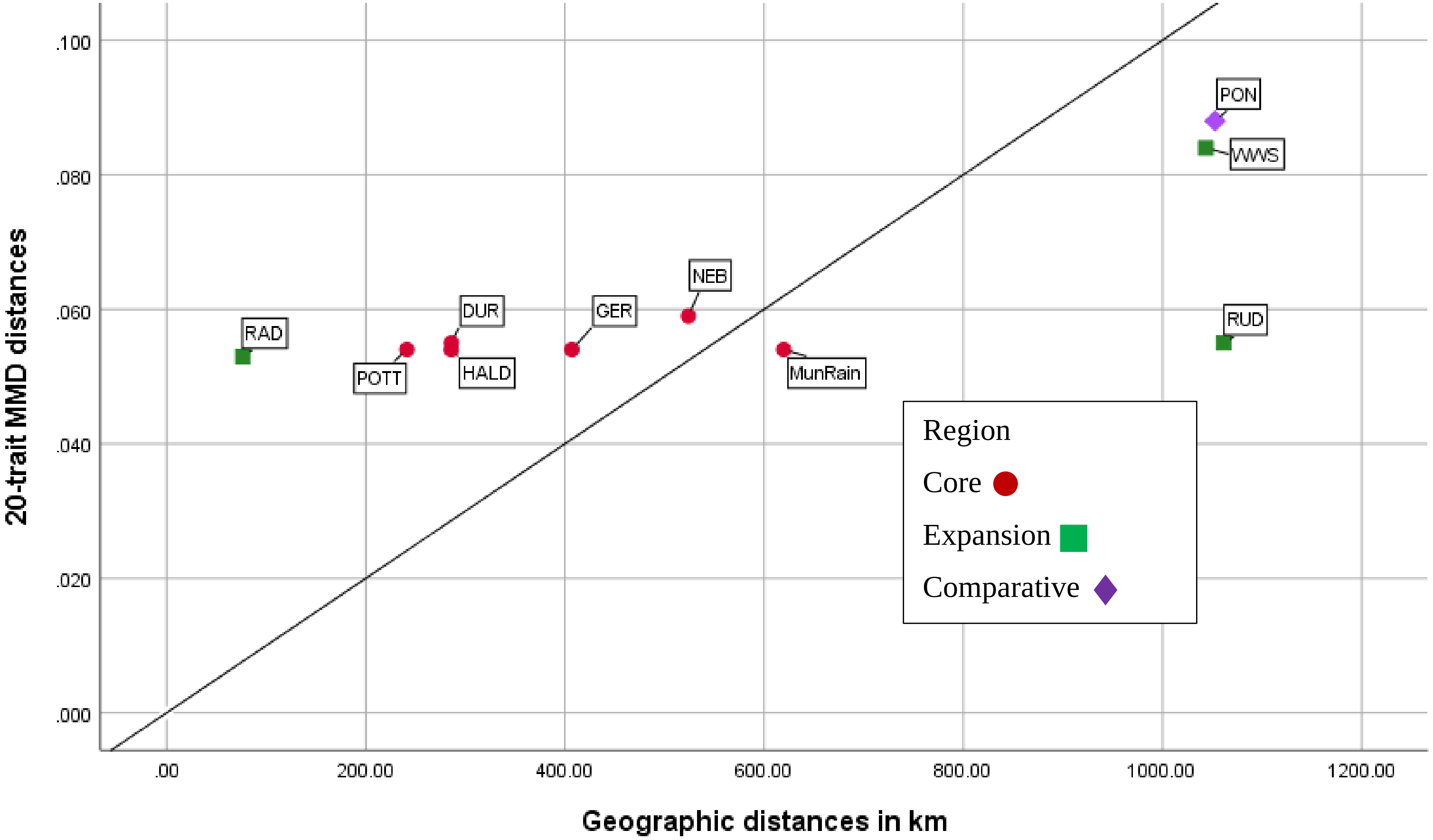


Figure 61. Two-dimensional scatterplot of the Rudston Makeshift (east Yorkshire, Britain) (RUD) sample relative to the other samples based on geographic (x-axis) versus phenetic (y-axis) distances. Solid black linear equation reference line with slope (b) of 1 and y-intercept (a) of 0 provided (i.e., y=0+1x, where y=a+bx) to illustrate where the other sample would be if a 1:1 correspondence existed between the distances. DUR (Dürrnberg); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); POTT (Pottenbrunn); RAD (Radovesice); KHK (Kutná-Hora-Karlov); WWS (Wetwang Slack); Pon (Pontecagnano).

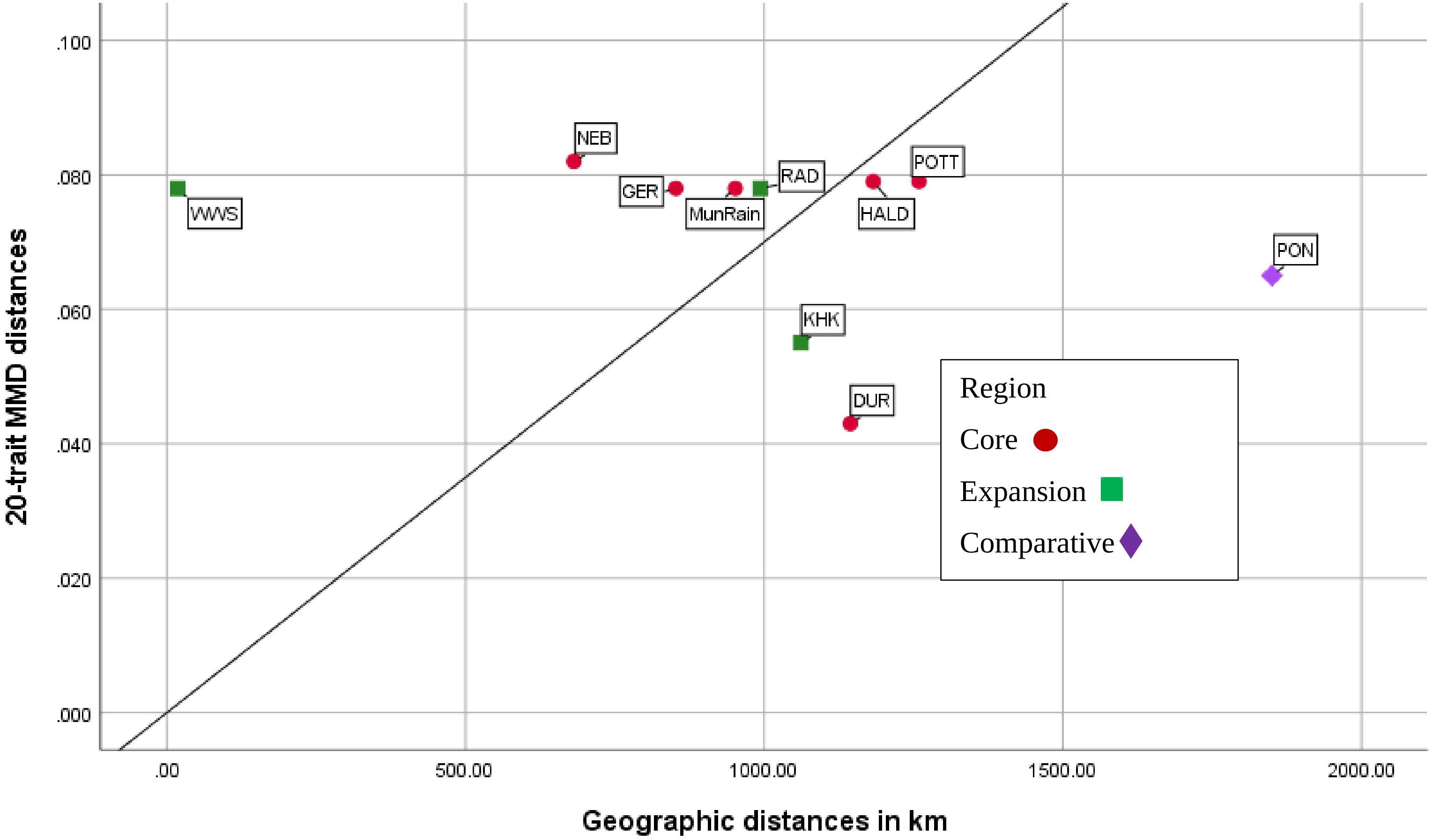
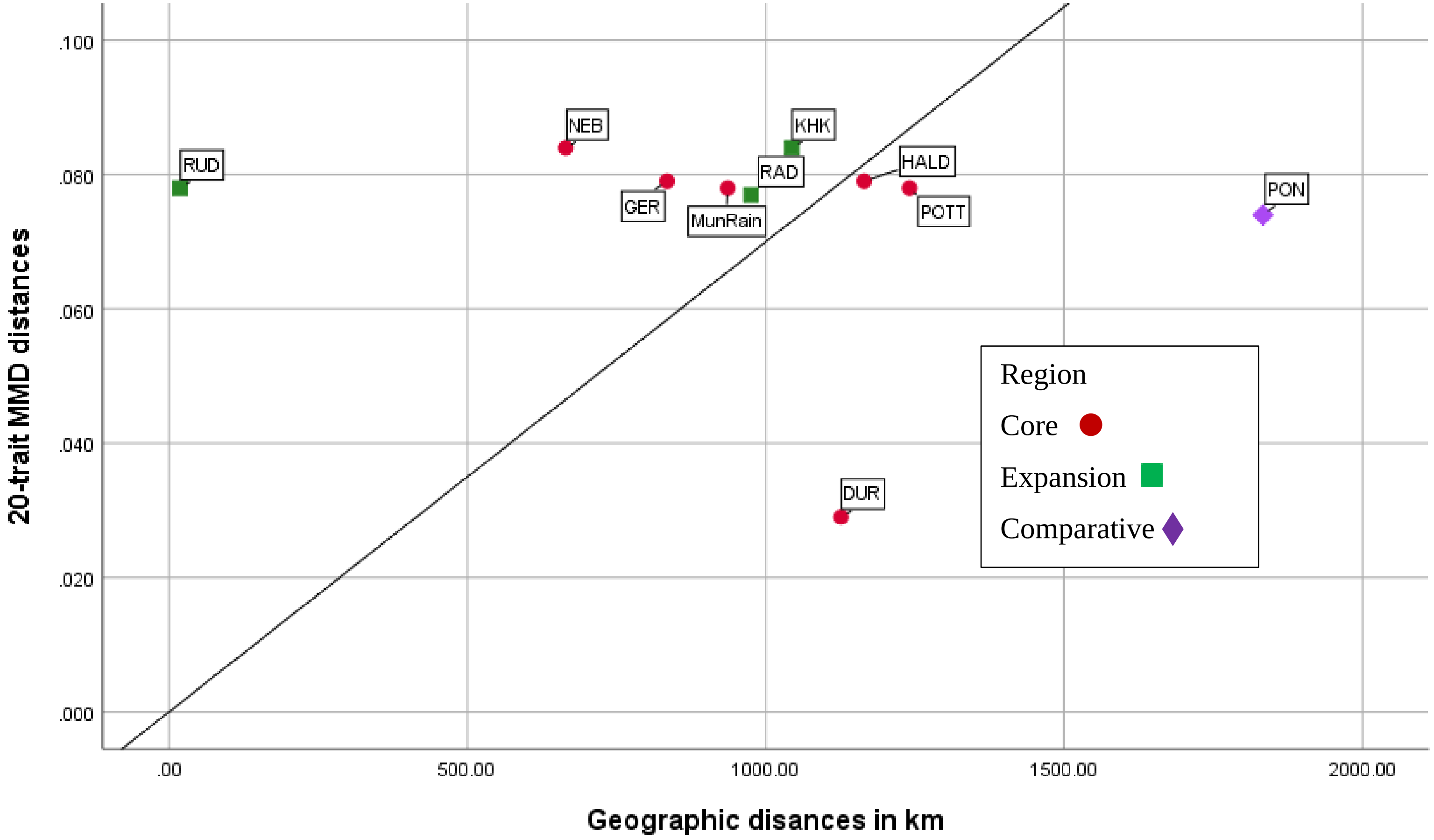


Figure 62. Two-dimensional scatterplot of the Wetwang Slack (east Yorkshire, Britain) (WWS) sample relative to the other samples based on geographic (x-axis) versus phenetic (y-axis) distances. Solid black linear equation reference line with slope (b) of 1 and y-intercept (a) of 0 provided (i.e., y=0+1x, where y=a+bx) to illustrate where the other sample would be if a 1:1 correspondence existed between the distances. DUR (Dürrnberg); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); POTT (Pottenbrunn); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); Pon (Pontecagnano).



Appendix V

Table 16. Rotated component matrix for the first 2 components.

	Component	
Trait *	**PCA 1**	**PCA 2**
Eigenvalue	10.285	6.225
Variance	47.855	34.277
Total Variance	47.855	82.133
Labial Curvature UI1	.361	**-.576**
Interruption groove UI2	-.146	.370
Tuberculum Dentale UI2*	.451	**-.889**
Distal accessory ridge UC*	.278	**-.805**
Hypocone UM2*	-.032	-.376
Cusp 5 UM1	**-.547**	.373
Carabelli's trait UM1	**-.777**	.401
Parastyle UM3*	**-.576**	**-.776**
Enamel extension UM1*	.016	**.696**
Root number UP1*	**.995**	-.116
Root number UM2*	**.802**	**.795**
Lingual cusp LP2*	**.992**	.034
Anterior fovea LM1*	**.996**	.027
Groove pattern LM2*	**.694**	**.721**
Rocker jaw	-.418	.398
Cusp number LM1*	.463	**.881**
Cusp number LM2*	-.456	**-.880**
Deflecting wrinkle LM*	**.976**	.211
C1–C2 crest LM1*	**.935**	-.348
Protostylid LM1*	**-.949**	-.318
Tome's root LP1*	**-.952**	.184
Root number LC*	-.153	**.949**
Root number LM1*	**-.968**	.210

*Denotes the 20 final traits used for MMD analysis after editing (Table 9). Boldface numbers indicate "strong" loadings (i.e., > |0.500|).

Table 16 continued. Rotated component matrix for the first 2 components.

	Component	
Trait *	**PCA 1**	**PCA 2**
Root number LM2*	**-.734**	-.093
Torsomolar angle LM3*	**-.916**	.392

*Denotes the 20 final traits used for MMD analysis after editing (Table 9). Boldface numbers indicate “strong” loadings (i.e., > |0.500|).

Appendix VI

Table 17. Component loadings, eigenvalues and variance for the for the first 3 components explained for the samples.

	Component		
Trait*	**1**	**2**	**3**
Eigenvalue	12.440	8.261	4.222
Variance	47.855	34.277	5.089
Total Variance	47.855	82.133	87.221
Labial Curvature UI1	.362	**-.556**	-.217
Interruption groove UI2	-.156	.416	-.461
Tuberculum dentale UI2*	.487	**-.866**	-.017
Distal accessory ridge UC*	.321	**-.832**	.169
Hypocone UM2	-.215	-.427	.421
Cusp 5 UM1	**-.511**	.464	-.004
Carabelli’s trait UM1*	**-.851**	.319	.101
Parastyle UM3*	**-.524**	**-.803**	.070
Enamel extension UM1*	.022	**.669**	.294
Root number UP1*	**.797**	-.056	-.039
Root number UM2*	**.790**	**.607**	-.009
Lingual cusp LP2*	**.994**	.090	.011
Anterior fovea LM1*	**.895**	.035	-.046
Groove pattern LM2*	**.648**	**.754**	-.014
Rocker jaw	-.432	.353	.111
Cusp number LM1*	.406	**.703**	-.017
Cusp number LM2*	-.416	**-.802**	.013
Deflecting wrinkle LM*	**.864**	.259	-.015
C1–C2 crest LM1*	**.752**	-.302	-.015
Protostylid LM1*	**-.729**	-.364	.013
Tome’s root LP1*	**-.882**	.164	-.018
Root number LC*	-.202	**.866**	-.014
Root number LM1*	**-.782**	.162	-.013
Root number LM2*	**-.735**	-.130	-.025
Torsomolar angle LM3*	**-.835**	.342	-.005

*Denotes the 20 final traits used for MMD analysis after editing (Table 9). Boldface numbers indicate “strong” loadings (i.e., > |0.500|).

Figure 63. Three-dimensional scatterplot of the first three components among the samples for 25 dental traits. The first three components account for 87.22% of the total variance (47.85% on the x-axis, 34.27% on the y-axis and 5.08% on the z-axis). Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

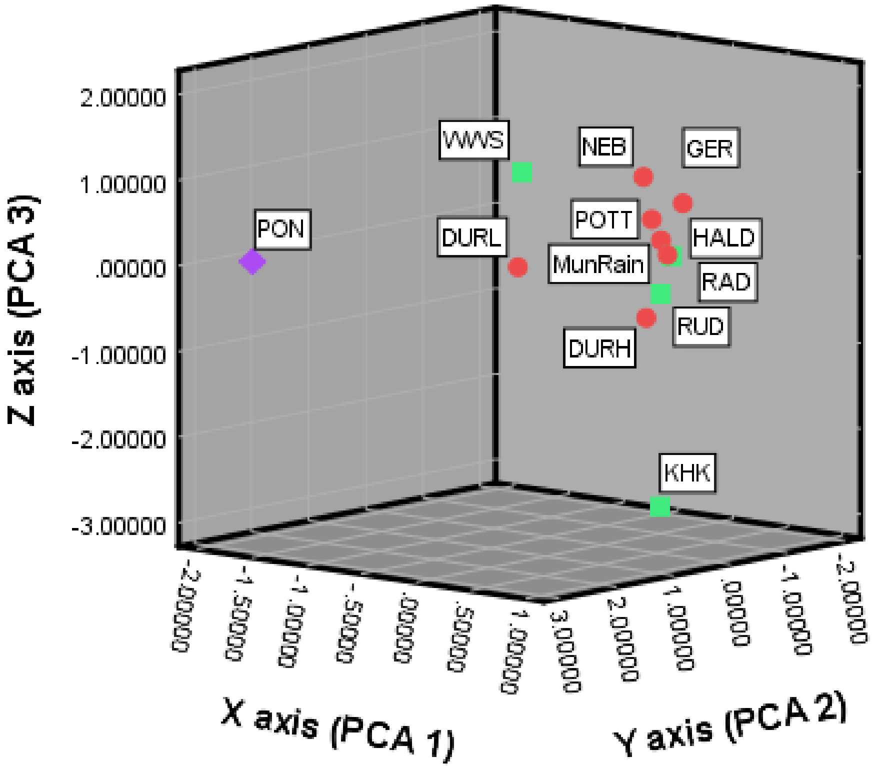


Table 18. Rotated component matrix for the first 3 components.

	Component		
Trait*	**PCA 1**	**PCA 2**	**PCA 3**
Eigenvalue	12.440	8.261	4.222
Variance	47.855	34.277	5.089
Total Variance	47.855	82.133	87.221
Distal accessory ridge UC*	.278	**-.805**	.274
Hypocone UM2*	-.032	-.376	.463
Cusp 5 UM1	**-.547**	.373	-.117
Carabelli's trait UM1	**-.777**	.401	.086
Parastyle UM3*	**-.576**	**-.776**	.130
Enamel extension UM1*	.016	**.696**	.216
Root number UP1*	**.995**	-.116	-.018
Root number UM2*	**.802**	**.795**	-.035
Lingual cusp LP2*	**.992**	.034	.051
Anterior fovea LM1*	**.996**	.027	-.036
Groove pattern LM2*	**.694**	**.721**	-.063
Rocker jaw	-.418	.398	.028
Cusp number LM1*	.463	**.881**	-.058
Cusp number LM2*	-.456	**-.880**	.090
Deflecting wrinkle LM*	**.976**	.211	-.006
C1–C2 crest LM1*	**.935**	-.348	-.065
Protostylid LM1*	**-.949**	-.318	.011
Tome's root LP1*	**-.952**	.184	-.008
Root number LC*	-.153	**.949**	-.0129
Root number LM1*	**-.968**	.210	-.080
Root number LM2*	**-.734**	-.093	-.051
Torsomolar angle LM3*	**-.916**	.392	-.089

*Denotes the 20 final traits used for MMD analysis after editing (Table 9). Boldface numbers indicate "strong" loadings (i.e., > |0.500|).

Appendix VII

Three-dimensional MDS ALASCAL graphs of the MMD distances among the samples.

Figure 64. Three-dimensional MDS graph of the 25 trait MMD distances among the samples. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

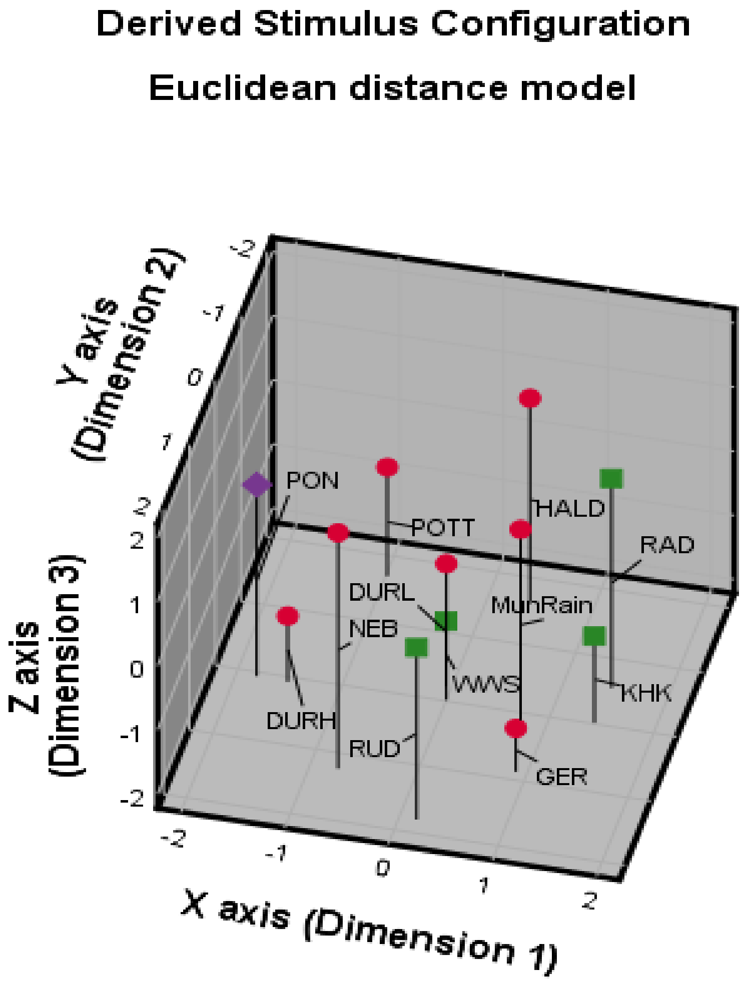


Figure 65. Three-dimensional MDS graph of the 20 trait MMD distances among all the samples. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).

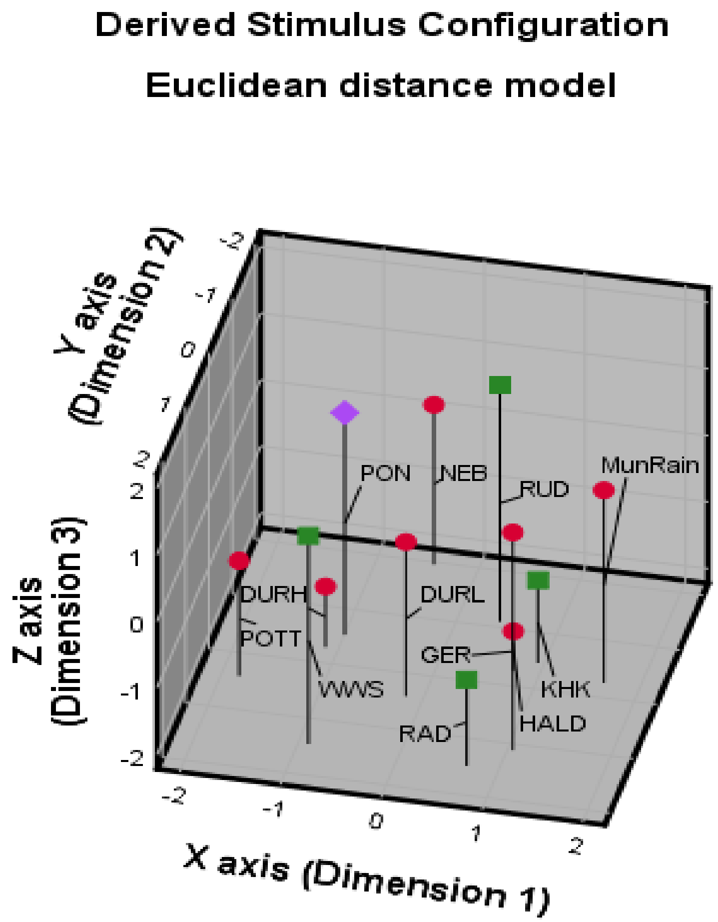
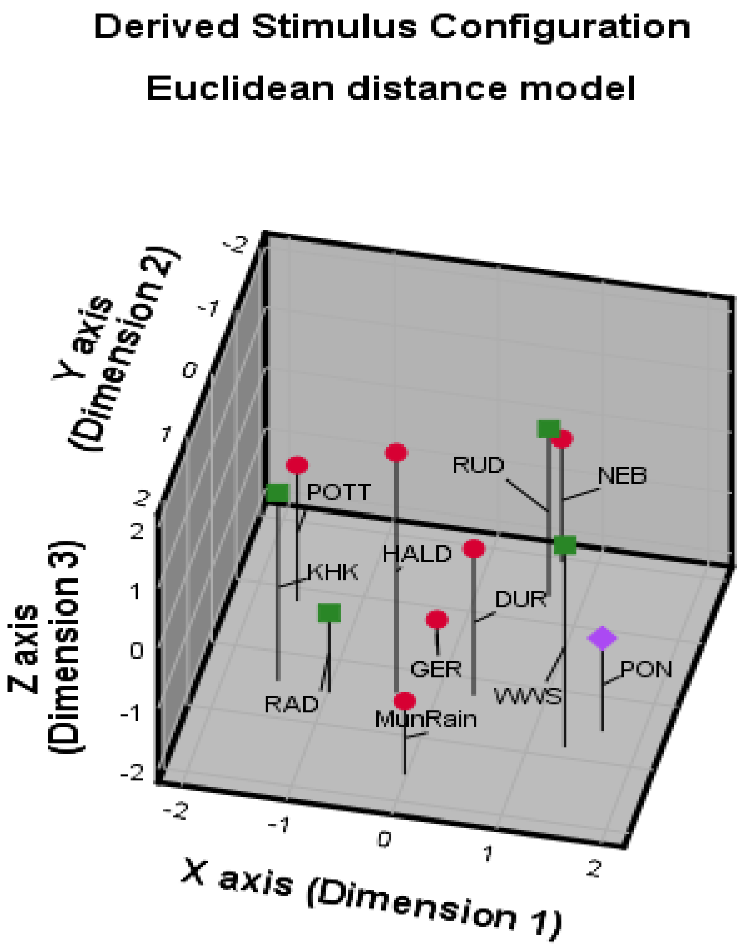


Figure 66. Three-dimensional MDS graph of the 20 trait MMD distances among the samples, with the Dürrnberg sample combined. Dürrnberg La Tène (DURL); Dürrnberg Hallstatt (DURH); Pottenbrunn (POTT); HALD (Hallstatt D); German (GER); NEB (Nebringen); MunRain (Münsingen-Rain); RAD (Radovesice); KHK (Kutná-Hora-Karlov); RUD (Rudston Makeshift); WWS (Wetwang Slack).



Appendix VIII

This appendix summarises information about the individuals excavated and the methods used by the recording osteologist to determine age-at-death and estimate sex for adults. It details the number of individuals included or excluded from this analysis, and sample demography.

Hallstatt D, Austria

Initial excavations led by Johann Georg Ramsauer were conducted from 1846-1863. Further excavations continued off and on until 1899. Further excavations were led by Frederick Morton and continued from 1937-1939 (See page 141) (Hodson, 1990). The burials analysed in this thesis comprise a group of 44 burials excavated by Frederick Morton.

Age-at-death determinations

The specific age-at-death categories in the original site reports for the Hallstatt cemetery are not present in the site archive (Hodson, 1990). Furthermore, the majority of the recovered skeletal material are too fragmentary to adequately determine these categories (See page 141). However, Hodson (1990) assigned age categories to the remains: sub-adult (juvenile 16-20 years old), adult (20-50 years old), and mature adult (50+ years old). These categories were based on tooth eruption, epiphyseal and cranial suture closure (Hodson, 1990, page 22). Consequently, those individuals, adults and sub-adults, with permanent dentitions were selected for this analysis (See page 141).

Sex estimations

Sex was estimated through examination of secondary sex characteristics of the skull and pelvis (Hodson, 1990, page 22). However, the specific methods used to estimate sex were not described (Hodson, 1990, page 22).

Number of individuals recovered

Although in total 1,045 burials were uncovered, the majority were cremations (Hodson, 1990). It is unknown how many inhumations were recovered from the other phases of excavation or temporal periods from the Hallstatt cemetery, as the initial excavation reports are not available (Hodson, 1990). In total 44 individuals were recovered from the HaD phase of this cemetery (See pages 138, 141, Table 8).

Total number of individuals, males, females and individuals of unknown sex, used in this analysis

In total 42 individuals, 12 males (11 adults, 1 sub-adult), 7 possible males (5 adults, 2 sub-adults), 6 females (4 adults, 2 sub-adults), 4 possible females (3 adults, 1 sub-adult), and 13 adult individuals of unknown sex, for whom nonmetric dental traits could be scored, were used in this analysis (Table 8). The 2 individuals excluded from this research represent 2 possible adult females.

German pooled sample, Stuttgart

These burials were excavated during the early to mid to late 1900s, in total 43 burials were uncovered (See page 143) (Balkwill, 1976; Burmeister, 2000; Dehn, 2013; Ebrecht et al., 2014; Gleirscher, 2006; Miron, 2012; Müller-Scheeßel, 2007; Paret, 1924, 1938; Stuck, 1985). As the excavation archive is not present (See below), the specific excavation locations and dates are not available (Burmeister, 2000; Gleirscher, 2006; Müller-Scheeßel, 2007).

Age-at-death determinations

The initial excavation reports for these burials have been lost, consequently the methods used to determine age-at death are unknown (archivist pers. comm Michael Franken) (Burmeister, 2000; Gleirscher, 2006; Müller-Scheeßel, 2007). Consequently, the age-at-death categories are described on an individual burial basis. These categories include, sub-adult (juvenile 17-20 years old) and adult (20-50 years old) **(**Burmeister, 2000; Dehn, 2013; Ebrecht et al., 2014; Gleirscher, 2006; Miron, 2012; Müller-Scheeßel, 2007; Stuck, 1985). The individuals recovered from these burials are commonly described based on sex and age categories e.g., adult male, but it is unknown how these designations were decided **(**Burmeister, 2000; Dehn, 2013; Ebrecht et al., 2014; Gleirscher, 2006; Miron, 2012; Müller-Scheeßel, 2007; Stuck, 1985). Due to this limitation, only individuals with permanent dentitions (adults and sub-adults), for whom age and sex designations had been provided were used in this analysis.

Sex estimations

Sex is presumed to have been estimated from examination of the pelvis and skull (Burmeister, 2000; Dehn, 2013; Ebrecht et al., 2014; Miron, 2012; Stuck, 1985).

Number of individuals recovered

In total, 43 inhumations were uncovered (Balkwill, 1976; Burmeister, 2000; Dehn, 2013; Ebrecht et al., 2014; Gleirscher, 2006; Miron, 2012; Müller-Scheeßel, 2007; Paret, 1924, 1938; Stuck, 1985) (See pages 138, 143, Table 8).

Total number of individuals, males, females and individuals of unknown sex, used in this analysis

Overall 35 individuals, 17 males (11 adults, 6 sub-adults), 7 possible adult males, 6 adult females, 2 possible adult females and 3 adult individuals of unknown sex for whom nonmetric dental traits could be scored, were used in this analysis (Table 8).The eight individuals included from this analysis include 3 adult females, 3 males (2 adults, 1 juvenile) and 2 adult individuals of unknown sex.

Münsingen-Rain, Switzerland

Excavations led by Jakob Wiedmer-Stern began in 1906 and subsequently uncovered 220 graves. However, only the skulls of 77 individuals determined to have “superior” preservation, were recovered and collected (See page 145) (Hodson, 1968; Jud, 1998).

Age-at-death determinations

The recovered individuals have been assigned to the following age-at-death categories, infant I (0-7 years old), infant II (7-12 years old), sub-adult (juvenile 12-20 years old), adult (20-50 years old), and mature (50+ years old) (Hodson, 1968, page 12; Jud, 1998; Müller et al., 2008). These categories were based on analyses of tooth eruption, and cranial suture closure (Hodson, 1968, page 12; Jud, 1998; Müller et al., 2008).

Sex estimations

Sex was determined through examination of secondary sex characteristics of the skull, as only the skulls are available for analysis (Hodson, 1968, page 12; Hung, 1962; Jud, 1998;

Müller et al., 2008). Consequently, the sex estimations are described as possible male, possible female and unknown (Hodson, 1968, page 12; Hung, 1962; Jud, 1998; Müller et al., 2008). However, the specific methods used to estimate sex were not described (Hodson, 1968, page 12; Hung, 1962; Jud, 1998; Müller et al., 2008).

Number of individuals recovered

Although 220 burials have been recorded from the Münsingen-Rain cemetery only 77 individuals were recovered and collected (See pages 138, 145, Table 8) (Hodson, 1968; Jud, 1998).

Total number of individuals, males, females and individuals of unknown sex, used in this analysis

In total 42 individuals, 21 possible males (17 adults, 4 sub-adults), 19 possible females (16 adults, 3 sub-adults) and 2 adult individuals of unknown sex, for whom nonmetric dental traits could be scored, were used in this analysis (Table 8). The 35 individuals excluded from this research include 12 possible females (8 adults, 4 sub-adults), 15 possible males (11 adults, 4 sub-adults) and 8 adult individuals of unknown sex.

Other/notes

Due to the global Covid-19 pandemic, the author is unable to provide images with a scale bar for Figures 33-35, 51-54 (See pages 183, 185-186, 394, 397, 399-400).

Individuals used in stable isotopic analysis, Scheeres (2014a), Scheeres et al (2014b) and Moghaddam et al (2014).

The bolded numbers represent those individuals also used in this analysis.

Scheeres (2014a), Scheeres et al (2014b) and Moghaddam et al (2014) conducted a stable isotopic analyses on several of the individuals from this cemetery including burials **6, 8a, 8b, 9, 10, 12, 13a, 14, 16, 17, 19, 20, 26, 28**, 31, 32, **40, 42, 43, 48, 52**, 56, 63, **69, 72, 78, 91, 121**, 122, **130, 134, 135, 149, 152, 156, 157, 158,** and **175** (See page 145).

Nebringen, Stuttgart, Germany

Rescue excavations were conducted in 1959 after road construction uncovered 6 graves (Krämer, 1964). Overall, 26 burials, 21 inhumations, 4 cremations and a few isolated skeletal fragments from an additional unidentified grave were recovered (See page 149, Table 8) (Krämer, 1964). Some burials are believed to have been lost due to construction, agricultural or taphonomic processes, such as erosion. Consequently, the number of burials is believed to have been as high as 35 (Krämer, 1964, 1966; Scholz et al., 1999).

Age-at-death determinations

The following age-at-death determinations have been used to describe the individuals recovered from Nebringen (Stuttgart, Germany), infant I (0-7 years old), infant II (7-14 years old), sub-adult (juvenile 14-21 years old), adult (21-45 years old), mature (45-60 years old) and senile (>60 years old) (Krämer, 1964, page 25, 1966; Scholz et al., 1999). The above categories were established based on tooth eruption, cranial suture, epiphyseal and cranial suture closure (Krämer, 1964, page 25, 1966; Scholz et al., 1999).

Sex estimations

Sex estimations were based on examination of the skull and pelvis, however, the specific methods above used to construct these categories is not recorded in the site archive (Krämer, 1964, 1966; Scholz et al., 1999).

Number of individuals recovered

In total 26 burials, 21 inhumations, 4 cremations were uncovered (See pages 138, 149, Table 8) (Krämer, 1964)

Total number of individuals, males, females and individuals of unknown sex, used in this analysis

In total 22 individuals, 8 males (7 adults, 1 sub-adults), 2 possible adult males, 6 females (5 adults, 1 sub-adult), 2 adult possible females, and 4 adult individuals of unknown sex, for whom nonmetric dental traits could be scored, were used in this analysis (Table 8). The remaining 4 individuals excluded from this research represent 1 adult female, 1 adult male and 2 adult individuals of unknown sex.

Other/notes

Due to the global Covid-19 pandemic, the author is unable to provide images with a scale bar for Figures 33-35, 51-54 (See pages 183, 185-186, 394, 397, 399-400).

Individuals used in stable isotopic analysis (Scheeres 2014a), Scheeres et al (2014b)

The bolded numbers represent those individuals also used in this analysis. Scheeres (2014a) and Scheeres et al (2014b) conducted a stable isotopic analysis on several of the burials from this cemetery including burials **1, 2, 3, 4, 5, 6, 8, 9, 12**, 14, 17, **18, 19, 20**, 23, **24**, and **25** (See page 149).

Pottenbrunn, Austria

Excavations, led by J Bayer in the early twentieth century, uncovered 2 burials dating to the HaC/HaD period and 12 dating to the La Tène period (See page 152) (Bayer, 1930; Neugebauer, 1991; Ramsl, 2002). Rescue excavations in the 1970s, led by JW Neugebauer and P Scherrer, continued off and on until 1982 (Neugebauer, 1991, 1992; Ramsl, 2002).

Age-at-death determinations

The age-at-death designations used for the recovered individuals from Pottenbrunn (Austria) include, infant I (0-7 years old), infant II (7-14 years old), sub-adult (juvenile 14-21 years old), adult (21-45 years old), mature adult (45-60 years old) and senile (>60 years old) (Ramsl, 2002, page 20). The above categories were established based on tooth eruption, epiphyseal and cranial suture closure (Ramsl, 2002, page 20).

Sex estimations

Sex was estimated using the morphology of the skull and pelvis (Ramsl, 2002, page 20). However, the specific methods used to estimate sex were not described (Ramsl, 2002, page 20).

Number of individuals recovered

In total, 46 inhumations, including several double burials, and 11 cremations were uncovered (Ramsl, 2002) (See pages 138, 152, Table 8).

Total number of individuals, males, females and individuals of unknown sex, used in this analysis

In total 41 individuals, 14 males (11 adults, 3 sub-adults), 3 possible adult males, 7 adult females, 4 possible adult females and 13 individuals (8 adults, 5 sub-adults) of unknown sex, for whom nonmetric dental traits could be scored, were used in this analysis (Table 8). The individuals excluded from this research include 2 adult females, 1 adult male and 2 adult individuals of unknown sex (n=5).

Dürrnberg, Austria

Rescue excavations, in response to construction, led by O Klose and E Penninger, began in the Eislfeld, Friedhof and Lettenbuhl grave fields between 1928-1932 (See page 155) (Klose, 1932; Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015). Further excavations, led by F Moosleitner, were conducted from 1979-1982 in the Romersteig grave field. Additional excavations, led by JW Neugebauer and K Zeller, in the Friedhof and Lettenbuhl grave fields were carried out from 1983-1984, briefly in 1987, and again from 1996-1997 (Neugebauer, 1983, 1984; Tiefengraber and Wiltschke-Schrotta, 2015; Zeller, 1997, 2001). Continuous excavations from 1963-1997 were conducted in the Eislfeld grave field (See page 155) (Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015).

Age-at-death determinations

The following age-at-death designations are used for the recovered skeletal material from Dürrnberg, infant I (0-2 years old), infant II (2-10 years old), sub-adult (juvenile 10-20 years old), adult (20-50 years old), and Mature adult (50+ years old) (Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015; Wendling et al., 2015). Several methods have been used to establish these categories such as, tooth eruption, epiphyseal and cranial suture closure (Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015; Wendling et al., 2015). However, the majority of the recovered individuals are not described by their specific age-at-death determinations, rather they are described as belonging to a particular age category, e.g., adult or juvenile (Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015; Wendling et al., 2015). Furthermore, the specific methods used to establish the above categories are not described (Thorsten et al., 2017, page

662; Tiefengraber and Wiltschke-Schrotta, 2015, page 259; Wendling and Wiltschke-Schrotta, 2015, page 170; Wendling et al., 2015, page 180).

Sex estimations

Sex was assessed through examination of secondary sex characteristics of the skull and pelvis (Thorsten et al., 2017; Tiefengraber and Wiltschke-Schrotta, 2015; Wendling and Wiltschke-Schrotta, 2015; Wendling et al., 2015). However, the specific methods used to estimate sex were not described (Thorsten et al., 2017, page 662; Tiefengraber and Wiltschke-Schrotta, 2015, page 259; Wendling and Wiltschke-Schrotta, 2015, page 170; Wendling et al., 2015, page 180).

Number of individuals recovered

Overall, 128 individuals, 48 dating to the Hallstatt period and 80 to the La Tène period, recovered from the Friedhof, Lettenbuhl, Romersteig and Eislfeld grave fields within the Dürrnberg cemetery and were used this analysis (See pages 138, 155, Table 8).

Total number of individuals, males, females and individuals of unknown sex, used in this analysis

In total 35 individuals from the Hallstatt period including 11 males (10 adults, 1 sub-adult), 3 possible males (2 adults, 1 sub-adult), 9 females (8 adults, 1 sub-adult), 2 possible adult females and 10 adult individuals of unknown sex, date to the Hallstatt period. The individuals excluded from this analysis include 3 adult females, 3 possible females (2 adults, 1 sub-adult), 3 adult males, 1 possible adult male and 3 adult unknown individuals (n=13). In total, 67 individuals from the La Tène period including 24 males (21 adults, 3 sub-adults), 8 possible males (5 adults, 3 sub-adults), 12 females (10 adults, 2 sub-adults), 7 possible adult females and 16 individuals (13 adults, 3 sub-adults), of unknown sex. The 13 individuals excluded from this analysis from the La Tène period include 4 females (3 adults, 1 sub-adult), 2 possible adult females, 3 adult males, 1 possible adult male and 3 adult individuals of unknown sex. These individuals include those for whom nonmetric dental traits could be scored, were used in this analysis (See page 155, Table 8). Overall, the Dürrnberg sample is comprised of 102 individuals from the above periods.

Other/notes

Due to the global Covid-19 pandemic, the author is unable to provide images with a scale bar for Figures 33-35, 51-54 (See pages 183, 185-186, 394, 397, 399-400).

Radovesice I and II, Czech Republic

Rescue excavations at the Radovesice I cemetery began in 1974 and further excavations were conducted in 1976 (Budinský and Waldhauser, 2004; Waldhauser, 1987, 1993, 1999). At Radovesice II excavations were carried out in 1981 (See page 164) (Budinský and Waldhauser, 2004).

Age-at-death determinations

The recovered individuals from Radovesice I and II have been categorized into the following age-at-death cohorts, infant I (0-6 years old), infant II (6-10 years old), sub-adult (juvenile 10-17 years old) adults (17-40 years old), and mature adult (40-60 years old) (Budinský and Waldhauser, 2004; Herrmann et al., 1990, page 25). These age designations were constructed based on epiphyseal and cranial suture closure (Budinský and Waldhauser, 2004; Waldhauser, 1993; Herrmann et al., 1990, page 25). However, the specific methods used to create the initial age-at-death determinations were not described (Budinský and Waldhauser, 2004; Waldhauser, 1993; Herrmann et al., 1990, page 25).

Sex estimations

Sex was estimated using the skull and pelvis morphology (Budinský and Waldhauser, 2004; Waldhauser, 1993; Herrmann et al., 1990, page 26). However, the specific methods used to achieve these designations were not described (Budinský and Waldhauser, 2004; Waldhauser, 1993; Herrmann et al., 1990, page 26).

Number of individuals recovered

The recovered skeletal material from Radovesice I and II is highly fragmented, therefore it is unknown whether the recovered individuals represent the entire cemetery population (Budinský and Waldhauser, 2004; Waldhauser, 1993). Although 34 inhumations, three cremations and 23 inhumations have been recovered from Radovesice I and II, respectively, only 33 individuals have been identified to a specific age-at-death category (21 adults, 2 sub-adults, 8 mature individuals, and 2 infants II (See page 164, Table 8) (Budinský and Waldhauser, 2004; Waldhauser, 1993; Herrmann et al., 1990; Scheeres et al., 2014b). In total 57 individuals were recovered from the Radovesice I and II cemeteries (See pages 138, 164) (Budinský and Waldhauser, 2004; Waldhauser, 1993; Herrmann et al., 1990; Scheeres et al., 2014b).

Total number of individuals, males, females and individuals of unknown sex, used in this analysis

In total 40 individuals, 12 males (10 adults, 2 sub-adults), 8 possible males (6 adults, 2 sub-adults), 9 females (8 adults, 1 sub-adult), 5 possible females (4 adults, 1 sub-adult), and 6 individuals (5 adults, 1 sub-adult) of unknown sex, for whom nonmetric dental traits could be scored, were used in this analysis (Table 8). The 17 individuals excluded from this research represent 6 females, 3 possible females, 2 males, 2 possible males and 4 individuals of unknown sex.

Other/notes

Individuals used in stable isotopic analysis, Scheeres (2014a), Scheeres et al (2014b)

The bolded numbers represent those individuals also used in this analysis.

Scheeres (2014a) and Scheeres et al (2014b) conducted a stable isotopic analysis on several of the burials from this cemetery including burials **1, 2, 3,** 11, 13, **14, 16, 20, 21, 22, 24, 25, 31a,** 31b, 33, **34, 35, 36, 5, 6, 7**, 8, **9, 10, 11, 12**, **13, 14, 15**, 17, **18, 19, 20**, **21, 22**, and 23 (See page 164).

Kutná-Hora-Karlov, Czech Republic

Rescue excavations were conducted from 1988-1989 (See page 168) (Valentová, 1991, 1993; Valentová and Sankot, 2012).

Age-at-death determinations

The following age-at-death categories have been used to describe the recovered individuals from Kutná-Hora-Karlov cemetery, infant I (0-2 years old), infant II (2-10 years old), sub-adult (juvenile 10-18 years old), adult (18-35 years old), mature I (35-50 years old) and mature II (50+ years old) (Valentová, 1991; Valentová and Sankot, 2012). These categories were constructed based on tooth eruption, epiphyseal and cranial suture closure (Valentová, 1991; Valentová and Sankot, 2012, page 286). However, the specific methods used to create the initial age-at-death cohorts were not described (Valentová, 1991; Valentová and Sankot, 2012, page 286).

Sex estimations

Sex was estimated through and examination of secondary sex characteristics of the skull and pelvis (Valentová, 1991; Valentová and Sankot, 2012, page 286). However, the specific methods used to estimate sex were not described (Valentová, 1991; Valentová and Sankot, 2012, page 286).

Number of individuals recovered

Some of the recovered skeletal material from Kutná-Hora-Karlov is highly fragmented, as the burials were discovered during the course of construction (Valentová and Sankot, 2012; Valentová, 2002, 2003). In total, 48 inhumation**s** and one cremation burial were recovered (Valentová, 1991; Valentová and Sankot, 2012). However, only 51 individuals have been identified to a specific age-at-death category (3 infants, 3 sub-adults, 18 adults, 17 mature I and 10 mature II adults (See pages 138, 168, Table 8) (Valentová, 1991; Valentová and Sankot, 2012).

Total number of individuals, males, females and individuals of unknown sex, used in this analysis

In total 37 individuals, 11 males (7 adults, 3 sub-adults), 9 possible males (8 adults, 1 sub-adult), 7 females (6 adults, 1 sub-adult), 4 possible females (2 adults, 2 sub-adults), and 6 individuals (4 adults, 2 sub-adults) of unknown sex, for whom nonmetric dental traits could be scored, were used in this analysis (Table 8). The 11 individuals excluded from this analysis represent 3 females, 4 possible females, 2 males and 2 individuals of unknown sex.

Other/notes

Due to the global Covid-19 pandemic, the author is unable to provide images with a scale bar for Figures 33-35, 51-54 (See pages 183, 185-186, 394, 397, 399-400).

Individuals used in stable isotopic analysis, Scheeres (2014a), Scheeres et al (2014b).

The bolded numbers represent those individuals also used in this analysis.

Scheeres (2014a) and Scheeres et al (2014b) conducted a stable isotopic analysis on several of the burials from this cemetery including burials **5, 8, 10, 14, 15, 17**, 18, **19, 20, 21**, 22, **24, 25, 26**, 28, **30, 32, 35, 36, 37**, 38, **39, 40, 43**, 45, **46, 47**, and **49** (See page 168).

Wetwang Slack, Britain

Initial excavations were led by JR and R Mortimer and continued from 1965-1975. Subsequent excavation from 1975-1981, were led by J Dent (See page 172) (Dent, 1982, 1984).

Age-at-death determinations

The following age-at-death determinations have been assigned to the individuals recovered from the Wetwang Slack cemetery, infant I (0-6), infant II (6-10), sub-adult (juvenile10-17), adult (17-35), mature adult (35-45) and senile (45+) (Dent, 1982, 1984; Giles, 2012; Good, 2005). These categories were based on tooth wear, dental eruption, epiphyseal and cranial suture closure (Dent, 1982, 1984). However, the cemetery population is commonly described according to a specific age range, rather than an age-at-death category.

Sex estimations

Sex was estimated through investigation of secondary sex characteristics of the skull and examination of the pelvis (Dent, 1982, 1984, page 94). However, the specific methods used to estimate sex were not described (See page 172) (Dent, 1982, 1984, page 94).

Number of individuals recovered/excavated

In total 180 individuals were recovered from the Wetwang Slack cemetery (See pages 138, 172, Table 8).

Total number of individuals, males, females and individuals of unknown sex, used in this analysis

In total 150 individuals, 60 males (57 adults, 3 sub-adults), 10 possible males (8 adults, 2 sub-adults), 57 females (48 adults, 9 sub-adults), 8 possible adult females and 15 adult individuals of unknown sex, for whom nonmetric dental traits could be scored, were used in this analysis (Table 8). The remaining 30 individuals represent 6 adult females, 16 adult males, 3 possible adult males and 5 adult individuals of unknown sex.

Other/notes

Individuals used in stable isotopic analysis, Jay et al (2013), Jay and Montgomery (2020)

The bolded numbers represent those individuals also used in this analysis.

Jay et al (2013) and Jay and Montgomery (2020) conducted a stable isotopic analysis on several of the burials from this cemetery including burials **13, 14,** 52, **59, 89, 98,** 117, **122, 143, 155,** 156, **223**, 236, **275, 301**, **327, 400**, **412, 430, 431**, 453, **454**, and 455 (See page 172).

Rudston Makeshift, Britain

Initial excavations began in 1967-1971 uncovered burials R68-114. Further excavations in 1973 and 1975 revealed burials R135-189 (See page 177) (Giles, 2012, Stead, 1991a)

Age-at-death determinations

Several age-at-death designations have been provided for the individuals recovered from Rudston Makeshift, including, infant (0-12 years old), sub-adult (juvenile 12-15 years old) and adults (15+ years old) (Stead, 1991a). However, the age-at-death of the cemetery population is frequently reported as a specific age range, e.g., 17-25 years old (Stead, 1991a). The above designations are based primarily on dental wear based on Brothwell and Payne (1982) dental wear chart. However, this system was modified to include a combined upper and lower dental wear score (Stead, 1991a, page 143).

Sex estimations

Sex was assessed through examination of the pelvis and of secondary sex characteristics of the skull (Stead, 1991a, page 143). However, the specific methods used to estimate sex were not described (Stead, 1991a, page 143).

Number of individuals recovered

In total, 180 individuals were recovered from the Rudston Makeshift (east Yorkshire, Britain) cemetery (Table 8). However, a random sub-sample of 45 individuals were selected for analysis (See pages 138, 177, Table 8).

Total number of individuals, males, females and individuals of unknown sex, used in this analysis

In total 40 individuals, 18 males (15 adults, 3 sub-adults), 6 possible males (4 adults, 2 sub-adults), 16 females (14 adults, 2 sub-adults), 3 possible females (2 adults, 1 sub-adult), and 2 adult individuals of unknown sex, for whom nonmetric dental traits could be scored, were used in this analysis (Table 8).

Other/notes

Along with the individual recovered from burial number, R99, two additional lower first premolars were present. These premolars were identified as additional as the individual recovered from this burial had all lower first and second premolars retained in the sockets within the mandible. The presence of these additional teeth was addressed and noted by the curator, (Dr. Julia Farley). It is unknown whether the premolars are still housed with the rest of the recovered remains from burial R99.

Individuals used in stable isotopic analysis, Jay et al (2013)

The bolded numbers represent those individuals also used in this analysis.

Jay et al (2013) conducted a stable isotopic analysis on several of the burials from this cemetery including burials **143, 175**, 178 and **180** (See page 177).

Due to the global Covid-19 pandemic, the author is unable to provide images with a scale bar for Figures 33-35, 51-54 (See pages 183, 185-186, 394, 397, 399-400).

Pontecagnano, Campania, Italy

Rescue excavations, due to highway construction, began in the 1960s and uncovered several graves (D'Agostino, 1974; Fredericksen, 1974). However, these initial excavations were unsystematic, consequently, the exact boundaries of the cemetery are still unknown (See page 179) (D’Agostino, 1974; Fredericksen, 1974). Subsequent excavations were conducted from 1973-1990, during which the Iron Age material was recovered, and were more systematic in nature (D’Agostino, 1974; Fredericksen, 1974). Therefore, more precise age and date categories were provided for the recovered individuals from this period (D’Agostino and Gastaldi, 1988; De Natale, 1992; Serritella, 1995) (See page 179).

Age-at-death determinations

Due to the more systematic 1973-1990 excavations more precise age-at-death categories have been provided for the individuals recovered during this phase of the archaeological work (D’Agostino and Gastaldi, 1988; De Natale, 1992; Serritella, 1995). These age-at-death categories include, infant I (0-8 years old), infant II (8-15 years old), sub-adult (juvenile 15-20 years old), adult (21-50 years old), and mature adult (>50 years old) (D’Agostino and Gastaldi, 1988; De Natale, 1992; Serritella, 1995). These categorise were based on tooth eruption, epiphyseal and cranial suture closure (D’Agostino and Gastaldi, 1988; De Natale, 1992; Serritella, 1995). However, the cemetery population is frequently described based on the above broad age-at-death designations, rather than by a specific age-at-death (D’Agostino and Gastaldi, 1988; De Natale, 1992; Serritella, 1995). Consequently, the number of individuals which correspond to the above age-at-death designations is not consistently documented (D’Agostino and Gastaldi, 1988, page 20; De Natale, 1992, page 15; Serritella, 1995, page 22).

Sex estimations

Sex was assessed through an examination of the skull and pelvis, however, the specific methods used are not described (D’Agostino and Gastaldi, 1988, page 20; De Natale, 1992, page 15; Serritella, 1995, page 22).

Number of individuals recovered

Due to the unsystematic nature of the initial excavations the total number of burials within this cemetery is unknown (D’Agostino, 1974; Fredericksen, 1974). However, it has been estimated that as many as 6,000 burials may have been originally present (See pages 138, 179, Table 8) (D’Agostino, 1974, 1988; Fredericksen, 1974). Only the skeletal remains of 700 individuals have been curated (D’Agostino and Gastaldi, 1988; De Natale, 1992; Serritella, 1995).

Total number of individuals, males, females and individuals of unknown sex, used in this analysis

It was considered appropriate to limit the analysed individuals, including adults and sub-adults (juvenile 17+ years old) with permanent dentitions, to burials from a discrete and roughly contemporaneous period, 650-260 BC. Consequently, due to the limited time available for recording, 45 randomly chosen individuals were analysed from the Pontecagnano cemetery population. However, only 35 individuals from this sub-sample could be scored for nonmetric traits (See page 179). The 35 individuals used in this analysis include 15 males (12 adults, 3 sub-adults), 4 possible adult males, 8 adult females, 4 possible females (3 adults, 1 sub-adult), and 4 adult individuals of unknown sex, for whom nonmetric dental traits could be scored, were used in this analysis (See page 179, Table 8). The remaining 10 individuals excluded from this analysis include 4 adult females, 1 possible adult female, 2 males (1 adult, 1 sub-adult), 1 possible adult male and 2 adult individuals of unknown sex.

Other/notes

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