Evolution of Asteraceae in the European Alps

Luca Pegoraro

School of Biological and Chemical Sciences
Queen Mary University of London
Mile End Road, London E1 4NS, UK

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Statement of originality

I, Luca Pegoraro, confirm that the research included within this thesis is my own work or that where it has been carried out in collaboration with or supported by others, that this is duly acknowledged below, and my contribution indicated. Previously published material is also acknowledged below.
Where not otherwise specified, I have provided the main data and material collection, analysis, manuscript drafting and revision. Experimental design has been collaborative but I always had ample freedom to direct it. Details of collaborations and publications:

Chapter 1 General introduction: Jaume Pellicer, Oriane Hidalgo and Andrew R Leitch have provided comments.

Chapter 2 The correlation of phylogenetics, elevation and ploidy on the incidence of apomixis in Asteraceae in the European Alps: Andrew R Leitch and Ilia J Leitch have provided insight and comments on the manuscript; Jaume Pellicer, Oriane Hidalgo and Luis Palazzesi have helped extensively during fieldwork and labwork a well as providing comments on the manuscript and analysis; Maïté Guignard helped with models validation; Ellen C Baker, Manica Balant, Rolland Douzet and Teresa Garnatje have contributed plant material to the research; David Aeschimann and Jean-Paul Theurillat have contributed data from Flora Alpina and comments. Two anonymous reviewers have contributed further comments.

Chapter 3 The evolution of genome size in alpine Asteraceae and its relationship with life history traits and ecological variables: Andrew R Leitch provided comments on the manuscript and analysis; Jaume Pellicer, Oriane Hidalgo have participated extensively in fieldwork and labwork, as well as commenting on manuscript and analysis; Robyn Powell helped with flow cytometry work in years 3-4 of the project; plant material and data providers contributions as for Chapter 2.

Chapter 4 Phenotypical and ecological differentiation of sympatric cytotypes of *Senecio doronicum*: Andrew R Leitch has provided comments on manuscript and analysis; Jaume Pellicer and Oriane Hidalgo have provided extensive help during fieldwork as well as comments on manuscript and analysis; Sarah Barlow has helped extensively during fieldwork and provided technical insight as well as comments for the analysis; Luis Palazzesi, Ellen C Baker took part in fieldwork and provided some initial comments; Robyn Powell provided the majority of flow cytometry readings for *Senecio doronicum* cytotype survey in the summer 2018.

Chapter 5 Automated video monitoring of insect pollinators in the field: Jaume Pellicer, Oriane Hidalgo, Sarah Barlow and Ilia J Leitch have provided comments on the manuscript.

Chapter 6 Rana automated pollinators monitoring on *Senecio doronicum* cytotypes: same as Chapter 4

Chapter 7 General discussion: Jaume Pellicer, Oriane Hidalgo and Andrew R Leitch have provided comments.

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Publications

Portions of the work detailed in this thesis have been presented at conferences and submitted as peer-reviewed publications, as follows:

- Chapter 2 is published as original research paper in Botanical Journal of the Linnean Society: L. Pegoraro, E. C. Baker, D. Aeschimann, M. Balant, R. Douzet, T. Garnatje, M. S. Guignard, I.J. Leitch, A. R. Leitch, L. Palazzesi, J.-P. Theurillat, O. Hidalgo, and J. Pellicer (2020) "The correlation of phylogenetics, elevation and ploidy on the incidence of apomixis in Asteraceae in the European Alps." *Botanical Journal of the Linnean Society*, 410-422, https://doi.org/10.1093/botlinnean/boaa058

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- Portions of Chapter 4 and 6 have been presented at international conferences Botanica Sudalpina[1] (November 2017) and Congresso Societá Botanica Italiana[2] (September 2019), as well as invited talk at the Department of Systematic and Evolutionary Botany, Universität Zürich (March 2018).

[1] https://www.botanicasudalpina.ch/en/2017
[2] http://www.societabotanicaitaliana.it/114/eng/detail.asp?idn=4819

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This thesis is typeset using LaTeX.

Abstract

We conducted an extensive flow cytometric survey of reproductive modes and genome sizes (GSs), combined with cytotype screenings for 100 genera and 335 Asteraceae species across elevation ranges in the Alps. We found that apomictic reproduction was tied to odd ploidy levels (e.g. 3x, 5x) and showed strong phylogenetic signal, but did not correlate with elevation or phenology. Most species analysed were diploid, with GSs skewed towards small values. Short life cycles (annual or biennial) and endemic status were linked to smaller GSs, while elevation, nitrogen soil content preference and phenology were not.

We analysed a sympatric mixed-ploidy population of *Senecio doronicum*, gathering ploidy and phenotype data. We found divergent phenology between cytotypes, with octoploid specimens flowering earlier than tetraploids. Also, cytotypes showed phenotype differences. Octoploids were taller and had larger capitula with more florets, and tetraploids had more numerous capitula with fewer florets and more pollen per floret. Likewise, cytotypes exhibited micro-niche differences: octoploids occupied a larger niche and grew in denser communities, while tetraploids occupied marginal habitats with sparse vegetation. Despite their abundance, reproductive success was lower in octoploids, that suffered attacks by a pre-dispersal seed predator.

Available automated pollinator monitoring systems were reviewed, and one of such systems (Rana) was deployed to monitor insect visits on *S. doronicum*. The main visitors were short-tongued insects (flies and small bees), mostly hoverflies. Octoploids received less visits and lower proportion of feeding visits than tetraploids. Most of the feeding visits to octoploids were made by *Syrphus* and to tetraploids by *Eristalis*. Overall, each cytotype showed distinct pollinators communities with similar extents of variation.

This thesis provides novel insights into how genomic processes, such as polyploidization, and ecological processes, such as pollination, can shape plant diversity both at the local (sympatric population micro-evolution) and geographical (Asteraceae family macro-evolution in the Alps) scales.

Contents

List of Figures

List of Tables

List of abbreviations

AI	Artificial Intelligence
ANN	Artificial Neural Network
GS	Genome Size
LGM	Last Glacial Maximum
MCMCglmm	Markov Chain Monte Carlo generalized linear mixed model
ML	Machine Learning
mya	millions of years ago
NMDS	Non-Metric Dimensional Scaling
PCA	Principal Component Analysis
PERMANOVA	PERMutational ANOVA (ANalysis Of VAriance)
QMUL	Queen Mary University of London
RBGK	Royal Botanic Gardens, Kew
WGD	Whole Genome Duplication

Chapter 1

Introduction

1.1 The study of evolution

Evolution is fuelled by heterogeneity in environmental conditions, interactions between species and genetic frequencies. With Darwin first ([1]) and the modern synthesis later ([2–4]), the sources of natural variation driven by the environment and the genome have provided a theoretical framework to model and test evolution. An influential idea proposed by Eldredge ([5]), termed the "sloshing bucket model", considers organisms as the meeting point of ecological (i.e. proteins to ecosystems) and evolutionary (i.e. genes to species) hierarchies. Change or evolution at any given level in these hierarchies can cause feedback into the other, driving diversity. One phenomenon that can have wide-ranging repercussions for both hierarchies is polyploidy, or Whole Genome Duplication (WGD) (i.e. the duplication of an entire set of chromosomes), a phenomenon which is a major focus of this thesis.

1.1.1 Polyploidy in plants

1.1.1.1 Polyploidy incidence and genomic impact

Genome-wide mechanisms such as polyploidy are one of the most dramatic genomic phenomena known, yet despite the enormous changes they stimulate polyploidy is tolerated and viable in many eukaryotes ([6, 7]). Polyploids can originate via somatic doubling (e.g. endopolyploidy), polyspermy or unreduced gametes, of which the latter seems to be the most common ([8, 9]). Polyploids are spontaneously generated in natural populations, and can arise from the same or closely related lineages (autoployploids) or from hybridization between different lineages (allopolyploids) ([10–12]). Polyploids often have complex patterns of hybridization (either with parental or different lineages), and can undergo subsequent genome reorganization ([13–15]), effectively generating genetic variation from different sources of genetic diversity ([16, 17]). Polyploidy is often accompanied over time by large-scale genome reorganization, including (but not limited to) gene silencing, gene expression diversification, dosage effects of multiple gene copies and epigenetic changes ([18–20]), that contribute to the phenotypic plasticity and rapid adaptation, as observed in neopolyploids ([21–23]).
In seed plants, after WGD there often follows a phase of diploidization that can involve neo- and subfunctionalization of genes where duplicate genes may take on tissue specific, new or different functions ([24–26]). There can also be genome downsizing occurring through the deletion of DNA during recombination (often repetitive sequences). Large-scale chromosomal rearrange-

ments may also follow polyploidy, with translocations between non-homologous chromosomes potentially causing chromosome number changes (dysploidy, [27–29]). Such mechanisms contribute to transforming a polyploid genome into a functionally "diploid" genome, and multiple cycles of polyploidization and subsequent diploidization are thought to have underpinned diversity and novelty in angiosperms ([30, 31], however [32] argues that this has only been tested indirectly). In fact, it is thought that polyploidy is one of the most prominent factors responsible for the evolution of flowering plants ([10, 16, 33]). It is probable that all eudicots have undergone ancient and/or recent polyploidization events in their ancestry ([34–36]). Chapters 2 and 3 of this thesis expand on the interactions between ploidy level, genome size (GS) and chromosome number changes in polyploid divergence. Whilst much is known about genome divergence in polyploid angiosperms, at least some of these processes are less frequent in ferns ([37, 38]), and WGD is rare in most lineages of gymnosperms ([38–40], but see [41, 42] for examples of polyploidy in this group).

1.1.1.2 Allopolyploids and autopolyploids

Allopolyploids have long been recognized in plants because they are often morphologically different from their parent lineages ([10, 16, 33]). In addition, the genetic and ecological implications of allopolyploidy have been intensely studied ([4, 14, 43, 44]). Autopolyploids have multiple sets of the homologous chromosomes, and at least in neoautopolyploids, polysomic inheritance (i.e. the formation of multivalents between more than two homologous chromosomes). In contrast, allopolyploids have sets of homeologous chromosomes, and are more likely to exhibit disomic inheritance (i.e. pairing between chromosome belonging to the same subgenome, [10]). Studies of hybrids indicate that they are more likely to produce unreduced gametes at high rates ([11, 45, 46]), a process that bypasses problems associated with imperfect homeologous pairing (i.e. pairs of chromosomes that share homology in some regions but are distinct from one another). This provides the opportunity for allopolyploid formation via diploid gamete formation ([6, 9]). Allopolyploids can in turn benefit from "hybrid vigor" and increased heterozygosity, traits that have been linked with polyploid establishment and success in ecological and evolutionary contexts ([16, 17, 47]).

Autopolyploidy in plants has been considered to be less frequent and an evolutionary dead-end ([4]), possibly because autopolyploids were rarely recognized in taxonomy, and it still remains difficult to detect cryptic autopolyploid cytotypes ([43, 48, 49]). However, evidence has been accumulating that autopolyploids are as common as allopolyploids in flowering plants (reviewed in [50]). The ecological changes brought about by autopolyploidy can be subtle ([49, 51]), and their demographical establishment could be subject to chance ([14, 47, 52]). However, novel allelic combinations and regulatory pathway alterations could produce advantageous phenotypes which selection can act upon, increasing the likelihood of polyploid population establishment ([18, 53]).

The success of allopolyploids in angiosperms could be due to their higher chance of establishment, by virtue of their immediate isolation from their parents' ecological niches and increased opportunity of intra-cytotype mating ([10, 54]). Nonetheless, autopolyploids are probably generated at a higher rate than allopolyploids, and could therefore have more opportunities to form long-lived lineages, potentially accounting for the observed parity in the occurrence of allo- and autopolyploids in angiosperms ([49, 50]).

1.1.1.3 Ecogeographical effects of polyploidy

The phenotypic manifestations of polyploidy were not lost on early researchers, who described the suite of changes in neopolyploids as the "gigas effect": increased cell size, slower cell division and tissue growth, larger organ size at maturity, reduced fertility and increased propensity to self-pollination (reviewed in [55]). Further correlations emerged in findings that polyploidy is more frequent in perennial taxa than short-lived taxa (that often lack vegetative reproduction). They are also more common in self-fertilizing than outcrossing groups, in groups that reside in recently glaciated areas (Pleistocene) and in taxa that occupy large geographical areas ([43, 56–60]). More recently, studies have leveraged flow cytometric screening of ploidy levels and showed that the effects of ploidy vary from taxon to taxon. Nevertheless, on average, polyploids tend to be taller, have larger and thicker (but fewer) leaves and floral structures, and initiate flowering later than diploids ([47, 61–65]). Polyploidy has also been linked to shifts to asexual reproduction via apomixis (reviewed in [66], see also Chapter 2) and with the likelihood of becoming invasive ([67–71]).

Early studies regarding the distribution of polyploids suggested that polyploids are more frequent at higher latitudes ([72–74]), however this could be driven by other factors correlated with latitude (reviewed in [10]). The relationship between polyploidy and elevation however is less clear, with some studies finding diploids ([75–77]) and others finding polyploids ([78–81]) to be more abundant and/or performing better at higher elevations, and such correlations are likely to be associated with covariates of elevation (reviewed in [82]).

Biotic interactions, such as competition, herbivory and pollination remain especially poorly investigated in relation to polyploidy, but they are likely to be important for polyploid establishment and evolution and remain a promising areas of study ([83–88], reviewed in [51]). Most investigations of polyploidy in an ecological context have studied established polyploids. Potentially, this has led to overestimates of the divergence caused by polyploidy, since these lineages will have evolved through selection and drift since they formed ([10, 11, 89]). However, the body of knowledge generated has highlighted how polyploidy is a possible path to speciation, provided that (neo)polyploids become reproductively isolated from their progenitors and can evolve independently.

1.1.1.4 Reproductive isolation and ecological reinforcement as a mechanism for polyploid speciation

Polyploidy is *de facto* the only widely accepted mechanism for sympatric speciation, as neopolyploids can be instantaneously separated from their progenitors via gametic incompatibility, hybrid sterility or ecological differentiation ([6, 14, 90]). However, in the early stages of establishment, neopolyploids will occur at low frequency in a diploid population and lack compatible mates (i.e. minority cytotype exclusion; [91]). In the absence of recurrent production of polyploid individuals, polyploid lineages are prone to extinction ([9, 89, 91]). Neopolyploid establishment can be facilitated by reproductive isolation mechanisms arising between them and the progenitor lineages, which can increase the probability of successful mating between polyploid individuals ([89]). The continuous production of unreduced gametes ([92–94]) and the occurrence of partially fertile triploids ([83, 94–96]) may result in the recurrent formation of polyploids, promoting their establishment by increasing the number of potential mates. Additionally, self-pollination may decrease the extinction rate of newly formed polyploid lineages ([91]), and autogamy has been found to be higher in polyploids than in diploids (e.g. [97]).

Other mechanisms may instead increase the chance of within-cytotype matings, reducing the expenditure of gametes delivered to the other cytotype (i.e. reinforcement, [90]). In entomophilous plants, assortative mating mediated by pollinators seems to be a major component of reproductive isolation between diploids and autopolyploids ([83, 98, 99]). Indeed, the few available studies investigating interactions with pollinators of different cytotypes suggest that pollinators may respond differently to different cytotypes when ploidy is associated with a difference in floral traits and/or in flowering phenology ([87, 100–102]).
Even though polyploid speciation has been theorized primarily in the context of strong post-zygotic reproductive isolation (e.g. triploid hybrid sterility, [94, 96]), the contribution of multiple components of reproductive isolation could be important (e.g. [102, 103]). An emerging trend from multiple studies is that pre-zygotic reproductive isolation between sympatric polyploid cytotypes could be more important than post-zygotic barriers ([98, 101, 103], but see [104]) and comparable in magnitude to pre-zygotic reproductive isolation between diploid cytotypes ([105–108]).

1.1.1.5 Intraspecific cytotype diversity and mixed-ploidy populations

Many taxa exhibit intraspecific cytotype diversity (e.g. [109–114], reviewed in [115]), and the contact zones between different cytotypes are of great evolutionary interest ([55, 116, 117]) as they represent a window on how polyploidy might have shaped plant diversity. In general, species with multiple cytotypes have one or more dominant cytotypes that are widespread, but they rarely occur in single-ploidy populations and rather tend to form contact (or hybrid) zones with other cytotypes ([10, 115, 118]). It is often unclear whether mixed-ploidy population are the result of polyploids being generated locally or if they have migrated from other, diverged populations (secondary contact in the latter case). Resolving these possibilities requires the age and occurrence of recent polyploids to be established ([119]).
Autopolyploids often share the ecological niche with their diploid progenitor, as seen in most studies of mixed-ploidy species (e.g. [14, 49, 120–123]). In sympatry, diploids and autopolyploids will compete for the same biotic and abiotic resources, generally resulting in the establishment of a more successful cytotype at the expense of the other. If the two cytotypes have no ecological differentiation, the newly formed autopolyploids could establish themselves by competitive superiority due, for instance, to higher relative fitness ([93, 124]) or to higher intrinsic plant vigour ([18]). Potentially, autopolyploids may establish simply through the power of genetic drift too ([125]). However, polyploids are often found to have higher seed set than their diploid progenitors in natural populations ([116, 126], but [127] reports the opposite in introduced *Centaurea*). Alternatively, the coexistence of diploids and autopolyploids can be stable due to ecological differentiation of cytotypes following adaptive processes (even at small spatial scales) that increase the chance of intra-cytotype mating ([111, 115, 128, 129]). This ecological divergence is driven by environment-dependent selection and can generate differentiation in microhabitat preference (both at the regional [130–132] and local [111, 133, 134] scales), floral morphology ([100, 135]) and flowering time ([101, 126]), as well as by the pollinators that occur and their choices ([98, 136]). Ecological divergence can also indirectly produce reproductive barriers that enforce assortative mating that favours stable cytotype coexistence so that, in mixed populations, cytotypes are ecologically and reproductively isolated (e.g. [102, 137, 138]). Furthermore, the phenotypes of cytotypes tend to be more divergent in sympatric populations than in allopatric populations ([113, 126, 132]), suggesting that interactions between cytotypes

enhances diverging selection. It is crucial for future studies of mixed-ploidy populations to explicitly distinguish between divergence caused by the polyploidy event *per se* (e.g. by synthesizing neopolyploids) and subsequent evolution, either by selection or drift ([115]).

1.1.2 Phylogenetic comparative methods

Since Felsenstein's seminal paper on independent contrasts ([139]), several more methods have developed tests for the independent evolution of traits in phylogenetically related organisms. The basic idea is to use a given (i.e. assumed known) phylogenetic structure to compute a "correction" that is applied to the trait values at the tips of the phylogenetic tree. In doing so, a statistically independent trait value is derived that has the same distribution as the original data. One of the most common applications of the method is PGLS (phylogenetic generalized least squares, [140, 141]), that extends generalized least squares regression that assumes residual errors are statistically independent and identically distributed. PGLS allows the residual error to vary proportionally to a variance-covariance matrix (V) derived from the phylogenetic tree and an assumed evolution model ([142]). The structure of V is independent of the trait values and is the part of the model that accounts for phylogenetic relationships ([143]). The value of V can be estimated with different models of trait evolution (e.g. Brownian motion, Pagel's lambda, Ornstein-Uhlbeck) and the models extended to non-continuous variables ([144]).
Further developments have seen the use of Monte Carlo (MC) simulations to create a large number of datasets that conform to the null hypothesis (e.g. traits are not correlated), against which the real data can be tested (i.e. the simulated datasets effectively constitute the null distribution; [145]). Modern implementations use tools developed in quantitative genetics, involving a Bayesian framework with a Markov Chain Monte Carlo sampler (MCMC, in which the state at each step depends solely on the state at the previous step). This generates null distributions and integrates the flexibility of generalized linear mixed models (GLMM) allowing for, amongst other things, multi-response (i.e. multiple dependent variables) and multinomial models (i.e. that can handle discrete traits and continuous traits) ([146]).
Particularly widespread in evolutionary studies are questions about the phylogenetic independence of traits (often referred to as phylogenetic signal), and two measures are widely used: Pagel's λ ([147]) and Blomberg's K ([148]). Pagel's λ measures the adherence of trait values to expected trait values under Brownian evolution model along a given phylogenetic tree, and varies from 0 (complete independence from phylogenetic structure) where traits of strict relatives are not more similar than those of distant relatives to 1 (complete dependence from phylogenetic structure), where traits of closely related taxa are much more similar than those of distantly related taxa. This statistic has been questioned in its power and applicability, but it has been proven to be robust even with incomplete phylogenies and sub-optimal branch length information, provided that the assumption of Brownian evolution is upheld ([149, 150]). Blomberg's K also assumes a Brownian model of evolution and uses the variance of the trait at the tips of the tree to be scaled to the variance of traits corrected by the phylogenetic structure; it ranges from 0 (absence of phylogenetic signal), where the variance within closely related taxa is similar to that of distantly related taxa to >1 (strong phylogenetic signal) where the variance within relatives is higher than expected under Brownian motion. This measure, K, although robust with respect to incomplete phylogenies, is not devoid of criticism and may provide inflated estimates in the case of deep polytomies ([151, 152]).

1.2 The European Alps

1.2.1 Geographical delimitation

The definition of "mountain" is a debated topic, and can accommodate both cultural and geographic definitions ([153]). For the study of biogeography a strict definition is necessary, and only recently have catalogues of mountain areas been compiled globally ([154]). The European Alps have been historically delimited by their geographical extent in a variety of ways, which are often discordant. Delimitations of mountain areas are given in many regional Floras of the alpine countries (France, Switzerland, Germany, Austria, Italy and Slovenia), see for example [155–157]. However, the most comprehensive treatise on the flora of the Alps is Flora Alpina ([158]). This provides a geographical delimitation of the Alps that has been widely adopted (albeit with modifications) by many recent works (Figure 1.1).

The most important features of the delimitation of the Alps in Figure 1.1 is the exclusion to

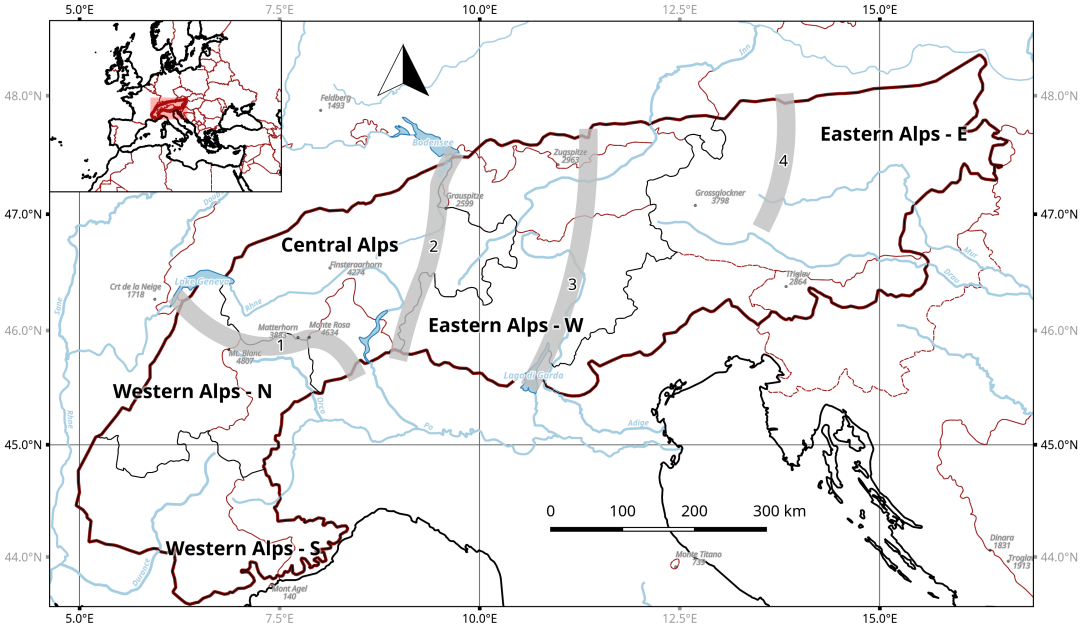

Figure 1.1: Map of Alps and their main geographic sectors, redrawn after [159]. The outline of the Alps is in dark red (solid line), and national borders are in light red (thin red line); thick grey lines represent notable biogeographical separations: 1 = from Lac Léman to Lago Maggiore, demarcating the separation of Western and Central Alps; 2 = from Bodensee to Lago di Como, diving Central and Eastern Alps; 3 = following the Isarco-Adige valleys, dividing the Eastern Alps in their Western and Eastern parts; 4 = from Traun to Lieser, separating the floristically distinct "noric province" to the East. Datum: WGS 84

the West of reliefs immediately contacting the Mediterranean in France (Provence-Alpes-Côte d'Azur) and Italy (Liguria), the exclusion of moraine hill systems to the South (especially in the Po valley, Italy) and to the East (Niederösterreich, just before reaching Vienna). This definition of the Alps encompasses an area of 171,000 km^2, stretching for ~800 km in length and ~200 km in width, divided among seven countries (in order of surface occupied): Austria, Italy, France, Switzerland, Germany, Slovenia and Leichtenstein (Figure 1.2).

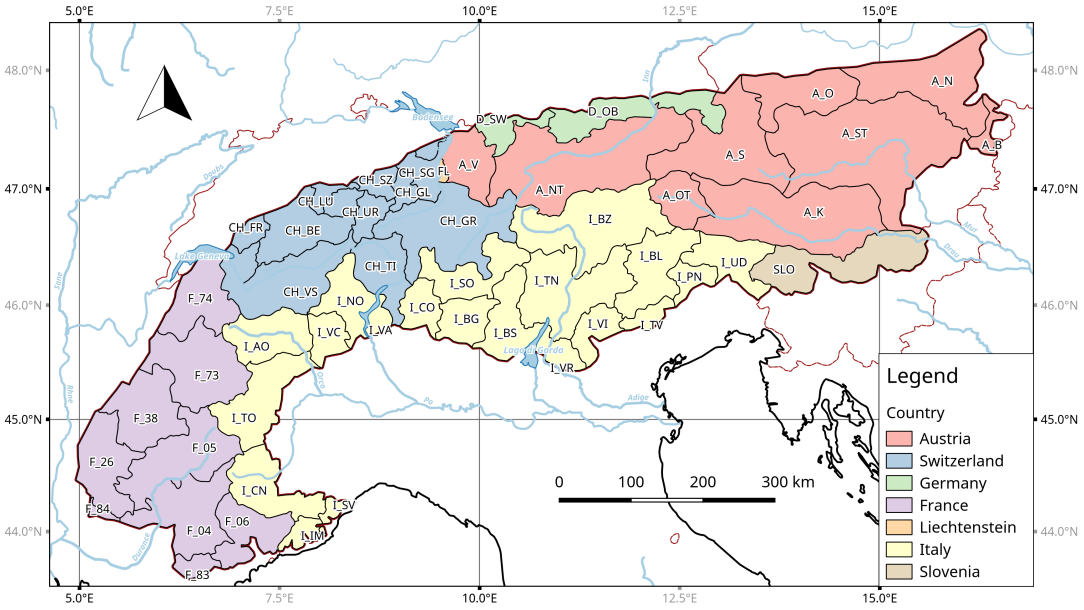

Figure 1.2: Map of the administrative sectors in the Alps and of the alpine Countries, redrawn after [159]. Administrative sectors are indicated by an acronym of their country and province, canton, land or other territorial division. Countries are indicated with different colours. Datum: WGS 84

1.2.2 Orogenesis and geology of the Alps

The European Alps are one of the best-known mountain ranges in the world, due to their location surrounded by densely populated areas. Naturalists began studying rocks and their formation in the Alps during the XVIII and XIX centuries, and many discoveries were made that lead to the formulation of modern geological theories ([160]).

The Alps are a "young" mountain chain, originated from orogenic processes in the Cretaceous and Cenozoic periods (145-66 mya and 66 mya-present, respectively) caused by the collision of the African and Eurasian plates [161]. Their rock composition is complex and reflects the multiple origins, ages and fates of the tectonic components. In broad terms, the oldest rocks form the lower layers and are of continental European origin, overlain with oceanic (Tethyan) sediments in the middle and younger rocks above derived from the African plate ([162]). The orogenic thrust starting in the Paleogene (∼35 mya) caused folding and fracturing of the layers, eventually leading to the uplift of the alpine belt, with subsequent erosion exposing the different layers (especially evident in the highest peaks of the Central Alps). This resulted in a variegated bedrock landscape, that in turn has influenced plant communities in the Alps (for a detailed map of bedrock types follow this link[1]).

Crystalline rocks (i.e. metamorphic) are more resistant to erosion, and that is in part the reason why the highest peaks in the Alps (with Mont Blanc as the highest, 4,808 m) are found in the Western and Central Alps, while calcareous rocks tend to form stark, acuminate peaks that are more prone to erosion and karst formation. The main edaphic factor is the pH from the bedrock type (e.g. acid substrates = silicicolous, generally crystalline or igneous rocks; basic substrates = calcicolous, mostly sedimentary rocks, like limestone and related to the proportion of calcareous rocks). The overall geology of the Alps (loosely based on [161–164]) reveals that the Southern Western Alps are characterized by mostly sedimentary calcareous rocks, but with the intrusion of crystalline rocks (i.e. not calcareous) corresponding with the

[1] https://perso.univ-rennes1.fr/romain.bousquet/Alps/Maps/tecto.html

high peaks at the Franco-Italian border. The Northern Western Alps are mostly crystalline, as are the Central Alps, with a high proportion of metamorphic rocks (i.e. granite) that host all the peaks >4,000m. All of the Eastern Alps are dominated by calcareous rocks, with only localized regions showing decalcification and intrusions of magmatic rocks. The Dolomites fall within this range and are the result of the most recent alpine uplift that exposed sedimentary rocks originating from ancient coral reefs, and the calcareous mineral bearing their name (dolomite) characterizes limestone massifs throughout the Eastern Alps.

1.2.3 Glaciations and plant biogeography

The current floristic arrangement in Europe (and in the Northern hemisphere in general) has been largely shaped by the last glacial cycle that began in the Pleistocene (2.58 mya), with the last glacial maximum in the Alps occurring around 21-24,000 years ago ([165, 166]). During this time, the vast majority of the Alps were covered in ice, reaching a maximum surface area of 163,000 km^2, stretching from the present-day location of Grenoble (France) to the West to roughly Graz (Austria) to the East (Figure 1.3).

Plant populations cannot survive in glaciated regions, but during interglacial periods plants

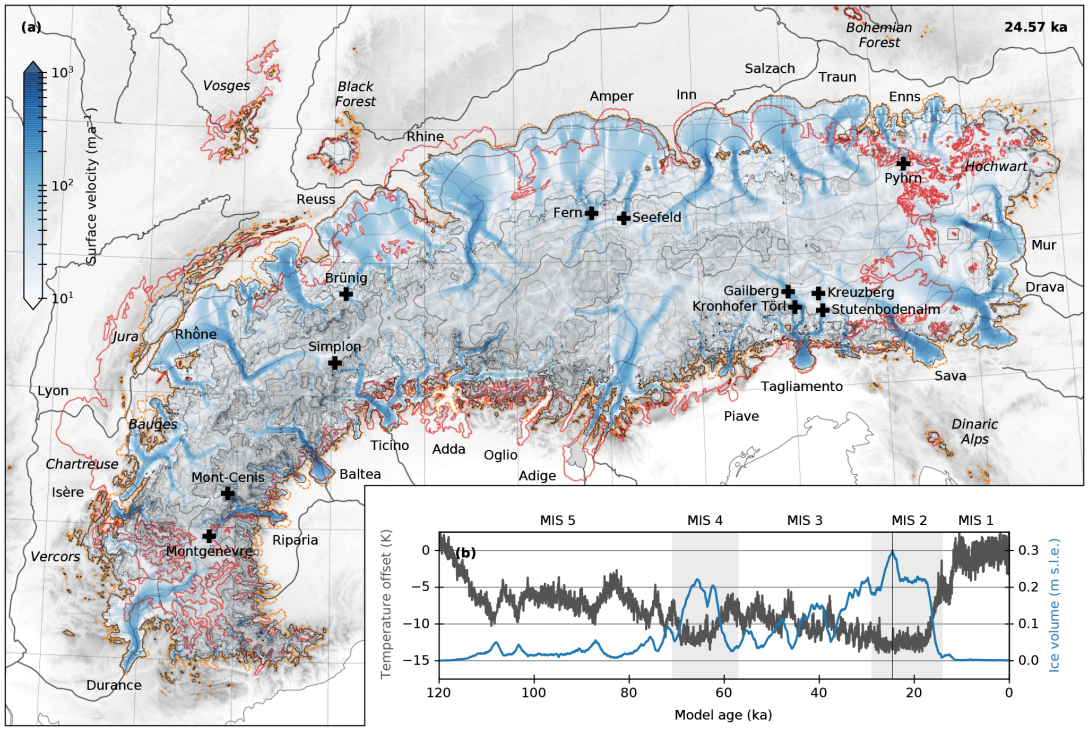

Figure 1.3: Last Glacial Maximum (LGM) 24,570 years ago, reproduced from [166]. a) the solid red line summarizes LGM extent from previous glaciation maps, and the orange dashed line is the newly modelled ice extent. Shades of grey represent the reconstructed relief topography, with grey lines representing ice surface topography, 200m apart from each other. Shades of blue indicate glacier flow, with crosses demarcating major transfluences. b) temperature offset series (black line) and total ice volume (blur line) over the past 120,000 years. The evolution of the ice sheet is also available as a video at this link[2].

recolonize the exposed land. This cycle has occurred multiple times in association with the glacial cycles across Northern Europe. During the LGM there was an almost uninterrupted ice sheet stretching from the British Isles to the Caucasus ([165, 167]), which resulted in the com-

[2]https://av.tib.eu/media/35164

plete eradication of plants, which only returned during the subsequent interglacial ([168–170], but see [171] for rare examples of *in situ* survival in *Sagina caespitosa* and *Arenaria humifusa*, two pioneer species with disjunct amphi-Atlantic distribution). The picture is however complicated in the Alps because of the terrain and glacier dynamics, which could have left refugial areas disjunct from one another and fostered independent population histories ([172–174]). The two alternative (but not mutually exclusive) biogeographical scenarios for the flora of the Alps following the quaternary glaciations therefore are: *tabula rasa*, with the complete eradication and subsequent recolonization from periglacial populations, or *in situ* survival in nunataks, with local populations surviving on unglaciated mountain peaks emerging from the ice sheet ([175–177]). These two should be regarded as extremes of a continuum rather than completely opposed situations ([174]), because ecological as well as reproductive traits have influenced the population history of each species during glaciations ([178]).

A great deal of effort has been spent inferring glacial refugia (i.e. areas in which plant populations survived glaciations, and from which recolonization began), with molecular as well as paleovegetation evidence establishing some areas as glacial refugia ([179–181]). Refugia are proposed in the South-Western Alps and in the easternmost Eastern Alps, as well as several smaller refugia scattered along the Southern border and few on the Northern side (Figure 1.4).

The contribution of nunataks to post-glaciation recolonization is a long-standing debate in

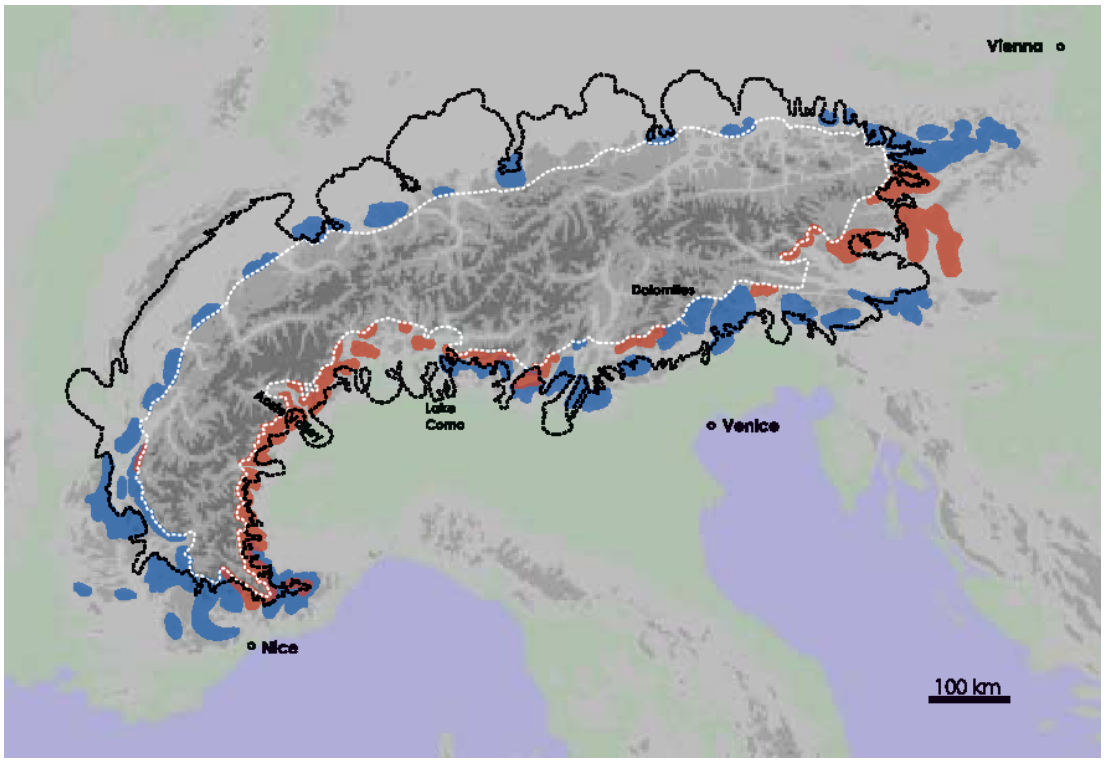

Figure 1.4: Pleistocene glacial refugia of the Alps, reproduced from [179]. Areas coloured in blue are glacial refugia on calcareous bedrock, areas in red are refugia on siliceous bedrock. The dashed black line indicates the estimated Last Glacial Maximum (LGM), and the dashed white line indicates the glacial snow line.

alpine botany ([175, 177, 182, 183]), but they seem to have been important in the evolution of some lineages at least in portions of the alpine arc ([184]). The most widely accepted proposition is that those genotypes that survived *in situ* integrated into the gene pool of postglacial immigrants from periglacial populations.

There are numerous studies tracing the history of specific species or lineages through the last

glaciations, a few examples: *Androsace alpina* (Alps endemic, Primulaceae, [184, 185]), *Primula marginata* (S-W Alps endemic, Primulaceae, [120, 186]), *Saxifraga florulenta* (Maritime Alps strict endemic, Saxifragaceae, [187]), *Phyteuma globularifolijm* (widespread, Campanulaceae, [181, 188, 189]), *Campanula rotundifolia* (widespread, Campanulaceae, [190]), *Bupleurum stellatum* (Alps endemic, Apiaceae, [191]), *Anthyllis montana* (widespread, Fabaceae, [192–194]), *Ranunculus kuepferi* (Alps endemic, Ranunculaceae, [195]), *Gentiana ligustica* (Maritime Alps strict endemic, Gentianaceae, [196]); for studies specific to the Asteraceae family, see Section 1.3.2. Only a handful of these works take into account many unrelated taxa in an effort to pick up general biogeographic patterns ([178, 181, 197]): it seems that each plant group is to some degree unique, without a clear general pattern emerging ([172, 198]). Nevertheless, is clear that repeated and severe glaciations cycles in the Alps impeded the undisturbed evolution of species rich lineages, resulting in the current melting pot of lineages seen today, originating from multiple glacial refugia ([199]).

1.2.4 The flora of the Alps

The unique flora of the Alps historically has attracted much attention, reaching as far back as the sixteenth century ([200, 201]), and many explanations have been offered for the extraordinary diversity and peculiarity of alpine plants, many of which are still debated today. The biodiversity is mainly the result of the multiple floristic influences, rather than speciation events *in situ* ([202]), and biogeographic patterns can only be appreciated by taking into account the entire European Alpine System (EAP). This includes not only the Alps, but also the Pyrenees, Apennines, Carpathians, Dinarids and Balkans, as well as other minor mountain groups (e.g. the Massif Central, the Jura mountains, the Vosges, the Black Forest mounts, [199, 202]).

Mountains can be divided in elevation zones, largely based on vegetation patterns (Figure 1.5)

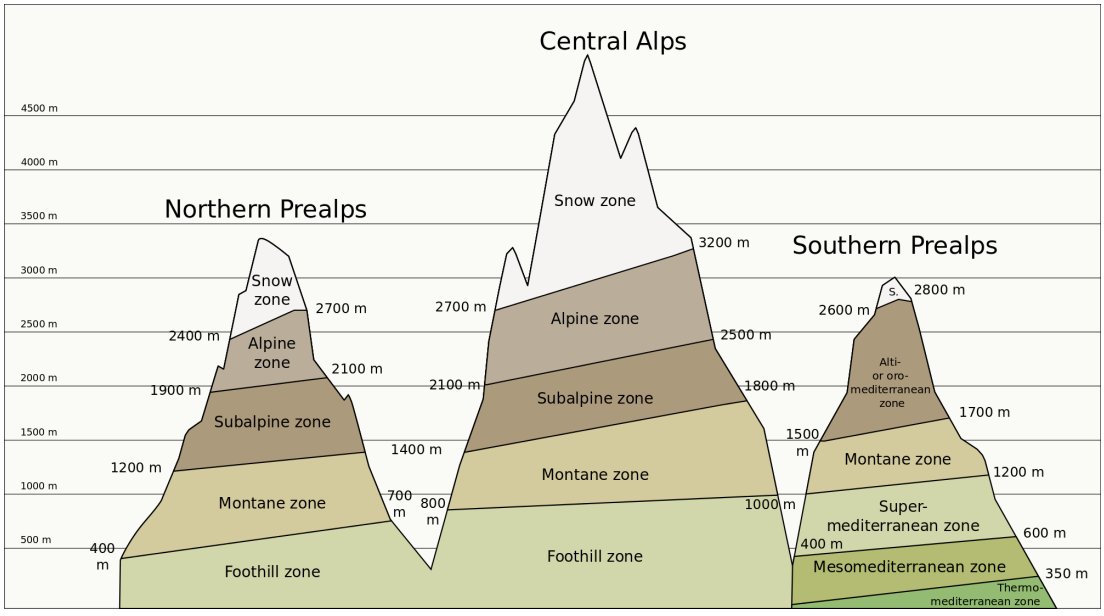

Figure 1.5: Elevational zonation in the European Alps, image from Wikipedia[3]. This schematic representation assumes that the Northern aspect is on the left-hand side, and the Southern aspect on the right-hand side. Elevation values are to be treated as indications only, and are largely based on values reported in [203]. The nomenclature for the Southern Prealps is not universally accepted, but is frequently found in regional floristic accounts of these regions.

which vary with latitude and exposure (i.e. Southern aspects receive more radiant heat from the sun and have higher mean temperatures than Northern aspects). Adopting the definition given in [202], five elevation zones can be distinguished in the Alps: the lowermost zone is the foothill (also called "colline", $\lesssim$800 m), with vegetation that is virtually the same as primary vegetation of adjacent flatland areas (mostly thermophilic broadleaf forest and sclerophyllous forest in the Mediterranean ranges); the montane zone occupies the middle elevations ($\sim$800-1,600 m) and its upper limit is demarcated by the timberline, and sees a gradual transition to more cold-tolerant tree species (mainly beech and spruce); the subalpine zone is broadly defined as the ecotone between the timberline and the tree species line (i.e. the transition between closed forest and the highest areas where tree saplings can establish, $\sim$1,600-2,300 m), and is characterized by a mosaic of trees of different statures and grass heath; the alpine zone ($\sim$2,300-2,800 m) is sometimes subdivided in lower, mid and upper alpine, and features dwarf-shrub communities (e.g. *Pinus mugo*) that give way to grassland, steppe-like vegetation (often dominated by sedges, e.g. *Carex curvula*) that becomes increasingly patchy at higher elevations; the nival zone ($\gtrsim$2,800 m) is dominated by rock and ice, with only isolated plants, frequently with rosette or cushion life forms ([202–205]). This general subdivision is influenced by heterogeneous landscapes and local microclimates that can locally change this overarching pattern of zones. Long-term anthropic activities (e.g. grazing, logging and reforestation) have also substantially altered the natural vegetational succession in many areas (especially the treeline ecotone has been affected, and its reliability as an ecological indicator is debated, [206–208]). Nevertheless, it remains useful for a general understanding of vegetational and floristic patterns to refer to elevational zonation.

1.2.4.1 Flora Alpina summary

A number of regional floras for the Alps have been published ([155, 156, 209, 210]), but to date the only work that encompasses the whole of the Alps remains Flora Alpina ([158]). The following subsections are largely based on the publications that accompanied the publication of Flora Alpina (*Analyse de la flore des Alpes* series, published in French in *Candollea* between 2011 and 2013: [159, 211–215]), that analyse in detail the floristic composition and its ecological relationships in the Alps. The focus of these subsections is a synopsis of the floristic and ecological aspects relevant to the present work, with emphasis on family Asteraceae where appropriate. Where presented, the numbers of taxa and percentages are not adjusted for any taxonomic changes that may have occurred and reflect the original figures in the articles.

The flora of the Alps is composed mainly of species typical of the montane zone across Southern European mountain ranges, by Mediterranean species and to a lesser extent by continental European and Asiatic species. Arctic species are represented only at the highest elevations (but make up a high proportion of species found there), and American species are frequent in the alien flora. The floristic diversity is highest where an essentially temperate flora is enriched by Mediterranean elements.

It is apparent that species diversity decreases with elevation and that endemics are more frequent at high elevations. Overall diversity is highest in endemism hotspots and occurs in areas that correspond with major glacial refugia. The flora of the Alps comprises $\sim$4,485 species level taxa, representing a little over two thirds of the European angiosperm flora. The most numerous family in the Alps is the Asteraceae ($\sim$557 taxa), and the most speciose genus is *Carex* ($\sim$115 taxa). There's a North-South diversity gradient in the Alps, with the Southern

[3] https://en.wikipedia.org/wiki/Altitudinal_zonation

margin harbouring more than 85% of the whole Alps' flora. The regions with higher taxa diversity extend from the southernmost belt from the South-Western Alps to the border with Friuli (highest diversity in the Maritime Alpes), while the lowest diversity is in the North-East (lowest in Niederösterreich, extreme excluded), see Figure 1.6.

The vast majority of species in the flora of the Alpes are perennial, and the proportion

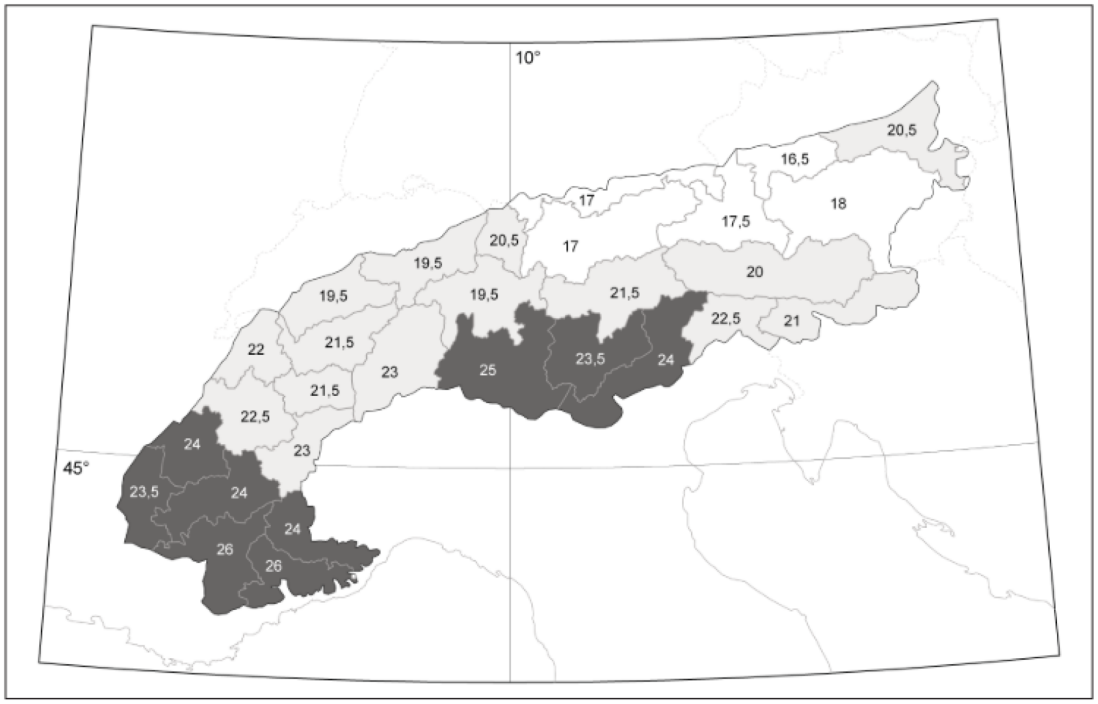

Figure 1.6: Figure reproduced from [159], representing the percentage of the total taxa occurring in the Alps that are present in each of the administrative sectors (see [159]). Colours represent the relative richness compared to the average: white = below average (<19.5% taxa/sector); light grey = average (19.5-23.5% taxa/sector); dark grey = above average (>23.5% taxa/sector).

of perennials increases with elevation. The most frequent life form is hemicryptophytes (e.g. herbaceous perennials), but chamephytes (e.g. cushion plants) are also well represented due to the prevalence of extreme habitats at high elevations. Most species concentrate their flowering time to June and July (except alien taxa, that tend to flower later in the year), in accordance with the short growing season at medium and high elevations. The lowering duration is inversely proportional to plant longevity.

Most species in the flora of the Alps prefer dry habitats, and this tendency is strongest amongst the endemics. Continental and South European montane plants have mesic requirements, and Mediterranean plants have a xerophilous propensity. Calcareous bedrock is the preferred substratum for the majority of taxa and endemics have an especially restricted preference, a feature that has probably been driven by the major glacial refugia being mostly calcareous. A medium soil nutrient content is the most widespread preference for the species of the Alps, and species with eutrophic (i.e. nutrient-rich) requirements decrease with elevation, mirroring the rarity of such habitats in the subalpine and alpine zones. Some life forms (e.g. chamephytes) are strictly oligotrophic (i.e. nutrient-poor soils), and drier, calcareous soils tend to contain less nutrients. Indigenous taxa are found mostly in grassland or eutrophic habitats and endemics occupy mostly rocky and grassland habitats (these types of habitats and endemicity increase with elevation). Mediterranean taxa are especially frequent in eutrophic communities which are often associated with anthropic activities and ruderal, i.e. weedy, habitats, common at lower elevations.

Arctic-alpine taxa constitute high proportions of grassy and rocky communities, reflecting the tundra-like vegetation in the upper alpine zone. Some habitats are specific to the Alps (e.g. rock faces, screes and alpine grasslands) that are stable in time, fostering a high proportion of endemic communities and species.

1.3 The Asteraceae family

1.3.1 Taxonomy, evolutionary history and worldwide distribution

The Asteraceae (syn. Compositae) is the focus of this thesis. It is one of the largest vascular plant families, with ∼24,000 species (some estimates are up to 30,000) worldwide, amounting to approximately 10% of known angiosperms. Species in the family occur in all continents except Antarctica ([216, 217]). The family is characterized by great floral diversity (see Figure 1.7), but all have: florets arranged on a receptacle developing from the inside out; anthers fused in a ring; achenes (i.e. dry fruits, called cypselae in this family) often accompanied by a pappus, which is a feathery or bristle-like structure that aids in seed dispersion ([217]). These typical characters have been recognized since the earliest efforts in species classifications, and the monophyly of the family was later confirmed by molecular studies ([218]).

Several crops and medicinal species belong to the Asteraceae family (e.g. sunflower, lettuce,

Figure 1.7: Inflorescence diversity of Asteraceae in the Alps. From top left to bottom right, row-wise: *Echinops sphaerocephalus*, *Saussurea discolor*, *Carduus nutans*, *Serratula tinctoria*, *Cyanus segetum*, *Crepis aurea*, *Pilosella aurantiaca*, *Urospermum dalechampii*, *Tragopogon pratensis*, *Doronicum grandiflorum*, *Senecio doronicum*, *Calendula arvensis*, *Anaphalis margaritacea*, *Leontopodium nivale*, *Aster alpinus*, *Erigeron uniflorus*, *Artemisia glacialis*, *Achillea clusiana*, *Achillea distans*, *Cota triumfetti*, *Santolina chamaecyparissus*, *Leucanthemum vulgare*, *Pulicaria dysenterica*, *Pentanema oculus-christi*, *Arnica montana*

Arnica) and many more are used as ornamentals (e.g. *Zinnia*, *Chrysanthemum*, *Leucanthemum*), and the family also includes some noxious weeds (e.g. *Taraxacum officinale*, *Cirsium arvense*, *Senecio vulgaris*).

The Asteraceae family diversity is the result of recent radiation, with their secondary chemistry, inflorescence structure and habit plasticity routinely assumed to be responsible for their evolutionary success ([217]). Polyploidy in Asteraceae is frequent ([219]), and it has been linked to an increase in speciation rates ([220]) that is likely to have contributed to the diversification of the family worldwide. Species in Asteraceae have a variety of breeding systems ([221]).

The family is placed within the Superasterids (Figure 1.8), one of the two major groups within Eudicots, and it is sister to Calycearaceae ([222]). The Asteraceae contains 43 tribes (according to [217]), and approximatively 1,700 genera ([217, 223]).

Recent discoveries have pushed back the origin of the Asteraceae family to the Cretaceous (most likely ∼83 mya, [224]). However the main diversification events took place after the K-Pg boundary, with the stem lineage accelerating its rate of diversification around ∼55 mya. Several WGD events have been identified after the divergence of the basal lineage Barnadesioideae ([219, 225]), with a concomitant acceleration in diversification within the lineages of the present-day crown group of the Asteraceae ([220]).

The centre of origin of Astearace is thought to be South America, and dispersal out of South America may have occurred around 50 mya. It remains unclear whether the family reached Asia through North America or Africa ([228, 229]). Regardless, the Asteraceae is thought to have reached Africa ∼42 mya where there was an explosive diversification, which over a relatively short period of time gave rise to 95% of the family's diversity. Following this massive radiation, the family rapidly colonized the rest of the world. A further major diversification event occurred ∼36 mya at the stem of African lineages, again underpinned by a WGD. Around 23 mya, the progenitor of the Heliantheae alliance diverged and colonized the New World, with the separate tribes emerging around 21 mya and coinciding with another major diversification event that gave rise to more than five thousand species ([223]).

1.3.2 Asteraceae in Europe and in the Alps

Europe hosts 20-25,000 species of vascular plants, of which 28% are endemic to the region (Biodiversity Information System for Europe[4]). Together with Poaceae, Asteraceae make up ∼30% of the biomass found above the treeline ([215]), making it an important component of high elevation communities.

In the Alps, the Asteraceae family is represented by 558 species and 110 genera (according to Flora Alpina, [158]). In contrast to the general tendencies for the flora of the Alps, Asteraceae seems to be well represented in the Eastern as well as in the Western Alps (both in terms of taxa diversity and genotypes), with a less pronounced diversity in the central Southern sectors (compare Figure 1.9 and Figure 1.6). Several studies in the tribes Cichorieae ([230–233]), Cardueae ([234–237]), Senecioneae ([112–114, 238, 239]) and Anthemidaeae ([240–244]) point towards Asteraceae surviving the glaciation cycles predominantly in Eastern and Western refugia. Southern refugia, which are generally thought to be important centres of diversity for vascular plant diversity), perhaps only play a minor role for Asteraceae, although harbouring several endemics.

[4]https://biodiversity.europa.eu/topics/species/vascular-plants

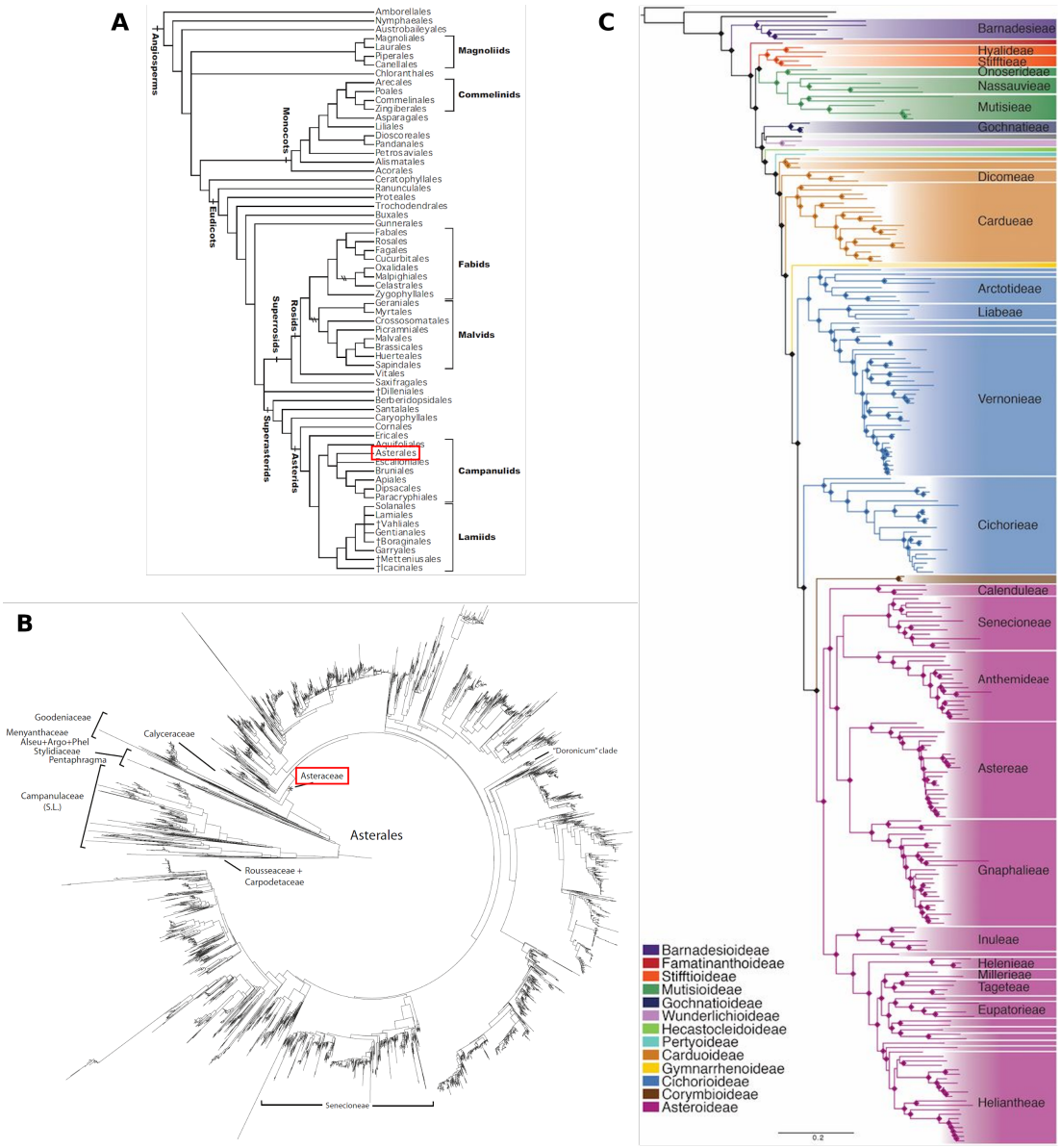

Figure 1.8: Taxonomic placement and composition of the Asteraceae family. Panel A: schematic representation of inter-relationships of orders and some families according to APG IV, reproduced from [226]. The Asterales order is highlighted in red. Panel B: maximum likelihood phylogeny of 4,954 species within Asterales, reproduced from [227]. The node giving rise to the Asteraceae is highlighted in red. Panel C: maximum likelihood tree of Asteraceae tribes, reproduced from [223]; colours correspond to subfamilies, with most tribe names reported.

1.3.3 Ploidy level and chromosomal variation in Asteraceae

Asteraceae are known for their staggering karyological diversity (reviewed in [245]), with more than 180 different mitotic chromosome counts and chromosome numbers, ranging from n=2 to n∼216. All base chromosome numbers through x=2 to x=11 occur in the family, and dysploidy decreases are common (21.9% of genera), as well as supernumerary chromosomes (14.6% of genera). Polyploidy occurs in 58.3% of genera of Asteraceae, including all the genera in the speciose Helenoid-Helianthoid clade. Ploidy levels range from 2x to 48x, with diploids being the most frequent (45%) and less than 30% of genera including ploidy levels 5x or higher ([245], In-

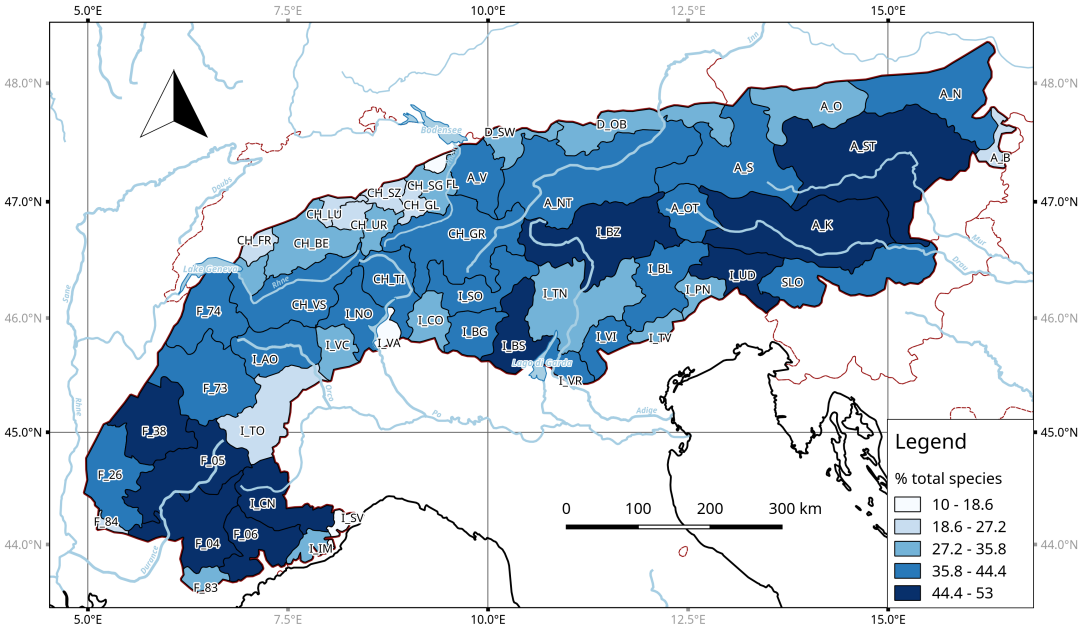

Figure 1.9: Map of the Asteraceae family diversity in the Alps, drawn after data from Flora Alpina [158]. The intensity of colour is proportional to the percentage of Asteraceae species over the total of Asteraceae species in the Alps occurring in that sector. Please note that larger sectors are more likely to host more species by only virtue of their areas. Datum: WGS 84.

dex to chromosome numbers in Asteraceae[5], Chromosome counts Database[6]). Correspondingly, several ancestral WGDs are documented for Asteraceae, with many attributed to dramatic eco-climatic changes associated with the glacial cycles, events that are thought to have contributed significantly to the family diversification ([225, 246]). Subsequent to ancestral WGD, dysploidy has occurred to different degrees in the clades of Asteraceae. For instance, early-branching tribes (e.g. Barnadesieae, Mutisieae) are n=27, while tribes of the Heliantheae alliance (most speciose in the Americas) have n=17 or 19, and the predominantly African tribes (e.g. Cichorioideae clade, the Anthemidae-Gnaphalieae clade, Inuleae) have reduced chromosome numbers of n=9 or 10 despite at least two WGDs ([245]). Whole genome duplications, chromosomal changes and diploidization processes have all generated enormous karyological and taxonomic diversity in Asteraceae ([27, 29, 246]), as exemplified by the numerous taxonomic studies that continue to find variation in chromosome numbers ([247–251]).

1.3.4 Apomixis in Asteraceae

1.3.4.1 Types of apomixis

The majority of plants have the ability to reproduce asexually via vegetative reproduction, although most species have a balance of clonal and sexual reproduction ([252]). The costs and advantages of sexual reproduction have long been debated ([253, 254]), however there remains many plant species that reproduce exclusively asexually. Species that only reproduce asexually by vegetative propagation are present in many angiosperm families ([255]). This mode of reproduction should not be confused with autogamous species (i.e. self-fertilizing), even when these species are obligate selfers (e.g. an extreme example are cleistogamous taxa, [256]).

[5]http://www.lib.kobe-u.ac.jp/infolib/meta_pub/G0000003asteraceae_e
[6]http://ccdb.tau.ac.il/home/

Besides vegetative reproduction, agamospermy is the most common mode of asexual reproduction in vascular plants. Agamospermy is the production of seeds without fertilization, and in seed plants this term is largely interchangeable with apomixis (however some authors use agamospermy to refer to the asexual formation of the embryo, and apomixis to the general process of asexual seed production without gamete fertilization, [257]).

There are two types of apomixis (Figure 1.10): sporophytic apomixis (also called adventitious embryony), in which the embryo forms directly from maternal tissues (generally the nucellus or inner integument) without the contribution of a gametophyte, and gametophytic apomixis, that is further divided into apospory and displospory ([258]). In both types of gametophytic apomixis, a megagametophyte (also called embryo sac in angiosperms) develops from an unreduced cell (i.e. a cell that did not undergo meiosis) and proceeds to form an embryo by parthenogenesis. In displospory, the megagametophyte originates from a cell of the archesporium (i.e. the cell or group of cells that would normally undergo meiosis and give rise to the megagametophyte), while in apospory the megagametophyte originates from some other cell ([66]). In further complications of apomixis, the central cell of the megagametophyte may require fertilization to form the endosperm (pseudogamous apospory, typical of Rosaceae, [259]), or the endosperm may form without the need for exogenous pollen (autogamous apospory, found in different lineages, [260]).

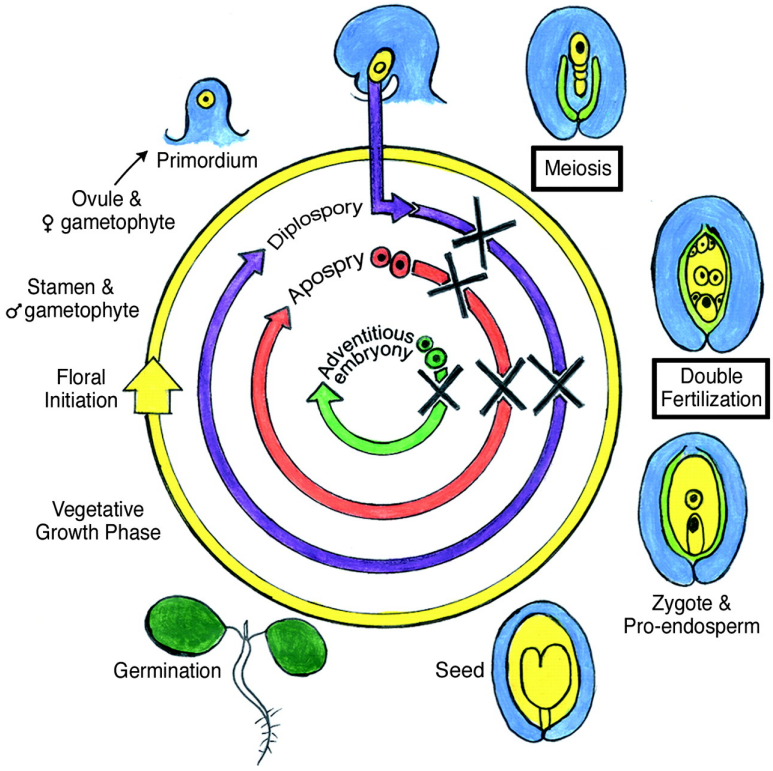

Figure 1.10: Schematic of apomixis events relative to the sexual life cycle (yellow), reproduced from [258]. Both diplospory (purple) and apospory (red) gametophytic apomixis pathways involve cells from the archesporium that bypass meiosis and double fertilization (represented by the black crosses) to form an unreduced embryo sac, that in turn will produce the embryo mitotically. Adventitious embryony (green) is also called sporophytic apomixis, in which the embryo forms directly by mitosis from the nucellar or integument tissues.

1.3.4.2 Agamic complexes in angiosperms and Asteraceae

Apomixis is widespread in angiosperms although occurring with low incidence (2% of genera are apomictic), with 326 genera reported worldwide (Apomixis Database[7]): 148 genera manifest sporophytic apomixis (adventitious embryony), 110 aposporous apomixis and 68 displosporous apomixis. Families containing apomicts tend to be more biodiverse, and apomictic groups are often highly cosmopolitan ([261]). The total number of apomicts tend to decrease with latitude, mirroring biodiversity, however some groups of apomicts have abundantly populated recently deglaciated areas ([262–264], but, for example, not the Himalayas [265]).
In Asteraceae, only gametophytic apomixis is found ([266]) and this mode of reproduction is common in the family, with 22 genera in seven tribes containing apomictic taxa ([266]). Although sexually-reproducing lineages are more numerous, apomictic lineages can include hundreds of taxa (e.g. *Taraxacum* and *Hieracium*). The taxonomic treatment of these "agamospecies swarms" is challenging, because lineages exhibit poor variation and complex hybridization histories ([243, 267]). *Hieracium* is characterized by aposporous apomixis, and the current view is that a restricted number of diploid, sexual lineages gave rise to groups of agamic, mostly triploid (micro)species through polyploidization and hybridization ([268, 269]). *Taraxacum* is the model genus for the characterization of diplosporous apomixis ([270, 271]), and, as for *Hieracium*, it includes strictly sexual diploids and asexual triploids, however the formation of triploid apomicts appears to happen via a tetraploid bridge ([272, 273]).
These apomictic taxa have often been grouped together for practical reasons based on overall morphology and distribution ([261, 267]). More recent treatments consider also taxa origin, balance of apomictic/sexual reproduction and morphological stability as grouping criteria. The approach has resulted in clusters of variants or "agamospecies swarms" around one or few diploid, sexual and morphologically stable progenitors (a criterion proposed by KH Zahn in 1921, [274], also adopted in modern floras [155, 209, 210]).

1.3.4.3 Ecological and evolutionary significance of apomixis

Apomixis combines the benefits of asexual reproduction with those of seed dispersal, but comes at the cost of the accumulation of deleterious mutations and reduced generation of genetic combinations ([258, 275, 276]).
Apomicts are invariably perennial and for the most part polyploid ([66, 252, 261]). Gametophytic apomixis is almost always tied to polyploidy and accompanied by facultative sexuality ([66, 255, 271]). Even in fully obligate apomixis, gene flow with sexual lineages is possible via pollen, where male meiosis and pollen maturation have not degenerated ([252, 255]). There is also a higher proportion of gametophytic apomicts at higher latitudes (and potentially elevations). This might be because the perennial habit is more frequent in these regions and the cold temperatures may enhance unreduced pollen formation and polyploidization, perhaps encouraging the formation of apomicts. Furthermore, large portions of the Northern hemisphere have been freed from ice relatively recently, and polyploid asexual lineages are thought to be excellent colonizers ([262–264], see also [277]).
Traditionally, agamic complexes have been regarded as evolutionary dead ends ([278]), however recent works have suggested that apomixis-inducing genes can escape an agamic lineage by infrequent hybridization with sexually-reproducing lineages (via fertile pollen). Selection and drift can then act to purge accumulated mutations and can lead to apomictic genes in a new

[7] https://uni-goettingen.de/en/423360.html

genomic backgrounds ([275, 279, 280]). Apomicts can also revert back to full sexuality, offering an additional pathway to speciation by predisposing these recombinant sexuals to diverging evolution from the parental species ([261, 271, 281]). Thus sexual and apomictic pathways can co-exist in parallel in the same lineage, with asexual reproduction playing a role in the rapid colonization of new or empty niches, and sexual reproduction having an advantage with selection pressure from competitors, pathogens and herbivores ([252]).

1.4 Aims and scope of the thesis

The aim of this thesis is to provide an integrated overview of macroevolutionary and microevolutionary processes shaping Asteraceae evolution in the European Alps, in turn contributing to the wider knowledge of plant evolution and diversification in heterogeneous environments with complex colonisation histories. Studies of the correlations between GS, ploidy level and reproductive mode with ecological variables in alpine Asteraceae, aimed to explore the interaction between these traits at the macroevolutionary scale. A microevolutionary experiment on the sympatric population of *Senecio doronicum* is by contrast examining in depth differences in phenotype, ecology and reproduction between cytotypes to explore the earliest stages of niche partitioning and mechanisms driving plant evolution and diversification.

Specifically, Chapter 2 focusses on the relationship between mode of reproduction (i.e. sexual or apomictic) and ploidy level, integrating elevation and phenology as ecological variables (derived from Flora Alpina, [158]) in phylogenetically informed models. Chapter 3 combines further ecological data from Flora Alpina and a modern phylogeny of alpine Asteraceae to capture correlations across taxa in the evolution of polyploidy and GS in high-elevation environments. Ultimately, Chapters 2 and 3 aim at uncovering what are the main factors influencing reproductive mode and genome evolution, and their role in adaptation to mountain environments, seeking to compare Asteraceae's trends with those of the flora of the Alps as a whole. Furthemore, these chapters aim at providing a comprehensive cytogenetic screen of ploidy levels and GSs of species in the Asteraceae family across the European Alps. The GS estimates will be included in the C-value database at Royal Botanic Gardens Kew (RBGK, currently v7.1 April 2019[8]). This is complemented by flow cytometric seed screening (FCSS) to ascertain mode of reproduction within the sampled populations.

Chapter 4 presents a detailed morphological and cytogenetic study of a high-elevation mixed-ploidy population of *Senecio doronicum* in SW France, where tetraploids and octoploids coexist but do not seem to produce hybrids, highlighting phenotypical, ecological and reproductive differences between these sympatric cytotypes. Chapter 5 is a review of available methods for monitoring invertebrate pollinators in the field, discussing state-of-the-art devices, techniques and opportunities for pollination ecology research. Chapter 6 is, to my knowledge, the first application of automated video monitoring of pollinators in high-elevation environments. The work studies the pollinators visiting the two cytotypes in the *Senecio doronicum* and explores whether insect visitation is influenced by morphological and ecological differences between the cytotypes. Thus Chapters 4 to 6 represent a look at polyploidy and pollination ecology at the microevolutionary scale, taking advantage of new technology.

Chapter 7 discusses the overarching implications of findings.

[8] https://cvalues.science.kew.org

Chapter 2

The correlation of phylogeny, elevation and ploidy on the incidence of apomixis in Asteraceae of the European Alps[1]

2.1 Summary

Asexual reproduction has often been associated with short-lived lineages, yet asexual complexes (most notably those that are apomictic) are present in several angiosperm families and often comprise a large number of taxa, both widespread and endemic. Investigating correlations between genetic, environmental and taxonomic factors and the incidence of apomixis has represented a challenge for many years, with previous analyses frequently omitting one or more of these variables. Here, flow cytometric seed screening, cytological data and ecological variables have been integrated within a phylogenetic framework to create a comprehensive dataset for 229 Asteraceae species of the European Alps. Data were analysed using phylogenetically-informed generalised linear mixed models (pMCMCglmm) where elevation, ploidy level and phenology were assessed for their potential correlation with asexual reproduction and apomixis type. Although apomixis is not dominant among the species studied, our results confirm that an uneven ploidy level (e.g. 3x), and to a lesser extent an even polyploid level (i.e. 4x), significantly increase its probability, most likely due to chromosome misalignments during meiosis. Apomictic species' distributions do not show any correlation with elevation, and there is a weak correlation between early flowering initiation and aposporous apomixis. While current and future changes in climate may severely impact the survival of the flora of the European Alps, asexual reproduction and polyploidisation may prove to be, at least temporarily, lifelines for a species' survival under the novel climatic conditions. Therefore, understanding how apomicts and polyploids evolve and persist will be essential for understanding the ecology of the European Alps and hence informing future conservation strategies.

[1]Pegoraro, L., Baker, E.C., Aeschimann, D., Balant, M, Douzet, R, Garnatje, T., Guignard, M.S., Leitch, I.J., Leitch, A.R., Palazzesi, L., Theurillat, J.-P., Hidalgo, O, Pellicer, J. (2020) The correlation of phylogenetics, elevation and ploidy on the incidence of apomixis in Asteraceae in the European Alps. *Botanical Journal of the Linnean Society*, 410-422, https://doi.org/10.1093/botlinnean/boaa058

2.2 Introduction

The environmental and genetic pressures behind the incidence and distribution of apomicts have long been a focus of intense debate and study. Plants that reproduce asexually via seed production (apomixis or agamospermy) often have greater ranges and occupy more extreme habitats (e.g. geographical parthenogenesis [282–285]), with the term 'extreme' used to embrace elevation, latitude, rainfall and soil content amongst other factors ([81, 263, 286]). Reasons for the success of apomicts in these environments ([287–289]) may include: (i) persistence of successful gene combinations, (ii) faster seed production in shorter growing seasons, (iii) more efficient dispersal and colonisation ability, (iv) no time or resources wasted in the production of sterile zygotes or pollen in autonomous apomicts and (v) freedom from pollinator dependence. In addition to these observations, an overwhelming majority of apomicts have been found to be polyploids ([73]), leading to the question as to whether apomixis combined with polyploidy play a role in enabling life in hostile environments.

While previous studies have led to significant progress in our understanding of the incidence and maintenance of apomixis in plants (see review [66]), efforts to disentangle the role that environment, polyploidy and phylogeny play have sometimes fallen short of providing a comprehensive answer ([81, 286]). For example, most studies have either taken a single species approach, or, when surveying across taxa, have failed to incorporate a phylogenetic framework into the statistical approaches used to quantify the relative influence of the factors studied. The present study aims to provide a comprehensive dataset to model the relative influence of environmental and cytogenetic variables with a phylogenetic perspective, to determine the probability of developing apomixis within a set of species in the Asteraceae family from the European Alps (hereafter alpine).

Flow cytometric seed screening (FCSS) has become established as a fast and reliable method for assessing the reproductive modes of large numbers of plant samples, including Asteraceae, without the need to dissect different seed tissues ([290]). However, this method can only be used to detect gametophytic apomixis, but not sporophytic, the latter being reported as rare in the family. It is thought that environmental pressures influence the frequency with which apomixis arises and their dispersal patterns after establishment. Many of the study systems used to explore apomixis and polyploidy have undergone recent range contractions and expansions due to glaciations and interglacial transitions during the Pleistocene, which created opportunities for divergence, secondary contact, hybridisation, and re-colonisation ([172, 285]). Lower temperatures, as experienced in areas closer to the poles and also in alpine environments, have been linked to increased rates of unreduced gamete formation ([82, 291]), and hybridisation has long been a known driver of polyploidisation ([9]). Polyploidy and hybridization are both thought to enhance the formation and subsequent dispersion of different cytotypes, creating 'postglacial colonisation patterns' ([172]) that strongly overlap with the distribution of apomictic polyploids ([292, 293]). The European Alps represent an excellent example of these phenomena ([294]), where increasing elevation has been used as a proxy for increasing environmental pressures due to its long-term influence on vegetation ([81, 286]) and its correlation with abiotic factors such as temperature, soil nutrients and CO_2 availability ([204]).

Polyploidy is a powerful genomic process that can buffer recessive deleterious mutations, mitigating against inbreeding depression, alter cell size and physiology ([295]), and potentially increase adaptive potential arising from the diversity of genomic changes which are triggered following polyploid formation ([296]). All of these can provide advantages to the neopolyploid when colonising hostile environments ([33, 72]), creating 'general purpose genotypes' ([297]) and

encouraging ecogeographical dispersal. Newly formed polyploids will be competing with their diploid counterparts, hence facing direct competition and possibly minority cytotype exclusion ([10]). In such a circumstance, the occupation of a new, and often more 'extreme' niche, may be a route to the successful establishment of neopolyploids ([294]). Given that polyploids may have perturbed meiotic processes, and through strong selection for increased fecundity, it may be a frequent outcome that neopolyploids are apomicts ([81, 298]). One developmental path that can lead to apomixis is for embryogenesis to occur prior to fertilisation ([293, 298]), which in turn, can become genetically fixed, enabling faster colonisation ability ([72]) through the avoidance of the cost of sexual reproduction and bypassing minority cytotype disadvantages ([91]).

Despite the ubiquitous nature of polyploidy across many plant lineages ([15]), there is still ongoing debate regarding its prevalence and incidence across different taxonomic groups ([10, 284]). Asteraceae represents a highly speciose and cosmopolitan family, with multiple independent episodes of polyploidy and apomixis ([225, 266]). Apomixis and polyploidy *per se*, might not guarantee success in colonising more 'extreme' or larger niches ([81, 262]). However, in combination, they may allow some species to occupy areas unavailable to their diploid, sexual progenitors, and to persist in the face of more extreme environmental conditions. This work builds on previous research that suggests a lack of a positive correlation between larger elevational ranges and occurrence of sexually reproducing polyploids ([81, 283]), while apomicts have higher seed set than sexuals at higher elevations and latitudes ([81, 271, 283]).

We test this hypothesis using a family-wide and multidisciplinary approach to quantifying the relative contribution of genetic, environmental and taxonomic variables that may influence the incidence of apomixis in Alpine Asteraceae, asking:

- Are some clades particularly rich in apomictic taxa (i.e. strong phylogenetic signal)?
- Is apomixis more frequent at higher elevation? Do apomictic species flower earlier in the year than sexual species?
- How does ploidy relate to frequency of apomictic reproduction?

2.3 Materials and methods

2.3.1 Plant material

For each plant population, we collected fresh leaves from 5-15 individuals and stored them in at 4°C until analysis. Mature seed heads were collected with a similar strategy from a minimum of five individuals, up to 30 individuals for taxa with very small seeds, and seeds were stored in silicate gel at 4°C. Multiple collections for the same species were carried out whenever possible, from population at least 50 km apart (see Table 2.1). Collection localities were chosen to maximise the number of Asteraceae species available, spanning the whole elevation range, with information based on vegetation and species occurrence maps available through various national and local services (e.g. Tela Botanica[2], France; InfoFlora[3], Switzerland; Acta Plantarum[4], Italy), as well as expert advice from collaborators in the field (please see 2.7). The areas surveyed included South East France (Alpes-Maritimes, Alpes-de-Haute-Provence, Hautes-Alpes), Southern Switzerland (Ticino and Valais), Austria (Niederösterreich

[2]https://www.tela-botanica.org/en/
[3]https://www.infoflora.ch/en/
[4]https://www.actaplantarum.org/

	Accessions per species		Elevation
Extended	All taxa	Subsp. lumped	Average elevation
Mean	1.899	1.974	1371.916
Range	1—15	1—15	350—2575
Median	1	1	1325
Strictly Alps	All taxa	Subsp. lumped	Field elevation
Mean	1.934	1.977	1702.843
Range	1—15	1—15	9—2951
Median	1	1	1890

Table 2.1: Average, median and range of number of accessions (i.e. populations) per species for the apomixis datasets, considering subspecies as separate taxa or lumping them together, as well as elevation average, median and range (computed elevation preference for 'Extended' dataset, field collected elevation for 'Strictly Alps' dataset)

and Kärnten), North East Italy (Veneto and Trentino-Alto Adige), and Slovenia, primarily from montane to sub-nival elevations (see Supplementary A.2 for collection details). Most seed collections were made from wild plants between March and September in 2016, 2017 and 2018. Wild seed collections were complemented with seeds from plants of known wild origin cultivated at the Jardin du Lautaret-SAJF (Hautes-Alpes) and other localities. See Figure 2.1 for a geographical overview of collections, and Supplementary section A.2 for a list of all accessions studied including collection details. Fresh leaf samples for DNA ploidy analyses (see Section 2.3.2 below) were also collected and processed within 7-10 days from harvesting.

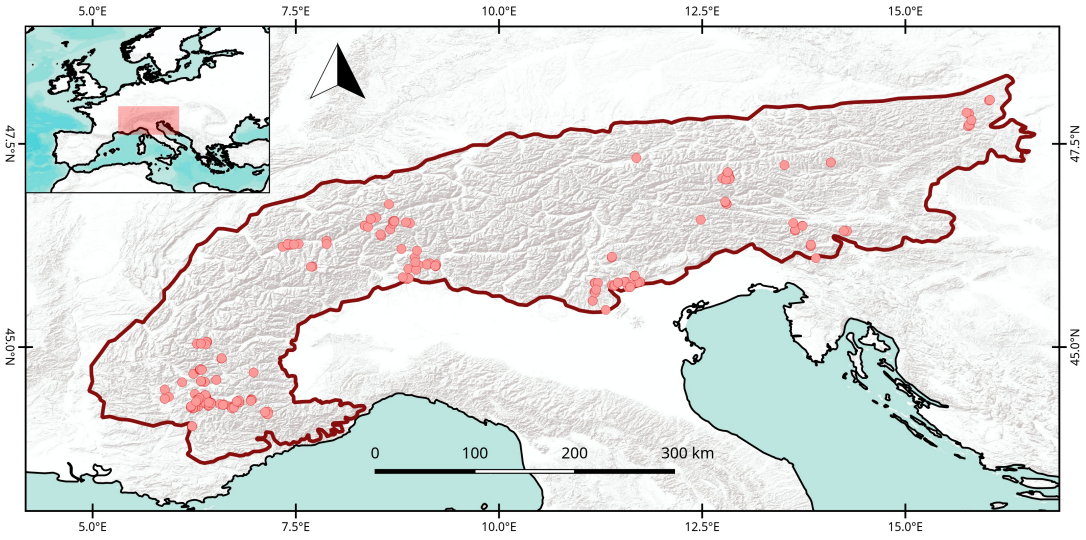

Figure 2.1: Overview of the Alpine arc (thick red outline). Circles represent accessions collected in the wild

2.3.2 Reproduction modes determined using flow cytometry seed screening (FCSS)

Seeds were individually assessed for reproductive modes by examining the ratio between endosperm (end) and embryo (emb) DNA contents using FCSS ([290]). In brief, one to five seeds were placed in a Petri dish with 1 ml general purpose buffer ([299]) supplemented with 3% PVP-

40 and chopped with a new razor blade on ice. The macerated seed suspension was then filtered through a 30 μm nylon mesh filter and stained with 50 μl of propidium iodide (PI, 1 mg/ml). For larger seeds, an additional 1 ml of buffer was used in combination with a further 50 μl of PI. The solution was then incubated on ice for 10 minutes to allow staining of nuclei. This was repeated for five seeds per population, or five sets of five to ten pooled seeds when these were of very small size. The mean end/emb fluorescence index was used to determine reproductive mode. In order to confirm that mixed reproductive modes were not present within capitula, preliminary tests were carried out in two species; the sexually reproducing species *Senecio viscosus* L. and the apomictically reproducing *Hieracium lawsonii* Vill. For each species, all seeds per capitulum were analysed and confirmed that stable reproductive modes in each case. In *S. viscosus*, the capitulum contained 74 seeds and the end/emb fluorescence indexes range was 1.495-1.672, indicative of sexual reproduction. In *H. lawsonii*, the capitulum contained 68 seeds, of which 58 showed a range of end/emb fluorescence indexes between 2.00-2.124, indicative of apomixis. Ten seeds failed to deliver any results (i.e. neither peaks for the embryo nor the endosperm were found, most likely due to seed abortion). Samples were analysed using a Partec CyFlow SL cytometer (Partec, GmbH, Münster, Germany), fitted with a 100 mW green solid-state laser (Cobolt Samba). FloMax software (v2.9, Partec GmbH) was used to analyse the histograms of mean relative fluorescence (1,000-3,000 particles) and calculate mean DNA amounts in the embryo and endosperm through either automatic Gaussian peak assignment or manual range setting when a reduced number of nuclei were released. Output fluorescence histograms from the samples analysed are available from the authors upon request.

2.3.3 Chromosome counts

Seeds of studied species were sown on agar petri dishes and incubated in the dark at room temperature until germinated. Seedlings were then transferred into pots and allowed to grow until root systems were fully developed. Healthy growing root tips were excised and pre-treated in 0.05% aqueous colchicine for 1-5 h in order to enhance accumulation of cells arrested in metaphase. Tips were then fixed in 2 ml glacial acetic acid and absolute ethanol (3:1) for 24 h at room temperature. For long-term storage, samples were transferred to 70% ethanol and stored at -20°C until use.

To make chromosome preparations, roots were rinsed in distilled water prior to hydrolysis in 1 M HCl in a 60°C water bath for 3-5 minutes, and then transferred to tubes containing Schiff's reagent, for a minimum of 30 minutes in the dark. Root tips were excised with a clean razor blade and squashed in a drop of either 45% acetic acid or 2% (v/v) aqueous aceto-orcein to increase staining contrast where needed. Chromosome counting was carried out using a Zeiss Axioplan-2 imaging light microscope, and photographs taken and edited using Jenoptik Progress Capture Pro (v2.9.0.1). Ploidy levels were determined karyologically wherever possible in at least one accession and associated to a given relative nuclear DNA content (estimated by flow cytometry, see Section 2.3.2 above), which was subsequently used to assess DNA ploidy in further accessions. For species which could not be grown, ploidy levels were allocated based on data available in databases containing (i) reports of previous chromosome counts and (ii) nuclear DNA contents linked to chromosome numbers: e.g. Chromosome Counts Database[5] ([300]), the Genome size in Asteraceae Database[6] and the Plant DNA C-value Database[7] ([301]).

[5] http://ccdb.tau.ac.il/
[6] https://www.asteraceaegenomesize.com/
[7] https://cvalues.science.kew.org/

2.3.4 Ploidy level estimation

Relative nuclear DNA contents of all accessions were estimated by flow cytometry using ∼1 cm^2 leaf material, as described for seeds, following [302] in order to allocate DNA ploidy levels. Each target sample was run alongside an internal standard: *Petroselinum crispum* (Mill.) Nyman ex A.W.Hill 'Champion Moss Curled' (2C=4.5 pg), *Pisum sativum* L. 'Ctirad' (2C=9.09 pg) or *Solanum lycopersicum* L. 'Stupiké polní rané' (2C=2 pg) [303].

2.3.5 Alpine Asteraceae phylogeny

The complete Asteraceae species list from Flora alpina ([158]) was screened against the Euro+Med PlantBase[8] for synonyms and a dataset was created. We adapted the phylogenetic tree of spermatophytes of Smith & Brown 2018 [304], that was obtained collating GenBank data using a hierarchical clustering method, and is, to date, the most comprehensive species-level phylogeny available for Angiosperms, comprising 353,185 taxa. We pruned from this supertree using the drop.tip function in *ape* ([305]).
Most species were available in this supertree, but for the ones missing, the closest available relative was replaced and used, since no ancestral state reconstruction analyses were carried out. Alternatively, tips were duplicated to include the sister missing taxa, and polytomies resolved for further analyses ([305]). In total, for the 'Extended' dataset, 48 taxa were added to the tree by renaming existing tips, and 11 taxa were added by duplicating tips, together amounting to 24.79% of the 238 taxa in the tree. For the 'Strictly Alps' dataset, 35 taxa were added by renaming tips, while 8 were added by duplicating tips, constituting 23.76% of the 181 taxa in the tree.

2.3.6 Flowering initiation, elevation and apomixis type

Data on flowering initiation time for all Asteraceae was extracted from Flora Alpina ([158]). Where taxa could not be found, we used the data from the most closely related species within the genus (e.g. for *Hieracium cydoniifolium* Vill., *H. glaucopsis* Gren. & Godr., *H. valdepilosum* Vill.), or a related subspecies (e.g. for *Senecio squalidus* L. subsp. *rupestris* (Waldst. & Kit.) Greuter). For every vegetation zone in Flora Alpina (e.g. foothill, montane, subalpine, alpine, nival) we calculated a single 'average elevation value' following delimitations given in [203]. For each taxon, we coded the 'elevation preference' as a factor with a value of 2 for its optimal vegetation zone(s), and 1 for its suboptimal vegetation zone(s), using data from Flora Alpina ([158]). We then multiplied the 'average elevation value' with the 'elevation preference' and divided this by the sum of the 'elevation preference' values, therefore obtaining the weighted mean to determine the 'average elevation preference' for each taxon. Analyses were also carried out on a reduced dataset, using field-collected elevation data (or its average for multiple accessions of the same taxon) of wild plants we collected within the alpine arc (*sensu* Flora Alpina, [158]). Using data for Asteraceae genera from [261] (Apomixis Database[9] accessed on April 15^{th}, 2020), we added a variable for each species specifying apomixis type: aposporous, apo-diplosporous, diplosporous or uncertain.

[8] http://www.emplantbase.org/home.html
[9] https://www.uni-goettingen.de/en/423360.html

2.3.7 Statistical analysis and phylogenetic modelling

All statistical analyses were carried out in R ([306]). The function phylosig ([307]) was used to assess phylogenetic signal in each of the variables separately. This is important to incorporate into multiple species analyses, as it weights variable effects using phylogenetic relatedness. Pagel's λ measures the deviation from correlation under Brownian motion (λ=1). Blomberg's K measures how variance is distributed (K>1 variance distributed mostly among clades, K<1 variance is distributed mostly within clades). To account for potential phylogenetic non-independence of tested variables, we used phylogenetic generalised linear mix models (pGLMM) with Markov Chain Monte Carlo techniques implemented in *MCMCglmm* ([308]), with dependencies: *ape* ([305]), *coda* ([309]), *Matrix* ([310]) and *phylolm* ([311]). Reproductive modes were coded as the binary dependent variable, with levels 'sexual' and 'apomictic'. Note that the latter was assigned to species in which at least one accession was reported as apomictic. Ploidy level (x), average elevation (m) and flowering initiation (month) were entered as explanatory variables into the model's formula. For this analysis, all ploidy levels of 6x or higher were collapsed into a single factor ('High ploidy'), otherwise the chains would not mix properly due to the scarcity of data points. These models used the threshold family and a weak prior: R structure had V and *fixed*=1, and G structure had V=1, *nu*=1000, with *alpha.nu*=0 and *alpha.V*=1. The chains were run for 10^6 cycles, with a burn-in of 2,500. Phylogeny was accounted for by using taxonomic positions as a random effect and including the tree as the *ginverse* error structure (phylogeny was transformed using the *inverseA* function). Default diagnostic plots and Geweke plots were used to check if chains were properly sampling the parameter space, as well as Heidel diagnostics for testing stationarity and autocorr.diag to check for signs of autocorrelation. Using the same model call, three chains with different starting points (*set.seed* of 111, 534, 386) were run, the *Sol* part of the models concatenated and ran through Gelman diagnostics to check if they converged to similar parameter estimates. To test the correlation of the explanatory variables (ploidy, elevation and flowering initiation) on each apomixis type, we ran an additional sets of models with *MCMCglmm* ([308]) using a multilevel response (apomixis type); for these analyses we excluded species with uncertain apomixis type, resulting in a response variable with four levels: sexual, aposporous, apo-diplosporous and diplosporous. We used the categorical family and a "close to flat" prior, running the chains for 107 cycles with a burn-in of $5{\cdot}10^5$, due to the high number of parameters to be estimated. For additional details please see Supplementary A.3 and Supplementary A.4.

2.4 Results

A total of 229 species (452 populations) from across 81 genera were studied (Supplementary A.2), out of ∼500 species and ∼112 genera recognised in Flora alpina ([158], updated to taxonomic criterion of Euro+Med PlantBase). Ploidy levels ranged from diploid (2x) to dodecaploid (12x) (Fig. 2.2A). Sexually produced seeds displayed an end/emb fluorescence index of ∼1.5 (ratio 3Cx:2Cx - endosperm:embryo) resulting from the double fertilization of the embryo and endosperm (see Supplementary Figure A.1 for illustration). Substantial deviation from this fluorescence index (i.e >1.8), when still showing a strong embryo peak was considered to be asexual reproduction (most likely apomixis). Note that the majority of apomictic species showed a relatively smaller endosperm peak signals at a fluorescence index ∼2 (ratio 4Cx:2Cx - endosperm:embryo), indicative of apomixis, whereby the endosperm is formed autonomously

via mitosis of maternal tissues, without contribution of pollen nuclei (Supplementary Figure A.1). The analyses of reproductive modes revealed a relatively low incidence of apomixis across samples, with only 20 species being exclusively apomictic, while 209 reproduced sexually (Supplementary A, Figure 2.3). In four taxa (*Centaurea scabiosa* L. subsp. *alpestris* (Hegetschw.) Nyman, *Crepis vesicaria* L., *Leucanthemopsis alpina* L. Heywood and *Picris hieracioides* L.), we detected multiple reproduction pathways. However, differences in reproduction were only found between populations, being consistently either sexual or apomictic within populations.

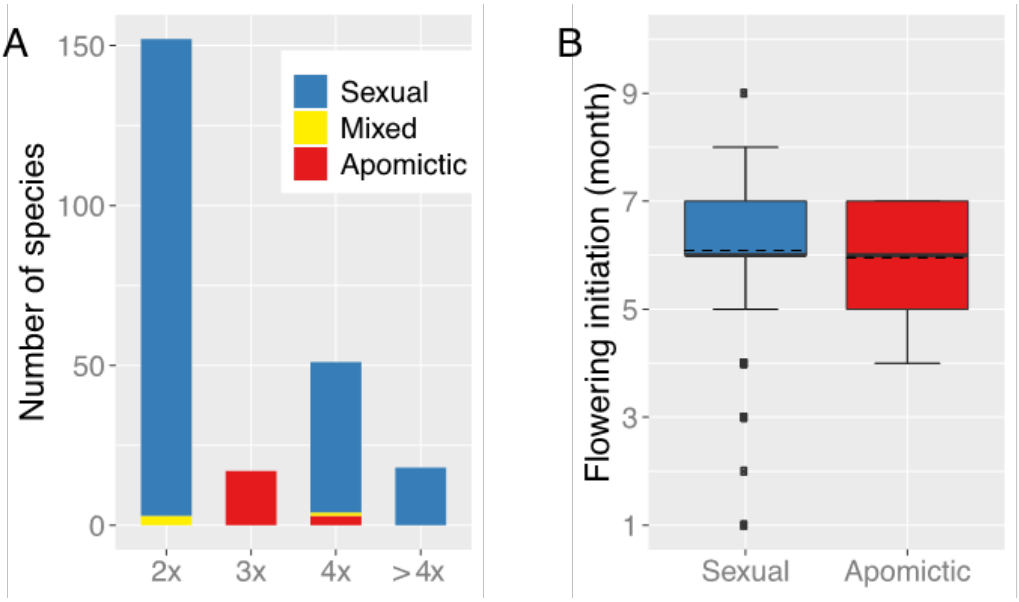

Figure 2.2: A: Stacked bar graphs showing the number of taxa (including subspecies) across different ploidy levels and the number of apomictics within them. B: Box plots showing the differences in the timing of flower initiation between sexual and apomictic species. Boxes display data distribution through median, upper (75%) and lower (25%) quartiles.

2.4.1 Evaluating the effects of ploidy level, elevation and flowering initiation

The results of the analysis for phylogenetic signal within model variables are presented in Table 2.2 for both the 'Extended' (i.e. 452 accessions, 81 unique genera and 229 species) and the 'Strictly Alps' datasets (comprising only those taxa collected from the wild in the Alps and hence with elevation data from the field; 350 accessions, 65 genera and 177 species). Apomixis type (e.g. sexual, aposporous, apo-diplosporous, displosporous) and reproduction mode (e.g. sexual, apomictic) showed the strongest phylogenetic bias, followed by phenology (flowering initiation) and ploidy. Our data suggested that most variance occurs within rather than between clades (Table 2.2, i.e. all Blomberg's K values were considerably less than 1).

The results of the Bayesian pGLMM threshold model outputs are summarised in Table 2.3. (N.B. all models passed Heidel's stationarity and halfwidth tests, and all factor levels converged to the same estimates in the Gelman's diagnostic. Model specifications and diagnostics are available in Supplementary A.4). Model results were similar using either the 'Extended' or 'Strictly Alps' datasets, with contributions from variables differing little (Table 2.3). Species reproducing apomictically were found across several ploidy levels, although their incidence of occurrence at each ploidy level was variable (apomixis recorded in 3 diploid accessions, 30

Extended	λ	**p-value λ**		**K**	**p-value K**	
Apomixis type	1.001	< 0.001	$***$	0.079	< 0.001	$***$
Reproductive mode	0.873	< 0.001	$***$	0.044	< 0.001	$***$
Ploidy	0.632	< 0.001	$***$	0.023	< 0.001	$***$
Elevation	0.452	< 0.001	$***$	0.023	< 0.001	$***$
Flowering initiation	0.736	0.002	$**$	0.023	< 0.001	$***$
Strictly Alps	λ	**p-value λ**		**K**	**p-value K**	
Apomixis type	1.003	< 0.001	$***$	0.312	< 0.001	$***$
Reproductive mode	0.851	< 0.001	$***$	0.054	< 0.001	$***$
Ploidy	0.567	< 0.001	$***$	0.025	0.004	$**$
Elevation	0.101	0.012	$*$	0.022	0.008	$**$
Flowering initiation	0.770	0.001	$**$	0.026	< 0.001	$***$

Table 2.2: Outputs of analysis for phylogenetic signal (Blomberg's K and Pagel's λ) within model variables for both datasets. Statistical significance is coded as follows: p≤0.001 = ∗∗∗; p≤0.01 = ∗∗; p≤0.05 = ∗

triploid accessions, and 6 tetraploid accessions; Fig. 2.2 and Supplementary A.2). Of all the variables analysed, only ploidy level had an effect on the likelihood of apomixis, with triploidy (3x) having a strong effect in both datasets (Table 2.3, p<0.001), with tetraploidy (4x) having a weaker effect in the Extended dataset only (Table 2.3, p=0.004). The variable 'elevation' had no effect on incidence of apomixis, as shown for species growing between 31 to 2,951 m, with most accessions being found above 1,000 m (Table 2.3). This is supported by the observation that there were only six examples of apomixis occurring <1,000 m. The timing of flowering initiation was also not significantly different between apomicts and sexual species (Table 2.3, Fig. 2.2B). The results of the categorical multilevel MCMCglmm models, using apomixis type as the response variable, are presented in Supplementary A.3. For both the 'Extended' and 'Strictly Alps' datasets, the triploid (3x) ploidy level had a strong positive interaction with diplosporous apomicts (Supplementary Table A.3, p=0.002), accompanied by a negative interaction between the diplod (2x) ploidy level and diplosporous apomicts ('Extended' dataset only). The variable 'elevation' did not have significant effects on any of the apomixis types in either dataset. The 'flowering initiation' variable manifested a weak negative association with aposporous apomicts only, in both datasets. It should be noted that, due to the high number of parameters to estimate, the chains did not mix as well as in the threshold models, resulting in large confidence intervals with relatively low statistical confidence, thus the output from this model is shown only in the supplementary.

2.5 Discussion

2.5.1 Taxonomic distribution of apomixis in the Asteraceae

Most recent reviews have considerably shortened the list of Asteraceae genera which include apomicts, from 70 ([266]) to 27 ([261], Apomixis Database[10] accessed on April 15th, 2020), nine of which have apomictic species present in the flora of the European Alps. Amongst them, we confirmed apomixis in *Crepis* L., *Chondrilla* L., *Hieracium*, *Pilosella* Hill and *Taraxacum* F.H.Wigg (all in the Cichorieae tribe), and *Erigeron* L. in the Astereae tribe (Fig. 2.3). In

[10]https://www.uni-goettingen.de/en/423360.html

Extended	**post.mean**	**l-95% CI**	**u-95% CI**	**eff.samp**	**pMCMC**	
Intercept	-1.506	-3.856	0.949	2127	0.192	
Elevation	$-2.845e^{-4}$	$-1.078e^{-4}$	$5.044e^{-4}$	1950	0.494	
Ploidy-3x	5.787	3.588	7.855	1950	$<5e^{-4}$	$***$
Ploidy-4x	1.270	0.313	2.184	1950	0.004	$**$
High ploidy	-0.178	-2.386	2.039	1730	0.890	
Flowering initiation	-0.165	-0.582	0.168	2157	0.395	
Strictly Alps	**post.mean**	**l-95% CI**	**u-95% CI**	**eff.samp**	**pMCMC**	
Intercept	0.088	-2.678	2.739	1950	0.929	
Elevation	$-2.352e^{-4}$	$-9.335e^{-4}$	$4.565e^{-4}$	2532	0.509	
Ploidy-3x	5.789	3.681	7.939	2156	$<5e^{-4}$	$***$
Ploidy-4x	0.996	-0.045	2.047	1950	0.054	
High ploidy	-0.688	-2.985	1.598	1950	0.587	
Flowering initiation	-0.390	-0.843	0.072	1936	0.090	

Table 2.3: pMCMCglmm models outputs for the 'Extended' and 'Strictly Alps' datasets. Statistical significance is coded as follows: p≤0.001 = $***$; p≤0.01 = $**$; p≤0.05 = $*$

contrast, we only found evidence of sexual reproduction in *Antennaria* Gaertn., *Arnica* L. and *Leontopodium* Cass., even though apomictic biotypes have been reported for some alpine species i.e. *Antennaria carpatica* (Wahlenb.) Bluff & Fingerh., *A. dioica* (L.) Gaertn., *Arnica montana* L. and *Leontopodium alpinum* Cass. ([266] and references therein). Furthermore, we detected apomixis in three additional genera: (i) *Centaurea* L. (where apomixis was considered doubtful, [266]), (ii) *Leucanthemopsis* (Giroux) Heywood (in the species *L. alpina* (L.) Heywood (discussed below)), previously reported to be strictly sexual ([262]) and (iii) *Picris* L. (in *P. hieracioides*), also considered as strictly sexual by [312]. Our results therefore provide preliminary evidence of apomixis in the Anthemideae and Cardueae tribes, despite previous doubts ([261, 266]). Altogether, 12 genera from six tribes of Asteraceae occurring in the European Alps are now known to contain apomictic biotypes (Fig. 2.3).

The incidence of Asteraceae genera containing apomictic species in the flora of the Alps is larger than for the family worldwide. About 10.71% of the genera contain apomictic taxa (nine genera of the Apomixis Database, [261], plus three genera we confirmed apomixis in the present study; total number of genera, ∼112, from Flora Alpina [158] updated to taxonomic criterion of Euro+Med PlantBase). For the family as a whole the percentage drops down to ∼1.85% (27 genera of the Apomixis Database, [261], plus three genera we confirmed apomixis in the present study; number of genera for the whole family, ∼1620, from [314]). However, there may be ascertainment bias because the Alps are the focus of considerable research into apomixis. Furthermore, it could be particularly easy to overlook apomixis in mixed reproducing biotypes, which are generally imbalanced towards sexual prevalence (Supplementary A.2). The Alpine flora includes widespread polyploid apomictic species, such as *Erigeron karvinskianus* DC. (introduced) or *Taraxacum officinale* F.H.Wigg., whose success has been linked to their reproductive mode and to a lesser extent to their ability to survive in alpine environments [262]. The tribe Cichorieae is one of the most numerous and particularly rich in apomictic taxa ([261, 266], Fig. 2.3). The centre of diversity of this tribe is in Europe [229] and the abundance of apomictic species found therein in the present study may be no higher in the Alps than elsewhere. Resolving this point would require a more comprehensive sampling across Cichorieae clades.

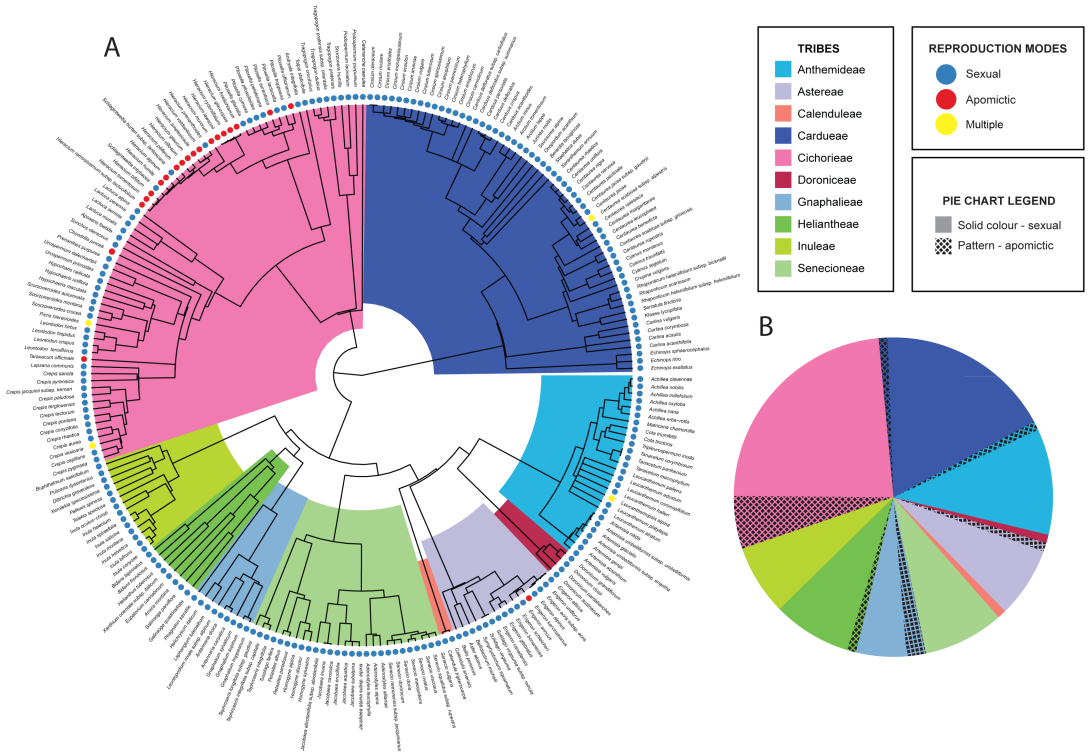

Figure 2.3: A. Phylogeny of alpine Asteraceae built from [313] for 238 taxa. The colour of the circles at the tips of each branch indicates the type of reproductive mode. Note that under the category "multiple" we refer to species where some populations shown exclusively sexual reproduction whilst other populations reproduce through apomixis, but not to detection of mixed reproductive pathways within populations. B. Pie chart illustrating the proportion of sexually reproducing genera (solid colour) and apomictically reproducing genera (black grid) for each tribe across the Asteraceae. Note that colour codes represent the same tribes as in the phylogeny.

2.5.2 Ecological and environmental implications

We found no correlation between flowering initiation time and apomixis overall, and a weak correlation between flowering initiation and aposporous apomicts only. It has been suggested that apomictic genotypes could flower earlier in the year than sexuals ([273, 315]), perhaps due to their independence from pollination; however, earlier phenologies were found only for diplosporous ("obligate") apomicts. Our results suggest instead that aposporous apomicts ("facultative", with sexual and asexual development in parallel), show a tendency to flower earlier in the year when compared to sexuals. However, the categorical models exploring these correlations have a high degree of uncertainty, with confidence intervals overlapping or very close to zero (meaning that the correlations could be zero, Supplementary A.3), therefore this trend is to interpreted with caution and merely as an indication. Future investigations looking at pairs of closely related sexual and apomictic species could analyze in detail their phenology and help ascertain if flowering time differences are widespread and linked to reproductive mode. We observed no correlation between elevation and the incidence of apomixis in Asteraceae, in agreement with the observations of [262], indicating that environmental pressures, or at least those associated with changes in elevation, do not seem to play a key role in contributing to shifts towards apomixis in Asteraceae populations in the Alps. Species can have sexual populations in one part of their distribution and apomictic populations in others (geographical parthenogenesis, [283] also described for Asteraceae in the Alps: [230, 233, 269]), and the majority of the species included in this study have ranges that extend past the Alps. It follows

that geographical trends in apomixis can only be addressed by sampling across each species full distribution range, and the results presented here should not preclude larger investigations. Further, in our study, elevation was used as a proxy for direct environmental pressures, such as temperature and rainfall. More focussed studies of specific ecoclimatic variables may reveal other trends, and perhaps a more comprehensive ecological niche modelling approach combined with comparative transcriptome gene analyses may yet reveal subtler differences. This could be especially informative given that recent studies have suggested that stress-associated genes are regulated in different ways in sexual and apomictic plants (e.g. [316, 317]).

2.5.3 The role of polyploidy in influencing apomixis

Hojsgaard and Hörandl ([66]) pointed out several indirect effects of polyploidy, which may be linked with the occurrence of apomixis in plants. Our results align with the current views that polyploidy, especially uneven ploidy levels (e.g. triploids), have the greatest influence on the incidence of apomixis. Certainly, the high incidence of diplosporous apomixis in triploids supports an hypothesis for selection pressures favouring unreduced gametes when meiosis is compromised by uneven ploidy levels, also supported by a correspondingly low incidence of displospory in diploids. While, in general, polyploidy seems to play a key role in influencing apomixis, recent evidence suggests that in some cases niche differentiation is more influenced by reproductive modes than cytotype diversity. A survey on *Potentilla puberula* Krašan in the Eastern Alps ([318]) found that ecological differentiation is stronger between sexuals and apomicts than between cytotypes with the same reproductive mode. Sexuals (i.e. 4x) occur in dry, primary habitats, while apomicts (5x, 6x, 7x and 8x) tend to occupy mesic, anthropogenic habitats with high disturbance. The study highlights the need to identify possible confounding factors, such as polyploidy, hybrid origin and spatial patterns, that could play a role in influencing the evolution of distinctive reproductive modes in different plant lineages.
Our study reports a case of apomixis in the otherwise sexually reproducing species *Leucanthemopsis alpina* (Supplementary A.2, Supplementary Figure A.2). Of the eight populations surveyed, both diploid and tetraploid cytotypes reproduced sexually, but the results from a triploid population (Alpes Maritimes, France) indicated asexual reproduction (i.e. apomixis). Previous work by Tomasello and Oberprieler ([319]) highlighted the high incidence of polyploidy across the distribution range of this species in the Alps, and the authors reported a single triploid individual in a diploid-dominated population from Baisse des Druos, also in the Alpes Maritimes. The fact that so far triploids seem to have arisen only within diploid populations suggests that the production of unreduced gametes might be underpinning their formation, as is the case for other members of the family ([269]). We also observed two diploid species with apomictic populations: *Crepis veiscaria* L. and *Picris hieracioides* L. (SupplementaryA.2), both belonging to the Cichorieae tribe, which presents the highest incidence of apomicts ([266], Fig. 2.3). Apomixis at the diploid level has been reported before in this clade in *Pilosella aurantiaca* L. ([320]), and outside the Asteraceae family in *Ranunculus kuepferi* Greuter & Burdet ([81]), however Mráz & Zdvořák ([269]) ruled out apomixis at the diploid level in *Hieracium* s.s. Diploid apomicts could also be the result of hybridisation between sexual and apomictic lineages ([271]), and indeed most natural diploid apomicts in *Boechera* A. Löve & D. Löve (Brassicacee) have a hybrid origin ([321]). Further studies are needed to assess how widespread apomixis is at the diploid level in Asteraceae, and whether hybrid in origin.

2.6 Conclusions

The present study points to a low incidence of apomixis in alpine Asteraceae, and the trait is tightly linked to phylogeny. Elevation is not correlated with the occurrence of apomixis in Asteraceae populations from the Alps, with ploidy level being the factor influencing most its occurrence. Aposporous apomicts tend to flower earlier in the year than sexuals, but with a high degree of uncertainty. This knowledge can help us move forward in our understanding of how apomixis can influence the evolutionary trajectory of several major plant families across a variety of environments, including mountain ecosystems. Likewise, combining insights from the genetic and environmental factors playing a role in the development of apomictic pathways across plants will help us to anticipate how resilient such plants will be in the face of ongoing global change.

2.7 Acknowledgements

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[11] https://www.winton.com/philanthropy

Chapter 3

The evolution of genome size in alpine Asteraceae and its relationship with life history traits and ecological variables

3.1 Summary

An organism's genome size (GS) is the result of processes that eliminate DNA (i.e. genome downsizing) and those increasing it (mainly (retro)transposon activity and polyploidization) in the ancestry of the lineage. Besides its role in storing genetic information ("genotype"), the genome can be treated as a phenotypical character ("nucleotype"), with important implications at the evolutionary, ecological and functional levels. The study of the relationship between GS, polyploidy and ecological indicators, integrated in a phylogenetic framework, is thus valuable to shed light into the multiple ways in which genomes and environment interact.

Here, a dataset of 335 species belonging to 100 genera of Asteraceae from the European Alps, comprising GS measurements, ploidy level and a number of ecological covariates, has been analysed together with a newly generated phylogeny including all species of Asteraceae in the Alps, to capture trends associated with GS.

GS ranged between species from very small (2C=0.98 pg) to large (2C=36.69 pg), with a median of 2C=5.06 pg and a skewed distribution towards small values, with intraspecific ploidy diversity found in nine species. Long-lived (i.e. perennial) species showed larger GSs than short-lived ones (e.g. ephemeral to biennial), with significant differences in GS between species preferring high-N substrates and others. However, GS, ploidy level, chromosome number, elevation, longevity, endemicity and phenology all exhibited strong phylogenetic bias (Pagel's λ), with variation distributed within clades (Blomberg's K). Therefore, data were analysed in a phylogenetic framework using Markov Chain Monte Carlo generalised linear mixed models, pMCMCglmms. Ploidy and chromosome number remained strongly linked with GS; an example of this can be observed in the *Leucanthemum* polyploid complex, where several species were polyploid (e.g. *L. adustum*, 8x) and included the largest GS values recorded in the dataset, albeit with indications of genome downsizing compared to closely related diploids. In addition, among the ecological covariates, short life cycles were associated with smaller genomes, as were

endemics. However, there was a weaker correlation between larger genomes and species having later flowering initiation. The differences in GS between different nitrogen content preference groups no longer held when species relatedness was taken into account, which was also the case in correlations between GS and elevation. Potentially, elevation is a poor variable to relate with GS, and instead more specific ecological indicators may reveal more focussed correlations with GS.

The study confirmed the general trend observed for all angiosperms, that alpine Asteraceae have a diverse range of GS and a prevalence of smaller genomes. The strong correlation between longevity (tightly linked to life cycles) and GS reflects the limitations imposed by ephemeral life cycles, with long-lived species being more variable. The trend observed with nitrogen content preference was driven by a group of related species with large genomes preferring nutrient-poor substrates, but in fact this was not evident in the phylogenetically corrected models.

3.2 Introduction

3.2.1 Genome size and polyploidy

Genome size (hereafter GS) is the amount of DNA contained in the cell's nucleus, which is frequently expressed as the C-value (i.e. the DNA amount of the unreplicated genome, [322]). The study of GS and its variation within and among taxa has been intensely studied and the results have revealed a staggering 2,400-fold variation in GS ([295, 323, 324]), from *Genlisea tuberosa* (Lentibulariaceae, 1C=61 Mb≈0.0624 pg, [325]) to *Paris japonica* (Melanthiaceae, 1C=150,000 Mb≈152.23 pg, [326]).

The extant diversity of plant GS is the result of the combined effect of mechanisms increasing the DNA content, such as polyploidization and (retro)transposon activity, with those mechanisms leading to genome contractions through DNA elimination ([323, 324, 327, 328]). Surprisingly, some of the very largest genomes known among plants are diploids (e.g. *Fritillaria koidzumiana*, 1C=87.16 pg, [40, 329–331]). These large genomes have presumably evolved as a result of the breakdown of genome downsizing mechanisms and through the proliferation of transposable elements ([328, 330, 332]). However, across land plants as a whole polyploidy is regarded as the predominant cause for increased GS ([28, 333, 334]). Polyploids are common in almost all land plant lineages ([15, 33, 36]), with some exceptions such as in gymnosperms ([41, 42]. In addition, it is now recognized that all angiosperms have undergone one or more rounds of polyploidization in their evolutionary history ([34, 39]). Nevertheless, the distribution of GS values is skewed towards small and very small values ([323, 324, 335]). Consequently, it is generally assumed that post polyploidy there is a phase of genome reduction. Polyploidy and post polyploid divergence mechanisms have contributed to the global success of angiosperms in colonizing a vast diversity of ecosystems ([24, 30, 336, 337]).

Together, GS and polyploidy influence many life history traits, but not always in a concerted manner ([338–340]). Potentially, the effect of GS on plant traits depends on the interplay between ploidy and 1Cx (monoploid genome) DNA content. Chromosome numbers generally correlate with ploidy level when closely related species are compared. Similarly, chromosome number and GS are correlated, but these relationship diminish as a consequence post-polyploid genome divergence, involving mechanisms influencing GS and rearrangements of chromosomes, leading to, for instance: dysploidy ([29]), Robertsonian translocations ([341]), chromosome length changes ([342, 343]), or B chromosomes, ([344]).

3.2.2 Genome size as a phenotypical trait and the large genome constraint hypothesis

GS is a product of a species ancestry, selection and drift. Indeed, it may be that that effective population sizes in multicellular eukaryotes are sufficiently small that the power of drift has resulted in the expansion of genomes ([345, 346]): in a process known as "random walk", if there is a limit on how small genomes can be and genome size varies randomly through time, then on average genomes would tend to become larger purely due to stochasticity ([347]). Despite that, there are many associations reported with GS, and some of the phenomena at least are difficult to be explained by genetic drift, especially when phylogenetic corrections are considered ([348, 349]).

GS can be seen as having a dual role in influencing an organism's phenotype, via its informational content (i.e. the DNA sequence itself, "genotype") and also via the physical effects of its mass and volume (i.e. the amount of DNA, "nucleotype", [350]). The "nucleotype" is thought to impose limitations on phenotypes at both the cellular and organism levels, reviewed in [351]. Large genomes may have a cost at (1) evolutionary level: larger genomes may have slower diversification rates and harbour less speciose genera; (2) ecological level: species with large genomes may be excluded from extreme habitats due to physiological limitations (e.g. large genomes are associated with drought sensitivity), and species with large genomes are found to be at higher extinction risk; (3) functional level: species with large genomes may exhibit reduced maximum photosynthetic rates and hydraulic performance ([351–353]), whilst species with smaller GS may have the potential to colonize new habitats ([354]) and have increased likelihood to become invasive ([68, 71, 355, 356]).

Perhaps one of the most widely accepted correlations is that between GS, cell size and stomatal density, with large genomes exhibiting larger cells and lower stomatal densities ([352]). Species with large genomes cannot produce small cells, therefore they offset water loss by producing fewer large stomata; this however reduces carbon uptake, affecting photosynthetic efficiency ([353]). Stomatal size is an important ecological attribute, which varies with life history traits and GS, influencing the breadth of ecological niches observed for angiosperms ([357]). It has been proposed that the evolution of small GS in early angiosperms contributed to their diversification and subsequent establishment across a diverse array of niches ([30]). In contrast, ferns, that typically have larger GS, have remained more limited in their ecological distribution throughout their geological history ([37, 358, 359]).

Relationships between GS and phenology varies between groups, with some authors reporting an early phenology for species with smaller GSs ([360]), whilst others find no correlation ([361]). Life form (also called biological form or growth habit, formulated by Raunkier, [362]) has also been shown to be linked to GS, with woody lineages having lower tempos of GS evolution and annuals having a lower maximum limit for GS ([363–365]). Generally, it is well established that species with annual life cycles are limited to small GS ([366–368]), while perennial species present a wider spectrum of GS, from very small to the largest genomes reported until present ([365, 368, 369]). The presence of storage organs (e.g. in geophytes) is associated with species with large genomes, perhaps slow growth and stored resources means that their genomes are free to expand by genetic drift, released from selective constraints imposed by limited nutrients in the environment ([247, 370, 371]). Conversely, aquatic and carnivorous species tend to have smaller than average genomes due to the oligotrophic habitats they occupy ([325, 372, 373]).

Elevation is frequently used as an "umbrella variable" that incorporates a variety of ecological pressures (short growing season, temperature, increased solar radiation, ice-cover, rainfall). Correlations between elevation and GS have frequently been found to be non-significant ([79, 230, 374, 375]), although there are studies that have highlighted an inverse relationship between elevation and GS (i.e. smaller genomes at higher elevations, [247, 376–379], but [367] reports larger genomes at higher elevations in *Centaurea* s.l. in Bulgaria). It is possible that shorter growing seasons could favour smaller genomes (i.e. faster cell cycles resulting in faster blooming and seed set), while large genomes are correlated with enhanced frost tolerance ([204, 342]). Large genomes could suffer more DNA damage due to increased solar radiation at high elevations (i.e. the chance of radiation-induced DNA mutation is higher the larger the genome is), and this has been hypothesized to influence genome reduction, given that UV-mediated DNA damage might result in higher rates of DNA damage and associated DNA deletion with repair ([380]). Given such a variety of ecological pressures in the term "elevation" it is likely that more specific ecological indicators are of greater use in analysis ([381], however see [382] for an example of high-resolution Digital Elevation Models, DEMs, that faithfully approximate ecological variables).
DNA is especially rich in Nitrogen (N) and Phosphorus (P), and both of these macronutrients can be limiting for plant growth ([383, 384]). Large genomes should therefore be more expensive in terms of N and P to build and maintain since they require more of these nutrients per cell cycle. Recent studies have found that substrates rich in N and P favour the growth of species with large genomes in temperate grassland communities ([385–387], but similar associations were not seen in Mediterranean species [388]). GS was correlated with available soil N in *Primulina* suggesting that there may be evolutionary selection on GS depending on availability of nutrients ([389]). Overall, species with large GS are usually considered to have more functional, ecological and evolutionary constraints ([351]) than species with smaller GS, being less adaptable and more likely to become under threat of extinction due to their longer life cycles and small population sizes ([390]).
Here we have conducted a survey of GS on species in Asteraceae as a model system for the European Alps. We have the following aims: (1) to uncover the diversity of GS in Asteraceae across alpine environments; (2) to evaluate any correlations between GS, cytogenetic (chromosome number and polyploidy) and biological (i.e. life cycle) traits, and; (3) to model the potential role of a range of eco-variables in influencing the distribution of species in relation to their GS.

3.3 Materials and methods

3.3.1 Plant Material

Fresh leaves were collected from wild plants between March and September in 2016, 2017 and 2018, concomitantly with seed collections (see Chapter 2 and Table 3.1, as well as Figure 3.1 for an overview of the field collections), in the same areas: South East France, Southern Switzerland, Austria, North East Italy and Slovenia. These collections were complemented with material from botanic gardens and wild plants collected in localities outside the alpine arc area (29.65% of total accessions). Fresh leaf material from 5 different individuals or more was harvested and stored in a small zip-lock bag with a small piece of humid paper to prevent wilting, and whenever possible refrigerated at +4°C until processing.

	Accessions per species		Individuals	Elevation
Extended	All taxa	Subsp. lumped	All taxa	Average elevation
Mean	3.172	3.558	7.893	1349.743
Range	1—65	1—65	1—65	350—2575
Median	2	2	7	1250
Strictly Alps	All taxa	Subsp. lumped	All taxa	Field elevation
Mean	3.274	3.536	8.299	1688.546
Range	1—61	1—61	1—65	9—2951
Median	2	2	8	1847

Table 3.1: Average, median and range of number of accessions (i.e. populations) per species for the genome size datasets, considering subspecies as separate taxa or lumping them together, as well as number of individuals per population and elevation average, median and range (computed elevation preference for 'Extended' dataset, field collected elevation for 'Strictly Alps' dataset)

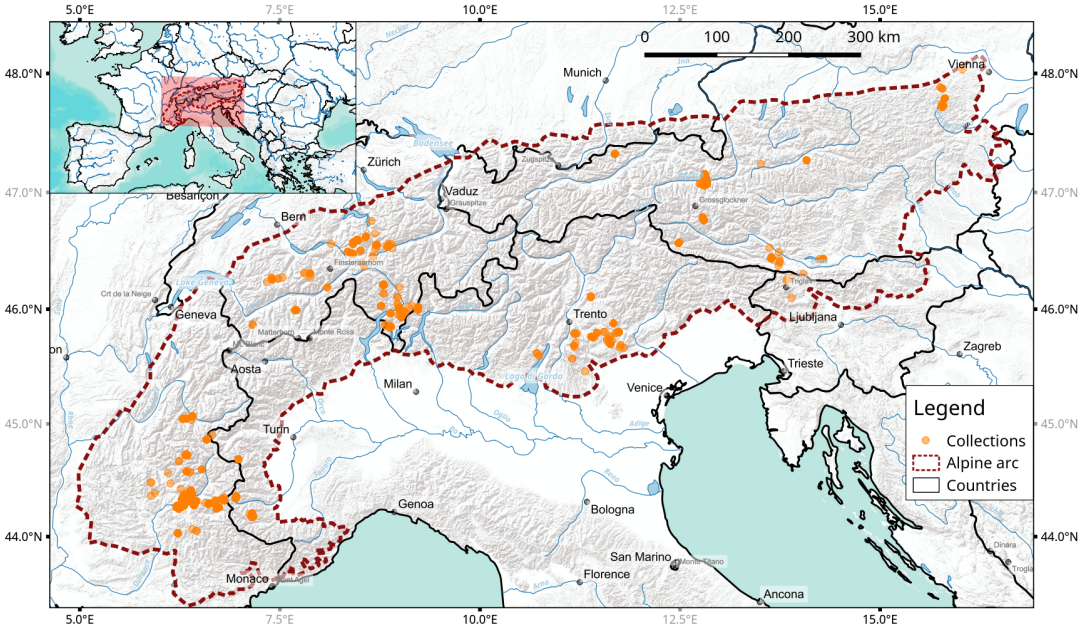

Figure 3.1: Overview map of all Asteraceae collections within the alpine arc. Datum: WGS 84

3.3.2 Flow cytometry analysis and chromosome counts

Nuclear DNA contents for all collected plants were estimated by flow cytometry following the one-step protocol ([303, 391]) at the Jodrell Laboratory of the Royal Botanic Gardens, Kew (RBGK) using fresh leaf materials, preserved up to 7-10 days from harvesting. Briefly, ~1 cm^2 of fresh leaf material was chopped with a new razor blade together with the selected reference standard (*Petroselinum crispum* (Mill.) Nyman ex A.W.Hill 'Champion Moss Curled' (2C=4.5 pg), *Pisum sativum* L. 'Ctirad' (2C=9.09 pg) or *Solanum lycopersicum* L. 'Stupiké polní rané' (2C=2 pg, [303]) directly into 2 mL of buffer (either GPB supplemented with 3% PVP-40, [299], Ebihara buffer, [392], or 'Cystain PI Absolute P kit' buffer, Sysmex UK) in a Petri dish over ice, then filtered through a 30 μm nylon mesh filter and stained with 100 μl of propidium iodide (PI, 1 mg/ml). For each species, two individuals from the same populations were anal-

ysed, and each sample was run for three times until at least 1,000 nuclei were included in each fluorescence peaks. Measurements were performed either with a Partec CyFlow SL cytometer (Partec, GmbH, Münster, Germany) or a Sysmex CyFlow Space cytometer (Sysmex UK Ltd, Milton Keynes, UK), both fitted with a 100 mW green solid-state laser (Cobolt Samba). The resulting flow histograms were analysed with FloMax software (v2.9, Partec GmbH). Mean 2C-values and standard deviations were calculated based on the fluorescence ratio between the sample and the reference standards used.
The GS of at least one accession of each of the species analysed was linked to a chromosome number, and hence to a given ploidy level (see details below). In order to allocate ploidy levels in subsequent accessions, the relative nuclear DNA contents were estimated as described in Chapter 2, following [302]. Briefly, up to 5 individuals were pooled and analysed together; wherever multiple peaks emerged, the samples were re-run separately to infer individual DNA contents and hence evaluate the presence of multiple DNA ploidies. Chromosomally-determined ploidy levels and their respective nuclear DNA contents were estimated and used as proxy for subsequent DNA ploidy allocations, based on relative DNA contents (see Chapter 2 for details). Chromosome counts were performed with the procedure described in Section 2.3.3, using root tips from seedlings grown from seed collections from the field. For species where seeds did not germinate or could not be collected, chromosome numbers were assigned based on the nuclear DNA content measured for the accession, after careful interpretation of data previously published (results available through Chromosome Count Database[1] [300], Genome size in Asteraceae Database[2] [393] and the Plant DNA C-value Database[3] [335]).

3.3.3 Ecological, phenotypical and biological data

Data on elevation preference, longevity, endemicity, phenology (flowering initiation) and edaphic requirements (nitrogen preference) were extracted from Flora Alpina ([158]). Data from Flora Alpina were summarized in the form of categorical variables, eventually simplifying them by reducing the number of factor levels (e.g. longevity, ploidy). An overall 'Average elevation preference' was calculated as described in Section 2.3.6, obtaining a number representing the "ideal" elevation value for each species. This variable, 'Elevation preference', was only used in the 'Extended' dataset (i.e. including all accessions), while the average value of field-collected elevation, simply called 'Elevation' was used in the 'Strictly Alps' dataset (i.e. restricted to accessions collected in the wild within the alpine arc). For species not present in Flora Alpina, data from the most closely related species within the genus or a related subspecies was used (see Supplementary B.1 for details). For agamospecies complexes (i.e. *Hieracium*, *Taraxacum*), the delineation of infrageneric sections adopted by JM Tison was used ([157, 210]) to guide in the selection of similar taxa.

3.3.4 Phylogenetic tree

The phylogenetic tree used in this analysis has been produced by Cristina Roquet (Laboratoide d'Ecologie Alpine, Grenoble, France & Universidad Autónoma de Barcelona, Spain) with sequences produced in the context of the projects PhyloAlps 2.0 (National Sequencing Center[4])

[1] http://ccdb.tau.ac.il/
[2] https://www.asteraceaegenomesize.com/
[3] https://cvalues.science.kew.org/
[4] http://phyloalps.org/index.html

and Origin-Alps (Agence Nationale de la Recherche[5]). The tree was built with RAxML ([394]) using 60 chloroplast markers, and includes 522 species from the Alps and two outgroups; see Supplementary Figure B.1 for the original tree.
Some species in the data were not present in the tree. For these, additional tips were introduced in the tree between the most closely related species. Resulting polytomies were randomly resolved using function *multi2d* (package *ape*, [305]); see Supplementary Figure B.2 for a comparison of the original tree and the modified tree.
In total, for the 'Extended' dataset, 36 taxa have been added to the tree (of which 13 are subspecies of taxa already included in the original tree), as well as 20 tips for non-subspecies level taxa (e.g. *Solidago virgaurea* added, while *Solidago virgaurea* subsp. *minuta* was present); overall, these constitute 14.85% of the 377 total taxa in the tree. For the 'Striclty Alps' dataset, 20 taxa have been added (of which 6 are subspecies), as well as 19 non-subspecies level taxa, amounting together to 15.35% of the 254 total taxa in the tree.

3.3.5 Statistical analysis

Statistical analyses were run in a similar fashion to Chapter 2 Statistical analyses 2.3.7. Data were split into two datasets: one including exclusively accessions from the wild collected material within the alpine arc ('Strictly Alps' dataset) and one also including accessions from botanic gardens and outside the alpine arc ('Extended' dataset). Where multiple GS measurements for the same taxon existed, these were averaged with respect to their ploidy level. For taxa with multiple ploidies, the lowest ploidy level was selected along with its corresponding chromosome and GS values. This was done in order to provide a conservative estimate on the effects of polyploidy. For 23 (6.86% of the total) species, GS measurements were not available for a set of individuals, and instead the ploidy estimate value was used. The same set of analyses has been carried out on each dataset. Phylogenetic signal was assessed for a reduced variable set (see details below) using the function *phylosig* (from package *phytools* v0.6-60, [307]), computing both Pagel's λ and Blomberg's K. Phylogenetically informed Markov Chain Monte Carlo generalized linear mixed models, as implemented in the package *MCMCglmm* v2.29 ([146]), were used to assess correlations within variables taking into account species relatedness. The natural logarithm of 2C genome size (GS) was used as the response variable: using the package *fitdistrplus* v1.0-14 ([395]), it was possible to determine that the best fit for the untransformed GS was a Gamma distribution (which is not supported in *MCMCglmm*), whilst the log-transformed data fitted a Gaussian distribution (which is supported), and this was therefore used as the family function for the models. Ploidy, chromosome number, elevation preference, longevity, life form, endemicity, indigeneity, phenology, hydric and edaphic requirements were entered as independent variables.
Fully specified models, that included all the genetic (i.e. ploidy level and chromosome number) and ecological (i.e. elevation, phenology, biological form, indigeneity and endemicity, soil pH, hydric and edaphic preferences) variables failed to converge due to the high number of parameters to estimate (see summary of these models in Supplementary B.3). Models were therefore separated into "genetic components" models, including ploidy level and chromosome number as the predictors, and "ecological components" models, including the ecological variables with the strongest relationship with GS, chosen by stepwise model reduction. This set of variables (both "genetic" and "ecological") was used for the phylogenetic signal analysis. For these last models, some variables underwent summarization to reduce the number of categories: for longevity,

[5]https://anr.fr/Project-ANR-16-CE93-0004

all factor levels that included annual or biennial life cycles were collapsed into a single level ("short"), and levels that included only perennial life cycles were grouped as well ("long"); for ploidy, all ploidy levels above the hexaploid (>6x) were grouped together. All models used the Gaussian family and a weak prior: both R and G structures had V=1 and nu=0.02; chains were run for $2 \cdot 10^6$ cycles, with a burn-in of 25,000 cycles, and the *trunc* parameter was set to 'TRUE'. Default model diagnostics were performed as well as Geweke plots, Heidel diagnostics and autocorrelation analysis. Multiple chain convergence diagnostics were carried out by running the same model calls with three different chains starting points (*set.seed* function) and examined with Gelman-Rubin diagnostics.
All models were diagnosed independently and achieved satisfactory chain mixing, passing stationarity tests as well as multiple chain diagnostics. For further details see Supplementary B.4. These results were congruent with the fully specified models (Supplementary B.3), albeit with better mixing and higher statistical significance, thanks to the re-parametrization and smaller parameter space to explore.
All data manipulation and statistical analyses were performed in R v3.6.2 ([306]) using RStudio v1.2.5033 ([396]). Additional data manipulation packages included: *plyr* v1.8.6 ([397]), *dplyr* v0.8.4 ([398]), *reshape2* v1.4.3 ([399]), *data.table* v1.12.2 ([400]), and *taxize* v0.9.7 ([401]). Data visualization was accomplished with *ggplot2* v3.3.1 [402] and additional packages *ggExtra* v0.9 ([403]), *ggpubr* v0.3.0 ([404]) and *ggtree* v2.3.0.991 ([405]).

3.4 Results

3.4.1 Genome size distribution and its relation with genetic and ecological covariates

A total of 335 species (1,225 distinct populations) from 100 genera were analysed, out of ∼500 species and ∼112 genera in Flora Alpina ([158], updated with Euro+Med taxonomic criteria). The 'Strictly Alps' dataset included a subset of these: 235 species and 74 genera (850 distinct populations). The figures shown here are from the 'Extended' dataset version unless otherwise specified.
Genome size (2C) ranged from 0.98 pg in *Erigeron canadensis* (2n=2x=18) to 36.69 pg in *Leucanthemum heterophyllum* (2n=8x=72), with a median of 5.06 pg, and it was skewed towards lower values (Figure 3.2A). Ploidy levels ranged from 2x (in ∼75% of the species) to 12x (in *Jacobaea incana*). We found intraspecific ploidy diversity in only nine species: *Artemisia campestris* and *Leucanthemopsis alpina* (Anthemideae), *Aster amellus* (Astereae), *Centaurea scabiosa* (Cardueae), *Pilosella autantiaca, P. cymosa* and *P. glacialis* (Cichorieae), *Senecio doronicum* and *Tephroseris integrifolia* (Senecioneae). Overall, GS scaled with ploidy level as well as with chromosome number (Figure 3.2B and Figure 3.2C). GS exhibited a positive relationship with elevation, in both the 'Extended' (Figure 3.3A) and 'Strictly Alps' (Figure 3.3B) datasets.

The distribution of GS values in relation to longevity, endemicity and substrate N content preference is shown in Figure 3.4. Species longevity was grouped together in a "short" category, that included all species that are capable of annual or biennial life cycles (irrespective of whether they could also live multiple years), and a "long" category, that included species incapable of annual or biennial life cycles. There were significant correlations between longevity and GS (Figure 3.4A) which become most apparent when the data are aggregated in two groups (Figure

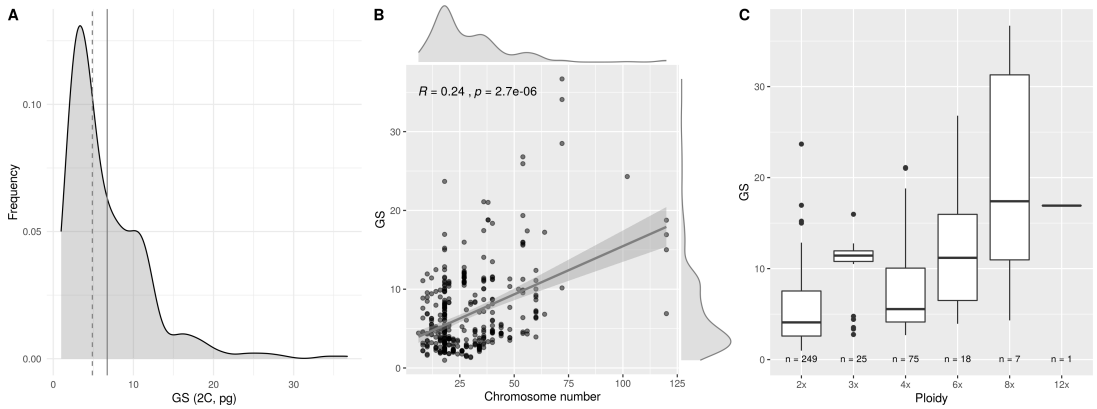

Figure 3.2: Genome size (GS) relationships of species of alpine Asteraceae. Panel A: density plot of untransformed GS, with on the y axis the frequency of values (as proportion of the total), the solid line representing the mean and the dashed line the median. Panel B: relationship between GS and chromosome number, with density plots along each axis (illustrating frequency of values for GS and Chromosome number), regression line with standard error and Spearman's correlation coefficient and significance. Panel C: boxplot showing the relationship between GS and ploidy, with sample sizes (n) for each ploidy level given.

3.4B), indicating that long-lived species tend to have larger GS than short-lived species. There is no apparent GS difference between endemics and not endemics (Figure 3.4C), but, strikingly, species preferring nitrogen-poor substrates tend to have larger genomes than those preferring medium and high nitrogen content substrates (Figure 3.4D).

3.4.2 Phylogenetic signal

The results of the phylogenetic signal analysis are reported in Table 3.2. For the 'Extended' dataset, all variables except N exhibited strong phylogenetic signal (i.e. λ close to 1), with GS

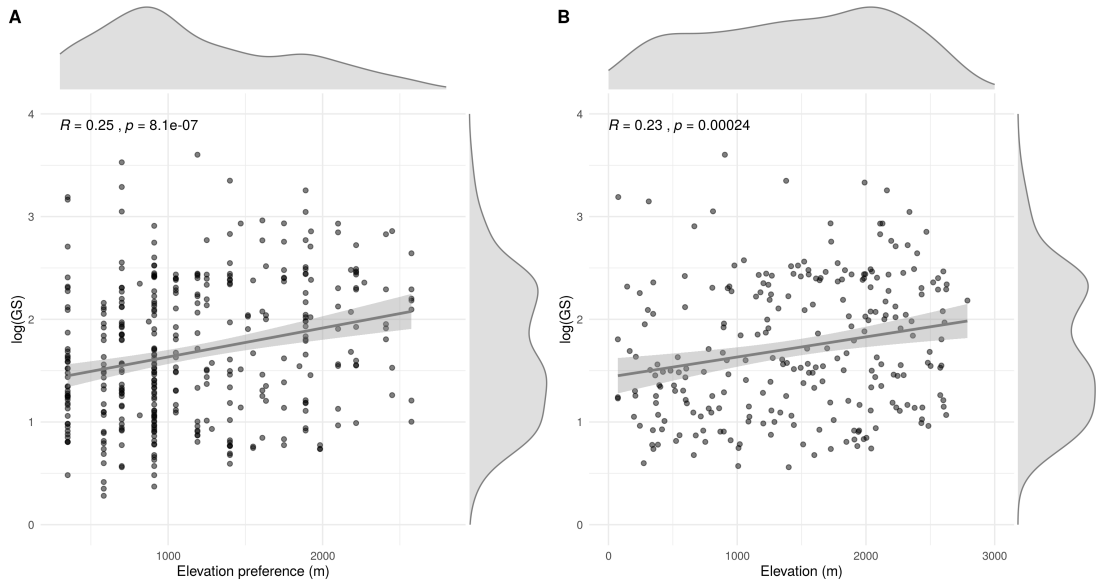

Figure 3.3: Scatterplots of log(GS) against elevation, with marginal density plots, regression line and correlation coefficients with significance reported. Panel A: log(GS) from the 'Extended' dataset, plotted against Elevation preference. Panel B: log(GS) from the 'Strictly Alps' dataset, plotted against field-collected Elevation.

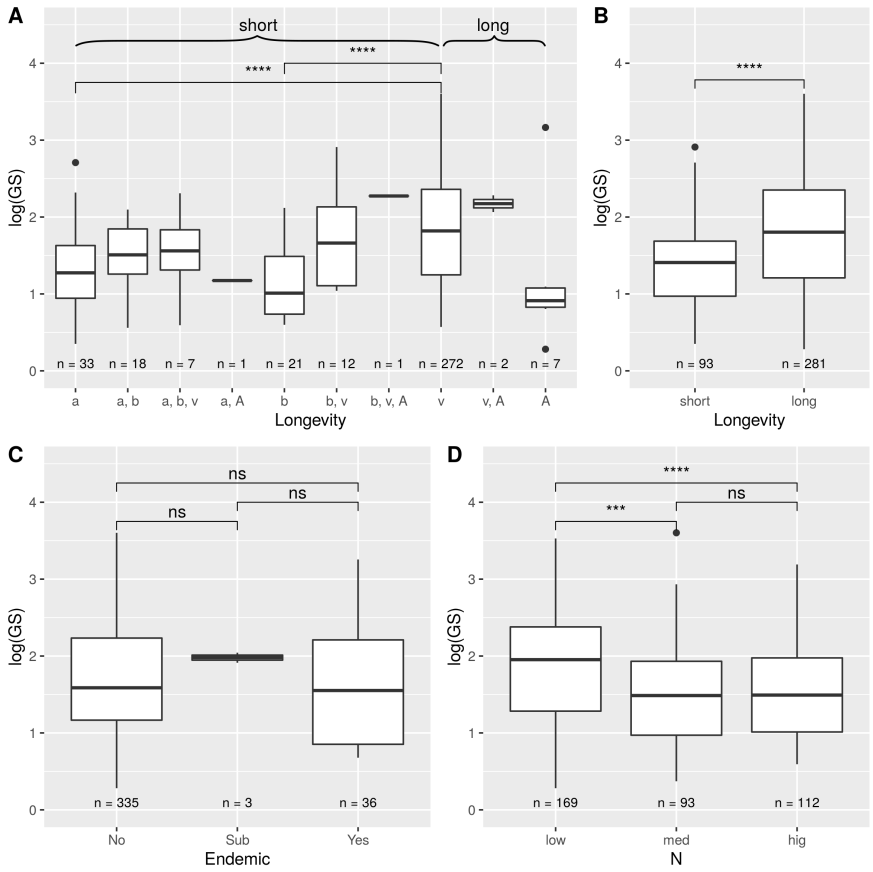

Figure 3.4: Boxplots illustrating the relationship between genome size and ecological variables, 'Extended' dataset. At the bottom of each box the sample size for that category is presented and above the boxes are pairwise Wilcoxon tests. Statistical significance is coded as follows: p≤0.0001 = ****; p≤0.001 = ***; p≤0.01 = **; p≤0.05 = *, p>0.05 = ns. Panel A: log(GS) and length of life cycle. Factor levels are interpreted as: a = annual, b = biennial, v = perennial, A = woody, and combinations of these. Brackets indicate how these levels were grouped together: "short" groups together species that include annual or biennial life cycles (i.e. annuals and biennials: a; a, b; a, b, v; a, A; b; b, v; b, v, A), and "long" groups together species that do not include annual or biennial life cycles (i.e. perennials and woody: v; v, A; A). Wilcoxon tests are shown only for highly significant (p≤0.001) differences. Panel B: presents the same data as in panel A but summarized in into two categories, "short" = capable of annual or biennial life cycle, "long" = incapable of annual or biennial life cycles. Wilcoxon tests as in panel A. Panel C: log(GS) and endemicity, where No = not endemic, Sub = Subendemic, Yes = Endemic. Panel D: log(GS) and substrate nitrogen level, where low = poor N levels, med = average N levels and high = rich N levels

and longevity being influenced the most. Variance mainly occurred within clades (i.e. K close to 0). Results are similar with the 'Strictly Alps' dataset, except for Endemic and N, which did not show strong phylogenetic signal. Variance was also found to be mainly within clades with this dataset. The results indicate that the taxonomic distribution of GS values is not random, a fact that is also visually apparent in Figure 3.5, which shows that the highest GS values (as well as ploidy levels) are found in the tribe Anthemideae, that the vast majority of triploid taxa occur in tribe Cichorieae (e.g. *Hieracium*), and that the tribe Cardueae is relatively uniform in terms of GS and cytotype diversity.

Figure 3.5: Phylogenetic tree of alpine Asteraceae. The GS of each species (2C, pg) is represented by bars, coloured by ploidy level. Poly = ploidy level >6x. Tribes are highlighted on the tree.

Extended	λ	λ **p-value**		**K**	**K p-value**	
Genome size	0.959	<0.001	$***$	0.0347	<0.001	$***$
Ploidy	0.605	<0.001	$***$	0.0147	<0.001	$***$
Chromosome number	0.672	<0.001	$***$	0.0153	<0.001	$***$
Elevation preference	0.942	<0.001	$***$	0.0198	<0.001	$***$
Longevity	0.959	<0.001	$***$	0.0192	<0.001	$***$
Endemic	0.780	<0.001	$***$	0.0125	<0.001	$***$
Flowering initiation	0.905	<0.001	$***$	0.0161	<0.001	$***$
Nitrogen	0.147	0.353		0.0123	<0.001	$***$
Strictly Alps	λ	λ **p-value**		**K**	**K p-value**	
Genome size	0.9473	<0.001	$***$	0.048	<0.001	$***$
Ploidy	0.7747	<0.001	$***$	0.026	<0.001	$***$
Chromosome number	0.8037	<0.001	$***$	0.027	<0.001	$***$
Elevation	0.8765	<0.001	$***$	0.026	<0.001	$***$
Longevity	0.9357	<0.001	$***$	0.028	<0.001	$***$
Endemic	$6.64e^{-5}$	1.000		0.017	0.025	$*$
Flowering initiation	0.9039	<0.001	$***$	0.025	<0.001	$***$
Nitrogen	0.0700	0.579		0.017	0.004	$**$

Table 3.2: Outputs of analysis for phylogenetic signal within model variables, for both datasets. Pagel's λ measures the deviation from correlation under Brownian motion (λ=0). Blomberg's K measures how variance is distributed (K>1 variance distributed mostly among clades, K<1 variance is distributed mostly within clades). Statistical significance is coded as follows: p≤0.001 = $***$; p≤0.01 = $**$; p≤0.05 = $*$.

3.4.3 Correlation between GS, genetic traits and ecological variables through phylogenetically-informed models (pMCMCglmm)

The relationships between GS, ploidy level and chromosome number, taking phylogeny into account, was explored by the "genetic components" models, reported in Table 3.3. Ploidies beyond diploid level had a highly significant and strong positive correlation with GS, with higher ploidies having a larger effect. Similarly, chromosome number had a highly significant correlation with GS, albeit weaker when compared to ploidy. The results are similar both with the 'Extended' and 'Strictly Alps' dataset, with the latter having lower effect sizes (except chromosome number).

To examine relationships between ecological variables and GS, taking into account phylogenetic structure, pMCMCglmms models were conducted (Table 3.4). A weak positive correlation was found between GS and elevation preference in the 'Extended' dataset, but it was not significant when elevation data was used in the 'Strictly Alps' datasets. For both datasets, there was a rather strong negative correlation between GS and short longevity (i.e. species having either annual or biennial life cycles), and between GS and endemics, meaning that species that have short life cycles or are endemic tend to have lower GS than average (weighing in the phylogenetic structure). There was also a small but positive correlation between GS and phenology (flowering initiation) in both datasets (i.e. species with larger GS tend to start flowering later). There was no significant relationship between GS and N content when taking into account phylogeny, despite being apparent with non-phylogenetically corrected comparisons.

Some ecological variables were dropped from further analyses at the stepwise model reduction stage (see Supplementary Table B.3). Among them were: life form, that is tightly linked with longevity (i.e. life cycle) and indigeneity, that is partially accounted for by the Endemic variable (e.g. an endemic has to be indigenous, but not vice versa). Water availability (e.g. dry,

Extended	**post.mean**	**l-95% CI**	**u-95% CI**	**eff.samp**	**pMCMC**	
Intercept	1.280	-0.377	3.020	3950	0.133	
Ploidy 3x	0.214	0.011	0.427	3950	0.048	$*$
Ploidy 4x	0.230	0.111	0.347	3950	<0.001	$***$
Ploidy (>6x)	0.452	0.240	0.658	4137	<0.001	$***$
Chromosome number	0.011	0.007	0.015	4174	<0.001	$***$
Strictly Alps	**post.mean**	**l-95% CI**	**u-95% CI**	**eff.samp**	**pMCMC**	
Intercept	1.2866	-0.3039	2.8109	3950	0.104	
Ploidy 3x	0.1528	-0.0862	0.3767	4671	0.209	
Ploidy 4x	0.2137	0.0560	0.3703	3950	0.012	$*$
Ploidy (>6x)	0.3398	0.0490	0.6538	3950	0.029	$*$
Chromosome number	0.0130	0.0078	0.0178	4202	<0.001	$***$

Table 3.3: pMCMCglmm models outputs for the 'Extended' and 'Strictly Alps' datasets, "genetic components" only. Statistical significance is coded as follows: p≤0.001 = $***$; p≤0.01 = $**$; p≤0.05 = $*$. Base level (Intercept) refers to: Ploidy 2x.

Extended	**post.mean**	**l-95% CI**	**u-95% CI**	**eff.samp**	**pMCMC**	
Intercept	1.127	-0.470	2.531	4405	0.137	
Elevation preference	$1.156e^{-4}$	$2.265e^{-5}$	$2.067e^{-4}$	3950	0.012	$*$
Longevity short	-0.237	-0.356	-0.125	3950	<0.001	$***$
Subendemic	-0.368	-0.866	0.070	3950	0.122	
Endemic	-0.210	-0.377	-0.058	4243	0.014	$*$
Flowering initiation	0.081	0.033	0.127	4008	0.002	$**$
Low N	0.037	-0.073	0.141	3950	0.509	
High N	0.040	-0.081	0.145	4178	0.482	
Strictly Alps	**post.mean**	**l-95% CI**	**u-95% CI**	**eff.samp**	**pMCMC**	
Intercept	1.332	-0.192	2.724	3950	0.070	
Elevation	$1.074e^{-5}$	$-7.510e^{-5}$	$1.056e^{-4}$	4034	0.811	
Longevity short	-0.295	-0.436	-0.134	4759	<0.001	$***$
Subendemic	-0.366	-0.837	0.125	3950	0.145	
Endemic	-0.215	-0.395	-0.047	3950	0.013	$*$
Flowering initiation	0.075	0.016	0.142	3950	0.018	$*$
Low N	0.083	-0.044	0.218	3950	0.242	
High N	-0.075	-0.219	0.070	3950	0.317	

Table 3.4: pMCMCglmm models outputs for the 'Extended' and 'Strictly Alps' datasets, "ecological components" only. Statistical significance is coded as follows: p≤0.001 = $***$; p≤0.01 = $**$; p≤0.05 = $*$. Base level (Intercept) refers to: Longevity long, Endemic No, N med.

medium, wet, etc) and pH (e.g. acid, neuter, basic) were also dropped as they did not exhibit much variation in the data for GS. The variables studied in detail are included in the models above.

3.5 Discussion

3.5.1 The diversity of genome size in alpine Asteraceae: polyploidy as the main driver of change

This study contributed with GS estimates for 319 species in the family, of which 186 had never been studied before from this viewpoint (based on available data on the GSAD database[6]). The distribution of GS values found in alpine Asteraceae was skewed towards smaller values (Figure 3.2A), in agreement with the general trend for the family ([406]) and angiosperms at large ([295, 324]), and only a small number of taxa showed relatively large GSs. Perhaps unsurprisingly, GS was strongly correlated with chromosome number and ploidy levels (Figure 3.2B and 3.2C), as polyploidization is the main driver of genome size increase in plants ([10, 12, 35]), and this was also confirmed by the phylogenetically-informed models ("genetic components", Table 3.3) that picked up strong relationships between these three variables, notwithstanding the strong phylogenetic signal characterizing them (Table 3.2); that is to say, the observed co-occurrence of high GS values in species with high chromosome counts and ploidy levels (and the opposite, low GS in low chromosome counts and ploidy species) was driven by a direct relationship and not purely due to species relatedness.
One example that clearly illustrates the impact of polyploidy in GS evolution was found in the *Leucathemum* polyploid complex, where several species (besides the diploid *L. atratum*) revealed polyploid cytotypes ranging from 4x to 8x, hence resulting in some of the largest genomes reported here (e.g. *L. adustum*, 2C=29.23 pg). Nevertheless, polyploid *Leucathemum*, albeit having large genomes, these were somewhat smaller than one would had predicted after genome duplication when compared with diploid accessions (e.g: *L. atratum*, 2n=2x=11.53 pg), evidencing a noticeable genome downsizing. Genome downsizing and post-polyploidization genome reorganizations have been now long reported in many plant groups, being indeed a general trend in angiosperms' evolution ([323, 328, 330, 332]), so this is not surprising in Asteraceae, especially given the high ploidy levels at which it has been recorded (e.g. 6x, 8x).

3.5.2 The correlation between nuclear DNA contents with life history, biological and ecological variables

Elevation and GS showed a positive correlation (Figure 3.3), both with the 'Elevation preference' (i.e. "ideal" elevation value inferred from Flora Alpina data) and the field-collected 'Elevation' varaibles (i.e. from wild collections, strictly within the alpine arc). This is in agreement with other studies that found higher ploidy levels (and/or higher GS) at higher elevations ([79, 351, 367, 378], but see [230, 375, 379] reporting lower ploidies at high elevations). However, elevation had strong phylogenetic signal (Table 3.2), and in fact the relationship between GS and elevation was very weak in the MCMCglmm results (Table 3.4), being entirely non-significant for the 'Strictly Alps' dataset. This means that the apparent trend observed in the

[6] https://www.asteraceaegenomesize.com/

data is mostly driven by phylogenetic relationships of the species, so that species with large GSs that occur at high elevations are also phylogenetically close to each other. The idea that mountain flora is predominantly made up of specialized lineages adapted to high-elevation environments (rather than species locally adapted to these habitats from lowland lineages) is not new ([182, 197, 199]), and the strong phylogenetic signal found here for elevation supports it. However, it is unclear whether high ploidies and large GS values are common among mountain species ([72, 79, 172, 183] in favour, in contrast with [247, 376–379]), and whether these traits confer an adaptive advantage in high-elevation habitats.

From this study of the Asteraceae family in the Alps, the phylogenetic relationships between species were the main driver of trait distribution for several variables. Nevertheless, a thorough understanding of the evolutionary dynamics of alpine plants must take into account the larger orographic context of Europe (e.g. Apennines, Massif Central, Balkans, Pyrenees, Carpathians, Caucasus, etc), as well as a broader taxonomic spectrum. Nonetheless, circumscribed studies such as the one here do provide insights into characteristics of a specific family or geographic area, and are of value in uncovering trends and associations between traits.

Most species in this study fall within the 'long-lived' category (i.e. perennials: 281 long-lived and 93 short-lived, Figure 3.4B), and GS was significantly smaller in 'short-lived' species. Furthermore, despite the fact that there was strong phylogenetic signal, that relationship remained significant in phylogenetically corrected models. Similarly, phenology (flowering initiation) had a small but significant correlation with GS (Table 3.4), revealing that species with larger genomes tend to start blooming later in the year. Curiously, the flowering asynchrony observed in the mixed-ploidy population of *Senecio doronicum* was in the opposite direction to this general trend, with larger genomes blooming earlier (see Chapter 4). Similar results were reported for other species with cytotypes mixed or in close vicinity ([101, 133]). This difference could be explained by the fact that phenology in mixed-ploidy species is shaped by additional constraints, bearing in mind that flowering asynchrony is an important mechanism to avoid inter-cytotype competition and support assortative mating ([102, 115]).

It has been suggested that some particular life forms (also called biological type or vegetative habit, formulated by Raunkiaer, [362]) tend to have large GS, for example geophytes (i.e. bulbous species, [357, 370, 371]) while other life forms may impose limitations on GS (e.g. annuals, [366–368] and aquatic plants, [325, 372, 373]). Species of the latter tend not to have short life cycles, and in general long-lived species tend to be more likely to have large GS, irrespective of life form ([365, 368, 369]). While the correlations found here do not inform about causes, a possible reason why long-lived species tend to have larger GS, is that larger genomes may be slower to replicate than smaller ones, slowing down the cell cycle and overall growth rate, effectively placing a selective pressure on GS for short-lived species. Similarly, the yearly growth cycle could be slowed by this physiological phenomenon, partially accounting for the small delay in flowering time initiation for species with large genomes.

On average, endemic species did not appear to have different GS than sub- and non-endemic species (Figure 3.4C), and endemicity displayed strong phylogenetic signal in the 'Extended' but not in the 'Strictly Alps' dataset (Table 3.2). In the phylogenetically corrected models, for both the 'Extended' and 'Strictly Alps' datasets, the endemic flora had smaller GS than non-endemics, albeit barely significant (Table 3.4), apparent when considering phylogenetic relationships, but not apparent when studied as two separate groups (Figure 3.4). Endemics in the Alps belong mostly to lineages that are widespread in mountain systems of Europe, rather than having evolved from relict populations that survived the glaciations *in situ* ([199]), and only investigations taking into account both nucleotype traits (e.g. GS and ploidy level) as well as

biogeography in the wider European mountain system could elucidate GS evolution dynamics in endemics in a meaningful way.

Given past studies showing that species with large GS are most abundant on soils rich in N and P ([385–387]), it is perhaps surprising that species preferring N-poor substrates also had significantly larger genomes that those preferring medium or N-rich substrates (Figure 3.4D). Nevertheless, this difference in GS between groups was not significant in the phylogenetically corrected models, meaning that species that prefer N-rich substrates tended to be related to each other, despite N not having a strong phylogenetic signal (Table 3.2). Potentially, the range of GS of the species analysed here does not impose severe nutrient limitations, and this, together with a group of species with large GS preferring N-poor substrates, could have driven the difference observed in the data. Indeed, this seem to be the case, as the *Leucanthemum* polyploid complex (that includes the biggest genomes in the dataset) is represented in the Alps by taxa preferring N-poor substrates. Furthermore, while nutrient limitation could be a strong selective pressure in lowland communities (that tend to be more dense and in which competition is more prominent, [204, 407]), in high-elevation environments the factors driving species habitat preferences could be different (e.g. low temperatures, number of snow-free weeks per year, shelter from wind, solar radiation, etc, [204]), with species with large genomes not being as disadvantaged as in more competition-driven communities.

Many of the effects of GS are reported for species with particularly large GS (e.g. Melanthiaceae, *Fritillaria*, some ferns, [330, 331, 359]). The size of even the largest genomes in the data presented here are substantially smaller (maximum here is 18.35 pg/1C in *Leucanthemum heterophyllum*, compared with the largest species in Melanthiaceae, *Paris japonica*=152.23 pg/1C). Nevertheless, the results presented here reaffirm some general trends observed for angiosperms (e.g. correlations between GS and longevity), as well as highlighting some peculiarities of the Asteraceae family (e.g. GS and nutrient level) that perhaps could be extended to other plant families in the Alps.

Chapter 4

Phenotypical and ecological differentiation of sympatric cytotypes of *Senecio doronicum*

4.1 Summary

Sympatric mixed-ploidy populations can be used as natural experiments, uncovering microevolutionary processes that, over long periods of time, can contribute to macroevolutionary patterns of plant evolution. In this study, a population in S-W France of the species *Senecio doronicum* showing multiple cytotypes was extensively studied. Our objective was to determine if ploidy level influenced phenotype, phenology and reproductive success in a high elevation area.

We conducted detailed phenotypic and cytological screening of ∼500 individuals of *Senecio doronicum* on Tête Grosse, Alpes Maritimes, S-W France in an area where we had previously identified mixed ploidy level cytotypes. The octoploid and tetraploid cytotypes of *Senecio doronicum* exhibit small but significantly different morphological characters and were clearly differentiated phenologically, with barely overlapping flowering times. They also differed in their reproductive success, with tetraploids producing more viable seeds per capitulum, despite the fact that they had lower potential reproductive output (fewer florets). Octoploids were more heavily attacked by pre-dispersal seed parasites, and these substantially lowered the reproductive output of these plants. Micro-niche distribution analysis revealed that some morphological traits differences (e.g. size of the capitulum) were less pronounced at the interface between the two cytotypes populations. This potentially suggests that octoploids were mostly influenced by environmental factors, while tetraploids were subject to density-dependent effects.

The outcome of competition between the two cytotypes in this local population seems to favour the octoploid cytotype, as they were more numerous. However, the tetraploid cytotype had higher viable seeds number, potentially an effect of the lower parasitization rates and different floral competition environment.

4.2 Introduction

4.2.1 Polyploidy and plant evolution

The high incidence of polyploidy in flowering plants is widely recognized ([33, 35]), and it is thought that all angiosperms have undergone at least one round of polyploidy or whole genome duplication in their ancestry, a process that has arguably fuelled their diversification, although the importance of polyploidy-driven diversification remains an ongoing debate ([15, 34, 408], but see Mayrose *et al.*'s critique [409] and the response to it by Soltis *et al.* [410]). Autopolyploidy is increasingly regarded as widespread in plants and is a process that, over time, can lead to the rise of new species ([8]). Over recent years there has been a growing number of studies investigating autopolyploid formation and establishment ([11, 49]). Autopolyploids generally result from unreduced gametes ([45]), and will arise in a population at low frequencies (potentially a single plant). Such individuals face problems associated with their 'minority cytotype disadvantage' ([91]). Consequently, without some form of selective advantage or reproductive isolation, autopolyploid lineages are prone to rapid extinction ([9]). In addition, autopolyploids often share their progenitors' ecological niche ([44]), and competition between the diploid and polyploid will generally result in the (local) extinction of one of the two cytotypes ([410]). In the absence of strong ecological differentiation, newly arisen autopolyploids can become established depending on their relative fitness compared with the lower ploidy level progenitor ([93, 100, 124]) or they may simply die out through the power of genetic drift. However, polyploids, especially allopolyploids, or autopolyploids formed from divergent parental genotypes can have higher intrinsic plant vigour ([18]). In fact, polyploids are generally found to have higher seed set in natural populations ([116, 126] but see [127]).

It is possible for autopolyploid cytotypes to show ecological differentiation, which can lead to reproductive isolation and diverging selective pressures. As a result, different cytotypes may diverge because of differing preferences for specific habitats ([82]), development of vegetative ([411]) and reproductive traits ([7]), or shifts in phenology ([88]). Ecological divergence can also indirectly produce assortative mating by increasing the chance of intra-cytotype mating ([98, 412]). When lineages are already isolated by strong post-mating barriers (e.g. inter-cytotype sterility, [11]), reinforcement of pre-mating barriers can prevent the waste of gametes in low-fitness crossings ([101, 413]), especially in species that experience pollen limitation. Potentially the evolution of pre-mating barriers between ploidy levels may be a strong selective pressure in species with a generalised pollination strategy ([414–416], however Hegland & Totalnd [417] found that pollen limitation was not prevalent in a natural plant community).

Compared with populations at the centre of the species distribution, those at the limit generally have lower densities and higher ecological stress because of sub-optimal environmental conditions, and depleted genetic diversity ([241, 418]). These characters can produce divergence and reproductive isolation if genetic flow with the central populations becomes limited (e.g. marginal speciation, [4, 419]). It has also been suggested that similar processes can operate at a smaller, local spatial scale ([241, 420, 421]).

4.2.2 *Senecio doronicum* s.l. on Tête Grosse

Senecio doronicum L. is a species of herbaceous perennial found throughout European mountain ranges between 1,000-2,400 m of elevation, exceptionally up to 3,000 m (chorological indication: European orophyte, [158]). Its habitat ranges from alpine meadows to rocky screes, typically on calcareous substrates.

The oval-lanceolate basal leaves have very short petioles and are truncate-attenuated, slightly fleshy and coriaceous at maturity. The indumentum is highly variable, with both entirely glabrous and densely pilose plants found. The species flowers in June and July, and bears 1-5 capitula on a stem 10-50 cm with progressively reduced leaves, all with slightly toothed margin. The capitula are radiate, yellow-orange in colour and 3-5 cm in diameter; they are arranged in a very loose corymb, flower basipetally (starting with the terminal capitulum downwards) and are heterogamous (ligulate or ray florets are female, while tubular or disk florets are hermaphroditic). When mature, seed heads expose a pure white pappus, with hairs on a single series and attached directly on the top of the achenes.
The *Senecio doronicum* material examined here was collected in the Maritime Alps of France, an area regarded as a biodiversity hotspot for the Alps ([157, 422]), with many endemic taxa derived from refugia associated with the last glacial maximum (e.g. for the Asteraceae family, *Berardia subacaulis*, [173, 187, 196]). The Maritime Alps are also the meeting point between Western and Eastern alpine floristic elements, and many plant groups have complex evolutionary histories associated with their population dynamics in the area ([186, 194, 423]).
A preliminary ploidy screening of *Senecio doronicum* in the Maritime Alps evidenced the presence of two cytotypes, including a tetraploid (4x) and an octoploid (8x) cytotype. This presented a natural experiment in which to explore phenotypic diversity and pollinator behaviour, with the potential to give insight into the early stages of evolution ([115, 118, 424, 425]).
The aim of this chapter is to combine comprehensive phenotypic data to examine in detail the dynamics of inter-cytotype competition and coexistence in a sympatric mixed-ploidy population, helping to shed light into the evolutionary processes that follow a polyploidization event.

4.3 Materials and methods

4.3.1 Plant tagging and cytotype screening

In 2016, 2017 and 2018 we carried out an extensive cytogenetic survey of the *Senecio doronicum* population on Tête Grosse and nearby areas. The survey followed our discovery that the population consisted of early- and late-flowering individuals, with a phenology lag which seemed to fit 4x and 8x cytotype differentiation in a preliminary ploidy screen. For areas outside of the main population on Tête Grosse, we adopted the same collection strategy as outlined in Chapters 2 and 3, i.e. collecting $\sim$10 individuals per population. During the summer of 2018, we focused on the Tête Grosse's population: from the beginning of June until mid-August. We labelled and numbered individual plants using electrician's tape as soon as they started to flower. For plants with more than one capitulum, we labelled each capitulum with letters, starting with the terminal capitulum (a), and progressing sequentially as capitula opened in secondary stems (ie: b, c and so on). As the season progressed and tetraploids started flowering, we focused on the portion of population where both cytotypes were in close proximity, labelling each individual plant, even if not flowering. Additionally, towards the end of the flowering season, we selected plants with maturing seeds that had not been previously analysed for ploidy and these were bagged to collect seeds (labelled as "silvertag").
DNA ploidy levels for all tagged plants were estimated from fresh leaf material within ten days from collection using flow cytometry at the Jodrell Laboratory of the Royal Botanic Gardens, Kew (RBGK). Measurements were performed with a Partec CyFlow SL cytometer (Partec, GmbH, Münster, Germany) fitted with a 100 mW green solid-state laser (Cobolt Samba). We

followed the one-step protocol described previously ([391]) with minor modifications ([37]). Measurements were made using the internal standard *Petroselinum crispum* "Champion Moss Curled" (4.401 Gbp/2C; [426]) and the "general purpose buffer" (GPB; [299]) supplemented with 3% (w/v) polyvinylpyrrolidone. Up to 5 individuals were pooled together and eventually re-run if multiple peaks emerged. Chromosomally-determined ploidy levels and their respective nuclear DNA contents were estimated and used as proxy for subsequent DNA ploidy allocations, based on relative DNA contents (see Chapter 2 for details).

4.3.2 Phenotype scoring and pollen counting

During summer 2018, we measured several morphological traits of *Senecio doronicum* plants in flower. Once the ligulate (ray) florets opened (i.e the capitulum fully expanded), and just before the tubular (disk) florets had fully opened, wherever possible, we took a series of measurements and pictures of each capitulum. The traits measured were as follows: diameter of capitulum (Ø.cap), height of capitulum (h.cap), diameter of the involucrum (Ø.inv), height of the involucrum (h.inv), height of the flowering stem (h.stem), number of caulinar leaves (n.leaves) and number of capitula (n.cap). A rigid metric tape was used to measure stem and leaf spacing to the nearest mm, and a digital caliper (DIN 862, Mib-Messzeuge GmbH, Spangenberg, Germany) was used for the capitulum measurements, to the nearest $1/100^{\text{th}}$ of mm.
As indicated above, in addition to the morphological measurements in the field, we took macrophotographs of the capitulum from above, making sure to include the entire corolla in the frame. We counted the number of ligulate and tubular florets using ImageJ 1.33 software (Rasband, National Institutes of Health, USA) and recorded whether the capitulum suffered from pre-dispersal seed predation (see 4.5 - Discussion).
For a selected number of plants of each cytotype we used flow cytometry to count the number of pollen grains, using the following protocol (Oriane Hidalgo, personal communication). First, we harvested the five un-dehisced anthers from florets, stored them into a 0.2 mL PCR tube in a hermetic container on a bed of silica gel, and let them dry at room temperature for approximatively one week. Lycopod spore tablets were used as a standard for pollen counting (9,666 ± 671 spores per capsule, batch 3862; Department of Quaternary Geology, Lund University, Lund, Sweden). One Lycopod tablet was placed in each flow cytometry tube, suspended in 1 mL of 1N HCl and vortexed until it had completely dissolved. The dry anthers were crushed with a dissection needle in the PCR tube, suspended in 200 μL of "General purpose buffer" (GPB, [299]) supplemented with 3% PVP-40, vortexed, sonicated for 1 min at 30 kHz (SFE 590/1 ultrasonicator, Ultrawave Ltd., Cardiff, UK), vortexed again and briefly spun in a mini-centrifuge to collect any liquid from the lid of the tube. The pollen suspension was then filtered through a 150 μm nylon mesh (Partec, Münster, Germany) into the Lycopod spore suspension. Anthers were rinsed with an additional 200 μL of GPB, vortexed and the suspension was filtered into the Lycopod spore suspension. The mesh was then rinsed with 600 μL of GPB. Propidium iodide (1 mg/mL; Sigma) was then added to the sample to stain the pollen exine and tubes were placed on ice for 30 min. Each sample was analysed using a CyFlow SL3 flow cytometer (Partec, Münster, Germany) fitted with a 100 mW green solid-state laser (Cobolt Samba, Solna, Sweden). Data were acquired using the logarithmic scale (FloMax software v2.7, Partec). Samples were run until a minimum of 200 pollen grains and 200 spores was reached. The total number of pollen grains per sample (representing the pollen production of five stamens) was calculated by multiplying the ratio between pollen and spore particle counted with the number of lycopod spores in the sample. Measurements were performed in triplicate for

each sample, taking their mean as the estimate of pollen production.

4.3.3 Flowering time

To determine the flowering phenology of tetraploid and octoploid plants, in 2018 we counted the number of individuals in bloom (i.e. with at least one floret open) per cytotype every 2/3 days. In the field, we assigned each individual to one or the other cytotype based on its location within the population, and this assignment was later corroborated with FCM ploidy estimation (see Cytotype Screening, Section 4.4.1).

4.3.4 Manual crossings and population fitness estimation

In 2017, we bagged 5 pre-anthesis capitula of the 4x cytotype to assess whether *Senecio doronicum* is capable of self-pollination, and harvested them after seed maturation. After confirming self-incompatibility, in 2018 we performed a series of cross-pollination experiments to assess the potential reproductive success (fitness) of intra-cytotype and inter-cytotype crossing. All crosses were performed when capitula were in full anthesis (i.e. up to the time when the oldest florets were starting to wither), by harvesting mature anthers from 5-10 florets of a donor capitulum and gently brushing them against the receptive stigmas of the receiving capitulum. Self-pollinations were performed in the same fashion, by taking dehisced anthers and pollinating mature stigmas from the same capitulum, for four capitula each per cytotype. Because of the phenology difference between cytotypes, a few capitula of octoploids (early flowering) had receptive stigmas when pollen of tetraploids was available, therefore we were able to perform four homoploid crosses and four heteroploid crosses in octoploids. For tetraploids, in which more capitula were available during the brief flowering time overlap, we performed seven homoploid crosses and seven heteroploid crossings. Pollination was conducted on capitula that were bagged with a fine soft mesh cloth secured with a cable tie to the stem before anthesis. The bag was then only opened briefly during the manual cross and then promptly re-closed to prevent access by pollinators. Plants monitored with Rana (see Section 6.3.3) were also bagged once the capitulum was no longer receptive for pollinators, and seeds collected after maturation. In addition, 30 capitula of octoploids and three capitula of tetraploids from different individuals were bagged when no longer receptive and collected after seed maturation. We inferred the number of predated capitula from the pictures taken for morphometrics (332 capitula). For all harvested capitula, the number of viable seeds was estimated under a stereomicroscope (Wild M8, Leica Biosystems, Nussloch, Germany)

4.3.5 Micro-niche mapping

A degree of spatial separation between tetraploid and octoploid *Senecio doronicum* was apparent in the Tête Grosse population. To quantify this, in 2018 we set up a system to map the position on the ground of each individual plant (or plant clusters, where more than two individual rosettes grew together). First, we established a principal axis approximatively running along the ridge of Tête Grosse's plateau (base transect). We used a Garmin eTrex 30 GPS unit to record latitude and longitude (decimal degrees, reference system WGS 84) of the starting and ending points of the base transect. The relative location of each individual plant of *Senecio doronicum* was measured using a 30 m metric tape laid on or parallel to the base transect (giving the x-coordinate) and using a rigid 5 m metric tape to measure each plant's perpendicular distance (the y-coordinate), to the closest cm. When plants grew less than 5 cm apart we

considered these as one cluster, and recorded the number of basal leaf rosettes to represent the number of individuals. These coordinates were then converted to GPS coordinates for each plant, and all tagged plants were recorded with their unique plant ID. In the westernmost part of the population, referencing from the base transect was difficult due to the steep declining slope, so GPS coordinates were calculated using triangles. GPS coordinates of all the vertices were recorded, and plants' locations inside each triangle were measured with their x-coordinate parallel to the base and y-coordinate measured along one of the sides (see Figure 4.1).
In order to collate all the individual positions of recorded plants under different transects, we converted the Cartesian metric coordinates x and y in latitude and longitude coordinates, on the basis of the GPS coordinates of the transects reference points. For the linear transects this is straightforward: let A and B be the reference points for the transect, each with latitude (Lat) and longitude (Lon) GPS coordinates, and let $\overline{AB}$ be the distance in metres between these two points as measured on the ground. Knowing the GPS coordinate of a point C on the perpendicular to the transect passing from A, and knowing the distance $\overline{AC}$, the longitude of of each plant P can be obtained as

$$P(\text{Lon}) = A(\text{Lon}) + \frac{x * (A(\text{Lon}) - B(\text{Lon}))}{\overline{AB}} + \frac{y * (A(\text{Lon}) - C(\text{Lon}))}{\overline{AC}}$$

equivalently, for the latitude:

$$P(\text{Lat}) = A(\text{Lat}) + \frac{x * (A(\text{Lat}) - B(\text{Lat}))}{\overline{AB}} + \frac{y * (A(\text{Lat}) - C(\text{Lat}))}{\overline{AC}}$$

Note that this method would not work if the reference transect points have the same latitude or the same longitude (i.e. the transect runs parallel to a parallel or a meridian). The ridge of Tête Grosse runs in direction NE-SW, so this was not the case for this study.
For the triangular transects an additional step was required: knowing the GPS coordinates of

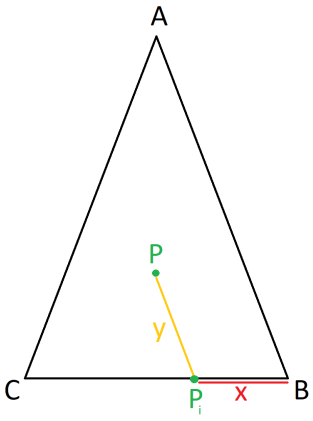

Figure 4.1: Diagram for GPS coordinate calculation in triangular transects

vertices ABC, and the distance x of P from AB (note that this was measured parallel to the base BC, and not perpendicular to the side AB, see Figure 4.1) and y of P from A (measured along the side AB) both in metres, the GPS coordinates of P can be calculated as follows.
Let Long be the longitude GPS coordinate, and Lat the latitude GPS coordinate; first, we calculate the coordinates of a point P_i on BC with distance x from B as:

$$P_i(\text{Lon}) = B(\text{Lon}) + \frac{x * (C(\text{Lon}) - B(\text{Lon}))}{\overline{CB}}$$

$$P_i(\text{Lat}) = B(\text{Lat}) + \frac{x * (C(\text{Lat}) - B(\text{Lat}))}{\overline{CB}}$$

Then P can be calculated as:

$$P(\text{Lon}) = P_i(\text{Lon}) + \frac{y * (B(\text{Lon}) - A(\text{Lon}))}{\overline{AB}}$$

$$P(\text{Lat}) = P_i(\text{Lat}) + \frac{y * (B(\text{Lat}) - A(\text{Lat}))}{\overline{AB}}$$

These steps were repeated with each separate transect, and plants latitude/longitude coordinates obtained collated in a single dataset. We assigned most of the mapped plants to the tetraploid or octoploid cytotype on the basis of their position and proximity with tagged plants of known ploidy level.

4.3.6 Marginality index

To examine if there was an effect of plant location within the population on its traits, we used the micro-niche data to compute a marginality index that reflects how close an individual plant is to the margin of the population with respect to the distribution of the other cytotype in the population. The numerical index gives a value close to 1 for plants of each cytotype at the edge of their respective population, and close to 0 for plants furthest from it.

The population on Tête Grosse roughly spreads along the Southern aspect of the plateau, that runs in direction NE-SW. For simplicity, we decided to use only the longitude (E) coordinate to estimate the marginality index. We established a breakpoint where the frequency of octoploids surpassed the frequency of tetraploids on the longitude axis, subdivided in 100 identical bins across the full extension of the population (irrespective of cytotype).

We defined the "breakpoint" as the longitude coordinate of the established split between tetraploid and octoploid populations, where "x" is the pool of longitude coordinates for the tetraploid population, and "y" is the pool of longitude coordinates for the octoploid population, and "x_i" and "y_i" are the i^{th} elements of their respective coordinate pools; we then calculated the marginality index for each element i as:

$$\text{Marginality}_{4\text{x},i} = \frac{x_i - \min(x)}{\text{breakpoint} - \min(x)}$$

$$\text{Marginality}_{8\text{x},i} = \frac{\max(y) - y_i}{\max(y) - \text{breakpoint}}$$

Note that the marginality index can have values larger than 1 if $x_i >$ breakpoint, or if $y_i <$ breakpoint. There were a few instances of plants occurring outside of their main cytotype population, and were surrounded by plants of the other cytotype. The reason we established an artificial breakpoint is that if we used $\max(x)$ and $\min(y)$ for tetraploids and octoploids respectively, the marginality index would have been skewed towards these few isolated plants, poorly representing the main population. Also note that the scaling of the index is not equivalent between tetraploids and octoploids, as they have largely different population areas and the index is calculated relative to population area (i.e. the spatial distance for an increase of 0.1 in marginality for a tetraploid does not equate to the same distance for an increase of 0.1 in marginality for an octoploid).

4.3.7 Statistical analyses

All data manipulation and statistical analyses were performed in R v3.6.2 ([306]) using RStudio v1.2.5033 ([396]). Additional packages data manipulation packages included: *plyr* v1.8.6 ([397]), *dplyr* v0.8.4 ([398]), *reshape2* v1.4.3 ([399]) and *data.table* v1.12.2 ([400]). Principal component analysis was conducted with function *princomp* (in R *stats* package), visualized with *ggfortify* ([427]). We visualized the results with *ggplot2* [402], with additional packages *ggExtra* ([403]), and *ggpubr* ([404]). The spatial structure of the *Senecio doronicum* population on Tête Grosse was visualized overlaying plants GPS coordinates onto satellite imagery (Google Maps) using *ggplot2* [402] and *ggmap* [428].

4.4 Results

4.4.1 Cytotype screening

We conducted a cytotype screening of *Senecio doronicum* focussed in SW France, with opportunistic collections across the Alps (Figure 4.2), surveying in total 56 distinct populations, of which only 15 contained tetraploids (including Tête Grosse). Overall, we analysed ploidy levels of 499 individual plants (excluding those on Tête Grosse), of which 443 were 8x and 56 were 4x. Tête Grosse had the most numerous population of tetraploids we found.

For the Tête Grosse population, we estimated DNA ploidy levels of 548 individual plants: 163

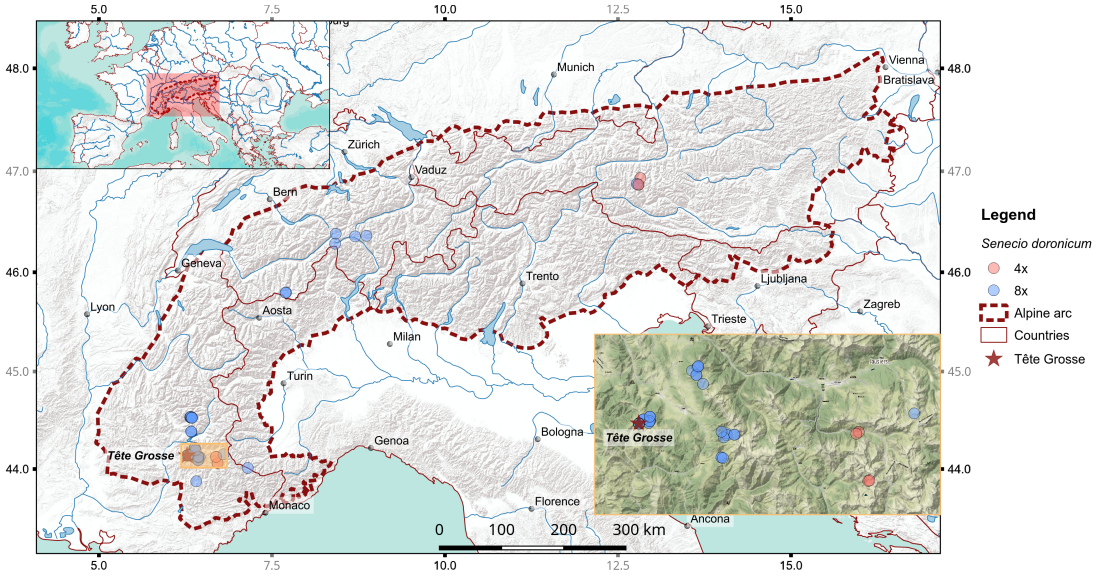

Figure 4.2: Overview of *Senecio doronicum* cytogenetic screening. Datum: WGS 84

tetraploids, 382 octoploids and 3 hexaploids (6x); see Supplementary Table C.1 and Figure 4.3 for illustration of the distribution of cytotypes in the population. Additionally, we counted chromosomes of one 4x and one 8x individual and linked the numbers to the nuclear DNA content to confirm the ploidy level estimation: 2n=4x=40 chromosomes≈8.9 pg/2C, and 2n=8x=80 chromosomes≈16.5 pg/2C.

4.4.2 Phenotype scoring

We collected morphometrics data from 372 unique capitula from 287 different plants (Supplementary Table C.2). For 175 of these capitula we counted florets from macrophotographs. The two cytotypes differed significantly in all the traits (Figure 4.4), except for the height of the involucrum. Octoploid plants tended to have larger capitula and taller stems. By contrast, 4x plants had more leaves and capitula, and also produced more pollen grains per floret.

In particular, we estimated the number of pollen grains per floret (98 florets for 4x, 91 for 8x) in 61 different plants: 31 4x and 30 8x; in one case (plant '432') we estimated pollen count for two capitula of the same plant. On average, 4x produced 3,480 pollen grains per floret and 8x produced 2,592 pollen grains (Wilcoxon rank test: W=791, p-value<0.001), with an average measurement error of 10.08% (standard deviation between the three repeated FCM measures of each floret), irrespective of ploidy level. Intra-individual variation (standard deviation between different florets of the same individual) was 22% for 4x and 27.8% in 8x.

There were only two plants for which we measured side capitula (different than the terminal capitulum, "a") for 4x and only one for 8x, and in neither case they had statistically different pollen counts than the terminal capitulum (data not shown).

The number of ligulate florets was larger for 8x polyploids than for 4x polyploids, these being 20 and 18 respectively (Wilcoxon test: W=2702, p-value=0.015), and the number of tubular florets was higher for 8x plants (127 florets) compared to 4x plants (87 florets; Wilcoxon test: W=1050, p-value<0.001, Figure 4.5). Accordingly, the total number of florets was higher in octoploids than tetraploids, these being 147 and 105 respectively (Wilcoxon test: W=1086, p-value<0.001).

The trends, which are larger overall size of the capitulum in 8x, as well as taller floral scapes, remain similar between terminal ("a") and side capitula ("b", "c", etc), with the exception of the number of tubular florets, that are similar for both cytotypes in the side capitula (Figure 4.6).

We then performed a PCA on fitness-related traits (i.e. thought to directly contribute to reproductive success) taken together: diameter of capitulum, height of capitulum, diameter of the involucrum, height of the involucrum, number of ligulate florets and number of tubular florets. The number of pollen grains per floret was excluded from this analysis as PCA analysis requires no missing values in the data, and including the pollen variable would make the sample size fall from 146 to 25 observations (Figure 4.7). The first two principal components accounted for 95.37% of variation, with number of tubular florets and stem height being the major drivers, respectively. Each cytotype tended to cluster together, but a certain degree of overlap exists, with a large portion of 4x's morphospace being contained in the 8x's morphospace.

In order to identify any differences between the morphospace of the terminal capitulum ("a") and the side capitula ("b", "c", etc), we plotted both terminal and side capitula to the same figure (Figure 4.8). The side capitula did not occupy a materially different morphospace than the terminal capitulum of the same plant.

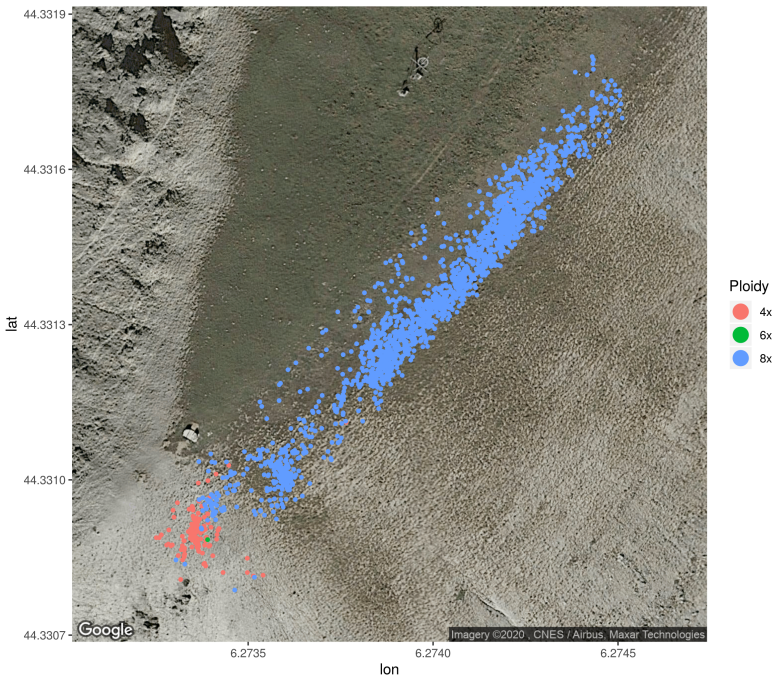

Figure 4.3: Map of the *Senecio doronicum* population on Tête Grosse. Each plants cluster (individual plants and plants occurring within 6 cm of each other) is plotted as a dot coloured by its ploidy. The number of plants is proportional to the size of the circle. Satellite imagery is from Google Earth.

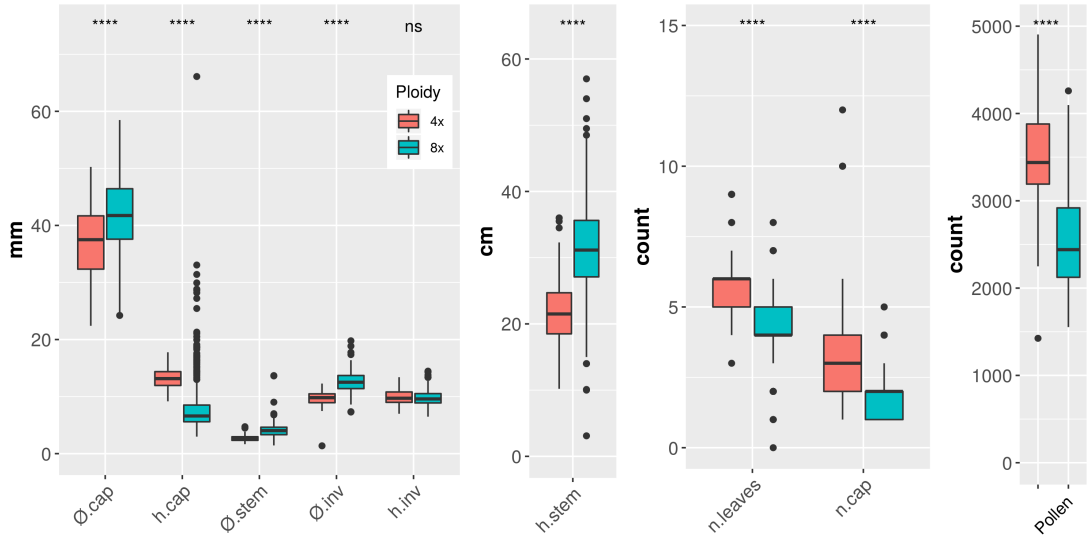

Figure 4.4: Boxplots presenting phenotypical traits per cytotype. Morphological traits are on the x-axes, and traits values on the y-axes. Box's middle lines represents the median, box extents represent the second to third quartiles, whiskers the first and fourth quartiles, while outliers are represented by points. For each trait, at the top of the plot is presented the p-value of a Wilcoxon test, coded as follows: $p \leq 0.0001$ = ****; $p \leq 0.001$ = ***; $p \leq 0.01$ = **; $p \leq 0.05$ = *; "ns" = $p > 0.05$. Abbreviations: Ø.cap = capitulum diameter; h.cap = capitulum height; Ø.stem = peduncle diameter at the base of capitulum; Ø.inv = diameter of the involucrum; h.inv = height of the involucrum; h.stem = height of the floral scape, from rosette to terminal capitulum; n.leaves = number of caulinar leaves along the floral scape; n.cap = number of capitula; Pollen = number of pollen grains per floret.

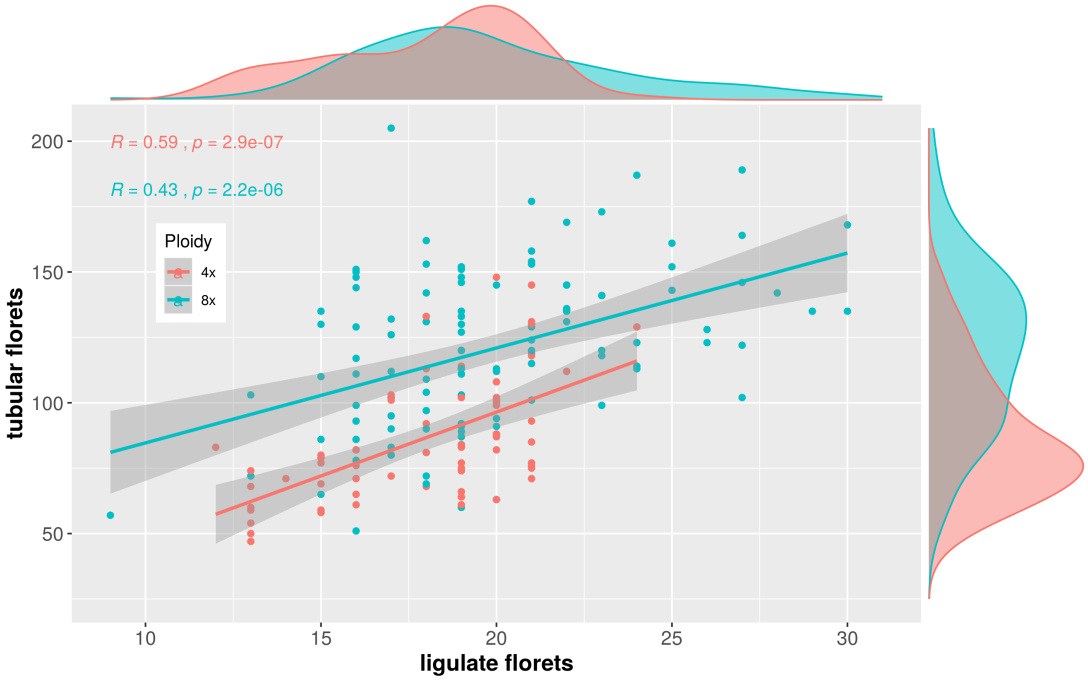

Figure 4.5: Scatterplot presenting the relationship between the two types of florets in *Senecio doronicum* capitula. Regression lines and 95% confidence intervals are plotted, as well correlation coefficients and associated p-values (Spearman's rank correlation) and marginal density plots, representing the distribution of each cytotype's trait on each axis.

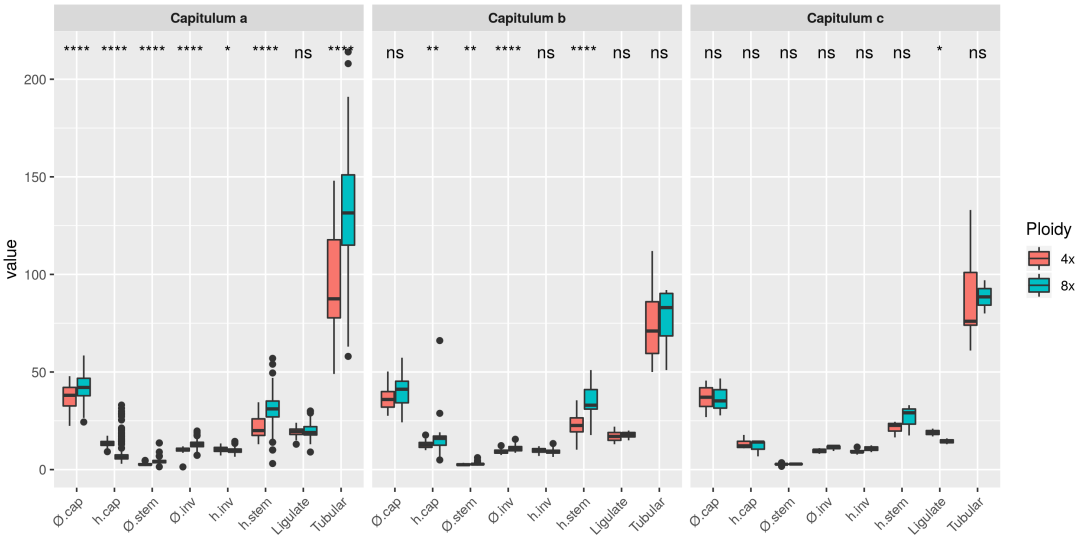

Figure 4.6: Boxplots presenting traits relationship of traits across capitula. "Capitulum a" is the terminal capitulum, "Capitulum b" is the first side capitulum, "Capitulum c" is the second side capitulum. For each trait, at the top of the plot is presented the p-value of a Wilcoxon test, coded as follows: p≤0.0001 = ****; p≤0.001 = ***; p≤0.01 = **; p≤0.05 = *; "ns" = p>0.05. Abbreviations: Ø.cap = capitulum diameter; h.cap = capitulum height; Ø.stem = peduncle diameter at the base of capitulum; Ø.inv = diameter of the involucrum; h.inv = height of the involucrum; h.stem = height of the floral scape, from rosette to terminal capitulum; Ligulate = number of ligulate (ray) florets; Tubular = number of tubular (disk) florets.

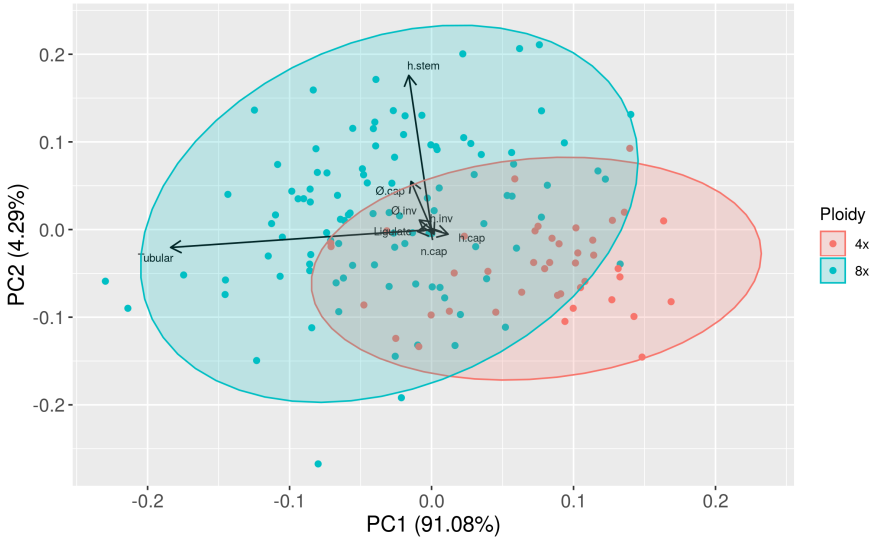

Figure 4.7: Principal Component Analysis (PCA) of fitness-related traits. The axes correspond to the first two Principal Components of variation (PC), and points are individual plants plotted according to their PC loadings. The relative contributions of traits to the PCs are plotted as vectors, and a 95% confidence interval ellipse is drawn around each cytotype's point cluster. Abbreviations: Ø.cap = capitulum diameter; h.cap = capitulum height; Ø.stem = peduncle diameter at the base of capitulum; Ø.inv = diameter of the involucrum; h.inv = height of the involucrum; h.stem = height of the floral scape, from rosette to terminal capitulum; Ligulate = number of ligulate (ray) florets; Tubular = number of tubular (disk) florets.

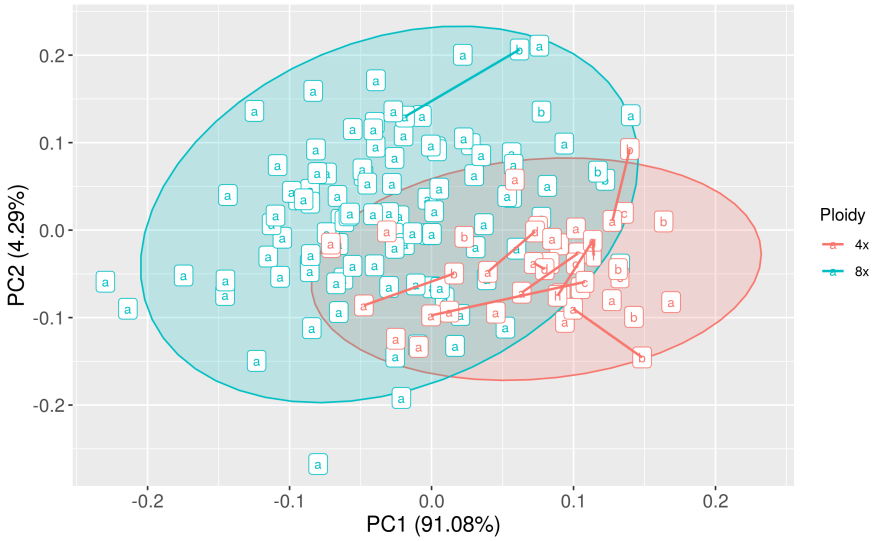

Figure 4.8: PCA of fitness related traits with capitula labelled as terminal (a), first (b) and second (c) side capitula, and so on. Different capitula of the same plant are linked by a line. PCs, ellipses and point locations are equivalent to Figure 4.7.

4.4.3 Flowering time

Octoploid plants flowered from 1st June to 17th July 2018 (35 days), and 4x flowered from 9th July to 6th August 2018 (28 days), see Figure 4.9 and Supplementary Material C.3. The 8x population was larger than 4x population, with flowering peaks at 227 and 46 individuals on the 28th June and 20th July respectively. There were 8 days (9th to 17th July 2018) in which both cytotypes were flowering at the same time (i.e. there was at least one individual in bloom per cytotype), encompassing the 22.86% and 28.57% of the total flowering period for 8x and 4x respectively. During this overlap period, up to 40 8x plants and up to 43 4x plants were co-flowering, corresponding to 17.62% and 93.48% of the number of individuals in bloom at peak flowering respectively.

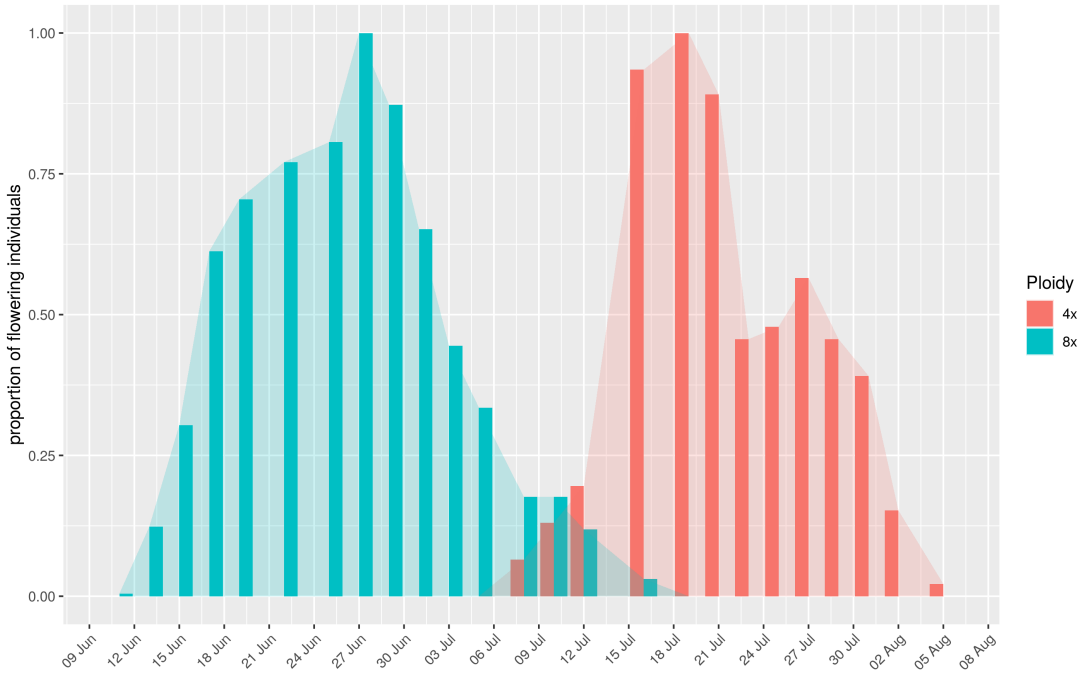

Figure 4.9: Barplot illustrating the flowering time of *Senecio doronicum* cytotypes on Tête Grosse. On the x-axis is the date (2018), and on the y-axis is plotted the proportion of individuals flowering on each day compared to the maximum number of individuals per cytotype observed throughout the flowering period.

4.4.4 Seeds and manual crossings

In total, 173 capitula were examined, counting a total of 2,451 viable seeds (Figure 4.10). For those plants that were naturally pollinated (labelled "Rana" and "silvertag", Supplementary Table C.4), the 4x plants had consistently higher numbers of viable seeds than the 8x plants. The results were similar when considering relative seed set per ploidy level, calculated as individual viable seeds / average number of florets of the population, per ploidy (data not shown).

No seeds were generated in self-polination experiments, confirming auto-incompatibility of *Senecio doronicum*. Overall, in all crosses fewer seeds were produced compared to plants exposed to natural pollinators, but intra-ploidy crosses produced more seeds than interploidy crosses (Table 4.1), even though differences were statistically insignificant (Wilcoxon tests, interploidy: W=18, p-value=0.147, intraploidy: W=6.5, p-value=0.409). It wasn't possible to

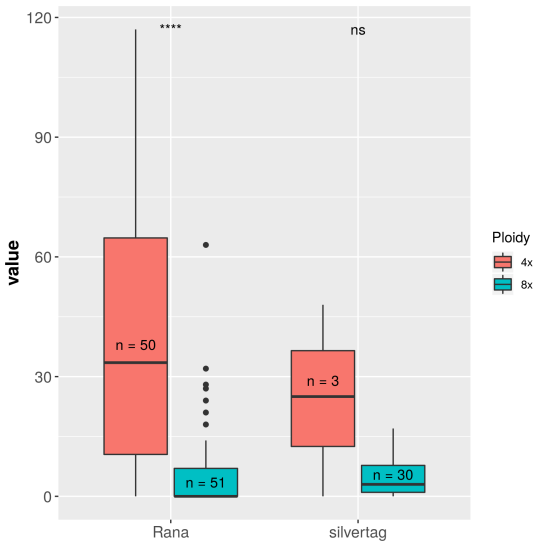

Figure 4.10: Boxplot of viable seed counts for plants exposed to natural pollination. Sample size for each group is reported above the median in each box, alongside the p-value of a Wilcoxon test, at the top of the plot, coded as follows: p≤0.0001 = ****; p≤0.001 = ***; p≤0.01 = **; p≤0.05 = *; "ns" = p>0.05. Plants exposed to natural pollinators were labelled as "Rana" if they had been monitored, and "silvertag" if only seeds were collected.

collect two of the capitula involved in manual crosses (one 4x heteroploid crossing and one 8x homoploid crossing).

	4x			**8x**		
Crossing	n plants	Mean n viable seeds	Mean % viable seeds	n plants	Mean n viable seeds	Mean % viable seeds
Self	4	0	0.00	4	0	0.00
Inter-ploidy	6	2.17	2.07	4	0	0.00
Intra-ploidy	7	2.43	2.32	3	2.00	1.36

Table 4.1: Manual crossings of *Senecio doronicum*. The number of plants used, the number of viable seeds counted and the percentage of viable seeds (calculated as % of the average floret number) is presented for self-crossings, interploidy crossings and intraploidy crossings, per cytotype.

4.4.5 Seed predation

Some *Senecio doronicum* capitula were attacked by a pre-dispersal seed parasite (larvae of a small beetle of the Curculionid group), with 8x plants being more affected than 4x plants.
The mean predation rate (capitula attacked / total capitula) per week was 37.07% for 4x plants and 73.97% for 8x plants, Figure 4.11, although this difference was not statistically significant (Wilcoxon test: W=4, p-value=0.343), likely due to too few datapoints (four for each ploidy, one for each week of flowering).

4.4.6 Micro-niche mapping

We recorded coordinates of 1,889 *Senecio doronicum* plant clusters (127 4x plants, 2,738 8x plants and 1 6x plant), of which 318 were labelled plants of known ploidy. For 23 plant clusters it was not possible to assign ploidy level unambiguously, and these have been removed from

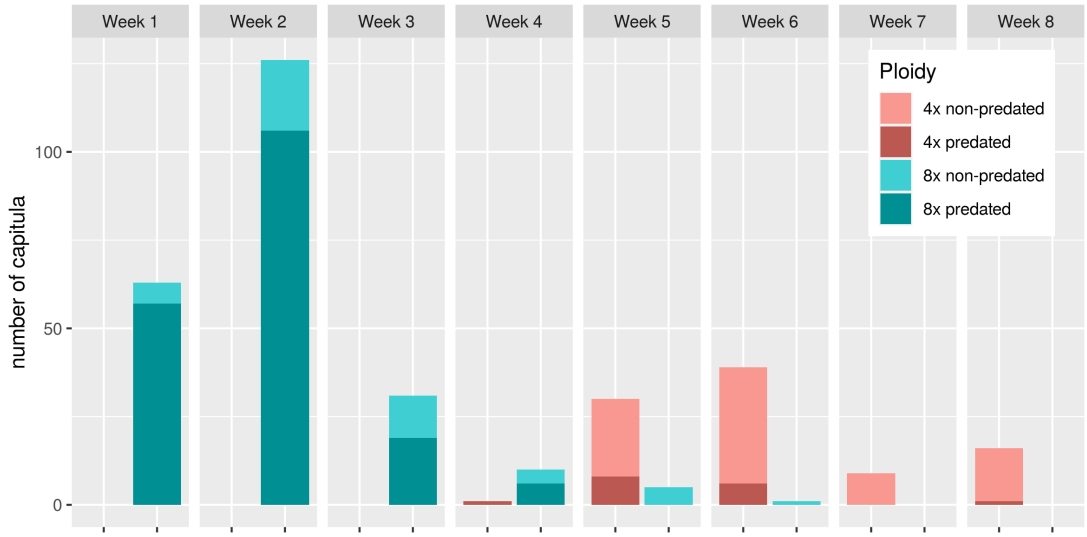

Figure 4.11: Barplot illustrating the pre-dispersal seed predation on *Senecio doronicum* capitula by cytotype. The number of attacked capitula (dark colour) and number of non-predated capitula (light colour) is plotted for each week of flowering.

the analysis. The conversion to latitude/longitude coordinates aligned well with the structure of the population on the ground, as seen by overlapping it with satellite imagery (Figure 4.3). On average, 4x plant clusters contained 2.14 individuals with median of 1, while 8x clusters contained 2.12 individuals with a median 2 (Wilcoxon test: W=96,772, p-value=0.014).

The marginality index measures the effect of plant location on its traits. The breakpoint chosen (i.e. the line chosen to split tetraploid and octoploid populations) to calculate the marginality index aligned reasonably well with the transition zone between cytotypes observed in the population, i.e. most of the 4x plants (red circles) occur on the left side, and most the 8x plants (blue circles) occur on the right side, as illustrated in Figure 4.12.

The marginality index ranged from 0 to 6.38 in 4x (two records with marginality >3) and from 0 to 1.09 in 8x (no records >3).

We then examined the relationships of phenotypical traits with the marginality index (Figure 4.12). Plants with high marginality (i.e. values ∼1) are close to the contact zone between the two cytotypes and are denoted by a white tint, while plants with low marginality (i.e. values ∼0) grow far from the contact zone, and are denoted by a deep blue tint. Octoploid plants tended to have smaller capitula traits (diameter of capitulum and involucrum) for plants with high marginality values (i.e. at the margin of the population, in Figure 4.14A and 4.14C), whereas 4x plant traits remained stable or increased (diameter of capitulum, Figure 4.14A) with high marginality values. The number of capitula was higher for 4x plants at the margin of the population, and constant for 8x plants (Figure 4.14E). Stem height decreased for high marginality values in 8x but remained constant for 4x plants (Figure 4.14F). The number of ligulate florets tended to decrease with marginality for both cytotypes (Figure 4.14G), while tubular florets number was lower for 8x plants but remained similar for 4x plants at the margin of the population (Figure 4.14H). Finally, the number of leaves decreased for 8x but not for 4x at the margin of the population (Figure 4.14I).

Figure 4.15 illustrates the variability of phenotypical traits in relation to marginality. The coefficients of variation (a proportional measure of variance, calculated as standard deviation divided by the mean) were almost constant across the distribution of plants of both ploidies for the diameter of capitulum and involucrum, height of the stem and number of tubular florets

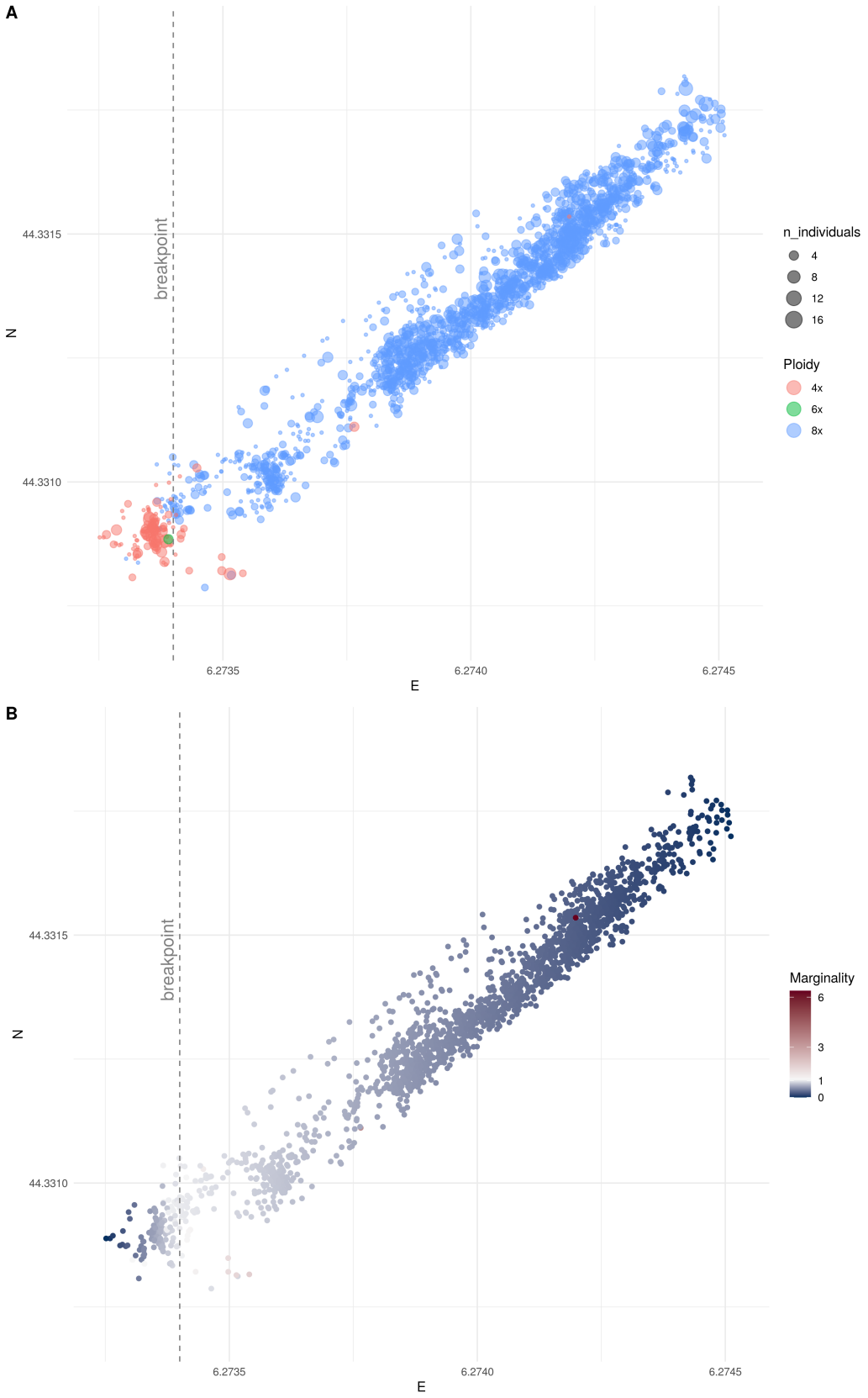

Figure 4.12: Marginality index and cytotype distribution of the *Senecio doronicum* population on Tête Grosse, with the artificial breakpoint drawn for both panels. Panel A illustrates the spatial structure of each cytotype's population, where each dot, coloured by ploidy, represents a plant cluster and its size is proportional to the number of individuals it contains. Panel B illustrates each plant cluster's marginality index; note that the scale goes up to values of 6 due to a few outliers occurring well beyond their population's limit (see Section 4.3.6 for further details), but the vast majority of plant clusters have marginality index values between 0 and 1.

(Figure 4.15B). For of the height of the involucrum , the number of tubular florets and number of capitula the variability of 8x plants decreased towards the edge of the population, while it increased for 4x. The opposite is true for number of leaves , with this trait being more variable for 8x plants than for 4x plants at the edge of the population.
Plants with higher marginality (i.e. values ∼1, meaning they are found closer to the edge of their respective population) do not seem to occupy a distinct part of the morphospace compared to plants with low marginality (Figure 4.13). Note that the morphospace of 4x includes more plants with high marginality than 8x's morphospace, although this effect does not seem dependent on the overlapping of the two morphospaces.

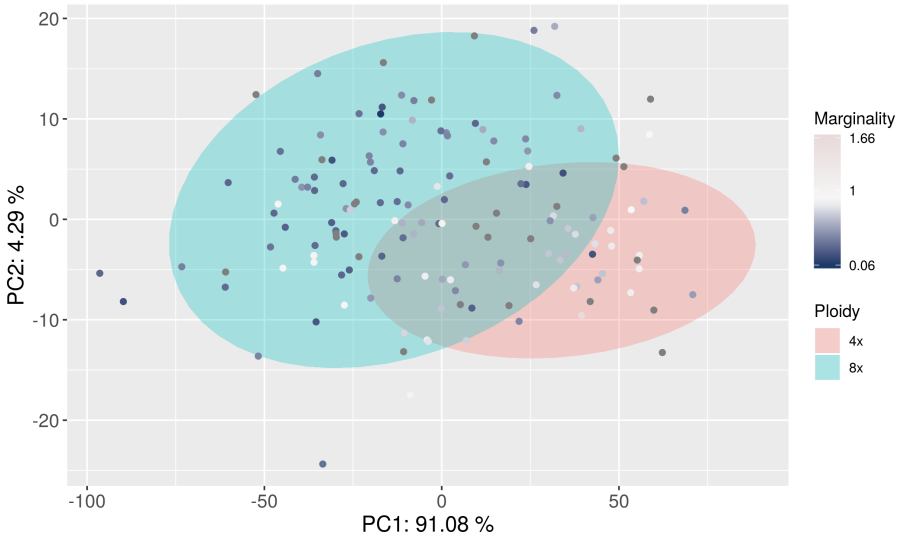

Figure 4.13: PCA analysis with individual capitula measurements coloured by their marginality index value. The PCs and ellipses are equivalent to those in Figure 4.7 and Figure 4.8, with individual points representing a unique capitulum, coloured by its plant marginality value. Note that the marginality scale does not cover the full range found in Figure 4.12 because morphological data was not available for all plants included in the micro-niche analyses.

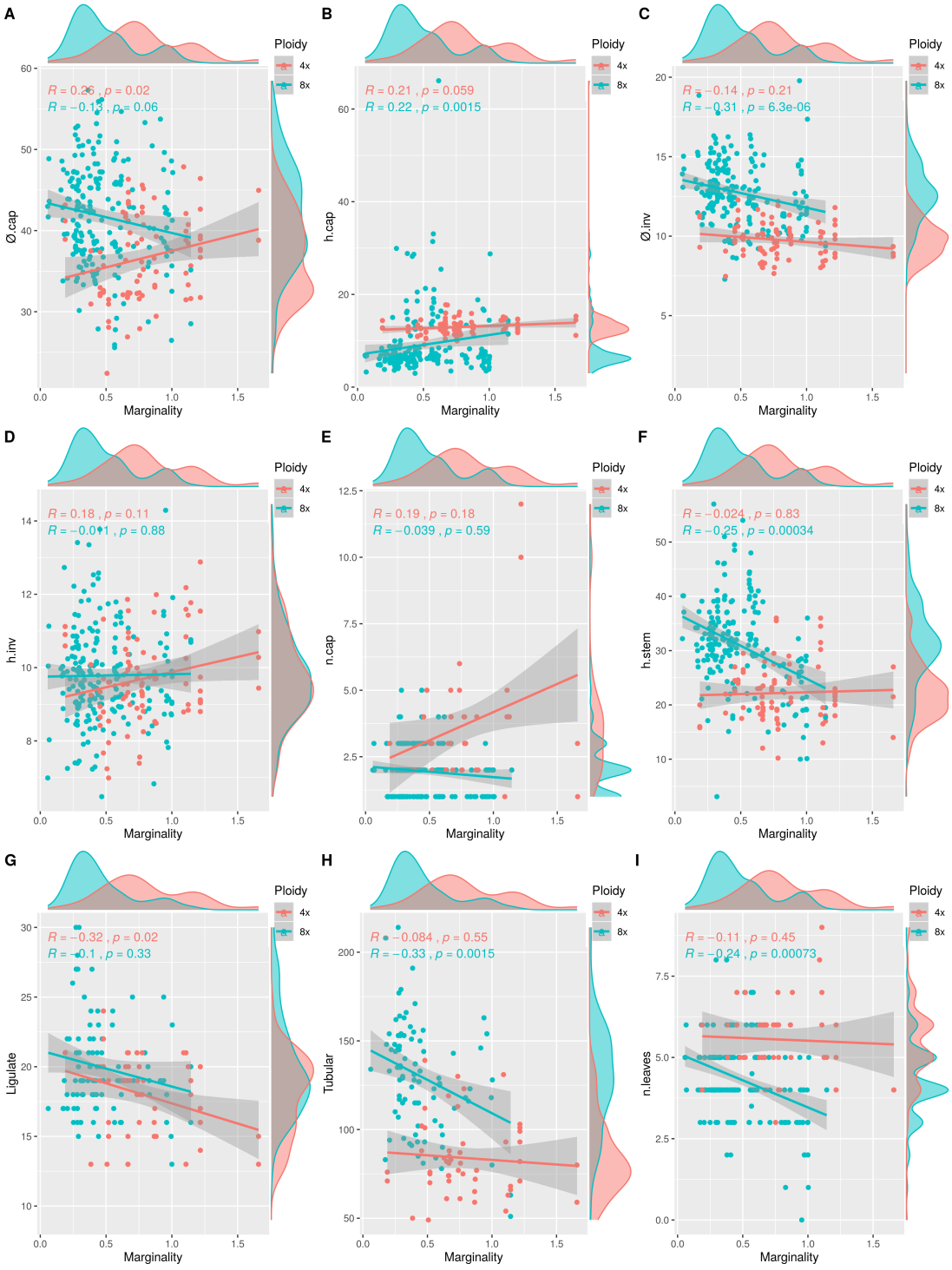

Figure 4.14: Phenotypical traits in relation to marginality index, by ploidy. In each panel, marginality index is on the x-axis, and the trait value on the y-axis. Marginal density plots illustrate the distribution of each variable on its respective axis. Regression lines with 95% confidence intervals are drawn, as well as their regression coefficients and statistical significance of the linear fit, coloured by ploidy.

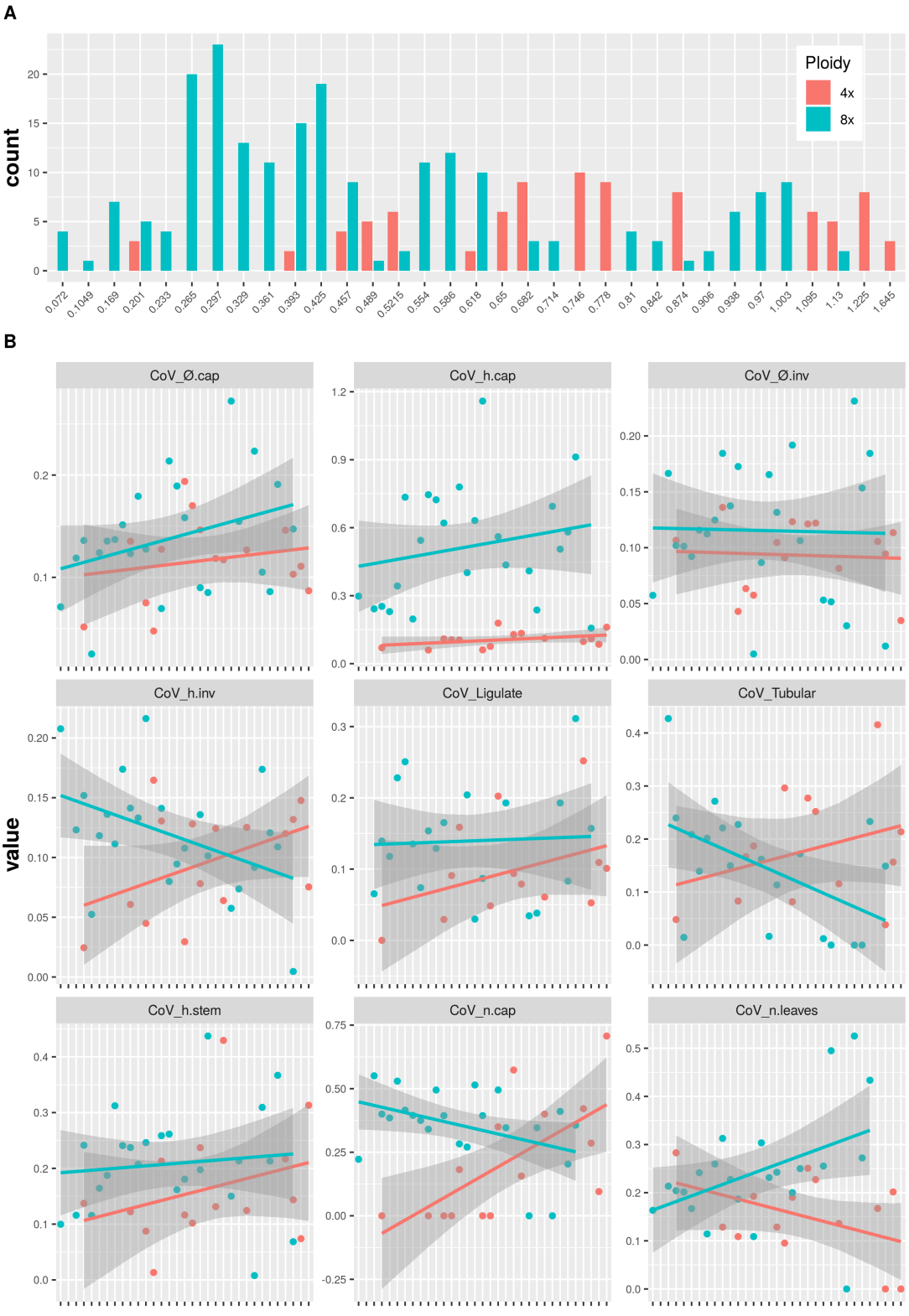

Figure 4.15: Phenotypical traits variability in relation to marginality index, by ploidy. Panel A illustrates the plant cluster density (y-axis) per marginality values bin (x-axis); note that number of bins was set to 50 to give the best resolution whilst maintaining an appropriate density per bin. Panel B presents the variability of each phenotypical trait, expressed as coefficient of variation (y-axis) per bin (x-axis), along with linear regressions and 95% confidence intervals; note that bins are equivalent to those of panel A

4.5 Discussion

4.5.1 Phenotypical differences between cytotypes of *Senecio doronicum* and reproductive success

The two cytotypes of *Senecio doronicum* are morphologically very similar, to the point that identification in the field can be difficult. Indeed, in the Maritime Alps several species of *Senecio* occur, and in particular a putative hybridization event is reported between *S. doronicum* and *S. provincialis* by molecular data ([429]).

Incorporating sequences from the mixed cytotype *S. doronicum* population on Tête Grosse to the ones previously published [429] and reported in Figure 7.3, reveals that the octoploid cytotype belongs to the *S. doronicum* clade and is not of hybrid origin (i.e. they are likely autopolyploids), albeit originating outside of the clade of the sampled tetraploids, i.e. the polyploidization event may not have occurred *in situ* at Tête Grosse (see also Section 7.2.1).

When *S. doronicum* phenology and other morphological traits were analysed differences emerged, with 8x plants exhibiting larger capitula and taller stems, and 4x plants having more capitula per plant and more pollen per floret. The number of ligulate florets is similar between 4x and 8x capitula, but the number of tubular florets is on average larger for the latter. Polyploids have often been found to have larger traits than their diploid, or in this case tetraploid, progenitors ([98–100], but Pegoraro *et al.* [101] detected the opposites in sympatric *Anacamptis* cytotypes), however the relationships between traits (phenotype integration [430] and references therein) can vary in different cytotypes, often with polyploids having less constraints in trait co-variance patterns ([102, 431, 432]). This could be the case for ligulate and tubular florets in *Senecio doronicum* cytotypes, with the two regression lines having different slopes (Figure 4.5) indicating a different degree of allometry within these two traits for each cytotype.

The two cytotypes also had diverging phenology, with plants at each ploidy level flowering for approximately one month, with only eight days of overlap (Figure 4.9). One of the ways for sympatric cytotypes to achieve reproductive isolation (or reinforcement of assortative mating, if they're already reproductively isolated) is diverging flowering times ([137, 424, 433, 434]). This effectively lowers the chance of exchanging heterospecfic pollen, and phenology is a trait upon which selection can act and drive diversification ([102, 126, 192, 435]). On the Tête Grosse population, due to the imbalance in population sizes among the two ploidy levels (see Section 4.5.2), the proportion of plants that were potentially exposed to heteroploid pollen (i.e. that were blooming during the overlap period) was higher for tetraploids. This could potentially expose the tetraploid population to strong heteroploid pollen competition, since the majority of the plants are exposed to it, and this can potentially exert an asymmetric selective pressure on the two cytotypes (e.g. tetraploids could be subject to stronger selective pressures than the octoploids because they are numerically in disadvantage). This might suggest different resource allocation strategies between the two cytotypes, that could be the results of direct competition between the two cytotypes or the effect of environmental factors (biotic or abiotic), or a combination of the two. Tetraploids had consistently higher numbers of viable seeds than octoploids despite of the fact that the latter had more tubular florets, therefore higher potential reproductive output. This can, at least in part, be attributed to the high predation rate for octoploid plants (73%), while tetraploid plants were less affected (37%). Capitula parasitized early on displayed malformations and could have been hindered in their capacity to attract pollinators. It could be that 2018 was a particularly bad year and parasitization rate is lower in general for octoploids, or that these rely on vegetative reproduction (e.g. rosettes side shoots). In any

case, the high parasitization rate does not seem to impact the octoploids' ability to maintain a viable population, since they were abundant at the study site.
Capitula fertilized via manual crossings had much lower numbers of viable seeds compared to open pollination capitula, and this could be because: i) the amount of pollen deposited was not sufficient to fertilize all the stigmas; ii) a high proportion of the stigmas were not receptive when pollinated; iii) the manipulation damaged the floral structures and prevented seed formation. Crossings between 4x plants showed slightly better seeds yields, likely due to the fact that capitula were more receptive, since 4x plants were at the beginning of their flowering period, rather than at the end, as was the case for 8x plants, when the pollination was conducted.

4.5.2 Micro-niche distribution

Mapping the spatial structure of the population on Tête Grosse evidenced that octoploid plants were numerically much more abundant than tetraploids (2,738 plant clusters VS 127). We quantified the spatial segregation of cytotypes, and a degree of differentiation was clearly evident (Figure 4.3), with 8x plants occupying the majority of the Southern aspect of the plateau and 4x plants limited to the westernmost portion. Satellite imagery confirmed the field observation that the transition zone between the 8x and 4x parts of the population is an ecotone where grass cover gives way to exposed rock with slopes becoming steeper. The differences in the habitat occupied by each ploidy level were also reflected in the wider plant community that were different in terms of species composition and abundance (see results further on in Chapter 6, Section 6.4.2).
To examine potential effects of spatial plant location for the two cytotypes we calculated the marginality index. Theory predicts that populations at the margin of a species range tend to have lower densities, are subject to higher stress and have higher phenotypical variability but lower genetic diversity, and this can apply to the population level too, between patches ([241, 418]). Both the mean value and the variability of phenotypical traits changed with proximity to the edge of the respective cytotype populations ("marginality"). Examining phenotypical traits (Figure 4.14), it is possible to see that 8x plants showed a tendency to have smaller capitula (diameter of capitulum and involucrum, number of tubular florets, height of the stem) at the interface between the two cytotype populations, as well as smaller plants (both in terms of height and number of caulinar leaves). This pattern was not reflected by 4x plants, which had a tendency for traits to either remain constant regardless of marginality or to even become larger (capitulum diameter) with marginality. Looking at the variability of traits (Figure 4.15), some traits had increasing variability as marginality increased for both ploidies, but others exhibited diverging trends between cytotypes: the number of tubular florets and number of capitula tended to be more variable at the edge of the population for 4x plants than 8x plants, and for the latter they actually tended to be less variable, while the opposite is true for the number of leaves.
It could be that the main influencing factors at the edge of the population are tied to habitat transition for the 8x plants (i.e. less favourable conditions resulting in fewer, smaller plants with relatively smaller traits), while the 4x suffer from competition with the other cytotype, having to increase their investment in floral display. The separation between 8x and 4x populations broadly corresponds with an ecological transition zone between alpine meadow and broken cover habitats (field observation). It is not clear whether the observed cytotype distribution is the result of different ecological preferences (both abiotic, i.e. drier conditions, and biotic, i.e. different plant community) or competition: the 8x plants could be outcompeting the 4x

plants, preventing them colonizing a potentially suitable part of their ecological niche. Indeed, polyploids have often been found to be more competitive than their progenitors ([115, 436]) and driving spatial occurrence patterns ([113, 114, 131]), although sympatric cytotypes coexistence is also possible ([102, 104, 120, 126, 437]).
Furthermore, it appears that traits directly involved in reproductive output (number of tubular florets and number of capitula) varied more with plant location within the tetraploid population, while number of leaves became more variable for 8x as marginality increased. The decoupling of reproductive (e.g. floral) and vegetative (e.g. leaves) traits is not surprising, and a relative independence of these flowering and vegetative characters is often found in natural plant populations (Berg's hypothesis, [438–440]).

In conclusion, *Senecio doronicum* 8x and 4x cytotypes differ in most phenotypical traits, in their spatial distribution and phenology and are effectively reproductively isolated from one another. This study contributes to the body of knowledge on the evolution following the establishment of sympatric polyploid populations, crucial in the understanding of plant speciation.

Chapter 5

Automated video monitoring of insect pollinators in the field[1]

5.1 Summary

Ecosystems are at increasing risk from the global pollination crisis. Gaining better knowledge about pollinators and their interactions with plants is an urgent need. However, conventional methods of manually recording pollinator activity in the field can be time- and cost-consuming in terms of labour.

Field-deployable video recording systems have become more common in ecological studies as they enable the capture of plant-insect interactions in fine detail. Standard video recording can be effective, although there are issues with hardware reliability under field-conditions (e.g. weatherproofing), and reviewing raw video manually is a time-consuming task.

Automated video monitoring systems based on motion detection partly overcome these issues by only recording when activity occurs hence reducing the time needed to review footage during post-processing. Another advantage of these systems is that the hardware has relatively low power requirements. A few systems have been tested in the field which permit the collection of large datasets. Compared to other systems, automated monitoring allows vast increases in sampling at broad spatiotemporal scales. Some tools such as post-recording computer vision software and data-import scripts exist, further reducing users' time spent processing and analysing the data.

Integrated computer vision and automated species recognition using machine learning models have great potential to further the study of pollinators in the field. Together, it is predicted that future advances in technology-based field monitoring methods will contribute significantly to understanding the causes underpinning pollinator declines and, hence, developing effective solutions for dealing with this global challenge.

5.2 Introduction

Pollinators provide a critical ecosystem service to 87% of angiosperms including 75% of crop species ([441–443]), and is mostly carried out by insects. Globally, pollinator populations are under threat from several interacting stressors, including: habitat loss, pesticides, pests and

[1]Pegoraro, L., Hidalgo, O., Leitch, I.J., Pellicer, J. and Barlow, S.E. (2020) Automated Video Monitoring of Insect Pollinators in the Field. *Emerging Topics in Life Sciences*, 1–11.https://doi.org/https://doi.org/10.1042/ETLS20190074

diseases, climate change and invasive alien species ([442, 444]).
Many government agencies have acknowledged the importance of pollinator conservation and pollination services in their biodiversity strategies, as their economic (estimated at US $ 200-600 billion/year) and societal value are being increasingly recognized ([442]). Correspondingly, it has become apparent that there are critical knowledge gaps in this area. For example, policies in the European Union (EU Pollinators Initiative, 2018), France (Plan national d'actions: France Terre de pollinisateurs, Opie 2016) and United Kingdom (National Pollinator Strategy, Defra 2014) have all called for more information about wild pollinators, with an increased focus on groups other than managed honeybees and bumblebees. However, wild pollinators such as solitary bees and hoverflies are challenging to study in the field with conventional methods, with comparatively little research focussing on them compared to managed honeybees and bumblebees. To overcome these challenges, novel technological approaches are urgently needed to study a broader range of pollinator taxa.
This short review focuses on novel technology-based methods for visual monitoring of invertebrate pollinators and their interactions with plants in the field. We review conventional camera systems that allow continuous video recording and recent advances being made in automated monitoring using computer vision. Conventional camera traps that use thermal sensing to monitor endothermic animals have not been reviewed in depth, as these approaches are not suitable for detecting small ectothermic animals such as insect pollinators. We also briefly discuss recent uses of machine learning models for automating the post-processing of video in pollinator studies.

5.3 Pollinator monitoring in the field

Studies of plant-pollinator interactions typically involve the collection of data using direct manual observations [445–447], which presents several issues. These include difficulties in achieving a sufficient sampling effort because manual observations are a time-consuming process and are logistically limited by labour force and environmental conditions. Manual observations are also difficult to carry out for long periods of time or at night, *ergo*, do not enable monitoring over large spatiotemporal scales. The observer must either identify the visitors *in situ* or capture them for identification in the laboratory, while still documenting pollinator events. This poses an extra challenge as the observer must follow and record simultaneous insect visitors and their behaviours. Furthermore, the presence of an observer may affect the pollinator's behaviour.
For all of these reasons, the collection of behavioural and visitation data of pollinators can be a challenging process that may result in insufficient sampling depending on the aims of the study. In particular, understanding the complexity of network interactions requires large ecological datasets to support meaningful hypotheses on ecosystem functioning and the drivers impacting pollination services.
The use of video recording systems to monitor animal activity is not a new field [448, 449], but takes advantage of widespread video monitoring technologies [450, 451] to facilitate the collection of wildlife data. Nevertheless, it is only recently that the availability of relatively inexpensive video recording devices has prompted their application for monitoring wild pollinators.

5.4 Video monitoring

5.4.1 Continuous video monitoring systems

A variety of continuous video monitoring systems are available that use low-cost commercial off-the-shelf (COTS) recording devices (such as digital cameras or camcorders). Typically, for field studies, the equipment requires protection from the environment (e.g. weather or animals) and a power supply. This type of monitoring has been used since the 1980s as a non-invasive technique for recording pollinators in the field.

Lortie *et al.* in 2012 ([452]) used Apple's iPod Nano (2.1 Mpx cameras, 8 GB capacity) equipped with small auxiliary battery packs to observe pollinators on focal plants of *Silene acaulis*, monitoring an area of $\sim$50 cm^2 for over five weeks and collecting a total of 450 hours of footage. Micheneau *et al.* in 2008 [453] monitored species of the orchid genus *Angraecum* using hard-disk camcorders with a night option and equipped with long-lasting batteries and waterproof casings. Recordings were made from 6:15 am to 6:30 pm, dictated by maximum battery duration. Flowers were observed for a total of 38 days (392.58 h) and four nights (44.83 h). Micheneau *et al.* ([454]) also used the same setup in 2010 to monitor *Angraecum cadettii*, an endemic orchid of Mauritius and Reunion Islands. The monitoring was split into 12 h periods (either day or night), to record eventual pollinia removal or deposition on flowers. This survey produced 48 days and 14 nights (577 h total) of footage obtained from the study of 508 flowers. In the context of a behavioural study of pollinators' predator avoidance strategy, Brechbühl *et al.* ([455]) monitored visitation to the capitula of two Asteraceae species in the presence or absence of predators (i.e. with or without paper crab spider models or dried spiders attached). Continuous video monitoring was conducted with wireless digital surveillance cameras, linked via an access point to a PC running a video surveillance software (go1984 v3.0 Pro). A total of 2,838 plant visits were recorded. A further example is given by Gula *et al.* ([456]) who reported seven years of experience using a video recording system to monitor endemic New Caledonian birds' nests. Although the study was not specifically used for studying pollinators, the approach is readily applicable to monitoring invertebrate pollinators. They used commercial surveillance cameras with an infrared (IR) illuminator and electret mini microphones, both connected to a Digital Video Recorder (DVR) through a RCA cable. The system was powered by two 12 V 100 Ah batteries in parallel, located 50 m from the camera and microphone setup. Events of interest were manually scored, watching the footage at 24-36x speed. In the seven years of work, with seven similar systems, 22,000 h of monitoring were accrued; the longest continuously monitored period was 58 days. The total cost of each unit was quoted at €520. Gilpin *et al.* ([457]) used weatherproof action cams (GoPro Hero 3) to monitor pollinator visitation to the inflorescences of two species (*Lavandula angustifolia* and *Canna sp*) and compared the recorded video footage to manual observations. These cameras performed identically to direct manual observations except for the number of flowers in the field of view, which was underestimated. Action cams were found to offer high resolution recordings and hardware robustness, but were limited in their depth of field, power supply and subsequent recording duration (1-2 h). Most recently, Zych *et al.* ([458]) published a study monitoring three flowering populations of *Angelica sylvestris* across a 700 km transect in three consecutive years. This study used a standard camcorder to perform 12 rounds of observations per year, each consisting of 15 min video recording, supplemented by direct insect sampling. Over the three years of monitoring, 8,477 visits were recorded, and visitors were manually scored into morphogroups.

Continuous video monitoring is a viable solution in many experimental systems, since com-

mercial video recorders can be adapted for field use. However, the success of these systems is determined, in part, by the duration of the standard batteries or the availability of long-lasting compatible battery packs (with the exception of [456] that used high-capacity vehicle batteries). This limits their application in the field, as they require the operator to visit the equipment frequently, unless, as in the case of [455], there is the option to take advantage of the proximity of an electrical grid which bypasses the need for batteries altogether.
It is noted that in the literature cited above, there was no specific mention of data storage capacity issues, and yet most modern camcorders support only limited storage capacity up to 64 GB (equivalent to 10-21 h of footage, depending on quality settings). The hardware used depends on the specific monitoring subject, but it requires few additional accessories besides the camcorder itself, therefore the total cost is typically not very high. The use of video recordings rather than photographs/images allows the researcher to view the pollinators in much more detail and from different angles, as well as observe their behaviour. Nevertheless, this method has one major downside: the need to manually examine all the footage and score pollinator visits and all other data of interest (e.g. identity of visitor, behaviour, time of visit, time spent visiting, etc), making it a time-consuming endeavour. Viewing the footage at increased speed can be useful, but is only suitable for systems where the events of interest are relatively infrequent and clearly visible (i.e. events unlikely to be missed when viewing the speeded-up video). Certainly, such an approach is unlikely to be practical for active systems with high rates and numbers of pollinator traffic (e.g. an inflorescence receiving simultaneous visits by several insects).

5.4.2 Computer vision-based systems

In recent years, ecologists have sought new approaches for automating the monitoring of pollinators in the field. One solution to overcome the time-consuming nature of manually examining continuous video is to automate the detection process so that the camera only records periods of activity when pollinators are present. This is made possible by using motion vision algorithms which detect the presence of a moving object of interest, e.g. a potential pollinator visiting a flower entering the camera's field of view based on changing pixel arrangement between consecutive frames relative to the previous frame.

5.4.2.1 DVR-based system for monitoring pollinators in the field

Motion detection features are commonly included in surveillance systems, such as DVRs that are widely available and relatively cheap. DVRs operate on low-voltage electric current (typically 12 V) and are connected to a CCD camera via RCA connections that allow the user to position the batteries and recording device far from the camera location. In addition, instead of drawing from the grid, the system can be powered by a 12 V battery, allowing deployment in remote sites. In 2009, Steen ([459]) used a COTS mini DVR and a CCD camera, powered by a 12 V 80 Ah lead battery, to monitor a Eurasian kestrel's nest. Parameters were set up in the field using a portable LCD. The detection area ('masking') divides the frame into a number of cells so that the user can choose which ones are active, and the level of sensitivity ('activation level'), which is determined by the change in the amount of pixels in an active cell needed to trigger recording. Each event was saved as a separate clip of 5 seconds. Removal of false positives was easily done using the thumbnail view in a file explorer, removing clips with no activity. The system could record 150 min of footage at the highest quality settings on a 2 GB SD card, and power consumption was modest, requiring batteries to be changed every 10-14

days. Over a monitoring period of 164 days, 0.009% failure rate was encountered due to battery or camera problems. For reviewing the material, a total of 130 h were spent, or 2 min/h of monitoring. In 2011, the same system was applied to study bumblebee visitations to a *Rhododendron* flower stand ([460]). The video signal from the same camera was split between two mini DVRs: one with the motion detection feature activated, the other recording continuously. This set-up simultaneously monitored a total of 98.5 h containing 75 insect visits, with a total of 35 min spent reviewing files and scoring the visitor's identity and behaviour. Approximately 85% of the recorded clips were false positives ('noise', e.g. events triggered by shadows, light changes and flower movement in the wind). All bumblebee visits were detected. A modified version of the system was deployed to monitor cavity usage by the European lobster ([461]), fitting the camera in a pressure-proof casing connected to the DVR in the coastal field station by a 70 m insulated cable. More recently, Steen ([462]) used two COTS devices with motion detection to monitor pollinators. He deployed the mini DVR system to monitor the diel activity pattern of bumblebees visiting white clover (*Trifolium repens*; Figure 1A), obtaining 514 clips over 193 h of monitoring, of which 210 were spurious (i.e. mistakenly triggered, containing either non-bumblebee insects or referring to the same prolonged visit). Using a digital camera and an open-source program (Canon Hack Development Kit, CHDK) that added new features such as motion detection to the 'standard' options, he also monitored honeybees visiting the capitula of thistle (*Cirsium arvense*; Figure 5.1B). The camera was set up to take a series of images, triggered by changes in luminance, adopting typical threshold values adjusted in the field. This system captured 145 unique visits over 336 min of monitoring, with 20 to 80% of unwanted clips (caused by wind or shadows), that were all filtered out using a thumbnail image viewer (XnView v2.25). The methods presented offer a time-efficient way of sorting and filtering the footage as well as preparing the datasets for analysis (see last paragraph of this section, 5.4.2.3). Recently, a similar system was used to monitor hawkmoth pollinators at night visiting *Platanthera clorantha* orchids ([463]), using an IR camera and concomitantly collecting floral volatiles. Eleven plants were monitored for 108 days (each for 24 h) over five years. Inflorescences were almost exclusively visited between 22:15-03:30 h (26 visits), while the quantity and composition of volatile compounds changed over the course of the day, with most volatile emissions coinciding with the increase in visitation by hawkmoths at night.

DVR-based monitoring systems have been extensively used to monitor wildlife activity in recent years, both vertebrates and invertebrates, and they are well suited for use in the field. The autonomy is dependent on battery capacity and data storage capacity, but rotating the batteries every ∼10 days allows continuous monitoring, while a 2 GB SD card can last up to 46 days (see [459]), depending on the level of activity at the monitored site. The setup and maintenance of the system is straightforward and quick, and the DVR unit and battery can be placed far away (up to 100 m) from the camera to minimize disturbance when access is necessary e.g. to change the battery. The motion detection feature was found to work well even for relatively small-bodied insects, but has so far only been tested with a relatively large pixel change threshold (i.e. sensitivity - the amount of change in one of the detection areas required to trigger the recording), and hence would miss small visitors (e.g. thrips, ants or small bees) when monitoring a large area, such as a whole inflorescence or multiple plants. Conversely, setting a low pixel change threshold would increase the amount of unwanted clips. The motion detection feature currently already yields a significant amount of unwanted clips, due to the relative insensitivity of the algorithm; however, these can be efficiently filtered out manually by viewing files' thumbnails and discarding spurious (i.e. 'empty') clips.

Automated data import into R ([306]) is also possible ([462]), although potential pitfalls arise

Figure 5.1: Example of image outputs from automated pollinator monitoring systems. (A) Bumblebee visiting a white clover inflorescence recorded with mini DVR-based system ([462]), (B) Honeybee visiting a thistle capitulum recorded with a digital camera with CHDK feature ([462]): note how in A and B large portions of the frame are taken up by the visitors to enable detection. (C) Bumblebee visiting an aconite's raceme recorded using Rana ([464]): the boundary box highlights the detected visitor, occupying only a small portion of the frame; (D) Hoverflies *Syrphus* (top) and *Eristalis* (bottom) visiting *Senecio doronicum*'s capitula: recorded using Rana (Pegoraro *et al.* unpublished), showing the detection of multiple visitors.

for clips obtained from busy periods of activity when several visitors may be overlapping on the same clip, or when visitors visit for longer than the specified clip length, thus triggering the creation of more than one clip per visit. This has to be checked manually and can potentially increase the time needed to process footage, depending on the study system. Finally, a potential downside can arise depending on the video motion detection software embedded in the DVR. This can be relatively inflexible in terms of the number of parameters that the user can adjust, and hence potentially underperform compared to a custom-built program. In his study, Steen ([462]) provided a data entry and analysis pipeline for mini DVR-based systems, or any monitoring system that outputs separate clips or stills of motion-triggered events, greatly facilitating data processing. A free software (XnView v2.25) was used to view, in thumbnail mode, the images and clips, allowing the user to discard frames in which no pollinators were present. Pollinator visits were archived manually in separate folders, according to a pollinator's taxonomic identification, e.g. order, genus, species, and whether it was male or female. Data entry was achieved with an R ([306]) script, using function *base::file.info()* to extract date, time and ID of each visit from the clips, hence avoiding manual data entry. Code to perform data aggregation by plant, hour-block and per day as well as statistical analysis was provided, including linear mixed-effect models (lme4) for analysing the diel activity of different pollinators. Streamlining the basic analysis of pollinator monitoring data in this way is useful, especially

for large datasets collated using automated monitoring. However, this method is limited to conspicuous visitors since small insects visiting flowers may not be discernible in thumbnail mode or identifiable from the image alone. Further, data extraction relating to the behaviour of the visitor (e.g. nectar or pollen foraging, investigative visit) is not automated.

5.4.2.2 Rana - a purpose-built automated pollinator monitoring system

To date, the only purpose-built solution for automated pollinator monitoring *in situ* is the (closed source) Rana system (Tumbling Dice Ltd, Newcastle upon Tyne, UK; [464]). Rana uses active motion vision to detect moving objects that fulfil programmable parameters based on target object size and shape (blob detection) and movement (automated tracking). The proprietary software, a C application, is bundled with a portable Linux operating system, and installed on a data logger compatible with COTS electronc platforms Rasperry Pi and O-Droid, connected to a COTS digital USB autofocus webcamera. For field-deployment, a 12 V 110 Ah lead acid battery provides power for approximately 7-10 days, or the system can be continuously solar-powered with a 12 V 50 W polycrystalline solar panel and 12 V 16 Ah lithium ion battery (S.E. Barlow, unpublished). The Rana web interface is accessed via USB connection (tethering) or a wireless link (WLAN) to a smartphone or laptop, where the user can view the video stream in real-time, tune the system and downland data remotely. The detection area and 'blob' size are adjustable, along with several other parameters (e.g. focus, brightness, contrast). The software will only trigger recording when a cluster of pixels (the blob) above a user-set threshold enters the field of vision, thus partially supressing the recording of spurious clips arising from extraneous movement such as shadows or the focal plant moving in the wind. The recorded footage is stored as time-compressed movies (i.e. recorded footage of motion events are joined into a single movie) which can be edited and images extracted using video-editing software (e.g. Virtualdub, Avidemux). Barlow *et al.* ([464]) used Rana in 2017 to monitor pollinating and nectar robbing bumblebees visiting flowers of two aconite species - *Aconitum napellus* and *A. lycoctotum* in a common garden environment (Figure 5.1C). This method generated a comprehensive dataset of 1340 visits and foraging patterns by the pollinator and robber during a total observation period of 293 h. In recent years, Rana has been applied to conservation studies of plant-pollinator interactions in remote locations in Utah ([465–467]). In 2016, Pavlik and Barlow ([467]) deployed several Rana units in the Rio Mesa reserve (Utah, USA) to monitor wild and cultivated populations of native wildflower species to assess each species' viability in supporting communities of pollinators. The units used were based on Rasperry Pi 1 model A and B, equipped with a 720p autofocus webcam (Logitech C525 HD), a 32 GB SDHC card and powered by a 12 V 100 Ah lead battery. In this study ([467]), 272 h of field monitoring data were collected, during which a total of 1613 visits to the ten target plant species were recorded. The time-compressed movies were then manually evaluated for visitor identity, behaviour and frequency (requiring a total of 96.5 person-hours for this study, although the time for analysis is likely to vary considerably between different studies depending on how busy the monitoring area is and how many different insect species visit). In 2017 ([465]), Rana was used to monitor populations of the Mojave desert endemic *Astragalus holmgreniorum*, collecting 1341 h of monitoring and recording 840 foraging visits by bees, moths and hummingbirds. The pollinator data, together with seed set data, informed recommendations for designing protected areas. In 2018 ([466]), within a study aimed at habitat restoration, twelve Rana units were deployed for 3 months at a broad landscape scale across northern Utah to monitor forb-pollinator interactions in sagebrush habitat. This method enabled the collation of a large ecological dataset based on

3,000 h of field monitoring and 1,818 foraging visits by insect pollinators. The plant-pollinator networks were informative for planning effective habitat restoration and pollinator conservation.

The Rana system has been tested in challenging conditions and in often remote sites with only rare hardware failures, hence validating its value for field use. Recently, Rana has been successfully deployed in a high elevation environment to simultaneously monitor multiple indivuals of *Senecio doronicum* (Asteraceae; L. Pegoraro *et al.*, unpublished), see Figure 5.1D and Supplementary Material of the article[2]. Tunable settings allow a great deal of flexibility and are remotely accessible in the field via WLAN or USB tethering; note that network connectivity is not required for communicating with the unit. The blob size threshold is a tuneable parameter which enables very small insects like *Perdita* bees, thrips and pollen beetles to be detected or excluded as desired ([465]). Some drawbacks of the system can include: COTS hardware failure and the need for effective weatherproofing in the field, choice of power supply, user-experience in tuning the system, and cost of the software. A potential limitation of collecting large image datasets is the workflow bottleneck involved in manually processing the time-compressed movies. To address this issue, work is underway to develop a machine learning model to semi-automate the processing of image data captured by Rana (see Box on automated insect identification for a brief overview). Recent improvements to the motion vision algorithms have also improved the sensitivity of the system, helping to reduce the detection of false positives (S.E. Barlow, unpublished). The latest iteration of Rana has several other improvements, which are beneficial for field-deployment including: solar power supply, optimised hardware, and better video compression (MP4/H264) (S.E. Barlow, unpublished).

5.4.2.3 Post-processing of continuous video recordings for pollinator monitoring

Weinstein ([468]) developed an open source motion detection program called MotionMeerkat[3] based on foreground changing pixel arrangement as a post-processor of continuous video. MotionMeerkat attempts to identify candidate motion frames containing a moving object in which the candidate organisms are detected via movement. It outputs timestamped files, with the blob outlined, which are reviewed manually and labelled as correct or incorrect detections to train and improve model accuracy. Blob size is adjustable, and the program includes an adaptive sensitivity control to change sensitivity at different times during the video. Tests revealed accuracy close to 100%, at times outperforming a human observer. An extension to the program is also available ([469]), called DeepMeerkat[4] that is based on Google's Inception neural network architecture and takes advantage of the pre-training done on ImageNet (an extensive set of images used to benchmark computer vision algorithms). It operates without the need for the user to set arbitrary initial values, while performance can still be improved with new labelled data. A pretrained DeepMeerkat GUI (Graphics User Interface) is freely available for download as well as reproducible code to train new models. The program can require significant computational resources (testing was done on 15-30 CPUs nodes), but identified >95% of frames correctly, while ignoring 76% of false positives.

Pairing continuous video monitoring or a motion triggered system (e.g. mini-DVR based or Rana) with MotionMeerkat or DeepMeerkat may yield good results and a reduction in human review time. Additionally, by moving the motion detection stage out of the recording system in the field, its power usage may be greatly reduced. Currently, this software is intended to run

[2] https://tinyurl.com/RanaExampleVideo
[3] http://benweinstein.weebly.com/motionmeerkat.html
[4] http://benweinstein.weebly.com/deepmeerkat.html

on workstations and not on low-power portable systems, thus limiting their application to the post-recording stage.

5.4.3 Visual monitoring of pollinator abundance

In a study where the focus was on pollinator abundance, activity and nest site rather than on identifying the pollinators and discerning different kinds of behaviour, e.g. foraging or investigative, Hart and Huang ([470]) used a time-lapse camera to record the number of pollinators visiting the canopies of manuka (*Leptospermum scoparium*) and kanuka (*Kunzea ericoides*) shrubs. The frame comprised the upper canopy of the plant with a fixed polysterene ball as a reference for size. Insects visiting the plant were recorded against the sky's background. Images were processed and stacked using ImageJ (Rasband, US National Institutes of Health, Bethesda, Maryland) and a Random Forest algorithm was trained on the first image of each stack. Accuracy in the number of insects counted was 98.91%, and was shown to closely follow the number of active nests observed at the same site. Hart *et al.* ([471, 472]) also developed a similar system to count the number of ground nests of New Zealand solitary bees: pre-processing of images with FIJI (ImageJ-based) followed by training of a Random Forest algorithm to count the number of nests on different soil types. Once again, the results were shown to be accurate and correlated with the number of bees in flight. Clearly these approaches do not inform about the pollinators' community composition, but have the potential to be used to assess the level of pollination services at a particular site using the number of insects in flight as a proxy.

5.5 Outlook and future

Recent developments in electronic hardware, imaging and data analysis mean that there are now several systems available, see Table 5.1, which can automatically monitor the numbers and types of invertebrate pollinators in the field, and hence overcome many of the shortcomings of traditional manual observations. The rapidly developing field of computer vision is providing new and better software to enhance data capture as well as power efficiency by obviating the need for continuous video recording. In addition, the development of automated pipelines which can integrate automated pollinator detection and identification have the exciting potential to open the door to a new epoch of study in plant-pollinator interactions. Such novel approaches will be able to address the emerging need to gather large datasets to document and act on the challenges faced by the current global decline in pollinators and the ecosystem services that they provide.

Monitoring System	Study system / Ecological application	Equipment and software	Cost	System overview
Standard video recording [452–458]	i) multiple plant and insect pollinator species including large herbaceous, alpines and epiphytes; and ii) New Caledonia endemic birds' nests. Nighttime monitoring with appropriate hardware.	Standard camcorder or action cam (see text for [456]), weatherproof enclosure; proprietary camera software.	50-520 €	Widely-available, low cost COTS hardware. Simple set-up. Limited battery power (but see [456]); manual review of continuous video is highly time-consuming.
DVR camera [459–463]	i) bumblebees visiting rhododendron and white clover; ii) nocturnal moth pollinators; iii) European raptor's nests; and iv) lobster dwellings.	CCD camera, mini DVR, 12 V battery, weatherproof enclosure; free thunmbnail viewer, R statistical software.	~650 €	Motion detection system using standard CCTV equipment. Battery power 10-14 days; quick sorting of records with thumbnail view. Limited tunable parameters; high volume of spurious events.
Motion-triggered time lapse camera [462]	Honeybees visiting thistle capitula.	CHDK-compatible camera, 12 V battery; free, open-source CHDK software and free thumbanail viewer, R statistical software.	50-400 €	COTS camera system using additional software to add motion detection function. High resolution images. Limited filter settings; time-lapse cycle may miss events.
Rana automated monitoring system [464–467]	Diverse range of visitors including tiny to very large insects and hummingbirds, studied in a variety of ecological contexts, including high desert, sagebrush and common garden environments.	WiFi-enabled Raspberry-Pi or Odroid datalogger, autofocus USB webcam, battery or solar-power, weatherproof enclosure. Proprietary Rana software, free open-source video editing software	~900 €	Motion vision software for automated monitoring of pollinators in the field. Wide range of tunable parameters; highly sensitive, capable of detecting (or filtering out) tiny insects; power supply options include battery or solar-power; up to 128 GB microSD data storage. Closed source (cost in the region of ~900 €); user learning curve to operate the system.
MotionMeerkat, DeepMeerkat [468, 469]	Post-processing of time-lapse video of foraging hummingbirds in Ecuadorian tropical forest	Standard video or time-lapse recording equipment; open-source MotionMeerkat and DeepMeerkat software available on GitHub	Open source (requires recording equipment)	Post-processing software based on motion vision and machine learning. Free software; range of filtering options; retraining machine learning models improves performance. Not available for direct deployment in the field; requires separate video recording equipment; model training is computationally expensive.
Time-lapse camera for counting bees [470–472]	Counting of native bee species at nests and tree canopies in New Zealand	Time-lapse camera, scale reference; open-source software FIJI for image analysis and WEKA for machine learning	Open source (requires recording equipment)	Post-processing image analysis software that estimates numbers of insects. Good performance of machine learning algorithms (time to build and accuracy). Not suited for species identification or behavioural studies.

Table 5.1: Summary of camera monitoring systems used to study pollinators and an overview of the main features. Asterisks indicate the cost of components from second-hand market.

5.6 Automatic insect identification

Recent developments in computer vision and machine learning models for automated species identification are an exciting prospect for ecological research involving field-based data acquisition ([473–476]). A significant challenge in developing these types of systems lies in training models with high volumes of classified images extracted from video (e.g. pollinator present/absent, [476]). Several machine learning models are available, and they differ in both scope and degree of accuracy. The ABIS system ([477–479]) uses wing venation to identify bee specimens in the field down to subspecies level, with 97% accuracy. DAISY ([480–483]) is an automated image recognition system that can be trained on a diverse range of taxa including insects, with accuracies in the range of 63-100%. Another system oriented towards higher taxonomic rank identification of insects is described by Wang ([484]). Machine learning has also been adopted by citizen science projects (e.g. iNaturalist; Snapshot Serengeti, Zooniverse) to streamline processing and improve the quality of records, as well as to create field guide apps (e.g. Pl@ntNet, Merlin Bird ID; Instant Wild). Coupling automatic recognition of insects (to species or higher taxonomic ranks) with an automated pollinator monitoring system is going to be one of the most important challenges for pollination ecology in the coming years ([485]). This would unlock unprecedented insights into the fundamental functioning of pollination networks, as well as providing large ecologiocal datasets on pollinators and their distributions, ultimately supplying the knowledge necessary to effectively conserve and manage pollinators and their habitats.

5.7 Summary Points

- Pollinator observations have traditionally been done manually but have been limited by the time investment required, its implicit biases and lack of scalability. This, in turn has limited the collection of large, high-quality datasets on pollinator-plant interactions.
- Continuous video monitoring has been applied with success to monitor pollinator visits, but manual post-processing of data is a time-consuming bottleneck.
- Computer vision methods which make use of motion detection systems overcome many of the issues of continuous recording, and several systems (mini DVR-based, Rana, MotionMeerkat) are now available for use.
- Mini DVR-based systems are most suited for detecting visitors whose size is comparable to the focal inflorescence, and enable the efficient sorting of spurious detections. In contrast, CHDK camera detection is more appropriate when the focus of study is on the identity rather than behaviour of visitors. The Rana system offers a flexible detection capability but software is closed source. MotionMeerkat software efficiently detects visits but cannot be deployed directly in the field.
- Integrated pipelines that make use of computer vision to automate the collection of data and identification of pollinators have the potential to bolster pollination ecology research and address crucial global challenges by informing policymakers.

Competing Interests

The authors declare that there are no competing interests associated with the manuscript.

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Abbreviations

CCD Charge Coupled Device, a device using a sensor that converts light into an electrical signal

CHDK Canon Hack Development Kit, a suite of applications to extend the functionalities of some Canon camera models

COTS Commercial Off-The-Shelf device

DVR Digital Video Recorder, a device used to record footage from a video source

GUI Graphics User Interface, a visual environment presented to the user, typically intended to be used with a mouse

IR Infrared, near infrared light with wavelength 700-1,000 nm

px pixel, a measure of an image resolution

RCA Radio Corporation America, standard connection used in TV systems and many video recording devices Waikato Environment for Knowledge Analysis, a platform for applied machine learning that includes several algorithms and tools.

[5]https://www.winton.com/philanthropy

Chapter 6

Rana automated pollinator monitoring on *Senecio doronicum* cytotypes

6.1 Summary

Building upon the detailed cytological and phenotypical screening of the mixed-ploidy population of *Senecio doronicum* on Tête Grosse (Chapter 4), we conducted an insect and vegetation survey on the study site, and monitored pollinators of *S. doronicum* deploying a state-of-the-art automated system (Rana).

The two cytotypes grew in different surroundings, with 8x plants occupying an habitat characterized by a more dense plant community, with higher floral resources available, while 4x plants occupied a more sparse habitat with less floral resources, but with higher species diversity. We found that insects captured at the site belonged to a mixture of different orders, but visitors to *Senecio doronicum* belonged mostly to the Diptera order, and in particular hoverflies (Syprhidae) were well represented. Tetraploid plants attracted a higher proportion of feeding visits than octoploids, and the latter received more investigative visits. Community analysis revealed that two genera of hoverflies were responsible for the majority of feeding visits: *Syrphus* for 8x plants and *Eristalis* for 4x plants.

The higher "effective" visitation rate of tetraploids could partially account for their higher reproductive success. The vegetation context in which each cytotype bloomed was different, and this could influence visitation rate. The two cytotypes had only small phenotypical differences but had largely non-overlapping pollinators communities, suggesting that even generalist plants benefit to a degree from pollinator preference. The two cytoypes are reproductively isolated (e.g. diverging phenology), and their differences in pollinators community are likely a result of increased ploidy level rather than predominantly driven by direct competition. This work exacerbates the potential of novel pollinator monitoring techniques in providing detailed insights into early stages of polyploid evolution and pollination, as well as their potential application in conservation and crop science.

6.2 Introduction

6.2.1 Pollination ecology

Pollinator-mediated assortative mating can be a major component of reproductive isolation between species ([107, 486–488]) and subspecies (e.g. cytotypes, [98, 99, 489], however Jersáková *et al.* [137] found no evidence of it in sympatric populations of *Gymnadenia*). Reproductive isolation can be achieved via differences in the pollinators that are attracted ([490, 491]), but can also potentially stem from behavioural differences within similar pollinator communities ([492, 493]). In recent years the cognitive abilities and capacity of pollinators to make choices about the plants they visit have received much attention ([494, 495] and [496] with references therein). Pollinators depend on floral resources to sustain their activity and feed their larvae, and are therefore under strong selection to make the most optimal feeding choice ([495, 497, 498]). This includes selecting floral resources based on their reward type (e.g. nectar, pollen, oil) and quality (e.g. nectar concentration, pollen amino acid content [54, 499, 500], see [501–503] for examples of floral rewards different than nutrients). Pollinators can also quickly change their choice to a different floral resource as it becomes available, and this creates a complex adaptive landscape ([504, 505]). Thus, small differences in floral rewards may alter the frequency of visits by certain pollinator species or functional groups.

In addition, plant community composition and floral density may have a feedback effect on pollinators choice, with both conspecific and heterospecific individual plants competing for pollination ([506–508]). The interaction can be negative (i.e. lower per-flower pollination success: competition) or positive (i.e. higher per-flower pollination success: facilitation), and it is density-dependent ([509, 510]). Specifically for pollination, in mixed patches a species can benefit from the vicinity to a more attractive flower resource (magnet species, [511–515]), and pollinators tend to be more attracted to dense patches, but at high plant densities the interaction can become competitive (Allee effect, [516–518]). Theory predicts that under certain conditions, e.g. when pollination is a function of combined densities and multiple species can occupy the same patch, two plant species can facilitate each other's pollination in a stable equilibrium ([445, 508, 510, 517, 519, 520]). In experimental patches, it has been proposed that density and diversity could increase pollinators attraction to a patch, but local foraging decision is more governed by plant identity than density factors ([521, 522]). Studies on an high alpine cushion plant (*Eritrichium nanus*, [523, 524]) confirmed these results, and found that a diverse plant neighbourhood attracts more overall visits, but focal plant fitness is dependent on intra-specific density.

High elevation habitats present unique challenges to pollinators and animal pollinated plants: strong winds, low temperatures, short favourable season and long distances between populations are all factors that could contribute to low and unpredictable pollinators visitation ([204, 525, 526], but a meta-analysis, [527], found no evidence of pollen limitation in alpine plants). However, alpine plants are able to achieve levels of reproductive success comparable to lowland plants thanks to a suite of adaptations ([528–530]). A possible plant response to varying pollination rates is flower longevity, and alpine plants tend to produce constitutionally long lived flowers ([531]), and it has been suggested that this trait is plastic in response to pollen limitation ([532]). For example, in a study on *Saussurea nigrescens* it was found that genotypes from high elevation (pollinator-poor) allocate more resources to nectar than to flower abundance than low-elevation genotypes, the latter having higher potential seed production (in hand-pollinated experiments, [533]).

The occurrence of pollinator-mediated selection in plant species with generalist pollination strategies has been the object of debate and its importance as an evolutionary driver is questioned by many authors ([534, 535], however some authors have already highlighted this issue [536–538]). In fact, compared to plants with specialised floral syndromes (i.e. the suite of traits that a particular group of pollinators prefers, [490, 539]), studies on plants with generalist pollination strategies have provided fewer conclusive results as to what are the drivers of floral trait diversification ([540, 541]). Nevertheless, it has been proposed that generalist plants can diverge phenotypically in response to slightly different local pollinator communities, thus increasing the pollination efficiency of the local pollinators without excluding other pollinators (i.e. adaptive wandering, [542]).

The aim of this chapter is to build upon the phenotypical study on the *Senecio doronicum* mixed-cytotype population on Tête Grosse and incorporate state-of-the-art pollinator monitoring technology to examine in detail the dynamics of inter-cytotype competition and coexistence in a sympatric mixed-ploidy population, helping to shed light into the implications for plant-pollinator interactions that follow from polyploidisation events.

6.3 Materials and methods

6.3.1 Insect collections

To complement monitoring records on *Senecio doronicum*, we collected insects flying on Tête Grosse and immediately adjacent areas with entomological nets (40 cm diameter). Collections were opportunistic, carried out predominantly in the morning and around midday, and deliberately focused on insects actively visiting or resting on flowers (including to species other than *Senecio doronicum*). Captured insects were placed in hermetic screwcap polyethylene bottles, filled to a third with cork chippings and a few drops of ethyl acetate.
In 2018 net collections were supported by 3 pan traps on Tête Grosse, deployed throughout the flowering season of *Senecio doronicum*. The trap locations were chosen to be: i) one within the predominantly tetraploid part of the population, ii) one in the predominantly octoploid part, and iii) one in the contact zone between the two. The pan traps were of sturdy constructions to withstand the strong winds and storms on the summit: they were built from yellow plastic plates (diameter ∼18 cm, depth ∼3 cm) fitted with strong adhesive Velcro strips on the bottom; the plates were affixed to a wooden pole (∼4 cm thick, ∼50 cm long) stuck in the ground with a small plywood platform screwed on top, which was fitted with adhesive Velcro strips. Early in the season we noticed birds picking insects from the traps, so we fitted them with chicken wire (25 mm mesh) folded on top to prevent birds from reaching in, but without hindering insects. Traps were filled up to ∼2 cm deep with water and a few drops of odourless transparent detergent (Tween 20, BDH Laboratory Supplies, Poole, UK), left exposed to insects for 2-4 days; after this time their contents were filtered to capture the insects, and refilled again. Insects captured with the pan traps were air dried for a few hours before preparation.
Insects were prepared within 48 h of capture using entomological black enamelled pins (size 0 or 2, depending on specimen size), holding the specimen legs and wings on polystyrene sheets. For Lepidoptera, individual small mounting boards were used made with thin sections of polystyrene sheets enveloped by ovenproof paper, and affixed to the main polystyrene sheet by pins; the body of the specimen was put between two makeshift mounting boards and their

wings spread on top of them, securing them with ovenproof paper strips, without piercing them. For specimens less than 5 mm in size, micropins (Minucie, stainless steel, No 15) were used, and specimens mounted on a plastazote foam strip, itself pinned on the main board (i.e. double mounting). Prepared insects were air dried at room temperature away from sunlight for up to a week, and then transferred to entomological boxes.
Identification and labelling of insects were performed on pinned specimens and validated at a later date by a specialist (Dr Daniele Sommaggio, personal communication). Each specimen received a unique number and was labelled with date of capture, location (with approximate GPS coordinates of locality) and collectors' names, as well as with an identification label with order, family and genus/species (sex was determined where possible).

6.3.2 Vegetation surveys

In order to examine the possible impact of nearby plant species co-flowering with *Senecio doronicum* we conducted in 2018 a plant community survey within the main population on Tête Grosse. We set up four transects, approximately 1 m wide and 25 m long, in the predominantly tetraploid part of the population, and four identical transects within the predominantly octoploid part of the population. This resulted in a 100 m^2 area surveys for each ploidy level. We marked the beginning and end of each transect with iron rods dug into the ground, and took GPS coordinates of each. From 15^{th} June to 4^{th} August, we surveyed all flowering species every 5-8 days, recording for all plant species in each transect number of individual plants in flower and number of floral units. We defined a floral unit as a group of flowers that a pollinator can visit without taking flight (e.g. one capitulum is one floral unit; a dense Fabaceae inflorescence is one floral unit). Plant identification was done mostly in the field, generally to genus level.

6.3.3 Rana pollinators monitoring system

In 2018, we used a novel automated pollinators monitoring system to record insect visits to *Senecio doronicum*. For details on Rana functioning as well as a comparison with other pollinators monitoring system see Chapter 5. Here we give a description of the equipment and deployment details for this specific experiment.
We used 8 Rana units, each composed of the Rana proprietary software (a C application, Tumbling Dice, Newcastle upon Tyne, UK) installed on a 64 GB microSD card (Samsung microSDXC class 10, 64 GB; three duplicates per unit), each run on a data logger (ODroid C1+, HardKernel, Anyang, South Korea) equipped with a WiFi dongle and enclosed in a protective case. Each unit was powered by a 12V 110Ah lead acid battery (YBX5000, Yuasa, Kyoto, Japan), connected by means of cable clamps. Each unit was fitted with a standard autofocus 720p webcam (C525, Logitech, Lausanne, Switzerland) connected via USB. Each unit's battery and data logger were housed in a large clear plastic box (∼60 L) with a clamp-down lid; a white polyester tablecloth was held in place by the closed lid so that it shaded the contents from direct sunlight. The webcam was held in place by a flexible camera clamp attached to a bucket filled with stones. The bucket was positioned so that the camera was ∼50 cm from the focus capitulum, casting the least possible shadow on the focus plant; for particularly tall plants we secured the stem to a wooden stick dug into the ground to prevent excessive movement caused by wind. When monitoring on steep slopes, the boxes and buckets were secured using iron rods dug into the ground, against which the equipment rested. When monitoring a

capitulum, we collected a leaf sample to confirm ploidy level and recorded its unique identifier, the Rana unit SD card's identifier, the monitoring starting date and hour and monitoring end date and hour, as well as battery voltage and SD card memory occupied. When simultaneously monitoring multiple capitula, we identified each capitulum regarding their position in the frame (e.g. bottom, right, left, etc) and its unique identifier. Each unit was accessible via WLAN (i.e. a short-range WiFi network) and could be accessed via smartphone or laptop browser. This allowed us to check the remaining memory capacity as well as testing the detection feature using the live video feed.
We visited the Rana units every 1-3 days, in order to avoid the microSD becoming full and stopping recording. When the occupied memory approached 80% we swapped microSD cards. To do so, we accessed that unit's WLAN network and shut it down via software, to prevent potential data loss or corruption. We then disconnected power, and swapped the microSD with its duplicate, reconnected power and eventually wiped the card prior to resume monitoring. At this time, we also checked the batteries voltage with a multimeter (Ultrics, Luton, UK), and replaced them when they fell below 12V. The data from the collected cards were downloaded to an external hard drive, and subsequently converted to MPEG-1 (25 FPS) using the free software *Avi to Mpeg* v3.5. Different capitula of the same plant were stored in separate directories. Depending on the meteorological conditions and the background (e.g. grass or bare rock), it was necessary to change Rana parameters in the field to achieve optimal detection. The main parameters that we adjusted were brightness, that was adjusted to 85 when monitoring plants against light-coloured rock background, and focus, toggled between autofocus on or off; when autofocus was disabled we also set an absolute focus of 65. Blob size was never altered.

6.3.4 Pollinators footage scoring

We manually examined the pollinators monitoring footage to record insect visits. We used the free software VirtualDub v1.1 (Avery Lee) to be able to play back the MPEG files frame-by-frame. For each file we recorded in two spreadsheets (one per plant cytotype) the plant ID, the filename, and the date and time of monitoring start and end (these latter from the video itself). While playing back the video, if extreme weather conditions (e.g. storm, heavy rain, very strong wind) occurred during the monitoring, how long these conditions lasted was subtracted from the effective monitoring time, because pollinators could not visit the plants in such conditions. When a pollinator entered the frame, the scoring process involved recording: the beginning time (to the nearest second) of the visit, the visitor's identity, its behaviour and the time when it left the capitulum.
Behaviour was scored as one of the following categories: "nectar feeding", when it was clearly visible that the visitor probed florets with its mouthparts; "pollen foraging", when the visitor adopted a particular behaviour to collect pollen (this was possible to assess only for bees and allies); "landed did not feed", when the visitor rested on the capitulum but did not adopt any feeding behaviours (note that sometimes visitors would spend several minutes resting this way); "flew by", when the visitor inspected the capitulum but decided not to make contact with it; "walked on", when a non-flying insect such as an ant or thrip climbed to the capitulum (note that no feeding behaviours were recorded for these visitors).
Visitors were identified to the lowest possible taxonomic rank that the footage permitted, although the most frequent identification was at genus level. We identified very small insects such as thrips or small ants by their vernacular names (e.g. thrips, winged ant). For each

visitor, a screenshot of a representative frame was taken (VirtualDub shortcut: Ctrl+1) and pasted in a PowerPoint presentation's slide. Each slide was given a unique identifier, and it could include several screenshot of different visits made by the same taxon. This, together with the timestamp in each screenshot, allowed to trace each visit.
Visitors identifications were checked with the help of the same entomologist who previously validated insect specimen identification (Dr. Daniele Sommaggio).

6.3.5 Statistical analyses

All data manipulation and statistical analyses were performed in R v3.6.2 ([306]) using RStudio v1.2.5033 ([396]). Additional packages data manipulation packages included: *plyr* v1.8.6 ([397]), *dplyr* v0.8.4 ([398]), *reshape2* v1.4.3 ([399]) and *data.table* v1.12.2 ([400]). Dates and times were converted to POSIX objects using *lubridate* v1.7.4 [543], and strings were handled with *stringr* v1.4 [544].
Community composition analysis were carried out using package *vegan* v2.5 ([545]), and taxonomic information was retrieved using *taxize* v0.9.7 ([401]). We visualized the results with *ggplot2* [402], with additional packages *ggExtra* ([403]), and *ggpubr* ([404]), *waffle* ([546]).

6.4 Results

6.4.1 Insect collections

We captured and mounted 287 insect specimens belonging to seven orders, 50 families and 90 genera (Supplementary Table D.1). The most represented orders were Diptera (flies), Hymenoptera (bees, wasps, ants and allies) and Lepidoptera (butterflies), with 102, 98 and 78 specimens respectively (Figure 1). It should be noted that the mixture of capture methods (net and pan traps) does not necessarily reflect the relative abundance of insects in the field.

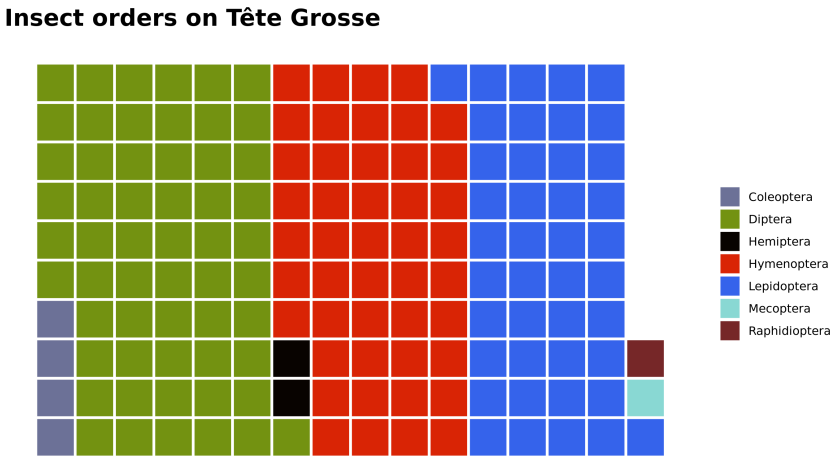

Figure 6.1: Waffle chart (square pie chart) showing the number of insect taxa belonging to each order collected on Tête Grosse. Each square represents one unique taxon (identified either at the family, genus or species level), not the number of specimens collected.

6.4.2 Vegetation survey

We recorded 53 plant taxa, mostly identified at genus level, of which 10 were unique to the early (8x) site and 19 unique to the late (4x) site (Supplementary Table D.2). The number of co-flowering taxa ranged from 9 to 23 species.

The main contributors to the total number of flowering units (i.e. a group of flowers that a pollinator can visit in one bout) and individuals were *Hippocrepis comosa, Thymus sp.* and two *Helianthemum* species, with *Euphrasia sp.* and *Myosotis sp.* having many individuals but few flower units.

The number of total flower units ranged from 1,090 to 7,514 (mean 3,754) for the site of the early flowering 8x population, and from 461 and 3,221 (mean 1,855) for the site of the late flowering 4x population, but these numbers were not significantly different (Wilcoxon test: W=22, p-value=0.164). Similarly, the number of co-flowering individuals ranged from 376 to 697 (mean 562) for the early site, and from 234 and 464 (mean 345) in the late site, but these were significantly different (Wilcoxon test: W=25, p-value=0.042).

We used the maximum number of flowering individuals per site as a measure of taxa abundance. With this data we calculated species richness: 34 species were in flower in association with the early, 8x population and 43 species for the late 4x population, giving Shannon-Weaver diversity indices of 2.14 and 2.56 respectively. Finally, we calculated community dissimilarity index as Jacccard's index: 0.68 (note that Jaccard's index close to 0 indicates no difference between sites, and 1 completely different communities).

6.4.3 Pollinator visits and behaviour

A total of 1,234.2 hours of Rana monitoring were recorded, which recorded a total of 5,457 insect visits (Table 6.1). A total of 3,091 insect visits were recorded for 4x plants, of which 1,065 were feeding visits (nectar feeding or pollen foraging, 34.44% of the total). A total of 2,366 insect visits were recorded for 8x plants, of which 206 were feeding visits (8.73% of the total). Even after removing 1,509 visits classified as "Walked over" which were performed by ants and thrips, the main contributors to non-feeding visits, the proportion of feeding visits for 8x plants was only 24.04%.

For feeding visits only, the mean visit duration was 168.17 seconds in 4x, and 84.84 seconds in 8x (Wilcoxon test W=85,304, p<0.001).

	4x (455.8 h)		**8x (320.3 h)**	
	n visits	% visits	n visits	% visits
Nectar feeding	919	29.73	182	7.69
Pollen foraging	146	4.72	24	1.01
Flew by	596	19.28	366	15.47
Landed did not feed	534	17.28	285	12.05
Walked over	896	28.99	1509	63.78
Total	3091	100	2366	100

Table 6.1: Summary of visits to *Senecio doronicum* capitula on Tête Grosse for each cytotype. Note that the number of hours of effective monitoring is indicated.

6.4.4 Visitation rate

Visitation rates are summarized in Figure 6.2. Considering only feeding visits, 4x plants had 8.15±7.37 visits/hour throughout the monitoring period, and 8x plants had 3.37±2.66 visits/hour, although these were not statistically different (Wilcoxon test: W=43, p-value=0.089). Tetraploid plants also attracted more investigative visits per hour than 8x: 15.27±11.89 and 8.69±3.97 respectively, although these too were not statistically different (Wilcoxon test: W=41, p-value=0.145). Nevertheless, 4x plants experienced on average a higher proportion of feeding visits over the total visits (59.26%) compared to 8x plants (44.91%).

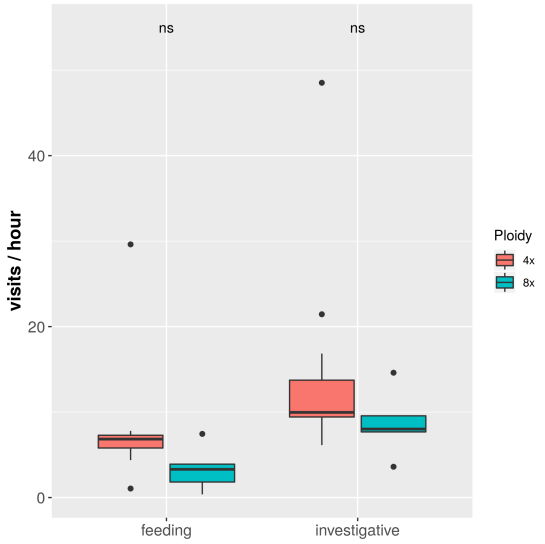

Figure 6.2: Visitation rate (visits / hour) for tetraploid and octoploid plants. For each group is presented the p-value of a Wilcoxon test, coded as follows: p≤0.0001 = ****; p≤0.001 = ***; p≤0.01 = **; p≤0.05 = *; "ns" = p>0.05.

6.4.5 Pollinators community composition

Visitors that fed on *Senecio doronicum* belonged to 7 orders, 31 families and 37 genera (Table 6.2. At the most granular identification level (that included sex and size designation for uncertain identifications, e.g. "*Eristalis tenax*, male, or "Anthomyiidae, medium") we identified 213 different visitor types.

The numbers of insect captured on Tête Grosse were similar across three orders (Diptera, Hymenoptera and Lepidoptera), but insects visiting *Senecio doronicum* (irrespective of cytotype)

Ploidy	Orders	Superfamilies	Families	Genera	Species	Types
4x	7 (1)	23 (9)	27 (14)	29 (12)	30	172 (112)
8x	6 (0)	19 (5)	17 (4)	25 (8)	15	101 (41)
All	7	28	31	37	36	213

Table 6.2: Summary of visitors by taxonomic rank. Some taxa were exclusive to one or the other cytotype, and the their number is indicated in brackets. The “Species” column indicates the number of unique visitors that was identified at species level, while the column “Types” indicates the most granular identification level, that includes sex and/or size specification for identification at the genus level and above (e.g. Apoidea, small).

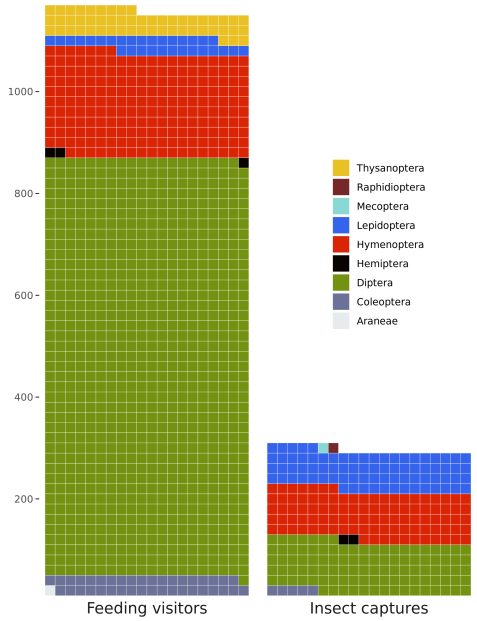

Figure 6.3: Waffle chart illustrating the number of visits to *Senecio doronicum* capitula (irrespective of ploidy) and number of insect specimens captured on Tête Grosse. Each individual square corresponds to one visit or one insect specimen respectively, and is coloured by which taxonomic order it belongs to.

belonged mostly to the Diptera and Hymenoptera orders, with Lepidoptera being underrepresented compared to insect captures (Figure 6.3).

Looking at the proportion of visits per taxonomic rank (see Supplementary D.3), at the order level (Figure 6.4), both ploidies were mostly visited by flies and bees, with 4x plants being more visited by Diptera (82%) than 8x plants (76%), and vice versa for Hymenoptera (13% for 4x plants, 19% for 8x plants). At the family level, the Syrphidae family dominated visits to both cytotypes (80% and 78% for 4x plants and 8x plants respectively), while the Apidae family was only found to visit 8x plants (8%). At the genus level (Figure 6.5), hoverflies were the most important pollinators for both cytotypes, but the most important contributor was *Eristalis* in 4x (64%) and *Syrphus* in 8x (44%); *Eristalis* also visitied 8x, but at a lower rate (25%).

When considering feeding visits only (behaviour scored as "Nectar feeding" or "Pollen foraging"), there was higher taxa richness and diversity in the visitors to the 4x plants than the 8x plants (20 and 12, respectively), but there was slightly lower species diversity (Shannon-Weaver index: 1.52 for 4x plants and 1.65 for 8x plants). Using individual monitored plants as "communities", grouped by ploidy level, the two cytotypes clustered separately in a NMDS analysis (Figure 6.6, Supplementary D.3.1; parameters: k=2, Bray-Curtis distance matrix, Stress=0.17), with clearly distinct centroids, confirmed by a PERMANOVA analysis (parameters: Bray-Curtis distance matrix, 106 permutations; p-value=0.004; Supplementary D.3.2). A multivariate dispersion analysis (PERMDISP) revealed comparable amounts of dispersion (0.39 for 4x and 0.45 for 8x), but these were largely non-overlapping in multidimensional space (Figure 6.7, Supplementary D.3.3). It is possible to see that the extent of dispersion, conceptually represented by the areas of the convex hulls encompassing the points of each group, is comparable between ploidy levels, but it is largely not overlapping, that is to say that the components contributing to variation are pulling in different directions for the two cytotypes.

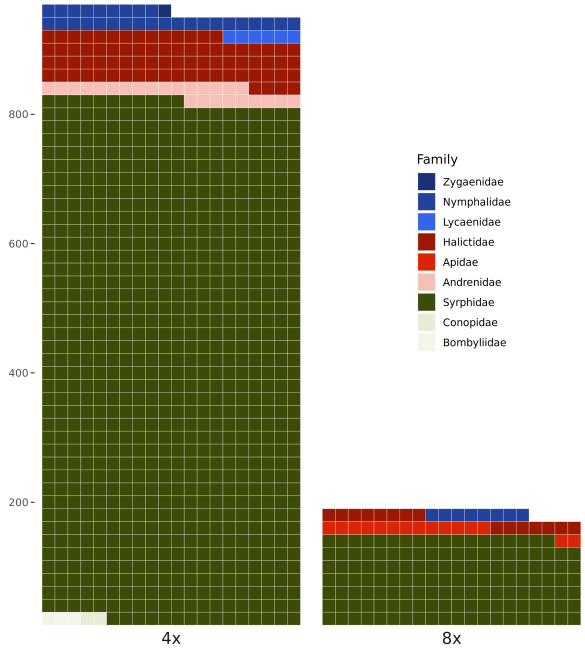

Figure 6.4: Waffle chart of feeding visits by family for ploidy level of *Senecio doronicum*. Families belonging to the same order are coloured with shades of the same colour (e.g. Lepidoptera is shaded in blues, Hymenoptera in reds, and Diptera in greens).

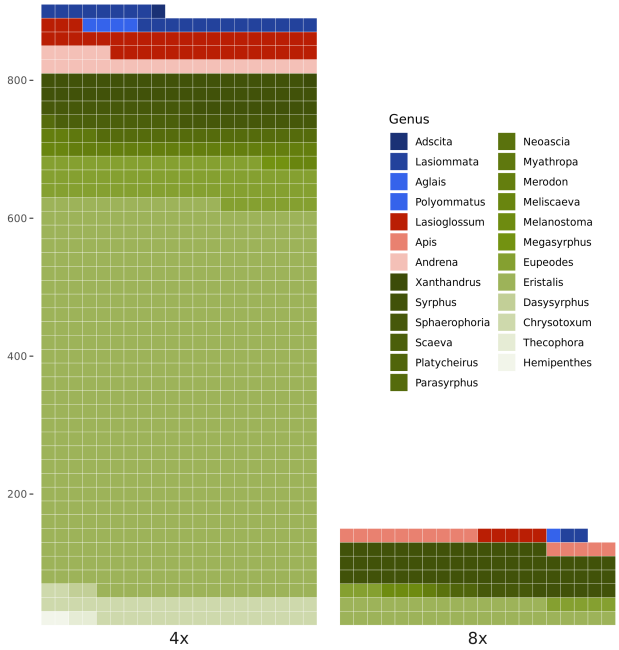

Figure 6.5: Waffle chart of feeding visits by genus for ploidy level of *Senecio doronicum*. Genera belonging to the same order are coloured with shades of the same colour. Note that *Syrphus* (dark green) and *Eristalis* (light green), both belong to the Syrphidae family and Diptera order. These insects make up substantial amounts of the total pollinators pool for the two cytotypes, but in different proportions.

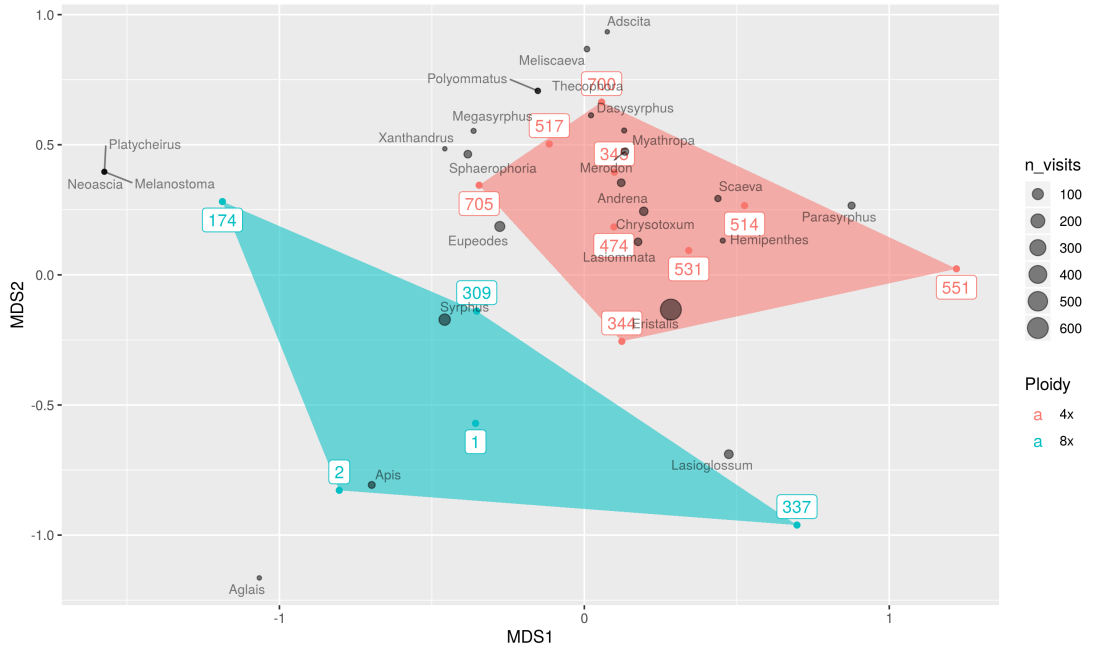

Figure 6.6: Non-Metric Dimensional Scaling (NMDS) analysis. The two axes are the two components of variation extracted. Individual plants (treated as "communities" in this analysis) are plotted as coloured dots and labels; convex hull encompassing all plants of each cytotype are also drawn. Insect genera (feeding visits only) are also plotted onto the multidimensional space in black, with their corresponding point's size proportional to their number of visits. Stress value: 0.17.

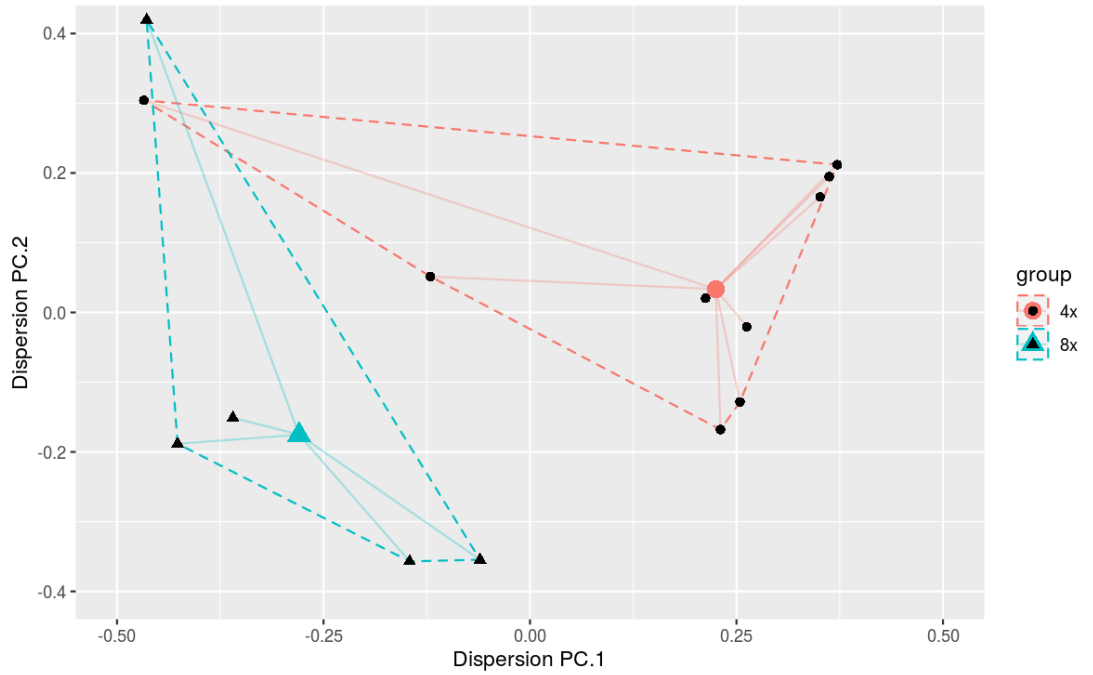

Figure 6.7: Dispersion around the median (centroid) of individual plants in multidimensional space (individual plants are treated as "communities" in this analysis). The extent of dispersion is visualized by the areas of the convex hulls encompassing the points of each group.

6.5 Discussion

Chapter 4 explored differences between the two sympatric cytotypes of *Senecio doronicum* on Tête Grosse. They manifested small but significant differences in most traits, notably: earlier flowering time in 8x, larger size of the capitula, number of tubular florets and height of the floral stem in 8x, as well as higher number of capitula in 4x. Octoploid plants (early flowering) were much more numerous and occupied a large portion of the study site, while tetraploid plants (late flowering) occupied a smaller area and were fewer.

The vegetation survey (Section 6.4.2) allowed us to quantify total floral display in the habitats occupied by each ploidy, and the octoploid part of the population had nearly twice the floral units of the tetraploid part. Pollinators respond to plant community density and composition (as well as pollinators density) by adapting their behaviour ([445, 508, 509, 524, 534, 547]). This could partially explain the lower visitation rate to 8x plants, as they were flowering in a community with more competition for pollinators than the 4x plants. The "patch attraction effect" could have been outweighed by intra and interspecific competition for 8x plants, given the relatively high density of plants in the majority of their part of the population, while 4x could have been benefited from a more sparse vegetation structure that allowed their floral displays to stand out more easily. The more intense floral display could also account for the lower feeding visits rate to 8x plants. With more options to choose from, pollinators may have been more selective and investigated several food sources before making a decision on which to use ([54, 500, 548]). The different scenarios that pollinators face when making feeding decisions could also be reflected by the average visits duration, that was approximately double in 4x plants than 8x plants, and this could be due to the fact that a pollinator would be more inclined to visit all the available florets of a capitulum when there are fewer options available, as opposed to moving on to a potentially more rewarding food source when plenty of other flowers are available.

The types of insects visiting *Senecio doronicum*, mainly flies and bees, was not surprising. Certainly, *Senecio*, like most Asteraceae, relies on a generalist pollination strategy and tends to attract insects with relatively short mouthparts (e.g. flies, short-tongued bees, [505, 536, 540, 541, 549]). We captured several butterfly species on Tête Grosse (Figure 6.1), but these were rarely observed visiting *Senecio* (Figure 6.3), as insects with long feeding organs prefer to visit plants with deeper corollas, where they have a higher chance of finding nectar, given the limited number of species that have access to it compared to an open inflorescence like those of Asteraceae.

Community composition analysis revealed significant differences in the pollinator pools between 4x and 8x plants. The communities differed in their composition and relative taxa abundance (Figure 6.6), but had comparable extent of variation (Figure 6.7). Whilst both ploidy levels were mostly visited by Diptera, and particularly by the Syrphideae family, the predominant pollinator was *Eristalis* for 4x and *Syrphus* for 8x plants. Differences in pollinator pools between sympatric cytotypes have been observed before, even though their effect on reproductive isolation is variable ([88, 98, 100, 137]). In the presence of existing pre-mating (e.g. spatial distribution and phenological differences) and post-mating (e.g. interploidy cross sterility) reproductive barriers between *Senecio doronicum* cytotypes, pollinator pool differences are unlikely to be the result of selection, but rather could be linked to pollinators preferences. *Eristalis* and *Syrphus* are two synanthropic genera (i.e. that thrive in association with human settlements and activities). Like several other hoverflies, they have a generalist niche at the adult stage

but at the larval stage they have entirely different ecological niches ([550]). *Eristalis* lays eggs near foul water, where the characteristically shaped rat-tail larvae feed on microorganisms, and overwinter as adults. *Syrphus*, by contrast, lays eggs on a variety of host plants and has larvae that are adept predators of aphids and overwinter as larvae. Environmental fluctuations could differentially influence the population dynamics of *Eristalis* and *Syrphus*, potentially having an impact on plants reproductive output. Plants with a generalist pollination strategy (like most Asteraceae) are generally regarded as being more resilient to variations in pollinator communities ([539, 551]). However, *Senecio doronicum* cytotypes were predominantly visited by one genus of hoverfly each, and the outcome of inter-cytotype competition could be impacted by their pollinator's demography in the long term.
The 8x plants were significantly more heavily predated than the 4x plants (Figure 4.11). Besides the direct damage to floral structures, the herbivory could have had an impact on floral scents or induced wound response (e.g. jasmonic acid pathways) in other, non-attacked capitula of the same plant, and that may have been detrimental to the attraction of pollinating insects ([552–554]), or perhaps influenced the numbers of individuals that are attracted. Pollination and herbivory interact with each other, and often plant signals like floral display or scent are exploited both by pollinators and predators ([555–557]), suggesting that plants are faced with a complex evolutionary landscape with multiple pressures acting at different hierarchies and scales ([558–560]), and further studies on the subject are likely to uncover fascinating dynamics. Beyond the fate of *Senecio doronicum*, its pollinators and the larger questions on the evolution of plant-pollinator interactions, a similar approach to that presented here can be valuable in a conservation framework. In the past 30 years insect numbers have plummeted dramatically ([443, 561, 562]), and this has been linked to a concomitant reduction in floral resources in a vicious cycle of secondary extinctions ([444, 563, 564]). The main drivers are habitat loss, agricultural intensification, pollution and introduced species (reviewed in [565]), and this decline in pollination services is threatening global food security ([442, 566]). Robust, easily scalable monitoring methods are necessary to address this biodiversity crisis (reviewed in [567], see also Section 7.2.4), and pollinators monitoring could be undertaken in species of conservation interest or on crops. An emerging theme is that generalist pollinators, and hoverflies in particular, are more resilient to anthropic activities disruption to ecosystems ([562, 568]). They have been found to provide a baseline pollination service to crops ([569, 570]), and therefore are likely to become increasingly important pollinators, if land use change continues on the current trajectory.

In conclusion, *Senecio doronicum* 8x and 4x cytotypes attract different pollinator communities (mostly hoverflies), and the majority of the feeding visits to each cytotype were performed by two genera: *Syrphus* for the 8x and *Eristalis* for the 4x. This study suggests that there might be more to generalist pollination strategies than plants attracting a wide variety of undiscriminating pollinators, and indeed they could benefit from specific pollinators preferences without precluding pollination from other species. Finally, the advent of new technologies in the field of pollination ecology is timely, given the global pollinator numbers decline.

Chapter 7

General Discussion

The results presented in Chapter 2 reported a higher proportion of apomictic taxa in alpine Asteraceae than previously reported for the family as a whole, and this trait was highly dependent on phylogeny. Apomixis was tightly correlated with polyploidy in general, mostly limited to the 3x and, to a lesser extent, to 4x, suggesting a link between WGD and shift in reproductive modes. We found no correlation between apomixis and preferences for higher elevations or earlier phenology.
In Chapter 3, the results indicate a prevalence of diploids in Asteraceae of the Alps, with a skewed distribution of GS towards smaller values, in agreement with general trends for angiosperms. The incidence of polyploidy varied by tribe, and is reflected in the diversity of GSs encountered. Polyploidy and genome size were highly correlated, supporting the importance of WGD as one of the main drivers of GS change in angiosperms. Short life cycle and endemic status were correlated with small GSs, however GS had no relationship with elevation or soil nutrient content.

7.1 Polyploidy, genome size and apomixis

7.1.1 General considerations

The interlinked phenomena of changes in ploidy, GS and chromosome numbers could all be driving factors with implications for ecological processes. For instance, inbreeding depression may be caused primarily by chromosomal changes that affect the inheritance of alleles (e.g. dysploidy, Robertsonian translocations). Likewise, restriction to humid and nutrient-rich habitats might be influenced by GS, as the result of associations between GS and gas exchange properties ([571]) or nutrient demands ([386]). It should be noted that polyploid status is assigned largely on the basis of comparisons with extant diploids in closely related taxa, and thus is only likely to reflect very recent radiations. Older WGD events are likely to be masked by diploidization processes ([25, 29, 31]). Consequently, ancient polyploids behave as diploids and are considered as such, meaning that estimates of polyploidy in recently diverged clades may overestimate the incidence of polyploidy compared with more ancient clades ([572]).
In recently diverged families like Asteraceae, phylogenetic signal is likely to override most ecological and/or genetic traits trends. This means that models require a large number of taxa and data from different, uncorrelated sources to tease apart correlation of variables from the effects of phylogeny. However, one advantage of recent radiations is that the majority of species are

more likely to be sampled because fewer lineages will have gone extinct than for ancient radiations. Any ecological study of natural populations is necessarily bound by the range of studied organisms, as well as spatial and temporal limitations. This is the case for the study of the mixed-cytotype *Senecio doronicum* population (Chapter 4). The analysis inevitably represents a snapshot in evolutionary time of the forces shaping the cytotype complex. Thus, ideally, a series of repeated studies over several years or decades should be conducted.

7.1.2 Longevity, polyploidy and floristic contingents

In the Asteraceae of the Alps, long-lived species were associated with higher GS than short-lived species (Figure 3.4), and this was also the case with ploidy (data not shown). This pattern reflects the trends for the arctic flora, in which high levels of polyploidy are found associated with perennial life forms ([58, 72, 573]).

At the last glacial maximum, the Arctic region was completely covered in a continuous sheet of ice, stretching from the British Isles to the Ural mountains ([165]). This is thought to have essentially eradicated all plant life in those regions, i.e. *tabula rasa* scenario ([573, 574]), with the contribution of *in situ* survival in "cryptic glacial refugia" thought to be negligible ([575, 576], but Schneeweiss & Schönswetter [183] provide evidence of *in situ* survival for two unrelated taxa in the Alps). Recolonization of the Arctic followed a clear South-North route, and this, together with the relatively low biodiversity of high-latitude regions, have provided an ideal model for the study of polyploidy speciation in relation to post-glacial recolonization ([72, 573, 574]). In contrast, the Alps have experienced a more complex recent biogeographic history than the arctic region (see Subsection 1.2.3). They are located at the very centre of Europe and have multiple botanical influences (i.e. floristic contingents). Consequently patterns of recolonization after the last glacial maximum in the Alps are less clear than for the Arctic, and are likely to have been heavily affected by the diversity surviving in glacial refugia, as well as by family or lineage-specific stochastic events ([172, 175, 197]).

Figure 7.1 illustrates the ploidy distribution in the various floristic contingents for Asteraceae in the Alps. What is interesting to note is that floristic contingents from provinces that have been less impacted by Quaternary glaciations (e.g. Eurasiatic, Mediterranean, S-European) have a higher proportion of diploid taxa, while floristic provinces of high latitudes (e.g. Arctic-Alpine, Eurosiberian) or typical of mountain ranges (e.g. East-Alpine, European-Montane, Mediterranean-Montane, South-East European-Montane, South-European Montane, West-Alpine) are richer in polyploid taxa.

What emerges from these data is an intricate mosaic of different botanical influences on the current species composition, each with their own separate evolutionary history. This pattern is common across plant families in the Alps, and is not restricted to Asteraceae ([172, 180, 197]), and is one of the reasons why the Alps host high vascular plant diversity.

We found that ploidy level correlates strongly with GS (see Chapter 3, Figure 3.2), and the diversity in GS and ploidy levels for Asteraceae in the Alps may be a result of the different prevalence of diploids and polyploids in different floristic contingents. This further remarks the idea of diversity (genetic as well as taxonomic) in the Alps being generated by migration rather than local evolution.

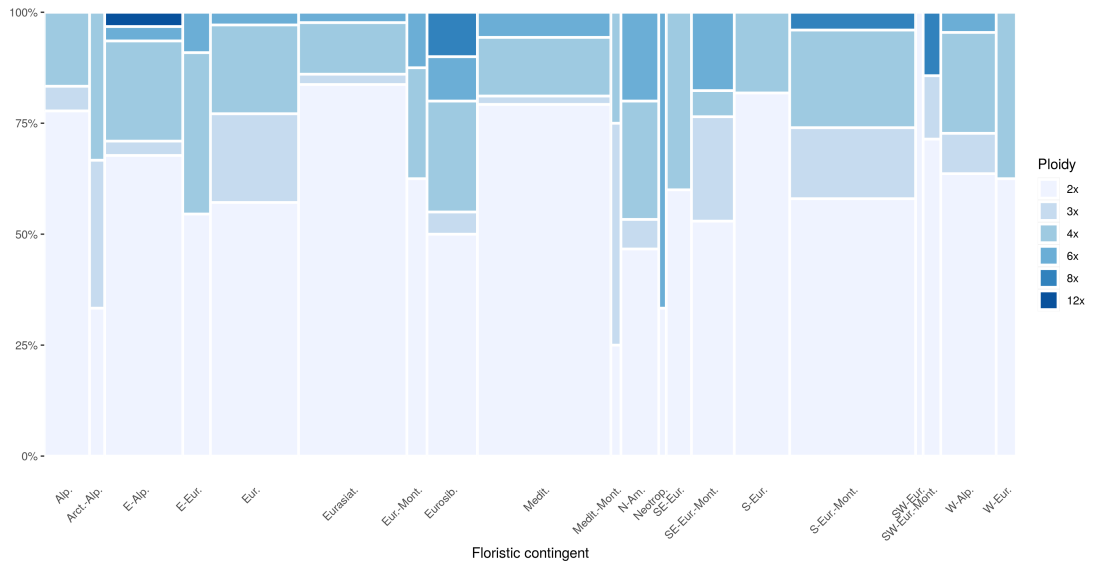

Figure 7.1: Spine plot of ploidy and floristic contingents of Asteraceae in the Alps, after data from Flora Alpina ([158]). Each column corresponds to one floristic contingent (i.e. provenance of the species, along the x axis), and column width is proportional to the number of taxa in that category. Each column's height is subdivided by ploidy level, expressed as a proportion of the total for each category (y axis). Floristic contingents represented by only one taxon have been excluded.

7.1.3 Apomixis distribution in Asteraceae and beyond

As stated above, apomixis has been traditionally linked to odd ploidy levels (e.g. 3x, 5x, 7x), that are thought to disrupt chromosome pairing during meiosis, resulting in unequal distribution of chromatids and ultimately in sterile gametes ([45, 257, 266]). While our survey of Asteraceae of the Alps is consistent with this hypothesis, with a high prevalence of apomictic triploids (Figure 2.2), apomixis was also found in diploid populations of *Picris hieracioides*, and in tetraploid populations of *Centaurea scabiosa*. *Picris* belongs to the Cichorieae tribe, which has a high incidence of apomixis, while *Centaurea* belongs to the Cardueae, where apomixis is much less common ([266]). We are not the first ones to report agamospermy in these tribes, and their inclusion in the list of apomictic taxa is contentious in the absence of further embryological evidence (reviewed in [266]). However, the recurrent finding of apomicts beyond the 3x level suggests flexibility between the sexual versus apomictic reproductive pathways in the Asteraceae family. While it appears that non-triploid populations do not exhibit stable apomixis reproduction as triploid populations do, the possibility of switching to asexual seed production could prove advantageous in certain scenarios ([66, 255, 577]). The phylogenetic distribution of apomixis in alpine Asteraceae (in the tribes Cichorieae, Senecioneae, Anthemideae and Cardueae) suggests multiple independent evolutions of apomixis, contributing to the impression of evolutionary lability of this trait in the family. Indeed, within the group formed by the closely related genera *Hieracium* and *Pilosella* (traditionally treated as two subgenera of *Hieracium*, [274]), *Pilosella* has aposporous apomixis and *Hieracium* is diplosporous, suggesting that agamospermy evolved at least twice in this group alone.

A comparison with the other major families containing a high proportion of apomictic genera (Poaceae and Rosaceae) reveals that autogamous endosperm formation and polyploidization lead to a high prevalence and diversity of apomictic lineages in these groups ([252, 261, 578], see also [579] for Poaceae and [580] for Rosaceae), much like Asteraceae. On the other hand, pseudogamous apomixis (i.e. where endosperm formation requires pollen from another individ-

ual) has the opposite effect ([260, 581]). For example, *Rubus* (Rosaceae) is a pseudogamous apomictic genus that harbours high diversity because of rampant polyploidy and hybridization coupled with occasional reversion to sexuality, and not because of apomixis. In fact, facultative apomictic lineages are more diverse than exclusively pseudogamous lineages, like in *Rubus* ([582–584]). Van Dijk ([585]) suggested that the evolution of apomixis in autonomous gametophytic lineages could be associated with tolerance of various proportions of maternal versus paternal genomes during endosperm formation, essentially constituting a 'preadaptation' (*sic.*) that facilitated a shift to apomixis, and could be a reason why agamospermy is widespread in the Asteraceae, Poaceae and Rosaceae family ([255, 258, 577]).

7.1.4 The paradox of flowers in apomictic plants

Apomictic plants produce costly flowers, pollen and nectar to attract pollinators, and are exposed to all the risks associated with pollinator visitation (e.g. transmission of pathogens and herbivory) while reaping none of the benefits associated with outcrossing ([66]). This could be easily dismissed as a case of "evolutionary history over adaptive optimality" (i.e. "phylogenetic inertia", see [586, 587]), and indeed there are examples of apomictic taxa going towards a reduction of floral display (e.g. Figure 7.2).

Many apomictic taxa can still produce (at least a portion) of viable pollen ([255, 258, 271]), and gene flow sporadically occurs between apomictic and sexual lineages ([279, 280]). This has been linked to reduced inbreeding depression by transferring apomictic genes to a new genomic context ([66, 252]). Further, there have been suggestions that Asteraceae capitula may also serve as solar radiation capturing devices, heating up beyond air temperature and thus accelerating seed development ([588]). Potentially, capitula may still play an adaptive role even in asexually reproducing lineages. In an evolutionary context, structures that exist as a by-product of selective pressures that drive the primary function of an organ can be referred to as "spandrels" ([589]), and these can take up new functions. Flowers (but not seeds and dispersal structures) in asexual lineages might be considered as spandrels, having lost their primary function (i.e. support outcrossing by cross-pollination). Such flowers can be considered vestigial in many respects, and their evolutionary trajectory could become driven by selective pressures other than sexual reproduction. Interesting parallels can be drawn with trends seen in sexually reproducing species, shedding new light into the multifaceted evolutionary landscape that has shaped flowers.

7.2 Sympatric mixed-cytotype populations and pollinator monitoring

The phenotypical scoring of the *Senecio doronicum* mixed-ploidy population on Tête Grosse (Chapter 4) revealed several differences between cytotypes. Plants of the 8x cytotype were taller, produced larger capitula with more tubular florets, while plants of the 4x cytotype had more capitula and produced more pollen per flower. The two cytotypes also manifested largely divergent phenology, with only one week of overlap. The 8x experienced higher predation rates than the 4x, and correspondingly seed set was higher for the latter. Micro-niche preferences were evident, and these paralleled plant community differences between the two micro-habitats. The 8x were numerically far more abundant, had more species in bloom as well as flower units

Figure 7.2: View of the capitulum of *Hieracium armerioides*, with visibly reduced and malformed ligulate florets (A frontal view, B side view); note that the capitulum was photographed at full anthesis and maximum expansion of the corolla; this is not a teratogenic individual, but all individuals of this taxon we observed exhibit such a floral phenotype. On the other hand, *Hieracium* sect. *alpina* occupies similar habitats and has a capitulum structure typical for the genus (C frontal view, D side view). Both species were collected during the same week in locations within a few km at similar elevations in Austria.

surrounding them (i.e. more competition for pollinators attraction), and their traits generally declined in size when plants grew at the margin of the population. By contrast, the 4x were less numerous and occupied a habitat with a sparser plant community, and their floral traits tended to remain constant or even increase with marginality. Both cytotypes were visited primarily by hoverflies (Chapter 6), however the composition of visitors differed between them: *Syrphus* was the main genus visiting the 8x, and *Eristalis* visiting the 4x. The 4x cytotype received more visits per hour as well as a higher proportion of feeding visits than the 8x.

7.2.1 Phenotypic differentiation and secondary contact: foundations for divergent selection?

Natural plant populations are subject to the forces of selection and genetic drift, and the observed divergence between 8x and 4x *Senecio doronicum* cytotypes could be the result of these

processes rather than a consequence of polyploidization ([55, 132, 590]). Figure 7.3 shows a ribotype analysis of the three cytotypes of *Senecio doronicum* from Tête Grosse and a phylogeny of the European clade of sect. *Crociseris*, to which *S. doronicum* belongs. Results clearly reveal that 8x and 4x cytotypes do not belong to the same genetic group. Furthermore, the 6x cytotype (constituted of only three individual plants) clusters together with the 4x, indicating that it is most likely derived from an unreduced 4x gamete crossing with a reduced 2x gamete. This means that the mixed ploidy population on Tête Grosse is likely of secondary contact origin, with 4x and 8x cytotypes originating from separate *Senecio doronicum* genetic lineages, and coming into contact later, potentially having evolved independently (i.e. in allopatry) for a period of time.

Interesting insights from mixed-cytotype populations have stemmed from comparisons with single-cytotype populations of the same species. In fact, several pairs of diploid-autopolyploid taxa are more strongly differentiated in sympatry than in allopatry ([90, 132, 591]), and it is thought that this is a result of competition, either for ecological space or sexual reproduction (reviewed in [115]). Indeed, it seems that evolution is faster in animal and plant populations in sympatric conditions ([592–594]), challenging the traditional view that sympatric speciation is rare and only results in weakly differentiated populations ([2–4], see also [595]).

It remains unclear whether the observed phenotypical differences between cytotypes of *Senecio doronicum* on Tête Grosse were pre-existing or if they evolved because of sympatry. It would be interesting to compare phenotype and phenology between the sympatric population of Tête Grosse and populations containing a single cytotype. However, our survey of the SW Alps (the geographic range where the two cytotypes are both reported, also see Figure 3.1) evidenced that the 4x cytotype was rare throughout, and it was never found without the widespread 8x. Clearly this should not be taken at face value, and it is possible that a wider sampling effort would reveal pockets of single-cytotype 4x populations. Nevertheless, comparing the phenotype of 8x single-ploidy populations within the SW Alps region and with 8x population from the Central or Eastern Alps could provide an indication whether 8x *Senecio doronicum* is subject to selective pressures in sympatric populations caused by the coexistence with the 4x, and if the magnitude and direction of selection differ between allopatric an sympatric populations.

It is possible to measure the effects of selection directly on phenotypical traits if a proxy for fitness can be estimated ([435, 596, 597]). If a trait has an effect on reproductive success (i.e. fitness), then its contribution to that individual's fitness can be calculated as a linear relationship between the trait's value and the individual's fitness deviation from the mean of the population ([596]). This can be expressed as a standardized measure, called "selection gradient", that is independent of the absolute values of the traits and fitness, and can be (with some caution) compared across taxa ([598]). Several studies have applied this method to natural plant populations, including sympatric autopolyploid cytotypes ([102, 599]). They have often found great variation in the strength and even direction of selection between years and locations ([542, 600], reviewed in [601]).

It could be that 8x and 4x *Senecio doronicum* have experienced asymmetrical selection forces, stemming from mainly environmental factors (e.g. micro-niche preference, predation) for the 8x cytotype and from biotic factors (e.g. direct competition, reinforcement) for the 4x cytotype. Indeed, phenotype diversification is a well-known effect of competition avoidance, and micro-niche differentiation is increasingly reported for autopolyploid cytotype pairs ([80, 101, 137]). When this is paired with pollinator preferences to forage on plants within the same patch, strong reproductive isolation can occur at small spatial scales ([98, 99, 106]).

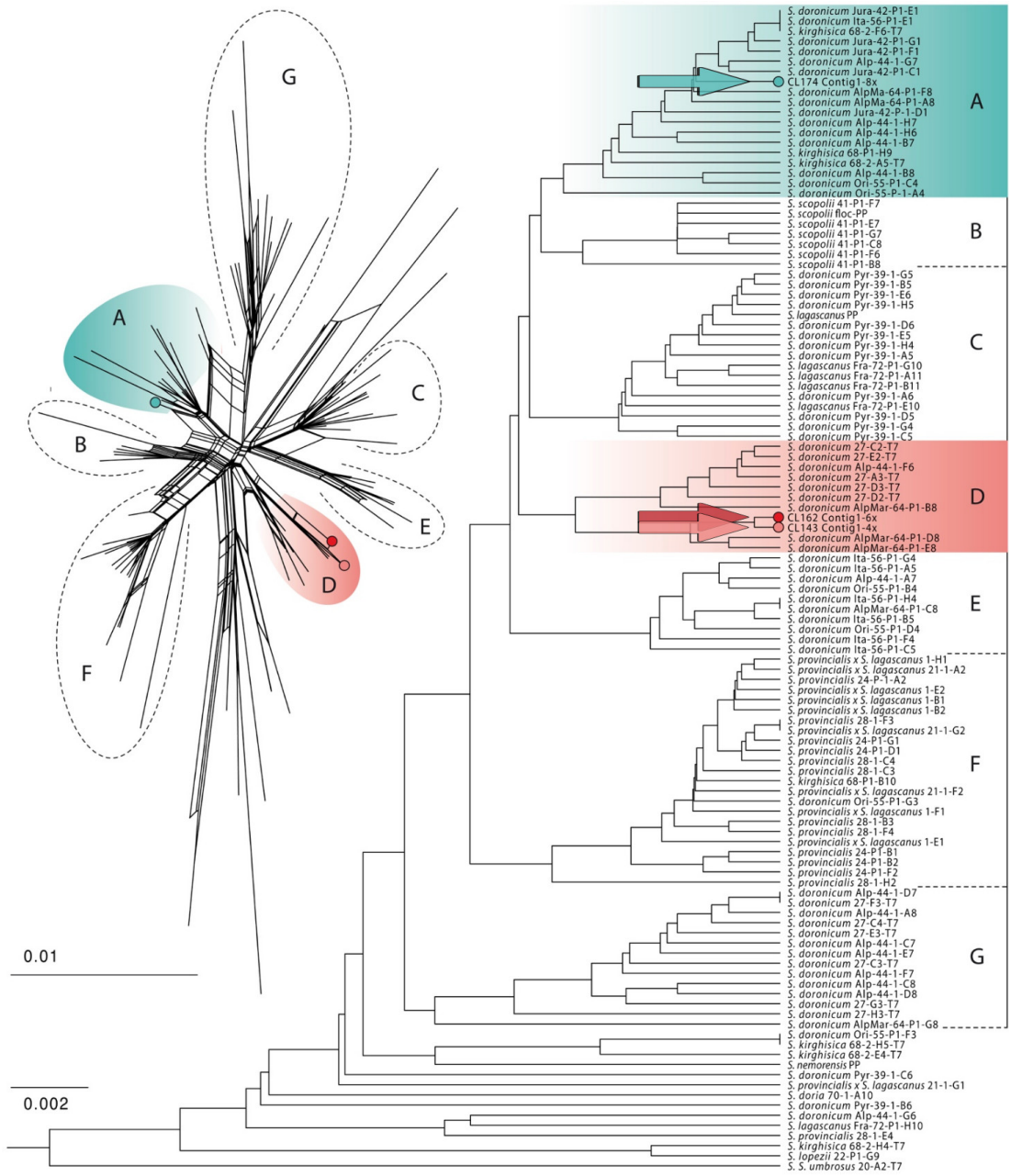

Figure 7.3: Phylogeny (right) and phylogenetic network (left) of the European clade of *Senecio* sect. *Crociseris* including 4x, 6x and 8x samples from Tête Grosse (indicated by arrow and dots at the tips of the tree, with membership clades highlighted). Sequences were retrieved from Calvo *et al.* ([429]), except those of Tête Grosse that we generated by NGS (Fernández *et al.*, in preparation).

7.2.2 Seed predation and floral constraints

Predation is one of the major driving forces in evolutionary arms races (Van Valen's Red Queen hypothesis, [602]), and both predator and prey are under selective pressures. Thus it is not surprising that plant phenotypes are constrained by selective pressures deriving from these plant-herbivore interactions, even when the organs affected have evolved principally under the influence of other forces, i.e. flowers have evolved to enhance outcrossing, yet they are also subject to selective pressures from herbivores. Seeds and other plant propagules are coveted by herbivores, as they are very nutrient-rich. Thus plants protect these energetically expensive organs with a variety of mechanical (e.g. thorns and though integuments, [603]), chemical (e.g.

alkaloids and other secondary metabolites, [604]) and temporal defences (e.g. many temperate tree species have "mast years" in which they produce more seeds than predators can consume, reducing overall predation rate through unpredictable food availability, [605]).
Fenner *et al.* ([606]) proposed that capitulum size in some widespread Asteraceae could be constrained by pre-dispersal seed predators (i.e. insects that prey on ovaries and maturing seeds, often by larvae hatching from eggs laid in or near the flowerhead), arguing that predators would prefer larger capitula as they represent a better effort/reward balance. This could explain the much higher pre-dispersal predation rate in 8x (Figure 4.11), as this cytotype had larger capitula than the 4x cytotype. Notably, the overall diameter of the capitulum and the diameter of the involucrum (Figure 4.4) were the most different traits, and are correlated with the number of florets per capitulum (Figure 4.5). However, it is also possible that seed predators were more abundant during the flowering period of the 8x cytotype. It is reasonable to expect seed predators to prefer the larger capitula of the 8x to lay their eggs in, because more resources would be available for the larvae (note that larvae must normally complete their development within the same inflorescence). Furthermore, 8x plants grew in a more dense plant community with more floral resources available to pollinators, and this could have caused them to have to invest more in floral display. But more visibility means it is easier for parasites to target the capitula as well as for pollinators, so there might be diminishing returns, so that herbivores limit and direct floral evolution ([455, 560, 607]).

7.2.3 Phenology: an all-too-often overlooked component of ecology and evolution

The analysis of pollinators communities revealed that while sharing several common visitors, the overall pollinator pools of the two cytotypes differed significantly (Figure 6.6, and Figure 6.7,). This is somewhat surprising given that Asteraceae species, and *Senecio* too, are notorious for their generalist pollination strategy, with weaker expected inter-species (and inter-cytotype) pollinators differentiation when compared to specialists ([608, 609]).
Only recently have pollination ecologists started to consider that generalist pollination is an adaptation to fluctuating pollinator populations, visitation rates and pollinator constancy, and not as a "lack of specialization" associated with lower efficiency ([505, 610, 611]). In fact, there are indications that the widely shared view that some important pollinators groups (first among them: flies, Diptera) are "super-generalists" is false, insofar that they visit indiscriminately a plethora of different plants ([536, 610]). The view is at a minimum inaccurate. For example, while it may be true that in its often short lifespan, an individual fly will visit many plant species, on short time scales its fidelity (i.e. flower constancy) is comparable with that of more well-known pollinator groups (e.g. bees). Indeed, within the same foraging bout and even the same day an individual fly may only visit one species ([538, 612]). This, coupled with the often high retention rate of pollen on flies' bodies (i.e. amount of pollen load released at every successive visit), guarantees that more pollen is dispersed overall, and also reduces the chances of geitonogamy (i.e. fertilization with pollen from a different flower of the same plant, normally achieved by pollinators visiting multiple flowers of the same plant in sequence) ([610]).
Temporal visitation patterns are crucially important in determining pollinators efficiency, and yet the phenology of pollination only receives a passing mention in many studies. Not only is it necessary for plants to synchronize flowering time with the emergence of suitable pollinators (most often mature or sexually maturing insect adults), but the timing and sequence of visits

is highly relevant too. Steen [462] proposed a method to model diel visitation patterns as a function of time of day and temperature. Small-scale temporal patterns are likely to be found in many pollinators formerly considered to be generalists. Furthermore, small temporal differences in visitation may be underlying reproductive isolation in co-flowering species with shared pollinator pools (e.g. [106, 107, 592]). Phenological patterns in pollinator visitation may be the result of optimization of foraging ([613, 614]). Recent sophisticated ethological experiments on insect cognition are investigating this topic, and indeed may well be universal in insects and not limited to bees ([615–617]). It seems that floral constancy is not fruit of cognitive limitations of pollinators, but rather a parsimonious exploration of a complex dynamic adaptive landscape ([548, 618–620]).

Concerning the mixed-ploidy population of *Senecio doronicum*, 8x flowered earlier than 4x plants. However, it is often reported that autopolyploids flower later than their diploid counterparts ([84, 126, 424], but see [102, 126] for examples of polyploids flowering earlier than diploids), revealing the unpredictable effects of polyploidy on phenotype (reviewed in [7]). As for morphological traits (Subsection 7.2.1), it would be interesting to compare phenology and pollinator pools of single-ploidy populations of *Senecio doronicum*. However, further complications would arise in this case as not only plants but also insect populations would be different in different localities, which would need to be controlled for.

Finally, considerations regarding climate change are especially poignant in the context of phenology. The general tendency is for the flowering season to start earlier every year ([621–623]), and the question is how this will impact pairs of polyploid-progenitor taxa. Will they respond in the same way to climate warming? Will their pollinators emerge earlier in the year as well, or will the synchrony between plants blooming and insects foraging be disrupted? These are questions that can and should be answered with novel automated monitoring methods and more studies on the topic of pollination ecology.

7.2.4 Technological perspectives in methods for pollination ecology

What was apparent during the pollinator visitation footage scoring of visitors of *Senecio doronicum* is that while automated monitoring systems greatly enhance the data collection step, the data processing step (i.e. manual scoring of insect behaviour and identity) is clearly a bottleneck. Algorithmic solutions are the next logical step for pollination data processing, and hold the promise to largely automate this stage, that was not possible until recently due to the complexity of the problem and the lack of large standardized datasets. Automated video monitoring (see Chapter 5) solves the problem of lack of data, and great advances in Machine Learning (ML) and Artificial Intelligence (AI) algorithms can efficiently tackle the complexity issue.

From an information theory point of view, the problem of species recognition is reducible to a pattern recognition problem, a field that has seen a great deal of interest recently with the rise of computer vision applications ([624]). In extremely simple terms, the process of pattern recognition is divided into the following stages: a pre-processing stage, in which images are standardized to reduce variance; a feature extraction stage, in which several image transformations are applied to extract as much information as possible and to enhance images' discriminatory power; a classification stage, in which the extracted features are grouped in different categories (i.e. insect species, types of behaviour) and a model applied to them to make a decision. Additionally, if artificial neural network (ANN) methods are used for the classification step, these

may need to be trained on a subset of the data for which the outcome is known before being able to make a decision (training dataset, i.e. a portion of the images for which the identity and/or behaviour of the visitor has been scored manually).
There are already a number of works applying these methods to insect recognition (reviewed in [567]), and at least two have seen some degree of application to real-world biological data. ABIS ([477]) is an automated system for the identification of honeybees and wild bees, that can be adapted for use in the field on anesthetized bees. It uses automatic forewing landmarks extraction and classifies them with a combination of LDA (linear discriminant analysis) and non-linear features analysis, achieving species or subspecies-level identification with accuracy over 99%, even in difficult species complexes ([478, 479, 625]). Another machine learning system applied to biological systems is DAISY ([480]), that uses principal component analysis (PCA) for features extraction and Kendall's τ rank correlation for classification. It can be applied to a variety of images of different kinds, from whole-specimen photographs to parts of the wing, and is able to achieve $\sim$80% accuracy for species-level identifications, with small training sets and in taxonomically difficult groups ([481–483]).
Other algorithms implemented different methodologies for feature extraction and classification, for instance: sparse signal analysis and support vector machines (SVM) in [626]; bag-of-features approach and scale-invariant feature transformation (SIFT) in [627]; sparse coding spatial pyramidal matching (ScSPM) with SIFT and local LBP (local binary pattern) descriptors in [628]; HOG (histogram of oriented gradients) and RCLP (robust complete local binary pattern) and SVM in [629]. Of particular interest are approaches involving ANNs, predominantly at the classification stage: [630] used a LBP descriptor and a multilayer perceptron architecture, obtaining good results on butterfly wings, while [631] used a pre-trained deep convolutional neural network architecture obtaining 100% accuracy and near-instantaneous results with Lepidopteran museum specimens. Other systems based on ANNs have tackled the problem with organism groups other than insects, like VeSTIS ([632]) on preserved specimens of polychaete worms, and SPIDA-web ([633]) on Trocantheriidae spiders' genitalia. Convolutional neural networks (CNN) are being increasingly adopted for a wide variety of applications, thanks to their moderate memory and computational requirements (relative to the complexity of the problem, i.e. number of parameters), and major software companies are investing in their development and implementing them in their products ([473, 474, 634]; Google offers a service to host and train your own CNN on their servers, complete with coding tutorials and templates: link[1]).
It is clear that there is a need to apply algorithmic solutions to the problem of biological species recognition. As reviewed by Martineau *et al.* ([635]), there are valid solutions for the classification stage of the process, but the problem lies mostly in the pre-processing and feature extraction stages that still pose significant software challenges, especially for video feature extraction. If these methods are to be applied to pollinators monitoring footage, they need to be able to deal with non-standard specimen poses, suboptimal focus, chromatic aberrations and many other sources of noise to isolate and extract a set of features of interest that can satisfactorily describe pollinators. If this challenge can be overcome, the study of pollination could experience a new era of scientific discovery, comparable perhaps to what next generation sequencing has made possible for the field of genetics.

[1] https://developers.google.com/machine-learning/practica/image-classification/convolutional-neural-networks

7.3 Final remarks

In this thesis I set out to examine the evolution of the Asteraceae family in the European Alps using a multidisciplinary approach, integrating evidence at the macroevolutionary and microevolutionary scales to provide insights into processes that drove and continue to shape plant traits, especially in geographic regions with a variety of environmental and migration influences. The experimental work has been structured in two main parts: the second and third chapter offer a top-down view of the current trait diversity in Asteraceae, focussing on cytological (GS and ploidy) diversity and reproductive mode and examining their correlation with elevation, phenology and other ecological covariates. Chapters four through to chapter six concern experimental and methodological aspects of a study of a sympatric population of Senecio doronicum, effectively presenting a window on recent evolutionary events and providing insights into some of the processes that have contributed to the diversity of traits and species observed today.

In Chapter 2, apomixis was strictly correlated with odd ploidy levels but not with elevation, and both ploidy level and mode of reproduction were strong influenced by the phylogeny. In Chapter 3, most alpine Asteraceae were found to have small GS and to be diploid, and chromosome number, ploidy and GS were all positively correlated with each other. Short-lived species and endemics tended to have small GSs, and these traits, together with elevation preference and phenology, manifested strong phylogenetic signal. These two chapters have provided a comprehensive dataset on alpine Asteraceae's GS, ploidy level and reproductive mode integrated in a modern phylogenetic framework, and they have provided novel insights into the relationship of genetic and ecological traits in high elevation environments.

In Chapter 4, the study of the sympatric mixed-cytotype population of *Senecio doronicum* has provided insights into the early stages of evolution of (potentially) incipient species. It reveals the importance of ecological components like phenology and micro-habitat preferences in driving cytotype divergence and shaping how plants adapt to their environment as well as biotic interactions. Chapter 5 is a review of automated pollinator monitoring techniques. It provides an overview of methods currently available, with particular attention to recent technological advances. In Chapter 6, the work with Rana provides the first extensive high elevation plant–pollinator interaction dataset, as far as I know. It records pollinators in high elevation environments and it exposes the clear need for new analytical technologies to be integrated into automated pollinator monitoring. It has highlighted how plants regarded as generalists can harbour divergent pollinator communities, and suggested that generalist pollinators could be exerting foraging preferences and play a role in such divergence. These chapters reveal the impact of WGD in a natural experiment, documenting its implications at multiple levels (e.g. habitat preferences, phenotype, pollinator attraction, reproductive success) and especially focussing on phenotype and pollination ecology.

By both examining in detail some of the processes potentially driving trait and species evolution in *Senecio doronicum* and more widely in alpine Asteraceae, this thesis has provided important clues into drivers of evolution in the European Alps, and more generally in mountain environments. This thesis highlights the role of polyploidy and genome size as phenotypic traits, with their own particular set of influences on plant life history, reproductive mode and phenotype, as well as the role of shared ancestry in explaining patterns.

In addition, this thesis has produced and collated a considerable amount of new data on GS, ploidy and reproductive mode for the Asteraceae of the Alps, that will be included in the main

global reference dataset for GS and ploidy levels (Plant DNA C-values database[2]) and apomixis (Apomixis database[3]). This data will be accessible for future studies and meta-analyses, and represents a useful reference to compare GS and ploidy composition of other plant families in the Alps and beyond. I also present the first automated pollinator monitoring data for high elevations (as well as one of the largest datasets on sympatric cytotypes). It reveals that the relationship between generalist floral morphologies and generalist pollinators is more complex that perhaps is generally acknowledged. This work thus contributes to our understanding of pollination networks resilience in the face of global climate change. Another important aspect highlighted in this work is that new tools to investigate plant-pollinator interactions are needed to harness the full potential of automated systems. Finally, this thesis highlights the extraordinary plant diversity in mountain environments, and especially in the European Alps can be regarded as the melting pot of much of European floristic diversity.

[2]https://cvalues.science.kew.org
[3]https://uni-goettingen.de/en/423360.html

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Appendices

Appendix A

Chapter 2 supplementary material

A.1 Flow histograms

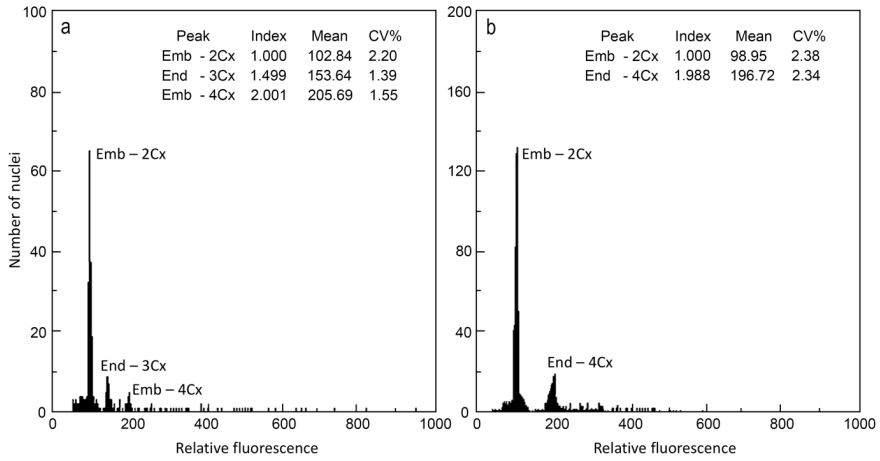

Figure A.1: Example of flow histograms for sexually produced seeds (a panel) with 3Cx endosperm peak visible and for apomictically produced seeds (b panel), with only 4Cx peak visible.

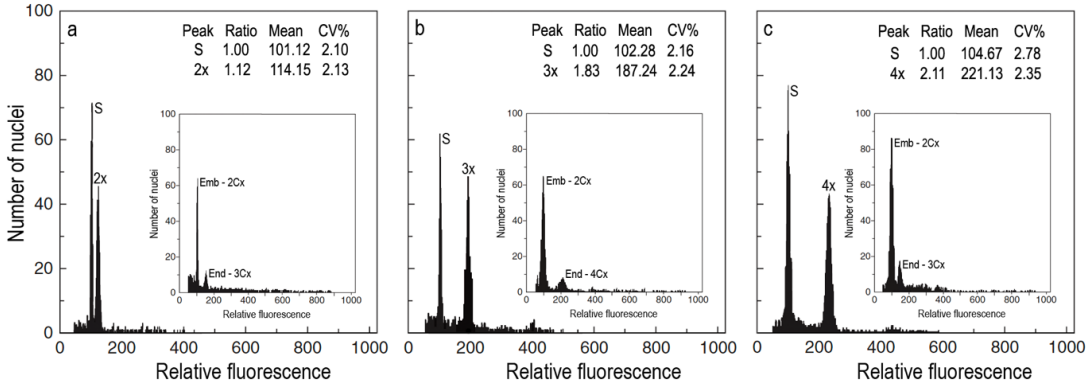

Figure A.2: Flow histograms of *Leucanthemopsis alpina* 2x, 3x and 4x cytotpyes (a, b and c panel respectively) with associated reproductive mode as insert (2x sexual, 3x apomictic, 4x sexual).

A.2 Data table for Chapter 2

Table A.1: Data table for Chapter 2 with sample origin, collection details and reproductive modes inferred.

ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.31.6.0	*Achillea clavennae*	Austria. L. Pegoraro et al. - A127	5	2x	3x	1.487	Sexual	2282	1890	18	6	47.0745	12.7498
124.31.2.0	*Achillea erba-rotta*	France. L. Pegoraro et al. - FR673	5	2x	3x	1.492	Sexual	2465	2100	18	7	44.2048	7.1561
124.31.11.0	*Achillea millefolium*	France. L. Pegoraro et al. - FR154	5	6x	9x	1.501	Sexual	1036	1250	54*	5	44.2584	6.2634
124.31.11.0	*Achillea millefolium*	France. L. Pegoraro et al. - FR182	5	6x	9x	1.512	Sexual	1380	1250	54*	5	44.2476	6.2349
124.31.11.0	*Achillea millefolium*	France. L. Pegoraro et al. - FR19	5	6x	9x	1.491	Sexual	1847	1250	54*	5	44.3400	6.2964
124.31.11.0	*Achillea millefolium*	France. L. Pegoraro et al. - FR253	5	6x	9x	1.493	Sexual	1961	1250	54*	5	44.3153	6.4422
124.31.11.0	*Achillea millefolium*	France. L. Pegoraro et al. - FR291	5	6x	9x	1.523	Sexual	2378	1250	54*	5	44.3158	6.4565
124.31.11.0	*Achillea millefolium*	France. L. Pegoraro et al. - FR305	5	6x	9x	1.504	Sexual	2505	1250	54*	5	44.4079	6.3854
124.31.11.0	*Achillea millefolium*	France. L. Pegoraro et al. - FR323	5	6x	9x	1.512	Sexual	1890	1250	54*	5	44.2608	6.2088
124.31.11.0	*Achillea millefolium*	France. L. Pegoraro et al. - FR612	5	6x	9x	1.489	Sexual	—	1250	54*	5	—	—
124.31.3.0	*Achillea nana*	France. L. Pegoraro et al. - FR539	5	2x	3x	1.506	Sexual	2623	2575	18	7	45.0641	6.4077
124.31.3.0	*Achillea nana*	France. L. Pegoraro et al. - FR630	5	2x	3x	1.492	Sexual	2428	2575	18	7	44.2541	6.7140
124.31.3.0	*Achillea nana*	France. R. Douzet s.n. 07-VII-2017	5	2x	3x	1.484	Sexual	2700	2575	18	7	45.0633	6.4137
124.31.3.0	*Achillea nana*	Switzerland. J. de Vos & A. Moerland s.n.	5	2x	3x	1.485	Sexual	—	2575	18	7	—	—
124.31.19.0	*Achillea nobilis*	Switzerland. L. Pegoraro et al. - CH163	5	2x	3x	1.507	Sexual	538	350	18	7	46.2620	7.4770
124.31.1.0	*Achillea oxyloba*	Switzerland. L. Pegoraro et al. - A93	5	2x	3x	1.503	Sexual	2219	2183	18	7	46.7637	12.8005
124.44.1.0	*Adenostyles alliariae*	France. L. Pegoraro et al. - FR203	5	4x	6x	1.502	Sexual	1772	1750	38	6	44.2847	6.4317
124.44.1.0	*Adenostyles alliariae*	France. L. Pegoraro et al. - FR52	5	4x	6x	1.510	Sexual	1802	1750	38	6	44.3417	6.2971
124.44.1.0	*Adenostyles alliariae*	France. L. Pegoraro et al. - FR613	5	4x	6x	1.515	Sexual	1583	1750	38	6	44.8621	6.5877
124.44.2.0	*Adenostyles alpina*	France. L. Pegoraro et al. - FR437	5	4x	6x	1.500	Sexual	1710	1470	38	6	44.2839	6.4345
124.44.3.0	*Adenostyles leucophylla*	France. L. Pegoraro et al. - FR290	5	4x	6x	1.612	Sexual	2378	1890	38	7	44.3158	6.4565

Table A.1: Data table for Chapter 2 with sample origin, collection details and reproductive modes inferred

ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.44.3.0	*Adenostyles leucophylla*	France. L. Pegoraro et al. - FR513	5	4x	6x	1.551	Sexual	2117	1890	38	7	44.3097	6.4554
124.44.3.0	*Adenostyles leucophylla*	France. L. Pegoraro et al. - FR629	5	4x	6x	1.553	Sexual	2428	1890	38	7	44.2541	6.7140
124.44.3.0	*Adenostyles leucophylla*	France. L. Pegoraro et al. - FR631	5	4x	6x	1.515	Sexual	2428	1890	38	7	44.2541	6.7140
124.98.1.0	*Andryala integrifolia*	Spain. O. Hidalgo 287	5	2x	3x	1.492	Sexual	—	350	18	6	—	—
124.12.2.0	*Antennaria carpatica*	France. L. Pegoraro et al. - FR293	25	8x	12x	1.464	Sexual	2378	1925	56	6	44.3158	6.4565
124.12.2.0	*Antennaria carpatica*	France. L. Pegoraro et al. - FR466	25	8x	12x	1.515	Sexual	2678	1925	56	6	44.7262	6.3237
124.12.2.0	*Antennaria carpatica*	France. R. Douzet s.n. 07-VII-2017	25	8x	12x	1.485	Sexual	2700	1925	56	6	45.0633	6.4137
124.12.1.0	*Antennaria dioica*	France. L. Pegoraro et al. - FR243	25	4x	6x	1.495	Sexual	1961	1633	28*	6	44.3153	6.4422
124.12.1.0	*Antennaria dioica*	France. L. Pegoraro et al. - FR248	25	4x	6x	1.536	Sexual	1961	1633	28*	6	44.3153	6.4422
124.12.1.0	*Antennaria dioica*	France. L. Pegoraro et al. - FR307	25	4x	6x	1.486	Sexual	2505	1633	28*	6	44.4079	6.3854
124.12.1.0	*Antennaria dioica*	France. L. Pegoraro et al. - FR45	25	4x	6x	1.529	Sexual	1966	1633	28*	6	44.3354	6.2957
124.12.1.0	*Antennaria dioica*	France. L. Pegoraro et al. - FR645	25	4x	6x	1.482	Sexual	2355	1633	28*	6	44.2477	6.7154
124.12.1.0	*Antennaria dioica*	France. L. Pegoraro et al. - FR669	25	4x	6x	1.485	Sexual	2354	1633	28*	6	44.2033	7.1513
124.80.1.0	*Aposeris foetida*	Italy. L. Pegoraro et al. - IT51	25	2x	3x	1.486	Sexual	1269	1400	16	6	45.7940	11.4628
124.56.2.0	*Arctium lappa*	Austria. L. Pegoraro et al. - CH135	5	2x	3x	1.491	Sexual	963	910	36*	7	46.2691	7.5357
124.56.2.0	*Arctium lappa*	France. L. Pegoraro et al. - FR140	5	2x	3x	1.520	Sexual	1172	910	36*	7	44.2574	6.2551
124.56.2.0	*Arctium lappa*	Slovenia. M. Balant 109	5	2x	3x	1.489	Sexual	—	910	36*	7	—	—
124.56.2.0	*Arctium lappa*	Slovenia. O. Hidalgo 488-1 & al.	5	2x	3x	1.493	Sexual	—	910	36*	7	—	—
124.56.3.0	*Arctium minus*	France. L. Pegoraro et al. - FR490	5	2x	3x	1.501	Sexual	1836	910	36	7	44.3574	6.9530
124.56.3.0	*Arctium minus*	France. L. Pegoraro et al. - FR523	5	2x	3x	1.509	Sexual	1440	910	36	7	44.3555	6.2935
124.56.1.0	*Arctium tomentosum*	Slovenia. O. Hidalgo 476 & al.	5	2x	3x	1.512	Sexual	—	1050	36	7	—	—
124.45.1.0	*Arnica montana*	France. L. Pegoraro et al. - FR205	5	4x	6x	1.478	Sexual	1772	1633	38*	6	44.2847	6.4317
124.45.1.0	*Arnica montana*	France. L. Pegoraro et al. - FR241	5	4x	6x	1.562	Sexual	1961	1633	38*	6	44.3153	6.4422
124.45.1.0	*Arnica montana*	France. L. Pegoraro et al. - FR258	5	4x	6x	1.472	Sexual	1961	1633	38*	6	44.3153	6.4422

Table A.1: Data table for Chapter 2 with sample origin, collection details and reproductive modes inferred

ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.45.1.0	*Arnica montana*	France. L. Pegoraro et al. - FR40	5	4x	6x	1.485	Sexual	1966	1633	38*	6	44.3353	6.2957
124.45.1.0	*Arnica montana*	France. L. Pegoraro et al. - FR436	5	4x	6x	1.485	Sexual	1710	1633	38*	6	44.2839	6.4345
124.45.1.0	*Arnica montana*	France. L. Pegoraro et al. - FR61	5	4x	6x	1.459	Sexual	—	1633	38*	6	—	—
124.45.1.0	*Arnica montana*	France. L. Pegoraro et al. - FR681	5	4x	6x	1.526	Sexual	2313	1633	38*	6	44.1738	7.1567
124.40.3.0	*Artemisia absinthium*	Cult. Royal Botanic Gardens Kew 1990-3675	5	2x	3x	1.510	Sexual	—	1050	18	7	—	—
124.40.3.0	*Artemisia absinthium*	Switzerland. L. Pegoraro et al. - CH138	5	2x	3x	1.503	Sexual	894	1050	18	7	46.3075	7.8777
124.40.13.0	*Artemisia genipi*	Italy. Index seminum. Cogne de Scaletta	5	2x	3x	1.489	Sexual	2280	2410	16	7	—	—
124.40.15.0	*Artemisia glacialis*	Italy. Index seminum. Valnontey	5	2x	3x	1.520	Sexual	2120	2410	16	7	—	—
124.40.11.0	*Artemisia nitida*	Cult. Botanical Garden Yves Rocher La Gacilly. Index seminum 2017-388	5	6x	9x	1.499	Sexual	—	1610	54	8	—	—
124.40.11.0	*Artemisia nitida*	Slovenia. O. Hidalgo 470 & al.	5	6x	9x	1.489	Sexual	—	1610	54	8	—	—
124.40.12.0	*Artemisia umbelliformis* subsp. *eriantha*	France. T. Garnatje & J. Vallès s.n.	5	2x	3x	1.489	Sexual	—	2100	18	6	—	—
124.40.10.0	*Artemisia umbelliformis* subsp. *umbelliformis*	France. L. Pegoraro et al. - FR698	5	4x	6x	1.526	Sexual	2560	2575	36	7	44.3321	6.7735
124.40.10.0	*Artemisia umbelliformis* subsp. *umbelliformis*	Switzerland. L. Pegoraro et al. - CH147	5	4x	6x	1.517	Sexual	2630	2575	36	7	45.9897	7.7047
124.40.1.0	*Artemisia vulgaris*	Switzerland. L. Pegoraro et al. - CH137	5	2x	3x	1.496	Sexual	894	910	16	7	46.3075	7.8777
124.4.6.0	*Aster alpinus*	France. L. Pegoraro et al. - FR200	5	2x	3x	1.512	Sexual	1772	1633	18*	6	44.2847	6.4317
124.4.6.0	*Aster alpinus*	France. L. Pegoraro et al. - FR263	5	2x	3x	1.494	Sexual	2127	1633	18*	6	44.3134	6.4484
124.4.6.0	*Aster alpinus*	France. L. Pegoraro et al. - FR321	5	2x	3x	1.491	Sexual	1888	1633	18*	6	44.2608	6.2087
124.4.6.0	*Aster alpinus*	France. L. Pegoraro et al. - FR325	5	2x	3x	1.585	Sexual	1456	1633	18*	6	44.2608	6.2088
124.4.6.0	*Aster alpinus*	France. L. Pegoraro et al. - FR391	5	2x	3x	1.524	Sexual	1968	1633	18*	6	44.3387	6.2928
124.4.6.0	*Aster alpinus*	France. L. Pegoraro et al. - FR8	5	2x	3x	1.502	Sexual	1970	1633	18*	6	44.3347	6.2955
124.4.6.0	*Aster alpinus*	France. O. Hidalgo 261	5	2x	3x	1.523	Sexual	—	1633	18*	6	—	—
124.4.7.0	*Bellidiastrum michelii*	France. L. Pegoraro et al. - FR415	5	2x	3x	1.530	Sexual	1811	1400	18	5	44.3144	6.4369

Table A.1: Data table for Chapter 2 with sample origin, collection details and reproductive modes inferred

ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.3.1.0	*Bellis perennis*	Czech Republic. J. Pellicer - CZ1	5	2x	3x	1.489	Sexual	—	910	18	1	—	—
124.55.1.0	*Berardia lanuginosa*	France. L. Pegoraro et al. - FR251	5	4x	6x	1.482	Sexual	1961	1890	36	7	44.3153	6.4422
124.55.1.0	*Berardia lanuginosa*	France. L. Pegoraro et al. - FR252	5	4x	6x	1.475	Sexual	1961	1890	36	7	44.3153	6.4422
124.23.5.0	*Bidens bipinnatus*	Italy. L. Pegoraro et al. - IT75	5	6x	9x	1.527	Sexual	145	350	72	7	45.7381	11.6150
124.23.4.0	*Bidens frondosus*	Italy. L. Pegoraro et al. - IT77	5	4x	6x	1.562	Sexual	—	350	48	8	—	—
124.19.1.0	*Buphthalmum salicifolium*	Austria. L. Pegoraro et al. - A9	5	2x	3x	1.485	Sexual	453	1050	20	6	48.0406	16.0416
124.19.1.0	*Buphthalmum salicifolium*	France. L. Pegoraro et al. - FR160	5	2x	3x	1.501	Sexual	1036	1050	20	6	44.2721	6.2988
124.19.1.0	*Buphthalmum salicifolium*	France. L. Pegoraro et al. - FR528	5	2x	3x	1.479	Sexual	1289	1050	20	6	44.3553	6.2900
124.19.1.0	*Buphthalmum salicifolium*	Italy. L. Pegoraro et al. - IT29	5	2x	3x	1.498	Sexual	890	1050	20	6	45.7981	11.7381
124.19.1.0	*Buphthalmum salicifolium*	Slovenia. M. Balant 97	5	2x	3x	1.515	Sexual	1706	1050	20	6	46.2426	13.8359
124.51.2.0	*Calendula arvensis*	Spain. O. Hidalgo 268	5	4x	6x	1.498	Sexual	—	350	44	4	—	—
124.51.2.0	*Calendula arvensis*	Spain. O. Hidalgo 269	5	4x	6x	1.501	Sexual	—	350	44	4	—	—
124.51	*Calendula tripterocarpa*	France. L. Pegoraro et al. - FR604	3	4x	6x	1.513	Sexual	1233	350	30	4	44.8593	6.5850
124.60.3.0	*Carduus acanthoides*	Austria. L. Pegoraro et al. - A1	5	2x	3x	1.489	Sexual	—	583	22	6	—	—
124.60.5.0	*Carduus crispus*	Switzerland. L. Pegoraro et al. - CH106	5	2x	3x	1.521	Sexual	667	910	16	7	46.7579	8.6461
124.60.9.0	*Carduus defloratus*	France. L. Pegoraro et al. - FR418	5	2x	3x	1.531	Sexual	1850	1400	22*	7	44.3121	6.4358
124.60.9.3	*Carduus defloratus* subsp. *carlinifolius*	France. L. Pegoraro et al. - R3	5	2x	3x	1.562	Sexual	—	1400	22*	7	—	—
124.60.9.5	*Carduus defloratus* subsp. *summanus*	Austria. L. Pegoraro et al. - A40	5	2x	3x	1.512	Sexual	695	1250	22*	7	47.8847	15.7541
124.60.4.0	*Carduus personata*	Austria. L. Pegoraro et al. - A111	5	2x	3x	1.540	Sexual	1848	1400	18	7	47.1300	12.8070
124.60.4.0	*Carduus personata*	Austria. L. Pegoraro et al. - A57	5	2x	3x	1.478	Sexual	1398	1400	18	7	46.5665	12.4825
124.52.5.0	*Carlina acanthifolia*	France. L. Pegoraro et al. - FR713	5	2x	3x	1.522	Sexual	1133	1050	20	7	44.4785	5.8887
124.52.4.1	*Carlina acaulis*	France. L. Pegoraro et al. - FR404	5	2x	3x	1.518	Sexual	1608	1400	20	6	44.3099	6.3885
124.52.4.1	*Carlina acaulis*	France. L. Pegoraro et al. - FR712	5	2x	3x	1.537	Sexual	1557	1400	20	6	44.3194	6.4284
124.52.1.0	*Carlina corymbosa*	Slovenia. M. Balant 122	5	2x	3x	1.510	Sexual	—	350	18	7	—	—
124.52.2.0	*Carlina vulgaris*	Slovenia. M. Balant 112	5	2x	3x	1.508	Sexual	—	910	20	7	—	—

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ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.75.1.0	*Catananche caerulea*	France. L. Pegoraro et al. - FR150	5	2x	3x	1.479	Sexual	1172	910	18*	7	44.2574	6.2551
124.75.1.0	*Catananche caerulea*	France. L. Pegoraro et al. - FR171	5	2x	3x	1.478	Sexual	1586	910	18*	7	44.2486	6.2295
124.75.1.0	*Catananche caerulea*	France. L. Pegoraro et al. - FR187	5	2x	3x	1.521	Sexual	1380	910	18*	7	44.2476	6.2349
124.75.1.0	*Catananche caerulea*	France. L. Pegoraro et al. - FR345	5	2x	3x	1.506	Sexual	1890	910	18*	7	44.0272	6.2248
124.70.1.0	*Centaurea benedicta*	Spain O. Hidalgo 367	5	2x	3x	1.522	Sexual	—	350	22	5	—	—
124.68.17.0	*Centaurea jacea*	Austria. L. Pegoraro et al. - A6	5	4x	6x	1.497	Sexual	154	700	44	5	48.0331	16.0297
124.68.17.0	*Centaurea jacea*	Slovenia. M. Balant 106	5	4x	6x	1.503	Sexual	—	700	44	5	—	—
124.68.17.0	*Centaurea jacea*	Slovenia. M. Balant 99	5	4x	6x	1.521	Sexual	1706	700	44	5	46.2603	13.8381
124.68.16.3	*Centaurea jacea* subsp. *gaudinii*	Italy. L. Pegoraro et al. - IT86	5	4x	6x	1.479	Sexual	648	910	44	6	45.8636	8.8164
124.68.16.3	*Centaurea jacea* subsp. *gaudinii*	Italy. L. Pegoraro et al. - IT97	5	4x	6x	1.526	Sexual	815	910	44	6	46.0065	9.2245
124.68.7.0	*Centaurea leucophaea*	France. L. Pegoraro et al. - FR603	5	2x	3x	1.561	Sexual	1233	700	18	6	44.8593	6.5850
124.68.14.0	*Centaurea margaritacea*	Switzerland. L. Pegoraro et al. - CH169	5	2x	3x	1.533	Sexual	274	583	18	7	46.1872	8.9919
124.68.25.0	*Centaurea nervosa*	Switzerland. L. Pegoraro et al. - CH118	5	2x	3x	1.499	Sexual	1754	1750	22	7	46.5371	8.8378
124.68.25.0	*Centaurea nervosa*	Switzerland. L. Pegoraro et al. - CH175	5	2x	3x	1.543	Sexual	1939	1750	22	7	46.5498	8.7009
124.68.21.0	*Centaurea nigra*	United Kingdom. O. Hidalgo 285	5	4x	6x	1.532	Sexual	—	910	44	7	—	—
124.68.26.0	*Centaurea pectinata*	Cult. Lautaret Botanical Garden. O. Hidalgo 333	5	2x	3x	1.503	Sexual	—	700	22	6	—	—
124.68.28.0	*Centaurea rhaetica*	Switzerland. L. Pegoraro et al. - CH69	5	2x	3x	1.498	Sexual	738	1190	22	6	45.9996	9.2165
124.68.4.0	*Centaurea rupestris*	Slovenia. M. Balant 120	5	2x	3x	1.543	Sexual	—	700	20	6	—	—
124.68.5.2	*Centaurea scabiosa* subsp. *alpestris*	France. L. Pegoraro et al. - FR124	5	4x	8x	1.899	Apomictic	1922	1750	20	6	44.3856	6.3909
124.68.5.2	*Centaurea scabiosa* subsp. *alpestris*	France. L. Pegoraro et al. - FR155	5	4x	6x	1.501	Sexual	1036	1750	20	6	44.2584	6.2634
124.68.5.2	*Centaurea scabiosa* subsp. *alpestris*	France. L. Pegoraro et al. - FR421a	5	4x	6x	1.523	Sexual	1850	1750	20	6	44.3121	6.4358
124.68.5.2	*Centaurea scabiosa* subsp. *alpestris*	France. L. Pegoraro et al. - FR421b	5	4x	8x	1.920	Apomictic	1850	1750	20	6	44.3121	6.4358
124.68.5.2	*Centaurea scabiosa* subsp. *alpestris*	France. L. Pegoraro et al. - FR58	5	4x	6x	1.499	Sexual	1802	1750	20	6	44.3417	6.2971
124.68.5.5	*Centaurea scabiosa* subsp. *grinensis*	Switzerland. L. Pegoraro et al. - CH46	5	2x	3x	1.520	Sexual	417	1050	20	6	45.9621	8.8851
124.68.24.0	*Centaurea uniflora*	France. L. Pegoraro et al. - FR15	5	2x	3x	1.482	Sexual	1847	1610	22*	7	44.3400	6.2964

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ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.68.24.0	*Centaurea uniflora*	France. L. Pegoraro et al. - FR211	5	2x	3x	1.486	Sexual	1772	1610	22*	7	44.2847	6.4317
124.68.24.0	*Centaurea uniflora*	France. L. Pegoraro et al. - FR22	5	2x	3x	1.492	Sexual	1893	1610	22*	7	44.3380	6.2963
124.68.9.0	*Centaurea valesiaca*	Switzerland. L. Pegoraro et al. - CH142	5	2x	3x	1.523	Sexual	663	910	18	7	46.3098	7.8040
124.94.1.0	*Chondrilla juncea*	France. O. Hidalgo 516 & J. Pellicer	5	3x	6x	1.959	Apomictic	—	700	15	6	—	—
124.94.1.0	*Chondrilla juncea*	Switzerland. L. Pegoraro et al. - CH133	5	3x	6x	1.883	Apomictic	600	700	15	6	46.2531	7.4057
124.61.13.0	*Cirsium acaulon*	France. L. Pegoraro et al. - FR198	5	2x	3x	1.496	Sexual	1772	1400	34*	7	44.2847	6.4317
124.61.13.0	*Cirsium acaulon*	France. L. Pegoraro et al. - FR249	5	2x	3x	1.487	Sexual	1961	1400	34*	7	44.3153	6.4422
124.61.13.0	*Cirsium acaulon*	France. L. Pegoraro et al. - FR320	5	2x	3x	1.512	Sexual	1980	1400	34*	7	44.2608	6.2087
124.61.13.0	*Cirsium acaulon*	France. L. Pegoraro et al. - FR617	5	2x	3x	1.492	Sexual	1716	1400	34*	7	44.3419	6.2941
124.61.7.0	*Cirsium alsophilum*	Cult. Lautaret Botanical Garden. L. Pegoraro et al. - FR585	5	2x	3x	1.499	Sexual	—	1190	34	6	—	—
124.61.7.0	*Cirsium alsophilum*	France. L. Pegoraro et al. - FR701	5	2x	3x	1.509	Sexual	1811	1190	34	6	44.2011	7.1226
124.61.7.0	*Cirsium alsophilum*	Italy. L. Pegoraro et al. - IT54	5	2x	3x	1.530	Sexual	980	1190	34	6	45.8781	11.6693
124.61.19.0	*Cirsium arvense*	France. L. Pegoraro et al. - FR423	5	2x	3x	1.489	Sexual	1613	910	34	7	44.3174	6.3850
124.61.19.0	*Cirsium arvense*	Italy. L. Pegoraro et al. - IT37	5	2x	3x	1.525	Sexual	—	910	34	7	—	—
124.61.10.0	*Cirsium carniolicum*	Cult. Lautaret Botanical Garden. L. Pegoraro et al. - FR591	5	2x	3x	1.562	Sexual	—	1190	34	6	—	—
124.61.10.0	*Cirsium carniolicum*	Slovenia. M. Balant 103	5	2x	3x	1.487	Sexual	1284	1190	34	6	46.4296	14.2438
124.61.3.0	*Cirsium eriophorum*	France. L. Pegoraro et al. - FR618	5	2x	3x	1.499	Sexual	1716	1190	34	6	44.3419	6.2941
124.61.8.0	*Cirsium erisithales*	Austria. L. Pegoraro et al. - A23	5	2x	3x	1.487	Sexual	553	1190	34	6	47.7283	15.7970
124.61.8.0	*Cirsium erisithales*	Slovenia. M. Balant 3	5	2x	3x	1.532	Sexual	236	1190	34	6	46.0941	13.8997
124.61.14.0	*Cirsium heterophyllum*	France. L. Pegoraro et al. - FR567	5	2x	3x	1.514	Sexual	1908	1190	34	6	45.0330	6.3940
124.61.17.0	*Cirsium monspessulanum*	France. L. Pegoraro et al. - FR195	5	2x	3x	1.482	Sexual	1358	910	34*	6	44.0272	6.2248
124.61.17.0	*Cirsium monspessulanum*	France. L. Pegoraro et al. - FR351	5	2x	3x	1.521	Sexual	1380	910	34*	6	44.2476	6.2349
124.61.17.0	*Cirsium monspessulanum*	France. L. Pegoraro et al. - FR449	5	2x	3x	1.488	Sexual	1052	910	34*	6	44.6704	6.2397

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ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.61.11.0	*Cirsium oleraceum*	Austria. L. Pegoraro et al. - A25	5	2x	3x	1.552	Sexual	552	910	34	7	47.7366	15.7847
124.61.11.0	*Cirsium oleraceum*	Austria. L. Pegoraro et al. - A55	5	2x	3x	1.498	Sexual	554	910	34	7	47.3258	11.6912
124.61.15.0	*Cirsium pannonicum*	Austria. L. Pegoraro et al. - A7	5	2x	3x	1.529	Sexual	453	700	34	5	48.0406	16.0416
124.61.6.0	*Cirsium rivulare*	Austria. L. Pegoraro et al. - A28	5	2x	3x	1.540	Sexual	736	700	34	6	47.8725	15.7842
124.61.12.0	*Cirsium spinosissimum*	France. L. Pegoraro et al. - FR643	5	2x	3x	1.478	Sexual	2692	2100	34	7	44.2595	6.7163
124.61.12.0	*Cirsium spinosissimum*	France. L. Pegoraro et al. - FR651	5	2x	3x	1.530	Sexual	2317	2100	34	7	44.2889	6.6046
124.61.5.0	*Cirsium tuberosum*	France. L. Pegoraro et al. - FR525	5	2x	3x	1.508	Sexual	1289	910	34	6	44.3553	6.2900
124.61.4.0	*Cirsium vulgare*	France. L. Pegoraro et al. - FR524	5	2x	3x	1.502	Sexual	1440	910	34	6	44.3555	6.2935
124.61.4.0	*Cirsium vulgare*	Slovenia. M. Balant 91	4	2x	3x	1.489	Sexual	—	910	34	6	—	—
124.30.7.1	*Cota tinctoria*	France. L. Pegoraro et al. - FR608	5	2x	3x	1.510	Sexual	1215	910	18	6	44.8628	6.5888
124.30.7.1	*Cota tinctoria*	France. L. Pegoraro et al. - FR624	5	2x	3x	1.506	Sexual	2000	910	18	6	44.2982	6.5684
124.30.8.0	*Cota triumfettii*	Switzerland. L. Pegoraro et al. - CH75	5	2x	3x	1.489	Sexual	550	700	18	6	45.9507	8.9807
124.97.7.0	*Crepis aurea*	Cult. Lautaret Botanical Garden. O. Hidalgo 294	5	2x	3x	1.510	Sexual	—	1890	10	6	—	—
124.97.7.0	*Crepis aurea*	France. L. Pegoraro et al. - FR546	5	2x	3x	1.511	Sexual	2601	1890	10	6	45.0641	6.4024
124.97.24.0	*Crepis capillaris*	Switzerland. L. Pegoraro et al. - CH76	5	2x	3x	1.509	Sexual	423	910	6	6	45.8378	8.8733
124.97.10.0	*Crepis conyzifolia*	Austria. L. Pegoraro et al. - A122	5	2x	3x	1.526	Sexual	2003	1750	8	6	47.0634	12.8259
124.97.10.0	*Crepis conyzifolia*	France. O. Hidalgo 311	5	2x	3x	1.520	Sexual	—	1750	8	6	—	—
124.97.5.0	*Crepis jacquinii* subsp. *kerneri*	Slovenia. M. Balant 123	5	2x	3x	1.479	Sexual	—	2217	12	7	—	—
124.97.1.0	*Crepis paludosa*	Austria. L. Pegoraro et al. - CH74	5	2x	3x	1.489	Sexual	740	1190	12	6	45.9728	9.0676
124.97.1.0	*Crepis paludosa*	Switzerland. L. Pegoraro et al. - CH112	5	2x	3x	1.508	Sexual	1785	1190	12	6	46.5925	8.4881
124.97.9.0	*Crepis pontana*	Austria. L. Pegoraro et al. - A129	5	2x	3x	1.499	Sexual	2087	1750	10	6	47.0609	12.7933
124.97.9.0	*Crepis pontana*	France. O. Hidalgo 429	5	2x	3x	1.487	Sexual	—	1750	10	6	—	—
124.97.2.0	*Crepis pygmaea*	France. L. Pegoraro et al. - FR278	5	2x	3x	1.502	Sexual	2378	1890	12	7	44.3158	6.4565
124.97.2.0	*Crepis pygmaea*	France. L. Pegoraro et al. - FR686	5	2x	3x	1.512	Sexual	2775	1890	12	7	44.3204	6.8070
124.97.11.0	*Crepis pyrenaica*	France. L. Pegoraro et al. - FR494	5	2x	3x	1.515	Sexual	1879	1517	8	6	44.3549	6.9572

Table A.1: Data table for Chapter 2 with sample origin, collection details and reproductive modes inferred

ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.97.11.0	*Crepis pyrenaica*	Switzerland. L. Pegoraro et al. - CH177	5	2x	3x	1.552	Sexual	1933	1517	8	6	46.5498	8.7009
124.97.6.0	*Crepis rhaetica*	Switzerland. L. Pegoraro et al. - CH153	5	2x	3x	1.511	Sexual	2788	2575	8	7	45.9896	7.6866
124.97.25.0	*Crepis sancta*	Italy. L. Pegoraro et al. - IT22	5	2x	3x	1.523	Sexual	—	350	10	4	—	—
124.97.19.0	*Crepis tectorum*	Switzerland. L. Pegoraro et al. - CH167	5	2x	3x	1.478	Sexual	324	700	8	5	46.0448	8.9723
124.97.3.0	*Crepis terglouensis*	Austria. L. Pegoraro et al. - A88	5	2x	3x	1.507	Sexual	2270	2217	12	7	46.7627	12.8026
124.97.27.1	*Crepis vesicaria*	France. L. Pegoraro et al. - FR432	5	2x	4x	2.059	Apomictic	1500	583	8	5	44.2783	6.4263
124.97.27.1	*Crepis vesicaria*	France. L. Pegoraro et al. - FR621	3	2x	3x	1.523	Sexual	1607	583	8	5	44.3466	6.2974
124.97.27.1	*Crepis vesicaria*	Italy. L. Pegoraro et al. - IT12	5	2x	3x	1.523	Sexual	980	583	8	5	45.7586	11.4231
124.97.27.1	*Crepis vesicaria*	Italy. L. Pegoraro et al. - IT17	5	2x	3x	1.533	Sexual	165	583	8	5	45.7384	11.5908
124.69.1.0	*Crupina vulgaris*	France. O. Hidalgo 377	5	2x	3x	1.526	Sexual	—	583	30	5	—	—
124.68.29.0	*Cyanus montanus*	France. L. Pegoraro et al. - FR412	5	4x	6x	1.488	Sexual	1752	1190	44	5	44.3187	6.3553
124.68.29.0	*Cyanus montanus*	France. L. Pegoraro et al. - FR493	5	2x	3x	1.489	Sexual	1879	1190	22	5	44.3549	6.9572
124.68.31.0	*Cyanus segetum*	France. L. Pegoraro et al. - FR384	5	2x	3x	1.540	Sexual	1096	910	24	5	44.3807	6.3266
124.68.31.0	*Cyanus segetum*	France. O. Hidalgo 308	5	2x	3x	1.561	Sexual	—	910	24	5	—	—
124.68.30.0	*Cyanus triumfettii*	Switzerland. L. Pegoraro et al. - CH48	5	2x	3x	1.479	Sexual	413	1050	22	5	45.9620	8.8847
124.16.14.0	*Dittrichia graveolens*	Slovenia. M. Balant 127	5	2x	3x	1.492	Sexual	—	350	18	8	—	—
124.46.1.0	*Doronicum austriacum*	Austria. L. Pegoraro et al. - A104	5	2x	3x	1.523	Sexual	1650	1190	60	6	47.1431	12.8154
124.46.8.0	*Doronicum clusii*	Austria. L. Pegoraro et al. - A64	5	4x	6x	1.502	Sexual	2110	2100	120	7	47.2716	14.0838
124.46.6.0	*Doronicum grandiflorum*	France. L. Pegoraro et al. - FR281	5	2x	3x	1.541	Sexual	2378	2575	60*	7	44.3158	6.4565
124.46.6.0	*Doronicum grandiflorum*	France. L. Pegoraro et al. - FR451	5	2x	3x	1.521	Sexual	2553	2575	60*	7	44.7225	6.3177
124.46.6.0	*Doronicum grandiflorum*	France. L. Pegoraro et al. - FR471	5	2x	3x	1.511	Sexual	2683	2575	60*	7	44.7299	6.3262
124.46.6.0	*Doronicum grandiflorum*	France. L. Pegoraro et al. - FR484	5	2x	3x	1.562	Sexual	2249	2575	60*	7	44.5806	6.3323
124.46.6.0	*Doronicum grandiflorum*	France. L. Pegoraro et al. - FR515	5	2x	3x	1.532	Sexual	2147	2575	60*	7	44.3091	6.4558
124.46.6.0	*Doronicum grandiflorum*	France. L. Pegoraro et al. - FR536	5	2x	3x	1.489	Sexual	2623	2575	60*	7	45.0641	6.4077
124.46.6.0	*Doronicum grandiflorum*	France. L. Pegoraro et al. - FR628	5	2x	3x	1.541	Sexual	2428	2575	60*	7	44.2541	6.7140

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ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.46.6.0	*Doronicum grandiflorum*	France. L. Pegoraro et al. - FR649	5	2x	3x	1.476	Sexual	2317	2575	60*	7	44.2889	6.6046
124.46.6.0	*Doronicum grandiflorum*	France. L. Pegoraro et al. - FR689	5	2x	3x	1.522	Sexual	2862	2575	60*	7	44.3215	6.8066
124.46.4.0	*Doronicum pardalianches*	Switzerland. L. Pegoraro et al. - CH22	5	2x	3x	1.552	Sexual	282	700	60*	5	46.0312	9.1485
124.54.2.0	*Echinops exaltatus*	Switzerland. L. Pegoraro et al. - CH68	5	2x	3x	1.497	Sexual	306	350	30	6	46.0090	9.0088
124.54.3.0	*Echinops ritro*	France. L. Pegoraro et al. - FR481	5	2x	3x	1.522	Sexual	1204	910	32	7	44.5716	6.3790
124.54.1.0	*Echinops sphaerocephalus*	Spain. T. Garnatje s.n. IX-2015	5	2x	3x	1.522	Sexual	—	700	30	7	—	—
124.6.3.1	*Erigeron acris* subsp. *acris*	France. L. Pegoraro et al. - FR352	5	2x	3x	1.561	Sexual	1358	910	18*	6	44.0272	6.2248
124.6.3.1	*Erigeron acris* subsp. *acris*	France. L. Pegoraro et al. - FR509	5	2x	3x	1.532	Sexual	2037	910	18*	6	44.3397	6.9475
124.6.6.0	*Erigeron alpinus*	France. L. Pegoraro et al. - FR265	5	2x	3x	1.485	Sexual	2127	1890	18*	7	44.3134	6.4484
124.6.6.0	*Erigeron alpinus*	France. L. Pegoraro et al. - FR318	5	2x	3x	1.541	Sexual	1980	1890	18*	7	44.2608	6.2087
124.6.6.0	*Erigeron alpinus*	France. L. Pegoraro et al. - FR677b	5	2x	3x	1.525	Sexual	2465	1890	18*	7	44.2048	7.1561
124.6.6.0	*Erigeron alpinus*	France. L. Pegoraro et al. - FR8d	5	2x	3x	1.510	Sexual	1970	1890	18*	7	44.3347	6.2955
124.6.1.0	*Erigeron annuus*	Spain. T. Garnatje GR558	5	2x	3x	1.522	Sexual	—	583	18*	6	—	—
124.6.4.0	*Erigeron atticus*	France. L. Pegoraro et al. - FR286	5	2x	3x	1.532	Sexual	2378	1750	18	7	44.3158	6.4565
124.7.3.0	*Erigeron bonariensis*	Switzerland. L. Pegoraro et al. - CH134	5	6x	9x	1.498	Sexual	604	350	54	6	46.2533	7.4060
124.7.1.0	*Erigeron canadensis*	Italy. L. Pegoraro et al. - IT78	5	2x	3x	1.522	Sexual	343	910	18	6	45.8460	8.8905
124.7.1.0	*Erigeron canadensis*	Switzerland. L. Pegoraro et al. - CH132	5	2x	3x	1.540	Sexual	593	910	18	6	46.2531	7.4064
124.6.8.0	*Erigeron glabratus*	Slovenia. M. Balant 7	5	2x	3x	1.527	Sexual	—	1890	18	7	—	—
124.6.2.0	*Erigeron karvinskianus*	Switzerland. L. Pegoraro et al. - CH39	5	4x	8x	1.899	Apomictic	881	350	36	4	46.0086	8.9852
124.6.5.0	*Erigeron schleicheri*	France. L. Pegoraro et al. - FR492	5	2x	3x	1.534	Sexual	1836	1470	18	7	44.3574	6.9530
124.6.5.0	*Erigeron schleicheri*	France. L. Pegoraro et al. - FR506	5	2x	3x	1.541	Sexual	2035	1470	18	7	44.3407	6.9471
124.6.9.0	*Erigeron uniflorus*	France. L. Pegoraro et al. - FR453	5	2x	3x	1.474	Sexual	2553	2575	18	7	44.7225	6.3177
124.6.9.0	*Erigeron uniflorus*	France. L. Pegoraro et al. - FR640	5	2x	3x	1.459	Sexual	2873	2575	18	7	44.2626	6.7096
124.1.1.0	*Eupatorium cannabinum*	Italy. L. Pegoraro et al. - IT71	5	2x	3x	1.536	Sexual	198	910	20	7	45.7603	11.6270

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124.28.1.0	*Galinsoga parviflora*	Italy. L. Pegoraro et al. - IT74	5	2x	3x	1.510	Sexual	145	583	16*	5	45.7381	11.6150
124.28.2.0	*Galinsoga quadriradiata*	France. L. Pegoraro et al. - FR487	5	4x	6x	1.522	Sexual	—	583	32	5	—	—
124.10.3.0	*Gnaphalium hoppeanum*	France. L. Pegoraro et al. - FR553	25	4x	6x	1.514	Sexual	2601	2217	28*	7	45.0641	6.4024
124.10.3.0	*Gnaphalium hoppeanum*	France. L. Pegoraro et al. - FR642	25	4x	6x	1.500	Sexual	2692	2217	28*	7	44.2595	6.7163
124.10.3.0	*Gnaphalium hoppeanum*	France. L. Pegoraro et al. - FR682	25	4x	6x	1.511	Sexual	2313	2217	28*	7	44.1738	7.1567
124.10.3.0	*Gnaphalium hoppeanum*	France. L. Pegoraro et al. - FR697	25	4x	6x	1.498	Sexual	2623	2217	28*	7	44.3450	6.8009
124.10.4.0	*Gnaphalium supinum*	France. L. Pegoraro et al. - FR552	15	4x	6x	1.521	Sexual	2601	2575	28	7	45.0641	6.4024
124.10.4.0	*Gnaphalium supinum*	France. L. Pegoraro et al. - FR660	25	4x	6x	1.511	Sexual	2354	2575	28	7	44.2584	6.7390
124.10.4.0	*Gnaphalium supinum*	France. L. Pegoraro et al. - FR678	25	4x	6x	1.565	Sexual	2338	2575	28	7	44.1753	7.1441
124.10.1.0	*Gnaphalium sylvaticum*	France. L. Pegoraro et al. - FR684	15	8x	12x	1.511	Sexual	2178	1400	56	6	44.1775	7.1725
124.25.2.0	*Helianthus tuberosus*	Italy. L. Pegoraro et al. - IT76	1	6x	9x	1.545	Sexual	—	350	102	8	—	—
124.11.2.0	*Helichrysum italicum*	Cult. Barcelona Botanical Garden. O. Hidalgo 371	5	4x	6x	1.523	Sexual	—	350	28	6	—	—
124.11.2.0	*Helichrysum italicum*	France. L. Pegoraro et al. - FR730	5	4x	6x	1.540	Sexual	659	350	28	6	44.4706	6.1301
124.11.2.0	*Helichrysum italicum*	Slovenia. M. Balant 92	5	4x	6x	1.489	Sexual	—	350	28	6	—	—
124.99.29.0	*Hieracium alpinum*	Slovenia. M. Balant 78	25	3x	6x	1.978	Apomictic	2036	2183	27	7	46.4351	13.6429
124.99.31.0	*Hieracium amplexicaule*	France. L. Pegoraro et al. - FR123	25	3x	6x	1.992	Apomictic	1985	1400	27	5	44.3793	6.3955
124.99.31.0	*Hieracium amplexicaule*	France. L. Pegoraro et al. - FR135	25	3x	6x	2.067	Apomictic	1922	1400	27	5	44.3856	6.3909
124.99.18.0	*Hieracium bifidum*	Switzerland. L. Pegoraro et al. - CH42	25	3x	6x	1.987	Apomictic	348	1550	27	6	46.0269	8.7665
124.99	*Hieracium cydoniifolium*	France. L. Pegoraro et al. - FR20	25	3x	6x	2.123	Apomictic	1847	1890	27	7	44.3400	6.2964
124.99	*Hieracium froelichianum*	France. L. Pegoraro et al. - FR120	25	3x	6x	2.078	Apomictic	1985	1890	27	7	44.3793	6.3955
124.99	*Hieracium glaucopsis*	France. L. Pegoraro et al. - FR328	25	3x	6x	1.965	Apomictic	1890	1890	27	7	44.2608	6.2088
124.99.35.0	*Hieracium glaucum*	France. O. Hidalgo 348 et al.	25	3x	6x	1.966	Apomictic	—	1190	27	6	—	—
124.99.30.0	*Hieracium humile*	France. L. Pegoraro et al. - FR427	25	3x	6x	1.897	Apomictic	1514	1400	27	6	44.3197	6.4320
124.99.23.0	*Hieracium lawsonii*	France. L. Pegoraro et al. - FR700	25	3x	6x	2.123	Apomictic	2560	1190	27	6	44.3321	6.7735

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124.99.16.0	*Hieracium murorum*	France. L. Pegoraro et al. - FR108	25	3x	6x	1.958	Apomictic	2119	1250	27	5	44.3833	6.3988
124.99.16.0	*Hieracium murorum*	France. L. Pegoraro et al. - FR134	25	3x	6x	1.980	Apomictic	1922	1250	27	5	44.3856	6.3909
124.99.16.0	*Hieracium murorum*	France. L. Pegoraro et al. - FR74	25	3x	6x	1.899	Apomictic	—	1250	27	5	—	—
124.99.16.0	*Hieracium murorum*	France. L. Pegoraro et al. - FR88	25	3x	6x	2.120	Apomictic	2219	1250	27	5	44.3862	6.3960
124.99.16.0	*Hieracium murorum*	Italy. L. Pegoraro et al. - IT11	25	3x	6x	1.988	Apomictic	730	1250	27	5	45.7538	11.4151
124.99.26.0	*Hieracium piliferum*	France. L. Pegoraro et al. - FR322a	25	3x	6x	1.968	Apomictic	1890	2217	27*	7	44.2608	6.2087
124.99.26.0	*Hieracium piliferum*	France. L. Pegoraro et al. - FR385	25	3x	6x	1.998	Apomictic	1991	2217	27*	7	44.3314	6.2924
124.99.37.0	*Hieracium prenanthoides*	France. L. Pegoraro et al. - FR572	25	2x	3x	1.498	Sexual	1380	1750	18	6	45.0415	6.2838
124.99	*Hieracium ramosissimum* subsp. *lactucifolium*	Cult. Lautaret Botanical Garden. L. Pegoraro et al. - FR580	25	3x	6x	2.098	Apomictic	—	1890	27	7	—	—
124.99.28.0	*Hieracium tomentosum*	France. L. Pegoraro et al. - FR231	25	3x	6x	1.999	Apomictic	1421	1050	27	5	44.2783	6.4237
124.99	*Hieracium valdepilosum*	Austria. L. Pegoraro et al. - A124	25	3x	6x	2.267	Apomictic	1954	1890	27	7	47.0559	12.8033
124.99.24.0	*Hieracium villosum*	France. L. Pegoraro et al. - FR214	25	3x	6x	1.929	Apomictic	1772	1890	27*	7	44.2847	6.4317
124.99.24.0	*Hieracium villosum*	France. L. Pegoraro et al. - FR44	25	3x	6x	2.132	Apomictic	1966	1890	27*	7	44.3354	6.2957
124.99.24.0	*Hieracium villosum*	France. L. Pegoraro et al. - FR500	4	3x	6x	2.080	Apomictic	1904	1890	27*	7	44.3527	6.9588
124.43.1.0	*Homogyne alpina*	France. L. Pegoraro et al. - FR473	25	6x	9x	1.562	Sexual	2463	1921	120	5	44.7232	6.3443
124.43.1.0	*Homogyne alpina*	France. L. Pegoraro et al. - FR547	20	6x	9x	1.561	Sexual	2601	1921	120	5	45.0641	6.4024
124.43.1.0	*Homogyne alpina*	France. O. Hidalgo 298	25	6x	9x	1.552	Sexual	—	1921	120	5	—	—
124.43.2.0	*Homogyne discolor*	Slovenia. M. Balant 86	25	4x	6x	1.499	Sexual	2108	1890	60	6	46.4460	13.6474
124.43.3.0	*Homogyne sylvestris*	Slovenia. M. Balant 45	5	4x	6x	1.537	Sexual	1146	1190	60	5	46.4284	14.2836
124.82.1.0	*Hypochaeris maculata*	France. L. Pegoraro et al. - FR333	5	2x	3x	1.487	Sexual	1890	1250	10*	5	44.2608	6.2088
124.82.1.0	*Hypochaeris maculata*	France. L. Pegoraro et al. - FR397	5	2x	3x	1.475	Sexual	1694	1250	10*	5	44.3291	6.3059
124.82.1.0	*Hypochaeris maculata*	France. L. Pegoraro et al. - FR438	5	2x	3x	1.488	Sexual	1710	1250	10*	5	44.2839	6.4345
124.82.5.0	*Hypochaeris radicata*	France. L. Pegoraro et al. - CH26	5	2x	3x	1.487	Sexual	328	910	8*	5	46.0190	9.2293
124.82.5.0	*Hypochaeris radicata*	United Kingdom. O. Hidalgo 286	5	2x	3x	1.513	Sexual	—	910	8*	5	—	—

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124.82.2.0	*Hypochaeris uniflora*	Austria. L. Pegoraro et al. - A120	5	2x	3x	1.499	Sexual	2203	1890	10	7	47.0675	12.8377
124.82.2.0	*Hypochaeris uniflora*	Switzerland. L. Pegoraro et al. - CH125	5	2x	3x	1.477	Sexual	2400	1890	10	7	46.5759	8.4224
124.82.2.0	*Hypochaeris uniflora*	Switzerland. L. Pegoraro et al. - CH179	5	2x	3x	1.509	Sexual	1927	1890	10	7	46.5493	8.7028
124.16.12.0	*Inula bifrons*	France. L. Pegoraro et al. - FR143	5	2x	3x	1.487	Sexual	1172	910	16	7	44.2574	6.2551
124.16.11.0	*Inula conyzae*	Italy. L. Pegoraro et al. - IT85	5	4x	6x	1.555	Sexual	595	700	32	6	45.8591	8.8161
124.16.11.0	*Inula conyzae*	Slovenia. M. Balant 111	5	4x	6x	1.532	Sexual	—	700	32	6	—	—
124.16.1.0	*Inula helenium*	Cult. Lautaret Botanical Garden	5	2x	3x	1.490	Sexual	—	700	20	7	—	—
124.16.2.0	*Inula helvetica*	France. L. Pegoraro et al. - FR522	5	2x	3x	1.499	Sexual	1440	583	16	7	44.3555	6.2935
124.16.10.0	*Inula montana*	France. L. Pegoraro et al. - FR193	5	2x	3x	1.550	Sexual	1380	910	16	6	44.2476	6.2349
124.16.9.0	*Inula oculus-christi*	Austria. L. Pegoraro et al. - A31	5	4x	6x	1.562	Sexual	—	350	32	6	—	—
124.16.4.0	*Inula salicina*	France. L. Pegoraro et al. - FR185	5	2x	3x	1.610	Sexual	1380	700	16	6	44.2476	6.2349
124.16.5.0	*Inula spiraefolia*	France. L. Pegoraro et al. - FR727	5	2x	3x	1.513	Sexual	609	700	16	6	44.3634	5.8873
124.48.22.0	*Jacobaea abrotanifolia* subsp. *abrotanifolia*	Cult. Lautaret Botanical Garden	5	8x	12x	1.489	Sexual	—	1890	80	7	—	—
124.48.22.0	*Jacobaea abrotanifolia* subsp. *abrotanifolia*	Italy. L. Pegoraro et al. - IT101	5	4x	6x	1.567	Sexual	1916	1890	40	7	45.7873	11.1819
124.48.22.0	*Jacobaea abrotanifolia* subsp. *abrotanifolia*	Switzerland. L. Pegoraro et al. - CH185	5	4x	6x	1.532	Sexual	1897	1890	40	7	46.5345	8.8540
124.48.15.0	*Jacobaea alpina* subsp. *alpina*	Switzerland. L. Pegoraro et al. - CH117	5	4x	6x	1.552	Sexual	1778	1470	40	7	46.6491	8.6873
124.48.15.0	*Jacobaea alpina* subsp. *alpina*	Switzerland. L. Pegoraro et al. - CH183	5	4x	6x	1.512	Sexual	1948	1470	40	7	46.5464	8.7136
124.48.18.0	*Jacobaea aquatica*	Switzerland. L. Pegoraro et al. - CH73	5	4x	6x	1.587	Sexual	746	583	40	6	45.9731	9.0669
124.48.2.2	*Jacobaea carniolica*	Austria. L. Pegoraro et al. - A65	5	12x	18x	1.495	Sexual	2110	2410	120	7	47.2716	14.0838
124.48.20.0	*Jacobaea erucifolia*	France. L. Pegoraro et al. - FR220	5	4x	6x	1.554	Sexual	1421	700	40*	6	44.2784	6.4237
124.48.20.0	*Jacobaea erucifolia*	France. L. Pegoraro et al. - FR349	5	4x	6x	1.567	Sexual	1358	700	40*	6	44.0273	6.2249
124.48.20.0	*Jacobaea erucifolia*	France. L. Pegoraro et al. - FR562	5	4x	6x	1.554	Sexual	—	700	40*	6	—	—
124.48.2.1	*Jacobaea incana*	Austria. L. Pegoraro et al. - A119	5	4x	6x	1.515	Sexual	2303	2410	40*	7	47.0692	12.8392
124.48.2.1	*Jacobaea incana*	France. L. Pegoraro et al. - FR301	5	4x	6x	1.520	Sexual	2505	2410	40*	7	44.4079	6.3854

Table A.1: Data table for Chapter 2 with sample origin, collection details and reproductive modes inferred

ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.48.2.1	*Jacobaea incana*	France. L. Pegoraro et al. - FR661	5	4x	6x	1.468	Sexual	2373	2410	40*	7	44.2571	6.7380
124.48.2.1	*Jacobaea incana*	France. L. Pegoraro et al. - FR662	5	4x	6x	1.558	Sexual	2349	2410	40*	7	44.2025	7.1503
124.48.2.1	*Jacobaea incana*	France. L. Pegoraro et al. - FR664	5	4x	6x	1.590	Sexual	2354	2410	40*	7	44.2033	7.1513
124.48.2.1	*Jacobaea incana*	France. L. Pegoraro et al. - FR672	5	4x	6x	1.497	Sexual	2465	2410	40*	7	44.2048	7.1561
124.48.2.1	*Jacobaea incana*	France. L. Pegoraro et al. - FR692b	5	4x	6x	1.502	Sexual	2862	2410	40*	7	44.3215	6.8066
124.48.2.1	*Jacobaea incana*	France. L. Pegoraro et al. - FR85	5	4x	6x	1.545	Sexual	2219	2410	40*	7	44.3862	6.3960
124.48.16.0	*Jacobaea subalpina*	Cult. Lautaret Botanical Garden. L. Pegoraro et al. - FR593	5	4x	6x	1.509	Sexual	—	1400	40*	7	—	—
124.59.1.0	*Jurinea mollis*	Slovenia. M. Balant 22	5	2x	3x	1.487	Sexual	—	350	34	5	—	—
124.65.3.0	*Klasea lycopifolia*	Slovenia. M. Balant 25	5	4x	6x	1.553	Sexual	—	700	60	6	—	—
124.90.1.0	*Lactuca alpina*	Austria. L. Pegoraro et al. - A85	5	2x	3x	1.567	Sexual	1638	1517	18	6	46.7828	12.7884
124.90.1.0	*Lactuca alpina*	Switzerland. L. Pegoraro et al. - CH107	5	2x	3x	1.512	Sexual	1437	1517	16	6	46.6232	8.5766
124.92.1.0	*Lactuca muralis*	France. L. Pegoraro et al. - FR121	5	2x	3x	1.499	Sexual	1985	910	18*	7	44.3793	6.3955
124.92.1.0	*Lactuca muralis*	France. L. Pegoraro et al. - FR159	5	2x	3x	1.632	Sexual	1036	910	18	7	44.2721	6.2988
124.89.7.0	*Lactuca perennis*	France. L. Pegoraro et al. - FR117	5	2x	3x	1.487	Sexual	1985	910	18*	5	44.3793	6.3955
124.89.7.0	*Lactuca perennis*	France. L. Pegoraro et al. - FR118	5	2x	3x	1.501	Sexual	1985	910	18*	5	44.3793	6.3955
124.89.7.0	*Lactuca perennis*	France. L. Pegoraro et al. - FR166	5	2x	3x	1.488	Sexual	1586	910	18*	5	44.2486	6.2295
124.89.3.0	*Lactuca serriola*	France. L. Pegoraro et al. - FR152	5	4x	6x	1.550	Sexual	1172	700	18*	7	44.2574	6.2551
124.89.3.0	*Lactuca serriola*	Italy. L. Pegoraro et al. - IT80	5	4x	6x	1.487	Sexual	345	700	18	7	45.8459	8.8902
124.10.6.0	*Laphangium luteoalbum*	Switzerland. L. Pegoraro et al. - CH157	5	2x	3x	1.543	Sexual	752	350	14*	6	46.2678	7.8803
124.96.1.0	*Lapsana communis*	Italy. L. Pegoraro et al. - IT43	5	2x	3x	1.551	Sexual	—	910	14*	5	—	—
124.96.1.0	*Lapsana communis*	Spain. T. Garnatje GR566	5	2x	3x	1.534	Sexual	—	910	14*	5	—	—
124.83.7.0	*Leontodon crispus*	France. L. Pegoraro et al. - FR217	5	2x	3x	1.552	Sexual	1772	910	8*	5	44.2847	6.4317
124.83.6.0	*Leontodon hirtus*	France. L. Pegoraro et al. - R9	5	2x	3x	1.478	Sexual	—	910	14*	5	—	—
124.83.5.0	*Leontodon hispidus*	France. L. Pegoraro et al. - FR340	5	2x	3x	1.552	Sexual	1890	1850	14*	6	44.2721	6.2117

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ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.83.5.0	*Leontodon hispidus*	France. L. Pegoraro et al. - FR69	5	2x	3x	1.448	Sexual	—	1850	14*	6	—	—
124.83.8.2	*Leontodon tenuiflorus*	Switzerland. L. Pegoraro et al. - CH34	5	2x	3x	1.568	Sexual	618	910	8	4	45.9965	9.2195
124.13.1.0	*Leontopodium nivale* subsp. *alpinum*	France. L. Pegoraro et al. - FR317	5	4x	6x	1.502	Sexual	1980	1633	24	7	44.2608	6.2087
124.13.1.0	*Leontopodium nivale* subsp. *alpinum*	France. L. Pegoraro et al. - FR327	5	4x	6x	1.555	Sexual	1890	1633	24	7	44.2608	6.2088
124.13.1.0	*Leontopodium nivale* subsp. *alpinum*	Italy. L. Pegoraro et al. - IT100a	5	4x	6x	1.610	Sexual	1987	1633	24	7	45.7899	11.1764
124.13.1.0	*Leontopodium nivale* subsp. *alpinum*	Slovenia. M. Balant 124	5	4x	6x	1.507	Sexual	—	1633	24	7	—	—
124.37.1.0	*Leucanthemopsis alpina*	Cult. Lautaret Botanical Garden. O. Hidalgo 330	5	2x	3x	1.520	Sexual	—	2270	18*	7	—	—
124.37.1.0	*Leucanthemopsis alpina*	France. L. Pegoraro et al. - FR310	5	2x	3x	1.562	Sexual	2505	2270	18*	7	44.4079	6.3854
124.37.1.0	*Leucanthemopsis alpina*	France. L. Pegoraro et al. - FR454	5	2x	3x	1.555	Sexual	2553	2270	18*	7	44.7225	6.3177
124.37.1.0	*Leucanthemopsis alpina*	France. L. Pegoraro et al. - FR538	5	2x	3x	1.531	Sexual	2623	2270	18*	7	45.0641	6.4077
124.37.1.0	*Leucanthemopsis alpina*	France. L. Pegoraro et al. - FR646	5	4x	6x	1.523	Sexual	2338	2270	36*	7	44.2892	6.6117
124.37.1.0	*Leucanthemopsis alpina*	France. L. Pegoraro et al. - FR663	5	3x	6x	2.103	Apomictic	2349	2270	27	7	44.2025	7.1503
124.37.1.0	*Leucanthemopsis alpina*	France. L. Pegoraro et al. - FR665	5	2x	3x	1.521	Sexual	2354	2270	18*	7	44.2033	7.1513
124.37.1.0	*Leucanthemopsis alpina*	France. L. Pegoraro et al. - FR688	5	2x	3x	1.662	Sexual	2862	2270	18*	7	44.3215	6.8066
124.39.2.0	*Leucanthemum adustum*	France. L. Pegoraro et al. - FR14	5	8x	12x	1.478	Sexual	1847	1400	72*	6	44.3400	6.2964
124.39.2.0	*Leucanthemum adustum*	France. L. Pegoraro et al. - FR210	5	8x	12x	1.468	Sexual	1772	1400	72*	6	44.2847	6.4317
124.39.2.0	*Leucanthemum adustum*	France. L. Pegoraro et al. - FR215	5	8x	12x	1.601	Sexual	1772	1400	72*	6	44.2847	6.4317
124.39.2.0	*Leucanthemum adustum*	France. L. Pegoraro et al. - FR250	5	8x	12x	1.532	Sexual	1961	1400	72*	6	44.3153	6.4422
124.39.2.0	*Leucanthemum adustum*	France. L. Pegoraro et al. - FR25a	5	6x	9x	1.499	Sexual	1893	1400	54	6	44.3380	6.2963
124.39.2.0	*Leucanthemum adustum*	France. L. Pegoraro et al. - FR25b	5	8x	12x	1.512	Sexual	1893	1400	72*	6	44.3380	6.2963
124.39.2.0	*Leucanthemum adustum*	France. L. Pegoraro et al. - FR322b	5	8x	12x	1.652	Sexual	1890	1400	72*	6	44.2608	6.2088
124.39.2.0	*Leucanthemum adustum*	France. L. Pegoraro et al. - FR330	5	8x	12x	1.552	Sexual	1890	1400	72*	6	44.2608	6.2087
124.39.2.0	*Leucanthemum adustum*	France. L. Pegoraro et al. - FR422	5	8x	12x	1.512	Sexual	1850	1400	72*	6	44.3121	6.4358

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124.39.2.0	*Leucanthemum adustum*	France. L. Pegoraro et al. - FR677	5	6x	9x	1.536	Sexual	2465	1400	54	6	44.2048	7.1561
124.39.8.0	*Leucanthemum atratum*	Cult. Lautaret Botanical Garden	5	6x	9x	1.562	Sexual	—	1890	54	7	—	—
124.39.8.0	*Leucanthemum atratum*	France. L. Pegoraro et al. - FR296	5	6x	9x	1.523	Sexual	2378	1890	54	7	44.3158	6.4565
124.39.8.3	*Leucanthemum coronopifolium*	France. L. Pegoraro et al. - FR444	5	6x	9x	1.562	Sexual	2070	1890	54*	7	44.2898	6.4356
124.39.8.3	*Leucanthemum coronopifolium*	France. L. Pegoraro et al. - FR634	5	6x	9x	1.551	Sexual	2428	1890	54*	7	44.2541	6.7140
124.39.8.3	*Leucanthemum coronopifolium*	France. L. Pegoraro et al. - FR650	5	6x	9x	1.521	Sexual	2317	1890	54*	7	44.2889	6.6046
124.39.8.2	*Leucanthemum halleri*	France. L. Pegoraro et al. - A63	5	2x	3x	1.601	Sexual	1973	1925	18	7	47.2394	13.5137
124.39.5.0	*Leucanthemum pallens*	France. L. Pegoraro et al. - FR191	5	6x	9x	1.526	Sexual	1380	700	54	5	44.2476	6.2349
124.39.8.5	*Leucanthemum platylepis*	Slovenia. M. Balant 114	5	8x	12x	1.534	Sexual	—	700	72	7	—	—
124.33.1.0	*Matricaria chamomilla*	Italy. L. Pegoraro et al. - IT38	5	2x	3x	1.552	Sexual	—	1050	18*	5	—	—
124.63.1.0	*Onopordum acanthium*	France. L. Pegoraro et al. - FR401	5	2x	3x	1.488	Sexual	809	910	34	7	44.4240	6.2590
124.63.1.0	*Onopordum acanthium*	Italy. L. Pegoraro et al. - IT62	5	2x	3x	1.478	Sexual	31	910	34	7	45.4575	11.3147
124.21.1.0	*Pallenis spinosa*	Spain. T. Garnatje GR565	5	2x	3x	1.526	Sexual	—	700	10	6	—	—
124.42.1.0	*Petasites albus*	Italy. L. Pegoraro et al. - IT26	5	2x	3x	1.526	Sexual	880	1050	60	3	45.8031	11.5638
124.42.3.0	*Petasites paradoxus*	Switzerland. L. Pegoraro et al. - CH13	5	4x	6x	1.599	Sexual	657	1633	120	3	46.3712	8.5503
124.15.3.0	*Phagnalon saxatile*	France. O. Hidalgo 370	5	2x	3x	1.487	Sexual	—	350	18	3	—	—
124.84.2.1	*Picris hieracioides*	France. L. Pegoraro et al. - FR156	5	2x	4x	2.005	Apomictic	1036	910	10*	6	44.2584	6.2634
124.84.2.1	*Picris hieracioides*	France. L. Pegoraro et al. - FR228	5	2x	4x	1.865	Apomictic	1421	910	10*	6	44.2783	6.4237
124.84.2.1	*Picris hieracioides*	Italy. L. Pegoraro et al. - IT70	5	2x	3x	1.556	Sexual	198	910	10*	6	45.7603	11.6270
124.99.14.0	*Pilosella aurantiaca*	Cult. Highgate Cemetry, London, UK. O. Hidalgo 290	25	4x	8x	2.123	Apomictic	—	910	36	6	—	—
124.99.14.0	*Pilosella aurantiaca*	Cult. Lautaret Botanical Garden. O. Hidalgo 315	25	4x	8x	1.889	Apomictic	—	910	36	6	—	—
124.99.12.0	*Pilosella cymosa*	France. L. Pegoraro et al. - FR71	25	2x	3x	1.571	Sexual	—	1250	18	5	—	—
124.99.8.0	*Pilosella glacialis*	France. L. Pegoraro et al. - FR107	25	2x	3x	1.532	Sexual	2119	2100	18	7	44.3833	6.3988
124.99.2.0	*Pilosella hoppeana*	Austria. L. Pegoraro et al. - A78	25	2x	3x	1.621	Sexual	2149	1400	18	5	47.0656	12.8325

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124.99.7.0	*Pilosella lactucella*	France. L. Pegoraro et al. - FR91	25	2x	3x	1.467	Sexual	2184	1250	18	5	44.3852	6.3964
124.99.4.0	*Pilosella officinarum*	France. L. Pegoraro et al. - FR447	25	4x	8x	2.087	Apomictic	997	1400	36	5	44.3724	6.3136
124.99.3.0	*Pilosella peleteriana*	France. L. Pegoraro et al. - FR501	25	2x	3x	1.498	Sexual	2184	1250	18	5	44.3852	6.3964
124.99.3.0	*Pilosella peleteriana*	France. L. Pegoraro et al. - FR96	25	2x	3x	1.512	Sexual	1904	1250	18	5	44.3527	6.9588
124.99.10.0	*Pilosella piloselloides*	Italy. L. Pegoraro et al. - IT28	25	4x	6x	1.532	Sexual	243	1050	36	5	45.7981	11.7381
124.85.2.1	*Podospermum laciniatum*	Spain. O. Hidalgo 277	5	2x	3x	1.479	Sexual	—	910	14	5	—	—
124.85.3.0	*Podospermum purpureum*	France. O. Hidalgo 378	5	2x	3x	1.468	Sexual	—	350	14	5	—	—
124.91.1.0	*Prenanthes purpurea*	France. L. Pegoraro et al. - FR527	5	2x	3x	1.522	Sexual	1289	1050	18	7	44.3553	6.2900
124.17.2.0	*Pulicaria dysenterica*	Slovenia. M. Balant 94	5	2x	3x	1.612	Sexual	—	700	18	7	—	—
124.17.2.0	*Pulicaria dysenterica*	Switzerland. L. Pegoraro et al. - CH158	5	2x	3x	1.631	Sexual	670	700	18	7	46.2339	7.3387
124.67.2.2	*Rhaponticum heleniifolium* subsp. *bicknellii*	Cult. Lautaret Botanical Garden	5	2x	3x	1.512	Sexual	—	1750	26	6	—	—
124.67.2.1	*Rhaponticum heleniifolium* subsp. *heleniifolium*	Cult. Lautaret Botanical Garden	5	2x	3x	1.499	Sexual	—	1400	26	6	—	—
124.67.1.0	*Rhaponticum scariosum*	Switzerland. L. Pegoraro et al. - CH171	5	2x	3x	1.567	Sexual	1933	1400	26	6	46.5498	8.7009
124.57.2.1	*Saussurea alpina*	France. L. Pegoraro et al. - FR637	5	4x	6x	1.551	Sexual	2951	2217	52	7	44.2642	6.7029
124.57.2.1	*Saussurea alpina*	France. L. Pegoraro et al. - FR647	5	4x	6x	1.523	Sexual	2539	2217	52	7	44.2943	6.6189
124.99	*Schlagintweitia huteri* subsp. *lantoscana*	France. L. Pegoraro et al. - FR667	5	2x	3x	1.521	Sexual	2354	1890	18	7	44.2033	7.1513
124.99.32.0	*Schlagintweitia intybacea*	Switzerland. L. Pegoraro et al. - CH123	5	2x	3x	1.544	Sexual	2383	1890	18	7	46.5759	8.4226
124.85.6.0	*Scorzonera humilis*	Switzerland. L. Pegoraro et al. - CH44	5	2x	3x	1.611	Sexual	978	910	14	5	46.1044	8.9661
124.83.4.0	*Scorzoneroides autumnalis*	Switzerland. L. Pegoraro et al. - CH180	5	2x	3x	1.567	Sexual	1950	1050	12	6	46.5541	8.7149
124.83.2.0	*Scorzoneroides crocea*	Austria. L. Pegoraro et al. - A12	5	2x	3x	1.678	Sexual	1530	1750	14	7	47.7173	15.7747
124.83.2.0	*Scorzoneroides crocea*	Switzerland. L. Pegoraro et al. - CH145	5	2x	3x	1.510	Sexual	2025	1750	14	7	45.9901	7.7049
124.83.3.1	*Scorzoneroides montana*	Austria. L. Pegoraro et al. - A116	5	4x	6x	1.555	Sexual	2338	2217	12	7	47.0979	12.8319
124.83.3.1	*Scorzoneroides montana*	France. L. Pegoraro et al. - FR532	5	4x	6x	1.504	Sexual	2601	2217	12	7	45.0641	6.4077

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ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.83.3.1	*Scorzoneroides montana*	France. L. Pegoraro et al. - FR83	5	4x	6x	1.562	Sexual	2219	2217	12	7	44.3862	6.3960
124.48.10.0	*Senecio doria*	Slovenia. M. Balant 95	5	4x	6x	1.633	Sexual	—	910	40	7	—	—
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR206	5	8x	12x	1.501	Sexual	1772	1890	80*	7	44.2847	6.4317
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR239	5	8x	12x	1.500	Sexual	1881	1890	80*	7	44.3178	6.4416
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR259	5	8x	12x	1.489	Sexual	1961	1890	80*	7	44.3153	6.4422
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR303	5	8x	12x	1.526	Sexual	2505	1890	80*	7	44.4079	6.3854
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR356	5	8x	12x	1.554	Sexual	1938	1890	80*	7	44.3366	6.2820
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR362	5	8x	12x	1.543	Sexual	1952	1890	80*	7	44.4033	6.3752
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR364	5	8x	12x	1.606	Sexual	2126	1890	80*	7	44.3975	6.3837
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR379	5	8x	12x	1.477	Sexual	2498	1890	80*	7	44.4094	6.3870
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR435	5	8x	12x	1.498	Sexual	1710	1890	80*	7	44.2839	6.4345
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR479	5	8x	12x	1.477	Sexual	2415	1890	80*	7	44.7204	6.3420
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR482	5	8x	12x	1.474	Sexual	2076	1890	80*	7	44.5761	6.3372
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR485	5	8x	12x	1.436	Sexual	2249	1890	80*	7	44.5806	6.3323
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR626	5	4x	6x	1.489	Sexual	2345	1890	40*	7	44.2524	6.7127
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR67a	5	8x	12x	1.525	Sexual	1974	1890	80*	7	44.3344	6.2905
124.48.14.0	*Senecio doronicum*	France. L. Pegoraro et al. - FR696	5	8x	12x	1.565	Sexual	2623	1890	80*	7	44.3450	6.8009
124.48.5.0	*Senecio inaequidens*	Spain. T. Garnatje GR557	5	4x	6x	1.523	Sexual	—	583	40	4	—	—
124.48.6.1	*Senecio nemorensis* subsp. *jacquinianus*	Austria. L. Pegoraro et al. - A41	5	4x	6x	1.511	Sexual	—	583	40	7	—	—
124.48.8.1	*Senecio ovatus*	France. L. Pegoraro et al. - FR571	4	4x	6x	1.478	Sexual	1380	910	40	7	45.0415	6.2838
124.48.21.0	*Senecio squalidus* subsp. *rupestris*	France. L. Pegoraro et al. - FR576	5	2x	3x	1.502	Sexual	—	1400	20	6	—	—
124.48.21.0	*Senecio squalidus* subsp. *rupestris*	Italy. L. Pegoraro et al. - IT104	5	2x	3x	1.503	Sexual	1400	1400	20	6	45.7891	11.2169
124.48.26.0	*Senecio viscosus*	France. L. Pegoraro et al. - FR489	5	4x	6x	1.562	Sexual	1610	1050	40	6	44.3464	6.2931
124.48.26.0	*Senecio viscosus*	France. L. Pegoraro et al. - FR620	5	4x	6x	1.540	Sexual	1615	1050	40	6	44.3464	6.2931

Table A.1: Data table for Chapter 2 with sample origin, collection details and reproductive modes inferred

ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.48.27.0	*Senecio vulgaris*	Italy. L. Pegoraro et al. - IT41	5	4x	6x	1.503	Sexual	—	910	40*	1	—	—
124.48.27.0	*Senecio vulgaris*	Spain. T. Garnatje GR564	5	4x	6x	1.545	Sexual	—	910	40*	1	—	—
124.48.27.0	*Senecio vulgaris*	United Kingdom. O. Hidalgo s.n.	5	4x	6x	1.521	Sexual	—	910	40*	1	—	—
124.65.1.0	*Serratula tinctoria*	Italy. L. Pegoraro et al. - IT96	5	2x	3x	1.602	Sexual	806	1610	22	7	46.0069	9.2258
124.2.1.0	*Solidago virgaurea*	France. L. Pegoraro et al. - FR111	5	2x	3x	1.523	Sexual	1985	1890	18	7	44.3793	6.3955
124.2.1.0	*Solidago virgaurea*	France. L. Pegoraro et al. - FR116	5	2x	3x	1.550	Sexual	1985	1890	18	7	44.3793	6.3955
124.2.1.0	*Solidago virgaurea*	France. L. Pegoraro et al. - FR238	5	2x	3x	1.521	Sexual	1881	1890	18	7	44.3178	6.4416
124.2.1.0	*Solidago virgaurea*	France. L. Pegoraro et al. - FR306	5	2x	3x	1.468	Sexual	2505	1890	18	7	44.4079	6.3854
124.2.1.0	*Solidago virgaurea*	France. L. Pegoraro et al. - FR341	5	2x	3x	1.520	Sexual	1890	1890	18	7	44.2721	6.2117
124.2.1.0	*Solidago virgaurea*	France. L. Pegoraro et al. - FR632	5	2x	3x	1.547	Sexual	2428	1890	18	7	44.2541	6.7140
124.2.1.2	*Solidago virgaurea* subsp. *minuta*	France. L. Pegoraro et al. - FR458	5	2x	3x	1.536	Sexual	2553	1890	18	7	44.7225	6.3177
124.88.2.0	*Sonchus oleraceus*	Italy. L. Pegoraro et al. - IT42	5	4x	6x	1.525	Sexual	—	910	32	5	—	—
124.88.2.0	*Sonchus oleraceus*	United Kingdom. O. Hidalgo s.n.	5	4x	6x	1.541	Sexual	—	910	32	5	—	—
124.58.1.0	*Staehelina dubia*	France. L. Pegoraro et al. - FR728	5	2x	3x	1.643	Sexual	609	583	30	5	44.3634	5.8873
124.58.1.0	*Staehelina dubia*	France. R. Douzet s.n. 05-VII-2017	5	2x	3x	1.578	Sexual	—	583	30	5	—	—
124.4.4.0	*Symphyotrichum squamatum*	Slovenia. M. Balant 128	5	2x	3x	1.458	Sexual	—	350	20	9	—	—
124.35.2.0	*Tanacetum corymbosum*	Austria. L. Pegoraro et al. - A11	5	4x	6x	1.556	Sexual	453	700	36	6	48.0406	16.0416
124.35.4.0	*Tanacetum macrophyllum*	Cult. Lautaret Botanical Garden. O. Hidalgo 323	5	2x	3x	1.499	Sexual	—	817	18	6	—	—
124.35.3.0	*Tanacetum parthenium*	Switzerland. L. Pegoraro et al. - CH170	5	2x	3x	1.564	Sexual	1356	700	18	6	46.5199	8.6964
124.93.15.0	*Taraxacum officinale*	Cult. Royal Botanic Gardens Kew	5	3x	6x	2.023	Apomictic	—	1250	24*	4	—	—
124.93.15.0	*Taraxacum officinale*	France. L. Pegoraro et al. - FR402	5	3x	6x	1.969	Apomictic	1602	1250	24*	4	44.3099	6.3885
124.93.15.0	*Taraxacum officinale*	Italy. L. Pegoraro et al. - IT18	5	3x	6x	1.856	Apomictic	—	1250	24*	4	—	—
124.93.15.0	*Taraxacum officinale*	United Kingdom. O. Hidalgo s.n.	5	3x	6x	2.189	Apomictic	—	1250	24*	4	—	—
124.20.1.0	*Telekia speciosa*	Slovenia. M. Balant 56	5	2x	3x	1.567	Sexual	—	817	20	6	—	—

Table A.1: Data table for Chapter 2 with sample origin, collection details and reproductive modes inferred

ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.49.1.0	*Tephroseris integrifolia*	Austria. L. Pegoraro et al. - A38	5	4x	6x	1.541	Sexual	1242	1250	48	5	47.7920	15.8145
124.49.3.0	*Tephroseris integrifolia* subsp. *capitata*	Cult. Lautaret Botanical Garden	5	8x	12x	1.560	Sexual	—	2100	64	6	—	—
124.49.9.0	*Tephroseris longifolia* subsp. *gaudinii*	Cult. Lautaret Botanical Garden. L. Pegoraro et al. - FR589	5	4x	6x	1.631	Sexual	—	1190	48	5	—	—
124.99.1.0	*Tolpis staticifolia*	France. L. Pegoraro et al. - FR218	5	2x	3x	1.667	Sexual	1772	1550	18	6	44.2847	6.4317
124.99.1.0	*Tolpis staticifolia*	France. L. Pegoraro et al. - FR342	5	2x	3x	1.487	Sexual	1890	1550	18	6	44.2721	6.2117
124.86.2.0	*Tragopogon crocifolius*	France. O. Hidalgo 518 & J. Pellicer	5	2x	3x	1.508	Sexual	—	910	12	5	—	—
124.86.3.0	*Tragopogon dubius*	France. L. Pegoraro et al. - FR722	5	2x	3x	1.489	Sexual	919	910	12*	5	44.5965	6.5232
124.86.4.0	*Tragopogon pratensis*	France. L. Pegoraro et al. - FR112	5	2x	3x	1.487	Sexual	1985	910	12*	5	44.3793	6.3955
124.86.4.0	*Tragopogon pratensis*	France. L. Pegoraro et al. - FR209	5	2x	3x	1.540	Sexual	1772	910	12*	5	44.2847	6.4317
124.86.4.0	*Tragopogon pratensis*	France. L. Pegoraro et al. - FR316	5	2x	3x	1.501	Sexual	1980	910	12*	5	44.2608	6.2087
124.86.4.0	*Tragopogon pratensis*	France. L. Pegoraro et al. - FR326	5	2x	3x	1.562	Sexual	1890	910	12*	5	44.2608	6.2088
124.86.4.0	*Tragopogon pratensis*	France. L. Pegoraro et al. - FR60	5	2x	3x	1.495	Sexual	—	910	12*	5	—	—
124.86.4.3	*Tragopogon pratensis* subsp. *orientalis*	Slovenia. M. Balant 58	5	2x	3x	1.543	Sexual	—	910	12	5	—	—
124.32.2.0	*Tripleurospermum inodorum*	France. L. Pegoraro et al. - FR400	5	4x	6x	1.562	Sexual	757	1050	36	6	44.5673	6.1023
124.32.2.0	*Tripleurospermum inodorum*	France. L. Pegoraro et al. - FR573	5	4x	6x	1.502	Sexual	1596	1050	36	6	45.0431	6.3318
124.32.2.0	*Tripleurospermum inodorum*	France. L. Pegoraro et al. - FR623	5	4x	6x	1.477	Sexual	—	1050	36	6	—	—
124.41.1.0	*Tussilago farfara*	France. L. Pegoraro et al. - FR709	5	6x	9x	1.578	Sexual	1581	1250	60	2	44.3473	6.2924
124.81.1.0	*Urospermum dalechampii*	Spain. J. Pellicer. Hostalets de Pierola. Spain. 2017	5	2x	3x	1.500	Sexual	—	583	14*	5	—	—
124.81.1.0	*Urospermum dalechampii*	Spain. O. Hidalgo 283	5	2x	3x	1.524	Sexual	—	583	14*	5	—	—
124.81.2.0	*Urospermum picroides*	Spain. O. Hidalgo 284	5	2x	3x	1.523	Sexual	—	350	10*	5	—	—
124.27.2.0	*Xanthium orientale* subsp. *italicum*	Italy. L. Pegoraro et al. - IT81	5	4x	6x	1.583	Sexual	345	350	36	7	45.8459	8.8902
124.27.2.0	*Xanthium orientale* subsp. *italicum*	Italy. L. Pegoraro et al. - IT73	5	4x	6x	1.525	Sexual	—	350	36	7	—	—
124.53.1.0	*Xeranthemum annuum*	Switzerland. L. Pegoraro et al. - CH161	5	2x	3x	1.640	Sexual	920	350	12	6	46.2674	7.3987

Table A.1: Data table for Chapter 2 with sample origin, collection details and reproductive modes inferred

ID FloraAlpina	Species	Collection ID	Seed number	Embryo ploidy	Endo-sperm ploidy	Ratio embryo/ endosperm	Reproductive mode	Field collected elevation	Average elevation preference	2n	Flowering initia-tion (month)	Latitude N	Longitude E
124.20.2.0	*Xerolekia speciosissima*	Italy. L. Pegoraro et al. - IT98	5	2x	3x	1.584	Sexual	801	1050	20	6	46.0072	9.2259

A.3 Additional model results for Chapter 2

Hereby are included results of modelling using apomixis type by genus, from: "Hojsgaard D, Klatt S, Baier R, Carman JG, Hörandl E. (2014) Taxonomy and biogeography of apomixis in angiosperms and associated biodiversity characteristics. *Critical Reviews in Plant Sciences* 33: 414-427", and available online: https://www.uni-goettingen.de/en/433689.html

Table A.2: Relative abundance of apomixis type per ploidy level in the dataset presented (extended version). Note that all triploids are diplosporous apomicts.

	Ploidy			
Apomixis type	*2x*	*3x*	*4x*	*> 4x*
Sexual	117	0	42	10
Aposporous	18	0	3	0
Apo-diplosporous	9	0	2	2
Diplosporous	1	17	2	0
Uncertain	7	0	2	6

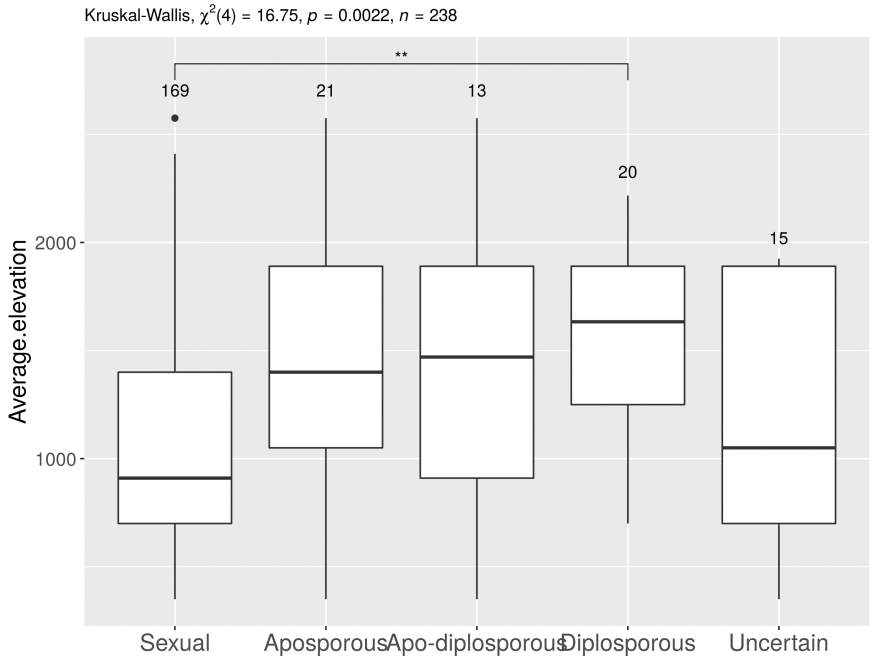


Figure A.3: Boxplot showing the distribution of elevation (m) for each type of apomixis. The result of Kruskal-Wallis one-way analysis of variance test is shown at the top of the plot; significant differences among groups are plotted, and coded as follows: p≤0.0001 = ****; p≤0.001 = ***; p≤0.01 = **; p≤0.05 = *; "ns" = p>0.05. Sample sizes for each group are reported above the corresponding box.

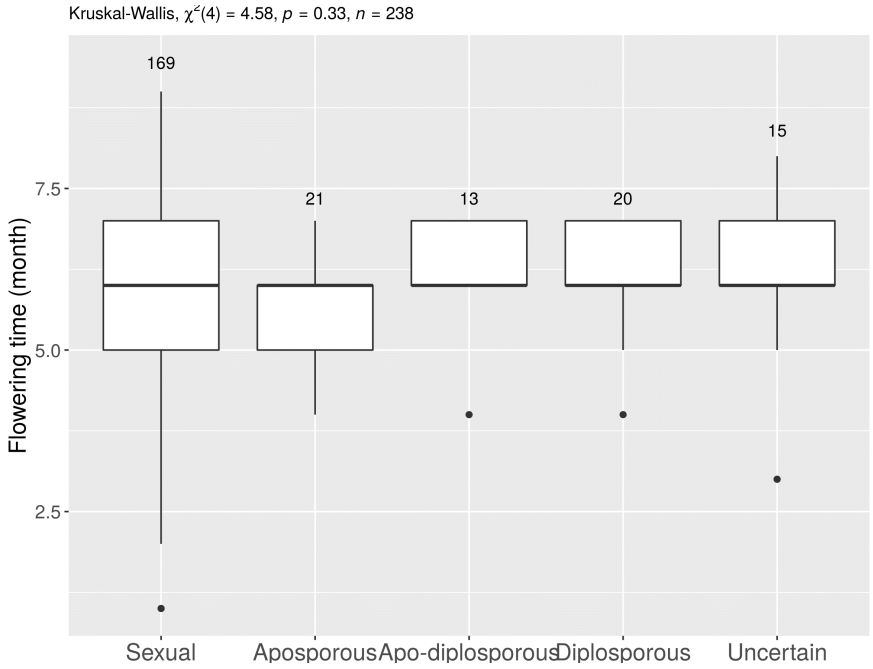


Figure A.4: Boxplot showing the distribution of flowering initiation time (month) for each type of apomixis. The result of Kruskal-Wallis one-way analysis of variance test is shown at the top of the plot; there are no significant differences among groups. Sample sizes for each group are reported above the corresponding box.

Table A.3: pMCMCglmm models outputs for the 'Extended' and 'Strictly Alps' datasets, using a categorical multilevel response model and a close to flat prior, chains run for 10^7 iterations, $5 * 10^5$ burn-in. For additional details see Supplementary A.4. Statistical significance is coded as follows: p≤0.001 = ∗∗∗; p≤0.01 = ∗∗; p≤0.05 = ∗. Please note that factor level "Uncertain" has been filtered out from the response variable, and tree pruned accordingly.

Extended	**post.mean**	**l-95% CI**	**u-95% CI**	**eff.samp**	**pMCMC**	
Apo-diplosporous:Elevation	0.00047	-0.00035	0.00132	16362	0.260	
Aposporous:Elevation	0.00067	-0.00017	0.00152	16543	0.110	
Diplosporous:Elevation	0.00043	-0.00041	0.00129	18043	0.314	
Apo-diplosporous:Flowering initiation	-0.32693	-0.74503	0.07769	16208	0.120	
Aposporous:Flowering initiation	-0.46790	-0.87890	-0.05135	14889	0.027	*
Diplosporous:Flowering initiation	-0.26469	-0.67265	0.15229	17577	0.210	
Apo-diplosporous:Ploidy 2x	-1.08367	-2.48261	0.33088	15454	0.130	
Aposporous:Ploidy 2x	-0.35868	-1.74339	1.14390	7570	0.623	
Diplosporous:Ploidy 2x	-1.46461	-2.87650	-0.01117	17781	0.045	*
Apo-diplosporous:Ploidy 3x	-0.76487	-2.99554	1.34410	2002	0.498	
Aposporous:Ploidy 3x	-0.98006	-3.26050	1.30719	1777	0.411	
Diplosporous:Ploidy 3x	2.91005	1.07117	4.77380	10505	0.002	**
Apo-diplosporous:Ploidy 4x	-0.77210	-2.26829	0.58664	14944	0.286	
Aposporous:Ploidy 4x	-0.14252	-1.63443	1.28913	7011	0.845	
Diplosporous:Ploidy 4x	-1.07481	-2.56251	0.36343	17069	0.151	
Apo-diplosporous:Ploidy >4x	0.61013	-1.34195	2.56856	2931	0.540	
Aposporous:Ploidy >4x	-0.91728	-3.29927	1.37467	1704	0.452	
Diplosporous:Ploidy >4x	-0.38240	-2.46916	1.69347	7949	0.729	
Strictly Alps	**post.mean**	**l-95% CI**	**u-95% CI**	**eff.samp**	**pMCMC**	
Apo-diplosporous:Elevation	0.00010	-0.00059	0.00077	17066	0.761	
Aposporous:Elevation	0.00023	-0.00046	0.00091	14231	0.493	
Diplosporous:Elevation	0.00005	-0.00064	0.00072	18057	0.885	
Apo-diplosporous:Flowering initiation	-0.46590	-0.98380	0.03705	16784	0.069	.

Table A.3: pMCMCglmm models outputs for categorical multilevel response model.

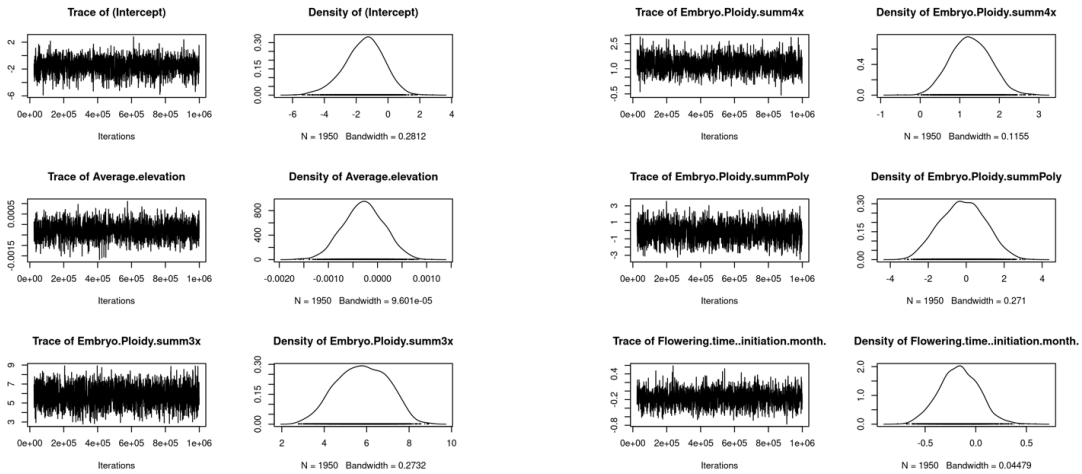
	post.mean	l-95% CI	u-95% CI	eff.samp	pMCMC	
Aposporous:Flowering initiation	-0.62090	-1.14800	-0.11060	14104	0.021	*
Diplosporous:Flowering initiation	-0.38110	-0.89050	0.12150	18543	0.136	
Apo-diplosporous:Ploidy 2x	-0.96780	-2.51900	0.57630	13553	0.215	
Aposporous:Ploidy 2x	-0.07315	-1.65600	1.56600	9237	0.927	
Diplosporous:Ploidy 2x	-1.48200	-3.04500	0.01853	16967	0.054	.
Apo-diplosporous:Ploidy 3x	-0.84220	-3.09700	1.25900	3279	0.439	
Aposporous:Ploidy 3x	-0.96320	-3.32700	1.31500	2799	0.416	
Diplosporous:Ploidy 3x	2.63600	0.77790	4.52800	11279	0.006	**
Apo-diplosporous:Ploidy 4x	-0.56550	-2.14300	0.99610	15181	0.479	
Aposporous:Ploidy 4x	0.13920	-1.48400	1.80800	10138	0.879	
Diplosporous:Ploidy 4x	-0.94800	-2.55500	0.61140	17644	0.243	
Apo-diplosporous:Ploidy >4x	0.52460	-1.56700	2.41200	6297	0.597	
Aposporous:Ploidy >4x	-0.94780	-3.30300	1.37200	4236	0.438	
Diplosporous:Ploidy >4x	-0.54970	-2.61900	1.52100	9507	0.613	

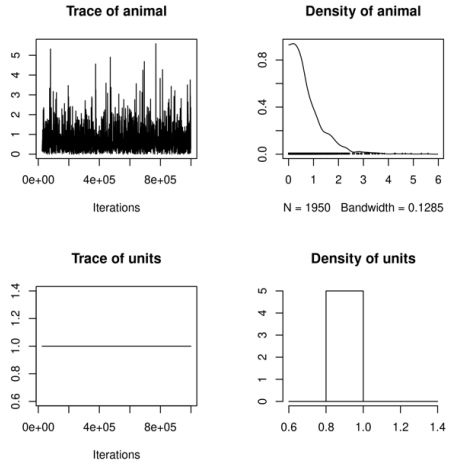
A.4 Model diagnostics for Chapter 2

Analyses have been run with R v3.6.1 and MCMCglmm v2.29. Only analysis for the 'Extended' dataset is reported.

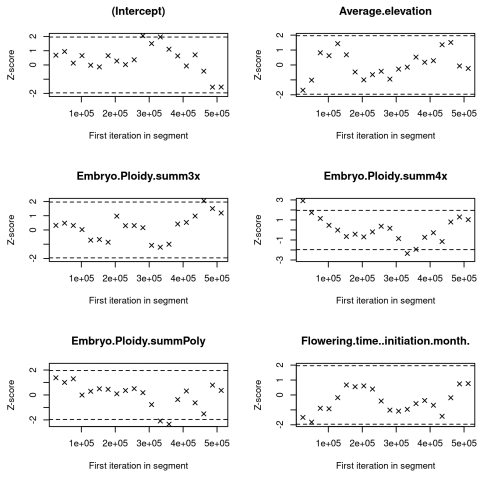
```
### THRESHOLD MODELS, RESPONSE VARIABLE WITH TWO LEVELS (SEXUAL VS APOMICTIC)

> prior_nu1000_1 <- list(R = list(V = 1, fix = 1), G = list(G1 = list(V = 1,
+     nu = 1000, alpha.mu = 0, alpha.V = 1)))

> set.seed(111)

> ext_mThre1.1 <- MCMCglmm(Reproductive.mode ~ Average.elevation +
+     Embryo.Ploidy.summ + Flowering.time..initiation.month.,
+     ginverse = list(species = invJanTree4_CC_online_tips$Ainv),
+     random = ~species, verbose = F, data = Online_v7_mean, family = "threshold",
+     trunc = T, prior = prior_nu1000_1, nitt = 10^6, thin = 500,
+     burnin = 25000)

> summary(ext_mThre1.1)

 Iterations = 25001:999501
 Thinning interval  = 500
 Sample size  = 1950

 DIC: 53.03027

 G-structure:  ~species

       post.mean l-95% CI u-95% CI eff.samp
species     0.733 3.01e-06     1.99     1476

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units         1        1        1        0

 Location effects: Reproductive.mode ~ Average.elevation + Embryo.Ploidy.summ +
```

```
 Flowering.time..initiation.month.

                                 post.mean   l-95% CI   u-95% CI eff.samp
(Intercept)                     -1.5064773 -3.8566343  0.9496854     2127
Average.elevation               -0.0002845 -0.0010781  0.0005044     1950
Embryo.Ploidy.summ3x             5.7873934  3.5876817  7.8550764     1950
Embryo.Ploidy.summ4x             1.2703863  0.3135906  2.1844798     1950
Embryo.Ploidy.summPoly          -0.1785097 -2.3864628  2.0397629     1730
Flowering.time..initiation.month. -0.1646853 -0.5822388  0.1683845     1950
                                 pMCMC
(Intercept)                     0.1918
Average.elevation               0.4944
Embryo.Ploidy.summ3x            <5e-04 ***
Embryo.Ploidy.summ4x            0.0041 **
Embryo.Ploidy.summPoly          0.8903
Flowering.time..initiation.month. 0.3949
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> plot(ext_mThre1.1, ask = F)
```





```
> heidel.diag(ext_mThre1.1$VCV)

       Stationarity start     p-value
       test         iteration
species passed        1        0.726
units  failed       NA           NA

       Halfwidth Mean  Halfwidth
       test
species passed    0.733 0.0343
units  <NA>         NA     NA

> heidel.diag(ext_mThre1.1$Sol)

                                Stationarity start     p-value
                                test         iteration
(Intercept)                     passed       1         0.441
Average.elevation               passed       1         0.554
Embryo.Ploidy.summ3x            passed       1         0.962
Embryo.Ploidy.summ4x            passed       1         0.232
Embryo.Ploidy.summPoly          passed       1         0.580
Flowering.time..initiation.month. passed     1         0.591

                                Halfwidth Mean      Halfwidth
                                test
(Intercept)                     passed    -1.506477 5.21e-02
Average.elevation               passed    -0.000285 1.83e-05
Embryo.Ploidy.summ3x            passed     5.787393 5.21e-02
Embryo.Ploidy.summ4x            passed     1.270386 2.20e-02
Embryo.Ploidy.summPoly          failed    -0.178510 5.48e-02
Flowering.time..initiation.month. passed  -0.164685 8.53e-03

> geweke.plot(ext_mThre1.1$Sol, ask = F)
```

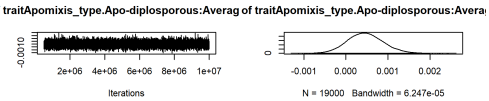


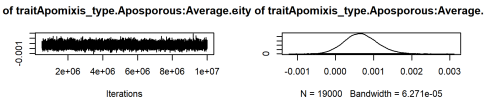

```
> autocorr.diag(ext_mThre1.1$Sol)

          (Intercept) Average.elevation Embryo.Ploidy.summ3x
Lag 0      1.000000000      1.0000000000          1.000000000
Lag 500   -0.043694371     -0.0025576579         -0.011721764
Lag 2500   0.030515827     -0.0002326107         -0.022908994
Lag 5000  -0.008904911     -0.0409927346          0.003905725
```

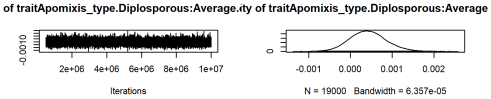
```
Lag 25000  0.006476335     -0.0059811204         -0.006633324
          Embryo.Ploidy.summ4x Embryo.Ploidy.summPoly
Lag 0              1.0000000000            1.000000000
Lag 500            0.0204273627            0.004727545
Lag 2500           0.0050215832            0.011628486
Lag 5000          -0.0119404306            0.014039114
Lag 25000          0.0001540036           -0.015943314
          Flowering.time..initiation.month.
Lag 0                              1.00000000
Lag 500                           -0.01468169
Lag 2500                           0.04171433
Lag 5000                          -0.04002078
Lag 25000                          0.02322205

#####
### Model runs with set.seed(534) and set.seed(386) are not shown
#####

> chainListTre2_Sol <- mcmc.list(ext_mThre1.1$Sol, ext_mThre2.1$Sol,
+     ext_mThre3.1$Sol)

> chainListTre2_VCV <- mcmc.list(ext_mThre1.1$VCV, ext_mThre2.1$VCV,
+     ext_mThre3.1$VCV)

> gelman.diag(chainListTre2_Sol)
Potential scale reduction factors:

                                  Point est. Upper C.I.
(Intercept)                                1       1.01
Average.elevation                          1       1.00
Embryo.Ploidy.summ3x                       1       1.00
Embryo.Ploidy.summ4x                       1       1.00
Embryo.Ploidy.summPoly                     1       1.00
Flowering.time..initiation.month.          1       1.01

Multivariate psrf

1

> gelman.diag(chainListTre2_Sol)
Potential scale reduction factors:

                                  Point est. Upper C.I.
(Intercept)                                1       1.01
Average.elevation                          1       1.00
Embryo.Ploidy.summ3x                       1       1.00
Embryo.Ploidy.summ4x                       1       1.00
Embryo.Ploidy.summPoly                     1       1.00
Flowering.time..initiation.month.          1       1.01

Multivariate psrf

1

##### ~ #####


### CATEGORICAL MODELS, MULTILEVEL RESPONSE VARIABLE (APOMIXIS TYPE)
### NOTE: Only analysis for the extended dataset is reported.
```

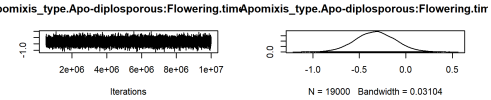
```
> levels(Online_v7_mean_ApomixisType_red4$Apomixis_type)
[1] "Sexual"           "Apo-diplosporous" "Aposporous"       "Diplosporous"

> j = 3 # dimensionality of the matrix, number of response variable levels - 1
> IJ <- (1/(j + 1)) * (diag(j) + matrix(1, j, j))
> k = 6 # number of fixed effects to estimate (including separate levels of categorical variables)
> prior_flat <- list(R = list(V = IJ, fix = 1),
+                    G = list(G1 = list(V = 1, nu = 1000, alpha.mu = 0, alpha.V = 1)),
+                    B = list(mu = rep(0, j*k), V = kronecker(IJ, diag(k)) * (1.7 + pi^2/3))
+ )

### For "close to flat" prior specifications see J. Hadfield's MCMCglmm course
### notes pp 97-99 (available in the R package support page)
> mCat_1_red4 <- MCMCglmm(Apomixis_type ~ trait:Average.elevation +
trait:Flowering.time..initiation.month. + trait:at.level(Ploidy_summ, "2x") +
trait:at.level(Ploidy_summ, "3x") + trait:at.level(Ploidy_summ, "4x") +
trait:at.level(Ploidy_summ, "Poly") - 1,
+                         ginverse = list(animal = invJanTree4_CC_red4$Ainv), random = ~animal,
+                         rcov = ~us(trait):units,
+                         verbose = T,
+                         data = Online_v7_mean_ApomixisType_red4,
+                         family = "categorical",
+                         trunc = T,
+                         prior = prior_flat,
+                         nitt = 10^7, thin = 500, burnin = 5*10^5)

> summary(mCat_1_red4)

 Iterations = 500001:9999501
 Thinning interval  = 500
 Sample size  = 19000

 DIC: 158.3556

 G-structure:  ~animal

       post.mean l-95% CI u-95% CI eff.samp
animal     18.28    10.62     26.1     6055

 R-structure:  ~us(trait):units
                                                                                post.mean l-95% CI u-95% CI
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Apo-diplosporous.units      0.50     0.50     0.50
traitApomixis_type.Aposporous:traitApomixis_type.Apo-diplosporous.units            0.25     0.25     0.25
traitApomixis_type.Diplosporous:traitApomixis_type.Apo-diplosporous.units          0.25     0.25     0.25
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Aposporous.units            0.25     0.25     0.25
traitApomixis_type.Aposporous:traitApomixis_type.Aposporous.units                  0.50     0.50     0.50
traitApomixis_type.Diplosporous:traitApomixis_type.Aposporous.units                0.25     0.25     0.25
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Diplosporous.units          0.25     0.25     0.25
traitApomixis_type.Aposporous:traitApomixis_type.Diplosporous.units                0.25     0.25     0.25
traitApomixis_type.Diplosporous:traitApomixis_type.Diplosporous.units              0.50     0.50     0.50
                                                                               eff.samp
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Apo-diplosporous.units        0
traitApomixis_type.Aposporous:traitApomixis_type.Apo-diplosporous.units              0
traitApomixis_type.Diplosporous:traitApomixis_type.Apo-diplosporous.units            0
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Aposporous.units              0
traitApomixis_type.Aposporous:traitApomixis_type.Aposporous.units                    0
traitApomixis_type.Diplosporous:traitApomixis_type.Aposporous.units                  0
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Diplosporous.units            0
```

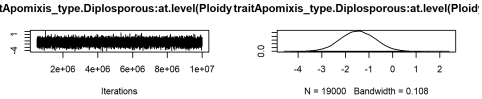
```
traitApomixis_type.Aposporous:traitApomixis_type.Diplosporous.units                  0
traitApomixis_type.Diplosporous:traitApomixis_type.Diplosporous.units                0

 Location effects: Apomixis_type ~ trait:Average.elevation + trait:Flowering.time..initiation.month. +
 trait:at.level(Ploidy_summ, "2x") + trait:at.level(Ploidy_summ, "3x") +
 trait:at.level(Ploidy_summ, "4x") + trait:at.level(Ploidy_summ, "Poly") - 1

                                                          post.mean   l-95% CI   u-95% CI
traitApomixis_type.Apo-diplosporous:Average.elevation                 0.0004674 -0.0003461  0.0013195
traitApomixis_type.Aposporous:Average.elevation                       0.0006690 -0.0001711  0.0015221
traitApomixis_type.Diplosporous:Average.elevation                     0.0004275 -0.0004065  0.0012920
traitApomixis_type.Apo-diplosporous:Flowering.time..initiation.month. -0.3269335 -0.7450290  0.0776892
traitApomixis_type.Aposporous:Flowering.time..initiation.month.       -0.4679027 -0.8789015 -0.0513462
traitApomixis_type.Diplosporous:Flowering.time..initiation.month.     -0.2646854 -0.6726530  0.1522905
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "2x")       -1.0836716 -2.4826099  0.3308832
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "2x")             -0.3586824 -1.7433909  1.1439000
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "2x")           -1.4646143 -2.8764973 -0.0111689
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "3x")       -0.7648735 -2.9955411  1.3441039
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "3x")             -0.9800572 -3.2604999  1.3071868
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "3x")            2.9100519  1.0711726  4.7737982
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "4x")       -0.7720982 -2.2682855  0.5866411
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "4x")             -0.1425245 -1.6344265  1.2891262
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "4x")           -1.0748113 -2.5625106  0.3634313
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "Poly")      0.6101276 -1.3419534  2.5685591
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "Poly")           -0.9172771 -3.2992714  1.3746723
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "Poly")         -0.3823971 -2.4691645  1.6934720
                                                         eff.samp   pMCMC
traitApomixis_type.Apo-diplosporous:Average.elevation       16362 0.26032
traitApomixis_type.Aposporous:Average.elevation             16543 0.11011
traitApomixis_type.Diplosporous:Average.elevation           18043 0.31421
traitApomixis_type.Apo-diplosporous:Flowering.time..initiation.month.    16208 0.11958
traitApomixis_type.Aposporous:Flowering.time..initiation.month.          14889 0.02747 *
traitApomixis_type.Diplosporous:Flowering.time..initiation.month.        17577 0.20979
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "2x")          15454 0.12968
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "2x")                 7570 0.62337
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "2x")              17781 0.04547 *
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "3x")           2002 0.49821
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "3x")                 1777 0.41147
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "3x")              10505 0.00158 **
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "4x")          14944 0.28600
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "4x")                 7011 0.84526
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "4x")              17069 0.15105
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "Poly")         2931 0.53958
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "Poly")               1704 0.45211
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "Poly")             7949 0.72905
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> plot(mCat_1_red4, ask = T)
```

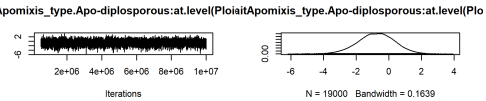

of traitApomixis_type.Apo-diplosporous:Averag
of traitApomixis_type.Apo-diplosporous:Avera
Iterations
N = 19000 Bandwidth = 6.247e-05

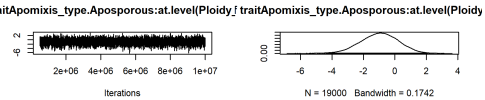

e of traitApomixis_type.Aposporous:Average.
eity of traitApomixis_type.Aposporous:Average.
Iterations
N = 19000 Bandwidth = 6.271e-05

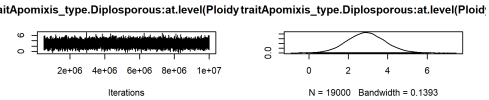

e of traitApomixis_type.Diplosporous:Average.
ty of traitApomixis_type.Diplosporous:Average
Iterations
N = 19000 Bandwidth = 6.357e-05

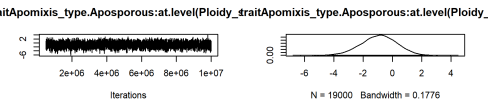

pomixis_type.Apo-diplosporous:Flowering.tim
Apomixis_type.Apo-diplosporous:Flowering.tim
Iterations
N = 19000 Bandwidth = 0.03104

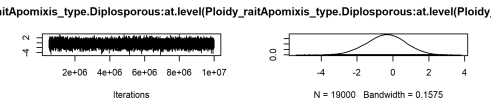

raitApomixis_type.Diplosporous:at.level(Ploidy
traitApomixis_type.Diplosporous:at.level(Ploid
Iterations
N = 19000 Bandwidth = 0.108

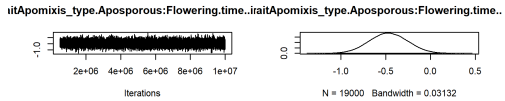

itApomixis_type.Apo-diplosporous:at.level(PloiaitApomixis_type.Apo-diplosporous:at.level(Plo
Iterations
N = 19000 Bandwidth = 0.1639

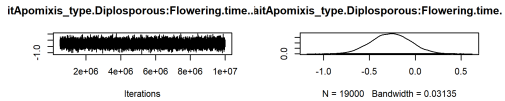

traitApomixis_type.Aposporous:at.level(Ploidy_f
traitApomixis_type.Aposporous:at.level(Ploidy
Iterations
N = 19000 Bandwidth = 0.1742

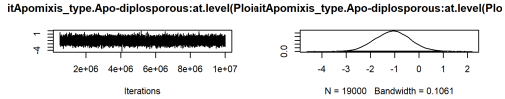

raitApomixis_type.Diplosporous:at.level(Ploidy
traitApomixis_type.Diplosporous:at.level(Ploid
Iterations
N = 19000 Bandwidth = 0.1393

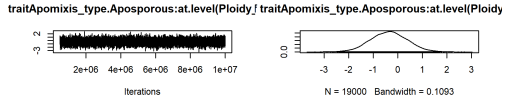

raitApomixis_type.Aposporous:at.level(Ploidy_f
traitApomixis_type.Aposporous:at.level(Ploidy_
Iterations
N = 19000 Bandwidth = 0.1776

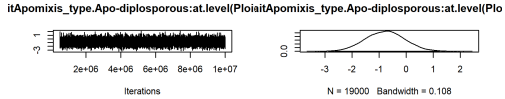

aitApomixis_type.Diplosporous:at.level(Ploidy_f
raitApomixis_type.Diplosporous:at.level(Ploidy_
Iterations
N = 19000 Bandwidth = 0.1575

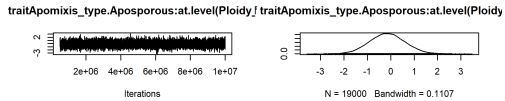

itApomixis_type.Aposporous:Flowering.time..
iraitApomixis_type.Aposporous:Flowering.time..
Iterations
N = 19000 Bandwidth = 0.03132

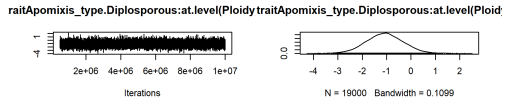

itApomixis_type.Diplosporous:Flowering.time..
aitApomixis_type.Diplosporous:Flowering.time.
Iterations
N = 19000 Bandwidth = 0.03135

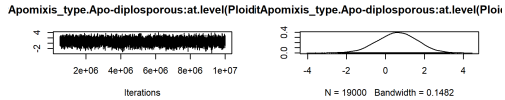

itApomixis_type.Apo-diplosporous:at.level(Ploi
aitApomixis_type.Apo-diplosporous:at.level(Plo
Iterations
N = 19000 Bandwidth = 0.1061

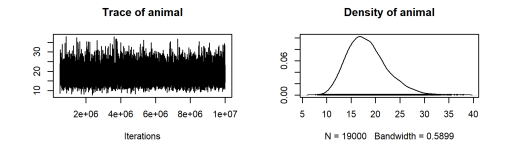

traitApomixis_type.Aposporous:at.level(Ploidy_f
traitApomixis_type.Aposporous:at.level(Ploidy
Iterations
N = 19000 Bandwidth = 0.1093

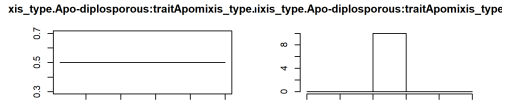

itApomixis_type.Apo-diplosporous:at.level(Ploi
aitApomixis_type.Apo-diplosporous:at.level(Plo
Iterations
N = 19000 Bandwidth = 0.108

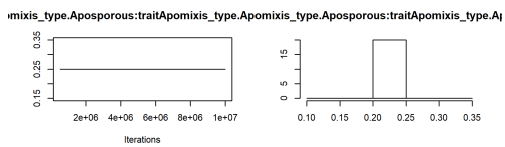

traitApomixis_type.Aposporous:at.level(Ploidy_f
traitApomixis_type.Aposporous:at.level(Ploidy
Iterations
N = 19000 Bandwidth = 0.1107

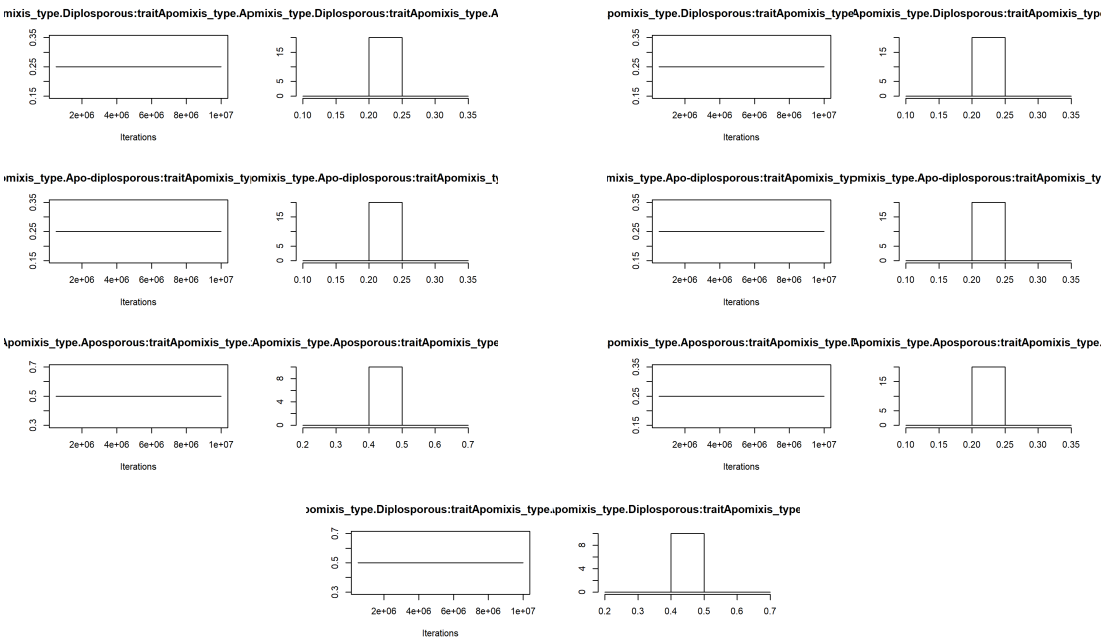

raitApomixis_type.Diplosporous:at.level(Ploidy
traitApomixis_type.Diplosporous:at.level(Ploid
Iterations
N = 19000 Bandwidth = 0.1099


Apomixis_type.Apo-diplosporous:at.level(PloiditApomixis_type.Apo-diplosporous:at.level(Ploi
Iterations
N = 19000 Bandwidth = 0.1482


Trace of animal
Density of animal
Iterations
N = 19000 Bandwidth = 0.5899


xis_type.Apo-diplosporous:traitApomixis_type.i
ixis_type.Apo-diplosporous:traitApomixis_type
Iterations


mixis_type.Aposporous:traitApomixis_type.Apomixis_type.Aposporous:traitApomixis_type.Ap
Iterations




```
> heidel.diag(mCat_1$VCV)
                                                                                Stationarity start
                                                                                test         iteration
animal                                                                          passed        1
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Apo-diplosporous.units failed       NA
traitApomixis_type.Aposporous:traitApomixis_type.Apo-diplosporous.units       failed       NA
traitApomixis_type.Diplosporous:traitApomixis_type.Apo-diplosporous.units     failed       NA
traitApomixis_type.Uncertain:traitApomixis_type.Apo-diplosporous.units        failed       NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Aposporous.units       failed       NA
traitApomixis_type.Aposporous:traitApomixis_type.Aposporous.units             failed       NA
traitApomixis_type.Diplosporous:traitApomixis_type.Aposporous.units           failed       NA
traitApomixis_type.Uncertain:traitApomixis_type.Aposporous.units              failed       NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Diplosporous.units     failed       NA
traitApomixis_type.Aposporous:traitApomixis_type.Diplosporous.units           failed       NA
traitApomixis_type.Diplosporous:traitApomixis_type.Diplosporous.units         failed       NA
traitApomixis_type.Uncertain:traitApomixis_type.Diplosporous.units            failed       NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Uncertain.units        failed       NA
traitApomixis_type.Aposporous:traitApomixis_type.Uncertain.units              failed       NA
traitApomixis_type.Diplosporous:traitApomixis_type.Uncertain.units            failed       NA
traitApomixis_type.Uncertain:traitApomixis_type.Uncertain.units               failed       NA

                                                                                p-value
animal                                                                          0.914
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Apo-diplosporous.units    NA
traitApomixis_type.Aposporous:traitApomixis_type.Apo-diplosporous.units          NA
traitApomixis_type.Diplosporous:traitApomixis_type.Apo-diplosporous.units        NA
traitApomixis_type.Uncertain:traitApomixis_type.Apo-diplosporous.units           NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Aposporous.units          NA
traitApomixis_type.Aposporous:traitApomixis_type.Aposporous.units                NA
traitApomixis_type.Diplosporous:traitApomixis_type.Aposporous.units              NA
traitApomixis_type.Uncertain:traitApomixis_type.Aposporous.units                 NA
```

```
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Diplosporous.units        NA
traitApomixis_type.Aposporous:traitApomixis_type.Diplosporous.units              NA
traitApomixis_type.Diplosporous:traitApomixis_type.Diplosporous.units            NA
traitApomixis_type.Uncertain:traitApomixis_type.Diplosporous.units               NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Uncertain.units           NA
traitApomixis_type.Aposporous:traitApomixis_type.Uncertain.units                 NA
traitApomixis_type.Diplosporous:traitApomixis_type.Uncertain.units               NA
traitApomixis_type.Uncertain:traitApomixis_type.Uncertain.units                  NA
```

	Halfwidth test	Mean	Halfwidth
animal	passed	17	0.1
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Apo-diplosporous.units	<NA>	NA	NA
traitApomixis_type.Aposporous:traitApomixis_type.Apo-diplosporous.units	<NA>	NA	NA
traitApomixis_type.Diplosporous:traitApomixis_type.Apo-diplosporous.units	<NA>	NA	NA
traitApomixis_type.Uncertain:traitApomixis_type.Apo-diplosporous.units	<NA>	NA	NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Aposporous.units	<NA>	NA	NA
traitApomixis_type.Aposporous:traitApomixis_type.Aposporous.units	<NA>	NA	NA
traitApomixis_type.Diplosporous:traitApomixis_type.Aposporous.units	<NA>	NA	NA
traitApomixis_type.Uncertain:traitApomixis_type.Aposporous.units	<NA>	NA	NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Diplosporous.units	<NA>	NA	NA
traitApomixis_type.Aposporous:traitApomixis_type.Diplosporous.units	<NA>	NA	NA
traitApomixis_type.Diplosporous:traitApomixis_type.Diplosporous.units	<NA>	NA	NA
traitApomixis_type.Uncertain:traitApomixis_type.Diplosporous.units	<NA>	NA	NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Uncertain.units	<NA>	NA	NA
traitApomixis_type.Aposporous:traitApomixis_type.Uncertain.units	<NA>	NA	NA
traitApomixis_type.Diplosporous:traitApomixis_type.Uncertain.units	<NA>	NA	NA
traitApomixis_type.Uncertain:traitApomixis_type.Uncertain.units	<NA>	NA	NA

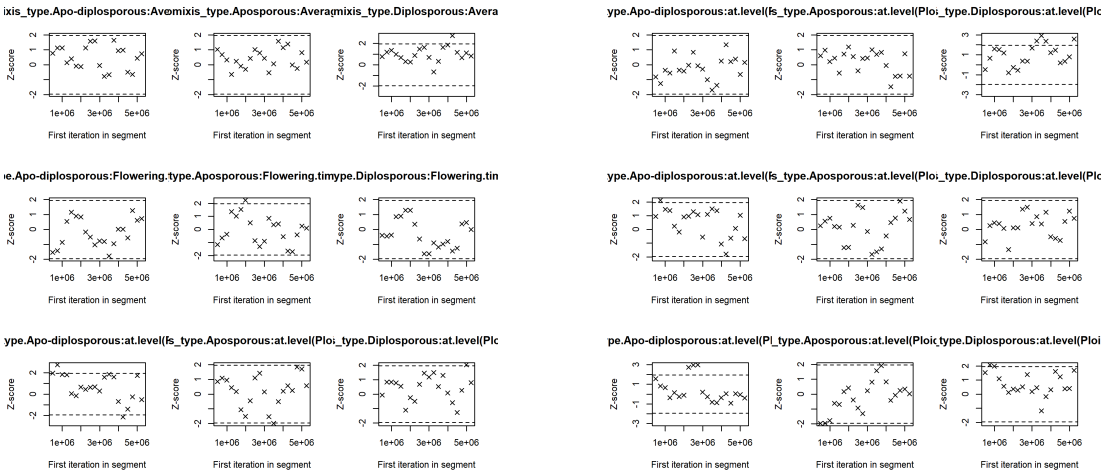
```
> heidel.diag(mCat_1$Sol)
```

	Stationarity test	start iteration	p-value
traitApomixis_type.Apo-diplosporous:Average.elevation	passed	1	0.683
traitApomixis_type.Aposporous:Average.elevation	passed	1	0.472
traitApomixis_type.Diplosporous:Average.elevation	passed	1	0.458
traitApomixis_type.Uncertain:Average.elevation	passed	1	0.470
traitApomixis_type.Apo-diplosporous:Flowering.time..initiation.month.	passed	1	0.653
traitApomixis_type.Aposporous:Flowering.time..initiation.month.	passed	1	0.609
traitApomixis_type.Diplosporous:Flowering.time..initiation.month.	passed	1	0.835
traitApomixis_type.Uncertain:Flowering.time..initiation.month.	passed	1	0.145
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "2x")	passed	1	0.594
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "2x")	passed	1	0.190
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "2x")	passed	1	0.647
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "2x")	passed	1	0.362
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "3x")	passed	1	0.401
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "3x")	passed	1	0.857
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "3x")	passed	7601	0.163
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "3x")	passed	1	0.271
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "4x")	passed	1	0.520
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "4x")	passed	1	0.142
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "4x")	passed	1	0.904
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "4x")	passed	1	0.375
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "Poly")	passed	1	0.803
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "Poly")	passed	1	0.087
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "Poly")	passed	5701	0.220
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "Poly")	passed	1	0.851

	Halfwidth test	Mean	Halfwidth
traitApomixis_type.Apo-diplosporous:Average.elevation	passed	0.000265	5.13e-06

```
traitApomixis_type.Aposporous:Average.elevation                          passed     0.000425 5.10e-06
traitApomixis_type.Diplosporous:Average.elevation                        passed     0.000234 4.98e-06
traitApomixis_type.Uncertain:Average.elevation                           passed     0.000239 5.06e-06
traitApomixis_type.Apo-diplosporous:Flowering.time..initiation.month.    passed    -0.337185 2.83e-03
traitApomixis_type.Aposporous:Flowering.time..initiation.month.          passed    -0.417900 3.02e-03
traitApomixis_type.Diplosporous:Flowering.time..initiation.month.        passed    -0.238360 2.63e-03
traitApomixis_type.Uncertain:Flowering.time..initiation.month.           passed    -0.301242 2.64e-03
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "2x")          passed    -0.509013 1.47e-02
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "2x")                failed    -0.131012 1.37e-02
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "2x")              passed    -1.129824 9.08e-03
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "2x")                 passed    -0.717390 1.05e-02
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "3x")          passed    -0.812746 5.62e-02
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "3x")                passed    -0.620993 4.26e-02
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "3x")              passed     2.956341 2.07e-02
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "3x")                 passed    -0.760299 5.27e-02
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "4x")          passed    -0.381313 1.26e-02
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "4x")                failed    -0.056862 1.30e-02
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "4x")              passed    -0.909731 9.10e-03
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "4x")                 passed    -0.555721 1.14e-02
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "Poly")        passed     0.570035 2.78e-02
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "Poly")              passed    -0.833973 4.16e-02
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "Poly")            passed    -1.251309 3.02e-02
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "Poly")               passed     1.359896 2.02e-02
```

```
> geweke.plot(mCat_1_red4$Sol, ask = T)
```




```
> heidel.diag(mCat_1$VCV)
```

```
                                                                         Stationarity start
                                                                         test         iteration
animal                                                                   passed        1
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Apo-diplosporous.units failed       NA
traitApomixis_type.Aposporous:traitApomixis_type.Apo-diplosporous.units       failed       NA
traitApomixis_type.Diplosporous:traitApomixis_type.Apo-diplosporous.units     failed       NA
traitApomixis_type.Uncertain:traitApomixis_type.Apo-diplosporous.units        failed       NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Aposporous.units       failed       NA
traitApomixis_type.Aposporous:traitApomixis_type.Aposporous.units             failed       NA
traitApomixis_type.Diplosporous:traitApomixis_type.Aposporous.units           failed       NA
traitApomixis_type.Uncertain:traitApomixis_type.Aposporous.units              failed       NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Diplosporous.units     failed       NA
traitApomixis_type.Aposporous:traitApomixis_type.Diplosporous.units           failed       NA
```

```
traitApomixis_type.Diplosporous:traitApomixis_type.Diplosporous.units         failed       NA
traitApomixis_type.Uncertain:traitApomixis_type.Diplosporous.units            failed       NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Uncertain.units        failed       NA
traitApomixis_type.Aposporous:traitApomixis_type.Uncertain.units              failed       NA
traitApomixis_type.Diplosporous:traitApomixis_type.Uncertain.units            failed       NA
traitApomixis_type.Uncertain:traitApomixis_type.Uncertain.units               failed       NA

                                                                              p-value
animal                                                                        0.914
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Apo-diplosporous.units    NA
traitApomixis_type.Aposporous:traitApomixis_type.Apo-diplosporous.units          NA
traitApomixis_type.Diplosporous:traitApomixis_type.Apo-diplosporous.units        NA
traitApomixis_type.Uncertain:traitApomixis_type.Apo-diplosporous.units           NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Aposporous.units          NA
traitApomixis_type.Aposporous:traitApomixis_type.Aposporous.units                NA
traitApomixis_type.Diplosporous:traitApomixis_type.Aposporous.units              NA
traitApomixis_type.Uncertain:traitApomixis_type.Aposporous.units                 NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Diplosporous.units        NA
traitApomixis_type.Aposporous:traitApomixis_type.Diplosporous.units              NA
traitApomixis_type.Diplosporous:traitApomixis_type.Diplosporous.units            NA
traitApomixis_type.Uncertain:traitApomixis_type.Diplosporous.units               NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Uncertain.units           NA
traitApomixis_type.Aposporous:traitApomixis_type.Uncertain.units                 NA
traitApomixis_type.Diplosporous:traitApomixis_type.Uncertain.units               NA
traitApomixis_type.Uncertain:traitApomixis_type.Uncertain.units                  NA

                                                                              Halfwidth Mean Halfwidth
                                                                              test
animal                                                                        passed    17   0.1
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Apo-diplosporous.units <NA>      NA    NA
traitApomixis_type.Aposporous:traitApomixis_type.Apo-diplosporous.units       <NA>      NA    NA
traitApomixis_type.Diplosporous:traitApomixis_type.Apo-diplosporous.units     <NA>      NA    NA
traitApomixis_type.Uncertain:traitApomixis_type.Apo-diplosporous.units        <NA>      NA    NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Aposporous.units       <NA>      NA    NA
traitApomixis_type.Aposporous:traitApomixis_type.Aposporous.units             <NA>      NA    NA
traitApomixis_type.Diplosporous:traitApomixis_type.Aposporous.units           <NA>      NA    NA
traitApomixis_type.Uncertain:traitApomixis_type.Aposporous.units              <NA>      NA    NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Diplosporous.units     <NA>      NA    NA
traitApomixis_type.Aposporous:traitApomixis_type.Diplosporous.units           <NA>      NA    NA
traitApomixis_type.Diplosporous:traitApomixis_type.Diplosporous.units         <NA>      NA    NA
traitApomixis_type.Uncertain:traitApomixis_type.Diplosporous.units            <NA>      NA    NA
traitApomixis_type.Apo-diplosporous:traitApomixis_type.Uncertain.units        <NA>      NA    NA
traitApomixis_type.Aposporous:traitApomixis_type.Uncertain.units              <NA>      NA    NA
traitApomixis_type.Diplosporous:traitApomixis_type.Uncertain.units            <NA>      NA    NA
traitApomixis_type.Uncertain:traitApomixis_type.Uncertain.units               <NA>      NA    NA
> heidel.diag(mCat_1$Sol)

                                                                              Stationarity start     p-value
                                                                              test         iteration
traitApomixis_type.Apo-diplosporous:Average.elevation                         passed          1      0.683
traitApomixis_type.Aposporous:Average.elevation                               passed          1      0.472
traitApomixis_type.Diplosporous:Average.elevation                             passed          1      0.458
traitApomixis_type.Uncertain:Average.elevation                                passed          1      0.470
traitApomixis_type.Apo-diplosporous:Flowering.time..initiation.month.         passed          1      0.653
traitApomixis_type.Aposporous:Flowering.time..initiation.month.               passed          1      0.609
traitApomixis_type.Diplosporous:Flowering.time..initiation.month.             passed          1      0.835
traitApomixis_type.Uncertain:Flowering.time..initiation.month.                passed          1      0.145
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "2x")               passed          1      0.594
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "2x")                     passed          1      0.190
```

```
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "2x")          passed          1      0.647
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "2x")             passed          1      0.362
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "3x")      passed          1      0.401
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "3x")            passed          1      0.857
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "3x")          passed       7601      0.163
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "3x")             passed          1      0.271
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "4x")      passed          1      0.520
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "4x")            passed          1      0.142
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "4x")          passed          1      0.904
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "4x")             passed          1      0.375
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "Poly")    passed          1      0.803
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "Poly")          passed          1      0.087
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "Poly")        passed       5701      0.220
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "Poly")           passed          1      0.851

                                                                     Halfwidth Mean      Halfwidth
                                                                     test
traitApomixis_type.Apo-diplosporous:Average.elevation                passed     0.000265 5.13e-06
traitApomixis_type.Aposporous:Average.elevation                      passed     0.000425 5.10e-06
traitApomixis_type.Diplosporous:Average.elevation                    passed     0.000234 4.98e-06
traitApomixis_type.Uncertain:Average.elevation                       passed     0.000239 5.06e-06
traitApomixis_type.Apo-diplosporous:Flowering.time..initiation.month. passed    -0.337185 2.83e-03
traitApomixis_type.Aposporous:Flowering.time..initiation.month.       passed    -0.417900 3.02e-03
traitApomixis_type.Diplosporous:Flowering.time..initiation.month.     passed    -0.238360 2.63e-03
traitApomixis_type.Uncertain:Flowering.time..initiation.month.        passed    -0.301242 2.64e-03
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "2x")      passed    -0.509013 1.47e-02
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "2x")            failed    -0.131012 1.37e-02
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "2x")          passed    -1.129824 9.08e-03
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "2x")             passed    -0.717390 1.05e-02
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "3x")      passed    -0.812746 5.62e-02
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "3x")            passed    -0.620993 4.26e-02
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "3x")          passed     2.956341 2.07e-02
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "3x")             passed    -0.760299 5.27e-02
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "4x")      passed    -0.381313 1.26e-02
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "4x")            failed    -0.056862 1.30e-02
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "4x")          passed    -0.909731 9.10e-03
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "4x")             passed    -0.555721 1.14e-02
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "Poly")    passed     0.570035 2.78e-02
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "Poly")          passed    -0.833973 4.16e-02
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "Poly")        passed    -1.251309 3.02e-02
traitApomixis_type.Uncertain:at.level(Ploidy_summ, "Poly")           passed     1.359896 2.02e-02


#####
### Model runs with set.seed(534) and set.seed(386) are not shown
#####

> chainListTre2_Sol <- mcmc.list(mCat_1_red4$Sol, mCat_2_red4$Sol, mCat_3_red4$Sol)
> chainListTre2_VCV <- mcmc.list(mCat_1_red4$VCV, mCat_2_red4$VCV, mCat_3_red4$VCV)

> gelman.diag(chainListTre2_Sol)

Potential scale reduction factors:

                                                                     Point est. Upper C.I.
traitApomixis_type.Apo-diplosporous:Average.elevation                      1.00       1.01
traitApomixis_type.Aposporous:Average.elevation                            1.01       1.02
traitApomixis_type.Diplosporous:Average.elevation                          1.00       1.01
traitApomixis_type.Apo-diplosporous:Flowering.time..initiation.month.      1.00       1.00
traitApomixis_type.Aposporous:Flowering.time..initiation.month.            1.00       1.01
```

```
traitApomixis_type.Diplosporous:Flowering.time..initiation.month.           1.00       1.00
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "2x")             1.00       1.00
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "2x")                   1.00       1.00
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "2x")                 1.00       1.00
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "3x")             1.00       1.00
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "3x")                   1.00       1.00
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "3x")                 1.00       1.00
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "4x")             1.00       1.00
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "4x")                   1.00       1.01
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "4x")                 1.00       1.00
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "Poly")           1.00       1.00
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "Poly")                 1.00       1.00
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "Poly")               1.00       1.00

Multivariate psrf

1.01
> gelman.diag(chainListTre2_Sol)
Potential scale reduction factors:
                                                                      Point est. Upper C.I.
traitApomixis_type.Apo-diplosporous:Average.elevation                       1.00       1.01
traitApomixis_type.Aposporous:Average.elevation                             1.01       1.02
traitApomixis_type.Diplosporous:Average.elevation                           1.00       1.01
traitApomixis_type.Apo-diplosporous:Flowering.time..initiation.month.       1.00       1.00
traitApomixis_type.Aposporous:Flowering.time..initiation.month.             1.00       1.01
traitApomixis_type.Diplosporous:Flowering.time..initiation.month.           1.00       1.00
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "2x")             1.00       1.00
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "2x")                   1.00       1.00
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "2x")                 1.00       1.00
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "3x")             1.00       1.00
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "3x")                   1.00       1.00
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "3x")                 1.00       1.00
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "4x")             1.00       1.00
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "4x")                   1.00       1.01
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "4x")                 1.00       1.00
traitApomixis_type.Apo-diplosporous:at.level(Ploidy_summ, "Poly")           1.00       1.00
traitApomixis_type.Aposporous:at.level(Ploidy_summ, "Poly")                 1.00       1.00
traitApomixis_type.Diplosporous:at.level(Ploidy_summ, "Poly")               1.00       1.00

Multivariate psrf

1.01

##### ~ #####
```

Appendix B

Chapter 3 supplementary material

B.1 Selection tables

Table B.1: Table illustrating which taxa have been selected to fill in data for subspecies not found in Flora Alpina (or where subspecies is not known). "ID_mod" is the modified Flora Alpina ID corresponding to the taxon, "Name_EuroMed" is the Euro+Med name adopted in the data, "ID_original" is the original Flora Alpina ID for the subspecies selected, "Name_FloraAlpina" is the original name in Flora Alpina.

ID_mod	**Name_EuroMed**	**ID_original**	**Name_FloraAlpina**
124.2.1.0	*Solidago virgaurea*	124.2.1.2	*Solidago virgaurea subsp. minuta*
124.30.4.0	*Anthemis arvensis*	124.30.4.1	*Anthemis arvensis subsp. arvensis*
124.31.11.0	*Achillea millefolium*	124.31.11.1	*Achillea millefolium subsp. millefolium*
124.31.19.0	*Achillea nobilis*	124.31.19.1	*Achillea nobilis subsp. nobilis*
124.31.9.1	*Achillea distans subsp. tanacetifolia*	124.31.9.0	*Achillea distans*
124.35.2.0	*Tanacetum corymbosum*	124.35.2.1	*Tanacetum corymbosum subsp. corymbosum*
124.39.2.0	*Leucanthemum adustum*	124.39.2.1	*Leucanthemum adustum subsp. adustum*
124.39.8.0	*Leucanthemum atratum*	124.39.8.3	*Leucanthemum coronopifolium*
124.40.19.0	*Artemisia campestris*	124.40.19.1	*Artemisia campestris subsp. campestris*
124.46.7.0	*Doronicum glaciale*	124.46.7.1	*Doronicum glaciale subsp. glaciale*
124.46.8.0	*Doronicum clusii*	124.46.8.2	*Doronicum clusii subsp. villosum*
124.48.14.0	*Senecio doronicum*	124.48.14.1	*Senecio doronicum subsp. doronicum*
124.48.2.0	*Jacobaea incana*	124.48.2.1	*Jacobaea incana subsp. incana*

Table B.1: Taxa selected to fill in data for subspecies not found in Flora Alpina

ID_mod	Name_EuroMed	ID_original	Name_FloraAlpina
124.48.6.0	*Senecio nemorensis subsp. jacquinianus*	124.48.6.1	*Senecio nemorensis subsp. jacquinianus*
124.48.8.0	*Senecio ovatus*	124.48.8.1	*Senecio ovatus subsp. ovatus*
124.52.4.0	*Carlina acaulis*	124.52.4.1	*Carlina acaulis subsp. acaulis*
124.54.3.1	*Echinops ritro subsp. ruthenicus*	124.54.3.0	*Echinops ritro*
124.56.3.0	*Arctium minus*	124.56.3.1	*Arctium minus subsp. minus*
124.57.2.0	*Saussurea alpina*	124.57.2.1	*Saussurea alpina subsp. alpina*
124.60.1.4	*Carduus nutans subsp. leiophyllus*	124.60.1.2	*Carduus nutans subsp. alpicola*
124.60.4.0	*Carduus personata*	124.60.4.1	*Carduus personata subsp. personata*
124.60.9.0	*Carduus defloratus*	124.60.9.1	*Carduus defloratus subsp. defloratus*
124.60.9.6	*Carduus defloratus subsp. rhaeticus*	124.60.9.3	*Carduus defloratus subsp. carlinifolius*
124.6.1.0	*Erigeron annuus*	124.6.1.1	*Erigeron annuus subsp. annuus*
124.61.3.0	*Cirsium eriophorum*	124.61.3.1	*Cirsium eriophorum*
124.6.3.0	*Erigeron acris*	124.6.3.1	*Erigeron acris subsp. acer*
124.65.1.0	*Serratula tinctoria*	124.65.1.2	*Serratula tinctoria subsp. monticola*
124.67.1.0	*Rhaponticum scariosum*	124.67.1.1	*Rhaponticum scariosum subsp. rhaponticum*
124.68.16.0	*Centaurea jacea*	124.68.16.1	*Centaurea jacea subsp. jacea*
124.68.18.1	*Centaurea nigrescens subsp. ramosa*	124.68.18.0	*Centaurea nigrescens*
124.68.25.0	*Centaurea nervosa*	124.68.25.1	*Centaurea nervosa subsp. nervosa*
124.68.5.0	*Centaurea scabiosa*	124.68.5.1	*Centaurea scabiosa subsp. scabiosa*
124.83.3.0	*Scorzoneroides montana*	124.83.3.1	*Scorzoneroides montana*
124.83.5.1	*Leontodon hispidus subsp. hispidus*	124.83.5.0	*Leontodon hispidus*
124.84.2.0	*Picris hieracioides*	124.84.2.1	*Picris hieracioides subsp. hieracioides*
124.85.2.0	*Podospermum laciniatum*	124.85.2.1	*Scorzonera laciniata subsp. laciniata*
124.86.4.0	*Tragopogon pratensis*	124.86.4.3	*Tragopogon orientalis*
124.89.1.0	*Lactuca viminea*	124.89.1.1	*Lactuca viminea subsp. viminea*
124.96.1.0	*Lapsana communis*	124.96.1.1	*Lapsana communis subsp. communis*
124.97.27.0	*Crepis vesicaria*	124.97.27.2	*Crepis vesicaria subsp. taraxacifolia*

Table B.1: Taxa selected to fill in data for subspecies not found in Flora Alpina

ID_mod	Name_EuroMed	ID_original	Name_FloraAlpina
124.99.26.1	*Hieracium piliferum subsp. glanduliferum*	124.99.26.0	*Hieracium piliferum*
124.99.26.2	*Hieracium piliferum subsp. subnivale*	124.99.26.0	*Hieracium piliferum*

Table B.2: Table illustrating which taxa have been selected to fill in data for species not found in Flora Alpina. Columns are analogous to the one in Table B.1.

ID_mod	Name_EuroMed	ID_original	Name_FloraAlpina
124.39.10.0	*Leucanthemum graminifolium*	124.39.7.0	*Leucanthemum burnatii*
124.39.11.0	*Leucanthemum icurtianum*	124.39.1.0	*Leucanthemum vulgare*
124.4.10.0	*Symphyotrichum pilosum*	124.4.2.0	*Symphyotrichium laeve*
124.48.28.0	*Jacobaea adonicifolia*	124.48.22.0	*Senecio abrotanifolius*
124.51.3.0	*Calendula tripterocarpa*	124.51.1.0	*Calendula officinalis*
124.82.6.0	*Hypochaeris maculata subsp. pelivanovicii*	124.82.1.0	*Hypochaeris maculata*
124.93.16.0	*Taraxacum carinthiacum*	124.93.1.0	*Taraxacum handelii*
124.93.17.0	*Taraxacum venustum*	124.93.1.0	*Taraxacum handelii*
124.99.43.0	*Hieracium armerioides*	124.99.26.0	*Hieracium piliferum*
124.99.44.0	*Hieracium caesioides*	124.99.19.0	*Hieracium caesium*
124.99.44.1	*Hieracium caesioides subsp. rionii*	124.99.19.0	*Hieracium caesium*
124.99.46.0	*Hieracium erioleucum*	124.99.24.0	*Hieracium villosum*
124.99.48.0	*Hieracium froelichianum*	124.99.20.0	*Hieracium lachenalii*
124.99.49.0	*Hieracium glaucopsis*	124.99.35.0	*Hieracium glaucum*
124.99.52.1	*Hieracium ramosissimum subsp. lactucifolium*	124.99.37.0	*Hieracium prenanthoides*
124.99.53.0	*Hieracium valdepilosum*	124.99.24.0	*Hieracium villosum*
124.99.54.0	*Pilosella x officinarum*	124.99.4.0	*Pilosella officinarum*
124.99.55.0	*Schlagintweitia huteri subsp. lantoscana*	124.99.32.0	*Schlagintweitia intybaceum*

B.2 Phylogenetic tree

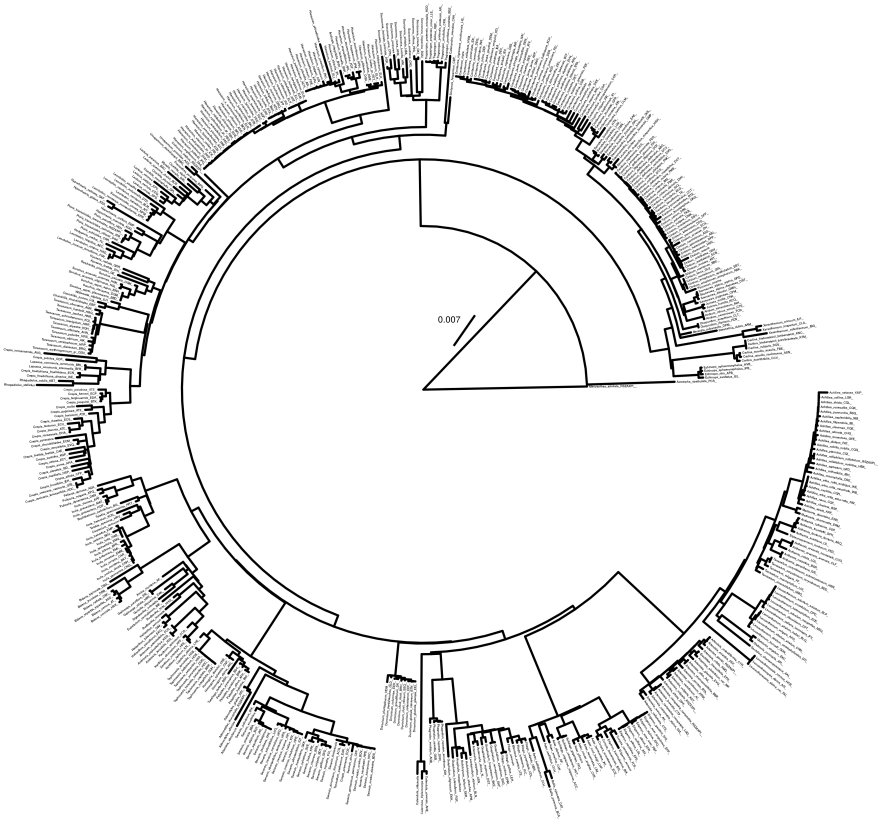


Figure B.1: Original ML phylogenetic tree of 522 taxa (+2 outgroups) built with 60 *cp* markers by Cristina Roquet.

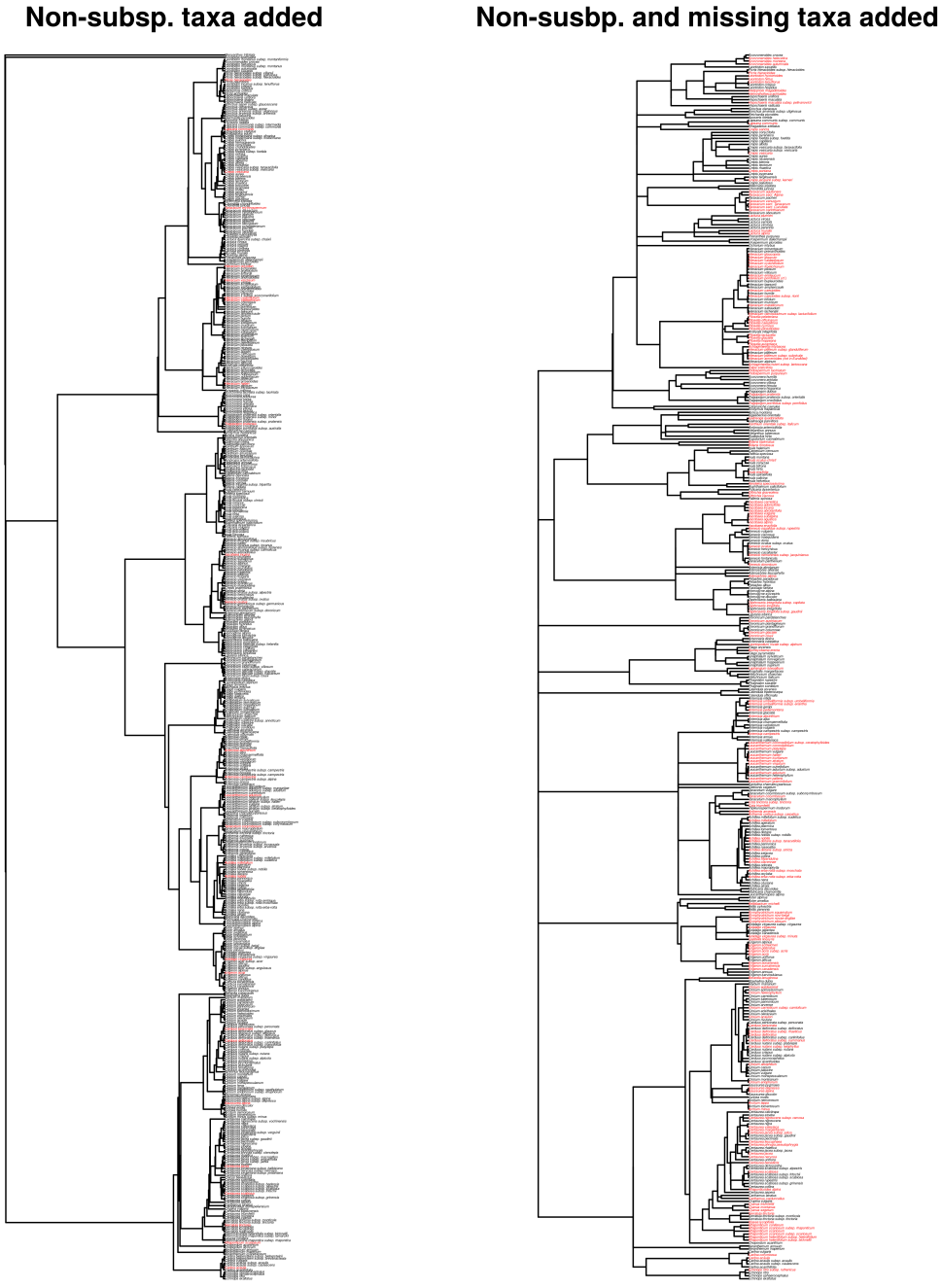


Figure B.2: Phylogenetic trees from Figure B.1 modified to include accessions of undetermined subspecies (left) and taxa present in the data but missing from the tree (right), highlighted in red in both cases.

B.3 Expanded MCMCglmm model summary

Table B.3: pMCMCglmm summaries for the fully specified models, including "genetic components" and "ecological components". Statistical significance is coded as follows: p≤0.001 = ∗∗∗; p≤0.01 = ∗∗; p≤0.05 = ∗. Base level (Intercept) refers to: Ploidy 2x, Longevity annual, Biological form therophyte, not Endemic, not Indigenous, pH neuter, medium N, average water availability.

Extended	**post.mean**	**l-95% CI**	**u-95% CI**	**eff.samp**	**pMCMC**	
Intercept	4.29E-01	-1.40E+00	2.04E+00	3950	0.6086	
Ploidy3x	2.88E-01	-2.96E-01	8.42E-01	3684	0.3119	
Ploidy4x	1.48E-01	-2.30E-01	5.36E-01	3950	0.4511	
Ploidy6x	3.62E-01	-3.53E-01	1.01E+00	3950	0.2987	
Ploidy8x	5.48E-01	-4.43E-01	1.52E+00	3692	0.2704	
Ploidy12x	-1.81E-02	-2.37E+00	2.38E+00	3722	0.998	
Chr_num	1.09E-02	-2.60E-03	2.37E-02	3595	0.0972	
Elevation_pref	9.01E-05	-1.86E-04	3.55E-04	3950	0.523	
Longevitya, b	1.04E+00	-1.57E+00	3.43E+00	3950	0.4172	
Longevitya, b, v	1.04E+00	-1.50E+00	3.56E+00	3950	0.4197	
Longevitya, A	-2.91E-01	-2.30E+00	1.83E+00	4211	0.7944	
Longevityb	8.95E-01	-1.26E+00	3.12E+00	3950	0.4162	
Longevityb, v	1.07E+00	-9.80E-01	3.46E+00	3950	0.3387	
Longevityb, v, A	5.46E-01	-1.42E+00	2.68E+00	3950	0.6132	
Longevityv	9.94E-01	-1.17E+00	3.08E+00	3950	0.3509	
Longevityv, A	1.03E+00	-1.54E+00	3.74E+00	3950	0.4385	
LongevityA	4.92E-01	-1.80E+00	2.93E+00	3950	0.6633	
BiologicalFormT, H	-8.64E-01	-3.30E+00	1.62E+00	3950	0.4911	
BiologicalFormH	-6.78E-01	-2.76E+00	1.40E+00	3950	0.5271	
BiologicalFormG	-6.94E-01	-2.90E+00	1.53E+00	3950	0.5453	
BiologicalFormG, H	-8.82E-01	-3.20E+00	1.48E+00	3950	0.4608	
BiologicalFormC	-4.20E-01	-2.67E+00	1.73E+00	3950	0.7165	
EndemicSub	-7.20E-02	-1.33E+00	1.05E+00	3950	0.9119	
EndemicYes	-2.12E-01	-6.51E-01	1.75E-01	3950	0.3114	
IndigenousYes	-7.15E-02	-5.44E-01	3.96E-01	3950	0.7732	
Tot.months	8.72E-02	-6.22E-01	8.00E-01	3950	0.8111	
Init.month	1.52E-01	-5.39E-01	8.67E-01	3950	0.681	
End.month	-8.87E-02	-7.70E-01	6.26E-01	3950	0.7985	
pHaci	-7.17E-02	-4.66E-01	3.39E-01	3950	0.7266	
pHbas	3.63E-02	-1.99E-01	2.98E-01	3950	0.7792	
Nlow	1.74E-01	-1.41E-01	4.91E-01	3964	0.2992	
Nhig	3.98E-02	-2.95E-01	3.35E-01	3950	0.7878	
WaterveryDry	-2.99E-02	-4.57E-01	3.58E-01	4187	0.8648	
WaterDry	-2.04E-02	-3.35E-01	2.77E-01	3950	0.883	
WaterWet	-1.17E-02	-3.64E-01	3.79E-01	4182	0.9413	
Strictly Alps	**post.mean**	**l-95% CI**	**u-95% CI**	**eff.samp**	**pMCMC**	
Intercept	3.09E-01	-1.37E+00	1.82E+00	3950	0.6957	
Ploidy3x	1.29E-01	-1.09E-01	3.42E-01	3722	0.26937	
Ploidy4x	2.13E-01	4.70E-02	3.85E-01	3950	0.01367	*
Ploidy6x	4.67E-01	1.76E-01	7.78E-01	3950	0.00304	**
Ploidy8x	6.65E-01	2.06E-01	1.07E+00	3950	0.00304	**
Ploidy12x	2.96E-01	-5.88E-01	1.07E+00	4168	0.46835	
Chr_num	1.04E-02	4.36E-03	1.59E-02	3950	0.00101	**
Elevation_pref	5.96E-05	-5.45E-05	1.69E-04	3950	0.29367	
Longevitya, b	3.04E-01	-4.91E-01	1.12E+00	4405	0.46582	
Longevitya, b, v	6.90E-01	-5.69E-02	1.45E+00	3422	0.07342	.
Longevitya, A	-2.81E-01	-9.50E-01	3.01E-01	3821	0.37418	
Longevityb	2.83E-01	-4.03E-01	9.30E-01	3950	0.40608	
Longevityb, v	4.88E-01	-2.04E-01	1.13E+00	3950	0.1681	

Table B.3: pMCMCglmm summaries for the fully specified models.

	post.mean	l-95% CI	u-95% CI	eff.samp	pMCMC	
Longevityb, v, A	2.65E-01	-4.04E-01	9.14E-01	4643	0.43595	
Longevityv	4.26E-01	-1.87E-01	1.09E+00	3741	0.21215	
Longevityv, A	4.76E-01	-4.36E-01	1.23E+00	3182	0.25418	
LongevityA	3.53E-01	-4.72E-01	1.20E+00	3950	0.4243	
BiologicalFormT, H	-5.66E-01	-1.33E+00	1.56E-01	3951	0.14177	
BiologicalFormH	-1.14E-01	-7.40E-01	4.45E-01	3950	0.7038	
BiologicalFormG	-2.15E-02	-6.81E-01	6.80E-01	3151	0.95899	
BiologicalFormG, H	-2.20E-01	-9.80E-01	5.14E-01	3950	0.55696	
BiologicalFormC	2.23E-01	-5.02E-01	8.85E-01	3950	0.52861	
EndemicSub	-2.39E-01	-6.35E-01	1.28E-01	3950	0.2081	
EndemicYes	-1.64E-01	-3.03E-01	-1.50E-02	3950	0.0243	*
IndigenousYes	-4.38E-04	-2.09E-01	2.05E-01	3950	0.99241	
Tot.months	1.21E-01	-8.89E-02	3.41E-01	3218	0.26684	
Init.month	1.77E-01	-3.17E-02	3.95E-01	3445	0.10835	
End.month	-9.46E-02	-2.94E-01	1.13E-01	3277	0.36253	
pHaci	-5.58E-02	-1.99E-01	9.35E-02	3950	0.44253	
pHbas	-3.92E-02	-1.40E-01	5.79E-02	3372	0.41772	
Nlow	6.41E-02	-5.99E-02	1.79E-01	3950	0.29873	
Nhig	-8.68E-02	-2.08E-01	3.34E-02	3950	0.17975	
WaterveryDry	-2.86E-03	-1.65E-01	1.75E-01	3950	0.97772	
WaterDry	7.79E-02	-2.88E-02	1.87E-01	3631	0.16101	
WaterWet	1.09E-01	-1.27E-02	2.38E-01	3891	0.08456	.

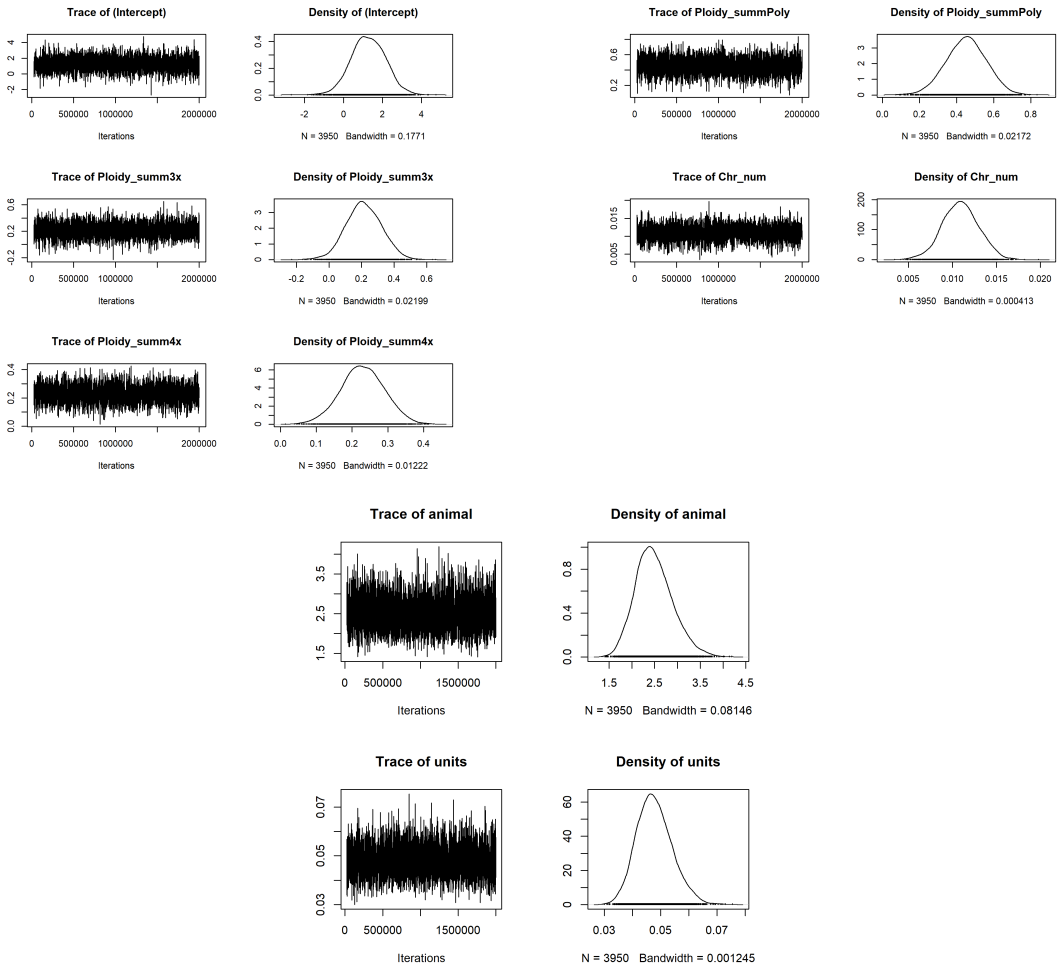
B.4 MCMCglmm models details

All analyses have been run with R v3.6.1 and MCMCglmm v2.29. Only diagnostics for the 'Extended' dataset are reported.

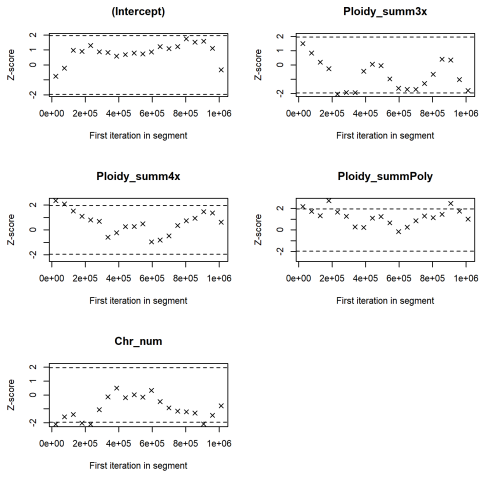
B.4.1 "Genetic components" only

```
### MCMCglmm_extended_noDbt_red2_priorchange_onlyLog.R

prior_V1_nu02 <- list(R = list(V = 1, nu = 0.02),
                      G = list(G1 = list(V = 1, nu = 0.02))
)
set.seed(111)

ext_mGauss1.1 <- MCMCglmm(log(GS_unified) ~ Ploidy_summ + Chr_num,
                          ginverse = list(animal = invFlorAlpes_Phylo_addTips2_ext_noDbt_tips$Ainv),
                          random = ~ animal, verbose = F,
                          data = DATA_extended_noDbt_cc,
                          family = "gaussian", trunc = T,
                          prior = prior_V1_nu02,
                          nitt = 2*10^6, thin = 500, burnin = 25000)
> summary(ext_mGauss1.1)

 Iterations = 25001:1999501
 Thinning interval  = 500
 Sample size  = 3950

 DIC: 82.14335

 G-structure:  ~animal
```

```
       post.mean l-95% CI u-95% CI eff.samp
animal     2.492    1.744    3.328     3696

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units   0.04778  0.03585  0.06013     3996

 Location effects: log(GS_unified) ~ Ploidy_summ + Chr_num

               post.mean  l-95% CI  u-95% CI eff.samp  pMCMC
(Intercept)      1.279504 -0.377483  3.019516     3950 0.1332
Ploidy_summ3x    0.214299  0.010821  0.426507     3950 0.0476 *
Ploidy_summ4x    0.229551  0.110845  0.347074     3950 <3e-04 ***
Ploidy_summPoly  0.452217  0.239556  0.658088     4137 <3e-04 ***
Chr_num          0.010924  0.007044  0.015034     4174 <3e-04 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> plot(ext_mGauss1.1, ask = F)
```



```
> heidel.diag(ext_mGauss1.1$VCV)

       Stationarity start     p-value
       test         iteration
animal passed       1         0.598
units  passed       1         0.640

       Halfwidth Mean   Halfwidth
       test
animal passed    2.4918 0.013160
units  passed    0.0478 0.000193

> heidel.diag(ext_mGauss1.1$Sol)

               Stationarity start     p-value
               test         iteration
(Intercept)    passed         1       0.3131
Ploidy_summ3x  passed         1       0.1953
Ploidy_summ4x  passed         1       0.2587
Ploidy_summPoly passed       396       0.1159
Chr_num        passed         1       0.0583

               Halfwidth Mean   Halfwidth
               test
(Intercept)    passed    1.2795 2.73e-02
Ploidy_summ3x  passed    0.2143 3.39e-03
Ploidy_summ4x  passed    0.2296 1.88e-03
Ploidy_summPoly passed    0.4513 3.53e-03
Chr_num        passed    0.0109 6.22e-05

> geweke.plot(ext_mGauss1.1$Sol, ask = F)
```



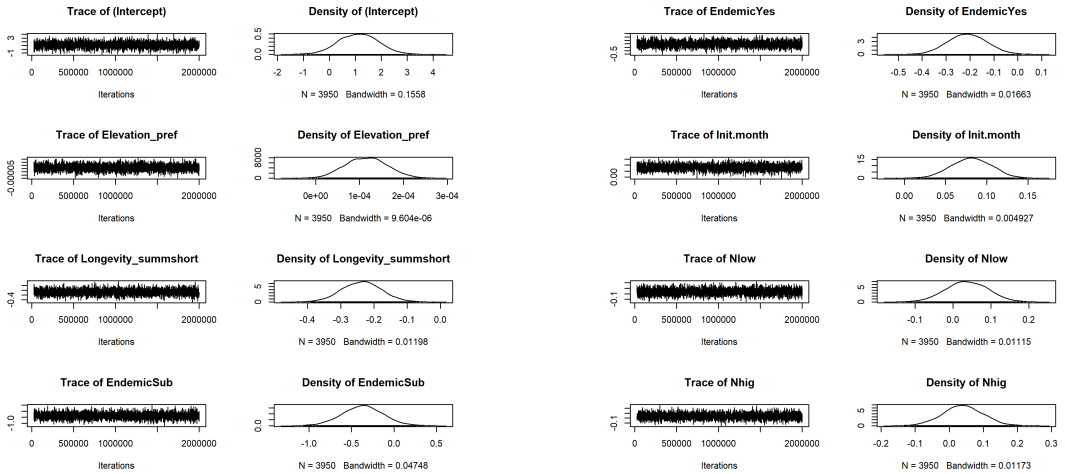

```
> autocorr.diag(ext_mGauss1.1$Sol)

           (Intercept) Ploidy_summ3x Ploidy_summ4x Ploidy_summPoly      Chr_num
Lag 0      1.000000000   1.000000000  1.0000000000     1.000000000  1.000000000
Lag 500   -0.017725357  -0.013089531 -0.0027143938    -0.023217554 -0.027652524
Lag 2500  -0.001434893  -0.002084306  0.0219010608     0.018530772  0.003848186
Lag 5000   0.015944502   0.009903679  0.0004972879    -0.016656415 -0.014498540
Lag 25000  0.002187930   0.030466022  0.0265317401    -0.007647882  0.011665441
```

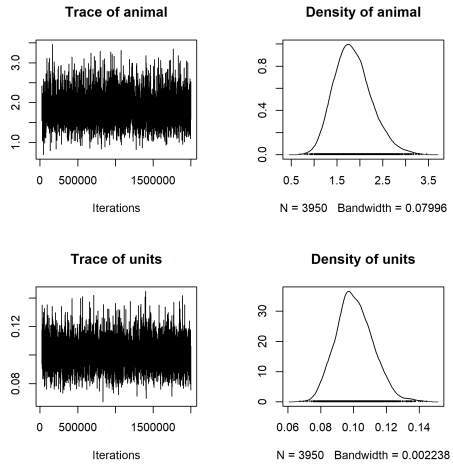
```
> raftery.diag(ext_mGauss1.1, q = 0.025, r = 0.005, s = 0.95)

Quantile (q) = 0.025
Accuracy (r) = +/- 0.005
Probability (s) = 0.95
You need a sample size of at least 3746 with these values of q, r and s

### Model runs with set.seed(534) and set.seed(386) are not shown

chainListTre2_Sol <- mcmc.list(ext_mGauss1.1$Sol, ext_mGauss2.1$Sol, ext_mGauss3.1$Sol)
chainListTre2_VCV <- mcmc.list(ext_mGauss1.1$VCV, ext_mGauss2.1$VCV, ext_mGauss3.1$VCV)

> gelman.diag(chainListTre2_Sol)
Potential scale reduction factors:

               Point est. Upper C.I.
(Intercept)             1          1
Ploidy_summ3x           1          1
Ploidy_summ4x           1          1
Ploidy_summPoly         1          1
Chr_num                 1          1

Multivariate psrf

1
> gelman.diag(chainListTre2_Sol)
Potential scale reduction factors:

               Point est. Upper C.I.
(Intercept)             1          1
Ploidy_summ3x           1          1
Ploidy_summ4x           1          1
Ploidy_summPoly         1          1
Chr_num                 1          1

Multivariate psrf

1
```

B.4.2 "Ecological components" only

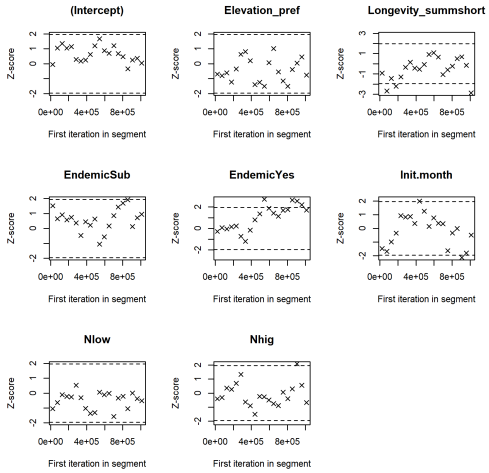
```
### MCMCglmm_extended_noDbt_red_priorchange_onlyLog.R

prior_V1_nu02 <- list(R = list(V = 1, nu = 0.02),
                      G = list(G1 = list(V = 1, nu = 0.02))
)

set.seed(111)

ext_mGauss1.1 <- MCMCglmm(log(GS_unified) ~ Elevation_pref + Longevity_summ + Endemic + Init.month + N,
                          ginverse = list(animal = invFlorAlpes_Phylo_addTips2_ext_noDbt_tips$Ainv),
                          random = ~ animal, verbose = F,
                          data = DATA_extended_noDbt_cc,
                          family = "gaussian", trunc = T,
                          prior = prior_V1_nu02,
                          nitt = 2*10^6, thin = 500, burnin = 25000)

> summary(ext_mGauss1.1)
```

```
 Iterations = 25001:1999501
 Thinning interval  = 500
 Sample size  = 3950

 DIC: 312.9906

 G-structure:  ~animal

       post.mean l-95% CI u-95% CI eff.samp
animal      1.85    1.087    2.639     3793

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units    0.1007  0.07967   0.1217     3950

 Location effects: log(GS_unified) ~ Elevation_pref + Longevity_summ + Endemic + Init.month + N

                   post.mean   l-95% CI   u-95% CI eff.samp   pMCMC
(Intercept)        1.127e+00 -4.700e-01  2.531e+00     4405 0.13722
Elevation_pref     1.156e-04  2.265e-05  2.067e-04     3950 0.01165 *
Longevity_summshort -2.366e-01 -3.564e-01 -1.250e-01     3950 < 3e-04 ***
EndemicSub        -3.683e-01 -8.655e-01  7.005e-02     3950 0.12152
EndemicYes        -2.103e-01 -3.769e-01 -5.764e-02     4243 0.01367 *
Init.month         8.139e-02  3.334e-02  1.270e-01     4008 0.00152 **
Nlow               3.673e-02 -7.268e-02  1.410e-01     3950 0.50937
Nhig               4.019e-02 -8.051e-02  1.451e-01     4178 0.48203
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> plot(ext_mGauss1.1, ask = F)
```






```
> heidel.diag(ext_mGauss1.1$VCV)

       Stationarity start     p-value
       test         iteration
animal passed       1         0.432
units  passed       1         0.827

       Halfwidth Mean  Halfwidth
       test
animal passed    1.850 0.012877
units  passed    0.101 0.000345

> heidel.diag(ext_mGauss1.1$Sol)

                  Stationarity start     p-value
                  test         iteration
(Intercept)       passed       1         0.6360
Elevation_pref    passed       1         0.7969
Longevity_summshort passed     1         0.4166
EndemicSub        passed       1         0.3402
EndemicYes        passed       1         0.0819
Init.month        passed       1         0.7457
Nlow              passed       1         0.3457
Nhig              passed       1         0.9459

                  Halfwidth Mean      Halfwidth
                  test
(Intercept)       passed     1.126504 2.27e-02
Elevation_pref    passed     0.000116 1.48e-06
Longevity_summshort passed  -0.236600 1.85e-03
EndemicSub        passed    -0.368291 7.44e-03
EndemicYes        passed    -0.210308 2.47e-03
Init.month        passed     0.081393 7.54e-04
Nlow              passed     0.036732 1.72e-03
Nhig              passed     0.040187 1.77e-03

> geweke.plot(ext_mGauss1.1$Sol, ask = F)
```




```
> autocorr.diag(ext_mGauss1.1$Sol)
           (Intercept) Elevation_pref Longevity_summshort    EndemicSub
Lag 0      1.000000000   1.0000000000          1.00000000  1.0000000000
Lag 500    0.001456649  -0.0034590602         -0.01123220  0.0102178720
Lag 2500  -0.007011594   0.0070430432         -0.01280447 -0.0098182936
Lag 5000   0.018984633  -0.0006284083         -0.01419519  0.0003430096
Lag 25000 -0.005928479  -0.0223529343          0.01681833 -0.0266606950
            EndemicYes   Init.month         Nlow         Nhig
Lag 0      1.000000000  1.000000000  1.000000000  1.000000000
Lag 500   -0.014725122 -0.014177018  0.015773496  0.006161546
Lag 2500   0.028827202  0.021301935 -0.016424356 -0.030653264
Lag 5000   0.001617485  0.006431117 -0.003747703 -0.006823819
Lag 25000 -0.009422187 -0.004581721  0.005867119 -0.018584160

> raftery.diag(ext_mGauss1.1, q = 0.025, r = 0.005, s = 0.95)

Quantile (q) = 0.025
Accuracy (r) = +/- 0.005
Probability (s) = 0.95
You need a sample size of at least 3746 with these values of q, r and s

### Model runs with set.seed(534) and set.seed(386) are not shown

chainListTre2_Sol <- mcmc.list(ext_mGauss1.1$Sol, ext_mGauss2.1$Sol, ext_mGauss3.1$Sol)
chainListTre2_VCV <- mcmc.list(ext_mGauss1.1$VCV, ext_mGauss2.1$VCV, ext_mGauss3.1$VCV)

> gelman.diag(chainListTre2_Sol)
Potential scale reduction factors:

                   Point est. Upper C.I.
(Intercept)                 1          1
Elevation_pref              1          1
Longevity_summshort         1          1
EndemicSub                  1          1
EndemicYes                  1          1
Init.month                  1          1
Nlow                        1          1
Nhig                        1          1

Multivariate psrf

1
```

```
> gelman.diag(chainListTre2_Sol)
Potential scale reduction factors:

                    Point est. Upper C.I.
(Intercept)                  1          1
Elevation_pref               1          1
Longevity_summshort          1          1
EndemicSub                   1          1
EndemicYes                   1          1
Init.month                   1          1
Nlow                         1          1
Nhig                         1          1

Multivariate psrf

1
```

B.5 Data table for Chapter 3

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae. Note that for phylogenetic analysis the data has been summarized by taxon. Variables with values "T" denote "TRUE", and "F" denote "FALSE". Column headers legend: Name EuroMed = species name, following the Euro+Med database; ID Collectors = unique identifier for the field collection; ID FloraAlpina = unique taxon identifier according to Flora Alpina, adapted where necessary; GS approx = 2C value in pg for the ploidy screening; n ind = number of separate plant individuals analysed for ploidy; GS = 2C genome size value in pg, averaged over the three repeated measures for two distinct individuals; GS StdErr = standard error on the GS value; Sample CV = average coefficient of variation for the sample's peaks; Standard CV = average coefficient of variation for the internal standard's peaks; Chr num = 2n chromosome number; Ploidy = Ploidy level; Date = Date; Lat N = Latitude North, in decimal degrees, datum WGS84; Long E = Longitude E, in decimal degrees, datum WGS84; Elevation = elevation of field collected accessions (m above sea level); Elevation pref = elevation preference as calculated from Flora Alpina data (m above sea level); Init month = flowering time initiation month (phenology); Longevity = life cycle length; BiologicalForm = vegetative form; Endemic = "No" denotes non-endemic, "Sub" subendemics and "Yes" denotes endemics; Indigenous = indicates whether the taxon is indigenous from the Alps; pH = summary variable for taxon's preference for substrate pH, "aci" is acidic, "neu" is neuter and "bas" is basic; N = taxon's substrate nitrogen content preference, "low" is nitrogen-poor, "med" is medium nitrogen, "hig" is nitrogen-rich; Water = summary variable for water availability preference, "VeryDry", "Dry", "Average", "Wet", "Aquatic"; Sect Occ = number of sectors occupied, according to Flora Alpina; Chr inferred = indicates whether the chromosome number was inferred from literature ("T") or experimentally determined ("F", one accessions per taxon); StrictlyAlps = indicates whether the accessions is of wild origin and collected within the alpine arc.

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Achillea ageratum	FR609	124.31.22.0	6.49	NA	6.49	0	2.79	3.01	18	2x	NA	44.8622	6.58772	1222	350	5	v	H	No	Yes	bas	low	Dry	1	F	T
Achillea atrata	A74	124.31.4.0	6.75	5	NA	NA	NA	NA	18	2x	17/07/2018	47.12224	12.82704	2361	2410	7	v	H	Sub	Yes	bas	low	Average	31	F	T
Achillea atrata	A117	124.31.4.0	NA	NA	6.66	0.05	4.97	4.04	18	2x	20/07/2018	47.0979	12.83191	2338	2410	7	v	H	Sub	Yes	bas	low	Average	31	F	T
Achillea atrata	MB87	124.31.4.0	NA	NA	6.86	0	2.54	2.4	18	2x	22/07/2018	46.44608	13.64746	2108	2410	7	v	H	Sub	Yes	bas	low	Average	31	F	T
Achillea atrata	JB Lautaret6	124.31.4.0	6.79	NA	6.79	0.04	1.51	2.3	18	2x	NA	NA	NA	NA	2410	7	v	H	Sub	Yes	bas	low	Average	31	F	F
Achillea clavennae	A18	124.31.6.0	7.94	10	7.74	0.08	2.33	1.75	18	2x	15/06/2018	47.71736	15.77347	1561	1890	6	v	H	No	Yes	bas	low	Dry	17	F	T
Achillea clavennae	A34	124.31.6.0	7.59	5	7.48	0.1	2.51	2.28	18	2x	17/06/2018	47.78864	15.81158	1455	1890	6	v	H	No	Yes	bas	low	Dry	17	F	T
Achillea clavennae	MB13	124.31.6.0	7.4	NA	7.4	0.02	2.31	1.99	18	2x	17/06/2018	NA	NA	NA	1890	6	v	H	No	Yes	bas	low	Dry	17	F	F
Achillea clavennae	CH61	124.31.6.0	7.81	9	NA	NA	NA	NA	18	2x	23/06/2018	45.93156	9.01994	1673	1890	6	v	H	No	Yes	bas	low	Dry	17	F	T
Achillea clavennae	A71	124.31.6.0	7.43	11	NA	NA	NA	NA	18	2x	17/07/2018	47.12388	12.82635	2354	1890	6	v	H	No	Yes	bas	low	Dry	17	F	T
Achillea clavennae	A127	124.31.6.0	7.52	12	NA	NA	NA	NA	18	2x	21/07/2018	47.07452	12.74988	2282	1890	6	v	H	No	Yes	bas	low	Dry	17	F	T
Achillea clavennae	IT102	124.31.6.0	7.61	7	NA	NA	NA	NA	18	2x	20/09/2018	45.78554	11.18503	1876	1890	6	v	H	No	Yes	bas	low	Dry	17	F	T
Achillea clusiana	JB Lautaret7	124.31.5.0	6.86	NA	6.86	0.06	2.16	2.39	18	2x	NA	NA	NA	NA	2217	7	v	H	Yes	Yes	bas	low	Average	1	F	F
Achillea collina	JB Lautaret5	124.31.17.0	11.13	NA	11.13	0.1	2.64	3.11	36	4x	NA	NA	NA	NA	910	6	v	H	No	Yes	bas	low	veryDry	15	F	F
Achillea distans	OH338	124.31.9.0	15.59	NA	15.59	0.09	2.89	2.71	54	6x	NA	NA	NA	NA	910	6	v	H	No	Yes	bas	hig	Average	17	F	F
Achillea distans subsp. stricta	OH339	124.31.10.0	15.73	NA	15.73	0	2.77	2.52	54	6x	NA	NA	NA	NA	1750	6	v	H	No	Yes	neu	hig	Average	26	F	F
Achillea distans subsp. tanacetifolia	RD7	124.31.9.1	11.26	NA	11.26	0.04	2.32	2.14	54	6x	NA	NA	NA	NA	910	6	v	H	No	Yes	bas	hig	Average	17	F	F
Achillea erba-rotta subsp. erba-rotta	FR503	124.31.2.1	8.37	25	8.37	0.09	2.9	3.1	18	2x	NA	44.34199	6.94715	1992	2100	7	v	H	Yes	Yes	aci	low	Average	6	F	T
Achillea erba-rotta subsp. erba-rotta	FR673	124.31.2.1	7.99	6	NA	NA	NA	NA	18	2x	NA	44.20487	7.1561	2465	2100	7	v	H	Yes	Yes	aci	low	Average	6	F	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Achillea erba-rotta subsp. moschata	CH94	124.31.2.2	7.52	5	NA	NA	NA	NA	18	2x	24/07/2018	46.47752	8.4128	2237	1921	6	v	H	Yes	Yes	aci	low	Average	24	F	T
Achillea erba-rotta subsp. moschata	CH105	124.31.2.2	7.52	4	NA	NA	NA	NA	18	2x	25/07/2018	46.56559	8.41424	2490	1921	6	v	H	Yes	Yes	aci	low	Average	24	F	T
Achillea erba-rotta subsp. moschata	CH128	124.31.2.2	NA	NA	7.54	0	1.89	1.83	18	2x	27/07/2018	45.86387	7.15902	2258	1921	6	v	H	Yes	Yes	aci	low	Average	24	F	T
Achillea erba-rotta subsp. moschata	CH173	124.31.2.2	7.55	2	NA	NA	NA	NA	18	2x	29/08/2018	46.54982	8.70094	1933	1921	6	v	H	Yes	Yes	aci	low	Average	24	F	T
Achillea filipendulina	OH424	124.31.23.0	6.5	NA	6.5	0.01	2.28	2.12	18	2x	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	F	F
Achillea macrophylla	RD6	124.31.7.0	7.69	NA	7.69	0.08	2.14	2.39	18	2x	NA	NA	NA	1517	7	v	H	No	Yes	neu	hig	Average	39	F	F
Achillea millefolium	FR0	124.31.11.0	15.91	NA	NA	NA	NA	NA	54	6x	24/07/2016	44.33469	6.29546	NA	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR55	124.31.11.0	15.82	NA	NA	NA	NA	NA	54	6x	24/07/2016	44.34171	6.29706	1802	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR34	124.31.11.0	15.82	NA	NA	NA	NA	NA	54	6x	24/07/2016	44.33598	6.29635	1987	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR23	124.31.11.0	15.91	NA	NA	NA	NA	NA	54	6x	24/07/2016	44.33802	6.29635	1893	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR19	124.31.11.0	15.45	NA	NA	NA	NA	NA	54	6x	24/07/2016	44.34002	6.29641	1847	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR16b	124.31.11.0	15.82	NA	NA	NA	NA	NA	54	6x	24/07/2016	44.34002	6.29641	1847	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR41	124.31.11.0	15.73	NA	NA	NA	NA	NA	54	6x	24/07/2016	44.33535	6.29567	NA	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR63	124.31.11.0	16.18	NA	NA	NA	NA	NA	54	6x	24/07/2016	NA	NA	NA	1250	5	v	H	No	Yes	neu	med	Dry	50	T	F
Achillea millefolium	FR102	124.31.11.0	15.7	NA	NA	NA	NA	NA	54	6x	25/07/2016	44.38339	6.39886	2119	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR109	124.31.11.0	16.04	NA	NA	NA	NA	NA	54	6x	25/07/2016	44.37932	6.3955	1985	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR81	124.31.11.0	15.95	NA	NA	NA	NA	NA	54	6x	25/07/2016	44.38621	6.39601	2219	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR133	124.31.11.0	15.78	NA	NA	NA	NA	NA	54	6x	25/07/2016	44.38569	6.39095	1922	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR182	124.31.11.0	15.6	NA	NA	NA	NA	NA	54	6x	26/07/2016	44.2476	6.23499	1380	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR180	124.31.11.0	15.77	NA	NA	NA	NA	NA	54	6x	26/07/2016	44.2486	6.22959	1586	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR167	124.31.11.0	15.9	NA	NA	NA	NA	NA	54	6x	26/07/2016	44.2486	6.22959	1586	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR154	124.31.11.0	15.95	NA	NA	NA	NA	NA	54	6x	26/07/2016	44.25846	6.26345	1036	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR207	124.31.11.0	15.64	NA	NA	NA	NA	NA	54	6x	27/07/2016	44.28474	6.4317	1772	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR226	124.31.11.0	15.92	NA	NA	NA	NA	NA	54	6x	27/07/2016	44.27839	6.4237	1421	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR208	124.31.11.0	15.61	NA	NA	NA	NA	NA	54	6x	27/07/2016	44.28474	6.4317	1772	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR291	124.31.11.0	15.25	NA	NA	NA	NA	NA	54	6x	28/07/2016	44.31586	6.4565	2378	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR253	124.31.11.0	15.41	NA	NA	NA	NA	NA	54	6x	28/07/2016	44.31535	6.44221	1961	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR236	124.31.11.0	15.5	NA	NA	NA	NA	NA	54	6x	28/07/2016	44.31782	6.44161	1881	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR305	124.31.11.0	15.74	NA	NA	NA	NA	NA	54	6x	29/07/2016	44.40792	6.385497	2505	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR323	124.31.11.0	15.66	NA	NA	NA	NA	NA	54	6x	29/07/2016	44.26081	6.20881	1888	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	A58	124.31.11.0	15.62	6	NA	NA	NA	NA	54	6x	16/07/2018	46.56657	12.48257	1398	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	IT67	124.31.11.0	17.41	11	NA	NA	NA	NA	54	6x	NA	45.6833	11.17753	635	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	IT39	124.31.11.0	NA	NA	NA	NA	NA	NA	54	6x	NA	45.696	11.6343	73	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	FR668	124.31.11.0	14.31	11	NA	NA	NA	NA	54	6x	NA	44.20338	7.1513	2354	1250	5	v	H	No	Yes	neu	med	Dry	50	T	T
Achillea millefolium	RBGK2014-526	124.31.11.0	15.97	NA	15.97	0.05	2.3	1.89	54	6x	NA	NA	NA	NA	1250	5	v	H	No	Yes	neu	med	Dry	50	T	F
Achillea millefolium	GR556	124.31.11.0	15.95	NA	NA	NA	NA	NA	54	6x	NA	NA	NA	NA	1250	5	v	H	No	Yes	neu	med	Dry	50	T	F
Achillea millefolium subsp. sudetica	A77	124.31.11.2	NA	NA	15.86	0.05	2.53	2.03	54	6x	17/07/2018	47.06729	12.83774	2196	1610	6	v	H	No	Yes	neu	med	Average	19	F	T
Achillea millefolium subsp. sudetica	OH453	124.31.11.2	16.01	NA	16.01	0.02	1.85	1.64	54	6x	NA	NA	NA	NA	1610	6	v	H	No	Yes	neu	med	Average	19	F	F
Achillea nana	CH82	124.31.3.0	8.2	5	NA	NA	NA	NA	18	2x	24/07/2018	46.48152	8.38656	2438	2575	7	v	H	Yes	Yes	neu	low	Average	24	F	T
Achillea nana	CH104	124.31.3.0	8.15	10	NA	NA	NA	NA	18	2x	25/07/2018	46.56559	8.41408	2497	2575	7	v	H	Yes	Yes	neu	low	Average	24	F	T
Achillea nana	CH148	124.31.3.0	8.15	12	NA	NA	NA	NA	18	2x	23/08/2018	45.98976	7.70472	2630	2575	7	v	H	Yes	Yes	neu	low	Average	24	F	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Achillea nana	FR465	124.31.3.0	8.2	8	NA	NA	NA	NA	18	2x	NA	44.72623	6.32373	2678	2575	7	v	H	Yes	Yes	neu	low	Average	24	F	T
Achillea nana	FR630	124.31.3.0	7.82	11	NA	NA	NA	NA	18	2x	NA	44.25411	6.71406	2428	2575	7	v	H	Yes	Yes	neu	low	Average	24	F	T
Achillea nana	FR687	124.31.3.0	7.75	6	NA	NA	NA	NA	18	2x	NA	44.32157	6.80667	2862	2575	7	v	H	Yes	Yes	neu	low	Average	24	F	T
Achillea nana	FR539	124.31.3.0	7.92	8	NA	NA	NA	NA	18	2x	NA	45.06417	6.40772	2623	2575	7	v	H	Yes	Yes	neu	low	Average	24	F	T
Achillea nana	FR706	124.31.3.0	7.77	15	NA	NA	NA	NA	18	2x	NA	44.68684	6.98025	2616	2575	7	v	H	Yes	Yes	neu	low	Average	24	F	T
Achillea nana	RD5	124.31.3.0	8.13	NA	8.13	0.02	2.3	2.08	18	2x	NA	NA	NA	NA	2575	7	v	H	Yes	Yes	neu	low	Average	24	F	F
Achillea nobilis	CH163	124.31.19.0	5.11	12	NA	NA	NA	NA	18	2x	24/08/2018	46.26204	7.477	538	350	7	v	H	No	Yes	bas	low	Dry	14	F	T
Achillea nobilis subsp. nobilis	RBGK1978-4907	124.31.19.1	5.53	NA	5.53	0.07	2.78	2.45	18	2x	NA	NA	NA	NA	350	7	v	H	No	Yes	bas	low	Dry	14	F	F
Achillea oxyloba	A86	124.31.1.0	NA	NA	7.94	0.02	1.79	1.64	18	2x	19/07/2018	46.77042	12.79189	1930	2183	7	v	H	Yes	Yes	bas	low	Average	9	F	T
Achillea oxyloba	A93	124.31.1.0	NA	NA	NA	NA	NA	NA	18	2x	19/07/2018	46.76379	12.80059	2219	2183	7	v	H	Yes	Yes	bas	low	Average	9	F	T
Achillea ptarmica	CH136	124.31.8.0	7.43	2	7.09	0.04	2.85	2.89	18	2x	22/08/2018	46.30779	7.87707	897	875	6	v	H	No	Yes	aci	med	Wet	28	F	T
Achillea ptarmica	JB Lautaret8	124.31.8.0	7.36	NA	7.36	0.02	1.92	1.71	18	2x	NA	NA	NA	NA	875	6	v	H	No	Yes	aci	med	Wet	28	F	F
Achillea roseoalba	CH28	124.31.15.0	6.83	7	6.83	0.02	3.31	2.47	18	2x	22/05/2018	45.9917	9.2267	347	700	6	v	H	No	Yes	neu	low	Average	21	F	T
Achillea roseoalba	CH57	124.31.15.0	5.33	9	NA	NA	NA	NA	18	2x	22/06/2018	46.20733	8.80109	1441	700	6	v	H	No	Yes	neu	low	Average	21	F	T
Adenostyles alliariae	FR52	124.44.1.0	18.91	NA	18.91	0.06	2.13	1.96	38	4x	24/07/2016	44.34171	6.29706	1802	1750	6	v	H	No	Yes	neu	hig	Wet	46	F	T
Adenostyles alliariae	FR136	124.44.1.0	19.04	NA	NA	NA	NA	NA	38	4x	25/07/2016	44.38569	6.39095	1922	1750	6	v	H	No	Yes	neu	hig	Wet	46	F	T
Adenostyles alliariae	FR110	124.44.1.0	19.11	NA	NA	NA	NA	NA	38	4x	25/07/2016	44.37932	6.3955	1985	1750	6	v	H	No	Yes	neu	hig	Wet	46	F	T
Adenostyles alliariae	FR203	124.44.1.0	18.7	NA	18.7	0.04	1.93	1.96	38	4x	27/07/2016	44.28474	6.4317	1772	1750	6	v	H	No	Yes	neu	hig	Wet	46	F	T
Adenostyles alliariae	FR344a	124.44.1.0	19.09	NA	NA	NA	NA	NA	38	4x	29/07/2016	44.27214	6.21177	1651	1750	6	v	H	No	Yes	neu	hig	Wet	46	F	T
Adenostyles alliariae	CH56	124.44.1.0	18.11	NA	NA	NA	NA	NA	38	4x	22/06/2018	46.21189	8.79884	1500	1750	6	v	H	No	Yes	neu	hig	Wet	46	F	T
Adenostyles alliariae	MB51	124.44.1.0	18.45	2	NA	NA	NA	NA	38	4x	11/07/2018	NA	NA	NA	1750	6	v	H	No	Yes	neu	hig	Wet	46	F	F
Adenostyles alliariae	A96	124.44.1.0	18.75	9	NA	NA	NA	NA	38	4x	19/07/2018	46.78288	12.78845	1638	1750	6	v	H	No	Yes	neu	hig	Wet	46	F	T
Adenostyles alliariae	FR448	124.44.1.0	18.77	7	NA	NA	NA	NA	38	4x	NA	44.34146	6.294136	1672	1750	6	v	H	No	Yes	neu	hig	Wet	46	F	T
Adenostyles alliariae	FR613	124.44.1.0	NA	NA	NA	NA	NA	NA	38	4x	NA	44.86218	6.58773	1583	1750	6	v	H	No	Yes	neu	hig	Wet	46	F	T
Adenostyles alpina	FR280	124.44.2.0	19.4	NA	NA	NA	NA	NA	38	4x	28/07/2016	44.31586	6.4565	2378	1470	6	v	H	No	Yes	bas	med	Wet	49	F	T
Adenostyles alpina	MB53	124.44.2.0	18.88	3	NA	NA	NA	NA	38	4x	11/07/2018	NA	NA	NA	1470	6	v	H	No	Yes	bas	med	Wet	49	F	F
Adenostyles alpina	FR437	124.44.2.0	NA	NA	NA	NA	NA	NA	38	4x	NA	44.28397	6.43458	1710	1470	6	v	H	No	Yes	bas	med	Wet	49	F	T
Adenostyles alpina	FR518	124.44.2.0	18.78	3	18.78	0.04	3.63	2.33	38	4x	NA	44.049	6.45916	2297	1470	6	v	H	No	Yes	bas	med	Wet	49	F	T
Adenostyles leucophylla	FR290	124.44.3.0	21.02	NA	21.02	0.11	3.37	3.08	38	4x	28/07/2016	44.31586	6.4565	2378	1890	7	v	H	Yes	Yes	aci	low	Wet	23	F	T
Adenostyles leucophylla	FR631	124.44.3.0	18.37	6	NA	NA	NA	NA	38	4x	NA	44.25411	6.71406	2428	1890	7	v	H	Yes	Yes	aci	low	Wet	23	F	T
Adenostyles leucophylla	FR513	124.44.3.0	18.46	7	NA	NA	NA	NA	38	4x	NA	44.30975	6.45543	2117	1890	7	v	H	Yes	Yes	aci	low	Wet	23	F	T
Adenostyles leucophylla	FR629	124.44.3.0	18.57	7	NA	NA	NA	NA	38	4x	NA	44.25411	6.71406	2428	1890	7	v	H	Yes	Yes	aci	low	Wet	23	F	T
Adenostyles leucophylla	FR544	124.44.3.0	18.47	NA	NA	NA	NA	NA	38	4x	NA	NA	NA	NA	1890	7	v	H	Yes	Yes	aci	low	Wet	23	F	F
Ambrosia artemisiifolia	IT83	124.26.1.0	2.57	8	2.51	0.02	2.95	2.54	36	2x	25/08/2018	45.84595	8.8902	345	350	7	a	T	No	No	neu	hig	Dry	31	F	T
Ambrosia artemisiifolia	MC4	124.26.1.0	2.67	NA	2.67	0.11	2.4	1.91	36	2x	NA	NA	NA	NA	350	7	a	T	No	No	neu	hig	Dry	31	F	F
Anaphalis margaritacea	RBGK1979-4967	124.14.1.0	3.59	NA	3.59	0.02	2.98	2.55	28	2x	NA	NA	NA	NA	350	7	v	H	No	No	neu	hig	Average	6	F	F
Andryala integrifolia	OHÁ 287	124.98.1.0	3.38	NA	3.38	0.01	2.94	2.78	18	2x	NA	NA	NA	NA	350	6	a	T	No	Yes	aci	low	Dry	2	F	F
Antennaria carpatica	FR293a	124.12.2.0	17.02	NA	NA	NA	NA	NA	56	8x	28/07/2016	44.31586	6.4565	2378	1925	6	v	H	No	Yes	neu	low	Dry	40	F	T
Antennaria carpatica	A66	124.12.2.0	17.57	5	NA	NA	NA	NA	56	8x	17/07/2018	47.12253	12.82531	2318	1925	6	v	H	No	Yes	neu	low	Dry	40	F	T
Antennaria carpatica	FR466	124.12.2.0	17.51	16	NA	NA	NA	NA	56	8x	NA	44.72623	6.32373	2678	1925	6	v	H	No	Yes	neu	low	Dry	40	F	T
Antennaria carpatica	FR658	124.12.2.0	17.42	5	NA	NA	NA	NA	56	8x	NA	44.26042	6.7396	2372	1925	6	v	H	No	Yes	neu	low	Dry	40	F	T
Antennaria carpatica	FR557	124.12.2.0	17.06	10	NA	NA	NA	NA	56	8x	NA	45.06417	6.4024	2601	1925	6	v	H	No	Yes	neu	low	Dry	40	F	T
Antennaria carpatica	RD2	124.12.2.0	17.4	NA	17.4	0.14	3.14	1.94	56	8x	NA	NA	NA	NA	1925	6	v	H	No	Yes	neu	low	Dry	40	F	F
Antennaria dioica	FR45a	124.12.1.0	7.39	NA	7.39	0.01	2.18	1.92	28	4x	24/07/2016	44.33443	6.29046	NA	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	FR84	124.12.1.0	7.42	NA	NA	NA	NA	NA	28	4x	25/07/2016	44.38621	6.39601	2219	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Antennaria dioica	FR93	124.12.1.0	7.38	NA	NA	NA	NA	NA	28	4x	25/07/2016	44.38528	6.39642	2184	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	FR104	124.12.1.0	7.38	NA	NA	NA	NA	NA	28	4x	25/07/2016	44.38339	6.39886	2119	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	FR173	124.12.1.0	7.43	NA	NA	NA	NA	NA	28	4x	26/07/2016	44.2486	6.22959	1586	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	FR248	124.12.1.0	7.25	NA	NA	NA	NA	NA	28	4x	28/07/2016	44.31535	6.44221	1961	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	FR298	124.12.1.0	7.34	NA	NA	NA	NA	NA	28	4x	28/07/2016	44.31586	6.4565	2378	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	FR243	124.12.1.0	7.34	NA	NA	NA	NA	NA	28	4x	28/07/2016	44.31535	6.44221	1961	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	FR266	124.12.1.0	7.34	NA	NA	NA	NA	NA	28	4x	28/07/2016	44.31346	6.44843	2127	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	FR324	124.12.1.0	7.34	NA	NA	NA	NA	NA	28	4x	29/07/2016	44.26081	6.20881	1888	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	FR315	124.12.1.0	7.51	NA	NA	NA	NA	NA	28	4x	29/07/2016	44.26084	6.20877	1890	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	FR307	124.12.1.0	7.34	NA	NA	NA	NA	NA	28	4x	29/07/2016	44.40792	6.385497	2505	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	A76	124.12.1.0	7.43	3	NA	NA	NA	NA	28	4x	17/07/2018	47.06833	12.83988	2258	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	FR464	124.12.1.0	2.64	16	NA	NA	NA	NA	28	4x	NA	44.72623	6.32373	2678	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	FR645	124.12.1.0	7.48	10	NA	NA	NA	NA	28	4x	NA	44.24774	6.7154	2355	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	IT46	124.12.1.0	7.15	8	NA	NA	NA	NA	28	4x	NA	46.10193	11.38771	1803	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	IT45	124.12.1.0	7.29	4	NA	NA	NA	NA	28	4x	NA	46.10193	11.38771	1803	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	FR669	124.12.1.0	7.48	6	NA	NA	NA	NA	28	4x	NA	44.20338	7.1513	2354	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Antennaria dioica	FR374	124.12.1.0	7.29	9	NA	NA	NA	NA	28	4x	NA	44.40943	6.38709	2498	1633	6	v	C	No	Yes	aci	low	Dry	50	T	T
Anthemis arvensis	FR587	124.30.4.0	8.11	NA	8.11	0.01	2.6	2.5	18	2x	NA	NA	NA	NA	910	5	a, b	T, H	No	Yes	neu	low	Dry	41	F	F
Anthemis cretica	OH417	124.30.2.0	6.91	NA	6.91	0.01	1.93	1.64	18	2x	NA	NA	NA	NA	1400	6	v	H	No	Yes	neu	low	veryDry	3	F	F
Anthemis cretica subsp. carpatica	JB Lautaret2	124.30.1.0	17.44	NA	17.44	0.1	2.95	2.91	36	4x	NA	NA	NA	NA	2450	7	v	H	No	Yes	aci	low	Dry	1	F	F
Aposeris foetida	FR719	124.80.1.0	4.68	6	NA	NA	NA	NA	16	2x	17/05/2018	44.33186	6.27433	2025	1400	6	v	H	No	Yes	bas	med	Wet	31	F	T
Aposeris foetida	MB41	124.80.1.0	4.94	NA	4.94	0.03	2.56	1.62	16	2x	08/07/2018	46.43362	14.29131	1524	1400	6	v	H	No	Yes	bas	med	Wet	31	F	T
Aposeris foetida	IT51	124.80.1.0	4.79	7	NA	NA	NA	NA	16	2x	NA	45.79402	11.46281	1269	1400	6	v	H	No	Yes	bas	med	Wet	31	F	T
Aposeris foetida	IT1	124.80.1.0	5.05	12	5.05	0.02	2.81	2.05	16	2x	NA	45.75737	11.41748	579	1400	6	v	H	No	Yes	bas	med	Wet	31	F	T
Arctium lappa	FR140b	124.56.2.0	4.09	NA	4.09	0.05	2.9	2.45	36	2x	26/07/2016	44.25745	6.25511	1172	910	7	b	H	No	Yes	neu	hig	Average	43	T	T
Arctium lappa	CH135	124.56.2.0	3.97	1	NA	NA	NA	NA	36	2x	22/08/2018	46.26919	7.53579	963	910	7	b	H	No	Yes	neu	hig	Average	43	T	T
Arctium lappa	MB109	124.56.2.0	NA	NA	NA	NA	NA	NA	36	2x	24/08/2018	NA	NA	NA	910	7	b	H	No	Yes	neu	hig	Average	43	T	F
Arctium lappa	OH488-1	124.56.2.0	4.5	2	NA	NA	NA	NA	36	2x	NA	NA	NA	NA	910	7	b	H	No	Yes	neu	hig	Average	43	T	F
Arctium minus	FR161	124.56.3.0	4.64	NA	NA	NA	NA	NA	36	2x	26/07/2016	44.27211	6.29882	1083	910	7	a, b	T, H	No	Yes	neu	hig	Average	30	F	T
Arctium minus	FR523	124.56.3.0	same	NA	NA	NA	NA	NA	36	2x	NA	44.35559	6.29353	1440	910	7	a, b	T, H	No	Yes	neu	hig	Average	30	F	T
Arctium minus	FR406	124.56.3.0	4.61	NA	4.61	0.05	2.96	2.18	36	2x	NA	44.31742	6.38509	1613	910	7	a, b	T, H	No	Yes	neu	hig	Average	30	F	T
Arctium minus	FR490	124.56.3.0	4.46	NA	NA	NA	NA	NA	36	2x	NA	44.35742	6.95305	1836	910	7	a, b	T, H	No	Yes	neu	hig	Average	30	F	T
Arctium nemorosum	CH98	124.56.4.0	NA	NA	4.83	0.05	3.13	2.16	36	2x	24/07/2018	46.50385	8.50929	1386	1283	7	b	H	No	Yes	neu	hig	Average	40	F	T
Arctium tomentosum	CZ5	124.56.1.0	3.79	8	NA	NA	NA	NA	36	2x	NA	NA	NA	NA	1050	7	a, b	T, H	No	Yes	bas	hig	Dry	29	F	F
Arctium tomentosum	OH476	124.56.1.0	NA	NA	3.7	0.04	3.12	2	36	2x	NA	NA	NA	NA	1050	7	a, b	T, H	No	Yes	bas	hig	Dry	29	F	F
Arnica montana	FR27	124.45.1.0	3.22	NA	NA	NA	NA	NA	38	4x	24/07/2016	44.33802	6.29635	1893	1633	6	v	H	No	Yes	aci	low	Average	48	T	T
Arnica montana	FR40	124.45.1.0	3.39	NA	3.39	0.02	2.81	1.84	38	4x	24/07/2016	44.33535	6.29567	NA	1633	6	v	H	No	Yes	aci	low	Average	48	T	T
Arnica montana	FR61	124.45.1.0	3.28	NA	NA	NA	NA	NA	38	4x	24/07/2016	NA	NA	NA	1633	6	v	H	No	Yes	aci	low	Average	48	T	F
Arnica montana	FR205	124.45.1.0	3.37	NA	NA	NA	NA	NA	38	4x	27/07/2016	44.28474	6.4317	1772	1633	6	v	H	No	Yes	aci	low	Average	48	T	T
Arnica montana	FR258	124.45.1.0	3.22	NA	NA	NA	NA	NA	38	4x	28/07/2016	44.31535	6.44221	1961	1633	6	v	H	No	Yes	aci	low	Average	48	T	T
Arnica montana	FR241	124.45.1.0	3.3	NA	NA	NA	NA	NA	38	4x	28/07/2016	44.31535	6.44221	1961	1633	6	v	H	No	Yes	aci	low	Average	48	T	T
Arnica montana	CH54	124.45.1.0	3.6	4	NA	NA	NA	NA	38	4x	22/06/2018	46.21421	8.79385	1650	1633	6	v	H	No	Yes	aci	low	Average	48	T	T
Arnica montana	CH66	124.45.1.0	3.64	2	NA	NA	NA	NA	38	4x	23/06/2018	45.93961	9.02406	1562	1633	6	v	H	No	Yes	aci	low	Average	48	T	T
Arnica montana	MB47	124.45.1.0	3.29	NA	3.29	0	3.94	2.76	38	4x	08/07/2018	46.43203	14.29266	1454	1633	6	v	H	No	Yes	aci	low	Average	48	T	T
Arnica montana	CH96	124.45.1.0	3.4	24	NA	NA	NA	NA	38	4x	24/07/2018	46.47752	8.4128	2237	1633	6	v	H	No	Yes	aci	low	Average	48	T	T
Arnica montana	FR416	124.45.1.0	3.41	13	NA	NA	NA	NA	38	4x	NA	44.3128	6.43604	1852	1633	6	v	H	No	Yes	aci	low	Average	48	T	T
Arnica montana	FR681	124.45.1.0	NA	NA	NA	NA	NA	NA	38	4x	NA	44.17389	7.1567	2313	1633	6	v	H	No	Yes	aci	low	Average	48	T	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Arnica montana	FR390	124.45.1.0	3.55	18	NA	NA	NA	NA	38	4x	NA	44.332	6.29235	1988	1633	6	v	H	No	Yes	aci	low	Average	48	T	T
Arnica montana	FR436	124.45.1.0	NA	NA	NA	NA	NA	NA	38	4x	NA	44.28397	6.43458	1710	1633	6	v	H	No	Yes	aci	low	Average	48	T	T
Arnica montana	OH292	124.45.1.0	NA	NA	NA	NA	NA	NA	38	4x	NA	NA	NA	NA	1633	6	v	H	No	Yes	aci	low	Average	48	T	F
Artemisia absinthium	FR141	124.40.3.0	9.61	NA	9.61	0.08	2.87	2.1	18	2x	26/07/2016	44.25745	6.25511	1172	1050	7	v, A	C	No	Yes	bas	hig	Dry	45	F	T
Artemisia absinthium	FR353	124.40.3.0	9.84	NA	NA	NA	NA	NA	18	2x	29/07/2016	44.02726	6.22486	1358	1050	7	v, A	C	No	Yes	bas	hig	Dry	45	F	T
Artemisia absinthium	A43	124.40.3.0	9.96	3	9.99	0.03	1.76	2.06	18	2x	18/06/2018	NA	NA	NA	1050	7	v, A	C	No	Yes	bas	hig	Dry	45	F	F
Artemisia absinthium	CH138	124.40.3.0	9.87	4	NA	NA	NA	NA	18	2x	22/08/2018	46.30757	7.877726	894	1050	7	v, A	C	No	Yes	bas	hig	Dry	45	F	T
Artemisia absinthium	CH140	124.40.3.0	9.38	4	NA	NA	NA	NA	18	2x	22/08/2018	46.30733	7.87714	875	1050	7	v, A	C	No	Yes	bas	hig	Dry	45	F	T
Artemisia absinthium	MB116	124.40.3.0	10.27	4	NA	NA	NA	NA	18	2x	27/08/2018	NA	NA	NA	1050	7	v, A	C	No	Yes	bas	hig	Dry	45	F	F
Artemisia absinthium	FR703b	124.40.3.0	9.97	NA	NA	NA	NA	NA	18	2x	NA	45.04335	6.33181	1603	1050	7	v, A	C	No	Yes	bas	hig	Dry	45	F	T
Artemisia absinthium	RBGK1990-3675	124.40.3.0	NA	NA	NA	NA	NA	NA	18	2x	NA	NA	NA	NA	1050	7	v, A	C	No	Yes	bas	hig	Dry	45	F	F
Artemisia annua	CH168	124.40.17.0	3.57	8	3.58	0.1	2.2	2.6	18	2x	28/08/2018	46.04408	8.97431	337	350	8	a	T	No	No	neu	hig	Average	15	F	T
Artemisia annua	IT99	124.40.17.0	3.74	8	3.77	0	2.29	2.71	18	2x	20/09/2018	45.70928	11.61751	75	350	8	a	T	No	No	neu	hig	Average	15	F	T
Artemisia campestris	OH523	124.40.19.0	NA	NA	11.43	0.03	1.89	2.34	36	4x	NA	NA	NA	NA	910	7	v	C	No	Yes	bas	low	veryDry	32	F	F
Artemisia campestris subsp. campestris	CH131	124.40.19.1	10.89	3	11.26	0.16	1.87	1.98	36	2x	22/08/2018	46.25315	7.40649	593	910	7	v	C	No	Yes	bas	low	veryDry	32	F	T
Artemisia chamaemelifolia	FR605	124.40.9.0	7.37	NA	7.37	0.04	2.85	2.72	18	2x	NA	44.85933	6.58506	1233	1190	7	v, A	C	No	Yes	neu	low	veryDry	8	F	T
Artemisia chamaemelifolia	RBGK1987-1438	124.40.9.0	8.4	NA	8.4	0.01	2.77	3.1	18	2x	NA	NA	NA	NA	1190	7	v, A	C	No	Yes	neu	low	veryDry	8	F	F
Artemisia chamaemelifolia	FR565	124.40.9.0	6.43	NA	NA	NA	NA	NA	18	2x	NA	NA	NA	NA	1190	7	v, A	C	No	Yes	neu	low	veryDry	8	F	F
Artemisia genipi	A128	124.40.13.0	5.78	3	NA	NA	NA	NA	16	2x	21/07/2018	47.07504	12.75082	2348	2410	7	v	C	Yes	Yes	neu	low	Dry	33	F	T
Artemisia genipi	CH154	124.40.13.0	6.01	4	NA	NA	NA	NA	16	2x	23/08/2018	45.98968	7.68665	2788	2410	7	v	C	Yes	Yes	neu	low	Dry	33	F	T
Artemisia genipi	FR533	124.40.13.0	6.08	NA	6.08	0.03	2.78	2.1	16	2x	NA	45.06417	6.40772	2623	2410	7	v	C	Yes	Yes	neu	low	Dry	33	F	T
Artemisia genipi	RD9	124.40.13.0	NA	NA	NA	NA	NA	NA	16	2x	NA	NA	NA	NA	2410	7	v	C	Yes	Yes	neu	low	Dry	33	F	F
Artemisia glacialis	JB Lautaret11	124.40.15.0	9.89	NA	9.89	0.06	2.2	1.7	16	2x	NA	NA	NA	NA	2410	7	v	C	Yes	Yes	neu	low	Dry	10	F	F
Artemisia nitida	OH470	124.40.11.0	14.19	NA	19.35	0.07	2.03	1.98	54	6x	NA	NA	NA	NA	1610	8	v	C	No	Yes	bas	low	Dry	8	F	F
Artemisia pedemontana	RBGK1949-2903	124.40.16.0	9.02	NA	9.02	0.04	2.1	2.63	16	2x	NA	NA	NA	NA	700	5	v	C	No	Yes	bas	low	veryDry	1	F	F
Artemisia umbelliformis subsp. eriantha	NA	124.40.12.0	6.73	NA	6.73	0.04	2.76	3.11	18	2x	NA	NA	NA	NA	2100	6	v	C	No	Yes	aci	low	Dry	6	F	F
Artemisia umbelliformis subsp. umbelliformis	FR272	124.40.10.0	14.4	NA	NA	NA	NA	NA	36	4x	28/07/2016	44.31586	6.4565	2378	2575	7	v	C	No	Yes	neu	low	Average	37	F	T
Artemisia umbelliformis subsp. umbelliformis	CH186	124.40.10.0	14.43	3	NA	NA	NA	NA	36	4x	29/08/2018	46.53468	8.85178	1838	2575	7	v	C	No	Yes	neu	low	Average	37	F	T
Artemisia umbelliformis subsp. umbelliformis	FR636	124.40.10.0	14.09	13	NA	NA	NA	NA	36	4x	NA	44.2609	6.71199	2814	2575	7	v	C	No	Yes	neu	low	Average	37	F	T
Artemisia umbelliformis subsp. umbelliformis	FR698	124.40.10.0	14.05	NA	14.05	0.06	2.85	2.54	36	4x	NA	44.3321	6.7735	2560	2575	7	v	C	No	Yes	neu	low	Average	37	F	T
Artemisia vallesiaca	FR142	124.40.5.0	9.42	NA	9.42	0.02	2.98	2.65	36	4x	26/07/2016	44.25745	6.25511	1172	700	8	v	C	Yes	Yes	bas	low	veryDry	3	F	T
Artemisia vallesiaca	CH141	124.40.5.0	10.65	8	NA	NA	NA	NA	36	4x	22/08/2018	46.30972	7.80617	702	700	8	v	C	Yes	Yes	bas	low	veryDry	3	F	T
Artemisia vallesiaca	CH164	124.40.5.0	10.44	10	10.67	0.01	2.19	2.57	36	4x	24/08/2018	46.26176	7.47787	546	700	8	v	C	Yes	Yes	bas	low	veryDry	3	F	T
Artemisia vulgaris	CH137	124.40.1.0	6.62	7	NA	NA	NA	NA	16	2x	22/08/2018	46.30757	7.877726	894	910	7	v	H	No	Yes	neu	hig	Average	49	F	T
Artemisia vulgaris	FR568	124.40.1.0	6.77	NA	6.77	0.03	2.46	2.63	16	2x	NA	45.04589	6.32922	1590	910	7	v	H	No	Yes	neu	hig	Average	49	F	T
Artemisia vulgaris	MC6	124.40.1.0	6.66	NA	6.66	0.02	2.3	2.7	16	2x	NA	NA	NA	NA	910	7	v	H	No	Yes	neu	hig	Average	49	F	F

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Aster alpinus	FR21	124.4.6.0	7.77	NA	NA	NA	NA	NA	18	2x	24/07/2016	44.33802	6.29635	1893	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster alpinus	FR35	124.4.6.0	7.84	NA	NA	NA	NA	NA	18	2x	24/07/2016	44.33598	6.29635	1987	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster alpinus	FR37	124.4.6.0	7.77	NA	NA	NA	NA	NA	18	2x	24/07/2016	44.33535	6.29567	NA	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster alpinus	FR7	124.4.6.0	7.7	NA	NA	NA	NA	NA	18	2x	24/07/2016	44.33469	6.29546	NA	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster alpinus	FR127	124.4.6.0	7.7	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38569	6.39095	1922	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster alpinus	FR80	124.4.6.0	7.72	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38621	6.39601	2219	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster alpinus	FR100	124.4.6.0	7.67	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38339	6.39886	2119	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster alpinus	A113	124.4.6.0	7.72	4	NA	NA	NA	NA	18	2x	20/07/2018	47.12461	12.82355	2293	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster alpinus	A121	124.4.6.0	7.68	2	NA	NA	NA	NA	18	2x	20/07/2018	47.0675	12.83779	2203	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster alpinus	MB72	124.4.6.0	7.52	2	NA	NA	NA	NA	18	2x	22/07/2018	46.43517	13.64299	2036	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster alpinus	FR420	124.4.6.0	7.63	NA	NA	NA	NA	NA	18	2x	NA	44.31216	6.43589	1850	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster alpinus	FR382	124.4.6.0	7.63	4	NA	NA	NA	NA	18	2x	NA	44.40182	6.3838	2206	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster alpinus	FR391	124.4.6.0	7.69	10	7.69	0.02	2.22	2.46	18	2x	NA	44.3387	6.29283	1968	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster alpinus	FR462	124.4.6.0	7.9	19	NA	NA	NA	NA	18	2x	NA	44.72623	6.32373	2678	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster alpinus	FR531	124.4.6.0	7.43	6	NA	NA	NA	NA	18	2x	NA	45.06417	6.40772	2623	1633	6	v	H	No	Yes	bas	low	Dry	46	T	T
Aster amellus	RBGK2015-2549	124.4.5.0	27.48	NA	27.48	0.14	2.66	2.25	54	6x	NA	NA	NA	NA	910	7	v	H	No	Yes	bas	low	Dry	32	F	F
Aster amellus	NA	124.4.5.0	8.6	NA	NA	NA	NA	NA	18	2x	NA	NA	NA	NA	910	7	v	H	No	Yes	bas	low	Dry	32	F	F
Bellidiastrum michelii	CH20	124.4.7.0	3.42	8	NA	NA	NA	NA	18	2x	21/05/2018	46.45284	8.66036	1298	1400	5	v	H	No	Yes	bas	low	Average	48	F	T
Bellidiastrum michelii	A14	124.4.7.0	3.2	8	3.32	0	1.97	1.72	18	2x	15/06/2018	47.71728	15.77466	1530	1400	5	v	H	No	Yes	bas	low	Average	48	F	T
Bellidiastrum michelii	MB5	124.4.7.0	3.25	NA	3.25	0.01	2.71	2.4	18	2x	16/06/2018	46.433	13.74313	1619	1400	5	v	H	No	Yes	bas	low	Average	48	F	T
Bellidiastrum michelii	A70	124.4.7.0	3.34	10	NA	NA	NA	NA	18	2x	17/07/2018	47.12385	12.82639	2354	1400	5	v	H	No	Yes	bas	low	Average	48	F	T
Bellidiastrum michelii	FR415	124.4.7.0	3.53	14	NA	NA	NA	NA	18	2x	NA	44.31443	6.43696	1811	1400	5	v	H	No	Yes	bas	low	Average	48	F	T
Bellidiastrum michelii	OH297	124.4.7.0	3.24	NA	3.24	0.03	2.49	2.12	18	2x	NA	NA	NA	NA	1400	5	v	H	No	Yes	bas	low	Average	48	F	F
Bellis perennis	RBGK wild1	124.3.1.0	NA	NA	NA	NA	NA	NA	18	2x	NA	NA	NA	NA	910	1	v	H	No	Yes	neu	hig	Average	49	F	F
Bellis perennis	CZ1	124.3.1.0	NA	NA	NA	NA	NA	NA	18	2x	NA	NA	NA	NA	910	1	v	H	No	Yes	neu	hig	Average	49	F	F
Bellis perennis	JdV343	124.3.1.0	3.79	NA	3.79	0	2.27	2.64	18	2x	NA	NA	NA	NA	910	1	v	H	No	Yes	neu	hig	Average	49	F	F
Bellis sylvestris	FR486	124.3.2.0	3.21	5	NA	NA	NA	NA	36	2x	NA	44.57913	6.32992	2322	350	3	v	H	No	Yes	bas	low	veryDry	4	F	T
Berardia lanuginosa	FR213	124.55.1.0	2.95	NA	NA	NA	NA	NA	36	4x	27/07/2016	44.28474	6.4317	1772	1890	7	v	G	Yes	Yes	bas	low	Dry	8	F	T
Berardia lanuginosa	FR279	124.55.1.0	3	NA	NA	NA	NA	NA	36	4x	28/07/2016	44.31586	6.4565	2378	1890	7	v	G	Yes	Yes	bas	low	Dry	8	F	T
Berardia lanuginosa	FR252	124.55.1.0	3.03	NA	3.03	0.01	2.96	1.86	36	4x	28/07/2016	44.31535	6.44221	1961	1890	7	v	G	Yes	Yes	bas	low	Dry	8	F	T
Berardia lanuginosa	FR694b	124.55.1.0	3.07	1	NA	NA	NA	NA	36	4x	NA	44.32157	6.80667	2862	1890	7	v	G	Yes	Yes	bas	low	Dry	8	F	T
Berardia lanuginosa	FR366	124.55.1.0	3.18	4	NA	NA	NA	NA	36	4x	NA	44.40563	6.38222	2340	1890	7	v	G	Yes	Yes	bas	low	Dry	8	F	T
Berardia lanuginosa	OH307	124.55.1.0	NA	NA	NA	NA	NA	NA	36	4x	NA	NA	NA	NA	1890	7	v	G	Yes	Yes	bas	low	Dry	8	F	F
Bidens bipinnatus	IT75	124.23.5.0	10.16	15	10.16	0.09	2.36	2.66	72	6x	NA	45.73819	11.61502	145	350	7	a	T	No	No	neu	hig	Average	19	F	T
Bidens frondosus	IT82	124.23.4.0	3.37	4	NA	NA	NA	NA	48	4x	25/08/2018	45.84595	8.8902	345	350	8	a	T	No	No	neu	hig	Wet	24	F	T
Bidens frondosus	IT77	124.23.4.0	3.51	7	3.51	0.03	3.26	2.92	48	4x	NA	45.69664	11.63582	73	350	8	a	T	No	No	neu	hig	Wet	24	F	T
Bombycilaena erecta	OH405	124.9.1.0	NA	NA	1.59	0.01	4.68	3.6	28	2x	NA	NA	NA	NA	910	4	a	T	No	Yes	bas	low	veryDry	19	F	F
Bombycilaena erecta	MSB241824	124.9.1.0	1.65	NA	1.65	0.03	3.18	2.42	28	2x	NA	NA	NA	NA	910	4	a	T	No	Yes	bas	low	veryDry	19	F	F
Buphthalmum salicifolium	FR160	124.19.1.0	5.42	NA	5.42	0.04	2.61	1.64	20	2x	26/07/2016	44.27211	6.29882	1083	1050	6	v	H	No	Yes	bas	low	Dry	49	F	T
Buphthalmum salicifolium	A9	124.19.1.0	5.28	10	5.25	0.01	2.52	2.08	20	2x	14/06/2018	48.04065	16.04163	453	1050	6	v	H	No	Yes	bas	low	Dry	49	F	T
Buphthalmum salicifolium	A26	124.19.1.0	5.28	10	NA	NA	NA	NA	20	2x	15/06/2018	47.74579	15.77217	554	1050	6	v	H	No	Yes	bas	low	Dry	49	F	T
Buphthalmum salicifolium	MB97	124.19.1.0	NA	NA	NA	NA	NA	NA	20	2x	15/08/2018	46.24269	13.83591	1706	1050	6	v	H	No	Yes	bas	low	Dry	49	F	T
Buphthalmum salicifolium	FR528	124.19.1.0	5.09	9	NA	NA	NA	NA	20	2x	NA	44.35538	6.29001	1289	1050	6	v	H	No	Yes	bas	low	Dry	49	F	T
Buphthalmum salicifolium	IT29	124.19.1.0	NA	NA	NA	NA	NA	NA	20	2x	NA	45.79818	11.73817	243	1050	6	v	H	No	Yes	bas	low	Dry	49	F	T
Calendula arvensis	OH269	124.51.2.0	5.4	NA	5.4	0.05	2.71	2.99	44	4x	NA	NA	NA	NA	350	4	a	T	No	No	bas	med	veryDry	13	F	F
Calendula arvensis	OH268	124.51.2.0	5.43	NA	NA	NA	NA	NA	44	4x	NA	NA	NA	NA	350	4	a	T	No	No	bas	med	veryDry	13	F	F

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Calendula officinalis	MC7	124.51.1.0	3	NA	3	0.01	3.35	2.65	32	4x	NA	NA	NA	NA	583	6	a, b, v	T, H	No	No	neu	hig	Dry	13	F	F
Carduus acanthoides	A1	124.60.3.0	2	4	1.99	0	2.98	2.1	22	2x	14/06/2018	NA	NA	NA	583	6	b	H	No	Yes	neu	hig	Dry	15	F	F
Carduus crispus	CZ6	124.60.5.0	NA	NA	1.88	0.02	2.19	2.51	16	2x	NA	NA	NA	NA	910	7	b	H	No	Yes	neu	hig	Average	26	F	F
Carduus defloratus	CH45	124.60.9.0	2.1	8	2.11	0.03	3.66	2.71	22	2x	21/06/2018	46.10529	8.97186	1010	1550	5	v	H	No	Yes	bas	med	Dry	30	T	T
Carduus defloratus subsp. carlinifolius	FR6	124.60.9.3	2.15	NA	NA	NA	NA	NA	22	2x	24/07/2016	44.33469	6.29546	NA	1400	7	v	H	No	Yes	bas	med	Dry	9	T	T
Carduus defloratus subsp. carlinifolius	FR77a	124.60.9.3	2.18	NA	NA	NA	NA	NA	22	2x	25/07/2016	44.38621	6.39601	2219	1400	7	v	H	No	Yes	bas	med	Dry	9	T	T
Carduus defloratus subsp. carlinifolius	FR274	124.60.9.3	2.14	NA	NA	NA	NA	NA	22	2x	28/07/2016	44.31586	6.4565	2378	1400	7	v	H	No	Yes	bas	med	Dry	9	T	T
Carduus defloratus subsp. carlinifolius	FR254	124.60.9.3	NA	NA	NA	NA	NA	NA	22	2x	28/07/2016	44.31535	6.44221	1961	1400	7	v	H	No	Yes	bas	med	Dry	9	T	T
Carduus defloratus subsp. carlinifolius	FR418	124.60.9.3	2.25	7	NA	NA	NA	NA	22	2x	NA	44.31216	6.43589	1850	1400	7	v	H	No	Yes	bas	med	Dry	9	T	T
Carduus defloratus subsp. carlinifolius	FR393	124.60.9.3	2.1	10	2.1	0.05	3.11	2.74	22	2x	NA	44.34212	6.29506	1796	1400	7	v	H	No	Yes	bas	med	Dry	9	T	T
Carduus defloratus subsp. carlinifolius	FRR3	124.60.9.3	2.21	NA	2.21	0.05	3.39	1.96	22	2x	NA	NA	NA	NA	1400	7	v	H	No	Yes	bas	med	Dry	9	T	F
Carduus defloratus subsp. defloratus	CH55a	124.60.9.1	NA	NA	2.16	0.22	3.71	2.4	22	2x	22/06/2018	46.1341	8.7968	1535	1550	5	v	H	No	Yes	bas	med	Dry	30	F	T
Carduus defloratus subsp. defloratus	CH58	124.60.9.1	2.21	10	2.21	0	3.8	2.46	22	2x	22/06/2018	46.20733	8.80109	1441	1550	5	v	H	No	Yes	bas	med	Dry	30	F	T
Carduus defloratus subsp. defloratus	CH65	124.60.9.1	2.18	6	NA	NA	NA	NA	22	2x	23/06/2018	45.92674	9.01793	1560	1550	5	v	H	No	Yes	bas	med	Dry	30	F	T
Carduus defloratus subsp. defloratus	OH438	124.60.9.1	2.05	NA	2.05	0.01	2.57	2.03	22	2x	NA	NA	NA	NA	1550	5	v	H	No	Yes	bas	med	Dry	30	F	F
Carduus defloratus subsp. rhaeticus	CH55b	124.60.9.6	2.28	NA	2.28	0.02	2.47	3.61	22	2x	22/06/2018	46.1341	8.7968	1535	1400	7	v	H	No	Yes	bas	med	Dry	9	F	T
Carduus defloratus subsp. rhaeticus	IT55	124.60.9.6	2.27	NA	2.27	0	1.77	3.41	22	2x	NA	45.87816	11.66935	363	1400	7	v	H	No	Yes	bas	med	Dry	9	F	T
Carduus defloratus subsp. summanus	A15	124.60.9.4	2.05	7	2.05	0.03	3.1	2.41	22	2x	15/06/2018	47.71728	15.77466	1530	1400	6	v	H	NA	Yes	bas	low	Dry	17	F	T
Carduus defloratus subsp. summanus	A40	124.60.9.4	NA	NA	NA	NA	NA	NA	22	2x	17/06/2018	47.88478	15.75414	695	1400	6	v	H	NA	Yes	bas	low	Dry	17	F	T
Carduus defloratus subsp. summanus	MB71	124.60.9.4	NA	NA	2.15	0.03	2.68	3.05	22	2x	13/07/2018	46.40767	13.75068	1102	1400	6	v	H	NA	Yes	bas	low	Dry	17	F	T
Carduus defloratus subsp. summanus	A100	124.60.9.4	NA	NA	2.17	0.01	5.52	3.9	22	2x	19/07/2018	46.78347	12.788	1640	1400	6	v	H	NA	Yes	bas	low	Dry	17	F	T
Carduus nutans subsp. alpicola	FR394	124.60.1.2	2.09	10	2.09	0.01	1.79	3.66	16	2x	NA	44.34194	6.29082	1727	1983	6	b	H	Yes	Yes	bas	hig	Dry	5	F	T
Carduus nutans subsp. leiophyllus	IT63	124.60.1.4	1.95	10	NA	NA	NA	NA	16	2x	NA	45.5699	11.1536	458	1983	6	b	H	Yes	Yes	bas	hig	Dry	5	F	T
Carduus nutans subsp. leiophyllus	IT33	124.60.1.4	2.09	NA	2.09	0.01	3.1	2.58	16	2x	NA	45.80437	11.7325	240	1983	6	b	H	Yes	Yes	bas	hig	Dry	5	F	T
Carduus nutans subsp. nutans	OH450	124.60.1.1	1.93	NA	1.93	0.01	2.5	1.91	16	2x	NA	NA	NA	NA	910	6	b	H	No	Yes	bas	hig	Dry	28	F	F
Carduus personata	A57	124.60.4.0	NA	NA	1.97	0	3.45	2.25	18	2x	16/07/2018	46.56657	12.48257	1398	1400	7	v	H	No	Yes	bas	hig	Wet	43	F	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Carduus personata	A111	124.60.4.0	NA	NA	NA	NA	NA	NA	18	2x	20/07/2018	47.13009	12.807	1848	1400	7	v	H	No	Yes	bas	hig	Wet	43	F	T
Carduus personata	A103	124.60.4.0	2.03	NA	NA	NA	NA	NA	18	2x	20/07/2018	47.14296	12.81415	1601	1400	7	v	H	No	Yes	bas	hig	Wet	43	F	T
Carduus personata	CH100	124.60.4.0	2.08	12	NA	NA	NA	NA	18	2x	24/07/2018	46.61453	8.57122	1548	1400	7	v	H	No	Yes	bas	hig	Wet	43	F	T
Carduus personata subsp. personata	FR599	124.60.4.1	2	NA	2	0.01	3.26	2.55	18	2x	NA	NA	NA	NA	1400	7	v	H	No	Yes	bas	hig	Wet	43	F	F
Carduus pycnocephalus	GR05-2017a	124.60.13.0	6.82	NA	6.82	0.06	3.24	3.51	64	6x	NA	NA	NA	NA	583	5	a, b	T, H	No	Yes	bas	hig	veryDry	15	F	F
Carlina acanthifolia	FR713	124.52.5.0	NA	NA	NA	NA	NA	NA	20	2x	25/04/2018	44.47856	5.88877	1133	1050	7	v	H	No	Yes	neu	med	veryDry	13	F	T
Carlina acanthifolia	FR607	124.52.5.0	11.38	NA	11.38	0.02	2.62	3.16	20	2x	NA	44.86083	6.58783	1201	1050	7	v	H	No	Yes	neu	med	veryDry	13	F	T
Carlina acanthifolia	OH522	124.52.5.0	NA	NA	10.59	0.01	2.51	2.55	20	2x	NA	NA	NA	NA	1050	7	v	H	No	Yes	neu	med	veryDry	13	F	F
Carlina acaulis	CH156	124.52.4.0	10.38	7	NA	NA	NA	NA	20	2x	23/08/2018	45.98989	7.70511	2627	1400	6	v	H	No	Yes	neu	low	Dry	30	F	T
Carlina acaulis subsp. acaulis	A99	124.52.4.1	NA	NA	10.81	0.06	2.19	2.51	20	2x	19/07/2018	46.78347	12.788	1640	1400	6	v	H	No	Yes	neu	low	Dry	30	F	T
Carlina acaulis subsp. caulescens	FR261	124.52.4.2	11.07	NA	NA	NA	NA	NA	20	2x	28/07/2016	44.31535	6.44221	1961	1750	6	v	H	No	Yes	neu	low	Dry	42	F	T
Carlina acaulis subsp. caulescens	FR335	124.52.4.2	10.73	NA	NA	NA	NA	NA	20	2x	29/07/2016	44.26081	6.20881	1888	1750	6	v	H	No	Yes	neu	low	Dry	42	F	T
Carlina acaulis subsp. caulescens	FR319	124.52.4.2	10.74	NA	NA	NA	NA	NA	20	2x	29/07/2016	44.26084	6.20877	1890	1750	6	v	H	No	Yes	neu	low	Dry	42	F	T
Carlina acaulis subsp. caulescens	FR712	124.52.4.2	NA	NA	NA	NA	NA	NA	20	2x	23/04/2018	44.31944	6.42849	1557	1750	6	v	H	No	Yes	neu	low	Dry	42	F	T
Carlina acaulis subsp. caulescens	FR404	124.52.4.2	10.68	NA	10.68	0	2.2	3	20	2x	NA	44.30992	6.38858	1608	1750	6	v	H	No	Yes	neu	low	Dry	42	F	T
Carlina acaulis subsp. caulescens	FRR2	124.52.4.2	10.71	NA	NA	NA	NA	NA	20	2x	NA	NA	NA	NA	1750	6	v	H	No	Yes	neu	low	Dry	42	F	F
Carlina corymbosa	MB122	124.52.1.0	10.05	3	10.05	0.03	3.03	3.12	18	2x	13/09/2018	NA	NA	NA	350	7	v	H	No	Yes	bas	low	veryDry	8	F	F
Carlina vulgaris	FR163a	124.52.2.0	NA	NA	NA	NA	NA	NA	20	2x	26/07/2016	44.27211	6.29882	1083	910	7	b, v	H	No	Yes	bas	low	Dry	42	F	T
Carlina vulgaris	FR233	124.52.2.0	8.93	NA	8.93	0.03	2.54	2.31	20	2x	27/07/2016	44.27839	6.4237	1421	910	7	b, v	H	No	Yes	bas	low	Dry	42	F	T
Carlina vulgaris	MB112	124.52.2.0	9	1	NA	NA	NA	NA	20	2x	25/08/2018	NA	NA	NA	910	7	b, v	H	No	Yes	bas	low	Dry	42	F	F
Carlina vulgaris	OH5121	124.52.2.0	9	NA	8.62	0.04	2.12	2.12	20	2x	NA	NA	NA	NA	910	7	b, v	H	No	Yes	bas	low	Dry	42	F	F
Carpesium cernuum	OH527	124.18.1.0	8.23	3	8.14	0.07	3.43	3.83	40	2x	NA	NA	NA	NA	583	7	a, b	T, H	No	Yes	bas	hig	Average	22	F	F
Carthamus carduncellus	OH402	124.72.1.0	7.69	NA	7.69	0.02	2.56	2.51	48	4x	NA	NA	NA	NA	910	6	v	H	No	Yes	bas	low	veryDry	7	F	F
Carthamus lanatus	MB31	124.71.1.0	5.12	NA	5.12	0.04	2.33	1.56	44	4x	02/07/2018	NA	NA	NA	583	7	a	T	No	Yes	neu	hig	veryDry	15	F	F
Catananche caerulea	FR171	124.75.1.0	12.47	NA	12.47	0.06	1.76	1.74	18	2x	26/07/2016	44.2486	6.22959	1586	910	7	v	H	No	Yes	bas	med	veryDry	11	T	T
Catananche caerulea	FR345	124.75.1.0	12.61	NA	NA	NA	NA	NA	18	2x	29/07/2016	44.02726	6.22486	1358	910	7	v	H	No	Yes	bas	med	veryDry	11	T	T
Catananche caerulea	FR480	124.75.1.0	12.83	20	NA	NA	NA	NA	18	2x	NA	44.5716	6.37908	NA	910	7	v	H	No	Yes	bas	med	veryDry	11	T	T
Centaurea aspera	GR561	124.68.12.0	2.25	NA	2.21	0	3.09	2.12	22	2x	NA	NA	NA	NA	583	6	v	H	No	Yes	neu	med	veryDry	6	F	F
Centaurea benedicta	OH367	124.70.1.0	2.24	NA	2.24	0.07	5.48	1.9	22	2x	NA	NA	NA	NA	350	5	a	T	No	No	neu	hig	Dry	2	F	F
Centaurea calcitrapa	OH531	124.68.11.0	NA	NA	8.3	0.09	3.12	3.8	20	2x	NA	NA	NA	NA	583	7	b	H	No	Yes	bas	hig	Dry	13	F	F
Centaurea collina	OH Catalunya1	124.68.2.0	NA	NA	11.11	0.02	1.99	2.18	60	6x	NA	NA	NA	NA	350	6	v	H	No	Yes	neu	hig	veryDry	1	F	F
Centaurea dichroantha	MB70	124.68.3.0	NA	NA	3.69	0.02	2.9	2.48	20	2x	13/07/2018	46.37287	13.73543	580	700	7	v	H	No	Yes	bas	low	veryDry	3	F	T
Centaurea jacea	FR59	124.68.16.0	4.33	NA	NA	NA	NA	NA	44	4x	24/07/2016	44.34171	6.29706	1802	910	6	v	H	No	Yes	neu	med	Average	34	F	T
Centaurea jacea	FR130	124.68.16.0	4.21	NA	NA	NA	NA	NA	44	4x	25/07/2016	44.38569	6.39095	1922	910	6	v	H	No	Yes	neu	med	Average	34	F	T
Centaurea jacea	FR175	124.68.16.0	4.26	NA	NA	NA	NA	NA	44	4x	26/07/2016	44.2486	6.22959	1586	910	6	v	H	No	Yes	neu	med	Average	34	F	T
Centaurea jacea	A6	124.68.16.0	4.27	4	4.02	0.01	2.39	1.8	44	4x	14/06/2018	48.03317	16.02977	154	910	6	v	H	No	Yes	neu	med	Average	34	F	T
Centaurea jacea	MB2	124.68.16.0	NA	NA	4.04	0.01	3.29	2.59	44	4x	15/06/2018	NA	NA	NA	910	6	v	H	No	Yes	neu	med	Average	34	F	F
Centaurea jacea	CH42	124.68.16.0	4.59	4	NA	NA	NA	NA	44	4x	20/06/2018	46.02695	8.76651	380	910	6	v	H	No	Yes	neu	med	Average	34	F	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Centaurea jacea	MB99	124.68.16.0	NA	NA	NA	NA	NA	NA	44	4x	15/08/2018	46.26036	13.83811	1706	910	6	v	H	No	Yes	neu	med	Average	34	F	T
Centaurea jacea	OH419	124.68.16.0	NA	NA	4.17	0.01	2.02	1.77	44	4x	NA	NA	NA	NA	910	6	v	H	No	Yes	neu	med	Average	34	F	F
Centaurea jacea subsp. jacea	FR225	124.68.16.1	4.36	NA	NA	NA	NA	NA	44	4x	27/07/2016	44.27839	6.4237	1421	910	6	v	H	No	Yes	neu	med	Average	34	F	T
Centaurea jacea subsp. jacea	FR398	124.68.16.1	4.32	20	4.39	0	2.4	2	44	4x	NA	44.3291	6.30592	1694	910	6	v	H	No	Yes	neu	med	Average	34	F	T
Centaurea jacea subsp. jacea	OH397	124.68.16.1	NA	NA	4.24	0.03	2.6	1.91	44	4x	NA	NA	NA	NA	910	6	v	H	No	Yes	neu	med	Average	34	F	F
Centaurea leucophaea	FR151	124.68.7.0	2.58	NA	NA	NA	NA	NA	18	2x	26/07/2016	44.25745	6.25511	1172	700	6	b	H	No	Yes	bas	low	veryDry	8	F	T
Centaurea leucophaea	FR603	124.68.7.0	2.78	6	NA	NA	NA	NA	18	2x	NA	44.85933	6.58506	1233	700	6	b	H	No	Yes	bas	low	veryDry	8	F	T
Centaurea leucophaea	FR561	124.68.7.0	2.55	1	2.57	0.02	2.26	3.21	18	2x	NA	NA	NA	NA	700	6	b	H	No	Yes	bas	low	veryDry	8	F	F
Centaurea margaritacea	CH169	124.68.14.0	1.71	12	1.82	0.04	2.54	1.86	20	2x	28/08/2018	46.18729	8.99199	274	583	7	b	H	No	Yes	neu	med	veryDry	6	F	T
Centaurea nervosa	CH118	124.68.25.0	NA	NA	2.28	0.07	3.2	1.88	22	2x	26/07/2018	46.53711	8.8378	1754	1750	7	v	H	No	Yes	neu	med	Average	31	F	T
Centaurea nervosa	CH129	124.68.25.0	NA	NA	NA	NA	NA	NA	22	2x	27/07/2018	45.86374	7.15908	2255	1750	7	v	H	No	Yes	neu	med	Average	31	F	T
Centaurea nervosa	CH175	124.68.25.0	2.26	17	2.32	0.01	4.08	2.96	22	2x	29/08/2018	46.54987	8.70095	1939	1750	7	v	H	No	Yes	neu	med	Average	31	F	T
Centaurea nigra	A51	124.68.21.0	4.19	8	NA	NA	NA	NA	44	4x	19/06/2018	47.32495	11.68786	465	910	7	v	H	No	Yes	aci	med	Average	4	F	T
Centaurea nigra	A60	124.68.21.0	4.46	6	NA	NA	NA	NA	44	4x	16/07/2018	46.56657	12.48257	1398	910	7	v	H	No	Yes	aci	med	Average	4	F	T
Centaurea nigra	OH285	124.68.21.0	4.4	NA	4.4	0.07	3.04	2.48	44	4x	NA	NA	NA	NA	910	7	v	H	No	Yes	aci	med	Average	4	F	F
Centaurea nigrescens	IT56	124.68.18.0	4.28	NA	NA	NA	NA	NA	44	4x	NA	45.87816	11.66935	363	1050	7	v	H	No	Yes	neu	med	Average	31	F	T
Centaurea nigrescens	OH343	124.68.18.0	4.44	NA	4.44	0.04	3.25	2.63	44	4x	NA	NA	NA	NA	1050	7	v	H	No	Yes	neu	med	Average	31	F	F
Centaurea nigrescens subsp. ramosa	IT64	124.68.18.1	4.5	5	4.41	0.01	2.59	2.09	44	4x	NA	45.5699	11.1536	458	1050	7	v	H	No	Yes	neu	med	Average	31	F	T
Centaurea nigrescens subsp. ramosa	IT66	124.68.18.1	4.25	NA	NA	NA	NA	NA	44	4x	NA	45.6833	11.17753	635	1050	7	v	H	No	Yes	neu	med	Average	31	F	T
Centaurea pectinata	OH333	124.68.26.0	2.79	NA	2.79	0.08	3.79	1.69	22	2x	NA	NA	NA	NA	700	6	v	H	No	Yes	aci	low	veryDry	4	F	F
Centaurea phrygia pseudophrygia	A110	124.68.23.0	NA	NA	2.24	0.01	3.48	1.98	22	2x	20/07/2018	47.13009	12.807	1848	1190	7	v	H	No	Yes	neu	med	Average	13	F	T
Centaurea rhaetica	CH35	124.68.28.0	2.36	4	2.4	0.03	4.42	3.79	22	2x	22/05/2018	45.99658	9.21958	618	1190	6	v	H	Yes	Yes	bas	low	Dry	7	F	T
Centaurea rhaetica	CH69	124.68.28.0	NA	NA	2.37	0.01	2.28	1.9	22	2x	24/06/2018	45.99966	9.21657	738	1190	6	v	H	Yes	Yes	bas	low	Dry	7	F	T
Centaurea rupestris	MB22a	124.68.4.0	NA	NA	3.46	0.01	2.69	2.74	20	2x	24/06/2018	NA	NA	NA	700	6	v	H	No	Yes	bas	low	veryDry	2	F	F
Centaurea rupestris	MB35	124.68.4.0	NA	NA	3.75	0	3.12	2.76	20	2x	02/07/2018	NA	NA	NA	700	6	v	H	No	Yes	bas	low	veryDry	2	F	F
Centaurea rupestris	MB34	124.68.4.0	NA	NA	3.88	0.01	2.66	1.97	20	2x	02/07/2018	NA	NA	NA	700	6	v	H	No	Yes	bas	low	veryDry	2	F	F
Centaurea rupestris	MB33	124.68.4.0	NA	NA	3.8	0.02	2.52	2.16	20	2x	02/07/2018	NA	NA	NA	700	6	v	H	No	Yes	bas	low	veryDry	2	F	F
Centaurea rupestris	MB120	124.68.4.0	NA	NA	NA	NA	NA	NA	20	2x	24/08/2018	NA	NA	NA	700	6	v	H	No	Yes	bas	low	veryDry	2	F	F
Centaurea scabiosa	A8	124.68.5.0	3.63	10	3.63	0.01	2.34	2.25	20	2x	14/06/2018	48.04065	16.04163	453	910	6	v	H	No	Yes	bas	low	Dry	45	F	T
Centaurea scabiosa	A49	124.68.5.0	22.13	1	NA	NA	NA	NA	20	2x	19/06/2018	47.32495	11.68786	465	910	6	v	H	No	Yes	bas	low	Dry	45	F	T
Centaurea scabiosa	IT92	124.68.5.0	3.66	6	NA	NA	NA	NA	20	2x	27/08/2018	46.0054	9.22227	820	910	6	v	H	No	Yes	bas	low	Dry	45	F	T
Centaurea scabiosa	FR421	124.68.5.0	NA	NA	NA	NA	NA	NA	20	2x	NA	44.31216	6.43589	1850	910	6	v	H	No	Yes	bas	low	Dry	45	F	T
Centaurea scabiosa subsp. alpestris	JB Lautaret23	124.68.5.2	3.83	6	4	0.04	3.31	2.31	20	4x	NA	NA	NA	NA	1750	6	v	H	No	Yes	bas	med	Dry	33	F	F
Centaurea scabiosa subsp. fritschii	MB19	124.68.5.4	NA	NA	3.74	0.01	3.36	2.52	20	2x	24/06/2018	NA	NA	NA	583	6	v	H	No	Yes	bas	low	Dry	7	F	F
Centaurea scabiosa subsp. grinensis	CH36	124.68.5.5	3.74	3	3.68	0.06	2.77	2.82	20	2x	22/05/2018	45.99658	9.21958	618	1050	6	v	H	No	Yes	bas	low	veryDry	10	F	T
Centaurea scabiosa subsp. grinensis	CH46	124.68.5.5	4.02	10	NA	NA	NA	NA	20	2x	21/06/2018	45.96212	8.88513	417	1050	6	v	H	No	Yes	bas	low	veryDry	10	F	T
Centaurea scabiosa subsp. scabiosa	OH491	124.68.5.1	3.79	2	NA	NA	NA	NA	20	2x	NA	NA	NA	NA	910	6	v	H	No	Yes	bas	low	Dry	45	F	F

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Centaurea stoebe	MC8	124.68.8.0	3.19	NA	3.19	0.01	3.16	2.9	18	2x	NA	NA	NA	NA	700	6	b	H	No	Yes	neu	med	veryDry	21	F	F
Centaurea uniflora	FR15	124.68.24.0	2.25	NA	NA	NA	NA	NA	22	2x	24/07/2016	44.34002	6.29641	1847	1610	7	v	H	No	Yes	neu	med	Dry	9	T	T
Centaurea uniflora	FR5	124.68.24.0	2.26	NA	NA	NA	NA	NA	22	2x	24/07/2016	44.33469	6.29546	NA	1610	7	v	H	No	Yes	neu	med	Dry	9	T	T
Centaurea uniflora	FR10	124.68.24.0	2.25	NA	NA	NA	NA	NA	22	2x	24/07/2016	44.33469	6.29546	NA	1610	7	v	H	No	Yes	neu	med	Dry	9	T	T
Centaurea uniflora	FR39	124.68.24.0	2.26	NA	NA	NA	NA	NA	22	2x	24/07/2016	44.33535	6.29567	NA	1610	7	v	H	No	Yes	neu	med	Dry	9	T	T
Centaurea uniflora	FR54	124.68.24.0	2.28	NA	NA	NA	NA	NA	22	2x	24/07/2016	44.34171	6.29706	1802	1610	7	v	H	No	Yes	neu	med	Dry	9	T	T
Centaurea uniflora	FR22	124.68.24.0	2.24	NA	2.33	0.04	2	2.22	22	2x	24/07/2016	44.33802	6.29635	1893	1610	7	v	H	No	Yes	neu	med	Dry	9	T	T
Centaurea uniflora	FR66	124.68.24.0	2.23	NA	NA	NA	NA	NA	22	2x	24/07/2016	NA	NA	NA	1610	7	v	H	No	Yes	neu	med	Dry	9	T	F
Centaurea uniflora	FR211	124.68.24.0	2.29	NA	NA	NA	NA	NA	22	2x	27/07/2016	44.28474	6.4317	1772	1610	7	v	H	No	Yes	neu	med	Dry	9	T	T
Centaurea uniflora	FR242	124.68.24.0	2.26	NA	NA	NA	NA	NA	22	2x	28/07/2016	44.31535	6.44221	1961	1610	7	v	H	No	Yes	neu	med	Dry	9	T	T
Centaurea uniflora	FR273	124.68.24.0	2.25	NA	NA	NA	NA	NA	22	2x	28/07/2016	44.31586	6.4565	2378	1610	7	v	H	No	Yes	neu	med	Dry	9	T	T
Centaurea uniflora	FR308	124.68.24.0	2.26	NA	NA	NA	NA	NA	22	2x	29/07/2016	44.40792	6.385497	2505	1610	7	v	H	No	Yes	neu	med	Dry	9	T	T
Centaurea uniflora	FR331	124.68.24.0	2.32	NA	NA	NA	NA	NA	22	2x	29/07/2016	44.26081	6.20881	1888	1610	7	v	H	No	Yes	neu	med	Dry	9	T	T
Centaurea uniflora	FR389	124.68.24.0	2.33	30	NA	NA	NA	NA	22	2x	NA	44.332	6.29235	1988	1610	7	v	H	No	Yes	neu	med	Dry	9	T	T
Centaurea uniflora	FR676	124.68.24.0	2.42	4	NA	NA	NA	NA	22	2x	NA	NA	NA	NA	1610	7	v	H	No	Yes	neu	med	Dry	9	T	F
Centaurea uniflora	OH293	124.68.24.0	NA	NA	NA	NA	NA	NA	22	2x	NA	NA	NA	NA	1610	7	v	H	No	Yes	neu	med	Dry	9	T	F
Centaurea valesiaca	CH142	124.68.9.0	1.99	4	1.97	0.03	2.91	2.11	18	2x	22/08/2018	46.30989	7.80409	663	910	7	b	H	Yes	Yes	bas	low	veryDry	4	F	T
Chondrilla juncea	CH133	124.94.1.0	3.37	9	NA	NA	NA	NA	15	3x	22/08/2018	46.25319	7.40579	600	700	6	v	H	No	Yes	neu	med	veryDry	28	F	T
Chondrilla juncea	OH516	124.94.1.0	NA	NA	NA	NA	NA	NA	15	3x	NA	NA	NA	NA	700	6	v	H	No	Yes	neu	med	veryDry	28	F	F
Chondrilla juncea	OH345	124.94.1.0	NA	NA	4.42	0.03	3.66	2.11	15	3x	NA	NA	NA	NA	700	6	v	H	No	Yes	neu	med	veryDry	28	F	F
Cichorium intybus	OH265	124.74.1.0	3.22	NA	3.22	0.12	2.44	1.72	18	2x	NA	NA	NA	NA	910	7	v	H	No	Yes	bas	med	Dry	47	F	F
Cirsium acaulon	FR3	124.61.13.0	2.73	NA	NA	NA	NA	NA	34	2x	24/07/2016	44.33469	6.29546	NA	1400	7	v	H	No	Yes	bas	med	Dry	46	T	T
Cirsium acaulon	FR50	124.61.13.0	2.8	NA	NA	NA	NA	NA	34	2x	24/07/2016	44.34171	6.29706	1802	1400	7	v	H	No	Yes	bas	med	Dry	46	T	T
Cirsium acaulon	FR65	124.61.13.0	2.73	NA	NA	NA	NA	NA	34	2x	24/07/2016	NA	NA	NA	1400	7	v	H	No	Yes	bas	med	Dry	46	T	F
Cirsium acaulon	FR169	124.61.13.0	2.66	NA	NA	NA	NA	NA	34	2x	26/07/2016	44.2486	6.22959	1586	1400	7	v	H	No	Yes	bas	med	Dry	46	T	T
Cirsium acaulon	FR188	124.61.13.0	2.71	NA	NA	NA	NA	NA	34	2x	26/07/2016	44.2476	6.23499	1380	1400	7	v	H	No	Yes	bas	med	Dry	46	T	T
Cirsium acaulon	FR198	124.61.13.0	2.66	NA	2.77	0.01	3.67	2.71	34	2x	27/07/2016	44.28474	6.4317	1772	1400	7	v	H	No	Yes	bas	med	Dry	46	T	T
Cirsium acaulon	FR249	124.61.13.0	2.62	NA	NA	NA	NA	NA	34	2x	28/07/2016	44.31535	6.44221	1961	1400	7	v	H	No	Yes	bas	med	Dry	46	T	T
Cirsium acaulon	FR332	124.61.13.0	2.71	NA	NA	NA	NA	NA	34	2x	29/07/2016	44.26081	6.20881	1888	1400	7	v	H	No	Yes	bas	med	Dry	46	T	T
Cirsium acaulon	FR320	124.61.13.0	2.64	NA	NA	NA	NA	NA	34	2x	29/07/2016	44.26084	6.20877	1890	1400	7	v	H	No	Yes	bas	med	Dry	46	T	T
Cirsium acaulon	MB107	124.61.13.0	2.77	3	NA	NA	NA	NA	34	2x	24/08/2018	NA	NA	NA	1400	7	v	H	No	Yes	bas	med	Dry	46	T	F
Cirsium acaulon	FR617	124.61.13.0	2.79	4	NA	NA	NA	NA	34	2x	NA	44.3419	6.2941	1716	1400	7	v	H	No	Yes	bas	med	Dry	46	T	T
Cirsium alsophilum	IT54	124.61.7.0	2.62	15	2.73	0.05	3.21	2.46	34	2x	NA	45.87816	11.66935	363	1190	6	v	H	No	Yes	neu	hig	Wet	19	F	T
Cirsium alsophilum	FR701	124.61.7.0	2.35	11	NA	NA	NA	NA	34	2x	NA	44.20113	7.12267	1811	1190	6	v	H	No	Yes	neu	hig	Wet	19	F	T
Cirsium alsophilum	FR585	124.61.7.0	2.43	4	NA	NA	NA	NA	34	2x	NA	NA	NA	NA	1190	6	v	H	No	Yes	neu	hig	Wet	19	F	F
Cirsium arvense	FR1a	124.61.19.0	3.01	NA	NA	NA	NA	NA	34	2x	24/07/2016	44.33469	6.29546	NA	910	7	v	G	No	Yes	neu	hig	Average	49	F	T
Cirsium arvense	FR227	124.61.19.0	3.16	NA	NA	NA	NA	NA	34	2x	27/07/2016	44.27839	6.4237	1421	910	7	v	G	No	Yes	neu	hig	Average	49	F	T
Cirsium arvense	A2	124.61.19.0	2.95	2	3	0.01	2.54	2.15	34	2x	14/06/2018	NA	NA	NA	910	7	v	G	No	Yes	neu	hig	Average	49	F	F
Cirsium arvense	A56	124.61.19.0	3.18	7	NA	NA	NA	NA	34	2x	19/06/2018	47.32581	11.69125	554	910	7	v	G	No	Yes	neu	hig	Average	49	F	T
Cirsium arvense	IT65	124.61.19.0	3.08	65	NA	NA	NA	NA	34	2x	NA	45.6833	11.17753	635	910	7	v	G	No	Yes	neu	hig	Average	49	F	T
Cirsium arvense	FR423	124.61.19.0	NA	NA	NA	NA	NA	NA	34	2x	NA	44.31742	6.38509	1613	910	7	v	G	No	Yes	neu	hig	Average	49	F	T
Cirsium arvense	IT37	124.61.19.0	NA	NA	NA	NA	NA	NA	34	2x	NA	45.72603	11.64959	75	910	7	v	G	No	Yes	neu	hig	Average	49	F	T
Cirsium arvense	OH455	124.61.19.0	NA	NA	3.07	0.01	2.72	1.97	34	2x	NA	NA	NA	NA	910	7	v	G	No	Yes	neu	hig	Average	49	F	F
Cirsium arvense	OH328	124.61.19.0	NA	NA	NA	NA	NA	NA	34	2x	NA	NA	NA	NA	910	7	v	G	No	Yes	neu	hig	Average	49	F	F
Cirsium canum	CZ7	124.61.16.0	NA	NA	2.44	0.01	2.88	2.66	34	2x	NA	NA	NA	NA	583	6	v	G, H	No	Yes	neu	hig	Wet	2	F	F
Cirsium carniolicum	MB103	124.61.10.0	NA	NA	NA	NA	NA	NA	34	2x	31/07/2018	46.42961	14.24383	1284	1190	6	v	H	Yes	Yes	bas	hig	Wet	8	F	T
Cirsium carniolicum	FR591	124.61.10.0	2.58	NA	2.61	0.02	2.79	2.01	34	2x	NA	NA	NA	NA	1190	6	v	H	Yes	Yes	bas	hig	Wet	8	F	F

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Cirsium carniolicum subsp. carniolicum	A24	124.61.10.0	2.44	3	2.39	0.01	2.5	2.35	34	2x	15/06/2018	47.73669	15.78478	552	1190	6	v	H	Yes	Yes	bas	hig	Wet	8	F	T
Cirsium eriophorum	FR245	124.61.3.0	3.77	NA	NA	NA	NA	NA	34	2x	28/07/2016	44.31535	6.44221	1961	1190	6	b	H	No	Yes	bas	hig	Dry	33	F	T
Cirsium eriophorum	CH97	124.61.3.0	NA	NA	3.79	0.01	2.7	2.72	34	2x	24/07/2018	46.50387	8.50891	1389	1190	6	b	H	No	Yes	bas	hig	Dry	33	F	T
Cirsium eriophorum	MB115	124.61.3.0	3.79	2	NA	NA	NA	NA	34	2x	27/08/2018	NA	NA	NA	1190	6	b	H	No	Yes	bas	hig	Dry	33	F	F
Cirsium eriophorum	FR611	124.61.3.0	NA	NA	3.79	0.03	2.58	2.23	34	2x	NA	44.90103	6.654416	1327	1190	6	b	H	No	Yes	bas	hig	Dry	33	F	T
Cirsium eriophorum	FR618	124.61.3.0	3.76	9	NA	NA	NA	NA	34	2x	NA	44.3419	6.2941	1716	1190	6	b	H	No	Yes	bas	hig	Dry	33	F	T
Cirsium erisithales	CH37	124.61.8.0	2.56	7	2.56	0.03	4.03	3.43	34	2x	22/05/2018	45.95981	9.00145	654	1190	6	v	H	No	Yes	bas	med	Average	29	F	T
Cirsium erisithales	A23	124.61.8.0	2.41	10	2.44	0.01	2.29	2.05	34	2x	15/06/2018	47.72835	15.79708	553	1190	6	v	H	No	Yes	bas	med	Average	29	F	T
Cirsium erisithales	MB3	124.61.8.0	NA	NA	2.43	0.01	2.7	2.01	34	2x	16/06/2018	46.09419	13.8997	236	1190	6	v	H	No	Yes	bas	med	Average	29	F	T
Cirsium erisithales	MB50	124.61.8.0	2.42	NA	NA	NA	NA	NA	34	2x	11/07/2018	NA	NA	NA	1190	6	v	H	No	Yes	bas	med	Average	29	F	F
Cirsium erisithales	A61	124.61.8.0	2.63	6	NA	NA	NA	NA	34	2x	16/07/2018	46.56657	12.48257	1398	1190	6	v	H	No	Yes	bas	med	Average	29	F	T
Cirsium erisithales	A98	124.61.8.0	2.58	4	NA	NA	NA	NA	34	2x	19/07/2018	46.78288	12.78845	1638	1190	6	v	H	No	Yes	bas	med	Average	29	F	T
Cirsium heterophyllum	FR567	124.61.14.0	2.5	11	2.5	0.01	3.27	2.55	34	2x	NA	45.03308	6.39406	1908	1190	6	v	H	No	Yes	neu	hig	Wet	33	F	T
Cirsium hybrid?	OH467	124.61	NA	NA	2.84	0.01	3.44	2.53	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	F
Cirsium monspessulanum	FR195	124.61.17.0	2.3	NA	2.4	0.01	4.42	2.46	34	2x	26/07/2016	44.2476	6.23499	1380	910	6	v	H	No	Yes	neu	hig	Wet	11	T	T
Cirsium monspessulanum	FR351	124.61.17.0	2.29	NA	NA	NA	NA	NA	34	2x	29/07/2016	44.02726	6.22486	1358	910	6	v	H	No	Yes	neu	hig	Wet	11	T	T
Cirsium monspessulanum	FR449	124.61.17.0	2.51	15	NA	NA	NA	NA	34	2x	NA	44.67046	6.23971	1052	910	6	v	H	No	Yes	neu	hig	Wet	11	T	T
Cirsium monspessulanum	FR602	124.61.17.0	2.47	6	NA	NA	NA	NA	34	2x	NA	44.85825	6.57948	1257	910	6	v	H	No	Yes	neu	hig	Wet	11	T	T
Cirsium monspessulanum	OH456	124.61.17.0	NA	NA	2.34	0.01	2.74	2.35	34	2x	NA	NA	NA	NA	910	6	v	H	No	Yes	neu	hig	Wet	11	T	F
Cirsium morisianum	FR521	124.61.2.0	NA	NA	2.64	0.05	2.87	3.01	34	2x	NA	44.35559	6.29353	1440	910	6	b	H	No	Yes	neu	med	veryDry	5	T	T
Cirsium oleraceum	A27	124.61.11.0	2.48	10	2.4	0	2.81	2.22	34	2x	15/06/2018	47.8776	15.7701	719	910	7	v	H	No	Yes	bas	hig	Wet	37	F	T
Cirsium oleraceum	A25	124.61.11.0	2.56	5	2.55	0.01	2.13	2	34	2x	15/06/2018	47.73669	15.78478	552	910	7	v	H	No	Yes	bas	hig	Wet	37	F	T
Cirsium oleraceum	A55	124.61.11.0	NA	NA	NA	NA	NA	NA	34	2x	19/06/2018	47.32581	11.69125	554	910	7	v	H	No	Yes	bas	hig	Wet	37	F	T
Cirsium oleraceum	A105	124.61.11.0	2.46	3	NA	NA	NA	NA	34	2x	20/07/2018	47.14314	12.81543	1650	910	7	v	H	No	Yes	bas	hig	Wet	37	F	T
Cirsium palustre	CH59	124.61.18.0	NA	NA	2.8	0.04	3.15	3.17	34	2x	22/06/2018	46.20715	8.80046	1443	910	6	b	H	No	Yes	neu	med	Wet	45	F	T
Cirsium palustre	CH72	124.61.18.0	NA	NA	2.92	0.03	3.34	2.4	34	2x	24/06/2018	45.97311	9.066946	746	910	6	b	H	No	Yes	neu	med	Wet	45	F	T
Cirsium pannonicum	A7	124.61.15.0	2.64	10	2.59	0	2.69	2.18	34	2x	14/06/2018	48.04065	16.04163	453	700	5	v	H	No	Yes	bas	low	Dry	12	F	T
Cirsium pannonicum	MB20	124.61.15.0	NA	NA	2.51	0	3.55	3.04	34	2x	24/06/2018	NA	NA	NA	700	5	v	H	No	Yes	bas	low	Dry	12	F	F
Cirsium pannonicum	IT53	124.61.15.0	2.56	15	NA	NA	NA	NA	34	2x	NA	45.87816	11.66935	363	700	5	v	H	No	Yes	bas	low	Dry	12	F	T
Cirsium pannonicum	IT34	124.61.15.0	2.42	NA	2.47	0	3.14	2.83	34	2x	NA	45.79267	11.70271	431	700	5	v	H	No	Yes	bas	low	Dry	12	F	T
Cirsium rivulare	A28	124.61.6.0	2.49	10	2.5	0	3.08	2.43	34	2x	15/06/2018	47.87259	15.78424	736	700	6	v	H	No	Yes	neu	med	Wet	22	F	T
Cirsium spinosissimum	FR282	124.61.12.0	2.65	NA	NA	NA	NA	NA	34	2x	28/07/2016	44.31586	6.4565	2378	2100	7	v	H	Yes	Yes	neu	hig	Wet	44	F	T
Cirsium spinosissimum	FR651a	124.61.12.0	2.71	8	NA	NA	NA	NA	34	2x	NA	44.28896	6.60467	2317	2100	7	v	H	Yes	Yes	neu	hig	Wet	44	F	T
Cirsium spinosissimum	FR643	124.61.12.0	NA	NA	NA	NA	NA	NA	34	2x	NA	44.25952	6.71632	2692	2100	7	v	H	Yes	Yes	neu	hig	Wet	44	F	T
Cirsium spinosissimum	FR457	124.61.12.0	2.49	4	NA	NA	NA	NA	34	2x	NA	44.72252	6.31779	2553	2100	7	v	H	Yes	Yes	neu	hig	Wet	44	F	T
Cirsium spinosissimum	RD15	124.61.12.0	2.53	NA	2.63	0.02	2.09	3.3	34	2x	NA	NA	NA	NA	2100	7	v	H	Yes	Yes	neu	hig	Wet	44	F	F
Cirsium tuberosum	FR525	124.61.5.0	2.8	7	2.72	0.02	5	3.35	34	2x	NA	44.35538	6.29001	1289	910	6	v	G, H	No	Yes	bas	low	Average	17	F	T
Cirsium vulgare	FR75a	124.61.4.0	2.12	NA	NA	NA	NA	NA	34	2x	24/07/2016	NA	NA	NA	910	6	b	H	No	Yes	neu	hig	Average	49	F	F
Cirsium vulgare	FR113	124.61.4.0	2.18	NA	NA	NA	NA	NA	34	2x	25/07/2016	44.37932	6.3955	1985	910	6	b	H	No	Yes	neu	hig	Average	49	F	T
Cirsium vulgare	FR128	124.61.4.0	2.18	NA	NA	NA	NA	NA	34	2x	25/07/2016	44.38569	6.39095	1922	910	6	b	H	No	Yes	neu	hig	Average	49	F	T
Cirsium vulgare	FR114	124.61.4.0	2.15	NA	NA	NA	NA	NA	34	2x	25/07/2016	44.37932	6.3955	1985	910	6	b	H	No	Yes	neu	hig	Average	49	F	T
Cirsium vulgare	FR77b	124.61.4.0	2.19	NA	NA	NA	NA	NA	34	2x	25/07/2016	44.38621	6.39601	2219	910	6	b	H	No	Yes	neu	hig	Average	49	F	T
Cirsium vulgare	MB91	124.61.4.0	NA	NA	NA	NA	NA	NA	34	2x	26/07/2018	NA	NA	NA	910	6	b	H	No	Yes	neu	hig	Average	49	F	F
Cirsium vulgare	FR524	124.61.4.0	2.76	6	NA	NA	NA	NA	34	2x	NA	44.35559	6.29353	1440	910	6	b	H	No	Yes	neu	hig	Average	49	F	T
Cirsium waldesteinii	MB54	124.61.9.0	NA	NA	2.54	0.01	2.41	2.21	34	2x	11/07/2018	NA	NA	NA	1283	7	v	H	No	Yes	aci	med	Average	2	F	F
Cirsium waldesteinii x erisithales	MB49	124.61	NA	NA	2.44	0.01	3.73	2.92	NA	NA	11/07/2018	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	F

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Cota tinctoria subsp. tinctoria	A47	124.30.7.1	10.15	10	NA	NA	NA	NA	18	2x	19/06/2018	47.32495	11.68786	465	910	6	b, v, A	H, C	No	Yes	neu	low	veryDry	23	F	T
Cota tinctoria subsp. tinctoria	CH165a	124.30.7.1	9.71	4	NA	NA	NA	NA	18	2x	24/08/2018	46.18626	8.09195	1187	910	6	b, v, A	H, C	No	Yes	neu	low	veryDry	23	F	T
Cota tinctoria subsp. tinctoria	FR624	124.30.7.1	9.79	NA	NA	NA	NA	NA	18	2x	NA	44.29824	6.568403	NA	910	6	b, v, A	H, C	No	Yes	neu	low	veryDry	23	F	T
Cota tinctoria subsp. tinctoria	FR608	124.30.7.1	9.71	NA	9.71	0.02	2.57	3.02	18	2x	NA	44.86288	6.58887	1215	910	6	b, v, A	H, C	No	Yes	neu	low	veryDry	23	F	T
Cota tinctoria subsp. tinctoria	JB Lautaret3	124.30.7.1	9.5	8	NA	NA	NA	NA	18	2x	NA	NA	NA	NA	910	6	b, v, A	H, C	No	Yes	neu	low	veryDry	23	F	F
Cota tinctoria subsp. tinctoria	RBGK2001-1966	124.30.7.1	9.72	NA	9.72	0.05	2.5	2.53	18	2x	NA	NA	NA	NA	910	6	b, v, A	H, C	No	Yes	neu	low	veryDry	23	F	F
Cota triumfettii	RBGK1979-4599	124.30.8.0	9.67	NA	9.67	0.02	1.62	1.94	18	2x	NA	NA	NA	NA	700	6	b, v	H	No	Yes	neu	med	veryDry	9	F	F
Crepis albida	OH340	124.97.13.0	6.83	NA	6.83	0.07	2.24	1.69	10	2x	NA	NA	NA	NA	1050	6	v	H	No	Yes	bas	low	Dry	13	F	F
Crepis albida	OH380	124.97.13.0	NA	NA	6.87	0.08	4.37	3.49	10	2x	NA	NA	NA	NA	1050	6	v	H	No	Yes	bas	low	Dry	13	F	F
Crepis aurea	MB44	124.97.7.0	6.9	NA	6.9	0.01	2.88	2.17	10	2x	08/07/2018	46.43314	14.29066	1504	1890	6	v	H	No	Yes	neu	hig	Average	41	F	T
Crepis aurea	A89	124.97.7.0	4.64	3	NA	NA	NA	NA	10	2x	19/07/2018	46.76274	12.80268	2270	1890	6	v	H	No	Yes	neu	hig	Average	41	F	T
Crepis aurea	OH294	124.97.7.0	NA	NA	NA	NA	NA	NA	10	2x	NA	NA	NA	NA	1890	6	v	H	No	Yes	neu	hig	Average	41	F	F
Crepis biennis	CH16	124.97.15.0	19.14	17	18.28	0.26	3.88	2.51	40	4x	21/05/2018	46.37077	8.55672	667	910	5	b, v	H	No	Yes	neu	hig	Average	44	F	T
Crepis biennis	OH381	124.97.15.0	NA	NA	18.44	0.07	4.25	3.07	40	4x	NA	NA	NA	NA	910	5	b, v	H	No	Yes	neu	hig	Average	44	F	F
Crepis capillaris	CH76	124.97.24.0	4.43	NA	4.43	0.02	3.6	2.28	6	2x	25/06/2018	45.83786	8.87339	423	910	6	a, b	T, H	No	Yes	neu	med	Average	44	F	T
Crepis conyzifolia	CH122a	124.97.10.0	NA	NA	11.08	0.04	2	1.95	8	2x	26/07/2018	46.59242	8.46232	2086	1750	6	v	H	No	Yes	aci	med	Average	39	F	T
Crepis conyzifolia	OH311	124.97.10.0	NA	NA	NA	NA	NA	NA	8	2x	NA	NA	NA	NA	1750	6	v	H	No	Yes	aci	med	Average	39	F	F
Crepis foetida subsp. foetida	OH253	124.97.21.1	4.38	NA	4.38	0.03	2.54	1.72	10	2x	NA	NA	NA	NA	583	6	a, b	T, H	No	Yes	neu	hig	veryDry	29	F	F
Crepis jacquinii subsp. kerneri	MB113	124.97.5.0	NA	NA	11.36	0.02	2.29	1.94	12	2x	27/08/2018	NA	NA	NA	2217	7	v	H	No	Yes	bas	low	Average	19	F	F
Crepis jacquinii subsp. kerneri	MB123	124.97.5.0	11.29	6	11.2	0.02	4.03	3	12	2x	16/09/2018	NA	NA	NA	2217	7	v	H	No	Yes	bas	low	Average	19	F	F
Crepis jacquinii subsp. kerneri	IT103	124.97.5.0	11.72	NA	11.72	0.1	4.62	3.88	12	2x	20/09/2018	45.78399	11.19824	1687	2217	7	v	H	No	Yes	bas	low	Average	19	F	T
Crepis nicaeensis	OH394	124.97.23.0	NA	NA	6.34	0.01	2.92	2.77	8	2x	NA	NA	NA	NA	700	5	a, b	T, H	No	Yes	bas	hig	veryDry	15	F	F
Crepis paludosa	CH74	124.97.1.0	NA	NA	9.42	0.06	2.02	1.94	12	2x	24/06/2018	45.97283	9.06761	740	1190	6	v	H	No	Yes	neu	med	Wet	47	F	T
Crepis paludosa	CH112	124.97.1.0	9.41	5	NA	NA	NA	NA	12	2x	25/07/2018	46.59258	8.4881	1785	1190	6	v	H	No	Yes	neu	med	Wet	47	F	T
Crepis pontana	A129	124.97.9.0	12.64	2	11.76	0.01	1.91	1.99	10	2x	21/07/2018	47.06066	12.79168	2047	1750	6	v	H	No	Yes	bas	med	Average	31	F	T
Crepis pontana	OH429	124.97.9.0	12.11	NA	12.11	0.03	2.64	2.91	10	2x	NA	NA	NA	NA	1750	6	v	H	No	Yes	bas	med	Average	31	F	F
Crepis pygmaea	FR519	124.97.2.0	6.53	9	NA	NA	NA	NA	12	2x	NA	44.049	6.45916	2297	1890	7	v	G, H	No	Yes	bas	low	Average	19	F	T
Crepis pygmaea	FR433	124.97.2.0	6.2	NA	NA	NA	NA	NA	12	2x	NA	44.28397	6.43458	1710	1890	7	v	G, H	No	Yes	bas	low	Average	19	F	T
Crepis pygmaea	FR686	124.97.2.0	6.29	4	NA	NA	NA	NA	12	2x	NA	44.32045	6.80709	2775	1890	7	v	G, H	No	Yes	bas	low	Average	19	F	T
Crepis pygmaea	FR644	124.97.2.0	6.18	10	NA	NA	NA	NA	12	2x	NA	44.25936	6.71471	2675	1890	7	v	G, H	No	Yes	bas	low	Average	19	F	T
Crepis pygmaea	RD17	124.97.2.0	6.34	NA	6.26	0.1	3.04	2.98	12	2x	NA	NA	NA	NA	1890	7	v	G, H	No	Yes	bas	low	Average	19	F	F
Crepis pyrenaica	CH113	124.97.11.0	NA	NA	7.59	0.02	2.68	2.03	8	2x	25/07/2018	46.59128	8.47155	2057	1517	6	v	H	No	Yes	bas	hig	Wet	44	F	T
Crepis pyrenaica	CH177	124.97.11.0	7.66	5	NA	NA	NA	NA	8	2x	29/08/2018	46.54982	8.70094	1933	1517	6	v	H	No	Yes	bas	hig	Wet	44	F	T
Crepis pyrenaica	JB Lautaret25	124.97.11.0	NA	NA	NA	NA	NA	NA	8	2x	NA	NA	NA	NA	1517	6	v	H	No	Yes	bas	hig	Wet	44	F	F
Crepis rhaetica	CH153	124.97.6.0	8.73	19	8.87	0.08	2.54	3.13	8	2x	23/08/2018	45.98968	7.68665	2788	2575	7	v	H	Yes	Yes	bas	low	Wet	7	F	T
Crepis sancta	IT22	124.97.25.0	3.5	4	NA	NA	NA	NA	10	2x	NA	45.68636	11.75984	369	350	4	a	T	No	Yes	neu	hig	veryDry	13	F	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Crepis sancta	OH278	124.97.25.0	3.48	NA	3.48	0	2.93	2.94	10	2x	NA	NA	NA	NA	350	4	a	T	No	Yes	neu	hig	veryDry	13	F	F
Crepis tectorum	CH167	124.97.19.0	4.5	13	4.51	0.02	3.22	1.91	8	2x	28/08/2018	46.0448	8.9723	324	700	5	a	T	No	Yes	neu	hig	veryDry	16	F	T
Crepis terglouensis	A88	124.97.3.0	NA	NA	4.73	0.02	3.23	2.09	12	2x	19/07/2018	46.76274	12.80268	2270	2217	7	v	H	Yes	Yes	bas	low	Average	19	F	T
Crepis vesicaria subsp. taraxacifolia	FR621	124.97.27.2	NA	NA	NA	NA	NA	NA	8	2x	NA	44.34665	6.29747	1607	700	5	a, b	T, H	No	Yes	bas	hig	Dry	36	F	T
Crepis vesicaria subsp. taraxacifolia	IT12	124.97.27.2	3.7	1	NA	NA	NA	NA	8	2x	NA	45.75867	11.42311	NA	700	5	a, b	T, H	No	Yes	bas	hig	Dry	36	F	T
Crepis vesicaria subsp. taraxacifolia	FR432	124.97.27.2	3.16	NA	3.16	0.01	3.67	2.17	8	2x	NA	44.27833	6.42638	1500	700	5	a, b	T, H	No	Yes	bas	hig	Dry	36	F	T
Crepis vesicaria subsp. taraxacifolia	IT17	124.97.27.2	3.59	10	NA	NA	NA	NA	8	2x	NA	45.73841	11.59084	165	700	5	a, b	T, H	No	Yes	bas	hig	Dry	36	F	T
Crupina vulgaris	OH255	124.69.1.0	1.42	NA	NA	NA	NA	NA	30	2x	NA	NA	NA	NA	583	5	a	T	No	Yes	bas	low	veryDry	16	F	F
Cyanus montanus	A33	124.68.29.0	6	7	NA	NA	NA	NA	44	4x	17/06/2018	47.79037	15.81182	1334	1190	5	v	H	No	Yes	bas	med	Average	35	F	T
Cyanus montanus	FR412	124.68.29.0	5.59	27	5.55	0.04	2.84	2.84	44	4x	NA	44.31877	6.3553	1752	1190	5	v	H	No	Yes	bas	med	Average	35	F	T
Cyanus montanus	OH296	124.68.29.0	NA	NA	NA	NA	NA	NA	44	4x	NA	NA	NA	NA	1190	5	v	H	No	Yes	bas	med	Average	35	F	F
Cyanus segetum	FR724	124.68.31.0	1.78	12	NA	NA	NA	NA	24	2x	18/05/2018	44.59653	6.52327	919	910	5	a	T	No	Yes	neu	low	Dry	39	F	T
Cyanus segetum	FR384	124.68.31.0	1.74	7	1.77	0.03	3.79	2.68	24	2x	NA	44.38071	6.32661	1096	910	5	a	T	No	Yes	neu	low	Dry	39	F	T
Cyanus segetum	OH308	124.68.31.0	1.78	NA	NA	NA	NA	NA	24	2x	NA	NA	NA	NA	910	5	a	T	No	Yes	neu	low	Dry	39	F	F
Cyanus triumfettii	CH5	124.68.30.0	3.08	11	3.09	0.04	3.63	2.84	22	2x	19/05/2018	46.00686	8.98604	723	1050	5	v	H	No	Yes	bas	med	Dry	31	F	T
Cyanus triumfettii	CH48	124.68.30.0	3.14	9	NA	NA	NA	NA	22	2x	21/06/2018	45.96207	8.88476	413	1050	5	v	H	No	Yes	bas	med	Dry	31	F	T
Cyanus triumfettii	IT27	124.68.30.0	3.08	NA	3.11	0.03	3.1	3.08	22	2x	NA	45.80229	11.54553	1200	1050	5	v	H	No	Yes	bas	med	Dry	31	F	T
Cyanus triumfettii	OH469	124.68.30.0	NA	NA	2.96	0.02	2.79	1.94	22	2x	NA	NA	NA	NA	1050	5	v	H	No	Yes	bas	med	Dry	31	F	F
Dittrichia graveolens	MB127	124.16.14.0	1.97	NA	1.97	0.02	4.46	2.52	18	2x	20/09/2018	NA	NA	NA	350	8	a	T	No	NA	neu	med	Dry	6	F	F
Dittrichia viscosa	OH264	124.16.13.0	2.41	NA	2.41	0.01	2.98	1.96	18	2x	NA	NA	NA	NA	350	8	v	H	No	Yes	bas	low	veryDry	5	F	F
Doronicum austriacum	MB10	124.46.1.0	NA	NA	8.7	0.06	2.03	2.42	60	2x	17/06/2018	NA	NA	NA	1190	6	v	G	No	Yes	bas	hig	Wet	24	F	F
Doronicum austriacum	MB42	124.46.1.0	NA	NA	8.53	0.02	2.28	2.63	60	2x	08/07/2018	46.43362	14.29131	1525	1190	6	v	G	No	Yes	bas	hig	Wet	24	F	T
Doronicum austriacum	MB55	124.46.1.0	8.82	3	NA	NA	NA	NA	60	2x	11/07/2018	NA	NA	NA	1190	6	v	G	No	Yes	bas	hig	Wet	24	F	F
Doronicum austriacum	A104	124.46.1.0	8.64	7	NA	NA	NA	NA	60	2x	20/07/2018	47.14314	12.81543	1650	1190	6	v	G	No	Yes	bas	hig	Wet	24	F	T
Doronicum austriacum	FR581	124.46.1.0	8.7	NA	8.7	0	2.47	2.98	60	2x	NA	NA	NA	NA	1190	6	v	G	No	Yes	bas	hig	Wet	24	F	F
Doronicum clusii	A64	124.46.8.0	NA	NA	18.76	0.22	2.22	2.56	120	4x	15/07/2018	47.27167	14.08389	2110	2100	7	v	G	No	Yes	aci	low	Average	2	F	T
Doronicum columnae	OH384	124.46.2.0	NA	NA	6.46	0.04	3	2.6	60	2x	NA	NA	NA	NA	1190	5	v	G	No	Yes	bas	hig	Wet	13	F	F
Doronicum glaciale	A73	124.46.7.0	NA	NA	10.02	0.03	3.13	2.52	60	2x	17/07/2018	47.12247	12.82878	2431	2217	7	v	G	Yes	Yes	neu	med	Average	10	F	T
Doronicum grandiflorum	FR281	124.46.6.0	9.61	NA	NA	NA	NA	NA	60	2x	28/07/2016	44.31586	6.4565	2378	2575	7	v	G	No	Yes	bas	med	Average	45	T	T
Doronicum grandiflorum	MB83	124.46.6.0	9.5	3	NA	NA	NA	NA	60	2x	22/07/2018	46.43713	13.64375	1985	2575	7	v	G	No	Yes	bas	med	Average	45	T	T
Doronicum grandiflorum	CH101	124.46.6.0	9.77	8	NA	NA	NA	NA	60	2x	25/07/2018	46.55712	8.41407	2498	2575	7	v	G	No	Yes	bas	med	Average	45	T	T
Doronicum grandiflorum	CH121	124.46.6.0	9.86	5	NA	NA	NA	NA	60	2x	26/07/2018	46.55581	8.85203	2221	2575	7	v	G	No	Yes	bas	med	Average	45	T	T
Doronicum grandiflorum	FR515	124.46.6.0	9.81	7	NA	NA	NA	NA	60	2x	NA	44.30914	6.45588	2147	2575	7	v	G	No	Yes	bas	med	Average	45	T	T
Doronicum grandiflorum	FR689	124.46.6.0	8.83	7	NA	NA	NA	NA	60	2x	NA	44.32157	6.80667	2862	2575	7	v	G	No	Yes	bas	med	Average	45	T	T
Doronicum grandiflorum	FR649	124.46.6.0	9.31	8	NA	NA	NA	NA	60	2x	NA	44.28896	6.60467	2317	2575	7	v	G	No	Yes	bas	med	Average	45	T	T
Doronicum grandiflorum	FR628a	124.46.6.0	9.13	7	NA	NA	NA	NA	60	2x	NA	44.25411	6.71406	2428	2575	7	v	G	No	Yes	bas	med	Average	45	T	T
Doronicum grandiflorum	FR471	124.46.6.0	same ploidy	1	NA	NA	NA	NA	60	2x	NA	44.72993	6.32625	2683	2575	7	v	G	No	Yes	bas	med	Average	45	T	T
Doronicum grandiflorum	FR536	124.46.6.0	9.09	7	NA	NA	NA	NA	60	2x	NA	45.06417	6.40772	2623	2575	7	v	G	No	Yes	bas	med	Average	45	T	T
Doronicum grandiflorum	FR705	124.46.6.0	9.24	NA	NA	NA	NA	NA	60	2x	NA	44.68684	6.98025	2616	2575	7	v	G	No	Yes	bas	med	Average	45	T	T
Doronicum grandiflorum	RD11	124.46.6.0	9	NA	9.04	0.12	2.37	2.67	60	2x	NA	NA	NA	NA	2575	7	v	G	No	Yes	bas	med	Average	45	T	F
Doronicum grandiflorum	OH385	124.46.6.0	NA	NA	NA	NA	NA	NA	60	2x	NA	NA	NA	NA	2575	7	v	G	No	Yes	bas	med	Average	45	T	F
Doronicum pardalianches	CH22	124.46.4.0	7.02	15	7.04	0.05	2.59	2.76	60	2x	22/05/2018	46.03122	9.14852	282	700	5	v	G	No	Yes	neu	hig	Average	20	T	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Doronicum plantagineum	RBGK2001-4128	124.46.3.0	NA	NA	6.9	0.01	2.83	2.38	120	4x	NA	NA	NA	NA	700	4	v	G	No	Yes	neu	med	Average	1	F	F
Echinops exaltatus	CH68	124.54.2.0	8.15	2	8.09	0.05	2.22	2.43	30	2x	24/06/2018	46.00907	9.0088	306	350	6	v	H	No	No	bas	hig	Wet	2	F	T
Echinops exaltatus	OH489	124.54.2.0	7.73	3	NA	NA	NA	NA	30	2x	NA	NA	NA	NA	350	6	v	H	No	No	bas	hig	Wet	2	F	F
Echinops ritro	FR170	124.54.3.0	9.22	NA	NA	NA	NA	NA	32	2x	26/07/2016	44.2486	6.22959	1586	910	7	v	H	No	Yes	bas	low	veryDry	11	F	T
Echinops ritro	FR196	124.54.3.0	9.06	NA	NA	NA	NA	NA	32	2x	26/07/2016	44.2476	6.23499	1380	910	7	v	H	No	Yes	bas	low	veryDry	11	F	T
Echinops ritro	FR153	124.54.3.0	9.25	NA	9.25	0.04	1.68	1.76	32	2x	26/07/2016	44.25846	6.26345	1036	910	7	v	H	No	Yes	bas	low	veryDry	11	F	T
Echinops ritro	FR168	124.54.3.0	9.07	NA	NA	NA	NA	NA	32	2x	26/07/2016	44.2486	6.22959	1586	910	7	v	H	No	Yes	bas	low	veryDry	11	F	T
Echinops ritro	FR481	124.54.3.0	9.14	6	NA	NA	NA	NA	32	2x	NA	44.5716	6.37908	NA	910	7	v	H	No	Yes	bas	low	veryDry	11	F	T
Echinops ritro	OH347	124.54.3.0	8.98	2	NA	NA	NA	NA	32	2x	NA	NA	NA	NA	910	7	v	H	No	Yes	bas	low	veryDry	11	F	F
Echinops ritro subsp. ruthenicus	A44	124.54.3.1	8.25	9	8.41	0.02	1.87	3.17	32	2x	18/06/2018	NA	NA	NA	910	7	v	H	No	Yes	bas	low	veryDry	11	F	F
Echinops ritro subsp. ruthenicus	OH464	124.54.3.1	9.11	2	NA	NA	NA	NA	32	2x	NA	NA	NA	NA	910	7	v	H	No	Yes	bas	low	veryDry	11	F	F
Echinops sphaerocephalus	FR355	124.54.1.0	7.97	NA	NA	NA	NA	NA	30	2x	29/07/2016	44.02726	6.22486	1358	700	7	v	H	No	Yes	bas	hig	Dry	34	F	T
Echinops sphaerocephalus	A45	124.54.1.0	8.29	8	8.38	0.01	3.47	2.44	30	2x	18/06/2018	NA	NA	NA	700	7	v	H	No	Yes	bas	hig	Dry	34	F	F
Echinops sphaerocephalus	FR652	124.54.1.0	8.19	2	NA	NA	NA	NA	30	2x	NA	44.3197	6.69477	1689	700	7	v	H	No	Yes	bas	hig	Dry	34	F	T
Echinops sphaerocephalus	GR2015-Pyrenees	124.54.1.0	8.31	NA	8.31	0.01	2.2	2.28	30	2x	NA	NA	NA	NA	700	7	v	H	No	Yes	bas	hig	Dry	34	F	F
Erigeron acris	FR352	124.6.3.0	2.98	NA	NA	NA	NA	NA	18	2x	29/07/2016	44.02726	6.22486	1358	910	6	b, v	H	No	Yes	neu	low	Dry	35	F	T
Erigeron acris	A106	124.6.3.0	NA	NA	rotten	NA	NA	NA	18	2x	20/07/2018	47.15695	12.81345	1311	910	6	b, v	H	No	Yes	neu	low	Dry	35	F	T
Erigeron acris subsp. acris	FR509	124.6.3.1	3.02	14	3.04	0.02	3.06	2.15	18	2x	NA	44.3397	6.94757	2037	910	6	b, v	H	No	Yes	neu	low	Dry	35	T	T
Erigeron alpinus	FR8d	124.6.6.0	3.28	NA	3.28	0.04	3.02	2.15	18	2x	24/07/2016	44.33469	6.29546	NA	1890	7	v	H	No	Yes	neu	low	Dry	42	T	T
Erigeron alpinus	FR1c	124.6.6.0	3.05	NA	NA	NA	NA	NA	18	2x	24/07/2016	44.33469	6.29546	NA	1890	7	v	H	No	Yes	neu	low	Dry	42	T	T
Erigeron alpinus	FR73	124.6.6.0	3.45	NA	NA	NA	NA	NA	18	2x	24/07/2016	NA	NA	NA	1890	7	v	H	No	Yes	neu	low	Dry	42	T	F
Erigeron alpinus	FR256	124.6.6.0	3.12	NA	NA	NA	NA	NA	18	2x	28/07/2016	44.31535	6.44221	1961	1890	7	v	H	No	Yes	neu	low	Dry	42	T	T
Erigeron alpinus	FR265	124.6.6.0	3.1	NA	NA	NA	NA	NA	18	2x	28/07/2016	44.31346	6.44843	2127	1890	7	v	H	No	Yes	neu	low	Dry	42	T	T
Erigeron alpinus	FR289	124.6.6.0	3.12	NA	NA	NA	NA	NA	18	2x	28/07/2016	44.31586	6.4565	2378	1890	7	v	H	No	Yes	neu	low	Dry	42	T	T
Erigeron alpinus	FR287a	124.6.6.0	3.08	NA	NA	NA	NA	NA	18	2x	28/07/2016	44.31586	6.4565	2378	1890	7	v	H	No	Yes	neu	low	Dry	42	T	T
Erigeron alpinus	FR302	124.6.6.0	3.15	NA	NA	NA	NA	NA	18	2x	29/07/2016	44.40792	6.385497	2505	1890	7	v	H	No	Yes	neu	low	Dry	42	T	T
Erigeron alpinus	FR318	124.6.6.0	3.11	NA	NA	NA	NA	NA	18	2x	29/07/2016	44.26084	6.20877	1890	1890	7	v	H	No	Yes	neu	low	Dry	42	T	T
Erigeron alpinus	JB Lautaret17	124.6.6.0	3.27	14	NA	NA	NA	NA	18	2x	NA	NA	NA	NA	1890	7	v	H	No	Yes	neu	low	Dry	42	T	F
Erigeron alpinus	JB Lautaret16	124.6.6.0	3.35	NA	NA	NA	NA	NA	18	2x	NA	NA	NA	NA	1890	7	v	H	No	Yes	neu	low	Dry	42	T	F
Erigeron annuus	CH41	124.6.1.0	NA	NA	4.76	0.02	2.71	1.95	27	3x	20/06/2018	46.02695	8.76651	380	583	6	a, b, v	T, H	No	No	neu	hig	Dry	27	T	T
Erigeron atticus	FR286	124.6.4.0	3.13	NA	3.12	0.02	2.25	2.32	18	2x	28/07/2016	44.31586	6.4565	2378	1750	7	v	H	No	Yes	neu	low	Average	35	F	T
Erigeron bonariensis	FR488	124.7.2.0	4.35	NA	4.38	0.03	2.21	3.07	54	6x	NA	NA	NA	NA	350	7	a	T	No	No	bas	hig	veryDry	9	F	F
Erigeron canadensis	CH132	124.7.1.0	1	16	1	0.02	4.03	3.01	18	2x	22/08/2018	46.25315	7.40649	593	910	6	a, b	T, H	No	No	bas	med	Dry	49	F	T
Erigeron canadensis	IT78	124.7.1.0	0.95	10	0.97	0.04	3.92	2.72	18	2x	25/08/2018	45.84601	8.89057	343	910	6	a, b	T, H	No	No	bas	med	Dry	49	F	T
Erigeron glabratus	MB7	124.6.8.0	NA	NA	3.4	0	2.45	1.84	18	2x	17/06/2018	NA	NA	NA	1890	7	v	H	No	Yes	bas	low	Dry	42	F	F
Erigeron glabratus	CH83	124.6.8.0	NA	NA	3.13	0.01	2.79	2.22	18	2x	24/07/2018	46.48152	8.38656	2438	1890	7	v	H	No	Yes	bas	low	Dry	42	F	T
Erigeron karvinskianus	CH7	124.6.2.0	4	11	4.16	0.02	4.12	2.94	36	4x	19/05/2018	46.0013	8.98556	279	350	4	v	H	No	No	neu	low	Dry	16	F	T
Erigeron karvinskianus	CH4	124.6.2.0	3.93	6	4.24	0.01	3.52	2.28	36	4x	19/05/2018	46.00863	8.98528	881	350	4	v	H	No	No	neu	low	Dry	16	F	T
Erigeron karvinskianus	CH25	124.6.2.0	3.98	7	NA	NA	NA	NA	36	4x	22/05/2018	46.019	9.22938	348	350	4	v	H	No	No	neu	low	Dry	16	F	T
Erigeron karvinskianus	CH39	124.6.2.0	NA	NA	NA	NA	NA	NA	36	4x	20/06/2018	46.00863	8.98528	881	350	4	v	H	No	No	neu	low	Dry	16	F	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Erigeron karvinskianus	RBGK1967-12301	124.6.2.0	NA	NA	3.15	0.09	3.12	2.21	36	4x	NA	NA	NA	NA	350	4	v	H	No	No	neu	low	Dry	16	F	F
Erigeron schleicheri	CH151	124.6.5.0	3.21	12	NA	NA	NA	NA	18	2x	23/08/2018	45.98814	7.69263	2835	1470	7	v	H	No	Yes	neu	low	Dry	21	F	T
Erigeron schleicheri	FR492	124.6.5.0	2.96	7	NA	NA	NA	NA	18	2x	NA	44.35742	6.95305	1836	1470	7	v	H	No	Yes	neu	low	Dry	21	F	T
Erigeron schleicheri	FR506	124.6.5.0	3.09	NA	3.13	0.03	3.81	3.4	18	2x	NA	44.34076	6.94718	2035	1470	7	v	H	No	Yes	neu	low	Dry	21	F	T
Erigeron sumatrensis	CH134	124.7.3.0	4.57	1	NA	NA	NA	NA	54	6x	22/08/2018	46.25335	7.40602	604	350	6	a	T	No	No	bas	hig	Dry	19	F	T
Erigeron uniflorus	FR287b	124.6.9.0	3.11	NA	NA	NA	NA	NA	18	2x	28/07/2016	44.31586	6.4565	2378	2575	7	v	H	No	Yes	neu	low	Dry	39	F	T
Erigeron uniflorus	A84	124.6.9.0	3.07	4	NA	NA	NA	NA	18	2x	18/07/2018	47.08228	12.84261	2592	2575	7	v	H	No	Yes	neu	low	Dry	39	F	T
Erigeron uniflorus	FR540	124.6.9.0	3.18	14	NA	NA	NA	NA	18	2x	NA	45.06417	6.40772	2623	2575	7	v	H	No	Yes	neu	low	Dry	39	F	T
Erigeron uniflorus	FR453	124.6.9.0	3.19	11	NA	NA	NA	NA	18	2x	NA	44.72252	6.31779	2553	2575	7	v	H	No	Yes	neu	low	Dry	39	F	T
Erigeron uniflorus	FR640	124.6.9.0	3.22	12	NA	NA	NA	NA	18	2x	NA	44.26269	6.70966	2873	2575	7	v	H	No	Yes	neu	low	Dry	39	F	T
Erigeron uniflorus	RD16	124.6.9.0	3.23	NA	3.35	0.11	2.13	2.11	18	2x	NA	NA	NA	NA	2575	7	v	H	No	Yes	neu	low	Dry	39	F	F
Erigeron? sp.	GR558	124.7	4.51	NA	4.51	0.03	2.46	2.23	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	F	F
Eupatorium cannabinum	FR350	124.1.1.0	5.44	NA	5.43	0.03	2.52	2.12	20	2x	29/07/2016	44.02726	6.22486	1358	910	7	v	H	No	Yes	bas	hig	Wet	50	F	T
Eupatorium cannabinum	MB108	124.1.1.0	5.37	2	NA	NA	NA	NA	20	2x	24/08/2018	NA	NA	NA	910	7	v	H	No	Yes	bas	hig	Wet	50	F	F
Eupatorium cannabinum	IT71	124.1.1.0	5.66	8	5.63	0.07	2.93	2.5	20	2x	NA	45.76034	11.62708	198	910	7	v	H	No	Yes	bas	hig	Wet	50	F	T
Eupatorium cannabinum	RBGK1994-2784	124.1.1.0	NA	NA	NA	NA	NA	NA	20	2x	NA	NA	NA	NA	910	7	v	H	No	Yes	bas	hig	Wet	50	F	F
Filago arvensis	FR566	124.8.4.0	1.45	1	1.46	0.01	3.77	2.59	28	2x	NA	NA	NA	NA	910	6	a	T	No	Yes	aci	med	veryDry	25	F	F
Filago arvensis	OH519	124.8.4.0	NA	NA	1.44	0.02	4.3	1.94	28	2x	NA	NA	NA	NA	910	6	a	T	No	Yes	aci	med	veryDry	25	F	F
Filago pyramidata	OH256	124.8.3.0	1.54	NA	1.54	0.02	3.18	2.67	28	2x	NA	NA	NA	NA	583	7	a	T	No	Yes	neu	med	veryDry	17	F	F
Filago pyramidata	OH Catalunya2	124.8.3.0	1.49	NA	1.49	0.03	5.32	3.48	28	2x	NA	NA	NA	NA	583	7	a	T	No	Yes	neu	med	veryDry	17	F	F
Galatella linosyris	CH160	124.4.9.0	10.13	6	10	0.16	3.06	2.8	18	2x	24/08/2018	46.27114	7.39629	1029	700	8	v	H	No	Yes	bas	low	veryDry	24	F	T
Galatella linosyris	IT91	124.4.9.0	10.06	5	NA	NA	NA	NA	18	2x	27/08/2018	46.00549	9.22218	823	700	8	v	H	No	Yes	bas	low	veryDry	24	F	T
Galatella linosyris	NA	124.4.9.0	10.1	NA	10.1	0.11	2.37	2.93	18	2x	NA	NA	NA	NA	700	8	v	H	No	Yes	bas	low	veryDry	24	F	F
Galinsoga quadriradiata	CH49	124.28.2.0	4.48	10	NA	NA	NA	NA	32	4x	21/06/2018	45.96199	8.88022	482	583	5	a	T	No	No	neu	hig	Average	42	F	T
Galinsoga quadriradiata	FR487	124.28.2.0	4.21	5	4.19	0.02	4.04	3.47	32	4x	NA	NA	NA	NA	583	5	a	T	No	No	neu	hig	Average	42	F	F
Glebionis segetum	OH274	124.34.1.0	NA	NA	15	0.05	2.07	2.12	18	2x	NA	NA	NA	NA	350	5	a	T	No	No	neu	med	Average	6	F	F
Gnaphalium hoppeanum	A92	124.10.3.0	3.11	1	NA	NA	NA	NA	28	4x	19/07/2018	46.76379	12.80059	2219	2217	7	v	H	No	Yes	bas	low	Average	39	T	T
Gnaphalium hoppeanum	MB84	124.10.3.0	2.72	2	NA	NA	NA	NA	28	4x	23/07/2018	46.44608	13.64746	2109	2217	7	v	H	No	Yes	bas	low	Average	39	T	T
Gnaphalium hoppeanum	FR679	124.10.3.0	2.91	4	NA	NA	NA	NA	28	4x	NA	44.17535	7.1441	2338	2217	7	v	H	No	Yes	bas	low	Average	39	T	T
Gnaphalium hoppeanum	FR553	124.10.3.0	2.69	NA	2.69	0.02	3.8	2.98	28	4x	NA	45.06417	6.4024	2601	2217	7	v	H	No	Yes	bas	low	Average	39	T	T
Gnaphalium hoppeanum	FR642	124.10.3.0	2.86	8	NA	NA	NA	NA	28	4x	NA	44.25952	6.71632	2692	2217	7	v	H	No	Yes	bas	low	Average	39	T	T
Gnaphalium hoppeanum	FR697	124.10.3.0	2.81	5	NA	NA	NA	NA	28	4x	NA	44.34501	6.80097	2623	2217	7	v	H	No	Yes	bas	low	Average	39	T	T
Gnaphalium norvegicum	CH103	124.10.2.0	NA	NA	4.69	0.03	3.34	2.29	56	8x	25/07/2018	46.55985	8.41448	2502	2100	7	v	H	No	Yes	aci	med	Average	41	F	T
Gnaphalium supinum	A91	124.10.4.0	3.11	10	NA	NA	NA	NA	28	4x	19/07/2018	46.76143	12.80439	2267	2575	7	v	H	No	Yes	aci	low	Wet	40	F	T
Gnaphalium supinum	FR707	124.10.4.0	2.44	12	NA	NA	NA	NA	28	4x	NA	44.68684	6.98025	2616	2575	7	v	H	No	Yes	aci	low	Wet	40	F	T
Gnaphalium supinum	FR660	124.10.4.0	2.53	6	NA	NA	NA	NA	28	4x	NA	44.2584	6.73907	2354	2575	7	v	H	No	Yes	aci	low	Wet	40	F	T
Gnaphalium supinum	FR678	124.10.4.0	2.57	4	NA	NA	NA	NA	28	4x	NA	44.17535	7.1441	2338	2575	7	v	H	No	Yes	aci	low	Wet	40	F	T
Gnaphalium supinum	FR552	124.10.4.0	2.76	15	2.79	0.05	3.79	3.68	28	4x	NA	45.06417	6.4024	2601	2575	7	v	H	No	Yes	aci	low	Wet	40	F	T
Gnaphalium supinum	RD1	124.10.4.0	2.58	NA	2.66	0.07	3.64	2.08	28	4x	NA	NA	NA	NA	2575	7	v	H	No	Yes	aci	low	Wet	40	F	F
Gnaphalium sylvaticum	FR684	124.10.1.0	4.26	NA	4.26	0.03	3.51	2	56	8x	NA	44.1775	7.17254	2178	1400	6	v	H	No	Yes	aci	med	Average	47	F	T
Gnaphalium sylvaticum	FR682	124.10.1.0	2.93	6	NA	NA	NA	NA	56	8x	NA	44.17389	7.1567	2313	1400	6	v	H	No	Yes	aci	med	Average	47	F	T
Gnaphalium sylvaticum	FR595	124.10.1.0	4.34	2	4.36	0	3	2.52	56	8x	NA	NA	NA	NA	1400	6	v	H	No	Yes	aci	med	Average	47	F	F
Gnaphalium sylvaticum	OH336	124.10.1.0	4.18	NA	NA	NA	NA	NA	56	8x	NA	NA	NA	NA	1400	6	v	H	No	Yes	aci	med	Average	47	F	F
Hedypnois rhagadioloides	OH272	124.78.1.0	2.67	NA	2.67	0.1	2.64	3.64	16	2x	NA	NA	NA	NA	350	5	a	T	No	Yes	bas	med	veryDry	3	F	F
Helianthus annuus	MC3	124.25.1.0	7.12	NA	7.09	0.03	2.85	3.08	34	2x	NA	NA	NA	NA	583	7	a	T	No	No	neu	hig	Average	16	F	F

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Helianthus tuberosus	IT76	124.25.2.0	NA	NA	24.3	0.27	2.63	2.28	102	6x	NA	45.70782	11.61403	76	350	8	v	G	No	No	neu	hig	Average	30	F	T
Helichrysum italicum	FR730	124.11.2.0	NA	NA	2.98	0.03	2.49	2.59	28	4x	03/07/2018	44.47067	6.13017	659	350	6	A	C	No	Yes	bas	low	veryDry	2	F	T
Helichrysum italicum	MB92	124.11.2.0	NA	NA	NA	NA	NA	NA	28	4x	26/07/2018	NA	NA	NA	350	6	A	C	No	Yes	bas	low	veryDry	2	F	F
Helichrysum italicum	OH371	124.11.2.0	2.8	NA	2.8	0	2.92	2.27	28	4x	NA	NA	NA	NA	350	6	A	C	No	Yes	bas	low	veryDry	2	F	F
Helichrysum italicum	OH458	124.11.2.0	NA	NA	2.87	0	2.83	2.04	28	4x	NA	NA	NA	NA	350	6	A	C	No	Yes	bas	low	veryDry	2	F	F
Helichrysum stoechas	OH254	124.11.1.0	2.99	NA	2.99	0.02	2.85	2.42	28	4x	NA	NA	NA	NA	583	4	A	C	No	Yes	neu	low	veryDry	8	F	F
Helminthotheca echioides	MB125	124.84.1.0	NA	NA	1.47	0.01	5.27	3.4	10	2x	20/09/2018	NA	NA	NA	583	7	a, b	T, H	No	NA	neu	hig	Average	24	F	F
Helminthotheca echioides	OH289	124.84.1.0	1.5	NA	NA	NA	NA	NA	10	2x	NA	NA	NA	NA	583	7	a, b	T, H	No	NA	neu	hig	Average	24	F	F
Helminthotheca echioides	OH401a	124.84.1.0	NA	NA	1.4	0	4.08	3.34	10	2x	NA	NA	NA	NA	583	7	a, b	T, H	No	NA	neu	hig	Average	24	F	F
Hieracium	CH89	124.99	NA	NA	12.14	0.02	1.86	1.75	NA	NA	24/07/2018	46.47858	8.38898	2500	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	F	T
Hieracium alatum	JB Lautaret27	124.99.42.0	NA	NA	11.24	0	2.76	2.56	27	3x	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	F	F
Hieracium alpinum	MB78	124.99.29.0	NA	NA	12.03	0.01	1.73	1.79	27	3x	22/07/2018	46.43517	13.64299	2036	2183	7	v	H	No	Yes	aci	low	Average	40	F	T
Hieracium alpinum	JB Lautaret26	124.99.29.0	11.87	NA	11.87	0.01	2.75	2.7	27	3x	NA	NA	NA	NA	2183	7	v	H	No	Yes	aci	low	Average	40	F	F
Hieracium alpinum (cf.)	A118	124.99.29.0	NA	NA	11.9	0.12	3.64	3.95	27	3x	20/07/2018	47.06936	12.83927	2302	2183	7	v	H	No	Yes	aci	low	Average	40	F	T
Hieracium alpinum (cf.)	CH87	124.99.29.0	NA	NA	11.88	0.01	2.22	2.07	27	3x	24/07/2018	46.47858	8.38898	2500	2183	7	v	H	No	Yes	aci	low	Average	40	F	T
Hieracium amplexicaule	FR135	124.99.31.0	10.98	NA	10.98	0.03	1.82	2.1	27	3x	25/07/2016	44.38569	6.39095	1922	1400	5	v	H	No	Yes	neu	low	Dry	48	F	T
Hieracium amplexicaule	FR123	124.99.31.0	10.99	NA	NA	NA	NA	NA	27	3x	25/07/2016	44.37932	6.3955	1985	1400	5	v	H	No	Yes	neu	low	Dry	48	F	T
Hieracium amplexicaule	CH60	124.99.31.0	NA	NA	14.56	0.04	2.21	2	27	3x	22/06/2018	46.20391	8.79724	1433	1400	5	v	H	No	Yes	neu	low	Dry	48	F	T
Hieracium amplexicaule	FR578	124.99.31.0	11.43	17	NA	NA	NA	NA	27	3x	NA	NA	NA	NA	1400	5	v	H	No	Yes	neu	low	Dry	48	F	F
Hieracium amplexicaule (cf.)	CH79	124.99.31.0	NA	NA	10.93	0.02	1.44	1.34	27	3x	24/07/2018	46.49419	8.34802	1662	1400	5	v	H	No	Yes	neu	low	Dry	48	F	T
Hieracium armerioides (not in EuroMed)	A67	124.99.43.0	NA	NA	15.21	0.55	4.54	4.49	18	2x	17/07/2018	47.12227	12.82532	2324	2217	7	v	H	No	Yes	aci	low	Dry	36	NA	T
Hieracium bifidum	CH24	124.99.18.0	10.58	7	NA	NA	NA	NA	27	3x	22/05/2018	46.019	9.22938	348	1550	6	v	H	No	Yes	bas	low	Dry	46	F	T
Hieracium bifidum	OH389	124.99.18.0	NA	NA	10.79	0.02	2.49	23.07	27	3x	NA	NA	NA	NA	1550	6	v	H	No	Yes	bas	low	Dry	46	F	F
Hieracium bupleuroides	CH166	124.99.34.0	11.03	5	10.5	0.04	2.08	2.51	27	3x	24/08/2018	46.18626	8.09195	1187	1400	6	v	H	No	Yes	bas	low	Dry	38	F	T
Hieracium bupleuroides	CH184	124.99.34.0	11.21	5	NA	NA	NA	NA	27	3x	29/08/2018	46.52447	8.90469	1220	1400	6	v	H	No	Yes	bas	low	Dry	38	F	T
Hieracium caesioides	OH302	124.99.44.0	10.88	NA	10.84	0.04	2.28	2.34	27	3x	NA	NA	NA	NA	1050	6	v	H	No	Yes	bas	low	Dry	18	F	F
Hieracium caesioides (cf.)	OH301	124.99.44.0	10.78	NA	10.79	0.01	2.22	2.21	27	3x	NA	NA	NA	NA	1050	6	v	H	No	Yes	bas	low	Dry	18	F	F
Hieracium cydoniifolium	FR20	124.99.45.0	11.88	NA	NA	NA	NA	NA	27	3x	24/07/2016	44.34002	6.29641	1847	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	F	T
Hieracium erioleucum	JB Lautaret28	124.99.46.0	16	NA	15.97	0.02	2.49	2.89	27	3x	NA	NA	NA	NA	1890	7	v	H	No	Yes	bas	low	Average	45	F	F
Hieracium favratii	OH350	124.99.47.0	11.82	NA	11.87	0	1.99	1.93	27	3x	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	F	F
Hieracium froelichianum	FR120	124.99.48.0	11.01	NA	NA	NA	NA	NA	36	3x	25/07/2016	44.37932	6.3955	1985	1050	5	v	H	No	Yes	neu	med	Average	42	F	T
Hieracium glaucopsis	FR328	124.99.49.0	11.44	NA	NA	NA	NA	NA	27	3x	29/07/2016	44.26081	6.20881	1888	1190	6	v	H	No	Yes	bas	low	Dry	38	F	T
Hieracium glaucum	FR122a	124.99.35.0	11.46	NA	NA	NA	NA	NA	27	3x	25/07/2016	44.37932	6.3955	1985	1190	6	v	H	No	Yes	bas	low	Dry	38	F	T
Hieracium glaucum	OH348	124.99.35.0	11.53	NA	11.53	0.04	2.27	2.1	27	3x	NA	NA	NA	NA	1190	6	v	H	No	Yes	bas	low	Dry	38	F	F
Hieracium glaucum (cf.)	FR409	124.99.35.0	11.85	NA	11.85	0.02	2.16	2.37	27	3x	NA	44.31993	6.42753	1516	1190	6	v	H	No	Yes	bas	low	Dry	38	F	T
Hieracium humile	FR483	124.99.30.0	10.6	9	NA	NA	NA	NA	27	3x	NA	44.57639	6.3365	2114	1400	6	v	H	No	Yes	bas	low	Dry	42	F	T
Hieracium humile	FR427	124.99.30.0	10.79	NA	10.89	0.09	2.94	2.87	27	3x	NA	44.31974	6.43204	1514	1400	6	v	H	No	Yes	bas	low	Dry	42	F	T
Hieracium lawsonii	CH165b	124.99.23.0	14.23	NA	14.48	0.14	2.98	3.42	36	4x	24/08/2018	46.18626	8.09195	1187	1190	6	v	H	No	Yes	neu	low	Dry	10	F	T
Hieracium lawsonii	FR700	124.99.23.0	11.03	NA	11.03	0.03	2.69	2.73	27	3x	NA	44.3321	6.7735	2560	1190	6	v	H	No	Yes	neu	low	Dry	10	F	T
Hieracium metallicorum	FR508	124.99.50.0	9.39	5	9.5	0.15	3.29	2.84	27	3x	NA	44.3397	6.94757	2037	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	F	T
Hieracium murorum	FR74	124.99.16.0	10.82	NA	NA	NA	NA	NA	27	3x	24/07/2016	NA	NA	NA	1250	5	v	H	No	Yes	neu	med	Dry	48	F	F
Hieracium murorum	FR134	124.99.16.0	10.93	NA	NA	NA	NA	NA	27	3x	25/07/2016	44.38569	6.39095	1922	1250	5	v	H	No	Yes	neu	med	Dry	48	F	T
Hieracium murorum	FR88	124.99.16.0	10.88	NA	NA	NA	NA	NA	27	3x	25/07/2016	44.38621	6.39601	2219	1250	5	v	H	No	Yes	neu	med	Dry	48	F	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Hieracium murorum	FR108	124.99.16.0	10.79	NA	10.86	0.06	1.84	1.75	27	3x	25/07/2016	44.38339	6.39886	2119	1250	5	v	H	No	Yes	neu	med	Dry	48	F	T
Hieracium murorum	FR230	124.99.16.0	10.85	NA	NA	NA	NA	NA	27	3x	27/07/2016	44.27839	6.4237	1421	1250	5	v	H	No	Yes	neu	med	Dry	48	F	T
Hieracium murorum	FR219	124.99.16.0	10.83	NA	NA	NA	NA	NA	27	3x	27/07/2016	44.28474	6.4317	1772	1250	5	v	H	No	Yes	neu	med	Dry	48	F	T
Hieracium murorum	FR244	124.99.16.0	10.88	NA	NA	NA	NA	NA	27	3x	28/07/2016	44.31535	6.44221	1961	1250	5	v	H	No	Yes	neu	med	Dry	48	F	T
Hieracium murorum	FR339	124.99.16.0	10.74	NA	NA	NA	NA	NA	27	3x	29/07/2016	44.27214	6.21177	1651	1250	5	v	H	No	Yes	neu	med	Dry	48	F	T
Hieracium murorum	MB9	124.99.16.0	NA	NA	10.91	0.02	1.8	1.74	27	3x	17/06/2018	NA	NA	NA	1250	5	v	H	No	Yes	neu	med	Dry	48	F	F
Hieracium murorum	IT13	124.99.16.0	10.71	23	NA	NA	NA	NA	27	3x	NA	45.75819	11.42602	334	1250	5	v	H	No	Yes	neu	med	Dry	48	F	T
Hieracium murorum	FR385	124.99.16.0	10.93	10	11.13	0.06	2.3	2.05	27	3x	NA	44.33147	6.29244	1991	1250	5	v	H	No	Yes	neu	med	Dry	48	F	T
Hieracium murorum	IT11	124.99.16.0	11.06	15	NA	NA	NA	NA	27	3x	NA	45.7538	11.41511	730	1250	5	v	H	No	Yes	neu	med	Dry	48	F	T
Hieracium murorum	OH396	124.99.16.0	NA	NA	NA	NA	NA	NA	27	3x	NA	NA	NA	NA	1250	5	v	H	No	Yes	neu	med	Dry	48	F	F
Hieracium murorum	FRR6	124.99.16.0	10.83	NA	NA	NA	NA	NA	27	3x	NA	NA	NA	NA	1250	5	v	H	No	Yes	neu	med	Dry	48	F	F
Hieracium murorum (cf.)	CH23	124.99.16.0	10.63	8	NA	NA	NA	NA	27	3x	22/05/2018	46.01708	9.11012	271	1250	5	v	H	No	Yes	neu	med	Dry	48	F	T
Hieracium murorum subsp. oblongum	FR517	124.99.16.0	11.03	8	11.05	0.02	3.14	3.35	27	3x	NA	44.30914	6.45588	2147	1250	5	v	H	No	Yes	neu	med	Dry	48	F	T
Hieracium piliferum	FR293b	124.99.26.0	11.63	NA	NA	NA	NA	NA	27	3x	28/07/2016	44.31586	6.4565	2378	2217	7	v	H	No	Yes	aci	low	Dry	36	T	T
Hieracium piliferum	FR322a	124.99.26.0	11.68	NA	NA	NA	NA	NA	27	3x	29/07/2016	44.26084	6.20877	1890	2217	7	v	H	No	Yes	aci	low	Dry	36	T	T
Hieracium piliferum	FR550	124.99.26.0	11.88	1	11.61	0.21	2.98	3.79	27	3x	NA	45.06417	6.4024	2601	2217	7	v	H	No	Yes	aci	low	Dry	36	T	T
Hieracium piliferum	RD18	124.99.26.0	11.84	NA	11.7	0.23	2.73	3	27	3x	NA	NA	NA	NA	2217	7	v	H	No	Yes	aci	low	Dry	36	T	F
Hieracium piliferum subsp. glanduliferum	FR551	124.99.26.1	11.92	NA	11.78	0.05	2.44	3.2	27	3x	NA	45.06417	6.4024	2601	2217	7	v	H	No	Yes	aci	low	Dry	36	F	T
Hieracium piliferum subsp. subnivale	OH306	124.99.26.2	12.03	NA	12.06	0.07	2.7	2.82	27	3x	NA	NA	NA	NA	2217	7	v	H	No	Yes	aci	low	Dry	36	F	F
Hieracium pilosum	A75	124.99.25.0	12	5	NA	NA	NA	NA	27	3x	17/07/2018	47.12224	12.82704	2361	1890	7	v	H	No	Yes	bas	low	Average	37	F	T
Hieracium pilosum	FR370	124.99.25.0	11.9	10	12.05	0.02	1.95	1.89	27	3x	NA	44.40939	6.38183	2386	1890	7	v	H	No	Yes	bas	low	Average	37	F	T
Hieracium porrifolium (cf.)	OH468	124.99.33.0	NA	NA	8	0.04	3.1	2.26	18	2x	NA	NA	NA	NA	910	6	v	H	No	Yes	bas	low	Dry	15	F	F
Hieracium prenanthoides	FR122b	124.99.37.0	11.55	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.37932	6.3955	1985	1750	6	v	H	No	Yes	neu	hig	Average	45	F	T
Hieracium prenanthoides	FR129a	124.99.37.0	16.45	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38569	6.39095	1922	1750	6	v	H	No	Yes	neu	hig	Average	45	F	T
Hieracium prenanthoides	CH108	124.99.37.0	NA	NA	10.95	0.01	1.39	1.67	18	2x	25/07/2018	46.62268	8.57544	1477	1750	6	v	H	No	Yes	neu	hig	Average	45	F	T
Hieracium prenanthoides	CH109	124.99.37.0	NA	NA	10.91	0.08	2.93	2.85	18	2x	25/07/2018	46.62298	8.57598	1476	1750	6	v	H	No	Yes	neu	hig	Average	45	F	T
Hieracium prenanthoides	FR572	124.99.37.0	7.38	11	11.27	0.03	2.62	2.78	18	2x	NA	45.0415	6.28388	1380	1750	6	v	H	No	Yes	neu	hig	Average	45	F	T
Hieracium prenanthoides	OH443	124.99.37.0	NA	NA	10.97	0	1.98	2.53	18	2x	NA	NA	NA	NA	1750	6	v	H	No	Yes	neu	hig	Average	45	F	F
Hieracium sabaudum	CZ9	124.99.39.0	NA	NA	12.15	0.56	2.04	2.01	27	3x	NA	NA	NA	NA	700	8	v	H	No	Yes	aci	med	Dry	43	F	F
Hieracium tomentosum	FR231	124.99.28.0	11.42	NA	NA	NA	NA	NA	27	3x	27/07/2016	44.27839	6.4237	1421	1050	5	v	H	No	Yes	neu	low	veryDry	15	F	T
Hieracium tomentosum	FR264	124.99.28.0	11.44	NA	NA	NA	NA	NA	27	3x	28/07/2016	44.31346	6.44843	2127	1050	5	v	H	No	Yes	neu	low	veryDry	15	F	T
Hieracium tomentosum	FR726	124.99.28.0	NA	NA	NA	NA	NA	NA	27	3x	09/06/2018	44.48228	5.88837	1118	1050	5	v	H	No	Yes	neu	low	veryDry	15	F	T
Hieracium tomentosum (H. lanatum?)	FR597	124.99.28.0	11.61	3	11.6	0.02	2.5	2.69	27	3x	NA	NA	NA	NA	1050	5	v	H	No	Yes	neu	low	veryDry	15	F	F
Hieracium valdepilosum	A124	124.99.53.0	11.34	NA	NA	NA	NA	NA	27	3x	21/07/2018	47.05592	12.8033	1954	1890	7	v	H	No	Yes	bas	low	Average	45	F	T
Hieracium valdepilosum	MB77	124.99.53.0	NA	NA	11.47	0.02	2.77	2.49	27	3x	22/07/2018	46.43517	13.64299	2036	1890	7	v	H	No	Yes	bas	low	Average	45	F	T
Hieracium villosum	FR28	124.99.24.0	11.44	NA	NA	NA	NA	NA	27	3x	24/07/2016	44.33802	6.29635	1893	1890	7	v	H	No	Yes	bas	low	Average	45	T	T
Hieracium villosum	FR44b	124.99.24.0	11.54	NA	NA	NA	NA	NA	27	3x	24/07/2016	44.33443	6.29046	NA	1890	7	v	H	No	Yes	bas	low	Average	45	T	T
Hieracium villosum	FR214	124.99.24.0	11.62	NA	NA	NA	NA	NA	27	3x	27/07/2016	44.28474	6.4317	1772	1890	7	v	H	No	Yes	bas	low	Average	45	T	T
Hieracium villosum	FR247	124.99.24.0	12.07	NA	NA	NA	NA	NA	27	3x	28/07/2016	44.31535	6.44221	1961	1890	7	v	H	No	Yes	bas	low	Average	45	T	T
Hieracium villosum	FR246	124.99.24.0	11.75	NA	NA	NA	NA	NA	27	3x	28/07/2016	44.31535	6.44221	1961	1890	7	v	H	No	Yes	bas	low	Average	45	T	T
Hieracium villosum	A17	124.99.24.0	12.15	9	11.92	0.02	1.87	2.23	27	3x	15/06/2018	47.71728	15.77466	1530	1890	7	v	H	No	Yes	bas	low	Average	45	T	T
Hieracium villosum	MB8	124.99.24.0	NA	NA	11.78	0.05	1.97	1.69	27	3x	17/06/2018	NA	NA	NA	1890	7	v	H	No	Yes	bas	low	Average	45	T	F
Hieracium villosum	FR500	124.99.24.0	11.69	13	NA	NA	NA	NA	27	3x	NA	44.35271	6.95888	1904	1890	7	v	H	No	Yes	bas	low	Average	45	T	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Hieracium villosum	MB60	124.99.24.0	NA	NA	NA	NA	NA	NA	27	3x	NA	NA	NA	NA	1890	7	v	H	No	Yes	bas	low	Average	45	T	F
Hieracium villosum	OH303	124.99.24.0	11.5	NA	11.49	0.02	2.31	2.61	27	3x	NA	NA	NA	NA	1890	7	v	H	No	Yes	bas	low	Average	45	T	F
Hieracium villosum	FR381b	124.99.24.0	12.99	12	11.42	0.01	2.8	2.73	27	3x	NA	NA	NA	NA	1890	7	v	H	No	Yes	bas	low	Average	45	T	F
Hieracium villosum	NA	124.99.24.0	14.57	NA	14.82	0.05	2.6	2.52	27	3x	NA	NA	NA	NA	1890	7	v	H	No	Yes	bas	low	Average	45	T	F
Hieracium villosum	FRR8	124.99.24.0	11.5	NA	NA	NA	NA	NA	27	3x	NA	NA	NA	NA	1890	7	v	H	No	Yes	bas	low	Average	45	T	F
Homogyne alpina	CH52	124.43.1.0	12.63	8	NA	NA	NA	NA	120	4x	22/06/2018	46.21058	8.78732	1784	1921	5	v	H	No	Yes	neu	low	Average	47	F	T
Homogyne alpina	A72	124.43.1.0	15.17	6	NA	NA	NA	NA	120	4x	17/07/2018	47.12388	12.82635	2354	1921	5	v	H	No	Yes	neu	low	Average	47	F	T
Homogyne alpina	FR372	124.43.1.0	14.71	NA	14.86	0.01	2.61	2.67	120	4x	NA	44.40911	6.38253	2378	1921	5	v	H	No	Yes	neu	low	Average	47	F	T
Homogyne alpina	FR469	124.43.1.0	14.62	14	NA	NA	NA	NA	120	4x	NA	44.72731	6.32338	NA	1921	5	v	H	No	Yes	neu	low	Average	47	F	T
Homogyne alpina	FR473	124.43.1.0	same ploidy	NA	NA	NA	NA	NA	120	4x	NA	44.72324	6.3443	2463	1921	5	v	H	No	Yes	neu	low	Average	47	F	T
Homogyne alpina	IT44	124.43.1.0	15.79	10	15.23	0.09	2.87	2.64	120	4x	NA	46.10193	11.38771	1803	1921	5	v	H	No	Yes	neu	low	Average	47	F	T
Homogyne alpina	FR547	124.43.1.0	14.75	9	NA	NA	NA	NA	120	4x	NA	45.06417	6.4024	2601	1921	5	v	H	No	Yes	neu	low	Average	47	F	T
Homogyne alpina	OH298	124.43.1.0	14.83	NA	14.93	0.05	2.4	2.21	120	4x	NA	NA	NA	NA	1921	5	v	H	No	Yes	neu	low	Average	47	F	F
Homogyne discolor	A87	124.43.2.0	NA	NA	7.32	0.01	2.56	2.19	60	2x	19/07/2018	46.77042	12.79189	1930	1890	6	v	H	No	Yes	bas	low	Average	10	F	T
Homogyne discolor	MB86	124.43.2.0	7.27	NA	NA	NA	NA	NA	60	2x	22/07/2018	46.44608	13.64746	2108	1890	6	v	H	No	Yes	bas	low	Average	10	F	T
Homogyne discolor	OH492	124.43.2.0	NA	NA	7.21	0.05	2.9	2.77	60	2x	NA	NA	NA	1890	1890	6	v	H	No	Yes	bas	low	Average	10	F	F
Homogyne sylvestris	MB45	124.43.3.0	NA	NA	9.22	0.04	2.24	2.72	60	2x	08/07/2018	46.42847	14.28365	1146	1190	5	v	H	No	Yes	bas	low	Dry	2	F	T
Homogyne sylvestris	?	124.43.3.0	NA	NA	9.28	0	2.27	2.15	60	2x	NA	NA	NA	NA	1190	5	v	H	No	Yes	bas	low	Dry	2	F	F
Hypochaeris maculata	FR11b	124.82.1.0	8.46	NA	NA	NA	NA	NA	10	2x	24/07/2016	44.33469	6.29546	NA	1250	5	v	H	No	Yes	bas	med	Dry	40	T	T
Hypochaeris maculata	FR333	124.82.1.0	8.9	NA	8.9	0.11	2.77	3.11	10	2x	29/07/2016	44.26081	6.20881	1888	1250	5	v	H	No	Yes	bas	med	Dry	40	T	T
Hypochaeris maculata	FR392	124.82.1.0	8.96	10	8.96	0.02	2.73	2.54	10	2x	NA	44.3387	6.29283	1968	1250	5	v	H	No	Yes	bas	med	Dry	40	T	T
Hypochaeris maculata	FR438	124.82.1.0	NA	NA	NA	NA	NA	NA	10	2x	NA	44.28397	6.43458	1710	1250	5	v	H	No	Yes	bas	med	Dry	40	T	T
Hypochaeris maculata	FR397	124.82.1.0	8.86	12	NA	NA	NA	NA	10	2x	NA	44.3291	6.30592	1694	1250	5	v	H	No	Yes	bas	med	Dry	40	T	T
Hypochaeris maculata	FR419	124.82.1.0	7.88	2	NA	NA	NA	NA	10	2x	NA	44.31216	6.43589	1850	1250	5	v	H	No	Yes	bas	med	Dry	40	T	T
Hypochaeris maculata	OH433	124.82.1.0	NA	NA	9.08	0.03	3.24	2.75	10	2x	NA	NA	NA	NA	1250	5	v	H	No	Yes	bas	med	Dry	40	T	F
Hypochaeris maculata	OH314	124.82.1.0	NA	NA	NA	NA	NA	NA	10	2x	NA	NA	NA	NA	1250	5	v	H	No	Yes	bas	med	Dry	40	T	F
Hypochaeris maculata subsp. pelivanovicii	MB15	124.82.6.0	NA	NA	8.47	0.02	2.96	3.33	10	2x	21/06/2018	NA	NA	NA	1250	5	v	H	No	Yes	bas	med	Dry	40	F	F
Hypochaeris radicata	CH26	124.82.5.0	2.88	4	NA	NA	NA	NA	8	2x	22/05/2018	46.019	9.22938	348	910	5	v	H	No	Yes	aci	med	Average	48	T	T
Hypochaeris radicata	CH77	124.82.5.0	2.95	7	NA	NA	NA	NA	8	2x	25/06/2018	45.83786	8.87339	423	910	5	v	H	No	Yes	aci	med	Average	48	T	T
Hypochaeris radicata	OH286	124.82.5.0	2.89	NA	NA	NA	NA	NA	8	2x	NA	NA	NA	NA	910	5	v	H	No	Yes	aci	med	Average	48	T	F
Hypochaeris uniflora	A120	124.82.2.0	9.74	NA	NA	NA	NA	NA	10	2x	20/07/2018	47.0675	12.83779	2203	1890	7	v	H	No	Yes	aci	low	Average	40	F	T
Hypochaeris uniflora	A131	124.82.2.0	NA	NA	9.74	0.04	2.03	2.51	10	2x	21/07/2018	47.06135	12.79348	2108	1890	7	v	H	No	Yes	aci	low	Average	40	F	T
Hypochaeris uniflora	CH95	124.82.2.0	9.59	9	NA	NA	NA	NA	10	2x	24/07/2018	46.47752	8.4128	2237	1890	7	v	H	No	Yes	aci	low	Average	40	F	T
Hypochaeris uniflora	CH125	124.82.2.0	9.31	10	NA	NA	NA	NA	10	2x	26/07/2018	46.57597	8.42242	2400	1890	7	v	H	No	Yes	aci	low	Average	40	F	T
Hypochaeris uniflora	CH179	124.82.2.0	NA	NA	NA	NA	NA	NA	10	2x	29/08/2018	46.54935	8.70288	1927	1890	7	v	H	No	Yes	aci	low	Average	40	F	T
Hypochaeris uniflora	OH451	124.82.2.0	NA	NA	9.36	0.03	2.31	2.29	10	2x	NA	NA	NA	NA	1890	7	v	H	No	Yes	aci	low	Average	40	F	F
Inula bifrons	FR143	124.16.12.0	4.85	NA	5.07	0	2.26	1.75	16	2x	26/07/2016	44.25745	6.25511	1172	910	7	b, v	H	No	Yes	bas	low	Dry	9	F	T
Inula bifrons	FR192	124.16.12.0	4.88	NA	NA	NA	NA	NA	16	2x	26/07/2016	44.2476	6.23499	1380	910	7	b, v	H	No	Yes	bas	low	Dry	9	F	T
Inula conyzae	CH159	124.16.11.0	7.74	4	NA	NA	NA	NA	32	4x	24/08/2018	NA	NA	NA	700	6	b, v	H	No	Yes	bas	low	Dry	46	F	F
Inula conyzae	IT85	124.16.11.0	7.33	3	8.32	0.18	2.45	2.68	32	4x	25/08/2018	45.8591	8.8161	595	700	6	b, v	H	No	Yes	bas	low	Dry	46	F	T
Inula conyzae	MB111	124.16.11.0	7.87	1	NA	NA	NA	NA	32	4x	25/08/2018	NA	NA	NA	700	6	b, v	H	No	Yes	bas	low	Dry	46	F	F
Inula ensifolia	MB28	124.16.7.0	NA	NA	3.81	0.01	3.21	2.67	16	2x	29/06/2018	NA	NA	NA	700	7	v	H	No	Yes	bas	low	veryDry	11	F	F
Inula ensifolia	OH465a	124.16.7.0	3.96	2	NA	NA	NA	NA	16	2x	NA	NA	NA	NA	700	7	v	H	No	Yes	bas	low	veryDry	11	F	F
Inula ensifolia	RBGK1977-1183	124.16.7.0	NA	NA	4.02	0.05	3.56	2.71	16	2x	NA	NA	NA	NA	700	7	v	H	No	Yes	bas	low	veryDry	11	F	F
Inula helenium	MB57	124.16.1.0	NA	NA	4.8	0.03	5.54	3.65	20	2x	11/07/2018	NA	NA	NA	700	7	v	H	No	No	neu	hig	Average	14	F	F

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Inula helenium	JB Lautaret1	124.16.1.0	4.85	5	5.01	0.08	3.39	1.98	20	2x	NA	NA	NA	NA	700	7	v	H	No	No	neu	hig	Average	14	F	F
Inula helenium	RBGK2014-541	124.16.1.0	NA	NA	NA	NA	NA	NA	20	2x	NA	NA	NA	NA	700	7	v	H	No	No	neu	hig	Average	14	F	F
Inula helenium	RBGK2008-1457	124.16.1.0	NA	NA	4.63	0.08	3.14	1.96	20	2x	NA	NA	NA	NA	700	7	v	H	No	No	neu	hig	Average	14	F	F
Inula helvetica	FR522	124.16.2.0	4.54	16	4.55	0.01	3.7	2.55	16	2x	NA	44.35559	6.29353	1440	583	7	v	H	No	Yes	bas	med	Wet	10	F	T
Inula hirta	CH32	124.16.6.0	3.95	9	NA	NA	NA	NA	16	2x	22/05/2018	45.9941	9.22238	464	700	5	v	H	No	Yes	bas	low	veryDry	25	F	T
Inula hirta	IT32	124.16.6.0	3.88	NA	3.89	0.01	2.58	2.45	16	2x	NA	45.79985	11.73854	344	700	5	v	H	No	Yes	bas	low	veryDry	25	F	T
Inula hirta	IT58	124.16.6.0	3.93	4	NA	NA	NA	NA	16	2x	NA	45.87805	11.66908	376	700	5	v	H	No	Yes	bas	low	veryDry	25	F	T
Inula hirta	RBGK1977-1184	124.16.6.0	3.69	NA	3.69	0.02	2.94	2.92	16	2x	NA	NA	NA	NA	700	5	v	H	No	Yes	bas	low	veryDry	25	F	F
Inula montana	FR193	124.16.10.0	3.5	NA	3.5	0	2.94	2.2	16	2x	26/07/2016	44.2476	6.23499	1380	910	6	v	H	No	Yes	bas	low	veryDry	15	F	T
Inula montana	RD4	124.16.10.0	3.31	NA	3.3	0.05	2.86	2.46	16	2x	NA	NA	NA	NA	910	6	v	H	No	Yes	bas	low	veryDry	15	F	F
Inula oculus-christi	A31	124.16.9.0	NA	NA	4.88	0.04	3.18	2.25	32	4x	16/06/2018	NA	NA	NA	350	6	v	H	No	Yes	bas	low	veryDry	0	F	F
Inula oculus-christi	RBGK1978-4798	124.16.9.0	NA	NA	NA	NA	NA	NA	32	4x	NA	NA	NA	NA	350	6	v	H	No	Yes	bas	low	veryDry	0	F	F
Inula salicina	FR176	124.16.4.0	3.54	NA	NA	NA	NA	NA	16	2x	26/07/2016	44.2486	6.22959	1586	700	6	v	H	No	Yes	bas	low	Average	43	F	T
Inula salicina	FR186	124.16.4.0	3.52	NA	NA	NA	NA	NA	16	2x	26/07/2016	44.2476	6.23499	1380	700	6	v	H	No	Yes	bas	low	Average	43	F	T
Inula salicina	FR185	124.16.4.0	3.49	NA	NA	NA	NA	NA	16	2x	26/07/2016	44.2476	6.23499	1380	700	6	v	H	No	Yes	bas	low	Average	43	F	T
Inula salicina	A10	124.16.4.0	NA	NA	3.61	0.04	3.6	2.49	16	2x	14/06/2018	48.04065	16.04163	453	700	6	v	H	No	Yes	bas	low	Average	43	F	T
Inula salicina	RBGK1986-215	124.16.4.0	NA	NA	NA	NA	NA	NA	16	2x	NA	NA	NA	NA	700	6	v	H	No	Yes	bas	low	Average	43	F	F
Inula spiraeifolia	MB27	124.16.5.0	NA	NA	3.73	0.01	3.78	2.36	16	2x	29/06/2018	NA	NA	NA	700	6	v	H	No	Yes	bas	low	veryDry	22	F	F
Inula spiraeifolia	FR727	124.16.5.0	NA	NA	3.26	0.04	3.38	2.51	16	2x	03/07/2018	44.36342	5.88735	609	700	6	v	H	No	Yes	bas	low	veryDry	22	F	T
Jacobaea abrotanifolia	CH185	124.48.22.0	5.9	NA	6.01	0.01	1.87	1.84	40	4x	29/08/2018	46.53455	8.854	1897	1890	7	v	H	No	Yes	neu	med	Dry	25	F	T
Jacobaea abrotanifolia	IT101	124.48.22.0	6.06	8	NA	NA	NA	NA	40	4x	20/09/2018	45.78739	11.18196	1916	1890	7	v	H	No	Yes	neu	med	Dry	25	F	T
Jacobaea abrotanifolia	OH471	124.48.22.0	5.93	NA	NA	NA	NA	NA	40	4x	NA	NA	NA	NA	1890	7	v	H	No	Yes	neu	med	Dry	25	F	F
Jacobaea abrotanifolia	OH59	124.48.22.0	NA	NA	5.97	0.02	2.45	2.41	40	4x	NA	NA	NA	NA	1890	7	v	H	No	Yes	neu	med	Dry	25	F	F
Jacobaea adonicifolia	FR575	124.48.28.0	6.07	7	6.07	0.09	3.08	2.89	40	4x	NA	NA	NA	NA	1890	7	v	H	No	Yes	neu	med	Dry	25	F	F
Jacobaea alpina	CH117	124.48.15.0	NA	NA	4.5	0.02	2.97	2.81	40	4x	26/07/2018	46.64911	8.68736	1778	1470	7	v	H	No	Yes	bas	hig	Wet	32	F	T
Jacobaea alpina	CH119	124.48.15.0	4.52	7	NA	NA	NA	NA	40	4x	26/07/2018	46.55894	8.89328	1755	1470	7	v	H	No	Yes	bas	hig	Wet	32	F	T
Jacobaea alpina	CH183	124.48.15.0	4.76	4	NA	NA	NA	NA	40	4x	29/08/2018	46.5464	8.7136	1948	1470	7	v	H	No	Yes	bas	hig	Wet	32	F	T
Jacobaea alpina	FR594	124.48.15.0	4.57	NA	4.58	0.02	2.98	2.69	40	4x	NA	NA	NA	NA	1470	7	v	H	No	Yes	bas	hig	Wet	32	F	F
Jacobaea aquatica	A29	124.48.18.0	4.12	5	NA	NA	NA	NA	40	4x	15/06/2018	47.87259	15.78424	736	583	6	b	H	No	Yes	neu	hig	Wet	31	F	T
Jacobaea aquatica	CH73	124.48.18.0	NA	NA	4.43	0.02	2.84	1.73	40	4x	24/06/2018	45.97311	9.066946	746	583	6	b	H	No	Yes	neu	hig	Wet	31	F	T
Jacobaea carniolica	A65c	124.48.2.2	17.41	7	16.76	0.1	2.23	2.88	120	12x	15/07/2018	47.27167	14.08389	2110	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea carniolica	A65b	124.48.2.2	17.29	12	17.08	0.05	1.99	2.31	120	12x	15/07/2018	47.27167	14.08389	2110	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea carniolica	A65a-1	124.48.2.2	17.34	3	NA	NA	NA	NA	120	12x	15/07/2018	47.27167	14.08389	2110	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea carniolica	A65a-2	124.48.2.2	17.46	2	NA	NA	NA	NA	120	12x	15/07/2018	47.27167	14.08389	2110	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea erucifolia	FR562	124.48.20.0	4.66	2	4.76	0.05	2.06	1.72	40	4x	NA	NA	NA	NA	700	6	v	H	No	Yes	bas	med	Dry	40	T	F
Jacobaea incana	FR301	124.48.2.0	7.19	NA	NA	NA	NA	NA	40	4x	29/07/2016	44.40792	6.385497	2505	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea incana	FR708	124.48.2.0	7.1	11	NA	NA	NA	NA	40	4x	NA	44.68684	6.98025	2616	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea incana	FR692b	124.48.2.0	7.11	10	NA	NA	NA	NA	40	4x	NA	44.32157	6.80667	2862	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea incana	FR702	124.48.2.0	7.16	2	NA	NA	NA	NA	40	4x	NA	44.3321	6.7735	2560	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea incana	FR690	124.48.2.0	7.16	4	NA	NA	NA	NA	40	4x	NA	44.32157	6.80667	2862	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea incana	FR664	124.48.2.0	6.94	6	NA	NA	NA	NA	40	4x	NA	44.20338	7.1513	2354	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea incana	FR661	124.48.2.0	7.25	10	NA	NA	NA	NA	40	4x	NA	44.25714	6.73808	2373	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Jacobaea incana	FR692a	124.48.2.0	7.1	16	NA	NA	NA	NA	40	4x	NA	44.32157	6.80667	2862	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea incana	FR662	124.48.2.0	6.98	10	NA	NA	NA	NA	40	4x	NA	44.20259	7.1503	2349	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea incana	FR672	124.48.2.0	6.98	9	NA	NA	NA	NA	40	4x	NA	44.20487	7.1561	2465	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea incana	FR460	124.48.2.0	7.46	10	NA	NA	NA	NA	40	4x	NA	44.72422	6.31918	2625	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea incana	FR548	124.48.2.0	7.27	6	NA	NA	NA	NA	40	4x	NA	45.06417	6.4024	2601	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea incana	FR691	124.48.2.0	7.2	6	NA	NA	NA	NA	40	4x	NA	44.32157	6.80667	2862	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea incana	FR461	124.48.2.0	7.36	20	NA	NA	NA	NA	40	4x	NA	44.72573	6.32062	2648	2410	7	v	H	No	Yes	aci	low	Dry	15	F	T
Jacobaea incana	FR683	124.48.2.0	6.94	15	NA	NA	NA	NA	40	4x	NA	NA	NA	NA	2410	7	v	H	No	Yes	aci	low	Dry	15	F	F
Jacobaea incana	RD13	124.48.2.0	7.12	NA	7.05	0.05	2.06	2.25	40	4x	NA	NA	NA	NA	2410	7	v	H	No	Yes	aci	low	Dry	15	F	F
Jacobaea subalpina	A20	124.48.16.0	4.52	1	NA	NA	NA	NA	40	4x	15/06/2018	47.71691	15.76619	1608	1400	7	v	H	No	Yes	neu	hig	Wet	3	T	T
Jacobaea subalpina	A21	124.48.16.0	NA	NA	4.39	0.12	2.63	2.02	40	4x	15/06/2018	47.71784	15.77401	1564	1400	7	v	H	No	Yes	neu	hig	Wet	3	T	T
Jacobaea subalpina	FR576a	124.48.16.0	4.54	14	4.54	0.05	2.85	2.14	40	4x	NA	NA	NA	NA	1400	7	v	H	No	Yes	neu	hig	Wet	3	T	F
Jacobaea vulgaris	FR220	124.48.17.0	4.69	NA	NA	NA	NA	NA	40	4x	27/07/2016	44.27839	6.4237	1421	910	6	b, v	H	No	Yes	neu	med	Average	38	F	T
Jacobaea vulgaris	FR396	124.48.17.0	4.74	10	4.79	0.08	3.09	2.42	40	4x	NA	44.32618	6.31045	1675	910	6	b, v	H	No	Yes	neu	med	Average	38	F	T
Jurinea mollis	MB22b	124.59.1.0	NA	NA	3.46	0.01	2.69	2.74	34	2x	24/06/2018	NA	NA	NA	350	5	v	H	No	Yes	bas	low	veryDry	0	F	F
Jurinea mollis	MB24	124.59.1.0	NA	NA	3.56	0.02	2.54	2.41	34	2x	28/06/2018	NA	NA	NA	350	5	v	H	No	Yes	bas	low	veryDry	0	F	F
Klasea lycopifolia	MB25	124.65.3.0	NA	NA	7.12	0.01	2.17	2.53	60	4x	29/06/2018	NA	NA	NA	700	6	v	H	No	Yes	bas	low	Dry	4	F	F
Klasea lycopifolia	MB32	124.65.3.0	NA	NA	7.23	0.02	3.64	3.4	60	4x	05/07/2018	NA	NA	NA	700	6	v	H	No	Yes	bas	low	Dry	4	F	F
Lactuca alpina	FR584	124.90.1.0	6.77	3	6.72	0.03	2.84	3.43	18	2x	NA	NA	NA	NA	1517	6	v	H	No	Yes	neu	hig	Wet	43	F	F
Lactuca muralis	FR13b	124.92.1.0	3.83	NA	NA	NA	NA	NA	18	2x	24/07/2016	44.33469	6.29546	NA	910	7	v	H	No	Yes	neu	hig	Average	49	T	T
Lactuca muralis	FR121	124.92.1.0	3.76	NA	3.97	0.08	3.05	1.99	18	2x	25/07/2016	44.37932	6.3955	1985	910	7	v	H	No	Yes	neu	hig	Average	49	T	T
Lactuca muralis	FR125	124.92.1.0	3.84	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38569	6.39095	1922	910	7	v	H	No	Yes	neu	hig	Average	49	T	T
Lactuca muralis	FR131	124.92.1.0	3.79	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38569	6.39095	1922	910	7	v	H	No	Yes	neu	hig	Average	49	T	T
Lactuca muralis	FR138	124.92.1.0	3.82	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38569	6.39095	1922	910	7	v	H	No	Yes	neu	hig	Average	49	T	T
Lactuca muralis	FR159	124.92.1.0	3.8	NA	NA	NA	NA	NA	18	2x	26/07/2016	44.27211	6.29882	1083	910	7	v	H	No	Yes	neu	hig	Average	49	T	T
Lactuca muralis	CH11	124.92.1.0	3.79	6	NA	NA	NA	NA	18	2x	19/05/2018	46.00423	8.9963	289	910	7	v	H	No	Yes	neu	hig	Average	49	T	T
Lactuca muralis	CH111	124.92.1.0	3.87	10	NA	NA	NA	NA	18	2x	25/07/2018	46.62268	8.57544	1477	910	7	v	H	No	Yes	neu	hig	Average	49	T	T
Lactuca perennis	FR117	124.89.7.0	4.86	NA	4.9	0.03	2.32	1.95	18	2x	25/07/2016	44.37932	6.3955	1985	910	5	v	H	No	Yes	bas	low	veryDry	36	T	T
Lactuca perennis	FR166	124.89.7.0	4.83	NA	NA	NA	NA	NA	18	2x	26/07/2016	44.2486	6.22959	1586	910	5	v	H	No	Yes	bas	low	veryDry	36	T	T
Lactuca perennis	IT23b	124.89.7.0	5.02	4	5.02	0.09	2.2	1.79	18	2x	NA	45.61889	10.71152	384	910	5	v	H	No	Yes	bas	low	veryDry	36	T	T
Lactuca perennis	IT31	124.89.7.0	NA	NA	NA	NA	NA	NA	18	2x	NA	45.79874	11.73927	305	910	5	v	H	No	Yes	bas	low	veryDry	36	T	T
Lactuca serriola	FR152	124.89.3.0	6.01	NA	NA	NA	NA	NA	18	4x	26/07/2016	44.25745	6.25511	1172	700	7	a, b	T, H	No	Yes	bas	med	Dry	43	T	T
Lactuca serriola	IT80	124.89.3.0	6.16	5	NA	NA	NA	NA	18	4x	25/08/2018	45.84595	8.8902	345	700	7	a, b	T, H	No	Yes	bas	med	Dry	43	T	T
Lactuca serriola	FR428	124.89.3.0	NA	NA	NA	NA	NA	NA	18	4x	NA	44.31974	6.43204	1514	700	7	a, b	T, H	No	Yes	bas	med	Dry	43	T	T
Lactuca serriola	FR703a	124.89.3.0	6.37	NA	6.37	0.06	3.35	2	18	4x	NA	45.04335	6.33181	1603	700	7	a, b	T, H	No	Yes	bas	med	Dry	43	T	T
Lactuca viminea	OH HauteAlpes1	124.89.1.0	4.59	NA	4.57	0.02	3.79	2.33	18	4x	NA	NA	NA	NA	910	6	b	H	No	Yes	bas	low	veryDry	11	F	F
Lactuca virosa	RBGK wild3	124.89.6.0	6.03	NA	6.03	0.02	3.25	2.24	18	2x	NA	NA	NA	NA	700	6	a, b	T, H	No	Yes	neu	hig	veryDry	25	F	F
Laphangium luteoalbum	CH157	124.10.6.0	NA	NA	2.24	0.02	3.07	1.95	14	2x	23/08/2018	46.26782	7.88036	752	350	6	a	T	No	Yes	neu	med	Wet	24	T	T
Lapsana communis	CH6	124.96.1.0	2.52	3	NA	NA	NA	NA	14	2x	19/05/2018	46.0013	8.98556	279	910	5	a	T	No	Yes	neu	hig	Average	46	T	T
Lapsana communis	CH43	124.96.1.0	2.57	6	NA	NA	NA	NA	14	2x	20/06/2018	46.02695	8.76651	380	910	5	a	T	No	Yes	neu	hig	Average	46	T	T
Lapsana communis	IT43	124.96.1.0	2.58	NA	2.62	0.02	3.08	2.42	14	2x	NA	45.696	11.6343	73	910	5	a	T	No	Yes	neu	hig	Average	46	T	T
Lapsana communis	OH291	124.96.1.0	2.55	NA	2.55	0.01	3.37	2.35	14	2x	NA	NA	NA	NA	910	5	a	T	No	Yes	neu	hig	Average	46	T	F
Lapsana communis	MC11	124.96.1.0	2.54	NA	2.54	0.01	3.67	1.75	14	2x	NA	NA	NA	NA	910	5	a	T	No	Yes	neu	hig	Average	46	T	F
Lapsana communis subsp. communis	GR566	124.96.1.1	2.62	NA	2.62	0.01	2.65	2.75	14	2x	NA	NA	NA	NA	910	5	a	T	No	Yes	neu	hig	Average	46	F	F
Leontodon crispus	IT23a	124.83.7.0	2.18	NA	NA	NA	NA	NA	8	2x	NA	45.61889	10.71152	384	910	5	v	H	No	Yes	bas	low	veryDry	24	T	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Leontodon hispidus	FR48b	124.83.5.0	4.81	NA	NA	NA	NA	NA	14	2x	24/07/2016	44.34171	6.29706	1802	1850	6	v	H	No	Yes	neu	med	Average	50	T	T
Leontodon hispidus	FR13	124.83.5.0	4.76	NA	NA	NA	NA	NA	14	2x	24/07/2016	44.33469	6.29546	NA	1850	6	v	H	No	Yes	neu	med	Average	50	T	T
Leontodon hispidus	FR69b	124.83.5.0	4.9	NA	NA	NA	NA	NA	14	2x	24/07/2016	NA	NA	NA	1850	6	v	H	No	Yes	neu	med	Average	50	T	F
Leontodon hispidus	A16	124.83.5.0	4.67	9	4.68	0	3.71	1.92	14	2x	15/06/2018	47.71728	15.77466	1530	1850	6	v	H	No	Yes	neu	med	Average	50	T	T
Leontodon hispidus	FRR10	124.83.5.0	4.96	NA	NA	NA	NA	NA	14	2x	NA	NA	NA	NA	1850	6	v	H	No	Yes	neu	med	Average	50	T	F
Leontodon hispidus subsp. hispidus	CH17	124.83.5.1	4.82	7	4.97	0.06	4.32	3.11	14	2x	21/05/2018	46.38723	8.54227	741	1850	6	v	H	No	Yes	neu	med	Average	50	F	T
Leontodon hispidus subsp. hispidus	CH27	124.83.5.1	4.77	7	NA	NA	NA	NA	14	2x	22/05/2018	45.9917	9.2267	347	1850	6	v	H	No	Yes	neu	med	Average	50	F	T
Leontodon hispidus subsp. hispidus	OH481	124.83.5.1	NA	NA	4.58	0.03	3.31	2.67	14	2x	NA	NA	NA	NA	1850	6	v	H	No	Yes	neu	med	Average	50	F	F
Leontodon hispidus subsp. hispidus	OH312	124.83.5.1	GS?	NA	NA	NA	NA	NA	14	2x	NA	NA	NA	NA	1850	6	v	H	No	Yes	neu	med	Average	50	F	F
Leontodon hyoseroides	OH305	124.83.11.0	4.96	NA	5.03	0.06	2.66	1.99	14	2x	NA	NA	NA	NA	350	7	a, b, v	T, H	No	Yes	aci	med	Average	13	F	F
Leontodon saxatilis	MC9	124.83.11.0	4.5	NA	4.59	0.05	3.37	2.57	8	2x	NA	NA	NA	NA	350	7	a, b, v	T, H	No	Yes	aci	med	Average	13	F	F
Leontodon tenuiflorus	CH34	124.83.8.2	2.26	8	2.19	0.01	4.35	2.72	8	2x	22/05/2018	45.99658	9.21958	618	910	4	v	H	Yes	Yes	bas	low	veryDry	11	F	T
Leontodon tenuiflorus	CH47	124.83.8.2	2.26	4	NA	NA	NA	NA	8	2x	21/06/2018	45.96212	8.88513	417	910	4	v	H	Yes	Yes	bas	low	veryDry	11	F	T
Leontodon tenuiflorus	CH146	124.83.8.2	2.59	8	NA	NA	NA	NA	8	2x	23/08/2018	45.99006	7.704933	2025	910	4	v	H	Yes	Yes	bas	low	veryDry	11	F	T
Leontopodium nivale subsp. alpinum	FR327	124.13.1.0	3.99	NA	4.07	0.02	2.46	1.33	48	4x	29/07/2016	44.26081	6.20881	1888	1633	7	v	H	No	Yes	bas	low	Dry	45	F	T
Leontopodium nivale subsp. alpinum	FR317	124.13.1.0	4.03	NA	NA	NA	NA	NA	48	4x	29/07/2016	44.26084	6.20877	1890	1633	7	v	H	No	Yes	bas	low	Dry	45	F	T
Leontopodium nivale subsp. alpinum	A69	124.13.1.0	3.87	3	NA	NA	NA	NA	48	4x	17/07/2018	47.12328	12.82621	2337	1633	7	v	H	No	Yes	bas	low	Dry	45	F	T
Leontopodium nivale subsp. alpinum	MB85	124.13.1.0	NA	NA	3.75	0.02	2.82	1.71	48	4x	22/07/2018	46.43517	13.64299	2036	1633	7	v	H	No	Yes	bas	low	Dry	45	F	T
Leontopodium nivale subsp. alpinum	MB124	124.13.1.0	NA	NA	NA	NA	NA	NA	48	4x	16/09/2018	NA	NA	NA	1633	7	v	H	No	Yes	bas	low	Dry	45	F	F
Leontopodium nivale subsp. alpinum	IT100a	124.13.1.0	3.89	7	3.76	0.04	5.71	2.94	48	4x	20/09/2018	45.78997	11.17647	1987	1633	7	v	H	No	Yes	bas	low	Dry	45	F	T
Leontopodium nivale subsp. alpinum	FR534	124.13.1.0	4.06	10	NA	NA	NA	NA	48	4x	NA	45.06417	6.40772	2623	1633	7	v	H	No	Yes	bas	low	Dry	45	F	T
Leontopodium nivale subsp. alpinum	FR445	124.13.1.0	4.01	5	NA	NA	NA	NA	48	4x	NA	44.28983	6.43567	2070	1633	7	v	H	No	Yes	bas	low	Dry	45	F	T
Leontopodium nivale subsp. alpinum	RD3	124.13.1.0	NA	NA	NA	NA	NA	NA	48	4x	NA	NA	NA	NA	1633	7	v	H	No	Yes	bas	low	Dry	45	F	F
Leucanthemopsis alpina	FR310	124.37.1.0	10.57	NA	NA	NA	NA	NA	18	2x	29/07/2016	44.40792	6.385497	2505	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	A82	124.37.1.0	19.75	5	NA	NA	NA	NA	36	4x	18/07/2018	47.08244	12.84014	2586	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	CH88	124.37.1.0	10.44	8	NA	NA	NA	NA	18	2x	24/07/2018	46.47858	8.38898	2500	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	FR651b	124.37.1.0	20.06	NA	NA	NA	NA	NA	36	4x	NA	44.28896	6.60467	2317	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	FR659	124.37.1.0	19.77	3	NA	NA	NA	NA	36	4x	NA	44.26042	6.7396	2372	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	FR538	124.37.1.0	10.43	8	NA	NA	NA	NA	18	2x	NA	45.06417	6.40772	2623	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	FR688	124.37.1.0	10.41	9	NA	NA	NA	NA	18	2x	NA	44.32157	6.80667	2862	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	FR680	124.37.1.0	10.57	4	NA	NA	NA	NA	18	2x	NA	44.17535	7.1441	2338	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	FR663	124.37.1.0	17.01	11	NA	NA	NA	NA	27	3x	NA	44.20259	7.1503	2349	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	FR665	124.37.1.0	10.46	7	10.51	0.02	2.63	2.31	18	2x	NA	44.20338	7.1513	2354	2270	7	v	H	No	Yes	aci	low	Average	37	T	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Leucanthemopsis alpina	FR646	124.37.1.0	20	5	19.97	0.01	3.54	2.34	36	4x	NA	44.2892	6.61178	2338	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	FR454	124.37.1.0	10.8	8	NA	NA	NA	NA	18	2x	NA	44.72252	6.31779	2553	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	FR638	124.37.1.0	19.7	8	NA	NA	NA	NA	36	4x	NA	44.26269	6.70966	2873	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	FR635	124.37.1.0	19.29	3	NA	NA	NA	NA	36	4x	NA	44.26045	6.70982	2754	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	FR367	124.37.1.0	10.57	NA	10.66	0.04	1.78	1.74	18	2x	NA	44.40609	6.38279	2362	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	FR549	124.37.1.0	10.5	7	NA	NA	NA	NA	18	2x	NA	45.06417	6.4024	2601	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	FR704	124.37.1.0	19.49	4	NA	NA	NA	NA	36	4x	NA	44.68684	6.98025	2616	2270	7	v	H	No	Yes	aci	low	Average	37	T	T
Leucanthemopsis alpina	OH330	124.37.1.0	19.27	2	NA	NA	NA	NA	36	4x	NA	NA	NA	NA	2270	7	v	H	No	Yes	aci	low	Average	37	T	F
Leucanthemopsis alpina	FR675	124.37.1.0	16.55	2	NA	NA	NA	NA	27	3x	NA	NA	NA	NA	2270	7	v	H	No	Yes	aci	low	Average	37	T	F
Leucanthemopsis alpina	RD8	124.37.1.0	10.46	NA	10.52	0.04	2.59	2.64	18	2x	NA	NA	NA	NA	2270	7	v	H	No	Yes	aci	low	Average	37	T	F
Leucanthemum adustum	FR14	124.39.2.0	NA	NA	NA	NA	NA	NA	72	8x	24/07/2016	44.34002	6.29641	1847	1400	6	v	H	No	Yes	bas	low	Average	33	T	T
Leucanthemum adustum	FR189	124.39.2.0	29.23	NA	NA	NA	NA	NA	72	8x	26/07/2016	44.2476	6.23499	1380	1400	6	v	H	No	Yes	bas	low	Average	33	T	T
Leucanthemum adustum	CH130	124.39.2.0	28.22	10	NA	NA	NA	NA	72	8x	27/07/2018	45.86332	7.1595	2247	1400	6	v	H	No	Yes	bas	low	Average	33	T	T
Leucanthemum adustum	FR422	124.39.2.0	NA	NA	NA	NA	NA	NA	72	8x	NA	44.31216	6.43589	1850	1400	6	v	H	No	Yes	bas	low	Average	33	T	T
Leucanthemum adustum	FR541	124.39.2.0	26.5	8	NA	NA	NA	NA	72	8x	NA	45.06417	6.40772	2623	1400	6	v	H	No	Yes	bas	low	Average	33	T	T
Leucanthemum adustum	OH441	124.39.2.0	NA	NA	28.5	0.08	1.73	1.87	72	8x	NA	NA	NA	NA	1400	6	v	H	No	Yes	bas	low	Average	33	T	F
Leucanthemum atratum	A37	124.39.8.0	11.53	10	NA	NA	NA	NA	18	2x	17/06/2018	47.79323	15.81586	1225	1890	7	v	H	Yes	Yes	neu	low	Average	6	F	T
Leucanthemum coronopifolium	FR296	124.39.8.3	27.07	NA	NA	NA	NA	NA	54	6x	28/07/2016	44.31586	6.4565	2378	1890	7	v	H	Yes	Yes	neu	low	Average	6	T	T
Leucanthemum coronopifolium	FR269	124.39.8.3	26.14	NA	NA	NA	NA	NA	54	6x	28/07/2016	44.31346	6.44843	2127	1890	7	v	H	Yes	Yes	neu	low	Average	6	T	T
Leucanthemum coronopifolium	FR444	124.39.8.3	NA	NA	25.93	0.06	2.4	2.93	54	6x	NA	44.28983	6.43567	2070	1890	7	v	H	Yes	Yes	neu	low	Average	6	T	T
Leucanthemum coronopifolium	FR507	124.39.8.3	26.76	12	NA	NA	NA	NA	54	6x	NA	44.34076	6.94718	2035	1890	7	v	H	Yes	Yes	neu	low	Average	6	T	T
Leucanthemum coronopifolium	FR625	124.39.8.3	26.61	15	NA	NA	NA	NA	54	6x	NA	44.24644	6.70512	2249	1890	7	v	H	Yes	Yes	neu	low	Average	6	T	T
Leucanthemum coronopifolium	FR514	124.39.8.3	26.73	14	NA	NA	NA	NA	54	6x	NA	44.30975	6.45543	2117	1890	7	v	H	Yes	Yes	neu	low	Average	6	T	T
Leucanthemum graminifolium	OH258	124.39.10.0	12.85	NA	12.85	0.05	NA	NA	18	2x	NA	NA	NA	NA	700	5	v	H	Yes	Yes	bas	low	veryDry	3	F	F
Leucanthemum halleri	A63	124.39.8.2	NA	NA	10.85	0.05	2.4	2.22	18	2x	10/07/2018	47.23947	13.51375	1974	1925	7	v	H	Yes	Yes	bas	low	Average	17	F	T
Leucanthemum heterophyllum	CH70	124.39.3.0	NA	NA	36.69	0.13	1.99	2.07	72	8x	24/06/2018	46.0048	9.21802	904	1190	6	v	H	No	Yes	bas	med	Average	19	F	T
Leucanthemum pallens	FR191	124.39.5.0	28.47	NA	NA	NA	NA	NA	54	6x	26/07/2016	44.2476	6.23499	1380	700	5	v	H	No	Yes	bas	low	veryDry	8	F	T
Leucanthemum pallens	OH404	124.39.5.0	NA	NA	26.8	0.05	1.54	1.86	54	6x	NA	NA	NA	NA	700	5	v	H	No	Yes	bas	low	veryDry	8	F	F
Leucanthemum platylepis	MB114	124.39.8.5	NA	NA	34.08	0.53	2.39	2.29	72	8x	27/08/2018	NA	NA	NA	700	7	v	H	No	Yes	bas	low	Dry	2	F	F
Leucanthemum vulgare	CH124	124.39.1.0	NA	NA	11.42	0.04	1.81	2.24	18	2x	26/07/2018	46.57605	8.42245	2400	1250	5	v	H	No	Yes	neu	med	Average	50	F	T
Leucanthemum vulgare	CH181	124.39.1.0	11.87	7	NA	NA	NA	NA	18	2x	29/08/2018	46.55413	8.71491	1950	1250	5	v	H	No	Yes	neu	med	Average	50	F	T
Ligularia sibirica	FR600	124.50.1.0	22.97	NA	22.97	0.14	2.29	2.87	60	2x	NA	NA	NA	NA	1050	7	v	H	No	NA	neu	low	Aquatic	1	F	F
Matricaria chamomilla	IT38	124.33.1.0	6.08	NA	6.08	0.01	2.35	2.69	18	2x	NA	45.696	11.6343	73	1050	5	a	T	No	Yes	neu	med	Average	46	T	T
Matricaria discoidea	FR685	124.33.2.0	5.1	NA	5.1	0.01	2.45	2.19	18	2x	NA	44.18073	7.16402	2084	1050	6	a	T	No	No	neu	hig	Average	44	F	T
Onopordum acanthium	A4	124.63.1.0	2.74	2	NA	NA	NA	NA	34	2x	14/06/2018	NA	NA	NA	910	7	b	H	No	Yes	bas	hig	Dry	24	F	F
Onopordum acanthium	A52	124.63.1.0	2.79	2	NA	NA	NA	NA	34	2x	19/06/2018	47.32495	11.68786	465	910	7	b	H	No	Yes	bas	hig	Dry	24	F	T
Onopordum acanthium	IT62	124.63.1.0	2.73	2	2.72	0.01	2.56	1.98	34	2x	NA	45.45759	11.31472	31	910	7	b	H	No	Yes	bas	hig	Dry	24	F	T
Onopordum acanthium	FR401	124.63.1.0	2.77	10	2.77	0.01	3.19	2.02	34	2x	NA	44.42402	6.25908	809	910	7	b	H	No	Yes	bas	hig	Dry	24	F	T
Onopordum acanthium	OH452	124.63.1.0	NA	NA	2.75	0.01	2.61	2.09	34	2x	NA	NA	NA	NA	910	7	b	H	No	Yes	bas	hig	Dry	24	F	F
Pallenis spinosa	Hostalets	124.21.1.0	1.77	NA	NA	NA	NA	NA	10	2x	NA	NA	NA	NA	700	6	a, b	T, H	No	Yes	neu	med	veryDry	7	F	F

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Pallenis spinosa	GR565	124.21.1.0	1.77	NA	1.75	0	3.6	1.93	10	2x	NA	NA	NA	NA	700	6	a, b	T, H	No	Yes	neu	med	veryDry	7	F	F
Petasites albus	FR710	124.42.1.0	6.31	1	NA	NA	NA	NA	60	2x	23/04/2018	NA	NA	NA	1050	3	v	G	No	Yes	neu	hig	Wet	47	F	F
Petasites albus	CH21	124.42.1.0	6.23	8	NA	NA	NA	NA	60	2x	21/05/2018	46.44829	8.66247	1287	1050	3	v	G	No	Yes	neu	hig	Wet	47	F	T
Petasites albus	CH12	124.42.1.0	6.18	4	NA	NA	NA	NA	60	2x	21/05/2018	46.38902	8.53927	758	1050	3	v	G	No	Yes	neu	hig	Wet	47	F	T
Petasites albus	IT26	124.42.1.0	6.35	NA	6.32	0.01	3.11	2.73	60	2x	NA	45.80314	11.56389	1034	1050	3	v	G	No	Yes	neu	hig	Wet	47	F	T
Petasites hybridus	CZ3	124.42.2.0	NA	NA	6.43	0.21	3.36	2.63	60	2x	NA	NA	NA	NA	910	3	v	G	No	Yes	neu	hig	Wet	48	F	F
Petasites paradoxus	CH13	124.42.3.0	7.01	16	12.39	0.16	2.4	2.96	60	2x	21/05/2018	46.37127	8.55038	657	1633	3	v	G	No	Yes	bas	low	Wet	43	F	T
Petasites paradoxus	A95	124.42.3.0	11.58	10	NA	NA	NA	NA	60	2x	19/07/2018	46.77828	12.78971	1723	1633	3	v	G	No	Yes	bas	low	Wet	43	F	T
Petasites paradoxus	A134	124.42.3.0	11.46	1	NA	NA	NA	NA	60	2x	21/07/2018	47.06206	12.81731	1875	1633	3	v	G	No	Yes	bas	low	Wet	43	F	T
Petasites paradoxus	OH495	124.42.3.0	11.75	2	NA	NA	NA	NA	60	2x	NA	NA	NA	NA	1633	3	v	G	No	Yes	bas	low	Wet	43	F	F
Phagnalon rupestre	OH270	124.15.2.0	2.34	NA	2.34	0.08	3.65	2.5	18	2x	NA	NA	NA	NA	350	5	A	C	No	Yes	bas	low	veryDry	1	F	F
Phagnalon saxatile	OH370	124.15.3.0	2.49	NA	2.49	0.03	4.62	2.44	18	2x	NA	NA	NA	NA	350	3	A	C	No	Yes	neu	low	veryDry	1	F	F
Phagnalon sordidum	OH409	124.15.1.0	NA	NA	2.23	0.01	3.8	2.33	18	2x	NA	NA	NA	NA	350	6	A	C	No	Yes	bas	low	veryDry	7	F	F
Phagnalon sordidum	OH355	124.15.1.0	2.24	NA	2.24	0.03	2.67	3.04	18	2x	NA	NA	NA	NA	350	6	A	C	No	Yes	bas	low	veryDry	7	F	F
Picris hieracioides	MB110	124.84.2.0	2.24	1	NA	NA	NA	NA	10	2x	25/08/2018	NA	NA	NA	910	6	b, v	H	No	Yes	bas	hig	Dry	29	F	F
Picris hieracioides	IT70	124.84.2.0	2.86	11	2.86	0.03	3.28	2.85	10	2x	NA	45.76034	11.62708	198	910	6	b, v	H	No	Yes	bas	hig	Dry	29	F	T
Picris hieracioides	OH439	124.84.2.0	NA	NA	2.8	0	2.45	1.93	10	2x	NA	NA	NA	NA	910	6	b, v	H	No	Yes	bas	hig	Dry	29	F	F
Picris hieracioides subsp. hieracioides	FR228	124.84.2.1	2.79	NA	2.89	0.01	4.3	1.99	10	2x	27/07/2016	44.27839	6.4237	1421	910	6	b, v	H	No	Yes	bas	hig	Dry	29	F	T
Pilosella aurantiaca	A132	124.99.14.0	12.04	7	NA	NA	NA	NA	54	6x	21/07/2018	47.06081	12.79331	2078	910	6	v	H	No	Yes	aci	low	Average	38	F	T
Pilosella aurantiaca	CH116	124.99.14.0	12.19	5	NA	NA	NA	NA	54	6x	25/07/2018	46.59436	8.45847	2116	910	6	v	H	No	Yes	aci	low	Average	38	F	T
Pilosella aurantiaca	CH182	124.99.14.0	2.47	NA	NA	NA	NA	NA	18	2x	29/08/2018	46.55052	8.7172	1941	910	6	v	H	No	Yes	aci	low	Average	38	F	T
Pilosella aurantiaca	Chiltern seeds (comercial)	124.99.14.0	8.29	NA	8.29	0.03	2.5	2.69	36	4x	NA	NA	NA	NA	910	6	v	H	No	Yes	aci	low	Average	38	F	F
Pilosella aurantiaca	OH290	124.99.14.0	8.23	NA	8.17	0.07	2.67	3.23	36	4x	NA	NA	NA	NA	910	6	v	H	No	Yes	aci	low	Average	38	F	F
Pilosella aurantiaca	OH315	124.99.14.0	8.19	NA	8.24	0.05	2.7	2.84	36	4x	NA	NA	NA	NA	910	6	v	H	No	Yes	aci	low	Average	38	F	F
Pilosella caespitosa	OH393	124.99.13.0	NA	NA	8.69	0.02	1.74	2.14	36	4x	NA	NA	NA	NA	700	5	v	H	No	Yes	neu	low	Average	10	F	F
Pilosella cymosa	FR71	124.99.12.0	4.53	NA	4.53	0.17	2.92	2.11	18	2x	24/07/2016	NA	NA	NA	1250	5	v	H	No	Yes	bas	low	veryDry	28	F	F
Pilosella cymosa	FR388	124.99.12.0	6.57	10	NA	NA	NA	NA	36	4x	NA	44.332	6.29235	1988	1250	5	v	H	No	Yes	bas	low	veryDry	28	F	T
Pilosella cymosa	OH428	124.99.12.0	NA	NA	11.97	0.02	1.6	2.04	54	6x	NA	NA	NA	NA	1250	5	v	H	No	Yes	bas	low	veryDry	28	F	F
Pilosella glacialis	FR107	124.99.8.0	4.77	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38339	6.39886	2119	2100	7	v	H	Yes	Yes	aci	low	Dry	29	F	T
Pilosella glacialis	FR516	124.99.8.0	6.3	11	6.41	0.03	3.25	3.05	27	3x	NA	44.30914	6.45588	2147	2100	7	v	H	Yes	Yes	aci	low	Dry	29	F	T
Pilosella glacialis	FR554	124.99.8.0	8.77	NA	8.77	0.05	2.94	2.58	36	4x	NA	45.06417	6.4024	2601	2100	7	v	H	Yes	Yes	aci	low	Dry	29	F	T
Pilosella hoppeana	A78	124.99.2.0	NA	NA	3.81	0.07	2.34	1.73	18	2x	17/07/2018	47.06569	12.83252	2149	1400	5	v	H	No	Yes	neu	low	Dry	27	F	T
Pilosella hoppeana	CH176	124.99.2.0	2.5	6	NA	NA	NA	NA	18	2x	29/08/2018	46.54982	8.70094	1933	1400	5	v	H	No	Yes	neu	low	Dry	27	F	T
Pilosella lactucella	FR90	124.99.7.0	4.16	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38621	6.39601	2219	1250	5	v	H	No	Yes	aci	low	Average	46	F	T
Pilosella lactucella	FR105	124.99.7.0	4.16	NA	4.21	0	2.31	2.01	18	2x	25/07/2016	44.38339	6.39886	2119	1250	5	v	H	No	Yes	aci	low	Average	46	F	T
Pilosella lactucella	FR94	124.99.7.0	4.17	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38528	6.39642	2184	1250	5	v	H	No	Yes	aci	low	Average	46	F	T
Pilosella lactucella	FR91	124.99.7.0	4.81	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38528	6.39642	2184	1250	5	v	H	No	Yes	aci	low	Average	46	F	T
Pilosella lactucella	FR292	124.99.7.0	4.22	NA	NA	NA	NA	NA	18	2x	28/07/2016	44.31586	6.4565	2378	1250	5	v	H	No	Yes	aci	low	Average	46	F	T
Pilosella lactucella	CH64	124.99.7.0	19.43	10	NA	NA	NA	NA	18	2x	23/06/2018	45.93537	9.0219	1621	1250	5	v	H	No	Yes	aci	low	Average	46	F	T
Pilosella lactucella	FR545	124.99.7.0	4.5	5	NA	NA	NA	NA	18	2x	NA	45.06417	6.4024	2601	1250	5	v	H	No	Yes	aci	low	Average	46	F	T
Pilosella lactucella	IT50	124.99.7.0	NA	11	NA	NA	NA	NA	18	2x	NA	45.79402	11.46281	1269	1250	5	v	H	No	Yes	aci	low	Average	46	F	T
Pilosella officinarum	FR1d	124.99.4.0	7.14	NA	NA	NA	NA	NA	36	4x	24/07/2016	44.33469	6.29546	NA	1400	5	v	H	No	Yes	neu	low	Dry	49	F	T
Pilosella officinarum	FR98	124.99.4.0	3.71	NA	NA	NA	NA	NA	36	4x	25/07/2016	44.38528	6.39642	2184	1400	5	v	H	No	Yes	neu	low	Dry	49	F	T
Pilosella officinarum	FR96a	124.99.4.0	3.6	NA	NA	NA	NA	NA	36	4x	25/07/2016	44.38528	6.39642	2184	1400	5	v	H	No	Yes	neu	low	Dry	49	F	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Pilosella officinarum	FR178b	124.99.4.0	7.11	NA	NA	NA	NA	NA	36	4x	26/07/2016	44.2486	6.22959	1586	1400	5	v	H	No	Yes	neu	low	Dry	49	F	T
Pilosella officinarum	FR223	124.99.4.0	7.02	NA	NA	NA	NA	NA	36	4x	27/07/2016	44.27839	6.4237	1421	1400	5	v	H	No	Yes	neu	low	Dry	49	F	T
Pilosella officinarum	FR271	124.99.4.0	7.17	NA	NA	NA	NA	NA	36	4x	28/07/2016	44.31346	6.44843	2127	1400	5	v	H	No	Yes	neu	low	Dry	49	F	T
Pilosella officinarum	CH2	124.99.4.0	7.52	10	NA	NA	NA	NA	36	4x	19/05/2018	46.00833	8.98694	898	1400	5	v	H	No	Yes	neu	low	Dry	49	F	T
Pilosella officinarum	CH63	124.99.4.0	7.39	4	NA	NA	NA	NA	36	4x	23/06/2018	45.93537	9.0219	1621	1400	5	v	H	No	Yes	neu	low	Dry	49	F	T
Pilosella officinarum	MB126	124.99.4.0	5.38	1	NA	NA	NA	NA	36	4x	20/09/2018	NA	NA	NA	1400	5	v	H	No	Yes	neu	low	Dry	49	F	F
Pilosella officinarum	FR447	124.99.4.0	7.25	NA	NA	NA	NA	NA	36	4x	NA	44.37244	6.31362	997	1400	5	v	H	No	Yes	neu	low	Dry	49	F	T
Pilosella officinarum	OH375	124.99.4.0	NA	NA	7.17	0.06	3.26	3.81	36	4x	NA	NA	NA	NA	1400	5	v	H	No	Yes	neu	low	Dry	49	F	F
Pilosella officinarum	FRR11	124.99.4.0	11.91	NA	NA	NA	NA	NA	36	4x	NA	NA	NA	NA	1400	5	v	H	No	Yes	neu	low	Dry	49	F	F
Pilosella officinarum (cf.)	OH494	124.99.4.0	NA	NA	7.22	0.03	2.52	2.86	36	4x	NA	NA	NA	NA	1400	5	v	H	No	Yes	neu	low	Dry	49	F	F
Pilosella peleteriana	FR96b	124.99.3.0	3.62	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38528	6.39642	2184	1250	5	v	H	No	Yes	aci	low	Dry	16	F	T
Pilosella peleteriana	FR165b	124.99.3.0	7.19	NA	NA	NA	NA	NA	18	2x	26/07/2016	44.2486	6.22959	1586	1250	5	v	H	No	Yes	aci	low	Dry	16	F	T
Pilosella peleteriana	FR312	124.99.3.0	3.66	NA	NA	NA	NA	NA	18	2x	29/07/2016	44.40792	6.385497	2505	1250	5	v	H	No	Yes	aci	low	Dry	16	F	T
Pilosella peleteriana	FR501	124.99.3.0	3.45	14	NA	NA	NA	NA	18	2x	NA	44.35271	6.95888	1904	1250	5	v	H	No	Yes	aci	low	Dry	16	F	T
Pilosella piloselloides	IT28	124.99.10.0	9.45	NA	9.54	0.07	2.18	2.77	54	6x	NA	45.79818	11.73817	243	1050	5	v	H	No	Yes	bas	low	Dry	45	F	T
Pilosella piloselloides	OH398	124.99.10.0	11.12	NA	NA	NA	NA	NA	54	6x	NA	NA	NA	NA	1050	5	v	H	No	Yes	bas	low	Dry	45	F	F
Pilosella x officinarum	OH318	124.99.54.0	11.07	NA	11.05	0.02	2.19	2.59	54	6x	NA	NA	NA	NA	1400	5	v	H	No	Yes	neu	low	Dry	49	F	F
Podospermum laciniatum	OH277	124.85.2.0	3.91	NA	3.91	0.1	2.8	2.85	14	2x	NA	NA	NA	NA	910	5	a, b	T, H	No	Yes	bas	med	Dry	7	F	F
Podospermum purpureum	OH259	124.85.3.0	9.72	NA	9.72	0.23	2.37	2.38	14	2x	NA	NA	NA	NA	350	5	v	H	No	Yes	bas	low	Dry	2	F	F
Prenanthes purpurea	FR132	124.91.1.0	8.48	NA	8.29	0.04	3.41	2.52	18	2x	25/07/2016	44.38569	6.39095	1922	1050	7	v	H	No	Yes	neu	med	Average	50	F	T
Prenanthes purpurea	FR158	124.91.1.0	8.4	NA	NA	NA	NA	NA	18	2x	26/07/2016	44.27211	6.29882	1083	1050	7	v	H	No	Yes	neu	med	Average	50	F	T
Prenanthes purpurea	A22	124.91.1.0	8.34	10	8.13	0.04	3.65	2.85	18	2x	15/06/2018	47.72835	15.79708	553	1050	7	v	H	No	Yes	neu	med	Average	50	F	T
Prenanthes purpurea	A101	124.91.1.0	8.52	3	NA	NA	NA	NA	18	2x	19/07/2018	46.78423	12.78753	1636	1050	7	v	H	No	Yes	neu	med	Average	50	F	T
Prenanthes purpurea	CH110	124.91.1.0	8.66	12	NA	NA	NA	NA	18	2x	25/07/2018	46.62326	8.57667	1437	1050	7	v	H	No	Yes	neu	med	Average	50	F	T
Prenanthes purpurea	FR527	124.91.1.0	8.17	4	NA	NA	NA	NA	18	2x	NA	44.35538	6.29001	1289	1050	7	v	H	No	Yes	neu	med	Average	50	F	T
Prenanthes purpurea	OH486	124.91.1.0	8.74	2	NA	NA	NA	NA	18	2x	NA	NA	NA	NA	1050	7	v	H	No	Yes	neu	med	Average	50	F	F
Pulicaria dysenterica	MB94	124.17.2.0	NA	NA	2.1	0.09	3	2.47	18	2x	12/08/2018	46.52671	13.62151	9	700	7	v	H	No	Yes	neu	med	Wet	45	F	T
Pulicaria dysenterica	CH158	124.17.2.0	2.17	12	2.25	0.01	3.9	2.67	18	2x	24/08/2018	46.23394	7.33874	670	700	7	v	H	No	Yes	neu	med	Wet	45	F	T
Pulicaria dysenterica	MC1	124.17.2.0	2.15	NA	2.16	0.01	2.86	2.32	18	2x	NA	NA	NA	NA	700	7	v	H	No	Yes	neu	med	Wet	45	F	F
Reichardia picroides	OH282	124.87.1.0	NA	NA	3.1	0.01	2.21	2.07	14	2x	NA	NA	NA	NA	350	4	v	H	No	Yes	bas	low	veryDry	9	F	F
Rhagadiolus stellatus	OH273	124.79.1.0	2.67	NA	2.67	0.02	2.82	2.37	10	2x	NA	NA	NA	NA	350	4	a	T	No	Yes	neu	med	veryDry	5	F	F
Rhaponticoides alpina	OH475	124.68.1.0	NA	NA	2.66	0.01	2.89	2.79	30	2x	NA	NA	NA	NA	700	6	v	H	No	Yes	bas	low	Dry	7	F	F
Rhaponticoides alpina	OH490	124.68.1.0	NA	NA	2.66	0	2.07	2.29	30	2x	NA	NA	NA	NA	700	6	v	H	No	Yes	bas	low	Dry	7	F	F
Rhaponticum coniferum	OH257	124.66.1.0	NA	NA	1.79	0.01	2.83	1.84	26	2x	NA	NA	NA	NA	700	5	v	H	No	Yes	neu	low	veryDry	12	F	F
Rhaponticum coniferum	OH399	124.66.1.0	NA	NA	1.75	0.01	2.76	1.92	26	2x	NA	NA	NA	NA	700	5	v	H	No	Yes	neu	low	veryDry	12	F	F
Rhaponticum heleniifolium subsp. bicknellii	JB Lautaret21	124.67.2.2	NA	NA	2.17	0.01	3.46	2.61	26	2x	NA	NA	NA	NA	1750	6	v	H	Yes	Yes	bas	hig	Dry	2	F	F
Rhaponticum heleniifolium subsp. heleniifolium	JB Lautaret20	124.67.2.1	2.24	NA	2.23	0.02	3.73	2.84	26	2x	NA	NA	NA	NA	1400	6	v	H	Yes	Yes	bas	hig	Average	4	F	F
Rhaponticum scariosum	CH171	124.67.1.0	2.15	21	NA	NA	NA	NA	26	2x	29/08/2018	46.54982	8.70094	1933	1400	6	v	H	Yes	Yes	bas	hig	Average	15	F	T
Rhaponticum scariosum	JB Lautaret18	124.67.1.0	2.15	NA	2.16	0.02	2.7	2.04	26	2x	NA	NA	NA	NA	1400	6	v	H	Yes	Yes	bas	hig	Average	15	F	F
Rhaponticum scariosum subsp. rhaponticum	OH498	124.67.1.1	NA	NA	2.15	0	2.32	2.2	26	2x	NA	NA	NA	NA	1400	6	v	H	Yes	Yes	bas	hig	Average	15	F	F
Rhaponticum scariosum subsp. scariosum	JB Lautaret19	124.67.1.2	2.17	NA	2.17	0.02	2.7	2.04	26	2x	NA	NA	NA	NA	1983	7	v	H	Yes	Yes	aci	hig	Average	12	F	F

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Rudbeckia hirta	CH40	124.24.1.0	NA	NA	7.79	0.02	2.07	2.4	38	2x	20/06/2018	46.02692	8.76233	347	583	7	a, b, v	H	No	No	neu	hig	Wet	15	F	T
Santolina chamaecyparissus	CH9	124.29.1.0	23.29	1	23.29	0.17	3.99	3.07	18	2x	19/05/2018	46.00221	8.98815	313	350	7	A	C	No	No	bas	low	veryDry	3	F	T
Santolina chamaecyparissus	RBGK1969-18489	124.29.1.0	24.08	NA	24.08	0.05	2.78	1.62	18	2x	NA	NA	NA	NA	350	7	A	C	No	No	bas	low	veryDry	3	F	F
Saussurea alpina	A68	124.57.2.0	9.53	2	NA	NA	NA	NA	54	4x	17/07/2018	47.12227	12.82532	2324	2217	7	v	H	No	Yes	neu	med	Average	29	F	T
Saussurea alpina	A133	124.57.2.0	9.78	3	NA	NA	NA	NA	54	4x	21/07/2018	47.06167	12.79314	2122	2217	7	v	H	No	Yes	neu	med	Average	29	F	T
Saussurea alpina	FR694a	124.57.2.0	9.51	10	9.87	0.13	3.07	3.2	54	4x	NA	44.32157	6.80667	2862	2217	7	v	H	No	Yes	neu	med	Average	29	F	T
Saussurea alpina	FR637	124.57.2.0	9.61	10	NA	NA	NA	NA	54	4x	NA	44.26424	6.7029	2951	2217	7	v	H	No	Yes	neu	med	Average	29	F	T
Saussurea alpina	FR647	124.57.2.0	9.43	7	NA	NA	NA	NA	54	4x	NA	44.29436	6.61896	2539	2217	7	v	H	No	Yes	neu	med	Average	29	F	T
Saussurea depressa	FR535	124.57.2.3	9.89	15	9.89	0.08	3.74	3.67	54	4x	NA	45.06417	6.40772	2623	2575	7	v	H	Yes	Yes	bas	low	Average	8	F	T
Saussurea discolor	FR598	124.57.3.0	5.22	NA	5.24	0.06	3.22	2.91	26	2x	NA	NA	NA	1890	7	v	H	No	Yes	bas	low	Dry	31	F	F
Saussurea pygmaea	MB80	124.57.1.0	NA	NA	10.1	0.03	2.42	2.39	52	4x	22/07/2018	46.43517	13.64299	2036	2100	7	v	H	No	Yes	bas	low	Dry	5	F	T
Saussurea pygmaea	JB Lautaret15	124.57.1.0	NA	NA	9.9	0.05	2.91	2.71	52	4x	NA	NA	NA	NA	2100	7	v	H	No	Yes	bas	low	Dry	5	F	F
Schlagintweitia huteri subsp. lantoscana	FR667	124.99.55.0	7.25	NA	7.25	0	2.91	2.72	18	2x	NA	44.20338	7.1513	2354	1890	7	v	H	Sub	Yes	aci	low	Dry	27	F	T
Schlagintweitia intybacea	CH92	124.99.32.0	NA	NA	7.76	0	2.56	2.18	18	2x	24/07/2018	46.47733	8.41281	2235	1890	7	v	H	Sub	Yes	aci	low	Dry	27	F	T
Schlagintweitia intybacea	CH123	124.99.32.0	NA	NA	7.68	0.16	2.54	2.03	18	2x	26/07/2018	46.57594	8.42267	2383	1890	7	v	H	Sub	Yes	aci	low	Dry	27	F	T
Scolymus hispanicus	MB43	124.73.1.0	NA	NA	rotten	NA	NA	NA	20	2x	17/07/2018	NA	NA	NA	350	6	b	H	No	Yes	neu	hig	veryDry	3	F	F
Scolymus hispanicus	MB119	124.73.1.0	NA	NA	8.32	0.05	2.05	2.54	20	2x	27/08/2018	NA	NA	NA	350	6	b	H	No	Yes	neu	hig	veryDry	3	F	F
Scorzonera aristata	MB79	124.85.7.0	NA	NA	7.97	0.01	3.05	2.42	14	2x	22/07/2018	46.43517	13.64299	2036	1610	6	v	H	No	Yes	bas	hig	Dry	16	F	T
Scorzonera hirsuta	OH260	124.85.10.0	6.03	NA	6.03	0.02	2.58	2.65	12	2x	NA	NA	NA	NA	583	4	v	H	No	Yes	bas	low	veryDry	8	F	F
Scorzonera hispanica	A32	124.85.8.0	5.47	1	5.4	0.01	1.72	1.71	14	2x	16/06/2018	NA	NA	NA	910	5	v	H	No	Yes	bas	med	Dry	15	F	F
Scorzonera hispanica	JB Barcelona4	124.85.8.0	5.17	NA	5.17	0.05	2.92	2.36	14	2x	NA	NA	NA	NA	910	5	v	H	No	Yes	bas	med	Dry	15	F	F
Scorzonera hispanica	JB Barcelona5	124.85.8.0	5.17	NA	5.17	0.05	2.92	2.36	14	2x	NA	NA	NA	NA	910	5	v	H	No	Yes	bas	med	Dry	15	F	F
Scorzonera humilis	CH44	124.85.6.0	NA	NA	12.48	0.05	2.09	2.37	14	2x	21/06/2018	46.1044	8.96611	978	910	5	v	H	No	Yes	neu	low	Average	22	F	T
Scorzonera villosa	MB36	124.85.9.0	NA	NA	NA	NA	NA	NA	14	2x	29/06/2018	NA	NA	NA	700	4	v	G	No	Yes	bas	low	Dry	2	F	F
Scorzoneroides autumnalis	CH180	124.83.4.0	3.82	10	3.21	0.8	3.3	2.91	12	2x	29/08/2018	46.55413	8.71491	1950	1050	6	v	H	No	Yes	neu	med	Average	47	F	T
Scorzoneroides crocea	A12	124.83.2.0	4.6	9	4.98	0.06	3.53	1.82	14	2x	15/06/2018	47.71728	15.77466	1530	1750	7	v	H	No	Yes	neu	low	Average	1	F	T
Scorzoneroides crocea	CH145	124.83.2.0	3.93	5	5.12	NA	6.91	5.5	14	2x	23/08/2018	45.99006	7.704933	2025	1750	7	v	H	No	Yes	neu	low	Average	1	F	T
Scorzoneroides helevetica	CH50	124.83.1.0	NA	NA	4.28	0.03	3.43	2.37	12	2x	22/06/2018	46.21058	8.78732	1784	1921	7	v	H	No	Yes	aci	low	Average	46	F	T
Scorzoneroides helevetica	MB82	124.83.1.0	4.31	3	NA	NA	NA	NA	12	2x	22/07/2018	46.44608	13.64746	2108	1921	7	v	H	No	Yes	aci	low	Average	46	F	T
Scorzoneroides helevetica	FR556	124.83.1.0	4.26	NA	4.3	0.05	3.3	2.57	12	2x	NA	45.06417	6.4024	2601	1921	7	v	H	No	Yes	aci	low	Average	46	F	T
Scorzoneroides helevetica	FR468	124.83.1.0	4.18	5	NA	NA	NA	NA	12	2x	NA	44.72623	6.32373	2678	1921	7	v	H	No	Yes	aci	low	Average	46	F	T
Scorzoneroides montana	A116	124.83.3.0	NA	NA	4.84	0.06	4.28	3.75	12	2x	20/07/2018	47.0979	12.83191	2338	2217	7	v	H	No	Yes	bas	low	Average	39	F	T
Scorzoneroides montana	FR532	124.83.3.0	4.67	8	NA	NA	NA	NA	12	2x	NA	45.06417	6.40772	2623	2217	7	v	H	No	Yes	bas	low	Average	39	F	T
Scorzoneroides montana	OH304	124.83.3.0	4.88	NA	5.04	0.23	2.82	2.13	12	2x	NA	NA	NA	NA	2217	7	v	H	No	Yes	bas	low	Average	39	F	F
Senecio cacaliaster	A136	124.48.9.0	NA	NA	11.53	0.01	2.57	3.03	40	4x	22/07/2018	47.15162	12.81429	1494	1400	6	v	H	No	Yes	neu	hig	Wet	14	F	T
Senecio cacaliaster	FR571	124.48.9.0	11.63	NA	11.48	0.06	2.28	3.18	40	4x	NA	45.0415	6.28388	1380	1400	6	v	H	No	Yes	neu	hig	Wet	14	F	T
Senecio doria	FR194	124.48.10.0	12.92	NA	12.96	0.04	1.98	1.65	40	4x	26/07/2016	44.2476	6.23499	1380	910	7	v	HÃ©l	No	Yes	neu	med	Wet	7	F	T
Senecio doria	CH78	124.48.10.0	11.61	12	NA	NA	NA	NA	40	4x	24/07/2018	46.49405	8.3477	1660	910	7	v	HÃ©l	No	Yes	neu	med	Wet	7	F	T
Senecio doria	MB95	124.48.10.0	NA	NA	14.02	0.06	2.7	2.75	40	4x	14/08/2018	NA	NA	NA	910	7	v	HÃ©l	No	Yes	neu	med	Wet	7	F	F
Senecio doria	RD12	124.48.10.0	NA	NA	NA	NA	NA	NA	40	4x	NA	NA	NA	NA	910	7	v	HÃ©l	No	Yes	neu	med	Wet	7	F	F

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Senecio doronicum	FR67a	124.48.14.0	NA	NA	16.9	0.16	1.63	1.72	80	8x	24/07/2016	NA	NA	NA	1890	7	v	H	No	Yes	bas	low	Average	42	T	F
Senecio doronicum	FR67b	124.48.14.0	16.73	NA	8.75	0.18	1.95	2.22	40	4x	24/07/2016	NA	NA	NA	1890	7	v	H	No	Yes	bas	low	Average	42	T	F
Senecio doronicum	FR95	124.48.14.0	16.77	NA	NA	NA	NA	NA	80	8x	25/07/2016	44.38528	6.39642	2184	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR206	124.48.14.0	16.7	NA	NA	NA	NA	NA	80	8x	27/07/2016	44.28474	6.4317	1772	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR259	124.48.14.0	16.77	NA	NA	NA	NA	NA	80	8x	28/07/2016	44.31535	6.44221	1961	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR275	124.48.14.0	16.71	NA	NA	NA	NA	NA	80	8x	28/07/2016	44.31586	6.4565	2378	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR239	124.48.14.0	16.6	NA	NA	NA	NA	NA	80	8x	28/07/2016	44.31782	6.44161	1881	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR303	124.48.14.0	16.49	NA	NA	NA	NA	NA	80	8x	29/07/2016	44.40792	6.385497	2505	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR711a	124.48.14.0	15.97	5	NA	NA	NA	NA	80	8x	23/04/2018	44.32002	6.43188	1557	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR716b	124.48.14.0	16.09	20	NA	NA	NA	NA	80	8x	17/05/2018	44.33137	6.27408	2019	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR716a	124.48.14.0	15.92	3	NA	NA	NA	NA	80	8x	17/05/2018	44.33137	6.27408	2019	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR715	124.48.14.0	15.96	7	NA	NA	NA	NA	80	8x	17/05/2018	44.33681	6.2822	1934	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR718b-3	124.48.14.0	16.77	5	NA	NA	NA	NA	80	8x	17/05/2018	44.331	6.27342	2027	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR720	124.48.14.0	15.78	12	NA	NA	NA	NA	80	8x	17/05/2018	44.3342	6.29422	1968	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR714	124.48.14.0	NA	NA	NA	NA	NA	NA	NA	NA	17/05/2018	44.34028	6.29359	1766	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR718b-2	124.48.14.0	13.13	1	NA	NA	NA	NA	60	6x	17/05/2018	44.331	6.27342	2027	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR721	124.48.14.0	15.92	3	NA	NA	NA	NA	80	8x	17/05/2018	44.34052	6.29454	1818	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR718a	124.48.14.0	16.43	2	NA	NA	NA	NA	80	8x	17/05/2018	44.331	6.27342	2027	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR718b-1	124.48.14.0	9.05	7	NA	NA	NA	NA	40	4x	17/05/2018	44.331	6.27342	2027	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	MB18	124.48.14.0	NA	NA	8.71	0.07	3.96	3.78	40	4x	21/06/2018	NA	NA	NA	1890	7	v	H	No	Yes	bas	low	Average	42	T	F
Senecio doronicum	A112	124.48.14.0	8.91	10	NA	NA	NA	NA	40	4x	20/07/2018	47.12461	12.82355	2293	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	A125	124.48.14.0	8.94	1	NA	NA	NA	NA	40	4x	21/07/2018	47.05946	12.79703	2022	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	A130	124.48.14.0	8.89	10	NA	NA	NA	NA	40	4x	21/07/2018	47.06135	12.79348	2108	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	A126	124.48.14.0	15.1	10	NA	NA	NA	NA	80	8x	21/07/2018	47.06711	12.77199	2145	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	CH93	124.48.14.0	16.79	6	NA	NA	NA	NA	80	8x	24/07/2018	46.47733	8.41281	2235	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	CH126	124.48.14.0	16.19	10	NA	NA	NA	NA	80	8x	26/07/2018	46.57597	8.42242	2400	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	CH120	124.48.14.0	16.42	8	NA	NA	NA	NA	80	8x	26/07/2018	46.55568	8.86541	2109	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	CH155	124.48.14.0	15.93	7	NA	NA	NA	NA	80	8x	23/08/2018	45.98862	7.69558	2814	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	CH149	124.48.14.0	15.84	9	NA	NA	NA	NA	80	8x	23/08/2018	45.98976	7.70472	2630	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	CH174	124.48.14.0	16.76	7	NA	NA	NA	NA	80	8x	29/08/2018	46.54982	8.70094	1933	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR360	124.48.14.0	16.78	8	NA	NA	NA	NA	80	8x	NA	44.3405	6.29449	1820	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR463	124.48.14.0	16.72	23	NA	NA	NA	NA	80	8x	NA	44.72623	6.32373	2678	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR459	124.48.14.0	16.94	21	NA	NA	NA	NA	80	8x	NA	44.72351	6.31857	2607	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR626	124.48.14.0	8.55	NA	NA	NA	NA	NA	40	4x	NA	44.25249	6.71275	2345	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR417	124.48.14.0	16.26	13	NA	NA	NA	NA	80	8x	NA	44.31216	6.43589	1850	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR387	124.48.14.0	16.31	16	NA	NA	NA	NA	80	8x	NA	44.332	6.29235	1988	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR380	124.48.14.0	16.53	12	NA	NA	NA	NA	80	8x	NA	44.40943	6.38709	2498	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR364	124.48.14.0	16.26	21	NA	NA	NA	NA	80	8x	NA	44.39758	6.38375	2126	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR365	124.48.14.0	15.95	15	NA	NA	NA	NA	80	8x	NA	44.39758	6.38375	2126	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR379	124.48.14.0	16.44	11	NA	NA	NA	NA	80	8x	NA	44.40943	6.38709	2498	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR475	124.48.14.0	17.01	17	NA	NA	NA	NA	80	8x	NA	44.72992	6.32625	2431	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR476	124.48.14.0	16.87	30	NA	NA	NA	NA	80	8x	NA	44.72099	6.34373	2429	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR648a	124.48.14.0	8.61	4	NA	NA	NA	NA	40	4x	NA	44.29436	6.61896	2539	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR628b	124.48.14.0	8.7	8	NA	NA	NA	NA	40	4x	NA	44.25411	6.71406	2428	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR361	124.48.14.0	17.15	2	NA	NA	NA	NA	80	8x	NA	44.3405	6.29449	1820	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR627	124.48.14.0	8.61	8	NA	NA	NA	NA	40	4x	NA	44.25315	6.71517	2405	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR363	124.48.14.0	16.63	11	NA	NA	NA	NA	80	8x	NA	44.40339	6.37521	1952	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR479	124.48.14.0	16.76	23	NA	NA	NA	NA	80	8x	NA	44.72046	6.34202	2415	1890	7	v	H	No	Yes	bas	low	Average	42	T	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Senecio doronicum	FR601	124.48.14.0	16.55	6	NA	NA	NA	NA	80	8x	NA	44.06522	6.40574	2678	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR359	124.48.14.0	16.92	9	NA	NA	NA	NA	80	8x	NA	44.33462	6.29482	1981	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR356	124.48.14.0	16.27	12	NA	NA	NA	NA	80	8x	NA	44.33665	6.28209	1938	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR653	124.48.14.0	8.75	2	NA	NA	NA	NA	40	4x	NA	44.3197	6.69477	1689	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR472	124.48.14.0	16.99	2	NA	NA	NA	NA	80	8x	NA	44.72993	6.32625	2683	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR482	124.48.14.0	16.98	9	NA	NA	NA	NA	80	8x	NA	44.57619	6.33727	2076	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR357	124.48.14.0	16.45	12	NA	NA	NA	NA	80	8x	NA	44.33665	6.28209	1938	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR358	124.48.14.0	16.7	8	NA	NA	NA	NA	80	8x	NA	44.33462	6.29482	1981	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR386	124.48.14.0	16.65	19	NA	NA	NA	NA	80	8x	NA	44.332	6.29235	1988	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR654	124.48.14.0	8.85	6	NA	NA	NA	NA	40	4x	NA	44.31719	6.690034	1662	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR648b	124.48.14.0	16.62	NA	NA	NA	NA	NA	80	8x	NA	44.29436	6.61896	2539	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR485	124.48.14.0	17.2	2	NA	NA	NA	NA	80	8x	NA	44.58065	6.33232	2249	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR696	124.48.14.0	15.62	7	NA	NA	NA	NA	80	8x	NA	44.34501	6.80097	2623	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR435	124.48.14.0	17.4	5	NA	NA	NA	NA	80	8x	NA	44.28397	6.43458	1710	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR671	124.48.14.0	16.13	1	NA	NA	NA	NA	80	8x	NA	44.20338	7.1513	2354	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR362	124.48.14.0	NA	NA	NA	NA	NA	NA	NA	NA	NA	44.40339	6.37521	1952	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR478	124.48.14.0	16.84	9	NA	NA	NA	NA	80	8x	NA	44.72046	6.34202	2415	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR474a	124.48.14.0	17.08	1	NA	NA	NA	NA	80	8x	NA	44.72324	6.3443	2463	1890	7	v	H	No	Yes	bas	low	Average	42	T	T
Senecio doronicum	FR411	124.48.14.0	16.56	2	NA	NA	NA	NA	80	8x	NA	NA	NA	NA	1890	7	v	H	No	Yes	bas	low	Average	42	T	F
Senecio doronicum	OH299	124.48.14.0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1890	7	v	H	No	Yes	bas	low	Average	42	T	F
Senecio fontanicola	MB130	124.48.11.0	NA	NA	NA	NA	NA	NA	40	4x	31/07/2018	46.49127	13.73711	835	583	6	v	HÃ©l	Sub	Yes	bas	low	Wet	1	F	T
Senecio hercynicus	A135	124.48.7.0	NA	NA	11.22	0.07	2.71	2.71	40	4x	22/07/2018	47.15162	12.81429	1494	1400	7	v	H	No	Yes	neu	hig	Wet	23	F	T
Senecio hercynicus	NA	124.48.7.0	NA	NA	11.32	0.03	1.85	1.92	40	4x	NA	NA	NA	NA	1400	7	v	H	No	Yes	neu	hig	Wet	23	F	F
Senecio inaequidens	IT21	124.48.5.0	3.27	NA	3.27	0.01	3.37	3.09	40	4x	NA	45.68636	11.75984	369	583	4	a, A	T, C	No	No	neu	med	Dry	28	F	T
Senecio inaequidens	GR557	124.48.5.0	3.2	NA	3.2	0.02	2.95	2.62	40	4x	NA	NA	NA	NA	583	4	a, A	T, C	No	No	neu	med	Dry	28	F	F
Senecio inaequidens	OH262	124.48.5.0	3.19	NA	NA	NA	NA	NA	40	4x	NA	NA	NA	NA	583	4	a, A	T, C	No	No	neu	med	Dry	28	F	F
Senecio nemorensis subsp. jacquinianus	A41	124.48.6.0	8.55	10	8.67	0.03	1.92	2.07	40	4x	18/06/2018	NA	NA	NA	583	7	v	H	No	Yes	neu	hig	Wet	3	F	F
Senecio ovatus	FR450	124.48.8.0	13.13	8	NA	NA	NA	NA	40	4x	NA	44.67046	6.23971	1052	910	7	v	H	No	Yes	neu	hig	Average	22	F	T
Senecio ovatus	CZ4	124.48.8.0	NA	NA	11.21	0.05	1.77	1.91	40	4x	NA	NA	NA	NA	910	7	v	H	No	Yes	neu	hig	Average	22	F	F
Senecio ovatus subsp. ovatus	FR395	124.48.8.1	11.94	10	11.94	0.09	2.27	2.42	40	4x	NA	44.32827	6.31656	1553	910	7	v	H	No	Yes	neu	hig	Average	22	F	T
Senecio ovatus subsp. ovatus	OH473	124.48.8.1	NA	NA	11.21	0.09	1.82	2.85	40	4x	NA	NA	NA	NA	910	7	v	H	No	Yes	neu	hig	Average	22	F	F
Senecio squalidus subsp. rupestris	IT104	124.48.21.0	1.79	13	1.75	0.03	3.35	1.75	20	2x	20/09/2018	45.78917	11.21698	1400	1400	6	a, b, v	T, H	No	Yes	neu	hig	Average	22	F	T
Senecio squalidus subsp. rupestris	FR576b	124.48.21.0	1.92	NA	1.87	0.07	4.66	2.83	20	2x	NA	NA	NA	NA	1400	6	a, b, v	T, H	No	Yes	neu	hig	Average	22	F	F
Senecio squalidus subsp. rupestris	NA	124.48.21.0	NA	NA	NA	NA	NA	NA	20	2x	NA	NA	NA	NA	1400	6	a, b, v	T, H	No	Yes	neu	hig	Average	22	F	F
Senecio viscosus	FR620	124.48.26.0	4.8	NA	NA	NA	NA	NA	40	4x	NA	44.34648	6.2931	1610	1050	6	a	T	No	Yes	neu	med	Dry	45	F	T
Senecio viscosus	FR489	124.48.26.0	4.95	9	4.63	0.02	4.09	3.25	40	4x	NA	44.34648	6.2931	1610	1050	6	a	T	No	Yes	neu	med	Dry	45	F	T
Senecio vulgaris	IT41	124.48.27.0	3.42	NA	3.42	0	3.14	2.69	40	4x	NA	45.696	11.6343	73	910	1	a	T	No	Yes	neu	hig	Average	50	T	T
Senecio vulgaris	GR564	124.48.27.0	3.56	NA	3.56	0.04	3.19	1.76	40	4x	NA	NA	NA	NA	910	1	a	T	No	Yes	neu	hig	Average	50	T	F
Senecio vulgaris	RBGK wild4	124.48.27.0	3.75	NA	3.75	0.04	2.61	1.92	40	4x	NA	NA	NA	NA	910	1	a	T	No	Yes	neu	hig	Average	50	T	F
Serratula tinctoria	IT96	124.65.1.0	4.5	8	3.5	0.09	3.78	3.99	22	2x	27/08/2018	46.00695	9.2258	806	1610	7	v	H	No	Yes	bas	med	Average	20	F	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Serratula tinctoria	RBGK1998-2082	124.65.1.0	NA	NA	NA	NA	NA	NA	22	2x	NA	NA	NA	NA	1610	7	v	H	No	Yes	bas	med	Average	20	F	F
Serratula tinctoria subsp. monticola	OH499	124.65.1.2	NA	NA	3.74	0.01	3.1	2.51	22	2x	NA	NA	NA	NA	1610	7	v	H	No	Yes	bas	med	Average	20	F	F
Serratula tinctoria subsp. monticola	OH331	124.65.1.2	NA	NA	3.65	0	2.97	2.79	22	2x	NA	NA	NA	NA	1610	7	v	H	No	Yes	bas	med	Average	20	F	F
Serratula tinctoria subsp. tinctoria	MB48	124.65.1.1	NA	NA	3.58	0.01	2.8	2.71	22	2x	10/07/2018	NA	NA	NA	700	7	v	H	No	Yes	bas	low	Wet	38	F	F
Sigesbeckia orientalis	IT72	124	7.5	11	7.69	0.08	3.4	2.63	30	2x	NA	45.70683	11.61797	80	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	F	T
Silybum marianum	GR05-2017b	124.64.1.0	2.09	NA	2.09	0.02	3.51	2.28	34	2x	NA	NA	NA	NA	583	6	a, b	T, H	No	No	neu	hig	veryDry	23	F	F
Solidago canadensis	MB101	124.2.2.0	NA	NA	2.26	0	3.68	2.88	18	2x	15/08/2018	46.303	14.04706	525	583	7	v	H	No	No	neu	med	Average	37	F	T
Solidago gigantea	MB102	124.2.3.0	3.75	NA	3.88	0.01	2.67	2.64	36	4x	15/08/2018	46.2685	13.89856	509	583	7	v	H	No	No	neu	med	Wet	42	F	T
Solidago virgaurea	FR99	124.2.1.0	2.54	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38528	6.39642	2184	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea	FR116	124.2.1.0	2.54	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.37932	6.3955	1985	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea	FR111	124.2.1.0	2.49	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.37932	6.3955	1985	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea	FR139	124.2.1.0	2.52	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38569	6.39095	1922	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea	FR82	124.2.1.0	2.5	NA	NA	NA	NA	NA	18	2x	25/07/2016	44.38621	6.39601	2219	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea	FR204	124.2.1.0	2.55	NA	NA	NA	NA	NA	18	2x	27/07/2016	44.28474	6.4317	1772	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea	FR238	124.2.1.0	2.46	NA	NA	NA	NA	NA	18	2x	28/07/2016	44.31782	6.44161	1881	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea	FR270	124.2.1.0	2.47	NA	NA	NA	NA	NA	18	2x	28/07/2016	44.31346	6.44843	2127	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea	FR285	124.2.1.0	2.52	NA	NA	NA	NA	NA	18	2x	28/07/2016	44.31586	6.4565	2378	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea	FR251	124.2.1.0	2.51	NA	NA	NA	NA	NA	18	2x	28/07/2016	44.31535	6.44221	1961	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea	FR347	124.2.1.0	2.4	NA	NA	NA	NA	NA	18	2x	29/07/2016	44.02726	6.22486	1358	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea	FR341	124.2.1.0	2.46	NA	NA	NA	NA	NA	18	2x	29/07/2016	44.27214	6.21177	1651	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea	FR306	124.2.1.0	2.53	NA	NA	NA	NA	NA	18	2x	29/07/2016	44.40792	6.385497	2505	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea	CH67	124.2.1.0	2.53	6	NA	NA	NA	NA	18	2x	23/06/2018	45.94328	9.0313	1327	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea subsp. minuta	MB81	124.2.1.2	2.56	2	NA	NA	NA	NA	18	2x	22/07/2018	46.43517	13.64299	2036	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea subsp. minuta	FR526	124.2.1.2	NA	NA	NA	NA	NA	NA	18	2x	NA	44.35538	6.29001	1289	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea subsp. minuta	FR458	124.2.1.2	2.58	8	NA	NA	NA	NA	18	2x	NA	44.72252	6.31779	2553	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea subsp. minuta	FR537	124.2.1.2	2.67	NA	2.56	0.01	2.66	2.51	18	2x	NA	45.06417	6.40772	2623	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea subsp. minuta	FR496	124.2.1.2	2.5	2	NA	NA	NA	NA	18	2x	NA	44.35498	6.95723	1879	1890	7	v	H	No	Yes	aci	med	Average	38	F	T
Solidago virgaurea subsp. virgaurea	A97	124.2.1.1	NA	NA	2.52	0	2.82	2.08	18	2x	19/07/2018	46.78288	12.78845	1638	910	7	v	H	No	Yes	neu	med	Average	49	F	T
Sonchus arvensis subsp. uliginosus	OH454	124.88.4.2	NA	NA	6.39	0.01	2.66	2.3	54	6x	NA	NA	NA	NA	700	7	v	H	No	Yes	neu	hig	Wet	7	F	F
Sonchus oleraceus	IT42	124.88.2.0	3.37	NA	3.46	0.01	2.38	3.59	32	4x	NA	45.696	11.6343	73	910	5	a, b	T, H	No	Yes	bas	hig	Average	49	F	T
Sonchus oleraceus	RBGK wild5	124.88.2.0	NA	NA	NA	NA	NA	NA	32	4x	NA	NA	NA	NA	910	5	a, b	T, H	No	Yes	bas	hig	Average	49	F	F
Sonchus tenerrimus	OH BCN2	124.88.5.0	2.45	NA	2.45	0.09	3.43	2.43	14	2x	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	F	F
Staehelina dubia	OH400	124.58.1.0	NA	NA	1.34	0.05	2.81	2.08	30	2x	NA	NA	NA	NA	583	5	A	C	No	Yes	neu	low	veryDry	10	F	F
Staehelina dubia	RD14	124.58.1.0	1.3	NA	1.31	0.01	2.07	2	30	2x	NA	NA	NA	NA	583	5	A	C	No	Yes	neu	low	veryDry	10	F	F

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Symphyotrichum novae-angliae	RBGK1994-3723	124.4.1.0	3.45	NA	3.45	0	3.45	2.56	10	2x	NA	NA	NA	NA	350	8	v	H	No	No	neu	hig	Average	16	F	F
Symphyotrichum novi-belgii	RBGK2014-1412	124.4.3.0	4.89	NA	4.89	0.05	3.08	2.54	48	6x	NA	NA	NA	NA	350	8	v	H	No	No	neu	hig	Average	41	F	F
Symphyotrichum pilosum	IT84	124.4.10.0	3.93	8	3.83	0.09	3.4	3.64	48	4x	25/08/2018	45.8675	8.8588	403	350	9	v	H	No	No	neu	hig	Average	1	F	T
Symphyotrichum squamatum	MB128	124.4.4.0	NA	NA	3.26	0.01	2.4	1.74	18	2x	20/09/2018	NA	NA	NA	350	9	a, b	T, H	No	No	neu	hig	Average	2	F	F
Tanacetum corymbosum	FR163b	124.35.2.0	21.74	NA	20.9	0.11	2.07	1.9	36	4x	26/07/2016	44.27211	6.29882	1083	700	6	v	H	No	Yes	bas	low	Dry	26	F	T
Tanacetum corymbosum	CH8	124.35.2.0	21.69	5	NA	NA	NA	NA	36	4x	19/05/2018	46.00203	8.98751	288	700	6	v	H	No	Yes	bas	low	Dry	26	F	T
Tanacetum corymbosum	CH3	124.35.2.0	21.49	7	NA	NA	NA	NA	36	4x	19/05/2018	46.00833	8.98694	880	700	6	v	H	No	Yes	bas	low	Dry	26	F	T
Tanacetum corymbosum	CH38	124.35.2.0	20.93	7	NA	NA	NA	NA	36	4x	22/05/2018	45.95981	9.00145	654	700	6	v	H	No	Yes	bas	low	Dry	26	F	T
Tanacetum corymbosum	A11	124.35.2.0	20.83	5	21.39	0.03	2.85	2.68	36	4x	14/06/2018	48.04065	16.04163	453	700	6	v	H	No	Yes	bas	low	Dry	26	F	T
Tanacetum corymbosum	FR429	124.35.2.0	20.84	4	NA	NA	NA	NA	36	4x	NA	44.31974	6.43204	1514	700	6	v	H	No	Yes	bas	low	Dry	26	F	T
Tanacetum corymbosum	OH444	124.35.2.0	NA	NA	21.01	0.21	3.4	2.38	36	4x	NA	NA	NA	NA	700	6	v	H	No	Yes	bas	low	Dry	26	F	F
Tanacetum corymbosum	FR300	124.35.2.0	19.78	NA	NA	NA	NA	NA	36	4x	NA	NA	NA	NA	700	6	v	H	No	Yes	bas	low	Dry	26	F	F
Tanacetum corymbosum	OH472	124.35.2.0	22.06	1	NA	NA	NA	NA	36	4x	NA	NA	NA	NA	700	6	v	H	No	Yes	bas	low	Dry	26	F	F
Tanacetum corymbosum subsp. subcorymbosum	OH335	124.35.2.2	16.96	NA	NA	NA	NA	NA	18	2x	NA	NA	NA	NA	1400	6	v	H	No	Yes	bas	low	Average	9	F	F
Tanacetum macrophyllum	OH323	124.35.4.0	10.45	NA	10.45	0.07	2.41	1.99	18	2x	NA	NA	NA	NA	817	6	v	H	No	No	neu	hig	Average	1	F	F
Tanacetum parthenium	CH170	124.35.3.0	4.53	16	4.77	0	2.32	2.97	18	2x	29/08/2018	46.51995	8.69642	1356	700	6	v	H	No	No	neu	hig	Average	40	F	T
Tanacetum parthenium	OH401b	124.35.3.0	NA	NA	4.85	0.05	2.75	2.3	18	2x	NA	NA	NA	NA	700	6	v	H	No	No	neu	hig	Average	40	F	F
Tanacetum vulgare	FR530	124.35.1.0	10.5	NA	10.49	0.01	3.05	2.79	18	2x	NA	45.06417	6.40772	2623	910	6	v	H	No	NA	neu	med	Dry	40	F	T
Tanacetum vulgare	OH2017-21	124.35.1.0	10.32	NA	NA	NA	NA	NA	18	2x	NA	NA	NA	NA	910	6	v	H	No	NA	neu	med	Dry	40	F	F
Taraxacum aquilonare	CH86	124.93.14.0	NA	NA	5.38	0.01	3.55	1.86	40	4x	24/07/2018	46.47839	8.38935	2495	2183	5	v	H	No	Yes	neu	low	Dry	9	F	T
Taraxacum carinthiacum	A80	124.93.16.0	3.24	6	3.53	0.03	5.58	3.81	24	3x	18/07/2018	47.08244	12.8416	2577	2450	7	v	H	Yes	Yes	neu	low	Average	1	F	T
Taraxacum obovatum	FR542	124.93.5.0	2.9	NA	2.91	0	3.47	2.69	32	4x	NA	45.06417	6.40772	2623	583	5	v	H	No	Yes	neu	hig	veryDry	6	F	T
Taraxacum pacheri	A81	124.93.3.0	NA	NA	4.71	0.03	4.85	3.58	32	4x	18/07/2018	47.08249	12.84136	2586	2217	7	v	H	Yes	Yes	bas	med	Wet	9	F	T
Taraxacum sect. Alpina	OH329	124.93.8.0	3.13	NA	3.09	0.01	3.94	2.58	32	4x	NA	NA	NA	NA	2100	6	v	H	No	Yes	neu	hig	Wet	42	F	F
Taraxacum sect. Cucullata	FR559	124.93.11.0	3.32	NA	3.36	0.04	3.27	2.38	24	3x	NA	45.06417	6.4024	2601	1890	6	v	H	No	Yes	neu	hig	Wet	24	F	T
Taraxacum sect. Taraxacum	CH18	124.93.15.0	14.73	5	2.85	0.03	4.04	3.06	24	3x	21/05/2018	46.38723	8.54227	741	1250	4	v	H	No	Yes	neu	hig	Average	50	T	T
Taraxacum sect. Taraxacum	FR402	124.93.15.0	NA	NA	NA	NA	NA	NA	24	3x	NA	44.30992	6.38858	1608	1250	4	v	H	No	Yes	neu	hig	Average	50	T	T
Taraxacum sect. Taraxacum	IT18	124.93.15.0	3.16	10	NA	NA	NA	NA	24	3x	NA	45.66489	11.80406	1419	1250	4	v	H	No	Yes	neu	hig	Average	50	T	T
Taraxacum sect. Taraxacum	IT10	124.93.15.0	2.79	10	3.23	0.04	4.08	3.46	24	3x	NA	45.75958	11.39021	1294	1250	4	v	H	No	Yes	neu	hig	Average	50	T	T
Taraxacum sect. Taraxacum	CZ8	124.93.15.0	NA	NA	NA	NA	NA	NA	24	3x	NA	NA	NA	NA	1250	4	v	H	No	Yes	neu	hig	Average	50	T	F
Taraxacum sect. Taraxacum	JdV342	124.93.15.0	2.73	NA	2.73	0.03	2.61	1.86	24	3x	NA	NA	NA	NA	1250	4	v	H	No	Yes	neu	hig	Average	50	T	F
Taraxacum sect. Taraxacum	OH529	124.93.15.0	NA	NA	2.21	0.01	4.47	4	24	3x	NA	NA	NA	NA	1250	4	v	H	No	Yes	neu	hig	Average	50	T	F
Taraxacum sect. Taraxacum	MSB0492049	124.93.15.0	2.54	NA	NA	NA	NA	NA	24	3x	NA	NA	NA	NA	1250	4	v	H	No	Yes	neu	hig	Average	50	T	F

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Taraxacum venustum	A79	124.93.17.0	NA	NA	4.61	0.01	3.37	2.64	32	4x	18/07/2018	47.08244	12.8416	2577	2450	7	v	H	Yes	Yes	neu	low	Average	1	F	T
Telekia speciosa	MB56	124.20.1.0	NA	NA	2.83	0.02	3.24	2.62	20	2x	11/07/2018	NA	NA	NA	817	6	v	H	No	No	bas	hig	Wet	8	F	F
Telekia speciosa	IT68	124.20.1.0	2.95	13	2.87	0	3.09	2.38	20	2x	NA	45.6702	11.18369	717	817	6	v	H	No	No	bas	hig	Wet	8	F	T
Telekia speciosa	RBGK1994-467	124.20.1.0	3	NA	3	0	2.45	1.89	20	2x	NA	NA	NA	NA	817	6	v	H	No	No	bas	hig	Wet	8	F	F
Tephroseris integrifolia	A38	124.49.1.0	9.56	6	10.34	0.09	3.47	3.04	48	4x	17/06/2018	47.79204	15.81456	1242	1250	5	v	H	No	Yes	bas	low	Dry	6	F	T
Tephroseris integrifolia subsp. capitata	JB Lautaret14	124.49.3.0	17.23	NA	17.23	0.22	2.87	2.53	64	8x	NA	NA	NA	NA	2100	6	v	H	No	Yes	bas	low	Dry	12	F	F
Tephroseris longifolia	IT49	124.49.9.0	11.04	10	11.3	0.02	2.43	2.15	48	4x	NA	45.79402	11.46281	1269	1190	5	v	H	No	Yes	neu	hig	Average	5	F	T
Tolpis staticifolia	FR70	124.99.1.0	3.92	NA	NA	NA	NA	NA	18	2x	24/07/2016	NA	NA	NA	1550	6	v	H	No	Yes	neu	low	Dry	43	F	F
Tolpis staticifolia	FR218	124.99.1.0	5.2	NA	NA	NA	NA	NA	18	2x	27/07/2016	44.28474	6.4317	1772	1550	6	v	H	No	Yes	neu	low	Dry	43	F	T
Tolpis staticifolia	FR240	124.99.1.0	5.06	NA	NA	NA	NA	NA	18	2x	28/07/2016	44.31782	6.44161	1881	1550	6	v	H	No	Yes	neu	low	Dry	43	F	T
Tolpis staticifolia	FR342	124.99.1.0	5.09	NA	NA	NA	NA	NA	18	2x	29/07/2016	44.27214	6.21177	1651	1550	6	v	H	No	Yes	neu	low	Dry	43	F	T
Tolpis staticifolia	CH80	124.99.1.0	5.12	6	NA	NA	NA	NA	18	2x	24/07/2018	46.49419	8.34802	1662	1550	6	v	H	No	Yes	neu	low	Dry	43	F	T
Tolpis staticifolia	CH144	124.99.1.0	5.09	12	NA	NA	NA	NA	18	2x	23/08/2018	45.9899	7.7051	2614	1550	6	v	H	No	Yes	neu	low	Dry	43	F	T
Tolpis staticifolia	FR430	124.99.1.0	5.18	NA	5.31	0.18	3.16	2.79	18	2x	NA	44.31974	6.43204	1514	1550	6	v	H	No	Yes	neu	low	Dry	43	F	T
Tragopogon crocifolius	OH518	124.86.2.0	NA	NA	4.76	0.02	2.29	2.04	12	2x	NA	NA	NA	NA	910	5	a, b	T, H	No	Yes	bas	med	veryDry	11	F	F
Tragopogon dubius	FR722	124.86.3.0	4.96	7	4.96	0.01	3	2.02	12	2x	18/05/2018	44.59653	6.52327	919	910	5	b	H	No	Yes	neu	hig	veryDry	25	T	T
Tragopogon dubius	OH403	124.86.3.0	NA	NA	5.48	0.01	2.36	1.81	12	2x	NA	NA	NA	NA	910	5	b	H	No	Yes	neu	hig	veryDry	25	T	F
Tragopogon porrifolius subsp. porrifolius	MC10	124.86.1.1	6.3	NA	6.3	0.04	1.81	2.41	12	2x	NA	NA	NA	NA	583	5	a, b	T, H	No	No	neu	hig	Dry	2	F	F
Tragopogon pratensis	FR30	124.86.4.0	5.25	NA	NA	NA	NA	NA	12	2x	24/07/2016	44.33598	6.29635	1987	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	T	T
Tragopogon pratensis	FR53	124.86.4.0	5.08	NA	NA	NA	NA	NA	12	2x	24/07/2016	44.34171	6.29706	1802	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	T	T
Tragopogon pratensis	FR24	124.86.4.0	5.25	NA	NA	NA	NA	NA	12	2x	24/07/2016	44.33802	6.29635	1893	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	T	T
Tragopogon pratensis	FR16a	124.86.4.0	5.28	NA	NA	NA	NA	NA	12	2x	24/07/2016	44.34002	6.29641	1847	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	T	T
Tragopogon pratensis	FR60	124.86.4.0	5.14	NA	NA	NA	NA	NA	12	2x	24/07/2016	NA	NA	NA	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	T	F
Tragopogon pratensis	FR112	124.86.4.0	5.29	NA	5.57	0.03	2.04	1.62	12	2x	25/07/2016	44.37932	6.3955	1985	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	T	T
Tragopogon pratensis	FR179	124.86.4.0	5.15	NA	NA	NA	NA	NA	12	2x	26/07/2016	44.2486	6.22959	1586	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	T	T
Tragopogon pratensis	FR209	124.86.4.0	5.12	NA	NA	NA	NA	NA	12	2x	27/07/2016	44.28474	6.4317	1772	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	T	T
Tragopogon pratensis	FR237	124.86.4.0	5.18	NA	NA	NA	NA	NA	12	2x	28/07/2016	44.31782	6.44161	1881	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	T	T
Tragopogon pratensis	FR316	124.86.4.0	5.35	NA	NA	NA	NA	NA	12	2x	29/07/2016	44.26084	6.20877	1890	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	T	T
Tragopogon pratensis	FR326	124.86.4.0	5.18	NA	NA	NA	NA	NA	12	2x	29/07/2016	44.26081	6.20881	1888	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	T	T
Tragopogon pratensis	IT35	124.86.4.0	NA	NA	NA	NA	NA	NA	12	2x	NA	45.79267	11.70271	431	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	T	T
Tragopogon pratensis	FR431	124.86.4.0	5.58	3	NA	NA	NA	NA	12	2x	NA	44.27853	6.42408	1418	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	T	T
Tragopogon pratensis	LF2	124.86.4.0	5.19	NA	NA	NA	NA	NA	12	2x	NA	NA	NA	NA	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	T	F
Tragopogon pratensis subsp. orientalis	FR4	124.86.4.3	5.14	NA	NA	NA	NA	NA	12	2x	24/07/2016	44.33469	6.29546	NA	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	F	T
Tragopogon pratensis subsp. orientalis	MB58	124.86.4.3	5.57	NA	NA	NA	NA	NA	12	2x	13/07/2018	NA	NA	NA	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	F	F
Tragopogon pratensis subsp. orientalis	IT16	124.86.4.3	5.71	11	NA	NA	NA	NA	12	2x	NA	45.73841	11.59084	165	910	5	b, v	T, H	No	Yes	neu	med	Dry	41	F	T
Tripleurospermum inodorum	A3	124.32.2.0	9.66	17	9.9	0.02	1.81	2.06	36	4x	14/06/2018	NA	NA	NA	1050	6	a, b, v	T, H	No	Yes	neu	hig	Average	43	F	F
Tripleurospermum inodorum	A53	124.32.2.0	9.95	6	NA	NA	NA	NA	36	4x	19/06/2018	47.32495	11.68786	465	1050	6	a, b, v	T, H	No	Yes	neu	hig	Average	43	F	T
Tripleurospermum inodorum	FR400	124.32.2.0	9.78	NA	9.78	0.13	2.41	3.14	36	4x	NA	44.56739	6.10231	757	1050	6	a, b, v	T, H	No	Yes	neu	hig	Average	43	F	T

Table B.4: Data table with GS, ploidy level and chromosome number for alpine Asteraceae

Name EuroMed	ID Collectors	ID Flora Alpina	GS approx	n ind	GS	GS Std Err	Sample CV	Standard CV	Chr num	Ploidy	Date	Lat N	Long E	Elevation	Elevation pref	Init month	Longevity	Biological Form	End	Ind	pH	N	Water	Sect Occ	Chr inferred	Strictly Alps
Tripleurospermum inodorum	FR573	124.32.2.0	11	NA	10.57	0	2.57	2.84	36	4x	NA	45.04315	6.33186	1596	1050	6	a, b, v	T, H	No	Yes	neu	hig	Average	43	F	T
Tripleurospermum inodorum	FR623	124.32.2.0	NA	NA	NA	NA	NA	NA	36	4x	NA	NA	NA	NA	1050	6	a, b, v	T, H	No	Yes	neu	hig	Average	43	F	F
Tripleurospermum inodorum	OH426	124.32.2.0	NA	NA	10	0.01	1.93	1.93	36	4x	NA	NA	NA	NA	1050	6	a, b, v	T, H	No	Yes	neu	hig	Average	43	F	F
Tussilago farfara	FR711b	124.41.1.0	3.85	9	NA	NA	NA	NA	60	6x	23/04/2018	44.32002	6.43188	1557	1250	2	v	G	No	Yes	bas	med	Average	50	F	T
Tussilago farfara	FR709	124.41.1.0	3.89	3	NA	NA	NA	NA	60	6x	23/04/2018	44.34737	6.292483	1581	1250	2	v	G	No	Yes	bas	med	Average	50	F	T
Tussilago farfara	CH19	124.41.1.0	NA	NA	NA	NA	NA	NA	60	6x	21/05/2018	46.45368	8.66041	1348	1250	2	v	G	No	Yes	bas	med	Average	50	F	T
Tussilago farfara	CH90	124.41.1.0	4.16	10	NA	NA	NA	NA	60	6x	24/07/2018	46.47789	8.38879	2485	1250	2	v	G	No	Yes	bas	med	Average	50	F	T
Tussilago farfara	IT7	124.41.1.0	4.09	5	4.05	0.02	3.45	2.5	60	6x	NA	45.75943	11.39541	1126	1250	2	v	G	No	Yes	bas	med	Average	50	F	T
Tussilago farfara	FR383	124.41.1.0	3.96	10	4.03	0.05	3.51	2.08	60	6x	NA	44.40182	6.3838	2206	1250	2	v	G	No	Yes	bas	med	Average	50	F	T
Tussilago farfara	IT47	124.41.1.0	3.88	10	NA	NA	NA	NA	60	6x	NA	46.1124	11.3901	1777	1250	2	v	G	No	Yes	bas	med	Average	50	F	T
Tussilago farfara	IT9	124.41.1.0	NA	NA	NA	NA	NA	NA	60	6x	NA	45.76149	11.39232	1218	1250	2	v	G	No	Yes	bas	med	Average	50	F	T
Tussilago farfara	RD10	124.41.1.0	3.71	NA	3.73	0.01	3.11	2.53	60	6x	NA	NA	NA	NA	1250	2	v	G	No	Yes	bas	med	Average	50	F	F
Urospermum dalechampii	JP2	124.81.1.0	NA	NA	NA	NA	NA	NA	14	2x	NA	NA	NA	NA	583	5	v	H	No	Yes	neu	med	veryDry	6	T	F
Urospermum dalechampii	OH283	124.81.1.0	2.47	NA	2.47	0.03	2.72	3.65	14	2x	NA	NA	NA	NA	583	5	v	H	No	Yes	neu	med	veryDry	6	T	F
Urospermum picroides	OH284	124.81.2.0	1.62	NA	1.62	0.05	3.19	2.09	10	2x	NA	NA	NA	NA	350	5	a	T	No	Yes	neu	med	veryDry	4	T	F
Willemetia stipitata	A123	124.95.1.0	NA	NA	4.31	0.05	2.69	2.63	10	2x	21/07/2018	47.0691	12.84261	2215	1610	6	v	H	No	Yes	neu	med	Wet	21	F	T
Xanthium orientale subsp. italicum	IT81	124.27.2.0	5.03	7	4.87	0.09	2.85	3.66	36	2x	25/08/2018	45.84595	8.8902	345	350	7	a	T	No	No	neu	hig	Average	15	F	T
Xanthium orientale subsp. italicum	MB118	124.27.2.0	NA	NA	5.28	0.02	2.64	2.24	36	2x	27/08/2018	NA	NA	NA	350	7	a	T	No	No	neu	hig	Average	15	F	F
Xanthium orientale subsp. italicum	IT73	124.27.2.0	5.39	NA	5.39	0.13	2.75	2.37	36	2x	NA	45.70683	11.61797	80	350	7	a	T	No	No	neu	hig	Average	15	F	T
Xeranthemum annuum	MSB0266532	124.53.1.0	3.68	NA	4.21	0.01	2.71	2.1	12	2x	NA	NA	NA	NA	350	6	a	T	No	No	neu	low	veryDry	1	F	F
Xeranthemum inapertum	FR563	124.53.2.0	6.12	NA	6.07	0.03	4.73	3.57	28	4x	NA	NA	NA	NA	700	6	a	T	No	Yes	neu	low	veryDry	13	F	F
Xerolekia speciosissima	IT94	124.20.2.0	3	7	NA	NA	NA	NA	20	2x	27/08/2018	46.00716	9.22596	801	1050	6	v	H	Yes	Yes	bas	low	Dry	4	F	T
Xerolekia speciosissima	IT93	124.20.2.0	2.92	9	2.98	0.05	3.32	2.47	20	2x	27/08/2018	46.00719	9.22622	797	1050	6	v	H	Yes	Yes	bas	low	Dry	4	F	T
Xerolekia speciosissima	IT98	124.20.2.0	3.07	11	NA	NA	NA	NA	20	2x	27/08/2018	NA	NA	NA	1050	6	v	H	Yes	Yes	bas	low	Dry	4	F	F

Appendix C

Chapter 4 supplementary material

Table C.1: Ploidy estimaton of *Senecio doronicum* on Tête Grosse. Ratios reported refer to the internal standard *Petroselinum crispum* "Champion Moss Curled" (4.401 Gbp/2C), so that 4x have a GS ∼9pg and 8x ∼16pg. Plant IDs are sorted by number, and include an 'X' if the plant was included in manual crossings or 'R' if it has been monitored with the Rana system.

Plant ID	Ratio	Ploidy	Plant ID	Ratio	Ploidy	Plant ID	Ratio	Ploidy
343R	2.023	4x	418	1.873	4x	449	1.999	4x
344	2.015	4x	419	1.873	4x	450	1.952	4x
345R	2.046	4x	420	2.016	4x	451	1.893	4x
346X	1.914	4x	421	1.905	4x	452	1.917	4x
347	2.012	4x	422	2.007	4x	453	2.046	4x
348R	2.058	4x	423	1.987	4x	454	1.892	4x
355R	2.008	4x	424	1.969	4x	456	2.003	4x
357R	2.014	4x	425	1.881	4x	457	2.032	4x
358	2.034	4x	426	2.007	4x	458	2.013	4x
359	2.003	4x	427	2.028	4x	459	2.054	4x
360	1.930	4x	428	2.016	4x	460R	2.059	4x
362	2.057	4x	430	1.958	4x	462	2.014	4x
363R	2.068	4x	431	1.872	4x	463	1.963	4x
364	2.001	4x	432R	2.035	4x	464	1.950	4x
365	2.024	4x	433	1.881	4x	465	2.015	4x
366R	2.036	4x	434	1.892	4x	466	2.022	4x
367R	2.009	4x	435	1.893	4x	467	2.009	4x
368	1.997	4x	436	1.893	4x	468R	2.041	4x
369	1.973	4x	437	1.917	4x	469	1.906	4x
370	2.018	4x	438	1.917	4x	470	2.038	4x
371	1.988	4x	439R	1.952	4x	471	2.005	4x
372	2.043	4x	440	1.940	4x	472	2.001	4x
373	2.041	4x	441	1.892	4x	473	2.029	4x
374	2.009	4x	442	2.015	4x	474R	1.994	4x
403	1.979	4x	443R	2.041	4x	475	1.977	4x
412	1.998	4x	444	2.000	4x	476	2.011	4x
413R	2.006	4x	445	1.981	4x	477	1.997	4x
415	2.062	4x	446	2.028	4x	478	2.024	4x
416	2.048	4x	447	2.039	4x	479	2.036	4x
417	2.044	4x	448	1.963	4x	480	1.976	4x

Plant ID	Ratio	Ploidy
481	2.000	4x
482	2.001	4x
484	2.050	4x
485	2.018	4x
486	2.020	4x
487	1.937	4x
488	1.994	4x
489	1.997	4x
490	2.009	4x
491	1.996	4x
492	1.906	4x
493	2.035	4x
494	2.017	4x
495	1.973	4x
496	1.996	4x
497	1.986	4x
498	2.032	4x
499	1.935	4x
500	2.054	4x
501	2.038	4x
502	1.952	4x
503	1.945	4x
504	1.903	4x
505	1.983	4x
508	2.001	4x
509	1.946	4x
510	1.946	4x
511	1.946	4x
512	1.937	4x
513	1.946	4x
514	1.907	4x
515	2.017	4x
516	2.051	4x
517	1.963	4x
518	1.998	4x
519	2.027	4x
520	1.975	4x
521R	1.970	4x
522	2.035	4x
523	1.963	4x
524	1.981	4x
525	1.944	4x
526	1.991	4x
527R	2.058	4x
529R	2.056	4x
530	2.076	4x
531	1.992	4x
532	2.028	4x
533	1.937	4x
537	1.906	4x
538	1.940	4x
545	2.012	4x
549	2.033	4x
551	2.027	4x
552	2.034	4x
567R	1.983	4x
572	1.952	4x
602	2.002	4x
604	1.967	4x
605	2.029	4x
606	2.039	4x
607	2.032	4x
608	2.056	4x
609	1.975	4x
610	2.003	4x
611	1.873	4x
612	1.881	4x
700R	2.040	4x
702	1.971	4x
703	1.946	4x
705	2.058	4x
707X	1.875	4x
337R	2.888	6x
506	2.794	6x
507	2.755	6x
1R	3.748	8x
2R	3.718	8x
3R	3.665	8x
4R	3.783	8x
5R	3.679	8x
6R	3.688	8x
7R	3.723	8x
8R	3.721	8x
9	3.763	8x
10	3.763	8x
11	3.763	8x
12	3.763	8x
13	3.763	8x
14R	3.715	8x
15	3.788	8x
16	3.788	8x
18R	3.769	8x
19	3.788	8x
20	3.788	8x
21	3.788	8x
22	3.730	8x
23	3.730	8x
24R	3.801	8x
25	3.730	8x
26	3.730	8x
27	3.730	8x
28R	3.775	8x
29	3.810	8x
30	3.810	8x
31	3.810	8x
32	3.810	8x
33	3.810	8x
34	3.867	8x
35	3.867	8x
36	3.867	8x
37	3.867	8x
38	3.867	8x
39R	3.720	8x
41R	3.683	8x
43	3.804	8x
44	3.804	8x
46	3.804	8x
47R	3.785	8x
48	3.835	8x
51	3.590	8x
52	3.572	8x
53	3.572	8x
54	3.497	8x
55	3.497	8x
56	3.497	8x
57	3.497	8x
58	3.497	8x
59	3.502	8x
60	3.502	8x
61R	3.735	8x
62	3.502	8x
63	3.502	8x
64R	3.745	8x
65	3.502	8x
66	3.593	8x
67	3.593	8x
68	3.593	8x
69	3.593	8x
70R	3.550	8x
71	3.593	8x
72	3.540	8x
73	3.540	8x
74	3.540	8x
75	3.540	8x
76	3.540	8x
77	3.609	8x
78	3.609	8x
79	3.609	8x
80	3.609	8x
81	3.609	8x
82	3.473	8x
83	3.473	8x
84	3.473	8x
85	3.473	8x
86	3.473	8x
87	3.572	8x
88	3.572	8x
89	3.590	8x
90	3.590	8x
91	3.590	8x
92	3.590	8x
93	3.595	8x
94	3.572	8x
95	3.497	8x
96	3.497	8x
97	3.497	8x
98	3.497	8x
99	3.497	8x

Plant ID	Ratio	Ploidy
100R	3.721	8x
101R	3.827	8x
103	3.578	8x
104	3.578	8x
105	3.578	8x
106	3.578	8x
107	3.578	8x
108	3.639	8x
109	3.639	8x
110	3.639	8x
111	3.639	8x
112	3.639	8x
113	3.603	8x
114	3.603	8x
115	3.603	8x
116	3.603	8x
117	3.603	8x
118	3.563	8x
119	3.563	8x
120	3.563	8x
121R	3.804	8x
122	3.563	8x
123	3.563	8x
124	3.719	8x
125	3.719	8x
126	3.719	8x
127	3.719	8x
128	3.719	8x
129	3.766	8x
130	3.766	8x
131	3.766	8x
132	3.766	8x
133	3.766	8x
134	3.700	8x
135	3.700	8x
136	3.700	8x
137	3.700	8x
138	3.700	8x
139R	3.867	8x
141	3.734	8x
142	3.734	8x
143	3.734	8x
144	3.734	8x
145	3.734	8x
146	3.852	8x
147	3.852	8x
148	3.852	8x
149	3.852	8x
150	3.852	8x
151	3.690	8x
152	3.690	8x
153	3.690	8x
154	3.690	8x
155	3.721	8x
156	3.721	8x
157	3.721	8x
158	3.721	8x
159	3.721	8x
161	3.660	8x
162	3.660	8x
163	3.660	8x
164R	3.779	8x
165	3.660	8x
166	3.660	8x
167	3.743	8x
168	3.743	8x
169	3.743	8x
170	3.743	8x
171	3.743	8x
172R	3.706	8x
173R	3.806	8x
174	3.668	8x
175	3.677	8x
176	3.677	8x
177	3.677	8x
178	3.677	8x
179	3.677	8x
180	3.633	8x
181	3.633	8x
182	3.633	8x
183	3.633	8x
184	3.803	8x
186	3.633	8x
187	3.737	8x
188	3.737	8x
189	3.737	8x
190	3.737	8x
191	3.737	8x
192	3.460	8x
193	3.460	8x
194	3.460	8x
195	3.460	8x
196	3.460	8x
197	3.571	8x
198	3.571	8x
199	3.571	8x
200	3.494	8x
202	3.478	8x
203	3.472	8x
204	3.472	8x
205	3.500	8x
206	3.494	8x
207	3.612	8x
208	3.478	8x
209	3.574	8x
210	3.574	8x
211	3.612	8x
212	3.567	8x
213	3.654	8x
214	3.654	8x
215	3.500	8x
216	3.654	8x
217	3.571	8x
218	3.743	8x
219	3.571	8x
220	3.574	8x
221	3.494	8x
222	3.724	8x
223	3.457	8x
224	3.472	8x
225	3.574	8x
226	3.457	8x
227	3.472	8x
228	3.567	8x
229	3.567	8x
230	3.567	8x
231	3.743	8x
232	3.478	8x
233	3.567	8x
234	3.500	8x
235	3.478	8x
236	3.457	8x
237	3.457	8x
238	3.654	8x
239	3.457	8x
240	3.494	8x
241	3.472	8x
242	3.494	8x
243	3.478	8x
244	3.500	8x
245	3.500	8x
246	3.574	8x
247	3.535	8x
248	3.612	8x
249	3.612	8x
250	3.724	8x
251	3.793	8x
252	3.724	8x
253	3.766	8x
254	3.793	8x
256	3.724	8x
257	3.766	8x
258	3.766	8x
259	3.793	8x
260	3.793	8x
261	3.754	8x
270	3.754	8x
271	3.766	8x
272	3.766	8x
274	3.743	8x
275	3.724	8x
277	3.754	8x
278	3.754	8x
279	3.793	8x
280	3.754	8x
290	3.510	8x
301R	3.903	8x
302R	3.938	8x

Plant ID	Ratio	Ploidy
303R	3.705	8x
304R	3.882	8x
305R	3.579	8x
306R	3.874	8x
307R	3.789	8x
308	3.864	8x
309	3.759	8x
310Rapa	3.658	8x
311	3.752	8x
312	3.984	8x
313	3.705	8x
315	3.690	8x
318	3.508	8x
320	3.787	8x
321	3.451	8x
322x	3.865	8x
324	3.853	8x
325	3.776	8x
326	3.774	8x
327R	3.732	8x
328	3.744	8x
329R	3.508	8x
331R	3.545	8x
332	3.451	8x
333	3.609	8x
335R	3.752	8x
336	3.535	8x
338R	3.586	8x
340R	3.592	8x
341	3.510	8x
342	3.706	8x
351	3.754	8x
352	3.668	8x
353	3.789	8x
354	3.903	8x
376	3.507	8x
377	3.878	8x
380	3.872	8x
381	3.756	8x
382	3.510	8x
387	3.900	8x
388	3.742	8x
389	3.745	8x
390	3.688	8x
391	3.724	8x
392	3.627	8x
393	3.690	8x
394	3.716	8x
395	3.820	8x
396	3.753	8x
397	3.832	8x
398	3.767	8x
399	3.519	8x
400	3.747	8x
401	3.529	8x
402	NA	8x

Plant ID	Ratio	Ploidy
404	3.701	8x
405	3.722	8x
406	3.737	8x
407	3.384	8x
408	3.468	8x
409	3.704	8x
410	3.823	8x
411	3.570	8x
414	3.711	8x
528	3.765	8x
534	3.433	8x
535	3.685	8x
536	3.545	8x
539	3.784	8x
540	3.777	8x
541	3.708	8x
542	3.708	8x
543	3.765	8x
544	3.744	8x
546	3.584	8x
547	3.384	8x
548	3.763	8x
550	3.687	8x
553	3.620	8x
554	3.643	8x
555	3.887	8x
556	3.758	8x
558	3.830	8x
559	3.733	8x
560	3.841	8x
561	3.701	8x
563	3.857	8x
565	3.533	8x
566	3.451	8x
568	3.701	8x
570	3.971	8x
571	3.757	8x
573	3.742	8x
574	3.753	8x
576	3.709	8x
577	3.384	8x
578	3.808	8x
579	3.742	8x
580	3.800	8x
581	3.692	8x
583	3.759	8x
585	3.944	8x
586	3.902	8x
588	3.692	8x
591	3.727	8x
592	3.716	8x
593	4.011	8x
594	3.793	8x
595	3.848	8x
596	3.507	8x
597	3.551	8x

Plant ID	Ratio	Ploidy
598	3.633	8x
599	3.764	8x
600	3.662	8x
601	3.730	8x
603	3.716	8x
613	3.691	8x
708	3.642	8x
709	3.642	8x
711	3.642	8x

C.1 Phenotype scoring

Table C.2: Phenotypic measurements for *Senecio doronicum* on Tête Grosse. Note that capitulum number is expressed in sequential order of flowering, starting with the terminal capitulum (a). Week is expressed as n^{th} week of the year and refers to the date when the capitulum was morphometrized. Number of leaves (n.leaves) and number of capitula (n.cap) is indicated only once per individual plant, with the earliest capitulum measured. The variable Predated indicates whether the capitulum had been attacked by a pre-dispersal parasite (Yes or No), as discerned from macrophotograph of the capitulum in anthesis; when the number of florets is missing from the table and the capitulum was predated, it was impossible to accurately count florets.

ID_num	Capitulum	Ploidy	Week	Ø.cap	h.cap	Ø.stem	Ø.inv	h.inv	h.stem	n.leaves	n.cap	Ligulate	Tubular	Predated	Pollen_count
1	a	8x	24	54.525	8.745	2.91	11.905	10.735	32.1	3	3	20	115	Y	2111.63
2	a	8x	24	50.14	11.07	4.62	13.98	12.26	33	4	1	19	115	Y	
3	a	8x	24	56.14	6.76	4.56	13.1	9.18	30.5	4	2	21	156	Y	
3	b	8x	25	41.3	8.46	4.2	8.61	6.48	32			18	81	N	1870.56
4	a	8x	24	47.22	7.33	4.63	15.2	10.08	29.5	5	1	22	144	Y	
5	a	8x	24	33.46	6.54	4.26	10.67	11.22	22	3	2	17	115	Y	
6	a	8x	24	42.31	6.66	4.73	13.48	12.53	35.2	6	2	22	137	Y	
7	a	8x	24	47.22	5.61	5.14	12.69	9.96	23.1	4	2	16	144	N	2136.21
8	a	8x	24	38.11	6.4	3.8	13.43	10.12	30.2	5	1			Y	
9	a	8x	24	53.79	6.06	5.74	14.51	11.61	31.5	4	1				
10	a	8x	24	44.15	6.86	4.6	13.95	10.25	39.1	5	2				
11	a	8x	24	34.86	6.29	4.08	13.29	9.46	37.2	5	2				
12	a	8x	24	39.32	8.41	6.23	12.99	11	37.1	5	2	21	128	Y	
13	a	8x	24	54.24	7.15	4.48	14.13	12.73	41.3	5	2	19	132	Y	
14	a	8x	24	50.91	5.15	5.43	13.71	12.58	35.1	4	3	15	133	Y	
15	a	8x	24	43.02	4.54	4.17	10.7	13.41	29.1	4	2	28	147	Y	
16	a	8x	24	40.78	6.75	4.63	14.12	8.71	33.2	4	2				
17	a	8x	24	37.57	6.2	6.8	14.18	8.86	30	6	2				
18	a	8x	24	33.76	8.67	4.7	13.04	10.71	31.2	6	2				
19	a	8x	24	37.61	6.32	5.02	15.11	9.67	31.1	4	3	25	166	Y	
20	a	8x	24	36.23	6.66	5.6	14.8	12.08	35.3	5	2			Y	
21	a	8x	24	38.38	7.01	4.3	12.43	9.48	31.5	5	2			Y	
22	a	8x	24	38.39	6.2	3.9	10.27	8.86	22.1	3	1	23	118	N	
23	a	8x	24	37.67	6	3.5	11.95	8.92	21.2	4	1	19	102	Y	

Table C.2: Phenotypic measurements for *Senecio doronicum* on Tête Grosse.

ID num	Capitulum	Ploidy	Week	Ø.cap	h.cap	Ø.stem	Ø.inv	h.inv	h.stem	n.leaves	n.cap	Ligulate	Tubular	Predated	Pollen count
24	a	8x	24	53.31	6.96	4.23	10.19	8.8	27.2	3	1	21	118	Y	
25	a	8x	24	47.69	7.51	5.02	8.62	14.46	31.1	4	2	9	58	Y	
26	a	8x	24	35.56	6.72	4.08	11.28	9.44	22.6	3	1	20	116	Y	
27	a	8x	24	37.94	5.22	4.03	11.41	9.75	16.3	1	2	19	123	Y	
28	a	8x	24	42.57	5.33	5.16	14.79	10.54	27.1	3	2	16	154	Y	2393.18
29	a	8x	24	37.08	8.39	3.37	12.79	8.08	33.2	3	2	16	105	Y	
30	a	8x	24	47.06	7.26	3.35	12.75	9.89	39.1	4	1	22	133	Y	
31	a	8x	24	38.65	6.35	3.96	9.82	10.47	15.1	2	1	18	97	Y	
32	a	8x	24	45.44	5.22	4.34	14.55	10.53	29.1	5	2	26	148	Y	
33	a	8x	24	45.52	5.61	3.77	12.1	8.54	33	5	5	18	145	Y	
34	a	8x	24	35.53	6.92	4.65	15.26	9.92	29.1	3	3	30	179	Y	2013.99
34	b	8x	25	45.96	4.94	2.75	13.52	9.01	39.1					Y	
35	a	8x	24	45.26	7.73	5.83	14.5	9.84	29.6	3	3	24	191	Y	
36	a	8x	24	42.57	5.35	4.34	15.55	9.93	32.3	5	2	27	214	Y	
37	a	8x	24	37.39	7.9	4.82	15.24	9.67	26	4	3	30	146	Y	
38	a	8x	24	42.86	5.5	5.5	13.05	10.6	35.3	4	2	20	153	Y	
39	a	8x	24	49.34	6.19	4.5	13.08	9.51	3.1	5	2	19	153	Y	
40	a	8x	24	37.09	6.94	3.81	12.81	8.19	46.2	4	1			Y	
41	a	8x	24	46.36	7.09	3.71	12.27	10.67	31.3	4	1	19	93	Y	
42	a	8x	24	49.47	5.86	3.9	14.88	10.05	33.5	3	2	19	137	Y	
43	a	8x	24	38.66	5.24	4.23	12.42	10.8	27.1	4	2			Y	
44	a	8x	24	37.55	6.25	4.26	10.74	11.21	25.2	1	2	19	105	Y	
45	a	8x	24	40.35	4.11	5.15	14.11	10.92	27.1	4	2	18	154	Y	
45	b	8x	26	36.86	16.56	2.79	9.73	9.23	28.5					Y	
46	a	8x	24	37.97	5.87	4.44	13.91	9.09	24.2	3	2			Y	
46	b	8x	25	34.51	6.3	2.94	11.37	7.97	26.1					Y	
47	a	8x	24	41.98	3.49	5.68	12.8	9.15	14	2	2			Y	2276.03
48	a	8x	24	43.62	6.76	5.78	14.23	8.03	37.1	4	2			Y	
49	a	8x	24	50.98	6.82	4.41	13.69	7.98	31.1	4	2			Y	
50	a	8x	24	57.64	7.15	3.17	11.24	6.76	27.2	3	1			Y	
51	a	8x	24	38.44	3.75	4.24	9.98	6.58	23.3	3	1	15	93	Y	

Table C.2: Phenotypic measurements for *Senecio doronicum* on Tête Grosse.

ID num	Capitulum	Ploidy	Week	Ø.cap	h.cap	Ø.stem	Ø.inv	h.inv	h.stem	n.leaves	n.cap	Ligulate	Tubular	Predated	Pollen count
52	a	8x	24	48.68	7.14	2.94	10.01	9.23	26.1	3	1			N	
53	a	8x	24	45.3	5.6	4.05	9.99	7.18	25	4	1	23	141	N	
54	a	8x	24	42	5.1	4.51	13.07	7.38	33.1	3	1			Y	
55	a	8x	24	49.74	5.5	3.66	12.88	10.7	25.3	3	1			Y	
56	a	8x	24	43.86	5.98	4.12	11.43	9.41	28.2	4	1	22	145	N	
57	a	8x	24	43.35	4.9	2.94	11.97	9.89	29	4	3			Y	
58	a	8x	24	38.75	6.84	4.93	11.69	8.99	30.1	4	1	17	117	Y	
59	a	8x	24	34.16	5.99	4.05	11.8	8.43	29.2	4	1	16	119	Y	
60	a	8x	24	46.58	10.02	4.81	12.94	9.29	39.4	4	1	18	140	Y	
61	a	8x	24	50.98	6.59	5.85	14.27	11.84	33.1	4	3	21	158	N	
62	a	8x	24	33.71	6.6	3.33	9.6	9.15	29.1	4	2			Y	
63	a	8x	24	37.75	6.62	4.85	10.71	9	33.1	5	3			Y	
64	a	8x	24	48.68	6.93	5.05	12.06	8.2	33	4	2	17	105	Y	2986.02
64	b	8x	26	38.46	13.71	2.23	9.66	8.82	31					Y	
65	a	8x	24	38.05	5.46	3.33	10.32	10.84	15	3	2	19	112	Y	
66	a	8x	24	42.83	3.48	3.09	10.01	9.25	15	4	2			Y	
67	a	8x	24	35.07	6.6	3.41	11.72	8.17	16.1	3	2			Y	
67	b	8x	27	48.27	16.24	2.29	10.37	8.27	33					N	
68	a	8x	24	44.7	7.65	4.38	12.11	10.17	21.2	4	1			Y	
69	a	8x	24	37.47	5.59	4.67	11.37	8.74	28.1	4	2	15	118	Y	
70	a	8x	24	45.89	7.6	3.78	12.36	8.95	34	4	2			N	2767.17
71	a	8x	24	48.86	3.26	7	15.03	11.13	40.1	6	3			Y	
72	a	8x	24	41.69	6.68	5.24	13.08	10.04	40.1	5	2	17	134	Y	
73	a	8x	24	42.98	6.86	3.544	13.91	6.99	32.2	5	2			Y	
74	a	8x	24	48.57	6.15	5.54	13	9.77	31.1	5	3			Y	
75	a	8x	24	42.85	4.87	3.87	13.06	10.03	34.2	5	1			Y	
76	a	8x	24	33.8	4.9	4.09	15.28	9.3	30	5	1			Y	
77	a	8x	24	47.51	6.86	5.56	15.08	9.85	27	4	1	17	208	Y	
78	a	8x	24											Y	1978.99
78	b	8x	24	43.89	6.17	3.01	11.17	10.24	32.2	5	2				
79	a	8x	24	34.13	5.58	13.62	10.72	7.25	30.5	4	1	17	94	Y	

Table C.2: Phenotypic measurements for *Senecio doronicum* on Tête Grosse.

ID num	Capitulum	Ploidy	Week	Ø.cap	h.cap	Ø.stem	Ø.inv	h.inv	h.stem	n.leaves	n.cap	Ligulate	Tubular	Predated	Pollen count
80	a	8x	24	46.07	7.14	4.73	12.57	9.69	33.1	6	1			Y	
81	a	8x	24	37.08	5.82	4.02	12.84	10.86	28.3	5	1			Y	
82	a	8x	24	47.28	5.27	4.43	14.57	12.22	31	4	2			Y	
83	a	8x	24	39.3	6.03	4.13	14.34	11.1	32.1	4	3	17	162	Y	
84	a	8x	24	46.44	8.8	3	12.6	10.31	25	4	2			Y	
85	a	8x	24	45.14	5.74	4.18	10.76	9.07	35.1	5	3	21	107	Y	
86	a	8x	24	39.99	8.13	4.74	13.17	10.86	35	6	4	27	153	Y	
87	a	8x	24	39.52	5.48	3.56	12.48	10.28	37.1	4	2			Y	
88	a	8x	24	46.21	8.71	3.82	11.58	10.52	33.2	4	3	22	136	N	
89	a	8x	24	39.37	5.7	3.52	12.68	9.58	29	4	3	19	95	Y	
90	a	8x	24	37.13	8.41	5.43	12.18	10.98	41.1	5	3	18	163	Y	
91	a	8x	24	35.95	6.28	3.41	12.37	9.6	47	5	1	19	107	Y	
92	a	8x	24	42.93	6.86	3.78	12.38	10.19	36	4	1	19	117	Y	
93	a	8x	24	35.84	4.15	3.43	11.5	7.23	24.3	4	2	18	131	Y	
94	a	8x	24	37.63	5.56	4.45	13.14	9.34	31	5	2	21	127	Y	
95	a	8x	24	45.99	5.93	4.1	12.32	10.11	32.2	4	1	18	102	Y	
96	a	8x	24	37.4	6.42	5	14.69	10.05	29.3	4	2	19	129	Y	
97	a	8x	24	43.36	7.25	5.15	11.88	9.76	38	5	2	19	125	Y	
98	a	8x	24	54.68	8.48	5.9	13.49	11.22	31.2	5	4			Y	2410.80
98	b	8x	25	46.17	66.1	4.67	11.78	9.27	32			18	90	Y	
98	c	8x	25	46.68	6.79	2.84	11.94	8.93	29.1			16	97	Y	
99	a	8x	24	42.93	5.51	4.52	15.12	10.36	27.1	4	1			Y	
100	a	8x	24	45.04	8.51	4.52	12.14	9.04	30.2	5	1	25	143	N	
101	a	8x	24	40.32	6.19	4.19	11.26	9.1	22.3	3	2	18	123	Y	
102	a	8x	24	38.67	7	5.73	14.41	11.53	28.1	3	1	19	163	Y	2500.09
103	a	8x	25	45.01	4.81	4.41	13.56	9.97	34.2	4	2			Y	
104	a	8x	25	40.68	5	4.15	14.49	10.69	22	4	1			Y	
105	a	8x	25	39.6	3.81	3.12	13.26	8.56	21.1	3	1	18	154	Y	
106	a	8x	25	51.22	6.33	4.93	12.74	8.92	30.33	4	2	27	164	N	
107	a	8x	25	44.92	6.61	4.31	12.95	11.42	26	5	2			Y	
108	a	8x	25	37.65	6.07	4.12	12.05	9.35	31	5	1			Y	

Table C.2: Phenotypic measurements for *Senecio doronicum* on Tête Grosse.

ID num	Capitulum	Ploidy	Week	Ø.cap	h.cap	Ø.stem	Ø.inv	h.inv	h.stem	n.leaves	n.cap	Ligulate	Tubular	Predated	Pollen count
109	a	8x	25	52.88	7.64	4.61	12.78	8.89	30.1	4	2	27	128	Y	
110	a	8x	25	43.57	9.97	3.74	12.02	7.39	31	5	1			Y	
111	a	8x	25	47.13	3.64	4.25	13.06	10.84	36.1	4	1	21	177	N	
112	a	8x	25	30.91	4.74	3.11	10.96	8.25	37.2	5	1			Y	
113	a	8x	25	33.32	5.46	3.55	17.74	7.91	27	4	1			Y	
114	a	8x	25	44.06	6.66	3.89	13.5	9.51	38.1	5	2			Y	2905.97
114	b	8x	27	43.15	18.71	2.82	12.48	9.27	40	5	3			N	
115	a	8x	25	47.67	6.125	3.92	12.44	7.965	28.8	5	3			Y	
115	b	8x	26	57.32	7.32	2.72	11.25	8.69	32.1			19	92	N	
115	c	8x	26											Y	
116	a	8x	25	41.05	4.42	4.35	13.49	11.72	40	5	2	24	119	Y	
117	a	8x	25	34.92	5.43	4.16	14	9.22	37	5	2	27	155	Y	4096.40
118	a	8x	25	34.38	5.59	4.64	16.25	9.48	21	4	3	16	171	Y	
119	a	8x	25	33.88	6.11	3.58	12.72	8.76	30.1	5	3			Y	
120	a	8x	25	38.7	4.21	4.05	12.26	9.44	30.2	5	3			Y	
120	b	8x	27	34.69	13.93	2.5	9.67	7.59	39			17	85	Y	
121	a	8x	25	55.91	4.54	3.5	13.05	9.6	35.3	4	1	23	150	Y	
122	a	8x	25	37.59	5.29	3.65	12.12	8.08	24	3	1			Y	
123	a	8x	25	36.74	5.92	3.16	11	8.3	33.1	5	1	19	93	Y	
124	a	8x	25	39.75	6.16	4.04	13.11	9.61	37.3	6	2			Y	1553.51
125	a	8x	25	45.73	4.98	3.41	11.24	9.19	36.2	5	1			Y	
126	a	8x	25	34.18	6.22	4.21	12.41	8.94	29	5	3	20	126	Y	
127	a	8x	25	35.69	5.83	4.32	11.97	9.2	35.1	5	1			Y	
128	a	8x	25	41.5	6.94	3.66	12.43	7.09	35.2	5	3			Y	
129	a	8x	25	45.67	6.34	4.84	14.39	11.38	37.1	5	2			Y	
130	a	8x	25	36.8	5.11	3.99	15.17	11.51	38.8	5	3			Y	
131	a	8x	25	48.78	7.9	4.65	14.46	11.08	29.5	5	3			Y	
131	b	8x	27	41.17	15.99	2.39	10.4	8.46	39					Y	
132	a	8x	25	45.2	7.95	3.67	13.13	9.79	31.1	4	1			Y	
133	a	8x	25	46.43	10.97	5.61	12	9.1	22.1	4	1			Y	
134	a	8x	25	46.88	10.21	4.2	10.34	8.6	32	5	2			N	1798.97

Table C.2: Phenotypic measurements for *Senecio doronicum* on Tête Grosse.

ID num	Capitulum	Ploidy	Week	Ø.cap	h.cap	Ø.stem	Ø.inv	h.inv	h.stem	n.leaves	n.cap	Ligulate	Tubular	Predated	Pollen count
135	a	8x	25	50.44	6.88	4.04	11.08	9.03	29.5	5	1			Y	
136	a	8x	25	38.57	7.42	4.99	11.85	9.8	26	4	2			Y	
137	a	8x	25	49.63	8.21	5.05	11.12	8.73	25.2	4	2			N	2440.48
138	a	8x	25	41.26	6.62	4.35	11.76	9.75	10.1	1	1	23	128	Y	
139	a	8x	25	47.52	6.66	6	14.5	11.42	32.2	5	3	25	163	Y	
140	a	8x	25	41.28	4.72	3.25	11.47	8.88	28.1	3	1	17	83	N	
141	a	8x	25	37.22	4.59	3.99	12.63	10.83	30.1	4	1	23	179	Y	
142	a	8x	25	51.71	8.52	4.6	14.71	11.65	40.2	4	1			Y	
143	a	8x	25	52.66	7.11	3.26	13.09	8.46	26	4	1			N	
144	a	8x	25	49.27	6.97	5.32	14.73	11.45	33.1	5	4			Y	
145	a	8x	25	38.36	4.65	3.83	12.93	8.03	35.5	6	1			Y	1782.69
146	a	8x	25	37.93	4.21	2.85	11.34	7.05	20	4	2			Y	
147	a	8x	25	41.28	6.32	4.55	11.77	9.49	17.1	3	2	18	110	Y	
148	a	8x	25	40.15	6.51	4.8	13.3	10.49	20.1	3	2			Y	
149	a	8x	25	39.25	5.09	3.98	13.49	10.87	32.3	4	2	21	142	Y	
150	a	8x	25	38.71	5.92	5.17	13.28	9.53	28.4	4	1			Y	
151	a	8x	25	48.93	6.52	3.68	13.52	10.12	36.2	4	2			Y	
152	a	8x	25	35.74	6.18	3.74	12.59	8.53	28	4	2			Y	
153	a	8x	25	39.71	5.96	4.61	14.6	9.58	34.6	4	3			Y	
154	a	8x	25	50.49	5.97	3.85	14.27	9.85	39.2	5	2			Y	
155	a	8x	25	44.31	9.18	4.71	12.52	9.1	38.1	5	2			Y	
156	a	8x	25	42.21	5.91	4.84	15.33	9.1	46.1	5	3	22	151	Y	3490.25
156	b	8x	26	45.27	16.38	3.86	11.76	9.91	51					Y	
157	a	8x	25	39.81	6.17	4.69	14.73	11.07	39.4	5	2			Y	
158	a	8x	25	43.04	4.75	4.39	12.94	8.33	40	5	3	23	124	Y	
158	b	8x	26	43.55	28.83	3.39	14.05	9.13	44			20	91	N	
159	a	8x	25	38.53	6.09	4.04	12.75	8.35	31.1	4	2			Y	
161	a	8x	25	47.24	7.05	4.26	12.43	9.01	23	4	2			Y	
162	a	8x	25	46.27	7.46	13.68	12.65	9.76	40.1	5	2			Y	
163	a	8x	25	45.72	5.91	4.2	14.05	9.84	32.3	4	2			Y	
163	b	8x	26	49.5	19.1	2.84	12.42	9.41	48						

Table C.2: Phenotypic measurements for *Senecio doronicum* on Tête Grosse.

ID num	Capitulum	Ploidy	Week	Ø.cap	h.cap	Ø.stem	Ø.inv	h.inv	h.stem	n.leaves	n.cap	Ligulate	Tubular	Predated	Pollen count
164	a	8x	25	32.52	6.06	3.86	11.59	9.06	16.2	2	2			Y	
165	a	8x	25	31.92	5.45	4.65	13.09	9.58	23	2	2			Y	
165	b	8x	26	34.22	17.27	3.18	11.21	10.5	29.5			15	67	Y	
166	a	8x	25	28.76	6.13	3.25	11.41	8.2	20	4	1			Y	2241.55
167	a	8x	25	39.54	8.41	9.02	18.86	12.73	37.2	6	1	19	148	N	
168	a	8x	25	29.24	3.77	2.97	9.9	7.38	30	2	1	13	103	N	
169	a	8x	25	37.87	5.67	4.17	13.23	9.05	26.5	5	4	19	135	N	
170	a	8x	25	48.23	2.98	4.16	12.46	10.99	39.2	3	1	24	127	Y	2491.52
171	a	8x	25	40.36	5.76	4.39	12.84	10.08	40.1	4	2			Y	
172	a	8x	25	48.58	5.18	3.54	12.51	9.89	19.2	3	1			Y	
173	a	8x	25	26.47	3.82	3.04	10.3	8.71	29	3	1			Y	
174	a	8x	25	43.41	5.03	3.91	13.19	10.09	14	3	1	26	129	Y	
175	a	8x	25	39.07	5.56	3.67	12.51	7.4	34.2	4	1			Y	
176	a	8x	25	46.15	5.11	3.38	12.96	8.93	34.1	5	3			Y	
177	a	8x	25	30.15	4.77	3.29	12.79	7.45	32.2	3	1	21	154	N	3128.22
178	a	8x	25	37.52	4.97	4.6	16.15	9.91	31.5	4	2	19	130	N	
179	a	8x	25	41.81	5.82	4.89	14.56	10.15	31.2	4	2	16	115	Y	
180	a	8x	25	38.67	4.27	6.06	15.84	11.81	32.1	5	2			Y	
181	a	8x	25	42.44	6.29	4.39	14.15	10.61	26.3	4	1			Y	
182	a	8x	25	42.7	6.65	4.76	12.07	9.13	27.2	3	1	24	123	N	
183	a	8x	25	39.08	6.43	5.1	12.16	9.37	18.2	3	1			Y	
184	a	8x	25	42.86	4.63	4.32	19.78	10.33	28.3	4	2			Y	3547.98
185	a	8x	25	37.45	4.29	3.23	11.41	9.02	19.1	3	3			Y	2706.33
185	b	8x	26	35.65	14.42	2.42	10.55	9.9	21.5						
185	c	8x	26									13	80	Y	
186	a	8x	25	24.36	5.51	3.89	11.98	9.4	30.2	4	1	16	86	N	
187	a	8x	25	40.59	6.47	5.21	14.1	9.87	31.1	4	1	15	135	N	
188	a	8x	25	35.44	4	6.2	13.5	9.19	28.3	3	1	16	129	N	
189	a	8x	25	40.9	5.82	4.18	13.94	9.06	37.4	4	1	16	151	N	
190	a	8x	25	42.61	5.69	3.82	14.68	9.55	40.1	4	1			Y	
191	a	8x	25	40.14	4.91	4.78	13.18	9.25	32.2	4	1	29	141	Y	

Table C.2: Phenotypic measurements for *Senecio doronicum* on Tête Grosse.

ID num	Capitulum	Ploidy	Week	Ø.cap	h.cap	Ø.stem	Ø.inv	h.inv	h.stem	n.leaves	n.cap	Ligulate	Tubular	Predated	Pollen count
257	a	8x	25	44.2	6.7	4.81	13.14	12.7	32.1	3	2				2931.35
300	a	8x	26	40.24	4.23	3.11	10.14	6.83	20.1	4	1			Y	
301	a	8x	26	50.44	8.26	3.84	10.36	8.41	25.2	3	1			Y	
302	a	8x	26	48.9	8.16	4.49	12.2	9.9	44.2	6	2			Y	2337.79
302	b	8x	27	25.93	17.17	3.43	11.19	9.97	43	6	2				
303	a	8x	26	45.76	7.65	3.23	12.43	8.8	42.3	6	2	16	84	Y	2323.11
303	b	8x	27	25.58	16.91	2.67	12.23	9.99	39.5						
304	a	8x	26	37.59	6.97	2.78	9.99	7.82	19	2	2			N	
305	a	8x	26	43.83	5.05	3.78	11.88	9.85	34.3	4	2				
305	b	8x	27	24.22	11.96	2.77	9.16	7.54	33					Y	
306	a	8x	26	52.41	5.99	3.62	10.9	7.51	30.1	4	1				
307	a	8x	26	48.66	6.07	4.03	10.69	8.67	30	4	2				2478.19
307	b	8x	27	28.32	12.88	2.83	10.11	6.62	32.5			19	69	Y	
308	a	8x	26	41.1	4.7	3.28	11.39	9.23	30	4	1				
309	a	8x	26	53.74	18.84	3.96	12.69	10.67	18	3	1	19	146	N	
310	a	8x	26	47.15	28.75	3.95	17.36	11.91	36	5	1				
311	a	8x	26	38.31	15.61	2.9	11.4	12.45	38	5	1			Y	
312	a	8x	26	47.96	17.58	3.08	15.43	9.5	44.5	5	2	22	169	N	
313	a	8x	26	30.99	25.44	2.94	12.99	8.64	37	3	2			N	
313	b	8x	27	48.59	16.4	2.7	9.21	9.8	41						
314	a	8x	26	38.4	31.41	3.92	16.38	11.18	32	7	3			Y	
314	b	8x	27	38.005	15.755	3.045	10.775	9.185	41.5						
314	c	8x	28	27.78	14.2	3.23	9.51	10.81	33						
315	a	8x	26	45.96	33.06	3.46	16.13	11.79	41.5	7	1			Y	
316	a	8x	26	50.95	21.06	5.43	15.65	11.4	41	7	1			Y	
317	b	8x	26	41.18	18.65	6.13	15.55	13.35	46	4	2			Y	
327	a	8x	26	36.1	13.36	2.13	10.59	8.88	27.5	5	1			N	
329	a	8x	26	34.525	17.055	3.215	12.91	10.42	44.5	4	2			Y	
329	b	8x	26	31.96	17.06	2.73	12.42	9.5	40					N	
330	a	8x	26	38.43	27.21	2.44	14.81	10.01	32	6	1			Y	
331	a	8x	26	54.37	19.95	2.11	9.09	8.73	32.5	4	2			N	

Table C.2: Phenotypic measurements for *Senecio doronicum* on Tête Grosse.

ID num	Capitulum	Ploidy	Week	Ø.cap	h.cap	Ø.stem	Ø.inv	h.inv	h.stem	n.leaves	n.cap	Ligulate	Tubular	Predated	Pollen count
332	a	8x	26	29.19	18.29	2.77	14.87	9.69	33	4	1			Y	
333	a	8x	26	53.18	28.65	3.31	15.69	10.16	39	6	2			Y	
334	a	8x	26	48.23	28.21	3.52	12.28	7.29	35	6	2			N	
335	a	8x	26	58.47	18.68	3.47	11.5	9.72	26	3	2				2104.96
335	b	8x	26											N	
336	a	8x	26	50.38	29.93	3.48	16.31	10	57	8	2			N	
337	a	6x	27	37.03	16.97	3	10.51	10.08	16	4	1			Y	
338	a	8x	27	46.03	15.22	2.88	11.74	10.09	31	6	2	16	78	N	
339	a	8x	27	43.86	21.3	3.41	13.02	11.74	54	7	3			N	
340	a	8x	27	51.67	20.51	3.19	12.04	13.77	49.5	6	3			Y	4258.98
340	b	8x	27	46.42	18.58	2.91	9.59	11.62	48.5	6	3				
341	a	8x	27	36.46	16.06	2.87	11.26	8.57	32	5	1			Y	
343	a	4x	27	42.64	15.06	3.84	10.48	9.71	29	6	4	21	148	Y	3234.66
343	b	4x	28	39.82	13.54	2.3	9.24	10.68	30	6	4			N	
344	a	4x	28	32.615	12.575	3.44	11.63	8.79	24.6	5	5	24	139	Y	3063.05
344	b	4x	28	35.68	14.52	2.45	12.28	9.7	24			22	112	N	
344	c	4x	29	32.38	11.24	2.75	10.62	7.67	24			20	101	N	
344	d	4x	29	32.56	12.8	3.82	11.04	11.32	24.5					N	
345	a	4x	28	38.28	14.87	4.48	10.84	10.36	17.3	5	5	15	81	Y	
345	d	4x	29	32.36	14.23	2.68	9.05	9.94	18.01			13	74	N	
345	e	4x	29	32.1	10.39	2.25	8.02	9.32	12.03			13	71	Y	
346	a	4x	28								5				2953.20
346	d	4x	29	35.58	12.99	2.49	9.71	9.79	17						
348	a	4x	28	38.8	14.48	2.41	9.35	10.98	14	4	3	15	80	N	
348	b	4x	29	38.82	11.16	2.02	8.92	10.28	21.5			13	59	N	
349	a		28	53.88	3.43	3.35	13.74	12.14	48	5	3				
349	b		28	49.66	3.86	2.69	11.5	9.87	45.5			12	86	Y	
350	a	8x	28	36.81	4.82	2.67	9.68	8.96	34.5	5	2				
354	a	8x	28	42.16	16.84	2.51	11.77	14.29	10	0	1			N	
355	a	4x	28	43.7	14.37	2.82	10.48	11.91	29	6	4	20	148	N	3879.59
356	a		28	36.89	14.25	3.31	9.65	10.44	28	7	3			N	3243.85

Table C.2: Phenotypic measurements for *Senecio doronicum* on Tête Grosse.

ID num	Capitulum	Ploidy	Week	Ø.cap	h.cap	Ø.stem	Ø.inv	h.inv	h.stem	n.leaves	n.cap	Ligulate	Tubular	Predated	Pollen count
357	a	4x	28	43.95	16.08	3.06	10.42	10.88	28.5	6	4			Y	
357	b	4x	28	40.39	15.6	3.42	9.28	11.25	29					N	
358	a	4x	28	41.96	17.36	2.99	9.76	10.28	15	4	2			Y	3222.51
359	b	4x	29	27.58	10.58	2.17	8.54	8.83	15.62			13	60	N	
361	a		28	50.02	16.15	3.7	10.98	10.38	24	6	3	21	118	N	3393.09
361	b		28	42.54	12.87	3.08	9.62	9.94	23					N	
362	a	4x	28	41.99	14.15	2.92	1.37	10.99	20	9	2			Y	3771.21
363	a	4x	28	35.54	14.95	2.63	11.35	11.66	20	8	2	19	114	N	
364	a	4x	28	33.75	13.58	2.14	9.88	8.86	18.5	6	2				3191.27
365	a	4x	28	38.07	13.04	2.58	11.06	9.52	17.5	6	3	20	100	N	4592.72
365	b	4x	28	32.33	10.62	2.3	9.53	8.46	20.1						
366	a	4x	28	39.92	15.15	2.9	9.94	11.59	31.5	6	5			N	4580.96
366	b	4x	29	34.75	12.17	2.48	8.02	10.84	18.2			13	54	N	
367	a	4x	28	33.26	13	3.51	11.33	9.88	25	5	4			Y	2949.59
367	b	4x	28	33.25	11.91	2.51	10.49	8.53	27.5			17	72	N	
367	c	4x	29	33.03	11.84	2.88	10.27	9.69	24.5						
368	a	4x	28	34.46	13.48	2.29	9.59	7.56	24	6	2	18	81	N	
368	b	4x	29	27.91	9.96	2.09	8.03	8.64	24.5						
374	a	4x	28	44.96	15.31	2.38	8.74	9.44	27	4	1			N	
375	a	8x	28	45.7	12.99	2.69	8.66	8.6	24	4	1			N	
375	b	8x	28	27.88	12.49	2.14	9.55	9.26	18						
375	c	8x	28	35.21	14.11	2.36	12.06	12.43	17.5						
376	a	8x	28	41.78	14.48	3.49	7.35	9.77	39	4	2			N	
377	a	8x	28	46.74	14.65	1.44	7.29	10.05	30	2	2			N	
378	a	8x	28	51.8	15.03	2.59	11.97	10.56	26	5	1			N	
379	a		28	47.29	18.02	3.83	12.93	14.88	43	4	1			N	
380	a	8x	28	38.6	13.03	3.37	11.01	10.54	19	4	1			N	
413	a	4x	29	42.9	11.92	2.14	9.37	9.58	17.3	6	3	18	92	N	
413	b	4x	30	42.23	13.31	2.2	9.62	9.23	19.2						
413	c	4x	31	45.6	16.2	3.45	8.9	8.96	19			21	75	N	
421	a	4x	30	30.95	12	2.3	9.06	10.08	18.5	6	2				3985.70

Table C.2: Phenotypic measurements for *Senecio doronicum* on Tête Grosse.

ID num	Capitulum	Ploidy	Week	Ø.cap	h.cap	Ø.stem	Ø.inv	h.inv	h.stem	n.leaves	n.cap	Ligulate	Tubular	Predated	Pollen count
421	b	4x	31	37.5	13.07	2.88	7.47	9.25	22			13	50	N	
432	a	4x	29	43.15	12.8	3.08	11.31	11.12	16	6	3			N	2249.54
432	b	4x	29	41.2	12.7	2.97	11.2	10.9	15.8			21	71	N	
432	c	4x	30	38.92	14.36	2.74	9.3	10.59	20			21	76	N	1424.99
439	a	4x	28	31.59	11.95	2.97	9.23	9.83	27.5	3	2	20	87	N	2925.91
439	b	4x	29	32.34	10.76	1.77	7.65	7.39	29.5			16	61	N	
442	a	4x	29	37.74	13.73	2.76	11.57	12.37	15.3	4	2	21	77	N	
442	b	4x	31	29.38	14.08	2.59	8.08	11.08	10.5			15	58	N	
443	a	4x	29	37.38	12.96	2.38	10.5	9.34	22.5	6	4	20	102	N	3709.20
443	b	4x	29	32.97	10.99	1.82	9.74	8.65	22.6			19	102	N	
443	c	4x	29	31.98	10.9	2.69	10.29	8.94	24.5						
443	d	4x	30	32.24	13.45	2.13	9.6	8.42	27			20	88	N	
445	a	4x	29	30.94	10.57	1.99	9.8	7.95	19.5	7	2	19	75	N	
446	a	4x	30	28.08	11.81	2.32	9.14	8.54	29.5	5	3				3804.58
448	a	4x	29	22.41	9.17	1.88	9.92	7.24	17.5	5	3	13	49	Y	3508.91
450	a	4x	29	31.5	11.92	2.36	10.06	9.6	26	7	3	16	76	N	3465.33
450	b	4x	29	28.79	10.45	2.34	8.79	6.99	26.5						
457	a	4x	29	42.28	12.41	2.86	11.68	9.15	19.5	6	2			N	
457	b	4x	30	32.09	13.53	2.65	10.07	9.54	23			19	84	N	
460	a	4x	29	41.12	13.37	2.19	10.2	11.86	18.5	5	3	21	119	N	
460	b	4x	30	31.74	11.44	1.85	8.36	9.55	20.3						
460	c	4x	30	26.9	12	1.66	8.06	8.12	21.5			19	74	N	
468	a	4x	29	32.3	11.63	2.45	8.89	8.99	25.5	6	2	19	83	N	4274.10
473	a	4x	30	31.99	11.24	1.99	8.58	9.3	17.5	4	4				
474	a	4x	29	40.71	13.15	2.6	11.92	10.41	15.5	4	3	19	123	Y	
474	b	4x	30	45.16	13.89	3.09	12.19	8.25	10.2						
474	c	4x	30	35.22	11.29	2.6	10.12	8.81	16.5						
491	b	4x	31	39.74	17.71	2.12	8.3	10.05	28	4	2			N	
494	a	4x	29	44.72	13.56	2.83	11.37	10.96	19.5	6	4	20	88	N	
494	b	4x	29	46.33	12.68	3.08	10.8	10.81	18.9			20	88	N	
494	c	4x	30	43.31	17.77	2.9	10.13	11.55	23.5					N	

Table C.2: Phenotypic measurements for *Senecio doronicum* on Tête Grosse.

ID num	Capitulum	Ploidy	Week	Ø.cap	h.cap	Ø.stem	Ø.inv	h.inv	h.stem	n.leaves	n.cap	Ligulate	Tubular	Predated	Pollen count
494	d	4x	30	43.59	15.96	2.44	10.07	10.15	19			21	85	N	
512	b	4x	29	39.27	13.22	2.52	9.51	11.99	21.3						
514	b	4x	30	36.15	12.28	2.99	10.4	9.51	35.5	6	4				
514	d	4x	31	38.93	15.54	3.56	10.27	9.35	36	7	4			N	
517	a	4x	31	47.86	14.4	2.46	10.87	8.79	27	8	1	21	131	N	
521	a	4x	28	33.75	12.73	3.38	11.19	10.77	19.5	6	5	21	130	N	3643.97
521	b	4x	29											N	
521	c	4x	29	32.25	11.37	2.64	9.9	8.89	23.2			18	113	N	
521	d	4x	30	38.43	13.74	2.59	9.86	9.71	23						
521	e	4x	30	33.74	12.34	2.56	10.79	9.71	22.7						
521	f	4x	31	41.84	15.1	2.43	9.16	9.99	20.5	5	6			N	
527	a	4x	28	31.62	13.57	3.3	9.04	11.77	17			19	66	N	3438.52
527	b	4x	29	35.66	11.42	2.78	8.47	10.71	18			18	68	N	
528	a	8x	28	35.15	14.34	2.83	9.39	10.76	19.5	4	2	20	63	N	2708.90
528	b	8x	29	28.52	11.48	2.55	9.55	10.69	17.7			16	51	N	
529	a	4x	28	42.1	15.13	3.29	10.28	12.18	30.2	9	4	21	93	N	3383.23
531	a	4x	29	33.31	12.77	2.33	10.23	11.43	13	5	4			Y	
531	b	4x	31	38.42	14.9	3.08	8.13	8.99	19.5						
531	c	4x	31	40.74	14.93	2.91	8.41	8.84	16.5			20	63	N	
551	a	4x	29	42.09	13.65	2.55	9.25	10.5	18.3	5	3	20	82	N	
551	b	4x	30	36.34	11.97	2.61	9.16	9.83	23.1						
551	c	4x	31	41.68	13.54	2.58	8.27	9.22	23			19	61	N	
602	a	4x	28	26.2	14.55	2.69	10.4	12.09	20	7	3			Y	
602	b	4x	28	29.18	13.95	2.2	9.22	10.26	21			19	64	N	
607	a	4x	29	34.93	12.75	2.26	10.05	8.48	20.5	7	2			Y	4904.97
607	b	4x	29	29.44	11.32	2.05	9.92	9.7				15	77	N	
608	a	4x	29	36.58	14	2.54	9.84	10.27	24	6	2	16	65	N	
608	b	4x	31	44.04	15.89	2.23	8.49	11.51	29			15	59	N	
610	a	4x	29	46.42	14.68	4.72	11.8	12.88	21.5	6	12			N	2390.00
610	b	4x	29	31.75	12.66	2.64	9.81	9.08	23			16	93	N	
610	c	4x	29	42.64	12.38	3.53	11.02	9.74	22.3			17	101	N	

Table C.2: Phenotypic measurements for *Senecio doronicum* on Tête Grosse.

ID num	Capitulum	Ploidy	Week	Ø.cap	h.cap	Ø.stem	Ø.inv	h.inv	h.stem	n.leaves	n.cap	Ligulate	Tubular	Predated	Pollen count
610	d	4x	29	37.71	11.76	3.03	10.08	9.12	21.59			17	103	N	
610	e	4x	29	38.96	11.93	2.71	10.71	11.54	20			20	99	N	
610	f	4x	30	37.535	13.585	2.555	8.92	9.04	20.85			14	71	Y	
610	g	4x	31	39.34	14.57	2.83	8.67	9.36	22			16	71	N	
610	h	4x	31	36.69	13.34	2.96	8.89	8.8	18			16	82	N	
700	b	4x	29	50.26	13.03	3.49	10.33	10.79	23	9	3	20	108	N	
700	c	4x	29									18	133	N	
701	a	4x	29	40.41	13.83	3.25	10.94	11.37	32.3	7	2			N	4222.46
702	a	4x	29	39.07	12.26	2.45	9.61	10.21	20	6	2				
702	b	4x	31	43.64	14.86	2.96	8.72	10.32	26.5	6	2			N	
704	a	4x	29	43.96	13.66	2.54	10.44	13.4	23.5	5	2				3301.16
705	a	4x	30	31.47	12.28	2.87	9.55	10.25	34.5	7	4				3326.03
705	d	4x	31	38.82	14.47	3.36	8.93	9.56	36					N	
706	b	8x	31	41.52	15.23	2.53	9.17	8.44	22.5	5	2			N	
453	a	4x	29									15	70	Y	
467	b	4x	29									19	77	N	
703	a	4x	29											N	3360.42
213	a	8x	25												3604.58
434	d	4x	29												4496.28

C.2 Flowering time

Table C.3: Phenology monitoring of *Senecio doronicum* cytoypes on Tête Grosse. Please note that phenology monitoring commenced on June 1st, but no plants bloomed before June 12th

	early (8x)		**late (4x)**	
	individuals n	individuals %	individuals n	individuals %
12/06/2018	1	0.44	0	0.00
14/06/2018	28	12.33	0	0.00
16/06/2018	69	30.40	0	0.00
18/06/2018	139	61.23	0	0.00
20/06/2018	160	70.48	0	0.00
23/06/2018	175	77.09	0	0.00
26/06/2018	183	80.62	0	0.00
28/06/2018	227	100.00	0	0.00
30/06/2018	198	87.22	0	0.00
02/07/2018	148	65.20	0	0.00
04/07/2018	101	44.49	0	0.00
06/07/2018	76	33.48	0	0.00
09/07/2018	40	17.62	3	6.52
11/07/2018	40	17.62	6	13.04
13/07/2018	27	11.89	9	19.57
17/07/2018	7	3.08	43	93.48
20/07/2018	0	0.00	46	100.00
22/07/2018	0	0.00	41	89.13
24/07/2018	0	0.00	21	45.65
26/07/2018	0	0.00	22	47.83
28/07/2018	0	0.00	26	56.52
30/07/2018	0	0.00	21	45.65
01/08/2018	0	0.00	18	39.13
03/08/2018	0	0.00	7	15.22
06/08/2018	0	0.00	1	2.17

C.3 Seed counts

Table C.4: Number of viable seeds counted of indivudal *Senecio doronicum* plant. Where 'Category' is 'Rana' it means that the plant was subejct to automated pollinators monitoring, where it is 'silvertag' is means that the plant was subject to natural pollination

Plant_ID_num	**Capitulum**	**Ploidy**	**Category**	**viable seeds n**
47	a	4x	Rana	6
343	a	4x	Rana	2
344	a	4x	Rana	28
345	a	4x	Rana	0
345	b	4x	Rana	35
345	c	4x	Rana	29
345	d	4x	Rana	16
348	a	4x	Rana	48
355	a	4x	Rana	12

Table C.4: Number of viable seeds counted of indivudal *Senecio doronicum* plant.

Plant_ID_num	Capitulum	Ploidy	Category	viable seeds n
357	a	4x	Rana	0
357	b	4x	Rana	7
361	a	4x	Rana	33
363	a	4x	Rana	52
366	a	4x	Rana	25
367	a	4x	Rana	0
367	b	4x	Rana	34
413	a	4x	Rana	71
413	b	4x	Rana	81
413	c	4x	Rana	45
421	b	4x	Rana	0
421	b	4x	Rana	0
432	a	4x	Rana	105
432	c	4x	Rana	75
439	a	4x	Rana	56
442	b	4x	Rana	0
443	a	4x	Rana	65
443	d	4x	Rana	19
457	b	4x	Rana	59
460	a	4x	Rana	117
460	b	4x	Rana	80
468	a	4x	Rana	66
474	a	4x	Rana	43
474	b	4x	Rana	57
474	c	4x	Rana	70
494	a	4x	Rana	15
494	b	4x	Rana	65
494	c	4x	Rana	0
514	d	4x	Rana	10
514	a	4x	Rana	21
517	a	4x	Rana	0
521	a	4x	Rana	86
521	c	4x	Rana	19
521	d	4x	Rana	14
521	e	4x	Rana	0
521	f	4x	Rana	64
527	a	4x	Rana	65
529	a	4x	Rana	68
531	c	4x	Rana	20
551	b	4x	Rana	48
705	a	4x	Rana	50
337	a	6x	Rana	0
1	a	8x	Rana	0

Table C.4: Number of viable seeds counted of indivudal *Senecio doronicum* plant.

Plant_ID_num	Capitulum	Ploidy	Category	viable seeds n
2	a	8x	Rana	0
3	a	8x	Rana	0
4	a	8x	Rana	0
5	a	8x	Rana	0
6	a	8x	Rana	21
7	a	8x	Rana	27
14	a	8x	Rana	0
14	b	8x	Rana	0
14	c	8x	Rana	0
18	a	8x	Rana	7
24	a	8x	Rana	0
28	a	8x	Rana	0
39	a	8x	Rana	0
41	a	8x	Rana	2
45	a	8x	Rana	0
61	a	8x	Rana	8
64	a	8x	Rana	7
67	a	8x	Rana	1
70	a	8x	Rana	24
100	a	8x	Rana	0
101	b	8x	Rana	1
102	a	8x	Rana	0
115	a	8x	Rana	0
120	b	8x	Rana	0
121	a	8x	Rana	63
131	a	8x	Rana	0
134	a	8x	Rana	0
138	a	8x	Rana	7
139	a	8x	Rana	0
163	b	8x	Rana	28
165	b	8x	Rana	8
173	a	8x	Rana	13
174	a	8x	Rana	0
184	a	8x	Rana	14
300	a	8x	Rana	0
301	a	8x	Rana	0
302	a	8x	Rana	1
303	a	8x	Rana	1
304	a	8x	Rana	0
307	a	8x	Rana	0
309	a	8x	Rana	6
327	a	8x	Rana	1
329	a	8x	Rana	0

Table C.4: Number of viable seeds counted of indivudal *Senecio doronicum* plant.

Plant_ID_num	Capitulum	Ploidy	Category	viable seeds n
329	b	8x	Rana	1
330	a	8x	Rana	0
331	a	8x	Rana	0
335	a	8x	Rana	0
338	a	8x	Rana	0
340	ab	8x	Rana	18
528	a	8x	Rana	32
368	a	4x	silvertag	25
607	a	4x	silvertag	0
610	a	4x	silvertag	48
88	a	8x	silvertag	8
221	a	8x	silvertag	3
351	a	8x	silvertag	0
351	a	8x	silvertag	0
376	a	8x	silvertag	15
377	a	8x	silvertag	7
378	a	8x	silvertag	9
381	a	8x	silvertag	3
383	a	8x	silvertag	0
384	a	8x	silvertag	1
579	a	8x	silvertag	14
581	a	8x	silvertag	12
583	a	8x	silvertag	0
587	a	8x	silvertag	2
588	a	8x	silvertag	16
590	a	8x	silvertag	7
591	a	8x	silvertag	4
591	b	8x	silvertag	9
592	a	8x	silvertag	1
593	a	8x	silvertag	0
595	a	8x	silvertag	1
597	a	8x	silvertag	1
598	a	8x	silvertag	17
598	b	8x	silvertag	0
600	a	8x	silvertag	7
613	a	8x	silvertag	1
708	a	8x	silvertag	0
709	a	8x	silvertag	3
710	a	8x	silvertag	7
711	a	8x	silvertag	1

Appendix D

Chapter 6 supplementary material

D.1 Insect collections

Table D.1: Insect specimens collected on Tête Grosse. Captures were made with a hand net and with pan traps.

Specimen ID	Order	Family	Genus	Species	Sex
300	Diptera	Rhinophoridae			
53	Diptera	Sarcophagidae			
138	Diptera	Fanniidae			
42	Lepidoptera				
144	Hymenoptera	Formicidae			
89b	Diptera	Muscidae			
66	Lepidoptera				
295	Diptera	Anthomyiidae			F
41	Lepidoptera				
157	Hymenoptera				
71	Lepidoptera				
142	Diptera	Empididae			
100	Diptera	Anthomyiidae			
149	Hymenoptera	Formicidae			
191	Hymenoptera	Astatidae			
44	Lepidoptera	Noctuidae			
132	Hymenoptera	Anthomyiidae			F
52	Diptera	Sarcophagidae			
195	Diptera	Anthomyiidae			F
43	Lepidoptera				
226	Diptera	Anthomyiidae			
228	Diptera	Anthomyiidae			F
124	Diptera	Anthomyiidae			F
237	Diptera	Tachinidae			
86	Coleoptera	Chrysomelidae			

Table D.1: Insect specimens collected on Tête Grosse.

Specimen ID	Order	Family	Genus	Species	Sex
247	Lepidoptera	Noctuidae			
160	Hymenoptera	Formicidae			
79	Lepidoptera				
306	Hymenoptera	Formicidae			
293	Hymenoptera	Ichneumonidae			F
266	Diptera	Anthomyiidae			F
215	Hymenoptera	Ichneumonidae			
289	Hymenoptera	Ichneumonidae			F
196	Hemiptera	Lygaeidae			
305	Hymenoptera	Formicidae			
88	Hymenoptera	Ichneumonidea			
129	Diptera	Anthomyiidae			M
302	Hymenoptera	Formicidae			
304	Hymenoptera	Formicidae			
177	Diptera	Muscidae			M
301	Diptera	Anthomyiidae			
291	Diptera	Anthomyiidae			
125	Hymenoptera	Ichneumonidae			
147	Diptera	Muscidae			
78	Lepidoptera	Pterophoridae	-		
113	Lepidoptera	Zygaenidae	*Adscita*		
8	Lepidoptera	Zygaenidae	*Adscita*		
49	Lepidoptera	Zygaenidae	*Adscita*		
62	Lepidoptera	Nymphalidae	*Aglais*	*Aglais urticae*	
95	Hymenoptera	Andrenidae	*Andrena*		
169	Hymenoptera	Andrenidae	*Andrena*		M
151	Hymenoptera	Andrenidae	*Andrena*	*Andrena nigroaenea*	F
239	Diptera	Asilidae	*Antiphrisson*		F
238	Diptera	Asilidae	*Antiphrisson*		M
19	Hymenoptera	Apidae	*Apis*	*Apis mellifera*	
14	Hymenoptera	Apidae	*Apis*	*Apis mellifera*	
5	Hymenoptera	Apidae	*Apis*	*Apis mellifera*	
136	Hymenoptera	Apidae	*Apis*	*Apis mellifera*	F
15	Hymenoptera	Apidae	*Apis*	*Apis mellifera*	
190	Hymenoptera	Pompilidae	*Arachnospila*		M
181	Lepidoptera	Erebidae	*Arctia*	*Arctia plantaginis*	F
116	Lepidoptera	Nymphalidae	*Fabriciana*	*Fabriciana adippe*	
251	Lepidoptera	Nymphalidae	*Argynnis*	*Argynnis aglaja*	F
270	Lepidoptera	Nymphalidae	*Argynnis*	*Argynnis aglaja*	M
56	Lepidoptera	Nymphalidae	*Argynnis*	*Argynnis aglaja*	
272	Lepidoptera	Nymphalidae	*Argynnis*	*Argynnis aglaja*	F
58	Lepidoptera	Nymphalidae	*Argynnis*	*Argynnis aglaja*	
246	Lepidoptera	Nymphalidae	*Argynnis*	*Argynnis aglaja*	F

Table D.1: Insect specimens collected on Tête Grosse.

Specimen ID	Order	Family	Genus	Species	Sex
273	Lepidoptera	Nymphalidae	*Argynnis*	*Argynnis aglaja*	M
271	Lepidoptera	Nymphalidae	*Argynnis*	*Argynnis aglaja*	F
283	Hymenoptera	Crabronidae	*Astata*		F
277	Hymenoptera	Crabronidae	*Astata*		F
217	Hymenoptera	Crabronidae	*Astata*		F
280	Hymenoptera	Crabronidae	*Astata*		F
292	Hymenoptera	Tenthredinidae	*Athalia*	*Athalia cordata*	F
16	Lepidoptera	Sesiidae	*Bembecia*	*Bembecia albanensis*	
55	Diptera	Tachinidae	*Besseria*		
287	Diptera	Tachinidae	*Bithia*		F
82	Lepidoptera	Nymphalidae	*Boloria*	*Boloria napaea*	
265	Hymenoptera	Apidae	*Bombus*		F
23	Hymenoptera	Apidae	*Bombus*		
6	Hymenoptera	Apidae	*Bombus*	*Bombus lapidarius*	
24	Hymenoptera	Apidae	*Bombus*	*Bombus lapidarius*	
256	Hymenoptera	Apidae	*Bombus*	*Bombus lapidarius*	F
123	Hymenoptera	Apidae	*Bombus*	*Bombus lapidarius*	
261	Hymenoptera	Apidae	*Bombus*	*Bombus lapidarius*	F
259	Hymenoptera	Apidae	*Bombus*	*Bombus lapidarius*	F
260	Hymenoptera	Apidae	*Bombus*	*Bombus lapidarius*	F
4	Hymenoptera	Apidae	*Bombus*	*Bombus lapidarius*	
176	Hymenoptera	Apidae	*Bombus*	*Bombus lapidarius*	F
262	Hymenoptera	Apidae	*Bombus*	*Bombus lucorum*	F
255	Hymenoptera	Apidae	*Bombus*	*Bombus lucorum*	F
231	Hymenoptera	Apidae	*Bombus*	*Bombus mesomelas*	F
254	Hymenoptera	Apidae	*Bombus*	*Bombus mesomelas*	F
257	Hymenoptera	Apidae	*Bombus*	*Bombus mesomelas*	F
258	Hymenoptera	Apidae	*Bombus*	*Bombus mesomelas*	F
45	Hymenoptera	Apidae	*Bombus*	*Bombus sylvarum*	
46	Hymenoptera	Apidae	*Bombus*	*Bombus sylvarum*	
26	Hymenoptera	Apidae	*Bombus*	*Bombus sylvarum*	
153	Hymenoptera	Apidae	*Bombus*	*Bombus terrestris*	F
152	Hymenoptera	Apidae	*Bombus*	*Bombus terrestris*	F
203	Hymenoptera	Apidae	*Bombus*	*Bombus terrestris*	F
202	Hymenoptera	Apidae	*Bombus*	*Bombus terrestris*	F
47	Hymenoptera	Apidae	*Bombus*	*Bombus vestalis*	
48	Hymenoptera	Apidae	*Bombus*	*Bombus wurlfenii*	
18	Hymenoptera	Apidae	*Bombus*	*Bombus wurlfenii*	
148	Diptera	Syrphidae	*Callicera*	*Callicera rufa*	F
94	Diptera	Calliphoridae	*Calliphora*		
143	Diptera	Tachinidae	*Campylocheta*		
112	Hemiptera	Pentatomidae	*Carpocoris*	*Carpocoris mediterraneus*	
2	Diptera	Oestridae	*Cephenemyia*		

Table D.1: Insect specimens collected on Tête Grosse.

Specimen ID	Order	Family	Genus	Species	Sex
7	Diptera	Oestridae	*Cephenemyia*		
5b	Diptera	Oestridae	*Cephenemyia*		
6b	Diptera	Oestridae	*Cephenemyia*		
21	Diptera	Oestridae	*Cephenemyia*		
107	Diptera	Oestridae	*Cephenemyia*		
106	Diptera	Oestridae	*Cephenemyia*		
184	Diptera	Oestridae	*Cephenemyia*	*Cephenemyia stimulator*	
90	Coleoptera	Scarabaeidae	*Cetonia*	*Cetonia aurata*	
285	Diptera	Stratiomyidae	*Chloromyia*		M
192	Diptera	Stratiomyidae	*Chloromyia*		F
51	Diptera	Stratiomyidae	*Chloromyia*	*Chloromyia formosa*	
155	Diptera	Syrphidae	*Chrysotoxum*		F
204	Diptera	Syrphidae	*Chrysotoxum*		F
154	Diptera	Syrphidae	*Chrysotoxum*	*Chrysotoxum cautum*	M
173	Diptera	Syrphidae	*Chrysotoxum*	*Chrysotoxum cautum*	M
172	Diptera	Syrphidae	*Chrysotoxum*	*Chrysotoxum cautum*	M
98	Diptera	Syrphidae	*Chrysotoxum*	*Chrysotoxum intermedium*	
268	Lepidoptera	Nymphalidae	*Coenonympha*		
64	Lepidoptera	Nymphalidae	*Coenonympha*	*Coenonympha glycerion*	
63	Lepidoptera	Nymphalidae	*Coenonympha*	*Coenonympha glycerion*	
68	Lepidoptera	Nymphalidae	*Coenonympha*	*Coenonympha glycerion*	
60	Lepidoptera	Nymphalidae	*Coenonympha*	*Coenonympha glycerion*	
75	Lepidoptera	Nymphalidae	*Coenonympha*	*Coenonympha glycerion*	
73	Lepidoptera	Nymphalidae	*Coenonympha*	*Coenonympha pamphilus*	
243	Lepidoptera	Pieridae	*Colias*	*Colias hyale*	M
119	Coleoptera	Cerambycidae	*Corymbia*		
119	Coleoptera	Cerambycidae	*Corymbia*		
38	Diptera	Tachinidae	*Cylindromyia*		
197	Diptera	Tabanidae	*Dasyrhamphis*	*Dasyrhamphis ater*	F
294	Diptera	Tachinidae	*Drino*		
67	Lepidoptera	Tortricidae	*Eana*		
93	Diptera	Empididae	*Empis*		
92	Diptera	Syrphidae	*Epistrophe*	*Epistrophe grossulariae*	
161	Lepidoptera	Nymphalidae	*Erebia*		
59	Lepidoptera	Nymphalidae	*Erebia*	*Erebia albergana*	
69	Lepidoptera	Nymphalidae	*Erebia*	*Erebia cassioides*	
211	Lepidoptera	Nymphalidae	*Erebia*	*Erebia cassioides*	F
61	Lepidoptera	Nymphalidae	*Erebia*	*Erebia cassioides*	
276	Lepidoptera	Nymphalidae	*Erebia*	*Erebia gorgone*	M
182	Lepidoptera	Nymphalidae	*Erebia*	*Erebia medusa*	M
208	Lepidoptera	Nymphalidae	*Erebia*	*Erebia medusa*	
34	Diptera	Syrphidae	*Eristalis*		
250	Diptera	Syrphidae	*Eristalis*	*Eristalis tenax*	F

Table D.1: Insect specimens collected on Tête Grosse.

Specimen ID	Order	Family	Genus	Species	Sex
20	Diptera	Syrphidae	*Eristalis*	*Eristalis tenax*	
232	Diptera	Syrphidae	*Eristalis*	*Eristalis tenax*	M
175	Diptera	Syrphidae	*Eristalis*	*Eristalis tenax*	M
198	Diptera	Syrphidae	*Eristalis*	*Eristalis tenax*	M
27	Diptera	Syrphidae	*Eristalis*	*Eristalis tenax*	
165	Diptera	Syrphidae	*Eristalis*	*Eristalis tenax*	F
249	Diptera	Syrphidae	*Eristalis*	*Eristalis tenax*	M
31	Diptera	Syrphidae	*Eristalis*	*Eristalis tenax*	
185	Diptera	Syrphidae	*Eupeodes*	*Eupeodes luniger*	M
10	Diptera	Syrphidae	*Eupeodes*	*Eupeodes luniger*	
9	Diptera	Syrphidae	*Eupeodes*	*Eupeodes luniger*	
214	Hymenoptera	Halictidae	*Lasioglossum*		M
103	Hymenoptera	Formicidae	*Formica*	*Formica fusca*	
105	Hymenoptera	Formicidae	*Formica*	*Formica rufa*	
3	Diptera	Tachinidae	*Gonia*		
32	Diptera	Tachinidae	*Gonia*		
264	Hymenoptera	Halictidae	*Halictus*	*Halictus quadricinctus*	F
234	Diptera	Bombyliidae	*Hemipenthes*		F
222	Hymenoptera	Chrysididae	*Holopyga*		
146	Diptera	Muscidae	*Hydrotaea*		M
186	Hymenoptera	Colletidae	*Hylaeus*		
225	Hymenoptera	Colletidae	*Hylaeus*	*Hylaeus angustatus*	M
297	Hymenoptera	Colletidae	*Hylaeus*	*Hylaeus angustatus*	F
218	Hymenoptera	Colletidae	*Hylaeus*	*Hylaeus difformis*	F
36	Hymenoptera	Ichneumonidae	*Ichneumon*		
244	Lepidoptera	Nymphalidae	*Issoria*	*Issoria lathonia*	M
269	Lepidoptera	Nymphalidae	*Issoria*	*Issoria lathonia*	M
219	Hymenoptera	Halictidae	*Lasioglossum*		F
188	Hymenoptera	Halictidae	*Lasioglossum*	*Lasioglossum lativentre*	F
137	Hymenoptera	Halictidae	*Lasioglossum*	*Lasioglossum lativentre*	F
139	Hymenoptera	Halictidae	*Lasioglossum*	*Lasioglossum lativentre*	F
227	Hymenoptera	Halictidae	*Lasioglossum*	*Lasioglossum lativentre*	F
131	Hymenoptera	Halictidae	*Lasioglossum*	*Lasioglossum morio*	F
183	Hymenoptera	Halictidae	*Lasioglossum*	*Lasioglossum morio*	F
130	Hymenoptera	Halictidae	*Lasioglossum*	*Lasioglossum morio*	F
128	Hymenoptera	Halictidae	*Lasioglossum*	*Lasioglossum morio*	F
307	Hymenoptera	Halictidae	*Lasioglossum*	*Lasioglossum morio*	F
290	Hymenoptera	Halictidae	*Lasioglossum*	*Lasioglossum morio*	M
189	Hymenoptera	Halictidae	*Lasioglossum*	*Lasioglossum morio*	F
303	Hymenoptera	Halictidae	*Lasioglossum*	*Lasioglossum morio*	F
245	Lepidoptera	Nymphalidae	*Lasiommata*	*Lasiommata maera*	F
206	Diptera	Asilidae	*Lasiopogon*		F
118	Coleoptera	Cerambycidae	*Leptura*	*Leptura maculata*	

Table D.1: Insect specimens collected on Tête Grosse.

Specimen ID	Order	Family	Genus	Species	Sex
308	Hymenoptera	Crabronidae	*Lindenius*		F
252	Lepidoptera	Noctuidae	*Luperina*	*Luperina testacea*	
274	Lepidoptera	Noctuidae	*Luperina*	*Luperina testacea*	
8e	Lepidoptera	Lycaenidae	*Lycaena*	*Lycaena dispar*	
110	Lepidoptera	Lycaenidae	*Lycaena*	*Lycaena virgaureae*	
296	Diptera	Tachinidae	*Meigenia*		
242	Lepidoptera	Nymphalidae	*Melanargia*	*Melanargia galathea*	M
248	Lepidoptera	Nymphalidae	*Melanargia*	*Melanargia galathea*	F
37	Lepidoptera	Nymphalidae	*Melanargia*	*Melanargia russiae*	
57	Lepidoptera	Nymphalidae	*Mellicta*	*Mellicta deione*	
54	Diptera	Syrphidae	*Merodon*	*Merodon cinereus*	
96	Diptera	Syrphidae	*Merodon*	*Merodon cinereus*	
159	Diptera	Syrphidae	*Merodon*	*Merodon moenium*	M
288	Hymenoptera	Andrenidae	*Andrena*		F
223	Diptera	Muscidae	*Musca*		F
84	Diptera	Muscidae	*Musca*		
292	Diptera	Muscidae			F
193	Diptera	Muscidae	*Myospila*		M
224	Hymenoptera	Apidae	*Nomada*		M
309	Hymenoptera	Crabronidae	*Nysson*		F
180	Diptera	Tephritidae	*Orellia*	*Orellia falcata*	F
216	Hymenoptera	Crabronidae	*Oxybelus*		F
286	Hymenoptera	Crabronidae	*Oxybelus*		F
237	Hymenoptera	Crabronidae	*Oxybelus*		F
102	Mecoptera	Panorpidae	*Panorpa*	*Panorpa communis*	
220	Hymenoptera	Andrenidae	*Panurgus*		F
221	Hymenoptera	Andrenidae	*Panurgus*	*Panurgus dentipes*	F
278	Hymenoptera	Andrenidae	*Panurgus*	*Panurgus dentipes*	F
279	Hymenoptera	Andrenidae	*Panurgus*	*Panurgus dentipes*	M
187	Hymenoptera	Andrenidae	*Panurgus*	*Panurgus dentipes*	F
267	Lepidoptera	Papilionidae	*Papilio*	*Papilio machaon*	
33	Diptera	Tachinidae	*Peleteria*		
150	Diptera	Tachinidae	*Peleteria*	*Peleteria rubescens*	F
199	Diptera	Tabanidae	*Philipomyia*	*Philipomyia aprica*	F
200	Diptera	Tabanidae	*Philipomyia*	*Philipomyia aprica*	F
201	Diptera	Tabanidae	*Philipomyia*	*Philipomyia aprica*	F
162	Lepidoptera	Pieridae	*Pieris*	*Pieris brassicae*	F
83	Lepidoptera	Pieridae	*Pieris*	*Pieris brassicae*	
89	Lepidoptera	Lycaenidae	*Plebejus*		
74	Lepidoptera	Lycaenidae	*Plebejus*	*Plebejus argus*	
70	Lepidoptera	Lycaenidae	*Plebejus*	*Plebejus argus*	
88	Lepidoptera	Lycaenidae	*Plebejus*	*Plebejus argus*	
253	Lepidoptera	Lycaenidae	*Plebejus*	*Plebejus argyrognomon*	F

Table D.1: Insect specimens collected on Tête Grosse.

Specimen ID	Order	Family	Genus	Species	Sex
241	Lepidoptera	Lycaenidae	*Plebejus*	*Plebejus argyrognomon*	F
210	Lepidoptera	Lycaenidae	*Plebejus*	*Plebejus argyrognomon*	M
209	Lepidoptera	Lycaenidae	*Plebejus*	*Plebejus argyrognomon*	M
240	Lepidoptera	Lycaenidae	*Plebejus*	*Plebejus argyrognomon*	F
12	Hymenoptera	Sphecidae	*Ammophilinae*	*Podalonia hirsuta*	
35	Hymenoptera	Sphecidae	*Ammophilinae*	*Podalonia hirsuta*	
91	Hymenoptera	Vespidae	*Polistes*	*Polistes biglumis*	
87	Hymenoptera	Vespidae	*Polistes*	*Polistes biglumis*	
120	Lepidoptera	Lycaenidae	*Polyommatus*		
81	Lepidoptera	Hesperiidae	*Pyrgus*	*Pyrgus bellieri*	
109	Raphidioptera	Raphidiidae	*Raphidia*	*Raphidia ophiopsis*	
205	Diptera	Syrphidae	*Scaeva*	*Scaeva pyrastri*	F
99	Diptera	Syrphidae	*Scaeva*	*Scaeva pyrastri*	
85	Diptera	Conopidae	*Sicus*		
134	Hymenoptera	Halictidae	*Sphecodes*		F
104	Hymenoptera	Halictidae	*Sphecodes*	*Sphecodes ephippius*	
30	Diptera	Syrphidae	*Syrphus*	*Syrphus ribesii*	
163	Diptera	Syrphidae	*Syrphus*	*Syrphus ribesii*	M
168	Diptera	Syrphidae	*Syrphus*	*Syrphus ribesii*	F
166	Diptera	Syrphidae	*Syrphus*	*Syrphus torvus*	F
164	Diptera	Syrphidae	*Syrphus*	*Syrphus torvus*	M
157	Diptera	Syrphidae	*Syrphus*	*Syrphus torvus*	M
167	Diptera	Syrphidae	*Syrphus*	*Syrphus torvus*	M
158	Diptera	Syrphidae	*Syrphus*	*Syrphus torvus*	F
171	Diptera	Syrphidae	*Syrphus*	*Syrphus torvus*	F
179	Diptera	Syrphidae	*Syrphus*	*Syrphus vitripennis*	F
156	Diptera	Tabanidae	*Tabanus*		F
117	Diptera	Tabanidae	*Tabanus*	*Tabanus bromius*	
25	Diptera	Tachinidae	*Tachina*		
97	Diptera	Tachinidae	*Tachina*		
233	Diptera	Tachinidae	*Tachina*		F
111	Hymenoptera	Tenthredinidae	*Tenthredo*	*Tenthredo brevicornis*	
39	Lepidoptera	Hesperiidae	*Thymelicus*	*Thymelicus lineola*	
76	Lepidoptera	Hesperiidae	*Thymelicus*	*Thymelicus lineola*	
77	Diptera	Tipulidae	*Tipula*		
275	Lepidoptera	Nymphalidae	*Vanessa*	*Vanessa cardui*	M
170	Lepidoptera	Nymphalidae	*Vanessa*	*Vanessa cardui*	M
1	Diptera	Bombyliidae	*Villa*		
101	Diptera	Syrphidae	*Volucella*	*Volucella pellucens*	
121	Diptera	Syrphidae	*Volucella*	*Volucella pellucens*	
230	Lepidoptera	Zygaenidae	*Zygaena*		M
40	Lepidoptera	Zygaenidae	*Zygaena*		
108	Lepidoptera	Zygaenidae	*Zygaena*	*Zygaena viciae*	

Table D.1: Insect specimens collected on Tête Grosse.

Specimen ID	Order	Family	Genus	Species	Sex
115	Lepidoptera	Zygaenidae	*Zygaena*	*Zygaena filipendulae*	
11	Lepidoptera	Zygaenidae	*Zygaena*	*Zygaena filipendulae*	
114	Lepidoptera	Zygaenidae	*Zygaena*	*Zygaena filipendulae*	
65	Lepidoptera	Zygaenidae	*Zygaena*	*Zygaena purpuralis*	

D.2 Vegetation survey

Table D.2: Results of the vegetation survey of plants co-flowering with *Senecio doronicum* on Tête Grosse. Please note that 'Week' is expressed as week's number within a year, and 'Unit' indicates whether the figures refer to floral units ('flu') or individual plants ('ind') in flower. 'Species count' expresses the number of distinct taxa in flower at any given date for that site.

Date	Week	Site	Unit	Total	Species count
15/06/2018	24	EARLY	flu	1090	18
20/06/2018	25	EARLY	flu	7514	9
22/06/2018	25	LATE	flu	2293	19
30/06/2018	26	LATE	flu	1822	18
30/06/2018	26	EARLY	flu	2852	17
06/07/2018	27	LATE	flu	3221	13
06/07/2018	27	EARLY	flu	3562	21
14/07/2018	28	LATE	flu	2500	23
20/07/2018	29	LATE	flu	2136	17
28/07/2018	30	LATE	flu	461	19
04/08/2018	31	LATE	flu	553	15
15/06/2018	24	EARLY	ind	376	18
20/06/2018	25	EARLY	ind	680	9
22/06/2018	25	LATE	ind	239	19
30/06/2018	26	LATE	ind	366	18
30/06/2018	26	EARLY	ind	496	17
06/07/2018	27	LATE	ind	346	13
06/07/2018	27	EARLY	ind	697	21
14/07/2018	28	LATE	ind	464	23
20/07/2018	29	LATE	ind	386	17
28/07/2018	30	LATE	ind	234	19
04/08/2018	31	LATE	ind	383	15

D.3 Pollinators community composition

Table D.3: Feeding visits to *Senecio doronicum* cytotypes by insect Order.

	4x		**8x**	
	n visits	% visits	n visits	% visits
Coleoptera	4	0.38	1	0.49
Diptera	877	82.35	157	76.21
Hemiptera	3	0.28	0	0.00
Hymenoptera	144	13.52	40	19.42
Lepidoptera	37	3.47	8	3.88

Table D.4: Feeding visits to *Senecio doronicum* cytotypes by insect family.

	4x		**8x**	
	n visits	% visits	n visits	% visits
Chrysomelidae	3	0.30	0	0.00
Nitidulidae	1	0.10	0	0.00
Bombyliidae	3	0.30	0	0.00
Simuliidae	5	0.50	0	0.00
Conopidae	2	0.20	0	0.00
Empididae	20	1.98	1	0.56
Muscidae	13	1.29	0	0.00
Calliphoridae	2	0.20	0	0.00
Sarcophagidae	9	0.89	0	0.00
Tachinidae	1	0.10	0	0.00
Syrphidae	806	79.96	138	77.97
Pentatomidae	3	0.30	0	0.00
Andrenidae	25	2.48	0	0.00
Apidae	0	0.00	15	8.47
Halictidae	78	7.74	15	8.47
Geometridae	1	0.10	0	0.00
Lycaenidae	6	0.60	0	0.00
Nymphalidae	29	2.88	8	4.52
Zygaenidae	1	0.10	0	0.00

Table D.5: Feeding visits to *Senecio doronicum* cytotypes by insect genus.

	4x		**8x**	
	n visits	% visits	n visits	% visits
Hemipenthes	2	0.22	0	0.00
Thecophora	2	0.22	0	0.00
Chrysotoxum	38	4.27	0	0.00
Dasysyrphus	2	0.22	0	0.00
Eristalis	569	64.00	35	25.36
Eupeodes	63	7.09	8	5.80
Megasyrphus	2	0.22	0	0.00
Meliscaeva	4	0.45	0	0.00
Merodon	20	2.25	1	0.72
Myathropa	2	0.22	0	0.00
Parasyrphus	17	1.91	0	0.00
Scaeva	9	1.01	0	0.00
Sphaerophoria	21	2.36	4	2.90
Syrphus	48	5.40	61	44.20
Xanthandrus	1	0.11	0	0.00
Andrena	25	2.81	0	0.00
Lasioglossum	38	4.27	5	3.62
Polyommatus	4	0.45	0	0.00
Lasiommata	21	2.36	2	1.45
Adscita	1	0.11	0	0.00
Melanostoma	0	0.00	3	2.17
Neoascia	0	0.00	1	0.72
Platycheirus	0	0.00	2	1.45
Apis	0	0.00	15	10.87
Aglais	0	0.00	1	0.72

D.3.1 Non-Metric Dimensional Scaling (NMDS) diagnostics

```
Call:
metaMDS(comm = Genera_matrix_perPlant, k = 2, trymax = 999)

global Multidimensional Scaling using monoMDS

Data:     wisconsin(sqrt(Genera_matrix_perPlant))
Distance: bray

Dimensions: 2
Stress:     0.1285161
Stress type 1, weak ties
Two convergent solutions found after 20 tries
Scaling: centring, PC rotation, halfchange scaling
Species: expanded scores based on 'wisconsin(sqrt(Genera_matrix_perPlant))'
```

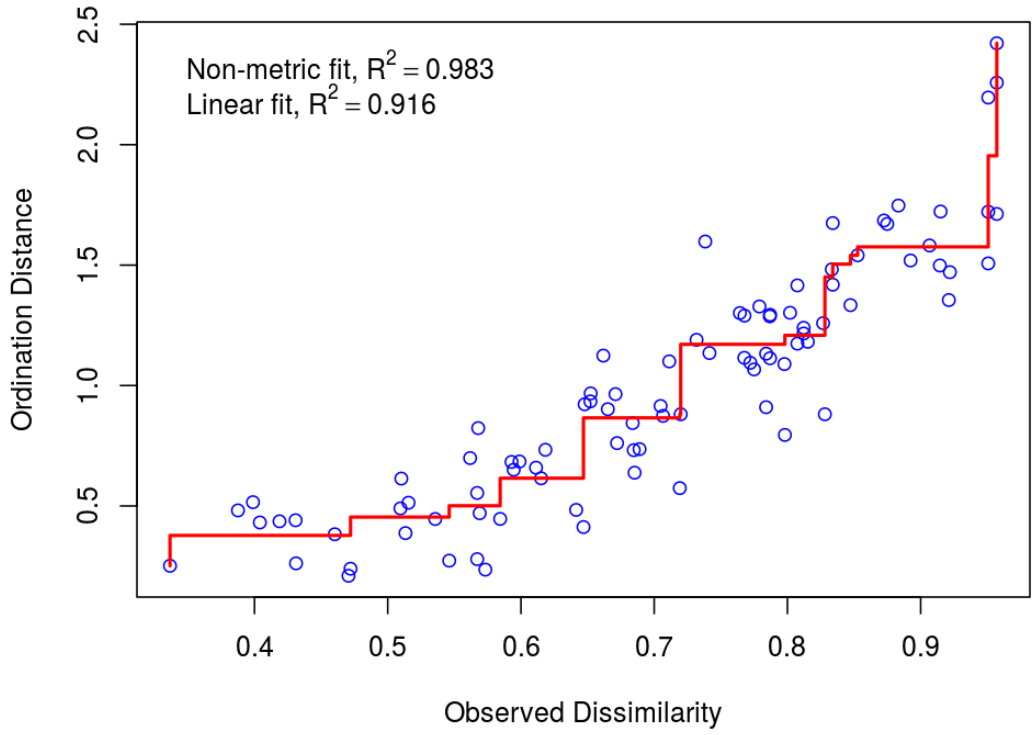


Figure D.1: Stress plot for NMDS analysis. Large scatter around the line would suggests that original dissimilarities are not well preserved in the reduced number of dimensions, but this is not the case here.

D.3.2 PERMANOVA analysis

```
Call:
adonis(formula = Genera_matrix_perPlant ~ Ploidy_temp,
       permutations = 10^6, method = "bray")
```

```
Permutation: free
Number of permutations: 1e+06

Terms added sequentially (first to last)

            Df SumsOfSqs MeanSqs F.Model      R2   Pr(>F)
Ploidy_temp  1    0.8822  0.8822  3.9331 0.24685 0.004047 **
Residuals   12    2.6916  0.2243         0.75315
Total       13    3.5738                 1.00000
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

D.3.3 Mutlivariate dispersion analysis

```
Homogeneity of multivariate dispersions

Call: betadisper(d = Distance_Genera_perPlant, group =
Ploidy_temp)

No. of Positive Eigenvalues: 10
No. of Negative Eigenvalues: 3

Average distance to median:
    4x     8x
0.3893 0.4488

Eigenvalues for PCoA axes:
(Showing 8 of 13 eigenvalues)
  PCoA1   PCoA2   PCoA3   PCoA4   PCoA5   PCoA6   PCoA7   PCoA8
1.40971 0.73846 0.45193 0.33433 0.22873 0.19271 0.12042 0.07896
```