

# BIOLOGICAL ANTHROPOLOGY IN THE INDO-PACIFIC REGION: NEW APPROACHES TO AGE-OLD QUESTIONS

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## ABSTRACT

*Biological anthropological research, the study of both modern and past humans, is a burgeoning field in the Indo-Pacific region. It is becoming increasingly apparent that the unique environments of the Indo-Pacific have resulted in an archaeological record that does not necessarily align with those in the northern hemisphere. New, regionally-specific archaeological models are being developed, and biological anthropological research has an important role to play in establishing past human experience within these models. In the Indo-Pacific, research using ancient and modern human tissues is adding insight into global processes of prehistoric settlement and migrations, subsistence change and human biosocial adaptation. This review synthesises current themes in biological anthropology in this region. It highlights the diverse methods and approaches used by biological anthropologists to address globally-relevant archaeological questions. In recent decades a collaborative approach between archaeologists, biological anthropologists and local communities has become the norm in the region. The many positive outcomes of this multi-disciplinary approach are highlighted here through the use of regionally-specific case studies. This review ultimately aims to stimulate further collaborations between archaeologists, biological anthropologists and the communities in the region, and demonstrate how the evidence from Indo-Pacific research may be relevant to global archaeological models.*

## INTRODUCTION

The Indo-Pacific region is broadly defined as encompassing eastern Asia and the Pacific (Figure 1), and is perhaps one of the most diverse biogeographical and cultural areas in the world (Lilley, 2017). It encompasses tropical, subtropical and temperate climates; landmasses ranging in scale from continental Southeast Asia to tiny coral atolls; and a vast array of endemic flora, fauna and pathogens.

This wide range of environmental variation provides unprecedented opportunities to assess human adaptation to a myriad of different conditions. The geographic isolation of most of the Pacific Islands and range of physical environments within island groups, has been particularly useful for characterising biological, cultural and linguistic diversity. Humans have a long history in the region, arriving with some of the earliest Out of Africa migrations in Australia and New Guinea (Malaspinas et al., 2016), and migrating through the Pacific to Remote Oceania in what many consider the last major phase of human migration (Matisoo-Smith and Daugherty, 2012). This extensive time-depth in the region means that biological anthropologists can explore biosocial adaptation using both skeletal remains and modern populations, shedding light on processes that began in the late Pleistocene and continue to influence lives today. This review explores the significance of current biological anthropological research in the Indo-Pacific region for both regional and global understanding of the human story.

In this review, we focus on biological anthropology in island and mainland Southeast Asia, and the Pacific Islands. While other areas of the Indo-Pacific such as South Asia have a long history of archaeological and biological anthropological research (Kennedy, 1980; Lovell and Kennedy, 1989; Mushrif-Tripathy et al., 2016), Southeast Asia and the Pacific have been traditionally under-explored and a review of current research is timely. In addition Southeast Asia and the Pacific are linked by a shared population history, the expansion of people into the Pacific had its origins in mainland and island Southeast Asia possibly occurring as early as 50,000 years ago (Kirch et al., 1989; Summerhayes et al., 2010).

Southeast Asia and the Pacific Islands are especially useful regions for evaluating archaeological paradigms regarding biological and cultural adaptations associated with changes in subsistence strategies. Recent evidence suggests that Southeast Asia may have been one of the locations for the early domestication of chickens (Pitt et al., 2016; Wang et al., 2015), and a route through which the



Figure 1: Map showing the Indo-Pacific region, with areas that this article focuses on shaded. Labelled regions and islands are those mentioned in-text.

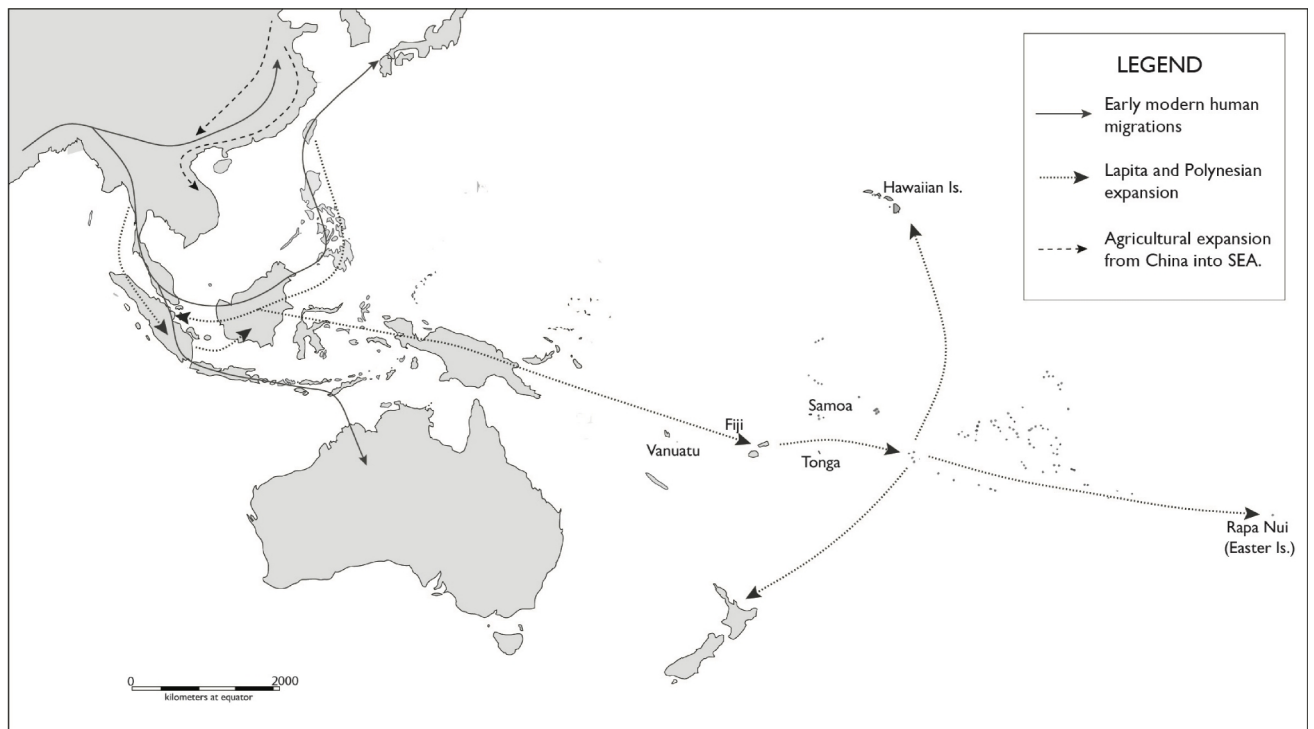


Figure 2: Map of the study area schematically showing major migrations from early modern human movement into the area (50,000-40,000BP) to movement of rice agriculturalists into mainland southeast Asia from China (~ 4000BP) and Austronesian/Polynesian expansion into the Pacific (3000-750BP).

domesticated dog was introduced to the Pacific (Greig et al., 2015; Oskarsson et al., 2011; Pang et al., 2009). In addition, both China and New Guinea are centres of independent plant domestication (Denham, 2011; Fuller et al., 2009; Fuller et al., 2014; Gross and Zhao, 2014; Perrier et al., 2011; Yen, 1991). Most archaeological research, and consequently the models drawn from them, is focused on areas in the world reliant on wheat or maize-based subsistence (Cohen and Armelagos, 1984; Roberts and Cox, 2003; Steckel and Rose, 2002). However, Southeast Asian populations generally have a rice-based economy, while the Pacific diet is primarily based on root crops, specifically yam, taro, and sweet potato, in addition to banana and breadfruit. The diversity in subsistence base within the Indo-Pacific region provides biological anthropologists with opportunities to assess human biosocial adaptation to these different subsistence strategies (Halcrow and Tayles, 2011; Kinaston et al., 2015; Kirch, 2010; Spriggs, 1997). This assessment is important as archaeological models based on subsistence change in the Americas, Europe or Near East may not be relevant worldwide, but in the absence of regionally-specific frameworks they are often applied regardless.

Biological anthropological research is significant because evidence obtained from the direct study of human tissues (both archaeological and modern), addresses additional aspects of the human experience to those that can be interpreted through material culture. These investigations include diverse techniques including macroscopic analysis of bone, chemical analysis of tissues, ancient and modern DNA analyses, and investigations of parasites and plant microfossils associated with human tissue as proxies for human health and behaviour. Research involving biological anthropology can provide direct insight into past human mobility, dietary transitions and related adaptations, the implications of climate or environmental change, nutritional deprivation, and the impact of these changes on general population stress and well-being.

There has been a global history of malpractice surrounding the ethical study and curation of human remains and this has included the Asia and Pacific region (see Larsen and Walker (2005) and Watkins (2003) for reviews). Biological anthropology in the Pacific region today involves taking into account the unique sets of beliefs surrounding human remains, death and the spirits of the ancestors (Gilmore et al., 2013; Ruckstuhl et al., 2016). Modern biological anthropologists must both acknowledge this history, and work to build new relationships with local communities. Initial research conducted in the area was colonial and 'race'-based, defined in part by a lack of community consultation regarding the study of populations in both the past and the present (Matisoo-Smith, 2015). A similar history of Western political and economic domination is seen in much of Southeast Asia (Peterson, 1982), with colonial attitudes seriously influencing early interpretations of the region's prehistory (Bayard, 1980; Peterson, 1982). From the mid-1980s onwards, however, biological anthropology began to develop into the research area it is today. In Southeast Asia, recent work is directly opposing

early (arguably ethnocentric) interpretations of foreign historical intervention in triggering the rise of complex stratified societies. Instead a long history of local innovation as the primary driver of social change is being revealed (Higham, 2014; O'Reilly, 2014). In the Pacific, biological anthropologists are developing strong research relationships with local communities, addressing the ghosts of past malpractice by working collaboratively to build both research and local identity (Ruckstuhl et al., 2016).

In summary, the Indo-Pacific region has been instrumental in addressing and extending our knowledge of universal archaeological and anthropological research questions; examining where people came from and how they moved around and adapted to their environments. This paper reviews the contribution that biological anthropological research in the Indo-Pacific region has made to the understanding of global archaeological paradigms, dividing this synthesis into three key themes: origins, migration, and biosocial adaptation. These themes are particularly pertinent and interlinked in Southeast Asia and the Pacific. Here researchers are beginning to focus on how population history (i.e. origins and movement of people groups) have impacted both culture and biology (biosocial adaptation), ultimately affecting health and disease outcomes in the region today. This review then uses the case study of archaeological work at Wairau Bar (New Zealand) to draw these themes together and illustrate the importance of inter-disciplinary and collaborative work with local communities and researchers.

## ORIGINS

Southeast Asia and the Pacific have highly diverse and deep population histories (see Matisoo-Smith, 2015; Bellwood, 2006), with multiple migrations into and through the area shaping the populations in the region today (Figure 2). Although new genetic data from modern populations is revealing more about human origins in this area, in order to fully address these questions, it is necessary to combine these data with archaeological and bioarchaeological data representing the early inhabitants of the region. Early models of human evolution traditionally focused on Africa and Europe, ignoring much of the evidence from the Indo-Pacific region despite its long human history (Marwick, 2009). Recent palaeontological and genetic research has identified numerous hominin species in the region, as well as evidence of some of the earliest modern human migrations out of Africa. (Malaspina et al., 2016; Sankararaman et al., 2016). Analysis of the remains from Denisova Cave, for example, has resulted in the discovery of genetic admixture between these previously unidentified hominins and *Homo sapiens* present in Southeast Asia and the Pacific (Reich et al., 2010). Recently, there have also been suggestions of additional, secondary Neanderthal admixture contributing to the genetic makeup of Asian populations (Vernot et al., 2016; Wall et al., 2013). In addition, the small-bodied hominin *Homo floresiensis* is also present in the region (Brown et al., 2004), though ancient DNA (aDNA) analyses of this species have to date been unsuccessful (Stringer, 2014). This kind of research highlights

the important role the Indo-Pacific region plays in understanding the role of admixture in the evolution of our species.

The current focus on palaeontological research in the region means that a new body of information is emerging in the form of combined morphological affinity and genetic work on evolutionary histories. For example, initial morphological studies in the region proposed two distinct migration events to Australia involving a gracile and more robust population (Thorne, 1980). Indeed, the first aDNA analyses of 10 ancient Australians from Lake Mungo and the Willandra Lakes found support for this two phase/ two population settlement scenario (Adcock et al., 2001). Recently, however, researchers have resequenced mitochondrial genomes (mitogenomes) from Mungo 3 and other Willandra Lakes remains (Heupink et al., 2016). Unlike the previous analyses (Adcock et al., 2001) they found continuity between the ancient and modern Australian mitochondrial DNA (mtDNA) sequences, and thus no support for two distinct migration events. Similarly, analyses of 83 whole genomes of modern Aboriginal Australians (Malaspinas et al., 2016) have found not only evidence of a single major migration event to Sahul, but have also identified variations in gene regions associated with thyroid hormone and elevated serum urate levels, which are suggestive of selective adaptations in Australian aboriginals for living in cold, desert environments and for dealing with dehydration. As these examples show, many of the advances in interpretation of population history in the region are being driven by new techniques in aDNA research, in particular the introduction of Next Generation Sequencing (NGS) technologies (Linderholm, 2016; Parks et al., 2015). These techniques give researchers the ability to sequence small pieces of fragmented DNA, which when pieced together can result in coverage of the complete mitogenome, or in some cases even coverage of the nuclear genome of typically degraded ancient samples including samples that would not have produced any reliable sequence data using traditional, Sanger sequencing methods (Koboldt et al., 2013).

Next Generation Sequencing methods also allow for the rapid and relatively inexpensive generation of data for large population level studies using modern DNA. For example, a large number of new complete mitogenomes have recently been generated for modern Pacific populations, which indicate much more mtDNA diversity and population complexity than previously recognised (Duggan et al., 2014). Combined with powerful new methods for statistical analysis, NGS allows for investigation of genome-wide diversity and estimation of levels of genetic admixture (Hellenthal et al., 2014; Lipson et al., 2014). Aboriginal genomes have also recently been sequenced revealing the deep antiquity of the human lineage in Australia, and shedding light on the timing and nature of the Out of Africa migration process (Malaspinas et al., 2016; Rasmussen et al., 2011).

This wealth of new genetic data means researchers can address a range of emerging questions about the evolution and dispersal of the human species (Huerta-Sánchez et al.,

2014; Malaspinas et al., 2016; Mallick et al., 2016; Pagani et al., 2016; Vernot et al., 2016; Xu et al., 2012). Improvements in laboratory techniques and sequencing technologies now allow us to incorporate both data derived from aDNA and sequence data available for contemporary populations when assessing these questions. For example, Pagani et al. (2016) detected admixture between Neanderthal and anatomically modern humans present in the genome sequence of present-day Papuans, suggesting this population derives from a migration earlier than the main migration of modern humans out of Africa. Similarly, admixture with Denisovans has been detected in modern Tibetan genomic data (Huerta-Sánchez et al., 2014) and with both Denisovan and Neanderthal in a contemporary Melanesian dataset (Vernot et al., 2016), highlighting the influence of archaic admixture on human evolution. While Southeast Asia and the Pacific are generally considered to be environments that are not conducive to aDNA preservation, recent analysis (Heupink et al., 2016; Knapp et al., 2012; Skoglund et al., 2016), and continued improvements suggest that it is possible to yield informative DNA sequences from archaeological material in this part of the world.

#### MIGRATION AND MOBILITY

Migration is a recurring theme in Indo-Pacific research. Genetic evidence regarding origins indicates that the colonisation of the Pacific through expansion of peoples from Southeast Asia was a multi-faceted process involving numerous populations and complex interactions between them (see Matisoo-Smith (2016) for a review). The movement of the Lapita people, the first colonists of Remote Oceania who are thought to be ancestral to Polynesian populations, began the last chapter of human global colonisation (McNiven et al., 2011; Spriggs, 2011; Figure 2). The geographic separation between the islands of the Indo-Pacific region is useful archaeologically as it allows the teasing apart of processes related to migration from those related to trade and other forms of contact. This is more difficult in mainland Southeast Asia (Fitzpatrick and Anderson, 2008), although it is now recognised that even in the Pacific most islands are unlikely to have ever been completely socioculturally and biologically isolated (Broodbank, 2002; Weisler et al., 2016). Current research in the Pacific is now showing extensive trade links after initial colonisation including retention of contact with the Southeast Asian mainland (Clark, G.R. et al., 2014; D'Arcy, 2006; Kirch, 1988; Lape, 2004). The Indo-Pacific region, therefore, is a dynamic area in which to study human mobility and interaction.

Biological anthropological research into migration has historically focused on cranial morphometrics and dental morphology to identify newcomers in an area, or migrating populations (Hanihara, 1992; Matsumura and Hudson, 2005; Pietrusewsky, 1996a; Pietrusewsky, 1996b; Stefan and Gill, 2016). Using these techniques, bioarchaeologists have demonstrated population affinities between the earliest inhabitants of mainland and island Southeast Asia (Barker et al., 2007; Matsumura et al., 2008b), with mor-

phometric work culminating in the development of explanatory models such as the Two-Layer hypothesis. This model posits the idea of replacement of Southeast Asian hunter-gatherer populations by agriculturalists (Matsumura et al., 2008a; Matsumura et al., 2011; Matsumura and Oxenham, 2014), and underpins the overarching narrative of population changes associated with agriculture in Southeast Asia.

More recently Southeast Asia and the Pacific have become a focus for genetic research into migrations, associated with both early Lapita settlers and more recent groups. The genetic sequencing of modern Pacific peoples has revealed previously unknown complexity in the histories of island populations (Duggan et al., 2014; Lipson et al., 2014). These modern studies are useful counterparts to aDNA work conducted in the region, especially as aDNA research is limited by poor preservation in the monsoonal and tropical environments of mainland Southeast Asia. The high level of past human mobility and complex migration history of the Indo-Pacific region means that multiple lines of evidence must be used in teasing apart processes of migration from those of trade or diffusion. These kinds of interdisciplinary projects are already well-underway in the region. Isotopic evidence for human movement, for example, is routinely combined with archaeological evidence to examine whether there was a permanent movement of people alongside material culture during trade and exchange processes, and separate this trade from idea diffusion. In the Bismarck Archipelago human and faunal isotopic studies have been used to compare the movement of valued animals and humans (Shaw et al., 2009) and human migration on the south coast of New Guinea (Shaw et al., 2011). Human isotopic values have also been considered in light of similarities and differences in mortuary material culture to differentiate long-distance trade from human migration in Tonga (Stantis et al., 2015), or to suggest groups of socially distinct females in northeast Thailand (Bentley et al., 2009).

The combination of craniometric and genetic evidence has been used to shed light on Lapita expansion and colonisation waves. For example, morphological analysis of five secondary burials of crania from the Lapita site of Teouma in Vanuatu seems to support the idea of a direct Lapita-Asian connection (Valentin et al., 2016). Most recently, researchers have also succeeded in extracting aDNA from the Teouma crania (Skoglund et al., 2016), the results of which may support the initial conclusions of the craniometric study showing Asian genetic affinities. These results, while interesting, derive solely from secondary burials and the burial practices at this site mean that the crania cannot be definitively associated with the postcranial remains. There is therefore much work to be done on fully establishing morphological and genetic affinities in early Pacific assemblages in general, and Teouma in particular. Future work will allow the teasing out of factors such as selective pressures contributing to the development of the Polynesian phenotype and possible Melanesian admixture during Lapita expansion. These latest genetic results, how-

ever, do present intriguing data that will generate much discussion regarding the origins, genetic makeup and the homogeneity of Lapita populations through time and space.

In addition to the combination of traditional biological anthropology techniques, the Indo-Pacific region has also been pivotal in the development of the commensal approach to study human migrations. Established in part due to the lack of access to human remains in the Pacific (see introduction), this approach uses aDNA and modern DNA of commensal animals and plants as a model to establish the human origins and settlement of the region (Larson et al., 2007; Matisoo-Smith et al., 2009; Oskarsson et al., 2011; Storey et al., 2013). Results of these studies indicate significant complexity and a range of origins of the different commensal animals in the region; with the origin and movement of pigs, dogs, chickens and rats all suggesting different ancestral sources, paths through island Southeast Asia into the Pacific, and differing timings and numbers of introductions (Matisoo-Smith, 2015). This DNA research has shown not only direct ties between the Pacific Islands, Southeast Asia and South America but also given insight into the timing of horticultural introductions and techniques (Chang et al., 2015; Clarke et al., 2006). The paper mulberry plant has been linked genetically to Taiwan (Chang et al., 2015), and Near Oceanic origins are indicated for taro, sugarcane and banana (Denham, 2011). The complexity of movement around the Pacific is also highlighted by genetic studies of sweet potato that reveal movement out of South America in prehistoric times and later interactions between Central America, the Caribbean, Southeast Asia and the Pacific via early European trade networks (Roullier et al., 2013). Recently, this commensal approach has been expanded to involve isotopic studies, with biological anthropologists using these techniques to trace not only human movement but also the movement of animals, showing continued trade-links between island populations after settlement (Shaw et al., 2009; 2010), or local residence of commensal animals (Kinaston et al., 2013c).

## BIOSOCIAL ADAPTATION

Most biological anthropological research in the Indo-Pacific region adopts a biosocial approach to the study of past populations to shed light on past human experiences. In this approach researchers use demographic factors, in addition to a number of accepted indicators of biological stress, as a measure of health and disease within a population (e.g. Clark, 2018). While “health” can be a problematic term when using a biosocial approach (see Temple and Goodman, 2014), here it is used as a holistic concept representing a general population-based measure of stress, illness and quality of life, based on a variety of skeletal and dental indicators. The biosocial model considers human health as an outcome of both factors of the physical environment and sociocultural context (Figure 3). This general model is not uniquely applied to the Indo-Pacific region (see Larsen, 2015), but is especially useful for the interpretations of health in an area that is both environmentally and culturally diverse.

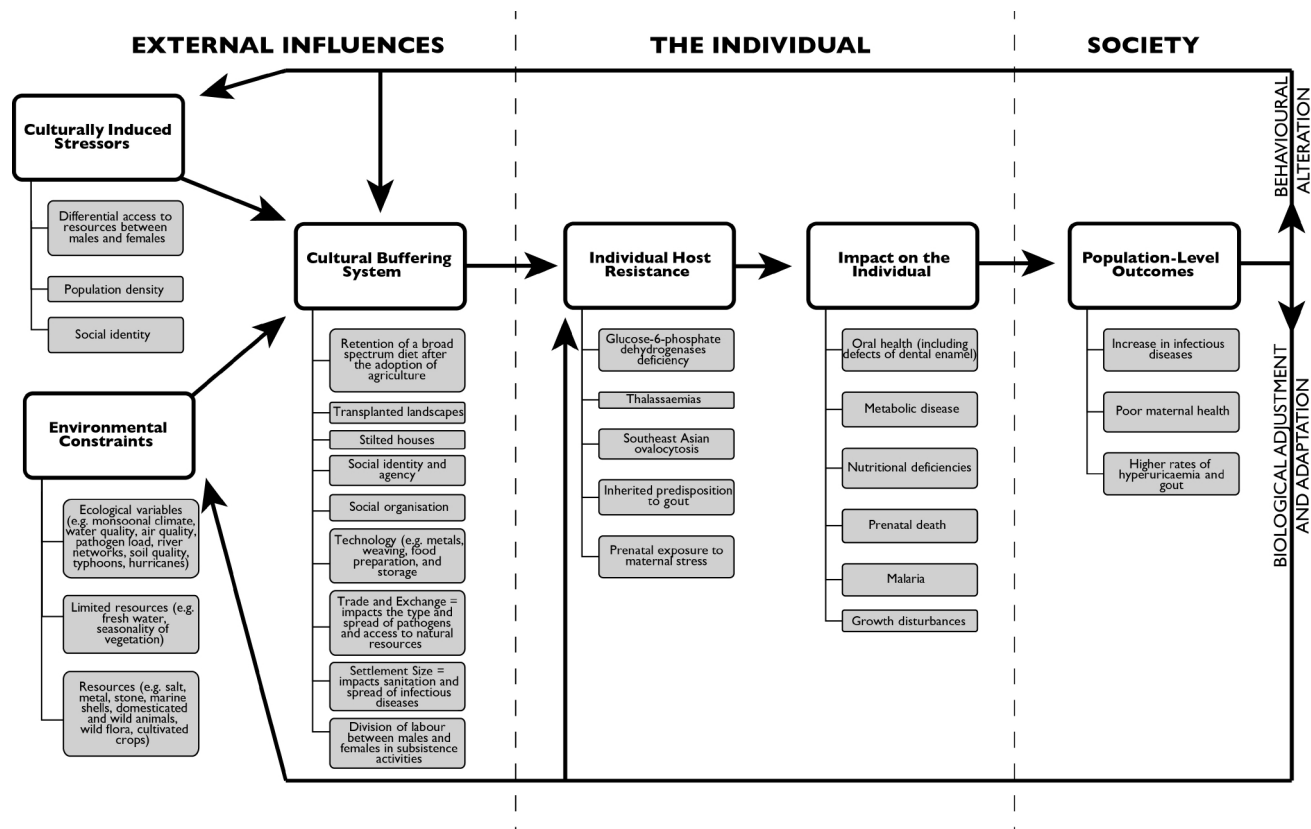


Figure 3. Factors of the physical environment and sociocultural context affecting health outcomes in the Southeast Asian and Pacific contexts.

The many different environments and complex population history of this region provide biological anthropologists with the ability to study the myriad of ways people adapt both biologically and socially to their environments. This discussion focuses on two major themes emerging from research within the Indo-Pacific region. The first of these is the significance of the region for assessing global paradigms relating subsistence change, population dynamics and human health and disease. The second relates to modern-day health in the region and how knowledge of the antiquity of disease and population history may affect current disease presence.

#### Adaptation to Subsistence Change, Demographic Change and Disease

A major theme in Southeast Asian and Pacific biological anthropology is the impact and significance of subsistence change on human populations. Here, the unique environments and atypical sociopolitical trajectories of the region allow assessment of global paradigms relating to the impact of agriculture. The environmental diversity within the Indo-Pacific region means that there is considerable variation in subsistence practices, social structure, and interaction spheres within the region. In Southeast Asia, the retention of a heavy reliance on broad-spectrum economies even after the adoption of agriculture led to a long, slow transi-

tion to full agricultural reliance. This means that the sociopolitical developments and subsequent impacts on health commonly observed elsewhere in the world are not uniformly present (e.g. Domett and Tayles, 2007; Halcrow and Tayles, 2011; Halcrow et al., 2016; Tayles et al., 2000). Similarly, subsistence in the Pacific region is equally complex and does not conform to more generalized global models of agricultural adoption. Here the colonisation of virgin environments gives biological anthropologists the chance to study how humans adapted to these new environments (Buckley et al., 2014). Modification of the environment in the form of transplanted landscapes in the Pacific shows how humans engineered their environment to suit their subsistence needs by translocating species.

The internationally applied subsistence change model posits that the transition to an agricultural-based economy resulted in significant changes to health and sociopolitical organisation (Pinhasi and Stock, 2011). This has implications for diet, weaning, fertility, population dynamics, pathogen-load and human health (Larsen, 1995). In essence, deterioration in the overall quality of life is commonly associated with the transition to a reliance on agricultural crops with a reduction in the nutritional value of food, and an increase in sedentary living arrangements and population size, leading to an increase in infectious disease (Larsen, 1995; Pinhasi and Stock, 2011). However, recent biological anthropological research in mainland Southeast

Asia and Taiwan has questioned the universal applicability of this central model by showing that human responses to the introduction of agricultural resources were more complex and regionally variable than previously thought (Cheng-Yi et al., 2016; Clark, 2014; Clark, A.L. et al., 2014; Dhavale et al., 2017; Domett, 2001; Domett and Tayles, 2006; Douglas, 1996; Halcrow et al., 2016; Tayles et al., 2009).

Some have argued, based on palaeodemography and female oral health, that there is a change in population dynamics in the Neolithic involving an increase in female fertility (e.g. Willis and Oxenham, 2013). However, this is hard to quantify given the comparative lack of pre-Neolithic samples to compare. Multiple lines of biological anthropological and archaeological evidence are now pinpointing the intensification of agriculture in Southeast Asia as occurring in the Iron Age (c. 500 BC to 500 AD), at which point a deterioration in health is observable in several regions (Halcrow et al., 2016; King et al., 2017). This change in population stress and disease is echoed in major cultural and environmental changes observed in the archaeological record during this transitional period (Boyd and Chang, 2010; Higham, 2016; Wohlfarth et al., 2016; Yamoah et al., 2017). Archaeological and biological anthropological analyses are now being combined to provide insight on health in relation to these social changes (Ward et al., In Press). Research from prehistoric mainland Southeast Asia highlights how the speed of agricultural resource uptake results in differential biosocial responses, and illustrates how important the consideration of environmental context is when applying generalised global models.

Historically, a paucity of founding population cemetery samples in the Pacific has limited the opportunities to assess the interactions between human subsistence choices and the island environments. However, recent excavations and analysis of human skeletal samples from Lapita contexts and post-Lapita cemetery sites are beginning to build a picture of early settler health, diet and adaptation (Horrocks et al., 2014; Kinaston et al., 2014a, 2014b; Kinaston et al., 2016; Valentin et al., 2010; Valentin et al., 2014). The Lapita colonists travelled with an agricultural package including tuberous crops, pigs, dogs, and chickens to new island environments where they also took advantage of diverse indigenous plants and animals. Multiple lines of biological anthropological research support the idea of crop translocation, including plant microfossils (starch grains and phytoliths) found in dental calculus (Dudgeon et al., 2016; Horrocks et al., 2014; Tromp and Dudgeon, 2015), and isotopic evidence for terrestrial crop use in some of the earliest Pacific settlers (Kinaston et al., 2013c).

The practice of translocating plant and animal species and relying on them for stable food sources may have had significant health implications for the early colonists. The introduced species are likely to have been vulnerable to the new conditions of each island environment, resulting in resource instability and consequent nutritional deficiencies (Buckley et al., 2014). Biological anthropological evidence is also revealing the use of endemic resources in mitigating

the effects of poor crop yield. Microfossil analysis indicates the importance of both wild and cultivated food sources on islands such as Efate, Vanuatu, generally showing a much broader plant diet than has been previously assumed in major migration models (Tromp, 2016). Furthermore, isotopic analysis indicates that on some islands where soils were poor, diverse human coping strategies were employed, including crop fertilisation (Commendador et al., 2013), and lessening reliance on agricultural crops in favour of using marine resources (Stantis et al., 2016b). In the Pacific, periods of social and environmental change have also provided biological anthropologists with the opportunity to study social inequality and its effect on food distribution and subsistence patterns (Fenner et al., 2015; Kinaston et al., 2013a, 2013b; Stantis et al., 2015; 2016a; Valentin et al., 2006). These studies have generally shown greater consumption of protein-rich foods in higher social classes and a ubiquitous lower consumption of protein in females compared to males.

Alongside investigations of the demographic effects of subsistence change, research is also being conducted to establish the impact of agriculture on human health. Commonly used indicators of health include stature and body size, oral health, developmental defects of dental enamel, metabolic disease, and the presence of infectious disease (Larsen, 2015). Within mainland Southeast Asia, there is no indication of a pattern of health change with the transition to agriculture. There is, however, some evidence for the increase in specific infectious disease in the Iron Age, including possible tuberculosis (or brucellosis) and leprosy (Oxenham et al., 2005; Tayles and Buckley, 2004). Metabolic disease, probable scurvy, has also been identified in the Iron Age Laos and historic period Cambodia (Halcrow and Boonlop, 2014; Halcrow et al., 2014). Recent work examines the individual and population level responses to infectious agents by modelling the effects of likely pathogens endemic to the region (Clark et al., 2015; King et al., 2017). By considering context-specific factors, biological anthropologists can characterise how health and disease may be impacted, providing a more detailed understanding of regional variation.

Biological anthropological research in the Pacific also focuses on the themes of health and population dynamics. However, the island environments of this region raise different questions than those addressed in Southeast Asia. In particular, research in this region focuses on how colonisation processes may have affected human health and population growth (e.g. Buckley 2016; Pietruszewsky et al., 2014). In moving to new islands and partially relying on a translocated horticultural package, early settlers will have experienced new pathogens, potential problems relating to lower genetic diversity of small founding populations, and environmental instability (Buckley et al., 2014). Small founding populations in the Pacific allow biological anthropologists to answer questions regarding how colonisation occurred and populations grew (Whyte et al., 2005). Similarly, to parts of Asia, the tropical environment of many of the Pacific Islands has implications for pathogen

distribution, and colonising and later populations were potentially burdened with a high levels of physiological and psychological stress (Buckley et al., 2008; Pietrusewsky et al., 1997; 2014). While we cannot confirm that we are examining psychosocial stress archaeologically, there are many aspects of health that can be examined using biological anthropological evidence. Large cemetery samples in the Pacific are rare, but those that do exist are allowing biological anthropologists to model and understand colonisation processes and health changes occurring in this area.

Research on the largest Lapita cemetery (Teouma in Vanuatu), for instance, has revealed a significant burden of prenatal death, likely reflecting poor maternal health in this population (Buckley et al., 2014; Kinaston et al., 2009). This may be related to differential access to resources between males and females during the initial colonisation phase (Kinaston et al., 2014b). Comparison to later Lapita sites is also beginning to allow the assessment of changes to health and diet as people become established in Vanuatu (Kinaston et al., 2014b; Valentin et al., 2014). There is also palaeopathological evidence for dietary insufficiencies in both the children and adults of founding Lapita populations, indicating that resource instability negatively affected health, resulting in scurvy or vitamin C deficiencies (Buckley et al., 2014).

#### Modern-day Health and Links to Evidence of Disease in the Past

Many countries in the Indo-Pacific region are at the forefront of global economic change. Yet more than a billion people in this region remain vulnerable to disease (World Health Organisation, 2014). Modern-day communicable diseases found in the Indo-Pacific perpetuate the cycle of poverty and poor health, and much of this disease burden today can be attributed to neglected tropical diseases (NTDs). NTDs are a group of diseases caused by parasites, bacteria, viruses, and other organisms. The most common NTDs in the Indo-Pacific region include: soil-transmitted helminthiasis (intestinal worms), foodborne trematodiasis (liver and lung flukes), leprosy, lymphatic filariasis (elephantiasis), schistosomiasis (snail fever), trachoma and yaws (World Health Organisation, 2014). Many of these diseases are associated with unsafe water and sanitation, and unique cultural practices of food preparation (i.e. eating raw fish in Thailand (Sithithaworn and Haswell-Elkins, 2003)) in a tropical environment. The disease burden of these pathogens in the present is likely to have been just as significant in the past (King et al. 2017), and although many of these diseases do not leave diagnostic traces on the skeleton, it may be plausible to infer their presence. Research into the antiquity of disease and population history in this region has the potential to inform clinical outcomes and models of modern-day epidemiology.

Differential diagnosis of skeletal evidence of diseases in archaeological samples is relatively commonplace in both the Pacific and Southeast Asia. This type of analysis is useful as it allows not only evaluation of archaeological hypotheses, but also has implications for human adaptation to disease and modern population health. In the Pacific, for

instance, the diagnosis of disease in the past has allowed assessment of migration-based hypotheses (Buckley and Tayles, 2003). It was assumed that treponemal diseases had a long history in the Pacific, entering with the first settlers ultimately originating from Southeast Asia (Tremblay, 1996). However, recent palaeopathological findings from pre-1500 AD skeletons from the region cast doubt on this assumption, suggesting that the transmission of treponemal diseases is much more recent and complex, perhaps reflecting later human interactions (Buckley and Oxenham, 2016). It has also been possible to use modern human genetic adaptations (e.g. Clark and Kelly, 1993) alongside the genetics of the pathogens themselves (Mokrousov et al., 2016) and palaeopathological evidence for disease (Gosling et al., 2014a) to trace human colonisation pathways.

Inherently, when organisms encounter new infectious pathogens, biological and/or social adaptations become fundamental to survival (Karlsson et al., 2014). The antiquity of certain diseases in the Indo-Pacific region, therefore, has resulted in biosocial adaptation that has had long-term impacts on culture, biology and disease experience. For example, malaria is currently recognised as one of the greatest evolutionary adaptive forces in the recent history of the human genome (Kwiatkowski, 2005). Malaria has a long, but undated, antiquity in the Indo-Pacific region. It is endemic to mainland and island Southeast Asia, coastal New Guinea, the Solomon Islands and Vanuatu. In these regions, malaria is likely to have affected both population growth and mortality rates in the past (Groube, 1993; Kirch, 2000; Pietrusewsky and Douglas, 2002; Tayles, 1999). Modern studies reveal that the long presence of malaria in the region has resulted in a wide-variety of genetic adaptations to malarial exposure, including glucose-6-phosphate dehydrogenase deficiency, the thalassaemias and Southeast Asian ovalocytosis (Flint et al., 1986; Fowkes and Day, 2008; Hill et al., 1985; Philippon et al., 1995; Ubalee et al., 2005). The high frequencies of some of these mutations found in populations of Remote Oceania, where malaria has never been endemic, provide additional support for models of population history. It is likely that the ancestral population of Remote Oceania were exposed to endemic malaria as they moved through the Pacific as they carry high levels of alpha thalassaemia mutations, which are advantageous for surviving in malarial environments (Flint et al., 1986; Hill et al., 1985). It has also recently been suggested that adaptation to malaria might also be an explanation for the high rates of hyperuricaemia and gout in Pacific populations (Gosling et al. 2014b). In addition to biological adaptation to malaria, there is also strong archaeological evidence for cultural responses to the disease, including the use of stilted houses in Lapita settlements to reduce the proximity to vector habitats (Kirch, 2000).

Metabolic disease research in the Pacific region is also shedding new light on the antiquity of disease and population responses. Many contemporary Pacific populations suffer a high prevalence of gout and other metabolic diseases (Buckley, 2011; Gosling et al., 2014a; Gosling et al.,



2014b). The high prevalence of gout was previously assumed to be primarily a result of transitioning to westernised diets and sedentary lifestyles. However, the integration of genetic and archaeological data with modern clinical research in the region is challenging this assumption. Historical research (Gosling et al., 2014b) combined with palaeopathological identification of diagnostic lesions (Buckley, 2011; Buckley, 2007; Snow, 1974) has established a deep time-depth for these conditions. It has therefore been proposed that the high rates of disease in modern populations may be a result of ancestry and an inherited genetic predisposition to disease (Hollis-Moffatt et al., 2009; Phipps-Green et al., 2010). These findings have been valuable in initiating discussions with communities about this disease burden and promoting education through community initiatives such as the Māori Gout Action Group (Winnard et al., 2008).

#### MOVING FORWARD WITH COMMUNITY-DRIVEN RESEARCH: WAIRAU BAR AS A CASE STUDY

The recent re-examination of *kōiwi tangata* (Māori ancestral remains) from Wairau Bar (New Zealand) prior to their return and reburial by their descendant community provides a useful example of how aspects of biological anthropology reviewed in this paper (origins, migration and bio-social adaptation) are being investigated in Indo-Pacific sites. Work at Wairau Bar is also an excellent illustration of how positive engagement between local groups and researchers can aid in interpretation of the past (Ruckstuhl et al., 2016). We expand upon this case study to explore some of the ways in which Indo-Pacific biological anthropology is moving forward, particularly in the field of community-driven research.

Wairau Bar is located on the northern coast of the South Island of New Zealand (Figure 4) and is one of the only founder-phase sites in New Zealand, inhabited during the earliest period of colonisation (Higham et al., 1999). The site was originally excavated in the 1940s to 1960s (Brooks et al., 2011; Duff, 1977) with limited consultation with descendant communities. Controversially, the 42 people represented by human remains recovered from Wairau Bar were held in a regional museum. However, in 2009 they were repatriated to the Māori community (*iwi*) who currently have guardianship over the area (Buckley et al., 2010). This process of repatriation involved re-excavation of part of the site in preparation for reinterment. During this time extensive consultation with local *iwi* was undertaken and a Memorandum of Understanding drawn-up to allow renewed biological anthropological study of the human remains from the site (Ruckstuhl et al., 2016).

The site's potential to answer important questions about early human colonisation of New Zealand, and the ways humans adapted to the environments they encountered there was recognised early on in the research process. As early coloniser sites in New Zealand are rare, there was a concerted effort for collaboration between archaeologists, biological anthropologists and the community at Wairau Bar, primarily because all parties recognise its importance. This collaborative approach involved multiple

lines of biological research including palaeopathological (Buckley et al., 2010), aDNA (Knapp et al., 2012), isotopic analyses (Kinaston et al., 2013c), and facial approximation (Hayes et al., 2012). The biological evidence was combined with analyses of material culture (Walter et al., 2006) and archaeozoological research relating to commensal and native species (Greig et al., 2015; Jacomb et al., 2014; Wilmshurst et al., 2008). The vast amount of data emerging from Wairau Bar means that research is ongoing, and there is still much to be discovered.

The reanalysis of the *kōiwi tangata* prior to reburial extended and, in some cases, clarified earlier analyses of the burials (Houghton 1975) including identification of gout and likely tuberculosis in the population, different demographic structure between the burial groups, and differential health patterns between males and females (Buckley et al., 2010). Isotopic studies have also indicated different patterns between the burial groups, with group 1, which contained not only the best-preserved remains, but also a large number of burial goods, having similar diets and similar childhood origins, which did not appear to be local. The isotopic results for burial groups 2 and 3 were much more variable in terms of diets and likely childhood environments (Kinaston et al., 2013c). The aDNA evidence from the Wairau Bar *kōiwi tangata* also provided some surprising results. Knapp et al. (2012) were able to obtain complete or near complete mitogenomes from four of the burials, and all four had different haplotypes, or maternal lineages. As the research continues several additional haplotypes have been found which together have implications regarding the number of founding females and ultimately for reconstructing the demographic history of New Zealand (Whyte et al., 2005).

The work being undertaken at Wairau Bar highlights the unique position of Pacific biological anthropology to shed light on processes of colonisation and human adaptation. The collaborative approach, in this instance, reveals a picture of a genetically diverse and mobile founding population. Research undertaken has enabled the exploration of the health and lifestyle in the earliest New Zealanders. Collaboration with descendant communities, including DNA sampling of *iwi* members means that cultural and genetic links between ancestral and modern population can be more fully explored. For the first time, the faces and lifestyles of the ancestors are being revealed to their descendants. As the usefulness of biological anthropology in constructing and supporting indigenous identity is highlighted, further community-lead research is being encouraged, and new research projects developed.

The work at Wairau Bar highlights the more general theme of community-based research emerging particularly in the Pacific region. Biological evidence and local involvement are no longer considered add-ons to the archaeology. Instead, community participation and biological anthropology are integral research components, which are beginning to drive research design in the Indo-Pacific region. The unethical manner in which human remains were collected throughout much of the Pacific region (see introduction) in the 19th and 20th century cannot be glossed over

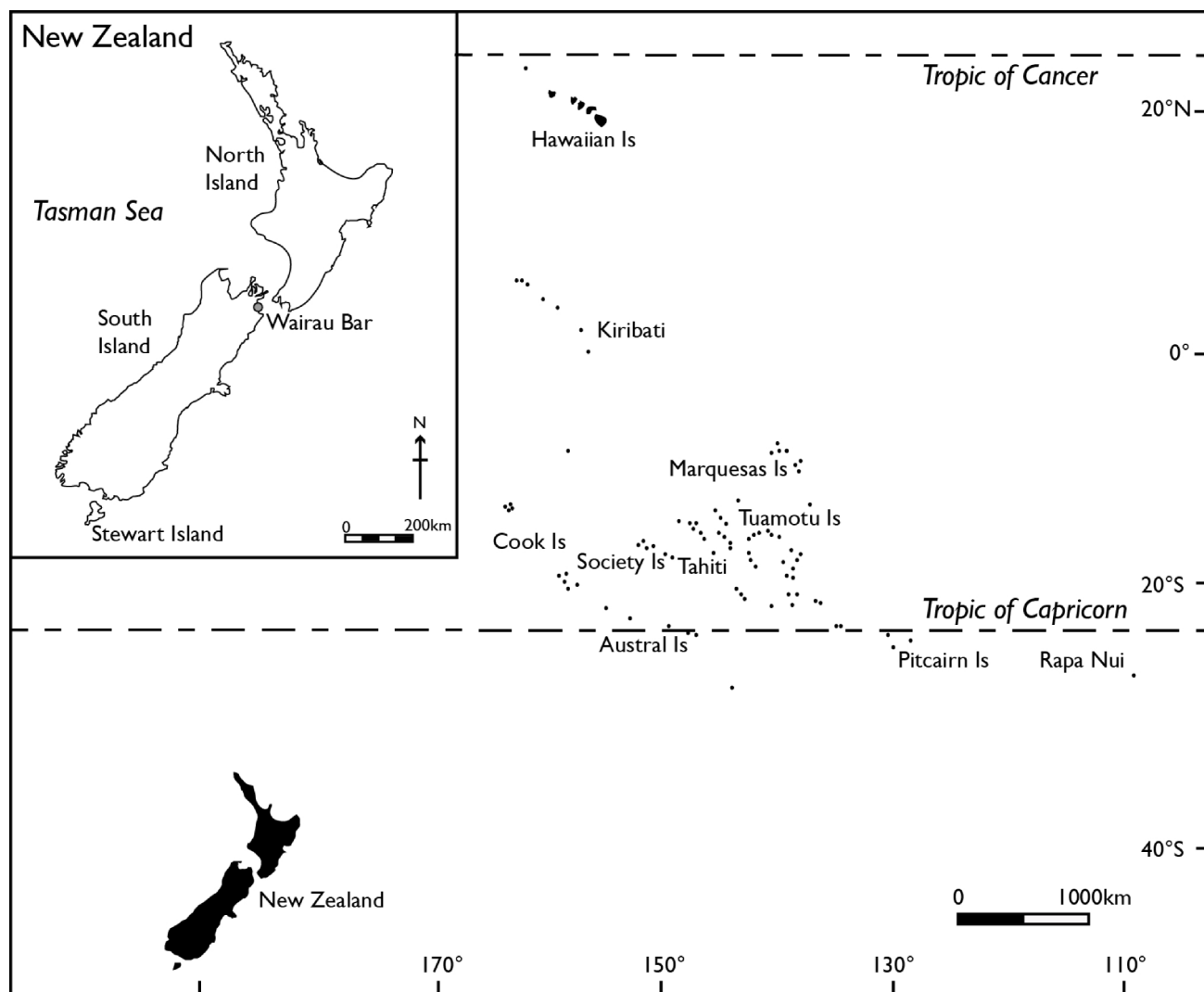


Figure 4: Location of Wairau Bar in the Pacific and New Zealand (inset). Figure reproduced with authors' permissions from Kinaston et al. (2013a).

or ignored, but it does appear we are entering a new chapter in research collaboration. Slowly trust is being regained and new relationships established (Bedford et al., 2011; Ruckstuhl et al., 2016) and we advocate for such approaches.

## CONCLUSION

Biological anthropological research in the Indo-Pacific region emphasises the diversity of life experiences and social changes during prehistory. Here, multiple lines of evidence are indicating retention of broad-spectrum subsistence choices in productive and diverse environments. Research in this region is allowing characterisation of subsistence diversity and demonstrating that models built using archaeological and biological anthropological evidence from Europe, the Near East and North America are not globally applicable.

Biological anthropological research has added new dimensions to the understanding of the human story in the

region. The biosocial approach provides essential context for understanding the cultural and biological complexity present not only in the past, but also in the modern world. For example, the study of biological and cultural adaptation to malaria in ancient and modern Pacific populations is shedding light on migration pathways and ancestral links in this region, as well as informing modern-day health research into the prevalence of disease.

This synthesis highlights the merits of biological anthropological research in the Indo-Pacific region. However, in order to make detailed and accurate interpretations, it is necessary to combine these data with other lines of evidence. There is growing recognition that investigation of the past needs to be multidisciplinary, incorporating evidence from archaeology with human remains and the perspectives of the descendent communities. The research undertaken at Wairau Bar epitomises this collaborative approach in combining archaeology, biological anthropology and community involvement. Research arising from

Wairau Bar is answering important academic questions regarding settlement processes and adaptation to the New Zealand environment. But, perhaps more significantly, the collaborative approach also has wider impacts, encouraging outreach and continued engagement with local and descendent communities.

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