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EVOLUTION AND CONSERVATION OF PLANT SPECIES ENDEMIC TO THE MEDITERRANEAN BASIN

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Abstract

Evolution and conservation are two aspects deeply interconnected: knowing the processes that drive the former, enables better management of the latter. Improve the knowledge about the vulnerability and future perspective for the species is indispensable to preserve the processes that generate biodiversity and thus biodiversity itself.

In this thesis, I investigated some Mediterranean endemic plant species, using an integrated study method, to assess their evolution and propose appropriate management strategies. Indeed, the lack of in-depth taxonomic knowledge, which does not consider biological and ecological aspects, makes species delimitation difficult and consequently slows down the proper conservation and protection. I aimed at: (a) providing information on *Santolina* genus that is taxonomically complex, to better understand plant evolution in the Mediterranean Basin and (b) assessing extinction risk of endemism to better manage conservation actions, decreasing risk and increasing cost effectiveness.

The investigation of *Santolina* genus, conducted using mainly phylogenetic analysis and ecological niche models, enriched considerably our knowledge of the relationships among species, shedding light on the processes that led to a current species framework. Additionally, the results demonstrated that in groups with taxonomic complexity an integrated study approach, based on the use of different and independent evidence, may provide important information to solve taxonomic problems.

Ecological niche models are a valid tool to assess extinction risk of species, providing information on crucial aspects of species distribution. Indeed, I used them to get information on the factors influencing the distribution of species and on the cost-effectiveness of assisted colonization and other conservation translocations.

Keywords: conservation, ecological niche models, evolution, integrated taxonomy, phylogenesis

List of Papers

This thesis is based on the following articles, which are referred to in the text by their Roman numerals.

I. Varaldo L., Baumel A., Guerrina M., Minuto L., Giacò A., Peruzzi L., Sáez L., Carballal R., Caputo P., De Luca D., Bacchetta G., Podda L., Conti F., Bartolucci F., Casazza G. Evolutionary relationship in the taxonomically complex genus *Santolina* endemic to the Mediterranean Basin (Manuscript)

II. Varaldo L., Calbi M., Guerrina M., Bonifazio C., Casazza G., Minuto L. *Santolina ligustica* Arrigoni: how climatic suitability and vegetation cover influence the distribution. (Manuscript)

III. Varaldo, L., Guerrina, M., Dagnino, D., Minuto, L., & Casazza, G. (2023). Dealing with disjunct populations of vascular plants: implications for assessing the effect of climate change. Oecologia, 1-14.

IV. Casazza, G., Abeli, T., Bacchetta, G., Dagnino, D., Fenu, G., Gargano, D., Minuto L., Montagnani C., Orsenigo S., Peruzzi L., Varaldo L., Rossi, G. (2021). Combining conservation status and species distribution models for planning assisted colonisation under climate change. Journal of Ecology, 109(6), 2284-2295.

Introduction

The history of the Mediterranean flora is complex and subject to many changes. During the Middle Miocene, the Middle\Late Pliocene and the Early\Middle Pleistocene numerous extinctions occurred involving whole taxonomic groups (Thompson, 2020) but, despite that, the current flora is extremely heterogeneous and rich. Endemism is a fundamental component of plant diversity of the Mediterranean region (Thompson et al., 2005), which harbours roughly 12,500 endemic species (Medail and Quezel, 1997), several of which have a distributed limited to a narrow biogeographical entity, the so-called narrow endemics. The main theory for the evolution of these endemic taxa relies on the hypothesis that a widespread ancestral taxon has fragmented, producing endemic taxa in different parts of the original distribution area (Favarger and Contandriopoulos, 1961). Under this assumption, several endemic species in the Mediterranean flora result from allopatric speciation in isolation after disappearance of previous connections between different regions. However, although allopatric speciation with geographic isolation has an important role in plants, some features of population ecology and evolution suggest that this mode of speciation is less important than in animals (Levin, 2000). Indeed, in plants the gene flow is often spatially limited and local genetic differentiation and adaptation could occur also in the absence of geographical barriers (Linhart and Grant, 1996). Additionally, several different types of evolutionary processes can conduct to local speciation: hybridisation, polyploidisation and inbreeding. Localised differentiation could be an important factor for endemism’s evolution, particularly in the

Mediterranean landscape where environmental gradients vary greatly. Despite the high biodiversity, this region faces significant challenges to supply the imminent global change. In fact, there are two main factors that can influence endemism distribution and dynamics in the Mediterranean basin: climate change and human activities. On one hand, the former involves not only increased mean temperatures and lower precipitation but also increased variability and a higher frequency of extreme climatic events (i.e., heat waves and droughts) (Field et al., 2012; Gao et al., 2006; Hoerling et al., 2012; Lloret et al., 2012). On the other hand, centuries of human activities have profoundly transformed the ecosystem, resulting in increased habitat fragmentation, deforestation, and land abandonment (Alodos et al., 2004; Blondel et al., 2010). Although land use change is one of the main drivers that affect biodiversity, climate change is the greatest threat to biodiversity now and in the nearest future (Leadley, 2010). Indeed, genetic patterns, physiological response, phenological behaviour, population dynamics, distribution of species and habitats can be affected by climate change (Bellard et al., 2012).

Given the current and future global change scenarios, Mediterranean plants may adopt resistance and tolerance strategies. In fact, plants can exhibit three main non mutually exclusive responses: 1) migrate to more favourable areas (Hampe and Petit, 2005; Jump and Peñuelas, 2005; Lenoir and Svenning, 2013; Parmesan, 2006); 2) producing different phenotypes in response to distinct environmental conditions (i.e., phenotypic plasticity); and 3) adapt to new conditions, driven by natural selection (Ghalambor et al., 2007; Hoffmann and Sgrò, 2011; Parmesan, 2006; Visser, 2008). The evolutionary adaptation can be an important way for natural population to cope with global change (Hoffmann and Sgrò, 2011; Reusch and Wood, 2007) and several studies have shown that evolutionary changes can be rapid in several taxa (Hansen et al., 2012; Hendry and Gonzalez, 2008; Jump and Peñuelas, 2005; Parmesan, 2006). Likewise, local adaptation shown from populations is a response to contrast novel pressures exerted by global change, and it is evidence of the genetic variation, hence the species' evolutionary potential (Jump and Peñuelas, 2005; Reusch and Wood, 2007).

Within this general framework, Mediterranean basin, despite the small area, is one of the major hotspots of biodiversity. Particularly, Italy represents one of the richest countries in the Mediterranean area for a number of endemic plant taxa (Medail and Quezel, 1997): indeed, there are more than 1,400 endemisms representing 18% of the national native vascular flora (Peruzzi et al., 2015). Many of these taxa have a strong nomenclatural ground, based on several years of intense collaborative studies, but have been described considering almost exclusively qualitative morphological characters, without considering biological and ecological aspects. Nevertheless, to better delimit species is important to consider the processes that lead to speciation for understanding what caused their origin and determined their evolutionary trajectories: indeed, taxonomy needs to be pluralistic, including several study approaches (Padial et al., 2010).

From these last considerations come the *Project of Relevant National Interest (Progetto di Rilevante Interesse Nazionale – PRIN) 2017JW4HZK - "PLAN.T.S. 2.0 - Towards a renaissance of PLANt Taxonomy and Systematics"* that involves several operating units spread across Italy: University of Genova, University of Cagliari, University of Camerino, University of Napoli, University of Pisa, University of Palermo. The goal is to propose an integrated systematic study on selected Italian endemic taxa to fill the current gaps. Part of the studies done in my doctoral project came out of this interesting collaboration. Below, I go on to describe in detail in what manner.

In conclusion, despite the widespread acknowledgment of the region's global importance of endemic plants and the threats exerted by climate change, there is still a lack of proper classification based on multiple aspects – not only morphological – which would then allow for proper management and protection.

My project

In my PhD project, I examined some Mediterranean endemic plant species, using an integrated study method. To study the species' evolution may allow us to understand the vulnerability of different populations and propose management strategies to better protect them and their diversity of ecological traits. Indeed, to preserve genetic diversity among populations, particularly that related to local adaptations, involves understanding the evolutionary forces that drive this diversity (Santamaria and Mendez, 2012).

Incorporating evolutionary processes to conserve areas in biodiversity hotspot is important, even if it could be challenging due to lack of in-depth taxonomic knowledge and consequently species extinction risk assessments are scarce. Therefore, the aims of my work were to:

a) Provide information on the taxonomically complex group of *Santolina*, helping to better understand plant evolution in the context of the Mediterranean Basin (I, II) and, in particular, to disentangle the genetic and phylogenetic relationships, providing a comprehensive picture of the phylogeny of *Santolina* (I).

b) Assess extinction risk of endemism to improve conservation actions, decreasing risks and increasing cost effectiveness and, in particular, to:

i. Investigate the relative role of climate and vegetation in determining the distribution of *Santolina ligustica*, an endemic rare species classified as Near Threatened by the International Union for Conservation of Nature (II).
ii. Evaluate the response of disjunct populations of endemics to future climate change (III).
iii. Inquire the role of translocation (moving population to suitable areas) to ensure the conservation of rare species (IV).

Material and Methods in a nutshell

This thesis is based on four papers, all concerning Mediterranean endemic plants. So, below I will briefly explain the main methods I used in the different studies. The detailed explanation of the methodological approaches implemented in the different analyses is reported in each article.

Study species

The articles I and II involve species belonging to *Santolina* genus. This genus was selected to study the evolutionary processes in the Mediterranean Basin. This Mediterranean endemic genus occurs in northern Africa (Morocco, Tunisia and Algeria), Iberian Peninsula, France and Italy. All the species are aromatic shrubs with diversification centre in the Iberian Peninsula, where the highest number of species occurs (Carbajal et al., 2017). Species within the genus are weakly defined both geographically and morphologically. *Santolina* is a diploid-polyploid genus with ploidy levels ranging from 2x (i.e., continental species of *S. chamaecyparissus* complex) to 6x (*S. villosa*). The different ploidy levels were considered in the interpretation of the results. This taxonomic complexity may result from rapid divergence, introgressive hybridisation and polyploidisation (Valente et al., 2010; Vasconcelos et al., 2020). Preferred habitats consist of garrigues, and these plants are generally pioneers occurring on degraded soils (Arrigoni 2018; Carbajal et al., 2019): the substrate preferences are not detected, even if many species occur on limestone while some on ophiolites and siliceous substrate (Arrigoni, 1982). Also, elevation range is rather wide, from 0 m a.s.l. (i.e., *S. ligustica, S. insularis, S. magonica*) to 2,000 m a.s.l. (i.e., *S. benthamiana, S. oblongifolia, S. rosmarinifolia*).

In the article III, I studied 12 plant species endemic or subendemic to the Mediterranean Basin characterized by a group of populations that is clearly geographically disjunct from the main range of the species. The distance between the two groups ranges from 30 to 500 km, spanning from Italy to the Pyrenees.

In the last article (IV), I considered 188 taxa endemic to Italy that, following the IUCN Red List Categories and Criteria, are categorized as Least Concern, Near Threatened, Vulnerable, Endangered or Critically Endangered, and represent the 14% of the Italian endemic vascular plants.

Study methods

To investigate evolution and conservation of Mediterranean endemic plant species I mainly used two different tools: molecular analysis (I), and ecological niche models (ENMs) (II-IV).

Molecular analyses were conducted to study the genome-wide phylogeny of *Santolina* (I) using restriction-site associated DNA sequencing (RADseq). This approach consists in subsampling homologous regions from the genome of several individuals with the aim of discovering and genotyping thousands of variable genetic markers that can be used for evolutionary, phylogenomic and population structure studies among others (Andrews et al., 2016). Among the reduced representation sequencing methods for generating genome-wide data, RADseq (Andrews et al., 2016) has demonstrated effective in resolving phylogenetic relationships in challenging taxonomic groups (Bombonato et al., 2020; Eaton et al., 2015; Hipp et al., 2020) and also for which no genomic resources are available (Davey et al., 2011). Moreover, RADseq has recently been used within Asteraceae with considerable success to reconstruct phylogenetic relationships within *Solidago* (Sakaguchi et al., 2018), *Phalacrocarpum* (Ruiz et al., 2021) and *Rhodanthemum* (Wagner et al., 2020).

Ecological niche models (ENMs) are a tool employed to explore the relationship between the distribution range of species and corresponding environmental variables, relying on the species-environment relationship that can explain and predict present and future species distribution (Peterson et al., 2011).

ENMs are widely used for various aims, including species conservation and assessment of climate change impact (Guisan and Zimmermann, 2000), also becoming an important management tool for identifying suitable areas to inform conservation decision and priorities (Austin, 2007; Carvalho et al., 2010). However, they usually do not consider intraspecific ecological variation exhibited by many species, among them also species with geographically disjunct populations. This lack could lead to misplacing any conservation actions: for this reason, I considered the intraspecific differentiation (III) that may enable to detect potential resilience units against climate change and thus to design targeted conservation strategies.

To combine the ENMs results with other information could lead to interesting considerations: indeed, combined with the IUCN red listing thresholds, they may provide a cost-benefit tool for planning assisted colonization and other conservation translocations (e.g., reintroduction, introduction, population reinforcement) (IV). Also including predictor variables derived from remotely sensed data improves the accuracy of the model (Pettorelli et al., 2011). Remotely sensed data provide measurements and surrogates directly related to vegetation type and structure, biomass and other ecosystem variables that collectively improve our understanding of habitat characteristics. Thus, I combined ENMs results with normalized difference vegetation index (NDVI) (II) to evaluate the role of climate and vegetation cover on the distribution of the species.

All the models were performed using different algorithms fulfilling the best-practice standards proposed by Araújo et al. (2019).

Conclusions and future perspective

In this thesis, I have investigated the evolution and conservation of Mediterranean endemic plant species, two aspects deeply connected. Indeed, to conserve the biodiversity we should aim at conserving evolutionary processes that generate it. Integrating many different complementary approaches, such as molecular and morphometrical analyses, to manage conservation practices is not an easy task, but the case studies presented in this thesis illustrate how a multidisciplinary study, which takes into account these aspects, proposes new deep information about the vulnerability and future perspective of species, allowing different management practices.

Through the study of *Santolina* genus, I explored several aspects of these complex interactions and feedbacks between genetics, evolution, and ecology: each facet enriched considerably our knowledge of the genus and set the stage for further investigations. Moreover, my study supports the idea that in groups where there is difficult to obtain a single, complete, and stable classification, a holistic approach based on the use of different and independent evidence, the so-called integrative taxonomy, may provide a reliable tool to solve taxonomic problems.

Because of increased threats across the Mediterranean region and the complex response of endemic species to climate change, it is crucial to observe, monitor and analyse changes in vegetation and plant biodiversity across ecological and environmental gradients. All the tree articles (III, IV, V) demonstrated that the ecological niche models are an important tool to identify crucial aspects for species distributions and manage habitat conservation appropriately.

Work on this argument was an exciting experience that I hope could lead to scientific benefits and benefits for the protection of biodiversity.

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Paper I

Evolutionary relationships in the taxonomically complex genus *Santolina* endemic to the Mediterranean Basin

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Abstract:

The genus *Santolina* L. (Asteraceae, Anthemidae) is distributed in the western part of the Mediterranean basin. *Santolina* has a long taxonomic history since Linnaeus (1753) described the genus and although over the years numerous studies aimed at clarifying the relationships among species, they have never led to a complete taxonomy and mostly remained limited to local studies. According to a recent taxonomic revision, the whole genus comprises 30 taxa, most of which are divided in two complexes: the *S. rosmarinifolia* one, which includes eleven taxa endemic to Iberian Peninsula and North Africa and was subject of extensive systematic and phylogenetic analysis, and the *S. chamaecyparissus* one, which includes fourteen taxa mainly narrow endemics occurring in Spain, France, and Italy. In addition, four taxa are not included in either complex. Recent diversification, incomplete speciation and/or reticulate evolution could explain the taxonomic issues related to species. Indeed, it was suggested that recurrent hybridization and polyploidization have played an important role in evolution of *Santolina*. In this study, for the first time we presented a phylogenetic analysis of the whole genus based on genetic data obtained through RADseq. We also investigated genome-wide diversity structure for evidence the reticulate evolution by computing a co-ancestry matrix between individuals with RADpainter software and by performing a principal component analysis of genotypes. To assess evidence of historical gene flow between species, we used Dsuite package performing the ABBA-BABA test.

Our phylogeny recognizes two main well-supported clades in *Santolina* roughly coinciding with the two main morphological complexes, and it confirms the monophyly of *S. rosmarinifolia* complex while *S. chamaecyparissus* complex seems to be polyphyletic. In particular, *S. villosa* belonging to the latter complex, shares common ancestor with species of *S. rosmarinifolia* complex. Our results suggests that ancient introgression may have played an important role in the evolution of *Santolina*. Moreover, we provide a first assessment of the taxonomic position of *S. africana*, a species omitted from all previous taxonomic considerations on the genus because of its mixed morphological features, now resulting sister of the *S. chamaecyparissus* complex. In conclusion, we build the first phylogenetic hypothesis for *Santolina chamaecyparissus* complex, which yields a much-increased understanding of phylogenetic relationships in this group. Taken together our results set the stage for further investigations of the evolutionary history of this circum-Mediterranean group.

Keywords: Asteraceae, diversification, endemism, Mediterranean Basin, RADSeq

Introduction

Phylogenetically complex groups are usually also taxonomically complex, with species weakly defined geographically and morphologically. The taxonomic complexity may result from rapid divergence, introgressive hybridisation and polyploidization (Valente et al., 2010; Vasconcelos et al., 2020). Moreover, in these taxonomically and evolutionary complex groups, the difficulty to classify species in stable and coherent taxa strongly affects the implementation of conservation measures for threatened, rare or endemic evolutionary significant units (Ennos et al., 2012). The study of taxonomically complex groups can thus shed new light on the role of interactions between hybridisation, genome multiplication and diversification in evolutionary processes, providing information on how to conserve the processes that lead to the generation of biodiversity.

Santolina L. (Asteraceae, Anthemidae) is a taxonomically complex genus distributed in the western part of the Mediterranean Basin, from Italian peninsula to Spain and North Africa. Linnaeus (1753) proposed seven species of which only *Santolina chamaecyparissus* L. and *Santolina rosmarinifolia* L. are still currently classified within *Santolina*. Over the centuries, several taxa of *Santolina* were described, but the studies were generally limited to single countries, except for Nyman (1879) that provided a taxonomic treatment of the genus for the whole Europe. The first taxonomic revision for the entire genus was attempted only in 1970's: indeed, Guinea (1970, 1976) tried to uniform the taxonomy by defining nine taxa and remaining nebulous on their distribution range. Thereafter, the numerous studies aiming at clarifying the relationships among species (Arrigoni, 1979a, 1977a; López-Udias and Fabregat, 2002; Marchi et al., 1979; Valdes-Bermejo and Antunez, 1981) mostly remained limited to the boundaries of each country.

According to a recent taxonomic revision (Carballal Vilaverde, 2022; Giacò et al., 2022a), the whole genus comprises 30 taxa, most of which are grouped in two complexes mainly on the basis of leaves shape. The *S. rosmarinifolia* complex includes 11 taxa endemic to the Iberian Peninsula and/or North Africa, while the S. *chamaecyparissus* complex includes 15 taxa, mainly narrow endemics occurring in Spain, France, and Italy. In addition, four taxa are not included in either complex (Carbajal et al., 2019; Greuter et al., 2003). Although the distinction between *S. chamaecyparissus* and S. *rosmarinifolia* complexes has been confirmed (Carbajal et al., 2017) there is an overall lack of phylogenetic studies on the entire *S. chamaecyparissus* complex (Carbajal et al., 2019), which was instead studied on nomenclatural (Giacò et al., 2021), morphometric (Giacò et al. 2022a), and karyological (Giacò et al., 2022b) grounds. Within these complexes the taxa circumscription is weak and morphologically some characters do not differ so clearly from one species to another (Rivero-Guerra, 2009; Giacò et al., 2022a). Recent diversification, incomplete speciation and/or reticulate evolution could explain taxonomic delimitation issues. Indeed it was suggested that recurrent hybridization and polyploidization have played an important role in evolution of *Santolina* (Rivero-Guerra, 2011; Rivero-Guerra and Laurin, 2012), as well as in other genera belonging to Anthemideae tribe (Funk et al., 2009). Hybridization and polyploidization are among the major drivers of speciation and diversification in plants (Soltis and Soltis, 2009) and they may result in complex pattern of relationship among species (Naciri and Linder, 2015). In fact, recurrent polyploidy and hybridization make extremely difficult a clear species delimitation in several representative polyploid complexes of Anthemideae (Oberprieler et al., 2018; Padilla-Garcia et al., 2018).

Recently, the *S. rosmarinifolia* complex has been the subject of an extensive systematic analysis (Rivero-Guerra, 2011) and morphology-based phylogenetic analyses suggested that it could be monophyletic (Rivero-Guerra and Laurin, 2012). This complex is divided in two main morphological clades which could be hypothetically considered as two evolutionary lineages. The first one, occurring in the central and south-eastern part of Iberian Peninsula, comprises *S. pectinata* Lag. and *S. ageratifolia* Barnades ex Asso and the second one, occurring in the central and north-west part of the Iberian Peninsula, comprises the other remaining taxa. However, Rivero-Guerra (2011) suggested that the poor morphological differentiation of these clades and generally of taxa belonging to *S. rosmarinifolia* complex and ensuing taxonomic complexity is due to recurrent hybridization and lack of geographical isolation between taxa. On the contrary, studies aimed at untangling species relationship for *S. chamaecyparissus* complex are few (De Giorgi et al., 2022; Giacò et al., 2023) and based on morphological and karyological evidence (Arrigoni, 1977b, 1979b; Giacò et al., 2022b; López-Udias and Fabregat, 2002). This complex occurs in different countries and systematic studies were carried out by local botanists only on part of the taxa. For instance, the Italian taxa belonging to *S. chamaecyparissus* complex have been considered as varieties or subspecies of *S. chamaecyparissus* for a long time (Bertoloni, 1847; Fiori, 1927; Fiori and Paoletti, 1903) and only in the second half of 20th century Arrigoni (1979b) recognized six species in Italy.

Species relationships within the whole genus of *Santolina* have never been investigated using molecular-based phylogenetic analyses and an overview of the evolutionary history of the genus is currently lacking. For these reasons, we investigate in this study the genome-wide phylogeny of *Santolina* using restriction-site associated DNA sequencing (RADseq) and a dense sample of *S. chamaecyparissus* complex taxa (90% of taxa). Among the reduced representation sequencing methods for generating genome-wide data, RADseq (Andrews et al., 2016) has demonstrated effective in resolving phylogenetic relationships in challenging taxonomic groups (Bombonato et al., 2020; Eaton et al., 2015; Hipp et al., 2020; Massatti et al., 2016). Moreover, RADseq has recently been used within Asteraceae with considerable success to reconstruct phylogenetic relationships within *Solidago* (Sakaguchi et al., 2018), *Phalacrocarpum* (Ruiz et al., 2021) and *Rhodanthemum* (Wagner et al., 2020). Our aims are to: (a) provide the first genome-wide based phylogeny of *Santolina*, gaining new insights into the relationships inside the *S. chamaecyparissus* complex, (b) investigate the role of hybridization in the evolution of *Santolina*.

Materials and methods

Plant material

We used material collected from 24 species of *Santolina* and three species selected as outgroup (Table S1 Mat. Sup.). Two of them belong to the tribe of Anthemideae, as *Santolina* (*Achillea millefolium* L., and *Tanacetum vulgare* L), one belongs to Senecioneae (*Euryops pectinatus* L.). We selected those species accepted in the Med-Checklist (Greuter et al., 2003) plus the three recently revised species *S. ericoides* Poir. (Pablo Ferrer-Gallego et al., 2021), *S. vedranensis* (O.Bolós & Vigo) L.Sáez, L.Sáez, M. Serrano, S. Ortiz & R. Carbajal (Carbajal et al., 2017), and *S. fruticosa* (Maire) R. Carballal, M. Serrano & S. Ortiz comb. & stat. nov. (Carbajal, 2022). Five species are missing because the leaf material needed for analysis could not be obtaines (*S. adscensionis* Sennen ex Maire; *S. virens* Mill.; *S. ageratifolia* Bernades ex Asso; *S. montiberica* (Riv-Guerra) R. Carballal L. Saez, M. Serrano & S. Oritz; *S. subclausa* (Linder) R. Carballal, M. Serrano & S. Ortiz). One species, *Santolina intricata* Jord. & Fourr., was excluded due to ongoing investigation regarding its taxonomic position at the time of our analysis (Giacò et al., 2022c). The different ploidy levels were considered in the interpretation of the results. A map of collected material is shown in Fig. 1.

DNA extraction, genomic library preparation and sequencing were conducted by Microsynth ecogenics GmbH (Blagach, Switzerland). The DNA was extracted from silica dried leaf materials from a total of 95 individuals (Table S1 Mat. Sup.) (92 individuals of *Santolina* and three individuals belonging to the outgroups) using NucleoSpin® 96 Plant II (Macherey Nagel). DNA extracts (200 ng input) were digested with the restriction enzymes EcoRI/MSeI following heat inactivation according to the manufacturer's protocol (New England Biolabs, NEB). Fragments between 500 and 600 bp were selected by automated gel cut, Illumina Y-shaped adaptors were ligated, and ligation products were bead purified. Each library was then individually barcoded by PCR using a dual-indexing strategy. Individually barcoded libraries were pooled and subsequently purified before single-end sequencing on an Illumina NextSeq platform (200 millions of 150 bp reads per run).

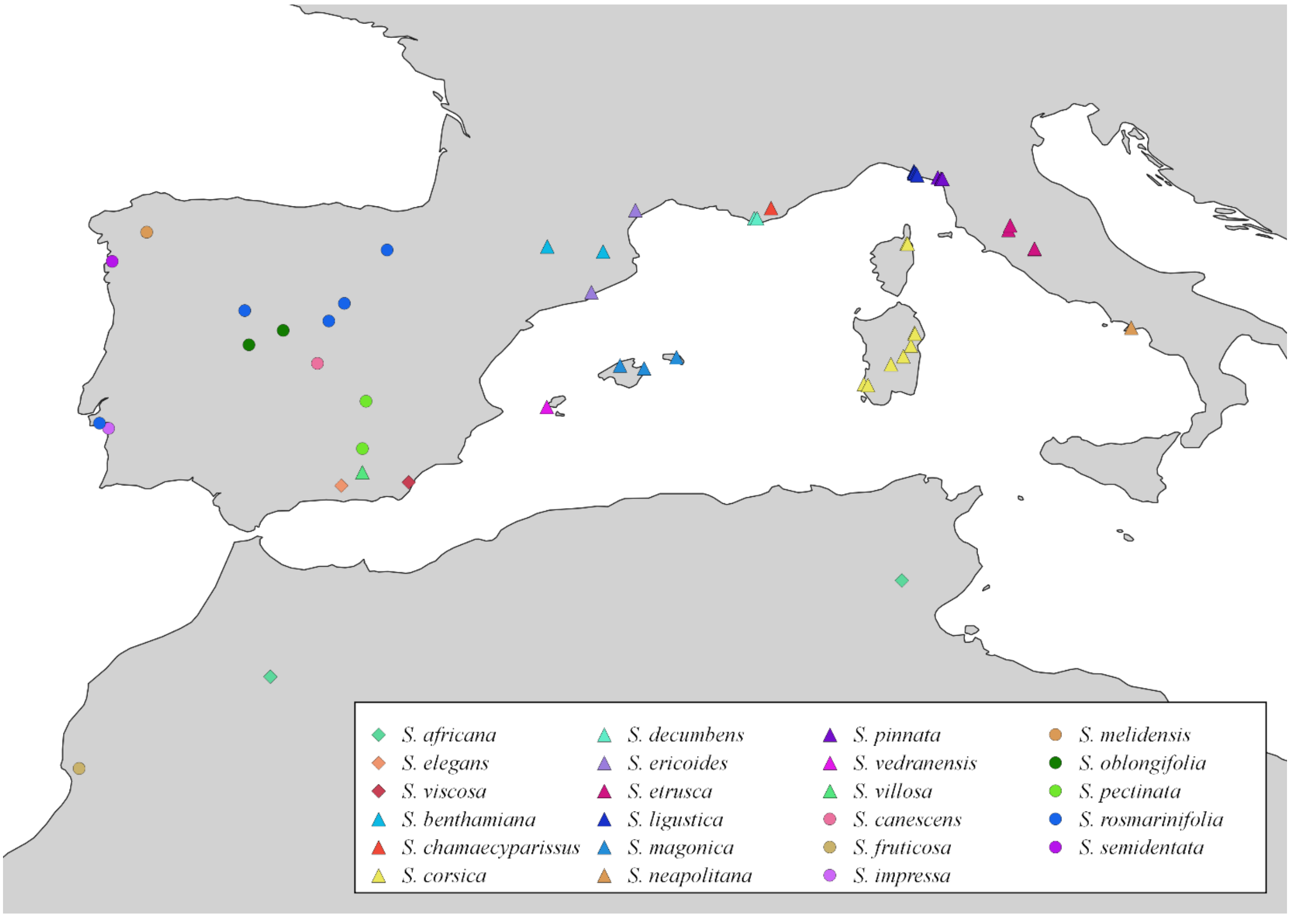

Figure 1: Map of Santolina samples collected from 24 species.

Bioinformatic pipeline to extract and filter SNPs from RADseq data

Quality of the reads was checked using FASTQC (multiqc) (Ewels et al., 2016) and samples with low coverage sequencing (i.e., less than 0.7 millions reads) were excluded after a preliminary assembly. Only the samples that passed the quality control were used in our subsequent analyses. Assembly was performed using IPYRAD software (v. 0.9.74, Eaton and Overcast, 2020) in the high-performance computing cluster OSU PYTHEAS (Aix Marseille University, Marseille, France). Following seven sequential steps, the raw data were demultiplexed, quality filtered and assembled with the IPYRAD pipeline (Eaton and Overcast, 2020). We conducted nine *de novo* assemblies using different combinations of: a) thresholds of clustering (0.85, 0.90, 0.95), because phylogenetic results are known to be sensitive to the similarity threshold employed for within-sample and across- sample sequence clustering (Mastretta-Yanes et al., 2015; Shafer et al., 2017; Takahashi et al., 2014); and b) minimal samples per locus (12, 24, 32). The other parameters required for assembly were kept by default: to avoid including potential paralogs, we excluded all loci with more than two alleles per individual, putative loci with heterozygous sites for more than 50% (in fact, heterozygous loci shared in many individuals potentially reflect clustering of paralogs rather than true heterozygous sites), or more than eight indels. For the nine datasets, we reported IPYRAD summary statistics such as error rate, heterozygosity, the number of RAD loci, the total number of SNPs and the missing data rate.

Phylogenetic analysis

Maximum likelihood (ML) phylogenetic inference was performed for each concatenated RADloci matrices resulting from the several datasets using. To conduct best molecular evolution model search and the ML phylogenetic analysis, we used a supermatrix approach with whole sequences of each loci and IQ-TREE software (Nguyen et al., 2015) setting 1,000 replicates of single branch test, 0.75 as perturbation strength for randomized NNI (nearest neighbor interchange), 1,000 as number of unsuccessful iterations to stop. We also estimated node robustness by ultrafast bootstrap analysis (1,000 iterations), writing the trees with branch lengths (adding *-wblt* option). Moreover, we used Quartet Sampling method (QS, Pease et al., 2018) to estimate the robustness of resolved relationships and select the dataset having the highest phylogenetic robustness. The QS method measures branch support in large sparse alignments by randomly sampling one taxon per subset to produce a quartet phylogeny. Discordance among topology of each quartet is evaluated by four metrics: quartet concordance (QC), quartet differential (QD), quartet informativeness (QI), and quartet fidelity (QF). These metrics allow the effective assessment of branch-related (QC, QD, and QI) and taxon-related (QF) discordance in the dataset. We performed Quartet Sampling on all datasets and the respectively resolved topologies, setting to 2 the minimum likelihood differential between the best and the second-best likelihood quartet tree and using 100 replicates per branch.

Based on the above-mentioned quartet scores, we kept the dataset with 0.95 as thresholds of clustering reads and 12 as minimal samples per locus for all the following analyses. On this data set we produced three phylogenetic trees: the IQ-TREE ML tree and two coalescent-based trees produced by the SVDquartets (Singular Value Decomposition Scores for Species Quartets) method (Chifman and Kubatko, 2014) implemented in PAUP* (Swofford, 2002). The first SVD tree was produced at the individual level, then after checking the congruence with the IQ-TREE ML tree, we performed a species phylogenetic tree using the SVDquartets method with samples grouped according to the 19 species. All possible quartets were analysed and node support was assessed based on 1,000 bootstrap replicates. We used the “distribute” option for heterozygous sites.

Detection and test of hybridization

In complement to phylogenetic analyses, we investigated the genome-wide diversity structure by computing a co-ancestry matrix between individuals with RADpainter software based on haplotype sequence differences (Malinsky et al., 2018). Because RAD loci were not mapped on a reference genome, we used the LD script, provided with RADpainter, to reduce as recommended the effect of linkage disequilibrium. After this step we used RADpainter with default settings to compute a co-ancestry matrix among each genotype. The matrix was re-organized in respect with the phylogenetic tree obtained with IQ-TREE and then used it to build a heatmap displaying shared ancestry among individuals using a custom R script.

To assess evidence of historical gene flow between species, we performed an ABBA-BABA test using Dsuite package (Malinsky et al., 2021). This test, used also for detection of polyploid hybrid speciation (Hühn et al., 2023), creates a four-taxon topology ([{P1, P2}, P3], O), for comparing the relative proportions of the derived traits that are shared by two lineages. The outgroup (O) is used to identify the ancestral allele (A) and the derived allele (B), and the site patterns (i.e., ABBA, BABA, BBAA) are counted among the SNPs. A significant Dstat value in Dsuite software indicates a bias in favor of the ABBA model, that is a contribution of P3 (donor) to P2 (receiver). For this analysis, we filtered the dataset to keep one SNP by locus and only SNP present in at least 8 samples. The tests were fitted onto the SVD quartet-based species phylogeny obtained previously and therefore provide a formal test of admixture into this phylogenetic context. The Outgroup (P4) chosen was *S. africana* Jord. & Fourr. because setting *A. millefolium*, *E. pectinatus*, and *T. vulgare* as outgroups limited too much the number of SNPs for the tests. The results were filtered to reduce the risk of false-positive: we selected only P2-P3 pairs with *Zscore* higher than 3 (all Pval < 0.01). Finally, the table of Dstats (Tab. S4 Mat Sup) was used to make a heatmap organized according to the species phylogeny.

Results

An average of 2,327,827 reads per sample was generated. After quality filtering using FASTQC, we retained 19 *Santolina* species and the three outgroup species to conduct the *de novo* assemblies on 46 samples. After filtering steps, the average number of retained loci varied between 109,715 (c085msl12) and 211,781 (c095msl12). The number of parsimony informative sites ranged between 7,017 (c085msl32) and 90,474 (c095msl12; Tab. S2 Mat. Sup.). Then, the selected dataset (c095msl12; Tab. S3 Mat. Sup.) contained 211,781 loci, 2,648,394 nucleotide sites (59% missing) of which 45,195 were parsimony informative.

Phylogenetic analysis

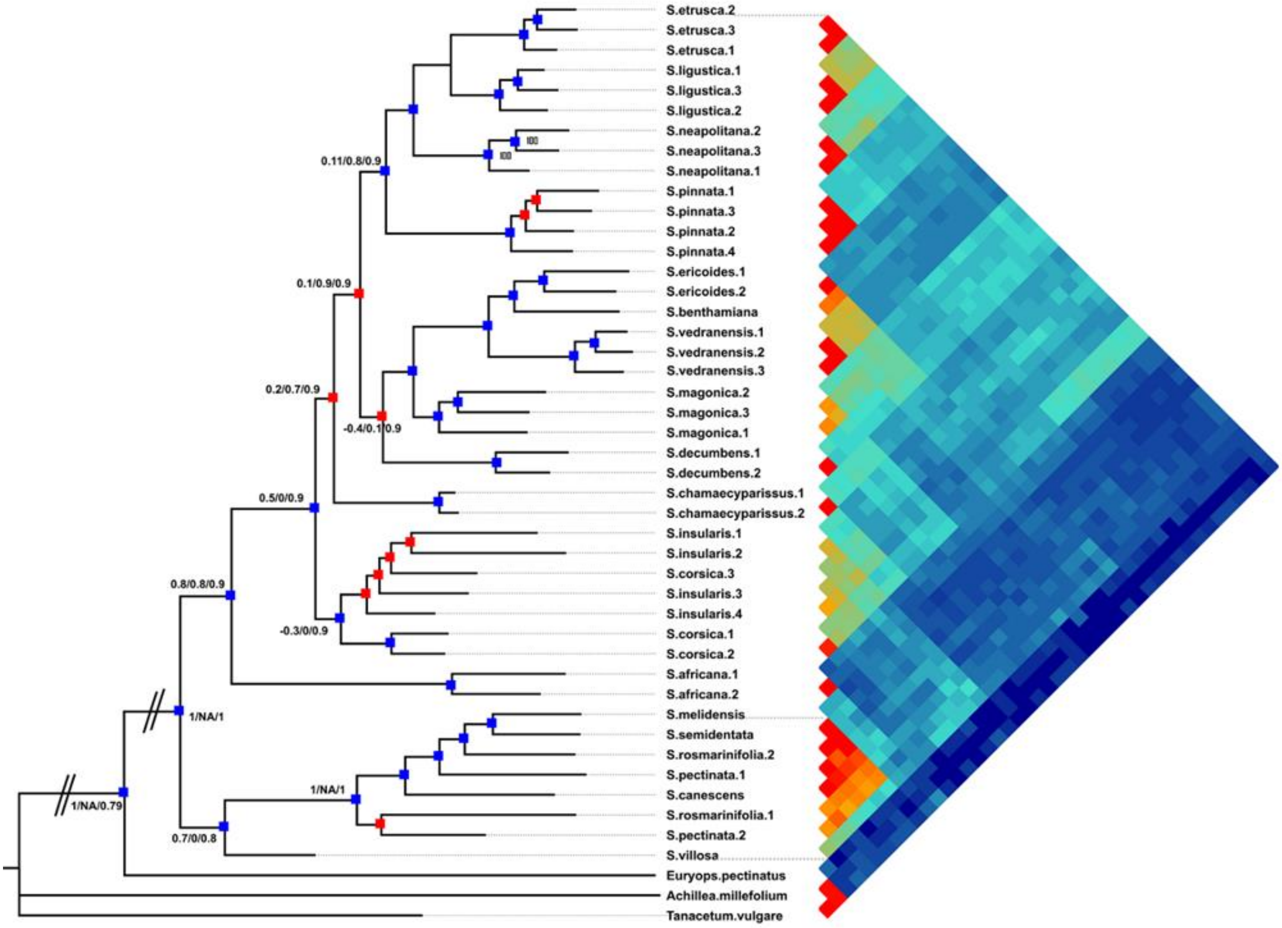

Figure 2: Genome-wide phylogenetic relationships versus co-ancestry matrix of Santolina RADseq data. The maximum likelihood tree (left) was obtained with IQ-TREE and based on a concatenated alignment of 17,806 RAD loci, derived from a further filtering aimed to retaining one SNP per locus, occurring in at least 8 samples (2,648,394bp, 45,195 parsimony informative sites, 59% of missing data) and a TVM+F+I+G4 model. Blue squares are indicating robust nodes (ultra-fast bootstrap values above 95%), red squares are indicating weak nodes. Numbers near the nodes are the Quartet Sampling estimate of robustness (QC/QD/QI), a tree with all QS values is available in Fig. S1 Mat. Sup. The RADpainter co-ancestry matrix (right) was ordered according to the IQ-TREE phylogeny (left) obtained on the same dataset. Genetic similarity between pairs of genotypes increases from blue to orange values.

According to the BIC criterion, IQ-TREE selected a TVM+F+I+G4 model and produced a phylogeny overall well supported by ultrafast bootstrap and Quartet Sampling robustness estimates (Fig. 2). Quartet Sampling inferred a consistently high QI (0.78-1) over the entire topology, suggesting that most of the quartets computed for a given branch are informative for the concerned branch. All the species belonging to the *S. rosmarinifolia* complex form a well-supported clade (Fig. 2). All but one species belonging to *S. chamaecyparissus* complex fall in a well-supported clade with *S. africana* as sister species. Indeed, *S. villosa* Mill., belonging to the *S. chamaecyparissus* morphological complex, is sister of the *S. rosmarinifolia* clade. The individuals of *S. corsica* Jord. & Fourr. from Sardinia fall in a clade with *S. insularis* (Gennari ex Fiori) Arrigoni (endemic to Sardinia). These two species form a clade sister to the species growing on the Italian peninsula. *Santolina pinnata* Viv. is sister to all the other Italian peninsular species. S*antolina decumbens* Mill., endemic to southern France, is sister to Iberian species (*S. benthamiama* Jord. & Fourr., *S. ericoides, S. vedranensis* (O.Bolós & Vigo) L.Sáez, M. Serrano, S. Ortiz & R. Carbajal, *S. magonica* (O.Bolòs, Molin. & P.Monts.) Romo. Moreover, *S. vedranensis* (endemic to Es Vedrà, Ibiza – Spain) clusters with species growing in the Pyrenees area.

The ML tree (Fig. 2) is almost identical to the SVD quartet phylogeny based on individuals (Fig. S1 Mat. Sup.). The main difference between the two trees is that in SVDquartets *S. corsica* from Sardinia and *S. insularis* fall in a well-supported clade (95%) and *S. corsica* from Corsica falls in a different clade. In ML tree all *S. corsica* and *S. insularis* fall in a well-supported clade.

The deep nodes are particularly well supported by both bootstrap and Quartet Sampling. Low values of QC were found in the central region of the tree indicating phylogenetic conflicts according to QC values (QC low) not caused by a lack of information (QI near 1), but by a phylogenetic conflict with one more supported alternative topology (QD low). In both complex the values become more stronger ascending to species subdivision.

Detecting hybridization and distinguishing it from incomplete lineage sorting

RADpainter analysis revealed genotypes groups of co-ancestry decreasing according to phylogenetic distance (red to turquoise squares). The *S. rosmarinifolia* and *S. chamaecyparissus* complex have a low co-ancestry (blue square) supporting the phylogeny and their deep genetic divergence (excepted for *S. villosa*, see below). The genotypes of the *S. rosmarinifolia* complex shown high level of co-ancestry supporting the phylogenetic closeness of these species. Species of *S. chamaecyparissus* cluster are genetically more heterogeneous and form multiple subclusters: the Italian peninsular species; the plants from Sardinia and Corsica, and French and Spanish species together.

Within the *S. chamaecyparissus* clade, but also between it and *S. villosa*, co-ancestrality as well low QC values suggest either introgression or incomplete lineage sorting. The ABBA-BABA tests (Fig. 3) confirmed the role played by introgression. The degree of introgression varies among species, being generally greater in *S. insularis/S. corsica*, *S. chamaecyparissus* and *S. benthamiana* with the *S. rosmarinifolia* complex and between *S. decumbens* and Italian species. Medium-low values of introgression were found between the Italian peninsular species (except for *S. pinnata*) and *S. magonica*. Significant introgression was also detected between *S. villosa* and almost all the species of *S. chamaecyparissus* complex.

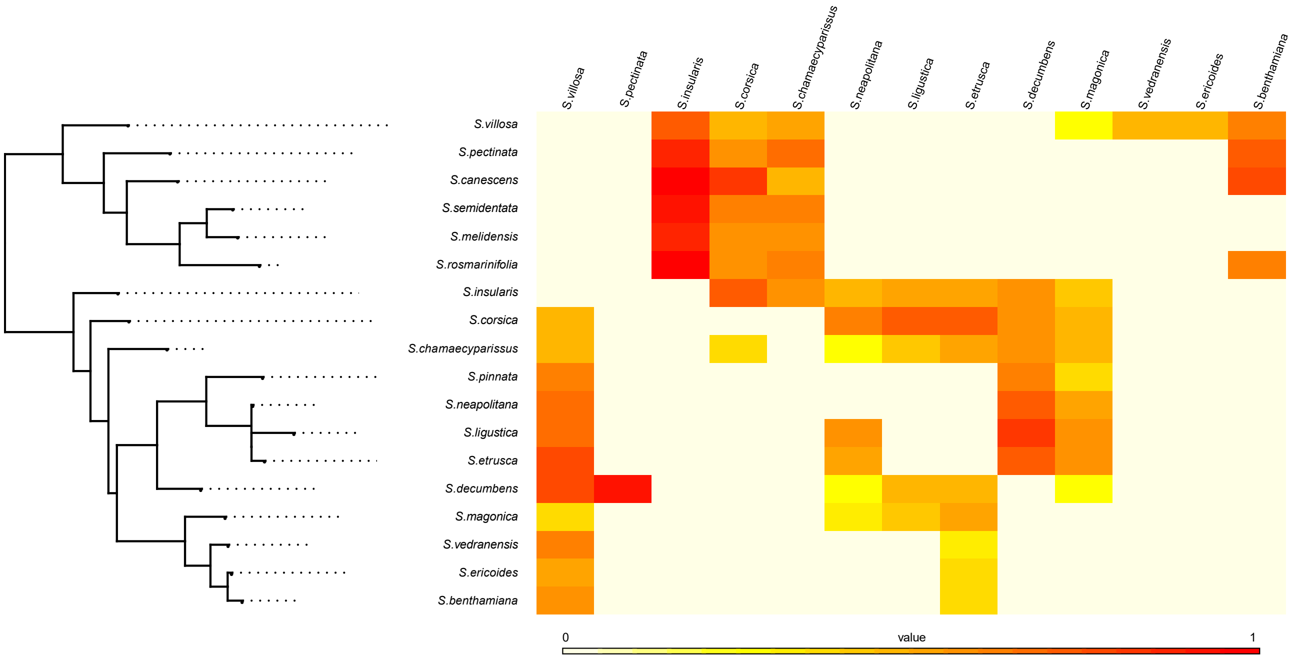

Figure 3: ABBA-BABA tests of introgression performed with Dsuite on 16,455 unlinked SNPs to test for introgression between Santolina species, only Dstat with Zscores above three were kept. S. africana was chosen as outgroup (P4) in the quartets and the analysis was conducted according to a species phylogenetic tree (left, SVD quartet tree). Positive Dstat scores (p-value>0.1) are indicating an excess of ABBA pattern and an introgression from donors (P3 in columns) to receivers (P2 in rows).

Discussion

In this study we presented for the first time a robust and genome-wide based phylogeny of the whole genus of *Santolina* relying on 19 species. Moreover, we also confirmed the role of hybridization and introgression in the evolution of the *Santolina*. Thus, our study improves the understanding of the phylogenetic relationships within the whole genus *Santolina*.

Phylogenetic relationships in Santolina

Our analysis corroborates the results of previous morphological analyses (Giacò et al., 2022a; Greuter et al., 2003; Jordan and Fourreau, 1868), confirming the existence of two main clades, one corresponding to the *S. rosmarinifolia* complex, which is monophyletic and the second to the *S. chamaecyparissus* complex which monophyletic if *S. villosa* is excluded. The latter species is assigned to the *S. chamaecyparissus* complex on a morphological basis, but according to our analysis it is found in an early branching position of the *S. rosmarinifolia* clade (Fig.2) with strong support (BS > 98%, QC 0.7). *Santolina villosa* is the only continental species of the S. *chamaecyparissus* complex that is reported both as tetraploid ($2n = 4x = 36$) and hexaploid ($2n = 6x = 54$), differently to the other species that are diploid (Afzal-Rafii and Vianot, 1985; Arrigoni, 1977a; Valdes-Bermejo and Antunez, 1981). In our analysis, we included an hexaploid individual of this species. According to a recent cytological study (Giacò et al., 2022b), *S. villosa* is supposed to be allopolyploid. Thus, the phylogenetic position of *S. villosa* is probably explained by its hybrid origin involving parents from the two clades. In particular, the tetraploids and the hexaploids of *S. villosa* occur in central-eastern and in southern Spain respectively, where most of the species belonging to the *S. rosmarinifolia* complex occur. So, the hexaploids of *S. villosa* may have been originated from a *S. villosa*-like ancestor belonging to *S. chamaecyparissus* clade and an ancestor belonging to the *S. rosmarinifolia* clade. Eventually, the inclusion of more individuals of *S. villosa* both hexaploids and tetraploids as well as analyses of chloroplast genes may further elucidate the evolution of this polyploid species.

According to our analyses, *S. africana* is sister to the *S. chamaecyparissus* clade and shows a low, but non null, co-ancestry with the *S. rosmarinifolia* clade. The taxonomic position of *S. africana* has long remained doubtful due to mixed features typical of both *Santolina* and *Chamaemelum* (Oberprieler, 2002). This species was originally described as *Santolina* by Jordan and Fourreau (1903, 1868), then in 1926 it was recombined by Maire under *Ormenis*, which at that time it included *Chamaemelum*. Oberprieler et al. (2002) pointed out that *S. africana* was sister to *S. rosmarinifolia* and that, consequently, the features shared with *Chamaemelum* should be interpreted as a symplesiomorphy. However, they included in the study only one another species of *Santolina* (i.e. *S. rosmarinifolia*). For this reason, they suggested performing further analyses including more species of *Santolina* to elucidate the proper classification of this species. Our data-rich analyses confirm that *S. africana* is indeed a *Santolina* species and revealed that it shares an ancestor closer to the *S. chamaecyparissus* clade rather than to *S. rosmarinifolia* clade. This result is in line with the previous observed similarity of this species with species belonging to the *S. chamaecyparissus* complex on the basis of its morphological features, in particular leaves of sterile stems well-markedly dentate and arranged in 4–6 series (Jordan and Fourreau, 1868). However, its incomplete differentiation from the *S. rosmarinifolia* clade can not be ruled out regarding co-ancestry values. ABBA-BABA tests without a phylogenetic guide (non-shown here) suggest that an ancient introgression between *S. africana* ancestor and the *S. rosmarinifolia* clade could be also possible.

Hybridization in Santolina

ABBA-BABA test, corroborated by low values of QC in the middle of the tree, supports that ancient admixture events involving extant taxa and/or extinct lineages have occurred within *Santolina*. In particular, our results showed that frequent hybridization events took place within the *S. chamaecyparissus* complex and between the two complexes. Hybridization and introgression have likely resulted in poorly defined species boundaries within *Santolina*, resulting in the long history of taxonomic uncertainty of this genus. Introgression resulting in poorly defined species is exemplified by the Italian peninsular species. These species were firstly included as varieties (Fiori, 1927; Fiori and Paoletti, 1903) or subspecies (Guinea 1970, 1976) of *Santolina chamaecyparissus.* They were recognized as different species by Arrigoni (1979), and recently they have been object of taxonomic revisions (Giacò et al., 2022c).

The introgression between the two early diverging lineages (i.e., *S. rosmarinifolia* and *S. chamaecyparissus* clades) was probably a crucial factor supplying the genetic diversity required for the radiation of *Santolina* lineages, particularly in the sympatric species of the *S. rosmarinifolia* complex. In fact, adaptive radiation and sympatric speciation may be facilitated by genetic variants that are older than the radiations themselves, via the reassembly of these old genetic variations into new combinations (Marques et al., 2019). The introgression between early diverging lineages, de-novo mutations and sorting of ancestral variation through speciation processes can promote rapid diversification and speciation in coincidence with ecological opportunity (Barrier et al., 1999; Caujapé-Castells et al., 2017; Lindqvist and Albert, 2002; Pease et al., 2016). Moreover, in the *S. chamaecyparissus* complex, where species are geographically isolated, ancient admixture followed by allopatric isolation in different ecological condition may have provided a suitable context for the isolation of hybrid lineages from parental populations and their persistence over time (Duenez-Guzman et al., 2009; James and Abbott, 2005; Noguerales and Ortego, 2022).

The phylogenetic position close to the *S. rosmarinifolia* clade and the high level of introgression with several *S. chamaecyparissus* lineages detected in the hexaploid of *S. villosa* may be explained with its supposed allopolyploid origin. Genome promiscuity is generated wherever different diploid lineages meet each other and give rise to tetraploids and whenever they meet other tetraploids to produce hexaploids. In allopolyploid species, the genomes of the parents may coexist for a long time without undergoing significant changes (Ainouche et al., 2004; Kryvokhyzha et al., 2019). Therefore, the high level of admixture detected in the hexaploid *S. villosa* can be explained by the maintenance of ancient introgressions favoured by genomic redundancy in polyploids.

Phylogenetic relationships within the S. chamaecyparissus complex

Within the *S. chamaecyparissus* clade, the plants from Corsica and Sardinia (i.e. *S. corsica*) are sister of the other species of the *S. chamaecyparissus* clade and one individual of *S. corsica* s.str. falls in the clade with the individuals of the formerly *S. insularis*. This result is in accordance with previous findings (Angiolini and Bacchetta, 2003; De Giorgi et al., 2022) suggesting that S. *corsica* ($2n = 4x = 36$) and *S. insularis* ($2n = 6x = 54$) are two cytotypes of the same species. Much uncertainty remains about the placement of *S. chamaecyparissus*, a cultivated pentaploid of unknown origin, that in SVD quartet tree (Fig. 1) is inferred to be close to *S. corsica/S. insularis* and in the ML tree (Fig.2) is inferred to be sister of the remaining species of the *S. chamaecyparissus* clade. However, the relationship we detected among *S. chamaecyparissus* and *S. corsica/S. insularis* is in line with a recent karyological study on this complex suggesting that *S. chamaecyparissus* is an allopolyploid and that at least one of the parental species is related to *S. corsica/S. insularis* (De Giorgi et al., 2022).

All the diploid species from the Italian peninsular fall in a well-supported clade [i.e. *S. pinnata*, *S. etrusca* (Lacaita) Marchi & D’Amato, *S. ligustica* Arrigoni and *S. neapolitana* Jord. & Fourr.] with *S. pinnata* sister of the other species. The distinction between *S. pinnata* and the other peninsular species is in line with the observations of Arrigoni (1979), which considered *S. pinnata* as a species more distinct from the other because of the absence of hairs, the bare stems in the upper part, the flowers single and white. Among the remnant Italian peninsular species, the most closely related are *S. etrusca* and *S. ligustica*, while S. *neapolitana* is sister of this group. These three species grow in allopatry in the Apennines (from Sorrento peninsula to Liguria) and are distinguished mainly for the color of flowers ranging from deep yellow to white.

The species ranging from southern France to Spain are closely related. The easternmost species *S. decumbens* diverged early in the clade, while the two westernmost species *S. ericoides* and *S. benthamiana* are closely related. Using NGS approach it was finally possible to recover the two lineages even though in previous analysis was demonstrated the impossibility to distinguish these species on molecular grounds (cpDNA) despite their clear morphological diagnosability (Giacò et al., 2022d)(Giacò et al., 2022a). Interestingly enough the two species occurring in the Balearic Islands are not closely related. This result conflicts with the previous studies that considered *S. vedranensis* as taxonomically related to the Balearic endemic *S. magonica* (Bolòs i Capdevila and Vigo, 1987; Romo i Díez and Sierra Ráfols, 1994) and gives further support to the study suggesting that *S. vedranensis* is closely related to the Iberian continental species (Carbajal et al., 2017). In particular, our phylogeny suggests that *S. vedranensis* (Islet of Es Vedrà, Ibiza) shares a common ancestor with *S. ericoides* and *S. benthamiana*, while *S. magonica* (Mallorca and Menorca) diverged early, pointing to a double colonization process of Balearic Islands from mainland.

Conclusion

Our findings provide a comprehensive picture of the phylogeny of *Santolina*. Our phylogeny recognizes two main well-supported clades in *Santolina*, roughly coinciding with the two main traditionally recognized morphological complexes. Moreover, our results suggest that ancient introgression may have played an important role throughout in the diversification of *Santolina*. We provide also a first assessment of the taxonomic position of *S. africana*, a species omitted from all taxonomic considerations on the genus because of its mixed morphological features. Moreover, we provide further evidence about the allopolyploid origin of *S. villosa*. Finally, we build the first phylogenetic hypothesis for *Santolina chamaecyparissus* complex, which yields a much-increased understanding of phylogenetic relationships in this group. Taken together our results set the stage for further investigations of the evolutionary history of this western Mediterranean group.

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Paper II

Santolina ligustica Arrigoni: how climatic suitability and vegetation cover influence the distribution

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Abstract:

Santolina ligustica Arrigoni is a rare endemic species of Liguria (North-west of Italy) and its distribution range is reducing over the past few years. Using species distribution models, land cover and normalized difference vegetation index (NDVI) data, we investigated the relative role of climate and vegetation in determining the distribution, namely how climate and vegetation cover changes may affect the distribution of the species. We observed a high range turnover in the last twenty years, related to change in climatic conditions. In addition, we observed that the overall habitat suitability slightly decreased over the past fifty years. The NDVI, based on the relationships between the absorption of the red radiation by photosynthetic pigments and the scattering of the near-infrared radiation caused by foliage, highlight – together with the land cover – the increasing in forest, shrubs, and built-up areas in the lost areas from 1970s until today. This greatly influences the distribution of *S. ligustica* that is generally located in sunny habitats. Our analysis evidence that the detected change in the species distribution was probably due to the interaction between climate and vegetation cover dynamics and, generalizing, climate change and land cover change interact to impact biodiversity with a wide range of mechanisms.

Key words: Asteracee, Endemism, Land Cover, NDVI, Species Distribution Models

Introduction

The Mediterranean Basin has long been recognized as one of the world's hotspots of plant biodiversity (Myers et al., 2000) hosting 10% of the world's vascular plants in an area that represents only 1.6 percent of the Earth's surface (Medail and Quezel, 1999). In particular, this hotspot is one of the richest in plant endemisms, being second to the tropical Andes with 13,000 endemisms (Myers et al., 2000). The high richness of this area is not only due to its environmental features but also to human activities that have affected environmental components and dynamics for centuries (Bagella et al., 2014; Blondel, 2006) . However, despite conservation efforts, its diversity is still highly threatened (Le Roux et al., 2019; Pimm et al., 1995). In fact, Mediterranean regions are disproportionately affected by climate change and land use changes (Newbold et al., 2020). In particular, change in land use is considered the main current driver of biodiversity loss (Sala et al., 2000; Zedan, 2004) because it is expected to be a major threat in the short term, whereas climate change will be more important on a longer time scale (Thuiller, 2007). However, relatively few studies have addressed how recent land-use change and human induced climate change have already affected present day species distributions.

The hilly areas of Liguria (N Tyrrhenian) underwent an intense change in land use during the second half of the 20th century, with the development of mass-oriented tourism in the post-war period. Since then, strong changes have occurred both in the vegetation cover (Roccati et al., 2018) and in landforms (Brandolini et al., 2017). In addition, a dramatic increase in temperatures has been observed since the 1980s (Fratianni and Acquaotta, 2017). It was recently recognized that species with restricted geographic range occurring in this area seem to be particularly prone to climate change effects (Casazza et al., 2014). Restricted range species are expected to be especially sensitive to climate changes due to their narrow ecological niche, circumscribed distribution and high habitat specificity (Essl et al., 2009). Furthermore, the low dispersal ability of most of these species affects their ability to keep up with ongoing environmental change (Engler et al., 2009; Ozinga et al., 2009).

In recent decades, species distribution models (SDMs) have come to the fore as tools to predict the distribution of species under different climates (Austin, 2007; Carvalho et al., 2010; Casazza et al., 2021; Raven, 2002). SDMs relate species occurrences to environmental data, usually climatic, to estimate the species' ecological requirements and project it in geographical space (Guisan and Zimmermann, 2000). Normalized difference vegetation index (NDVI) has been largely used to perform aboveground biomass and vegetation features assessments (Huang et al., 2021). NDVI is an index of primary production calculated from near-infrared (NIR) radiation (which vegetation strongly reflects) minus red radiation (which vegetation absorbs) divided by near-infrared radiation plus red radiation (Kriegler et al., 1969).

In this study we focused on *Santolina ligustica* Arrigoni, an endemic species with a narrow distribution, occurring on ophiolitic soils in the Eastern Riviera of Liguria. Despite no specific threats have been detected (Conti et al., 1997; Rossi et al., 2020), the species is rare (Conti et al., 1992), and its distributional range is diminishing rapidly (Torricelli et al., 1999). In this study we used SDMs and vegetation assessment by means of land cover mapping and NDVI analysis to unravel the relative role of climate and vegetation in determining the distribution of *S. ligustica*. In particular, we asked whether areas where the species has persisted over time, areas where the species has become extinct and areas where the species has migrated differ in terms of climatic suitability and vegetation features.

Material and methods

Study area and taxa

Santolina ligustica (Asteraceae) is a dwarf aromatic shrub with small capitula that grows in sunny pseudogarigues mostly on ophiolitic outcrops between Deiva Marina and Riomaggiore (Liguria, Northwestern Italy) from the coast up to 600 meters of altitude (Torricelli et al., 1999). As the other *Santolina* species of the Italian peninsula, *S. ligustica* is diploid (2n=18) but it differs from the other species for bearing white instead of yellow flowers and for having narrow sized capitula and tomentose branches (Arrigoni et al., 1980).

The species occur in an area characterized by a Mediterranean climate with summer droughts and four months with mean temperatures >20°C (Fratianni and Acquaotta, 2017). Part of the study area has been included in the Cinque Terre National Park since 1995. The areas where our study species occurred in the past were obtained from the literature (Torricelli et al., 1999). The areas where the species currently occurs were obtained from field surveys carried out in 2020 and 2021: we marked with GPS population distribution limits and then calculated the convex . The polygons encompassing the distribution of the species were rasterized using the same resolution of climatic and vegetation rasters. In total, we obtained 4,380 cells where the species was present in the past and 3,964 cells where the species is present today. We then intersected the past and current distribution to identify lost, gained and stable areas.

Bioclimatic variables

We downloaded nineteen bioclimatic variables for current (2000-2016) and past (1970-1990) timeframes at about 1x1 km spatial resolution from CHELSA v.1.2 dataset (Karger et al., 2017a; 2017b; www.chelsa-climate.org). To reduce collinearity and to minimize model overfitting, we removed highly correlated variables ($r \leq |0.80|$) performing a pairwise Pearson correlation between bioclimatic predictors. For the analysis, we retained the five least-correlated variables physiologically important for the species: mean diurnal range, minimum temperature of the coldest month, precipitation seasonality, precipitation of driest quarter, precipitation of coldest quarter (BIO2, BIO6, BIO15, BIO17, BIO19 respectively).

Because coarse-scale models may underestimate suitable areas in regions with high topographic heterogeneity by not taking microclimatic conditions into account, we statistically downscaled each selected predictor (for the past and the current timeframes) at 30-m resolution. We used a physiographically informed model fitted with a geographically weighted regression (GWR) technique (Fotheringham et al., 2003), as implemented in Lenoir et al. (2017). We calculated slope, eastness (as sin(aspect)), northness (as cos(aspect)) by using the terrain function in the R package “raster” and the distance from the coast. Then, we used GWR models to interpolate climatic variables on the physiographic variables previously calculated.

Species distribution models

Species distribution modelling was performed in R (R Core Team, 2019) using six different modelling techniques implemented in the ‘biomod2’ package (Thuiller et al., 2016). These modelling techniques belong to three different model classes, *i.e*., two machine learning methods (generalised boosted models—GBM, Ridgeway 1999, and random forest—RF, Breiman 2001), two regression methods (generalized linear models—GLM, McCullagh and Nelder 1989, and multivariate adaptive regression splines— MARS, Friedman 1991) and two classification methods (classification tree analysis—CTA, Breiman et al. 1984, and flexible discriminant analysis (FDA—Hastie et al., 1994). We generated 10,000 pseudo-absence data by randomly sampling points within the study area where the species was not recorded, repeating the selection process 10 times. For each set of pseudoabsences, we repeated 10 times a split-sample cross-validation by using a random subset (30%) of the initial data set. To assess model accuracy, we used two evaluation criteria included in biomod2: the area under the curve of relative operating characteristic (AUC; Hanley and McNeil, 1982) and true skill statistic (TSS; Allouche et al., 2006). For the final ensemble projection, we averaged all produced models for the same timeframe. To detect any possible change in suitable areas due to climate change, the models were calibrated with data on the presence of the species in the past and then projected for the two different periods.

Land cover mapping

After screening available SENTINEL images for completely cloudless images, two high-resolution adjacent SENTINEL tiles acquired on the 20th of July 2022 (T32TNP_20220720T101611 and T32TNQ_20220720T101611) were retrieved from the web portal (available at: https://scihub.copernicus.eu/). The downloaded tiles were then mosaicked using the function merge from the ‘raster’ package (Hijmans et al., 2015) with setting default in Rstudio v. 2021.9.2.382 to encompass the whole study area. Unsupervised classification was carried out using the k-means algorithm with the kmeans function of the 'stats' R package (R Core Team, 2018), specifying 10 centers and 500 iterations. After visually inspecting the resulting classification, the 10 classes obtained were then merged into the 5 final land cover classes (Forest, Grass, Maquis, Bare/Built-up and Sea).

Lastly, to ensure the adequacy of the classification accuracy for our scope, a visual stratified validation was carried out by extracting 100 random points for each land cover class and by subsequently verifying the attributed land cover class on a baseline, high resolution, Bing maps layer, as recommended by Olofsson et al. (2014). A confusion matrix was generated, and accuracy metrics were calculated with the confusionMatrix function of the broom R package (Robinson, 2014). The overall classification accuracy was 0.78 (95% CI: 0.7411, 0.8156) and Kappa = 0.725. Class-specific balanced accuracy values were 0.8400, 0.7613, 0.8326, 0.9084, 0.9808 for Forest, Grass, Maquis, Bare/Built-up and Sea respectively. The resulting land cover map was then cropped to match the study area and resampled to match the climatic layers resolution (Fig. 1).

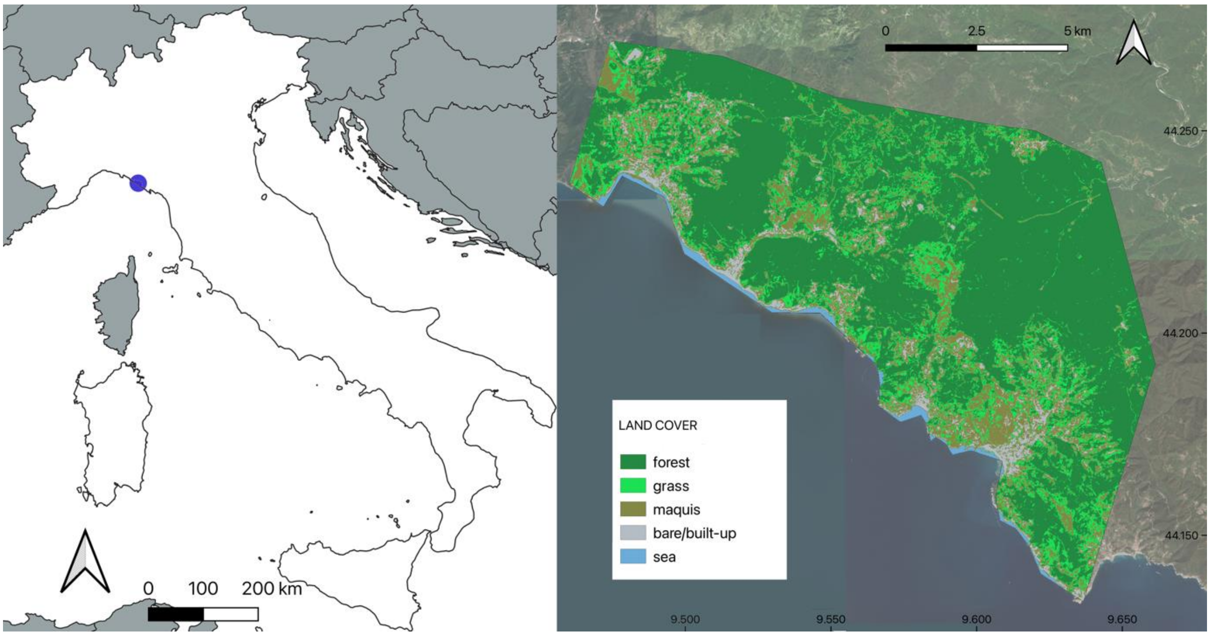

Figure 1 - Map of the study area location highlighted in blue and land cover map of the study area. Different land cover classes are color coded in the legend.

NDVI change mapping

The USGS portal was queried for 1970s and 2021 LANDSAT images of the study area (available at: https://earthexplorer.usgs.gov/). Six images were found to be suitable for our aim, three for each of the two timeframes (i.e., no clouds, spanning three different months of spring/early summer seasons to allow us to summarize the phenological variations of the main vegetative season). The retrieved images were:

PAST	LM01_L1TP_208029_19720813_20200909_02_T2
PAST	LM02_L1TP_208029_19750720_20200908_02_T2
PAST	LM02_L1TP_208029_19760608_20200907_02_T2
CURRENT	LC08_L2SP_193029_20210629_20210708_02_T1_SR

CURRENT	LC08_L2SP_193029_20210528_20210607_02_T1_SR
CURRENT	LC08_L1TP_193029_20210731_20210804_01_T1

The NDVI was then calculated in Rstudio for each image using the red (R) and near infrared (NIR) bands with the formula (NIR - R) / (NIR + R) and then averaged for each of the two timeframes (1970s and 2021). Obtained averaged NDVI rasters were then aligned and resampled to match the species distribution models.

Analysis of changes in suitability, land cover and NDVI values across stable, lost and gained distribution areas

First, rasters with past and current *S. ligustica* distribution were overlapped to obtain stable, lost and gained areas. Then, the values of land cover, 1970s and 2021 NDVI, and past and current habitat suitability were extracted for stable, lost and gained (Fig. 2). Thus, the possible changes in the land cover and NDVI are considered, in principle, independently from bioclimatic variables.

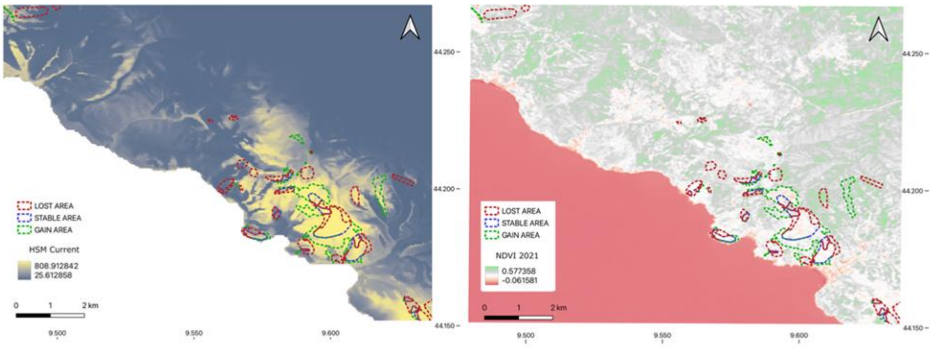

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Figure 2 - Intersection of habitat suitability values (left) and NDVI values (right) with stable, lost and gained distribution areas of S. ligustica

A threshold of 70% coverage was applied to pixel-based extracted values to filter only the most representative values. To test for statistically significant differences between stable, lost and gained areas in land cover, NDVI and habitat suitability (HSM) we performed a Kruskal-Wallis test (Kruskal and Wallis, 1952) and a post-hoc Dunn test (Dunn, 1964). These tests were computed using the kruskal.test function of the ‘stats’ R package (Team et al., 2018) and the dunnTest function of the ‘FSA’ R package (specifying method="bh" for ajdusted p-values) (Ogle and Ogle, 2017) respectively.

Secondly, a multinomial regression was fitted with stable, lost and gained areas as outcome and current NDVI values and HSM values as predictors (also including an interaction term), using the *multinom* function of the ‘nnet’ R package (Ripley et al., 2016). The baseline level of our outcome variable was specified as "lost" using the *relevel* function of the ‘stats’ R package. Z-values and P-values were subsequently calculated as zvalues = model$coefficients / model$standard.errors and pvalues= pnorm(abs(zvalues), lower.tail=FALSE)*2.

Results

The comparison between past and current distribution of the species underlines that *S. ligustica* still occurs in 1,869 pixels where it previously occurred, it disappeared in 2,511 pixels and now occurs in 2,095 new pixels, corresponding roughly to 43%, 57% and 47% of the past distribution, respectively.

Model performance

Model evaluation under current climatic conditions indicated an excellent model performance for the all the modelling techniques (Online Resource). For the current model, AUC values ranged from 0.92 to 0.98 (SD between 0.00 and 0.01) and TSS values from 0.68 to 0.88 (SD; 0.01) for the past models AUC ranged from 0.91 to 0.98 (SD between 0.00 and 0.01) and TSS from 0.65 to 0.81 (SD: 0.01).

Habitat suitability

The average habitat suitability in the stable areas passed from around 73% in the past to 69% in the current, remaining almost unchanged. In areas where the species is no longer present today, average habitat suitability decreased up to 40%. In the new gained areas habitat suitability is almost 70%.

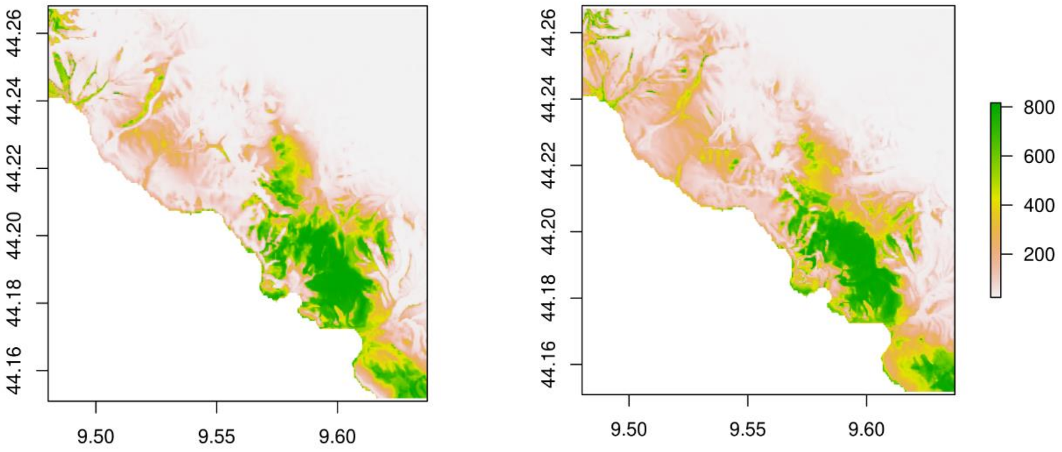

Figure 3 - Differences between stable, lost and gain areas in Land cover, NDVI and HSM values

For the present time, stable and gained areas are mainly associated with maquis and grass areas, while areas where the species disappeared are dominated by forests. Bare/Built-up areas are scarcely associated with either stable, lost or gained areas (Fig. 3).

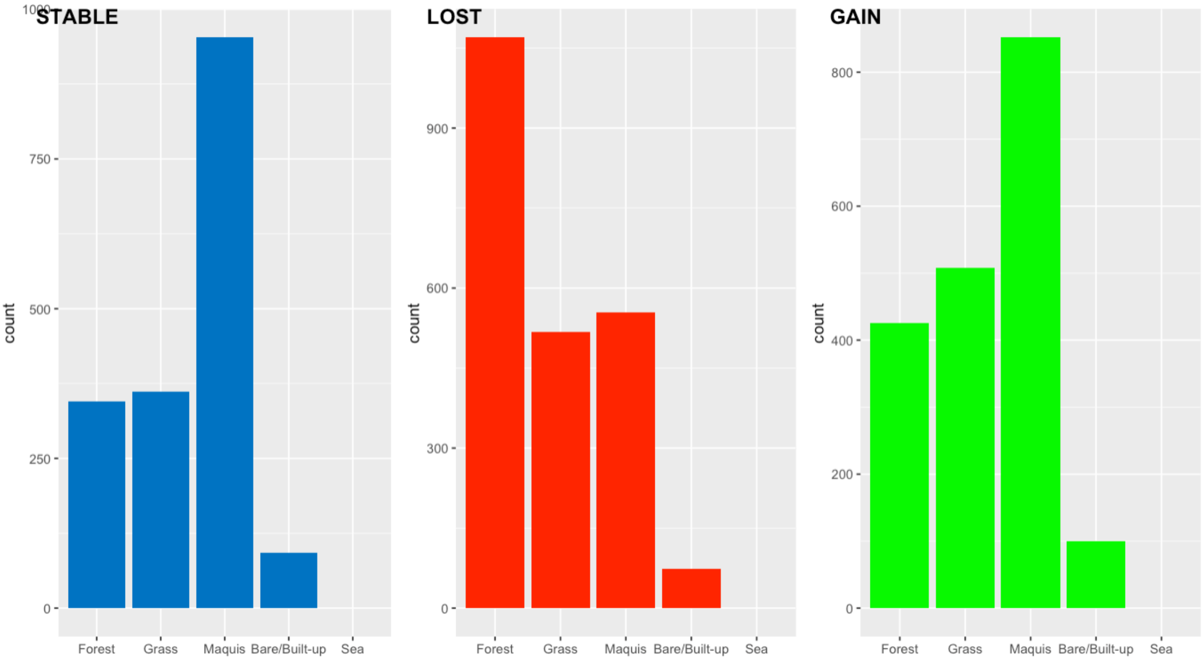

Figure 4 - Histograms of pixel count by land cover classes for stable, lost and gained areas of S. ligustica

For the 2021 timeframe, lost areas had highest NDVI values and stable areas the lowest ones (Fig. 4). In particular, lost areas were significantly different in NDVI values from both stable (Z=31.19, p-value <0.001) and gained (Z= -13.18, p-value <0.001) areas and, gained areas were significantly different from stable ones (Z= 17.60, p-value <0.001). The increase in NDVI values between periods was significantly lower in the lost areas than in the gained (Z= -10.81, p-value <0.001) and stable (Z=-15.17, p-value <0.001) areas. It was also slightly but significantly lower in the gained areas than in the stable areas (Z= -4.41, p-value <0.001).

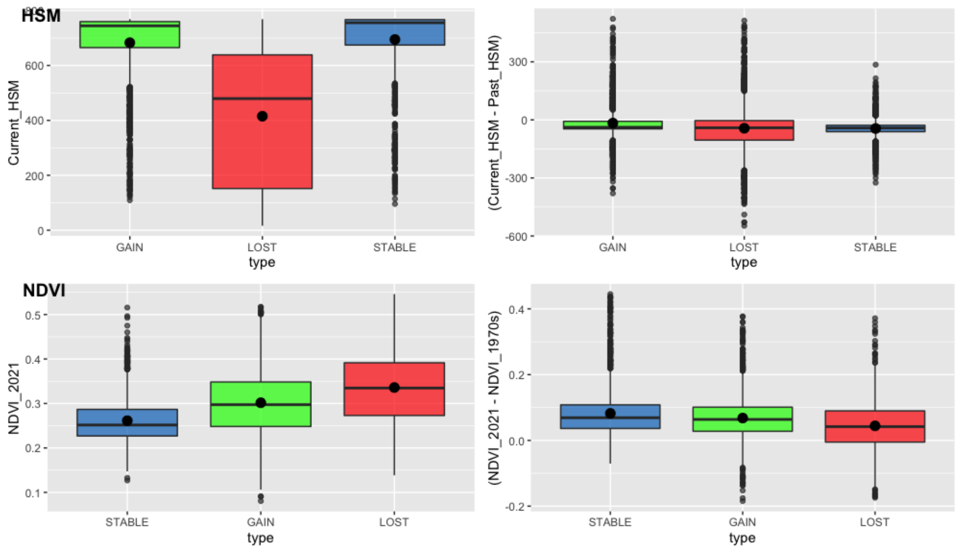

Figure 5 - Boxplots of pixel-based values of habitat suitability and NDVI for stable, lost and gained areas of S. ligustica for the current timeframe (left) and the difference between current and 1970s scenarios.

Moreover, gained (Z= 35.07, p-value <0.001) and stable (Z=-41.61, p-value <0.001) areas had significantly higher suitability values than lost areas (Fig. 4). Stable areas had significantly higher suitability values than gained ones (Z= -6.98, p-value <0.001).

Difference in habitat suitability over time showed that suitability decreased slightly in gained, stable and lost areas, having average values below zero in all cases, although the decrease was significantly higher in lost than in gained (Z= 8.59, p-value <0.001) and stable (Z= 1.07, p-value <0.001) areas. Moreover, the decrease was lower in gained than in stable areas (Z= 9.14, p-value <0.001).

Multinomial regressions

The multinomial model results (Table 1) showed that a one-unit increase in the variable NDVI_2021 was associated with the decrease in the log-odds of belonging to stable areas vs. lost areas in the amount of 2.283 (Z= -59.021, p-value <0.001) and with the increase of the log-odds of belonging to gain areas vs. lost areas in the amount of 1.311 (Z= 28.995, p-value <0.001). A one-unit increase in HSM values was linked to an increase of belonging to stable areas vs. lost areas and in the amount of 0.011 (Z= 30.988, p-value <0.001) and with the increase of the log-odds of belonging to gain areas vs. lost areas in the amount of 0.009 (Z= 28.672, p-value <0.001). Lastly, an increase in the product of NDVI_2021 and HSM values was linked to a decrease of the log-odds of belonging to gain areas vs. lost areas in the amount of 0.015 (Z= -16.049, p-value <0.001) and a decrease of the log-odds of belonging to gain areas vs. lost areas in the amount of 0.007 (Z= -9.334, p-value <0.001).

Table of regression

Coefficients

	Intercept	*NDVI_2021*	*Current_HSM*	*NDVI_2021*Current_HSM*
STABLE	-3.240	-2.823	0.011	-0.015
GAIN	-4.292	1.311	0.009	-0.007

Std. Errors:

	Intercept	*NDVI_2021*	*Current_HSM*	*NDVI_2021*Current_HSM*
STABLE	0.157	0.048	0.000	0.001
GAIN	0.134	0.045	0.000	0.001

Z-values

	Intercept	*NDVI_2021*	*Current_HSM*	*NDVI_2021*Current_HSM*
STABLE	*-20.701*	*-59.021*	*30.988*	*-16.049*
GAIN	*-32.067*	*28.995*	*28.672*	*-9.334*

P-values

	Intercept	*NDVI_2021*	*Current_HSM*	*NDVI_2021*Current_HSM*
STABLE	<0.001	<0.001	<0.001	<0.001
GAIN	<0.001	<0.001	<0.001	<0.001

Table 1 - Multinomial logistic regression analysis for the associations of habitat suitability values and NDVI values with stable, lost and gained areas of S. ligustica

Discussion

The aim of this study was to understand how climate and vegetation cover changes may affect the distribution of *S. ligustica*. In particular, we observed that the detected change in the species distribution was probably due to the interaction between climate and vegetation cover dynamics.

Driver of change in the distributional range

Comparing past and present species distribution, we observed a high range turnover in the last twenty years, despite the limited dispersal capabilities of the taxa that has seeds with a moderately efficient plume (Vittoz and Engler, 2007). These range changes seem to be related to changes in climatic conditions. In fact, the observed range shift has taken place toward areas with higher values of habitat suitability, while the areas where the species disappeared have the lowest values of habitat suitability. The high sensitivity of *S. ligustica* to climate change is congruent with the expectations for endemic species (Bellard et al., 2012; Cahill et al., 2013) and in particular with previous results on endemic species growing in the N Tyrrhenian (Casazza et al., 2014; Dagnino et al., 2020). In addition, we observed that the overall habitat suitability slightly decreased over the past fifty years.

The NDVI is based on the relationship between the absorption of the red radiation by photosynthetic pigments and the scattering of the near-infrared radiation caused by the foliage. Consequently, NDVI values increase when the vegetation cover increases but also when its structural complexity increases (Beck et al., 2006). Our results supported a negative relationship between the increase of vegetation cover and complexity (i.e., the increase of forested and closed cover) and the presence of *S. ligustica*. Indeed, land cover and NDVI analysis results highlight the occurrence of major changes in vegetation cover from the 1970s until today, in particular an increase in forest, shrubs, and built-up areas in lost areas. This condition has a great influence on distribution of *S. ligustica* that is generally found in open and sunny habitats. The regrowth of more closed and/or stratified vegetation has already been documented for the Province of La Spezia and in Cinque Terre National Park as a result of agricultural land abandonment (Agnoletti et al., 2019).

Overall, the magnitude of the impact of the interaction between climate and vegetation cover changes (NDVI) was lower than the magnitude of vegetation cover alone but also higher than the magnitude of climate alone, as evidenced by the higher absolute value of coefficients and Z-values of NDVI alone in the multinomial regression. This result implies a pivotal role of vegetation cover dynamics in shaping a species' range, nevertheless it is unclear to what extent these dynamics are also a result of climate-driven shifts or human-driven shifts.

Conclusion

Rapidly developing cities and infrastructures, changes in climate and land use/cover are posing serious challenges to biodiversity. In this study we analyzed remote sensing data and SDM tools conjunctly to effectively assess habitat suitability and its main drivers.

The analyses of the NDVI trajectories and of their relationship with climatic drivers performed on the distribution of *Santolina ligustica* highlighted an interplay between ecological and climatic changes over the past fifty years that is shrinking the species' habitat. This conjunt negative effect adds up to the scarcity of ophiolitic substrates and high sunny exposure substrates (growing condition of *S. ligustica*), further reducing the presence of the species (Torricelli et al., 1999).

Climate change and land cover change interact to impact biodiversity with a wide range of mechanisms. Proper consideration of these mechanisms is necessary to manage habitat appropriately.

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POPULATION ECOLOGY – ORIGINAL RESEARCH

Dealing with disjunct populations of vascular plants: implications for assessing the effect of climate change

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Abstract

Species distribution models are the most widely used tool to predict species distributions for species conservation and assessment of climate change impact. However, they usually do not consider intraspecific ecological variation exhibited by many species. Overlooking the potential differentiation among groups of populations may lead to misplacing any conservation actions. This issue may be particularly relevant in species in which few populations with potential local adaptation occur, as in species with disjunct populations. Here, we used ecological niche modeling to analyze how the projections of current and future climatically suitable areas of 12 plant species can be affected using the whole taxa occurrences compared to occurrences from geographically disjunct populations. Niche analyses suggest that usually the disjunct group of populations selects the climatic conditions as similar as possible to the other according to climate availability. Integrating intraspecific variability only slightly increases models' ability to predict species occurrences. However, it results in different predictions of the magnitude of range change. In some species, integrating or not integrating intraspecific variability may lead to opposite trend in projected range change. Our results suggest that integrating intraspecific variability does not strongly improve overall models' accuracy, but it can result in considerably different conclusions about future range change. Consequently, accounting for intraspecific differentiation may enable the detection of potential local adaptations to new climate and so to design targeted conservation strategies.

Keywords Intraspecific variation · Climatic niche · Species distribution model · Northern Mediterranean mountains

Introduction

Species distribution models (SDMs) are the most widely used tool to predict species distributions for various aims, including species conservation and assessment of climate change impact (Guisan and Zimmerman 2000). Most studies conducted using SDMs assume that all populations of the species would respond to the environment in the same way (Mota-Vargasa and Rojas-Soto 2016; Qiao et al. 2017). Actually, many species exhibit intraspecific ecological variation and to not consider this ecological differentiation may bias predictions obtained with models (D'Amen et al. 2013; Valladares et al. 2014). Consequently, SDMs at the species level may overlook any difference in relationship between groups of populations and climate and they may result in lower model sensitivity (i.e., lower ability to predict presences), affecting projections of future habitat suitability (Osborne and Suárez-Seoane 2002; Lecocq et al. 2019). Therefore, SDMs at the species level may lead to misplaced conservation plans (Hällfors et al. 2016). This issue may be particularly relevant in species in which few populations with potential local adaptation occur (Lecocq et al. 2019; Pearman et al. 2010). To increase the SDMs' performance (Gonzalez et al. 2011) and to provide a more robust basis for conservation plans, it is recommended to divide species into subunits with biological significance (Smith et al. 2019).

Defining subunits within a species is a major difficulty in integrating intraspecific niche divergences in SDMs. Ideally, subunits should be defined on the basis of the relationships between regional climate and populations of species (Pearman et al. 2010, Oney et al. 2013, Romero et al. 2014,

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Valladares et al. 2014). However, this information is almost never available for most species. Consequently, different approaches have been performed to define a priori species subunits, such as: (i) occurrences were spatially portioned into geographic quadrants (Osborne and Suárez-Seoane 2002); (ii) subunits were based on distinct genetic lineages or recognized subspecies (Hernandez et al. 2006; Gonzalez et al. 2011; Oney et al. 2013); or, (iii) they were based on biological differentiation (Lecocq et al. 2019; Marcer et al. 2016). However, few studies have considered disjunct populations as an effective way to integrate intraspecific differentiation into SDMs (but see Hällfors et al. 2016; Chen et al. 2020), although disjunct populations may be frequently locally adapted because of the divergent selection (Fang et al. 2013; Mimura and Aitken 2010; Veatch-Blohm et al. 2017).

Geographical disjunction occurs when individuals from a group of populations cannot interact or can interact very rarely with individuals from other groups because of the distance or physical barriers that prevent interaction (Wells and Richmond 1995). Geographical disjunction by distance may be due to historical (such as past climate change or human intervention) or ecological (such as substrate specificity and long-distance dispersal) factors. Past climate fluctuations may have fragmented previously continuous distributional range causing the extinction of intervening populations and enabling survival only in refugia and/or isolated areas with relictual suitable habitat (Comes and Kadereit 1998; Kropf et al. 2003; Schönswetter et al. 2003). In addition, stochastic long-distance dispersal may have enabled some individuals to reach suitable habitat far from the main distributional range of the species (Kropf et al. 2006; Sanz et al. 2014). Regardless of the causes of disjunction, the low number of immigrants and a possible unequal distribution of the species genetic diversity (Despres et al. 2002) between the disjunct groups result in genetic and demographic disjunctions. Moreover, the geographically distant populations may occur in different biotic contexts (Lozano-Jaramillo et al. 2014; Quiroga et al. 2021), being part of regionally distinct species pools (Gallien et al. 2010; Pellissier et al. 2010) or being exposed to different human pressure (Gehrig-Fasel et al. 2007). These factors might potentially lead to distinct competition regimes, which result in occupying different subset of the inhabitable conditions of the species. The interaction between the different genotypes with the local environments may result in the emergence of ecotypes through adaptations to local conditions (Billings 1973; Leinonen et al. 2009; Keir et al. 2011). These ecotypes are maintained because of the absence or the low level of gene flow (Kawecki and Ebert 2004; Tigano and Friesen 2016). Locally adapted genotypes are expected to have a higher relative fitness in their local habitat than genotypes from other habitats. Some locally adapted populations may become maladapted to new climates because of global warming, while others may be well adapted assuring species survival (Aitken and Whitlock 2013).

In this study, we analyzed how the projections of current and future climatically suitable areas can be affected using SDMs based on the whole species occurrences compared to occurrences' groups based on separate distribution ranges. We used twelve species with geographically disjunct populations distributed in the Southern European mountains, between the Pyrenees and the South-west Alps. In particular, we were asking the following questions: (1) Do disjunct populations experience different climatic conditions? (2) Do SDMs projections based on geographically disjunct populations differ from projections based on the whole species?

Materials and methods

Studied species, occurrence data and climatic layers

We selected 12 plant species characterized by a group of populations that is clearly geographically disjunct from the main range of the species. The distance between main group and disjunct populations ranges from 30 to 500 km (Table 1). Six species have a group of populations in the Alps and the other one in the Pyrenees (having the longest distance between the two groups), one species has a group of populations in the Alps and the other one in Corse. In these seven species, the large geographical distance between populations suggests a very reduced gene flow between groups. Differently, three species have groups of disjunct populations within Alps and two species between Alps and Apennines. In these cases, the distance between groups is shorter and a certain degree of gene flow might still occur. The two disjunct groups of populations were named "core populations" (the larger group) and "disjunct populations" (the smaller group) on the basis of the number of occurrences, without any inference about the genetic or biogeographic relationships between them. To the best of our knowledge, information about possible local adaptations is currently available for none of these studied species.

Occurrence data were obtained from both global and regional databases: Système d'Information et de Localisation des Espèces Natives et Envahissantes (SILENE—www.silene.eu); Sistema de información sobre las plantas de España (Anthos—www.anthos.es); Conservatoire Botanique de Corse (CBNC—http://cbnc.oec.fr); Osservatorio Ligure Biodiversità (Li.Bi.Oss.—ARPAL, Regione Liguria, Italy); and Wikiplantbase #Toscana (http://bot.biologia.unipi.it/wpb/toscana/index.html). For each species, occurrences were spatially filtered retaining randomly only one occurrence per grid cell of about 1 × 1 km. A final data

Table 1 Distributional features of the 12 studied species

Species	Core populations		Disjunct populations		Distance between core and disjunct populations (km)
	Number of occurrences	Distribution	Number of occurrences	Distribution	
Adonis pyrenaica DC.	41	Pyreneans	24	Southwestern Alps	475
Allium narcissiflorum Vill.	542	Southwestern Alps	27	Western Alps	70
Crocus ligusticus Mariotti	170	Southwestern Alps	22	Northern Apennines	65
Cytisus ardoinii E. Fourn.	98	Southwestern Alps	18	Southwestern Alps	30
Erysimum collisparsum Jord.	249	Southwestern Alps	26	Pyreneans	250
Eryngium spinalba Vill.	369	Southwestern Alps	43	Southwestern Alps	85
Gentiana alpina Vill.	387	Pyreneans	139	Alps	400
Potentilla nivalis Lapeyr.	476	Pyreneans	124	Southwestern Alps	360
Primula hirsuta All.	377	Pyreneans	252	Alps	500
Thymelaea dioica (Gouan) All.	343	Pyreneans	124	Southwestern Alps	400
Valeriana rotundifolia Vill.	286	Southwestern Alps	112	Corse	200
Valeriana saxatilis L.	104	Eastern Alps	20	Apennines	225

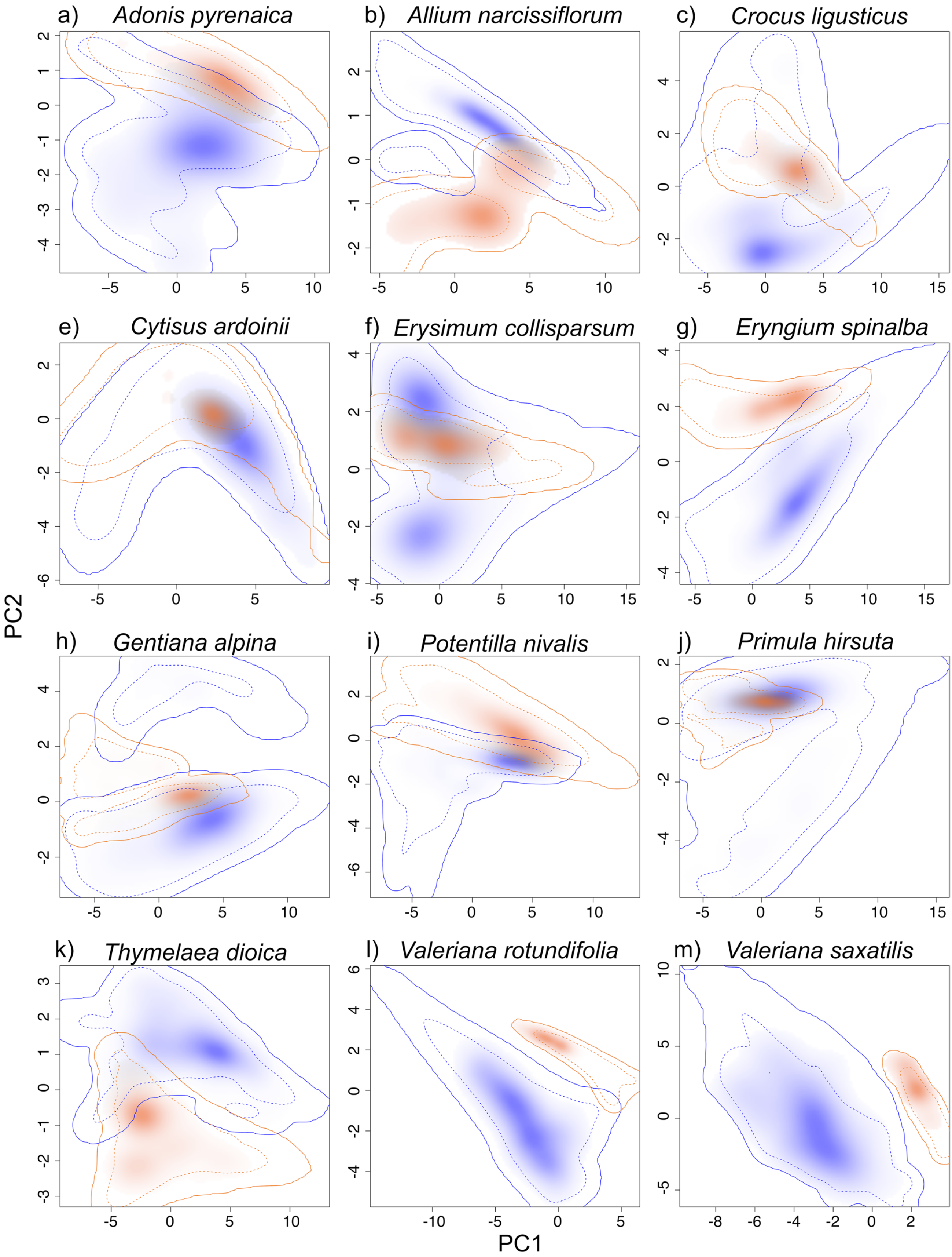
Core populations (the larger group) and disjunct populations (the smaller group) are defined on the basis of the number of occurrences

set of 4373 occurrences, ranging from 65 to 629 occurrences per species (Table 1), was used in the analyses.

From the WorldClim data set v.1.4 website (http://www.worldclim.org), we downloaded 19 bioclimatic variables representative of historic (1960–1990) climatic conditions at 1 × 1 km spatial resolution (Hijmans et al. 2005). Furthermore, we downloaded bioclimatic variables for two Representative Concentration Pathways (RCPs), representing moderate and extreme possible future emission trajectories and coded according to a possible range of radiative forcing values in the year 2100 relative to preindustrial values (+2.6 and +8.5 W/m^2, respectively; IPCC 2014). We used RCPs projections from four general circulation models (GCMs), which represent physical processes in the atmosphere, ocean, cryosphere, and land surface: IPSL-CM5A-LR, provided by Institut Pierre-Simon Laplace; MPI-ESM-LR, provided by Max Planck Institute for Meteorology; HadGEM2-ES, provided by Met Office Unified Model; and CCMS4, provided by Community Earth System Model. Following the approach of Hamann et al. (2015) and Maiorano et al. (2012), we used the first two axes of a principal component analysis (PCA) as environmental variables for species distribution modeling, harmonized on both current and future climates to reduce the transferability issue (Petitpierre et al. 2017). First, we pooled together all the bioclimatic variables for both current and each future scenario (i.e., all the combination of RCPs and GCMs); then, we selected the first two axes of the PCA and re-separated the scenarios. The PCA (see results in Online Resource Table S1) was carried out in R (R Core Team 2019) using the packages ‘ade4’ (Dray and Dufour 2007).

Niche analysis in environmental space

To test any differentiation in ecological niche in the environmental space between core and disjunct populations, we performed niche analysis in a multivariate space defined by the climatic conditions in which they occur, following the approach of Broennimann et al. (2012). First, for each couple of populations, we calculated the niche overlap using Schoener’s D index (Schoener 1970), which ranges from 0 (no overlap) to 1 (full overlap). This metric is based on the density of species occurrences along the environmental axes of a multivariate analysis (Broennimann et al. 2012) and it is considered one of the best niche overlap metrics (Rödder and Engler 2011). Finally, we used the similarity test to assess whether the observed overlap between the niches of the two groups is significantly higher or lower than expected at random from the backgrounds where the species occur (Warren et al. 2008; Broennimann et al. 2012). In short, the observed niche overlap between the two groups was compared with the overlap measured between the niche of one group and the niche obtained by randomly sampling occurrence points in the background area of the other group. This randomization was repeated 100 times. Significant results indicate that the ecological niches of species are either more or less similar than expected by chance. The similarity test indicates whether the observed niche differentiation is because of an actual selection of different habitats or simply an artifact due to habitat availability in the background areas (Warren et al. 2008). To test whether our results are robust to different choices of background, we defined three background areas using a 5, 10 and 15 km buffer zone around


a) Adonis pyrenaica
b) Allium narcissiflorum
c) Crocus ligusticus
e) Cytisus ardoinii
f) Erysimum collisparsum
g) Eryngium spinalba
h) Gentiana alpina
i) Potentilla nivalis
j) Primula hirsuta
k) Thymelaea dioica
l) Valeriana rotundifolia
m) Valeriana saxatilis
PC2
PC1

◂**Fig. 1** Niches of the core (blue) and disjunct (orange) populations of the 12 studied species. The solid and dashed lines represent 100 and 50% of the entire available environmental space (considering a background area of 10 km around occurrences), respectively. Color shadings illustrate the density of the occurrences of core and disjunct populations in each climatic cell

the occurrences of both core and disjunct populations. Both D overlap and similarity test were calculated in R (R Core Team 2019) using the "ecospat" package (Broennimann et al. 2016).

Species distribution modeling

Species distribution modeling was carried out in R (R Core Team 2019) using the Maxent algorithm (Phillips et al. 2004, 2006) as implemented in the 'Biomod2' package (Thuiller et al. 2016). We selected 10,000 random points as pseudo-absence data and a split-sample cross-validation was repeated 10 times, using a random subset (30%) of the initial data set. Model performance was evaluated using both the area under the relative operating characteristic curve (AUC—Hanley and McNeil 1982) and the true skill statistic (TSS—Allouche et al. 2006).

The suitability maps from model projections were converted into binary distribution maps using three different thresholds implemented in the 'PresenceAbsence' package (Freeman and Moisen 2008): sensitivity equals specificity (Sens = Spec), maximizing the sum of sensitivity and specificity (MaxSens + Spec), and minimizing the distance between the relative operating curve plot and the upper left corner of the unit square (MinROCdist). These thresholds outperform other commonly used thresholds (Cao et al. 2013; Liu et al. 2005).

We constructed SDMs of both the overall species (hereafter "species model") and each group of populations (hereafter "core model" and "disjunct model") over the entire distributional range of the species. In addition, following the approach of Pearman et al. (2010), we considered the area that was predicted to have suitable climatic conditions in one or both groups of populations as an "aggregate" model for the distribution of the species. To obtain a relative score of "goodness" of the aggregate model, we calculated the mean AUC and TSS values for core and disjunct models, according to Gonzalez et al. (2011). In addition, for each studied species, we calculated the sensitivity of all types of models as the proportion of occupied sites that are correctly predicted as suitable by the model under current climatic conditions (Pearman et al. 2010). For SDMs under future climates, we performed an ensemble combining all projections and species were considered occurring in a cell if at least 50% of models projected its occurrence there (i.e., a majority consensus rule).

Range analysis under future climate

To assess the impact of climate change on the potential distribution of each species, we calculated the percentage of overall range change (RC). This index was calculated separately for each type of model using the following formula: $RC = 100 \times (RG - RL)/CPR$, according to Casazza et al. (2014). RG (range gain) is the number of grid cells not suitable under current condition but suitable under future climate; RL (range loss) is the number of grid cells suitable under current climate but unsuitable under future climate; CPR (current potential range) is the number of grid cells suitable under current climate.

Results

Niche analysis

The niche overlap between the two groups of populations was low (Fig. 1). It ranged from 0 to 0.39 (Table 2, Online Resource Table S2) and was close to 0 in 5 out of 12 species (Table 2, Online Resource Table S2). The similarity test indicated that in 7 out of 12 species, the ecological niche of at least 1 group of populations was significantly more similar to the niche of the other one than expected by considering the differences in the surrounding environmental conditions (Table 2, Online Resource Table S2). Taken together, our results show that in these seven species, the overlap between the two groups is low, but the two groups of populations occupy environments that are significantly more similar to each other than expected by chance.

Model performance

With few exceptions, AUC and TSS indicated good to excellent performance under current climates for species, core and disjunct models (Table 3). In most cases, evaluation of core and disjunct models was slightly higher than their respective species models. Consequently, the performance of aggregate models (obtained averaging the AUC and TSS values of core and disjunct models) was equal to or higher than species models (Table 3). The sensitivity scores were high in all types of models, but in almost all species, the aggregate models outperformed the species models, better predicting the known species' occurrences (Table 3).

Table 2 Results of niche overlap and niche similarity test between core and disjunct populations

Species	Niche overlap	Similarity test	
		Core vs disjunct	Disjunct vs core
		10 km background	10 km background
Adonis pyrenaica	0.14	Ns	More
Allium narcissiflorum	0.16	More	Ns
Crocus ligusticus	0.30	More	Ns
Cytisus ardoinii	0.16	Ns	More
Erysimum collisparsum	0.08	Ns	Ns
Eryngium spinalba	0.06	Ns	Ns
Gentiana alpina	0.27	Ns	More
Potentilla nivalis	0.19	Ns	Ns
Primula hirsuta	0.39	More	More
Thymelaea dioica	0.06	More	More
Valeriana rotundifolia	0.00	Ns	Ns
Valeriana saxatilis	0.00	Ns	Ns

Background is defined by applying 10 km buffer zones around the occurrence points. Significant results are indicated by ‘less’ for significant divergence or ‘more’ for significant similarity between test and comparison taxa, ‘ns’ indicates not significant results

Range analysis under future climate

In most species, an overall range contraction (i.e., negative range change) was forecasted under both the moderate and the extreme scenarios, but some differences among model types were detected (Fig. 2). In general, all models projected the same trend in range change and species models projected a higher range contraction than aggregate models. However, despite both species and aggregate models had the same trend, in three cases, the disjunct model projected a range gain, while the core model projected a range loss (i.e., *Valeriana rotundifolia* in both scenarios, *Valeriana saxatilis* in moderate scenario and *Eryngium spinalba* in extreme scenario). Moreover, in four cases, species and aggregate model predicted opposite trends: in two cases (*Eryngium spinalba* and *Gentiana alpina* both under moderate scenario) contrasting range change trends occur also between the core and the disjunct models, while in the other two cases (*Adonis pyrenaica* under moderate scenario and *Gentiana alpina* under extreme scenario), the core and the disjunct models predicted a concordant range change trend. In *Eryngium spinalba, Valeriana saxatilis* and *Valeriana rotundifolia* the niche overlap was very low (0.00–0.06), and the disjunct populations occur under Mediterranean climatic conditions with low values of temperature seasonality and precipitation concentrated during wet period, while core populations occur under temperate (mountain) climate with high values of temperature seasonality (Fig. 3a–c). In *Adonis pyrenaica* and *Gentiana alpina* niche, overlap was higher (0.14 and 0.27, respectively), and the disjunct populations grow under a subset of marginal conditions of core populations having different optimal conditions (Fig. 3d, e).

Discussion

In this study, we assessed the importance of considering geographically separated populations to predict potential effects of future climate change using SDMs. In fact, these disjunct populations may respond differently to climate change because they may host local adaptation or because they may occur in more suitable climatic conditions in the future. Our results underline the importance of incorporating intraspecific variability in SDMs, given that it can provide different conclusions about future range changes.

Climatic niche differentiation within disjunct populations

Our results suggest that ecological differentiation among disjunct and core populations occurs, although disjunct populations grow under the available climatic conditions more similar to those of core populations (Table 2, Online Resource Table S2). The niche similarity is in line with previous studies suggesting that disjunct populations maintain the same climatic niche (e.g., arctic-alpine species—Wasof et al. 2015, Corso-Sardinian species—Piñeiro et al. 2007, species ranging from Pyrenees to Alps—Kropf et al. 2008), particularly when disjunctions result from paleoclimatic changes (Winkworth et al. 2015). In line with this observation, the disjunct populations of *Gentiana alpina*—the only studied species for which phylogeographic studies are available—were attributed to vicariance events (Kropf et al. 2006). The ecological differentiation among disjunct and core populations is irrespective of the distance between the central and disjunct populations. In fact, the

Table 3 Model performance evaluation

Species	Model	AUC (sd)	TSS (sd)	Sensitivity (%)
Adonis pyrenaica	Core	0.97 (0.02)	0.86 (0.07)	92.68
	Disjunct	0.99 (0.01)	0.96 (0.03)	95.83
	Species	0.97 (0.01)	0.85 (0.05)	90.77
	Aggregate	0.98 (0.02)	0.91 (0.05)	93.85
Allium narcissiflorum	Core	0.94 (0.01)	0.77 (0.02)	89.30
	Disjunct	0.92 (0.03)	0.76 (0.07)	81.48
	Species	0.93 (0.01)	0.74 (0.02)	88.75
	Aggregate	0.93 (0.02)	0.77 (0.05)	91.56
Crocus ligusticus	Core	0.98 (0.00)	0.89 (0.02)	95.29
	Disjunct	0.99 (0.00)	0.96 (0.02)	100.00
	Species	0.98 (0.01)	0.89 (0.04)	95.83
	Aggregate	0.99 (0.00)	0.93 (0.02)	95.83
Cytisus ardoinii	Core	0.99 (0.02)	0.99 (0.00)	96.94
	Disjunct	0.98 (0.00)	0.91 (0.02)	100.00
	Species	0.99 (0.00)	0.96 (0.01)	94.83
	Aggregate	0.99 (0.00)	0.95 (0.01)	97.41
Erysimum collisparsum	Core	0.93 (0.01)	0.73 (0.03)	87.95
	Disjunct	0.94 (0.02)	0.85 (0.04)	92.31
	Species	0.92 (0.01)	0.72 (0.03)	89.82
	Aggregate	0.94 (0.02)	0.79 (0.04)	91.27
Eryngium spinalba	Core	0.93 (0.01)	0.76 (0.04)	88.35
	Disjunct	1.00 (0.00)	0.97 (0.03)	97.67
	Species	0.92 (0.01)	0.74 (0.02)	88.83
	Aggregate	0.97 (0.01)	0.87 (0.03)	90.53
Gentiana alpina	Core	0.98 (0.00)	0.86 (0.02)	93.02
	Disjunct	0.98 (0.01)	0.88 (0.02)	92.81
	Species	0.96 (0.01)	0.83 (0.02)	90.68
	Aggregate	0.98 (0.01)	0.87 (0.02)	93.73
Potentilla nivalis	Core	0.97 (0.00)	0.87 (0.01)	94.75
	Disjunct	0.98 (0.00)	0.89 (0.02)	95.16
	Species	0.97 (0.00)	0.84 (0.01)	92.83
	Aggregate	0.98 (0.00)	0.88 (0.02)	95.33
Primula hirsuta	Core	0.97 (0.01)	0.84 (0.02)	92.31
	Disjunct	0.97 (0.02)	0.91 (0.03)	95.24
	Species	0.96 (0.01)	0.83 (0.02)	91.73
	Aggregate	0.97 (0.02)	0.88 (0.03)	93.8
Thymelaea dioica	Core	0.93 (0.01)	0.73 (0.02)	84.55
	Disjunct	0.91 (0.02)	0.73 (0.07)	86.29
	Species	0.90 (0.01)	0.66 (0.02)	86.51
	Aggregate	0.92 (0.02)	0.73 (0.05)	90.15
Valeriana rotundifolia	Core	0.86 (0.02)	0.58 (0.04)	83.92
	Disjunct	0.92 (0.13)	0.83 (0.25)	99.11
	Species	0.89 (0.01)	0.63 (0.04)	84.42
	Aggregate	0.89 (0.08)	0.71 (0.15)	88.19
Valeriana saxatilis	Core	0.89 (0.01)	0.70 (0.03)	86.54
	Disjunct	0.93 (0.04)	0.79 (0.09)	90.00
	Species	0.85 (0.02)	0.61 (0.03)	83.06
	Aggregate	0.91 (0.03)	0.75 (0.06)	89.52

The values of the area under the relative operating characteristic curve (AUC) and true skill statistic (TSS) are the means of the evaluation scores of the 100 runs performed for each type of model. The sensitivity of all types of models is estimated as the proportion of occupied sites that are correctly predicted as suitable by the model under current climatic conditions

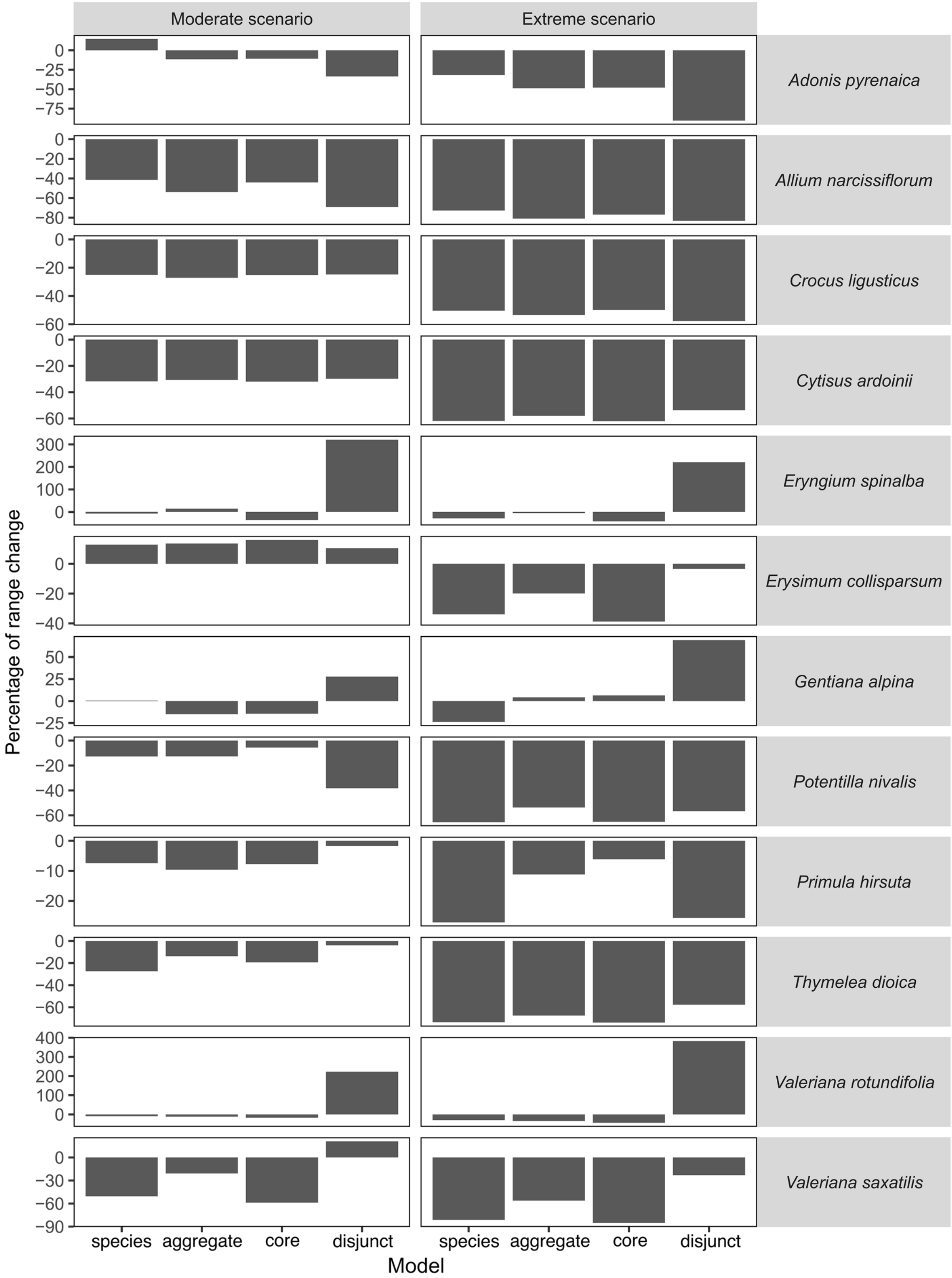


Fig. 2 Percentage of range change projected under moderate and extreme future scenarios

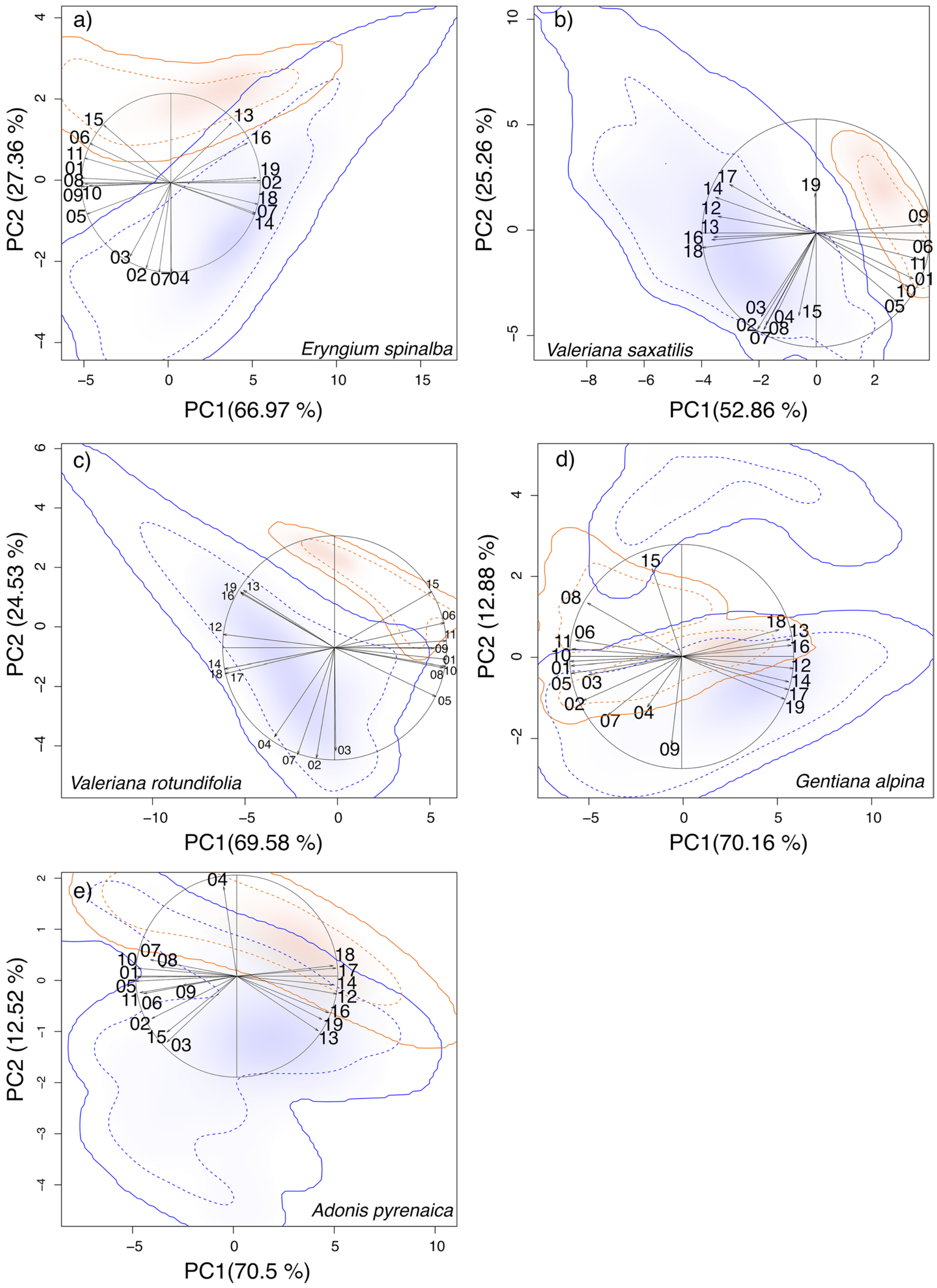
low degree of niche overlap between core and disjunct populations (Table 2, Online Resource Table S2) may occur because of differences in environmental availability across their geographic ranges (Murphy and Lovett Doust 2007; Dagnino et al. 2016), historical climate changes, or other non-climatic factors (e.g., dispersal limitation and biotic interactions) that limit the distributional range of species resulting in a climatic disequilibrium between populations (Shipley et al. 2013).

In our study, species occurrences are predicted better by the aggregate than by the species model, as suggested by the slightly highest values of sensitivity and accuracy detected in the aggregate model (Table 3). A higher accuracy in aggregate than in species models was observed in several other studies considering intraspecific variability as formally recognized subspecies (e.g., Gonzalez et al. 2011; Oney et al. 2013), genetic lineages (e.g., Marcer et al. 2016; Ikeda et al. 2017) or a combination of them (e.g., Pearman et al. 2010), underlying the importance of considering intraspecific variation to increase accuracy of predictive models (Smith et al. 2019). In fact, species model may underestimate the overall niche of a species having disjunct distribution, resulting in an under-prediction bias for the less widespread group of populations (Pearman et al. 2010; Oney et al. 2013). This may occur when one group of populations occupies a narrower range of climatic conditions than the other group, as observed in most of the studied species (Fig. 1). Conversely, the aggregate model is the sum of the independent core and disjunct models and, consequently, it maximizes the sensitivity value also for the group with the narrowest niche, thus reducing the under-prediction bias. Considerable intraspecific variability occurs in plant species growing along environmental gradients in Mediterranean mountains (Pironon et al. 2017; Casazza et al. 2021; Macrì et al. 2021). For this reason, although we detected niche conservatism in disjunct populations, these populations growing under marginal conditions may generate valuable adaptive genetic combinations because of differential selection pressures (Hereford 2009) and, therefore, they might respond in a different way to climate change (Morente-López et al. 2021; Papuga et al. 2018).

Intraspecific differentiation and future range changes

In general, the high AUC and TSS values suggest that model predictions are highly accurate. In six species (i.e., *Adonis pyrenaica*, *Allium narcissiflorum*, *Crocus ligusticus*, *Cytisus ardoinii*, *Erysimum collisparsum* and *Valeriana saxatilis*) the number of occurrences in the disjunct populations is closed to the number of occurrences expected to affect the reliability of species distribution models (i.e., 25 occurrences; van Proosdij et al. 2016). However, the high-performance values in disjunct models of these species suggest that the occurrences are not biased and that they adequately represent the environmental gradient used by disjunct populations. Our results suggest that the distributional range of most of studied species will be strongly negatively affected by the climate change (Fig. 2). Nevertheless, the aggregate models generally predicted a slightly less severe range change than the species models (Fig. 2). This result is in line with previous studies including intraspecific (i.e., populations or subspecies) or intra-clade (i.e., sister species) niche variability (Pearman et al. 2010, Benito Garzón et al. 2011, Oney et al. 2013, Valladares et al. 2014) in the models. This pattern may be due to the different ecological niche used by the core and disjunct populations under current climate, as previously discussed. In particular, in the aggregate models, the ecological conditions used by the disjunct populations, that use a narrower and different climatic space than core populations, contribute more to the overall niche of the species than in species models. Combining the separate models of core and disjunct populations, the aggregate model may project a broader suitable area into the future climate than the species model (Oney et al. 2013), resulting in a less negative future range change.

However, despite the low niche overlap between core and disjunct populations, we found the same trend (i.e., contraction, expansion, or stability) both in core and disjunct models and, consequently, in species and aggregate models in most of the cases (Fig. 2), as observed in previous studies (Pearman et al. 2010; Hällfors et al. 2016; Maguire et al. 2018). In four cases (i.e., *Eryngium spinalba* in the pessimistic scenario, *Valeriana saxatilis* in the moderate scenario and *Valeriana rotundifolia* in both scenarios), we detected a different trend in core and disjunct models, even if this difference does not result in a different trend between aggregate and species models. The disjunct populations of these species occur under more Mediterranean climatic conditions than core populations (Fig. 3a–c), so they might increase their suitable areas because of climate change. In fact, in the future, species growing under Mediterranean climate, characterized by hot and arid summer and mild to cool winter, will probably lie within the climatic conditions already experienced at least in some periods of the year and, consequently, these species may be less sensitive to climate change (Thuiller et al. 2006; Tielbörger et al. 2014; Dagnino et al 2020). However, this gain in range of disjunct populations will not be large enough to compensate the range loss of core populations growing under temperate conditions, resulting in an overall range loss both in aggregate and species models. Moreover, under the moderate scenario in *Eryngium spinalba* and *Gentiana alpina* contrasting directions of range change occurring between the core and disjunct models result in a different trend between species and aggregate models (Fig. 2). In *Eryngium spinalba*, under the extreme scenario, range gain is very low in disjunct populations (see above). Differently under the moderate scenario, the weak range loss of temperate core populations is counterbalanced by the high range gain of disjunct populations growing under Mediterranean conditions, resulting in an overall gain in the aggregate models. On the contrary, in the species model, the



niche was mainly affected by the temperate conditions under which most populations grow, resulting in an overall range loss. In *Gentiana alpina,* the disjunct populations thrive under a subset of conditions which constitute the marginal conditions for the core populations (Fig. 3d). The future climate change will affect in slightly different way the two groups of populations, resulting in a weak gain in the most thermophilous disjunct populations and in a weak loss of

◂**Fig. 3** Focus on the niches of the core (blue) and disjunct (orange) populations of five studied species with different trends predicted by SDMs. The correlation plot reporting the contribution of each bioclimatic variable in the niche space to the first and second principal components is shown. The solid and dashed lines represent 100 and 50% of the entire available environmental space (background), respectively. Color shadings illustrate the density of the occurrences of core and disjunct populations in each climatic cell. Bioclimatic variables are: 01 = annual mean temperature; 02 = mean diurnal range; 03 = isothermality; 04 = temperature seasonality; 05 = max temperature of warmest month; 06 = min temperature of coldest month; 07 = temperature annual range; 08 = mean temperature of wettest quarter; 09 = mean temperature of driest quarter; 10 = mean temperature of warmest quarter; 11 = mean temperature of coldest quarter; 12 = annual precipitation; 13 = precipitation of wettest month; 14 = precipitation of driest month; 15 = precipitation seasonality; BIO16 = precipitation of wettest quarter; 17 = precipitation of driest quarter; 18 = precipitation of warmest quarter; 19 = precipitation of coldest quarter

distributional range in the core populations (Fig. 3d). These results suggest that in some species, disjunct populations are likely to occur in new conditions that fall within their climatic tolerance. All the above can assure the survival of some lineages that may provide the raw genetic material enabling the species to adapt and/or shift in response to the climatic change (Budd and Pandolfi 2010). In two other cases (i.e., *Adonis pyrenaica* under moderate scenario and *Gentiana alpina* under extreme scenario), although both the core and the disjunct models projected range contraction, the species and the aggregate models projected a contrasting range change (i.e., range contraction in aggregate model and range expansion in species model) (Fig. 2). This may occur when disjunct and core populations share the same suboptimal conditions (Fig. 3d, e). These suboptimal conditions may be recognized as optimal in the species model but not in the populations models, resulting in an opposite trend of range change (Pearman et al. 2010; Valladares et al. 2014). Differently, because the aggregate model is the sum of the potential ranges provided by disjunct and core populations' models, the range changes detected by the aggregate model are in accordance with those predicted by the last two.

Conclusion

In conclusion, our results suggest that integrating intraspecific variability does not strongly improve overall accuracy of SDMs based on all species occurrences, but it can result in considerably different conclusions about future range change (Lecocq et al. 2019). However, the response of disjunct groups of populations to climate change largely depends on the difference between the current climate where they grow and the future climate more than on the difference between niches. Consequently, to account for intraspecific differentiation may enable to point out potential resilience units that may act as potential buffer against adverse effects of climate change and accordingly to design targeted conservation strategies (Chen et al. 2020).

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Author contribution statement DD and GC: originally formulated the idea. LV, MG and DD: performed the analyses. GC and LM: supervised the project. LV, MG, DD, GC and LM: wrote the paper.

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Availability of data and materials Occurrences data are owned by public institutions and can be obtained contacting: SILENE—www.silene.eu; Anthos—www.anthos.es; CBNC—http://cbnc.oec.fr); Li.Bi.Oss.—https://www.regione.liguria.it/open-data/item/7256-libioss-specie-animali-suddivise-nei-principali-gruppi-sistematici_7256.html; and Wikiplantbase #Toscana—http://bot.biologia.unipi.it/wpb/toscana/index.html.

Code availability Not applicable.

Declarations

Conflict of interest The authors declare that they have no conflict of interest.

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PLANT TRANSLOCATIONS AND CLIMATE CHANGE: BIOASSAY, SURVEILLANCE AND SOLUTION TO A GLOBAL THREAT?

Research Article

Combining conservation status and species distribution models for planning assisted colonisation under climate change

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Abstract

1. Effects of climate change are particularly important in the Mediterranean Biodiversity hotspot where rising temperatures and drought are negatively affecting several plant taxa, including endemic species. Assisted colonisation (AC) represents a useful tool for reducing the effect of climate change on endemic plant species threatened by climate change.
2. We combined species distribution models (SDMs) for 188 taxa endemic to Italy with the IUCN red listing range loss threshold under criterion A (30%) to define: (a) the number of AC (measured as 2 × 2 km grid cells that should be occupied by new populations, i.e. grid cells = new populations) required to fully compensate for predicted range loss and to halt the decline below the 30% of range loss; (b) The number of cells necessary to compensate for range loss was calculated as the number of currently occupied cells lost under future climate due to unsuitable conditions. We used two representative concentration pathways, +2.6 and +8.5 W/m^2, optimistic and pessimistic scenarios respectively. Availability of suitable areas for AC was also assessed within the current species distribution and within protected areas.
3. Under the optimistic scenario, no taxa would lose more than 30% of their range and AC would not be required. Under the pessimistic scenario, roughly the 90% of taxa showed a cell loss higher than 30%. Eight taxa were predicted to lose >95% of their range. For these species, AC was required from 13 to 16 new populations (=13–16 grid cells) per taxon to cap the range loss at 30%. For currently VU or EN species, an average number of 32–35 AC attempts would be necessary to fully compensate their range loss under a pessimistic scenario. Suitable recipient sites within protected areas falling in their projected range were identified, allowing for short-distance AC.

4. *Synthesis*. Combining species distribution models and red listing thresholds under Criterion A has enabled the strategic planning of multiple species assisted colonisation minimising the effort in terms of new populations to be created and maximising the conservation benefit in terms of range loss compensation.

KEYWORDS
climate change, conservation planning, conservation translocation, endemic plant, managed relocation, plant–climate interaction, prioritisation, red listing

1 | INTRODUCTION

Climate change poses serious threats to biodiversity. In general, species can either migrate with climate change by colonising new areas matching the species environmental requirements or adapt by surviving in situ through mechanisms involving phenotypic plasticity and selection (Giménez-Benavides et al., 2018; Thompson et al., 2013). Nevertheless, the high rates of climate change may prevent some species to dispersing or adapting fast enough to survive (Jiménez-Alfaro et al., 2016). In particular, narrow endemic plant species may not be able to track rapid shifts in climate having poor dispersal capability (Essl et al., 2011) and a restricted climatic niche (Thuiller et al., 2005), which compound the negative effects exerted by climate warming in fragmented landscapes (Ozinga et al., 2009; Pauli et al., 2012). Accordingly, a recent work on the Italian flora (Attorre et al., 2018) highlighted the highest potential for range reduction in species typical of lowlands, where fragmentation of natural habitats has occurred over the last few decades.

A basic foundation of conservation is that species should be maintained within their native ranges wherever possible. However, the rate of human-mediated environmental change (climate change in particular) may necessitate translocation of individuals into new suitable areas when adaptation and dispersal are not possible, an intervention known as assisted colonisation (AC; IUCN, 2013). AC raises several ethical and technical concerns (Schwartz, 2016), namely, the potential invasiveness of a translocated species when introduced into a new habitat (Ricciardi & Simberloff, 2009), the spreading of pathogens and pests (Champagnon et al., 2012), the disruption of recipient ecosystem functioning (Graham et al., 1996) and the hybridisation with local taxa (Ricciardi & Simberloff, 2009). As a consequence, the consideration of AC should follow a cautious approach (Butt et al., 2020) and it should be used as the absolute last attempt to avoid species extinction. Planning for AC is, therefore, important to avoid unnecessary movements of species and identify suitable sites that minimise the risks highlighted above. For instance, short-distance AC (e.g. movements to higher elevations than a species would normally occur, but within a species range, also known as ‘assisted range expansion’; Ste-Marie et al., 2011) is predicted to reduce several risks associated with long-distance movements of species (Mueller & Hellmann, 2008). Another benefit of AC planning across many species is the identification of suitable translocation sites within protected areas. Indeed, translocation is more effective when performed within protected areas (Fenu et al., 2019; Godefroid et al., 2011).

Species distribution models are statistical tools that associate species occurrence with environmental variables (Guisan & Zimmermann, 2000) to detect the environmental factors that account for species distributions, to map potential distribution of species and to estimate suitable areas for a species in the past or future and/or in different regions (Araújo et al., 2019; Zurell et al., 2020). SDMs assume that climate governs species distributions at large geographical scales, and usually do not take into account other influential factors like biogeographical history, dispersal or biotic interactions (Elith & Leathwick, 2009). They have been largely used to understand species' vulnerability to climate change, a key step in developing effective biodiversity conservation plans, and less frequently, to identify and implement management options, like translocation planning (Foden et al., 2019), and detect the role of climate change in translocations failure (Bellis et al., 2020). So far, SDMs have been used to select suitable sites for reintroduction of single species (Adhikari et al., 2012; Wilson et al., 2011), to identify potential source populations for translocation (Maes et al., 2019) and to predict range expansion after translocation (Smeraldo et al., 2017). SDMs have been used in combination with the IUCN Red List Categories and Criteria and related metrics for incorporating the impact of climate change on species extinction risk (Attorre et al., 2018) and other conservation purposes (e.g. Seddon, 2015; Shier, 2015). However, whilst SDMs are increasingly used in biodiversity assessments (Araújo et al., 2019), their reliability may be affected by four critical aspects: the quality of the species occurrence data, the quality of the environmental data, the model building (e.g. different modelling techniques) and the model evaluation (Araújo et al., 2019). All these issues have to be addressed to improve model quality and the options applied should be clearly stated to ensure transparency and reproducibility (Araújo et al., 2019; Zurell et al., 2020).

In this study, we used SDMs to identify the potential loss of current and future suitable climate space of 188 plant taxa endemic to Italy. We then combined the results of SDMs with the IUCN red listing thresholds for range loss under criterion A3(c) (IUCN, 2019) to define the minimum number of AC attempts (assuming that one attempt is needed per 2×2 km grid cell) required to maintain the risk of extinction at the current level (maintenance of the current IUCN category) and to compensate for the full range loss (a proactive intervention aimed at improving a species’ current conservation status).

We also evaluated the availability of suitable areas for AC within the species distribution range, and whether they are located inside or outside protected areas. Our approach will allow to better explore the use of SDMs in plant translocation and will provide a cost–benefit tool for planning AC and other conservation translocation.

2 | MATERIALS AND METHODS

2.1 | Studied species

All the Italian endemic vascular plants (1,340 taxa) have recently been assessed against the IUCN Red List Categories and Criteria (Orsenigo et al., 2018). Of these 1,340 taxa, 188 were selected for this study. Firstly, endemic taxa categorised as Extinct (EX), Extinct in the Wild (EW) Possibly Extinct (CR[PE]) or Data Deficient (DD) were not considered. Secondly, among the 300 taxa (22.4%) recorded in one of the main threat categories (CR, EN, VU), and 218 (16.3%) taxa listed as NT, those with fewer than 30 occurrences were excluded to avoid the risk of inaccurate SDMs. In fact, although sensitivity to sample size varies among algorithms, no algorithm predicts species distributions well with small sample sizes (i.e. roughly 30 occurrences; Jarnevich et al., 2015; Jiménez-Valverde, 2020). In addition, taxa showing gaps in distribution data or taxonomic uncertainties (i.e. genera *Hieracium* L. and *Pilosella* Hill) or typical of azonal wetland habitats (e.g. genus *Pinguicula* L.) were also excluded (see Supporting Information for the full list of taxa). In total, 188 LC, NT, VU, EN or CR Italian endemics (14% of the Italian endemic vascular plants) were used in this study (Table S1).

Occurrence data were obtained from published and unpublished data, herbarium specimens and recent field surveys (since the early 2000s onwards) and validated by groups of expert botanists. These records were organised into a 2 × 2 km grid geo-database (see also Orsenigo et al., 2021 for more details). The final dataset consisted of 12,221 occurrences, ranging from 30 to 471 occurrences for each species.

2.2 | Environmental layers

Cumulative monthly precipitation and monthly maximum and minimum temperature at 1 × 1 km spatial resolution for both current and future time slices were obtained from CHELSA version 1.2 (Karger et al., 2017a, 2017b; www.chelsa-climate.org) for Italy. We used the mean values to resample from 1 × 1 km to the 2 × 2 km resolution of the species data. We then obtained 19 bioclimatic variables for both current and future timeframes by using DISMO package (Hijmans et al., 2017) implemented in R (R Core team, 2017).

For the future climate, we used two representative concentration pathways (RCPs), which represent moderate and extreme possible future emission trajectories and encoded according to a possible range of radiative forcing values in the year 2080 relative to preindustrial values (+2.6 and +8.5 W/m^2, here optimistic and pessimistic scenarios, respectively; IPCC, 2014). We employed representative concentration pathway (RCP) projections from five general circulation models (GCMs), representing physical process in the atmosphere, the ocean, the cryosphere and the earth's surface. Specifically, we chose the following GCMs: CESM1-CAM5, FIO-ESM, IPSL-CM5A-MR, MIROC5, MPI-ESM-MR. The GCMs projections were chosen to minimise the model interdependence, following the recommendations of Sanderson et al. (2015; available on CHELSA website).

To improve transferability of models between species (Petitpierre et al., 2017), we used the first two axes of a principal component analysis (PCA) of bioclimatic variables as environmental variables for species distribution modelling. The PCA was obtained from the bioclimatic variables for current conditions and for each future scenario pooled together; then, a dataset for the current projections and five datasets each (corresponding to the five GCMs) for both future scenarios were obtained separating the values of the first two axes of PCA of each climate. The PCA was performed using ADE4 of R package (Dray & Dufour, 2007).

We identified the potential for undertaking assisted colonisations within range and within protected areas. The spatial extent of distributional range of each species was assessed combining the minimum convex polygon containing all the occurrences with the spatial distribution along the altitudinal range of the species. The altitudinal range (i.e. minimum and maximum elevation) of each taxon was defined according to Pignatti et al. (2017a), Pignatti et al. (2017b), Pignatti et al. (2018) and its spatial distribution was assessed by using the digital elevation model downloaded from Geoportale Nazionale\ Ministry of Environment (http://www.pcn.minambiente.it/mattm/servizio-di-scaricamento-wcs/) with a spatial resolution of 70 metres. The distribution of terrestrial protected areas (including protected natural areas—EUAP, and sites of the Natura 2000 Network) was downloaded from the website of the Italian Ministry of the Environment (https://www.minambiente.it/pagina/aree-naturali-protette).

2.3 | Species distribution models building and evaluation

Species distribution models were built using the bioclimatic variables from across an area describing each species' range plus a buffer of 50 km beyond the range edge. To account for uncertainties in the modelling process (Araújo & New, 2007; Petchey et al., 2015), six widely used SDM techniques (Figure S1) implemented in the R package BIOMOD2 v 3.3.7 (Thuiller et al., 2016) were used. We used modelling techniques belonging to three different model classes: two machine learning methods (Generalised Boosted Models—GBM and Random Forest—RF), two regression methods (Generalized Linear Models—GLM and Multivariate Adaptive Regression Splines—MARS) and two classification method (Classification Tree Analysis—CTA and Flexible Discriminant Analysis—FDA). To minimise the effects of spatial dependency, we randomly sampled 1,000 pseudo-absence data choosing between background points at distance of

5–50 km from any presence point and we generated 10 replicate sets. Then, a split-sample cross-validation was repeated 10 times, using a random subset (30%) of the initial dataset (Figure S1). To validate and interpret the model, we used two different measures implemented in BIOMOD2: ROC (Hanley & McNeil, 1982) and TSS (Allouche et al., 2006). The quality of modelling algorithms was then checked according to the values proposed by Araújo et al. (2005). Projections from different model techniques and environmental datasets were averaged using the mean of projections to implement an ensemble forecasting approach (Marmion et al., 2009), obtaining six current and 60 future projections for each species (Figure S1). Because the threshold choice may affect prediction bias, we transformed continuous probability values to binary presence–absence outputs using three different thresholds, which have been shown to perform equally well or better than others (Cao et al., 2013): the threshold selection method based on equal training sensitivity and specificity, the threshold selection method based on maximising training sensitivity and specificity and threshold selection method based on minimising the distance between the curve and the upper left corner of ROC plot (Figure S1). These were implemented in the R package PresenceAbsence (Freeman & Moisen, 2008). We then considered species as occurring in a cell if at least 50% of models predict its occurrence there (i.e. a majority consensus rule).

2.4 | Range loss and assisted colonisation effort estimation

For each taxon, we calculated the number of currently occupied cells which could be lost under future climate in two different ways: directly as the number of cells currently occupied and lost in the future (hereafter COL) and in proportion to the loss of suitable area (hereafter SAL). COL was calculated as the number of currently occupied cells that were projected to be unsuitable under the future climate. This value assumes that the loss of occupied cells may not be proportional to the loss of potential suitable area as not all of the projected area. SAL was calculated on the basis of the loss of the suitable area for a species (i.e. number of currently occupied cells*ratio of the number of grid cells projected to be suitable under present climate but becoming unsuitable under future climate, and the number of grid cells predicted suitable under present climate). By multiplying the number of currently occupied cells by a ratio derived from projected losses and current suitable habitat, this value assumes that the loss of currently occupied cells is proportional to the loss of predicted suitable area. COL might be more realistic because it is actual loss of occupancy, but less accurate relying more strictly on per cell precision of models and climatic data. Then, by using the two previous approaches, we calculated for each taxon: a) the number of grid cells that should be occupied to compensate for range loss; and b) the number of grid cells that should be occupied to halt the decline below the 30% of range loss. The latter threshold corresponds to the range loss required to a species to shift from LC to VU under Criterion A3(c) (IUCN, 2019), and to shift from a threat category to the immediately higher one (e.g. from EN to CR).

3 | RESULTS

3.1 | Species distribution models and assisted colonisation effort required to reduce the risk of extinction

The first two axes of the PCA calibrated over all climates and considering all variables accounted for 74.17% of the total variance (37.81% of variance along the first axis, 36.36% along the second axis), with precipitation variables mainly contributing to the first axis and temperature variables to the second (Table S2). Under current climate conditions, model evaluation indices (ROC and TSS) indicated a good model performance for almost all modelling algorithms, with exceptions of three algorithms out of five (CTA, RF and GLM) in nine taxa (Table S3). Both indices indicated only a fair performance in three taxa for CTA and GLM, ROC indicated a fair performance in three taxa for one algorithm and one taxa for two algorithms (CTA and RF) and TSS indicated a fair performance in two taxa for one algorithm (Table S4).

Under the optimistic scenario, no taxa would lose equal to or more than 30% of their cells both considering COL and SAL (Figure 1a,c). However, the intensity of range loss is different considering COL and SAL. In particular, COL was high, roughly 60% of taxa were predicted to lose at least the 10% of their currently occupied cells and only the 5% of taxa were projected to not lose cells. SAL was lower, roughly only 2% of taxa were projected to lose more than 1% of their currently occupied cells. Under the pessimistic scenarios, losses of more than 30% were found for 95% of taxa using the COL metric, and 88% of taxa using the SAL metric (Figure 1b,d).

Moreover, in the latter scenario, eight taxa (*Bellevalia webbiana*, *Brassica glabrescens*, *Centaurea aplolepa* subsp. *carueliana*, *Cerastium supramontanum*, *C. utriense*, *Salix arrigonii*, *Festuca riccerii* and *Viola bertolonii*) were projected to lose all or nearly all (>95%) of their currently occupied cells, that is, COL (Table S1). For these taxa, the effort required to halt the loss of range under the threshold of 30% would require on average, 13–16 new cells per taxon (considering SAL and COL respectively). For species currently listed as VU or EN, an average number of 35 and 32 new cells (using COL and SAL metrics, respectively) would be necessary to fully compensate their range loss under a pessimistic scenario. Nevertheless, the percentage of taxa expected to lose more than the 80% of their currently occupied cells was lower according to the COL method than when considering the SAL (7.5% and 20% respectively).

In a finding in line with the low losses of currently occupied cells under the optimistic scenario, there were no taxa that met the threshold of 30% loss that might then require compensatory assisted colonisation. Similarly, under the optimistic scenario, the number of cells needed to entirely compensate for COL and SAL was generally low (Figure 2a,c; Table S1). In particular, <10 cells were forecast to entirely compensate for COL and SAL in the 85% and 100% of taxa respectively.

Under the pessimistic scenario, roughly 30 cells were forecast to entirely compensate for COL and SAL in the 50% of taxa (Figure 2b,d; Table S1). Similarly, 20 cells had to be recovered to halt

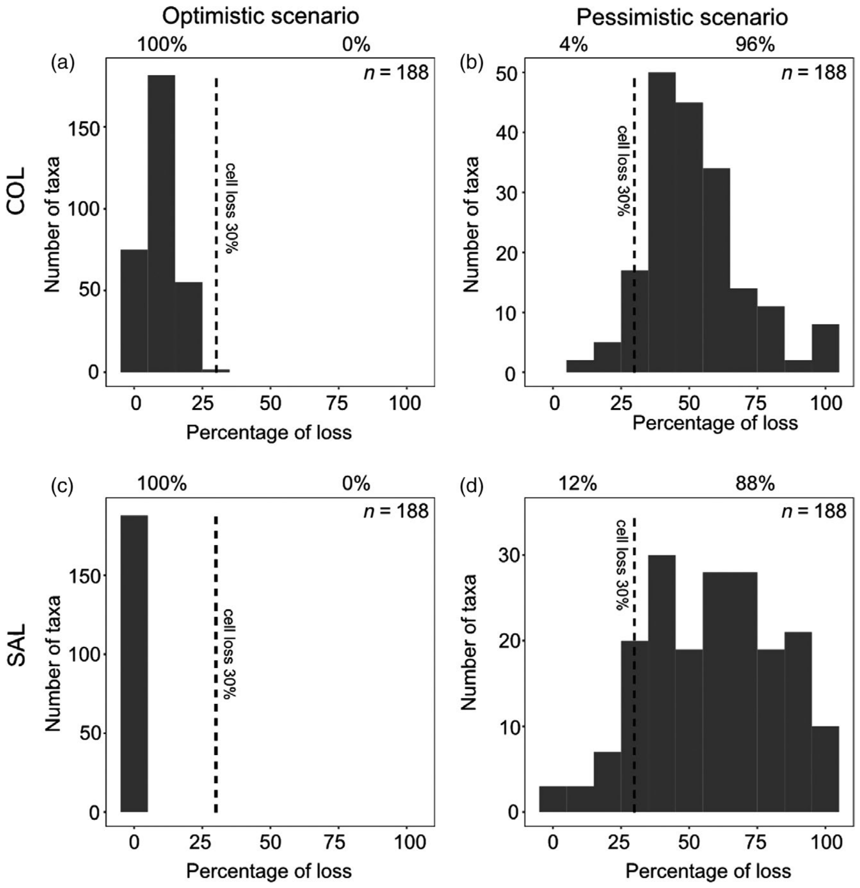

FIGURE 1 Frequency distribution of loss of currently occupied cells (COL; a and b) and loss of currently occupied cells proportional to the loss of suitable area (SAL; c and d) under future optimistic (a and c) and pessimistic (b and c) scenario. The dotted line shows the threshold of 30% of reduction. The percentage of species having a reduction lower (left) and higher (right) than 30% is reported above the plot

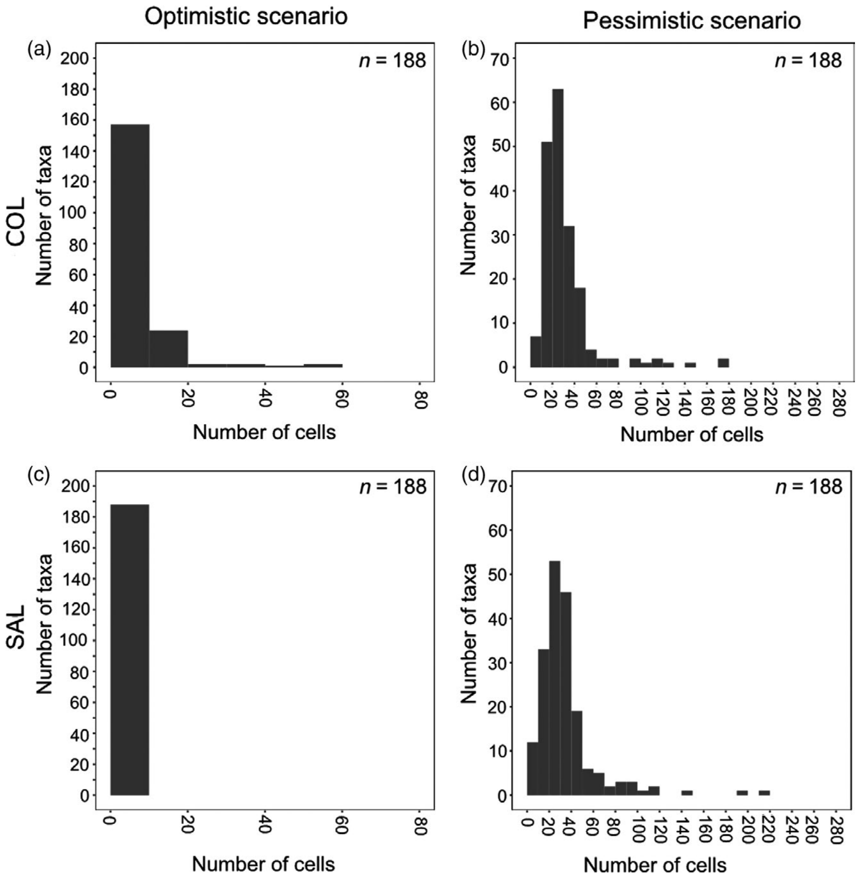

FIGURE 2 Frequency distribution of the number of cells required for translocation necessary to completely compensate for loss of currently occupied cells (COL; a and b) and loss of currently occupied cells proportional to the loss of suitable area (SAL; c and d) under optimistic (a and c) and pessimistic scenario (b and d)

the drop below 30% in the 85% and 68% of taxa considering COL and SAL respectively (Figure 3a,b).

3.2 | Within-range assisted colonisations and availability of suitable cells within protected areas

Most taxa were forecast to have suitable sites available for AC within protected areas in their distribution range. In an optimistic scenario, only two (*Ophrys passionis* subsp. *majellensis* and *Saxifraga presolanensis*) and seven (the previous two plus *Campanula sabatia*, *Limonium merxmuelleri* subsp. *sulcitanum*, *Laserpitium nitidum*, *Oenanthe lisae* and *Viola ferrarinii*) taxa were expected to have not enough cells in protected areas within the distribution range to entirely compensate for COL and SAL respectively (Figure 4a,b). Under the pessimistic scenario, roughly 10% of taxa were expected to have inadequate numbers of cells in protected areas within the range to halt the drop below 30% considering both calculation methods (Figure 4c,d). Similarly, roughly 25% of taxa were expected to have too few cells in protected areas within the range to entirely compensate for both COL and SAL (Figure 4e,f).

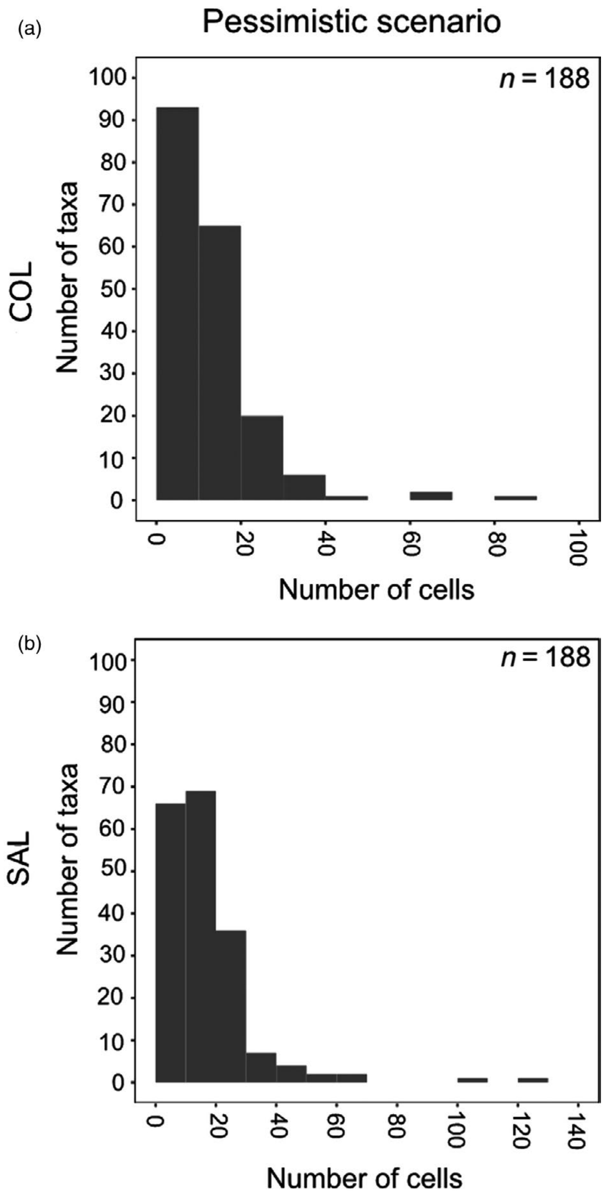

FIGURE 3 Frequency distribution of the number of translocation necessary to halt the decline below the 30% to completely compensate for loss of currently occupied cells (COL; a) and loss of currently occupied cells proportional to the loss of suitable area (SAL; b) under pessimistic scenario

4 | DISCUSSION

Climate change has been demonstrated to be an important driver of plant species distribution shift, local extirpation and colonisation (Parmesan & Hanley, 2015). Plants threatened by climate change may find their own way to escape global warming depending on their dispersal ability (Engler et al., 2009). However, in a highly fragmented landscape due to habitat destruction and degradation, migration to suitable areas may become impossible (Renton et al., 2013). It is therefore important to assess assisted colonisation as a proactive conservation activity for some highly threatened species (Butt et al., 2020).

In our study, SDMs revealed important differences between the two considered climate change scenarios in the future conservation status of 188 plant species endemic to Italy, which in turn is reflected in the opportunity to use AC to mitigate the effect of climate change. As explained below, our new approach for planning assisted colonisation, that combines IUCN red listing criterion A3 and SDMs, has the advantage of defining the expected outcomes to be achieved through AC (in terms of a species' future conservation status), and subsequently decides whether AC is needed or not. Under the optimistic scenario, AC would not be needed, whilst under the pessimistic scenario, AC may be useful, especially for eight taxa predicted to lose nearly all their range.

The limitations of the approach we adopted should be considered and addressed with particular attention. Our approach for planning assisted colonisation of multiple species is scale dependent; thus, the number of grid cells to be occupied by new populations of a given species to compensate for range loss depends on the grid size. Here, we used a grid resolution (i.e. 2 × 2 km) that has been demonstrated to be effective for calculating the AOO of species whose distribution is well known (Martín, 2009). In addition, we used climatic variables that may be only one part of a suite of predictor variables controlling species distribution. In fact, other processes like abiotic constraints, dispersal, biotic interactions, evolution under changing environmental conditions and population dynamics may affect reliability of species distribution projections (Akçakaya, 2000; Thuiller et al., 2013). Recently, considerable progress has been made towards the integration of population dynamics and dispersal in SDMs, as pointed out by recently developed approaches, including BioMove (Midgley et al., 2010), MigClim (Engler et al., 2012) and RangeShifter (Bocedi et al., 2014). Then, we suggest that, when this approach is used for planning of pre-emptive actions on single species, all these issues should be addressed using all available information.

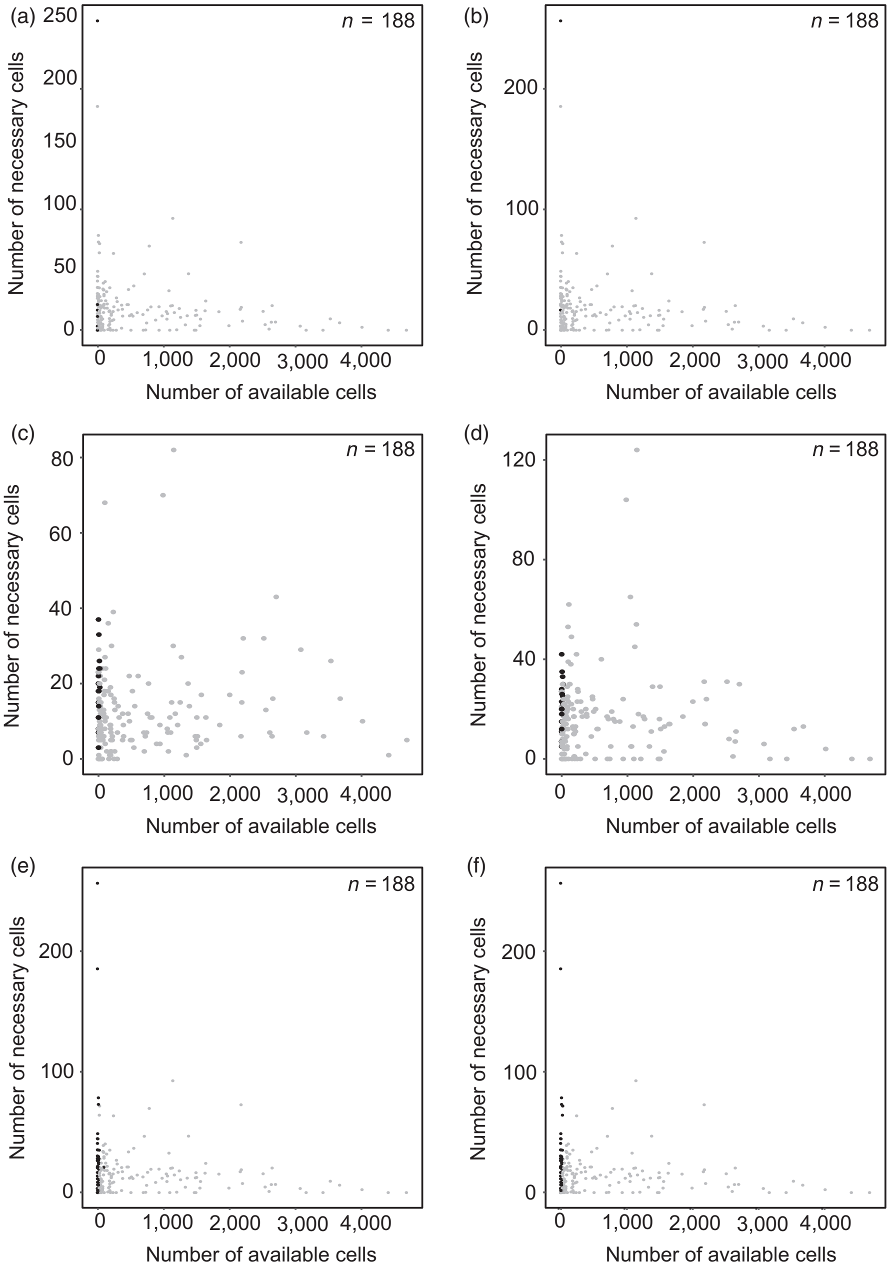

FIGURE 4 Scatterplot showing the relationship between the number of cells necessary to halt the decline below the 30% (c and d) and to completely compensate (a, b, e and f) both for loss of currently occupied cells (a, c and e) and loss of currently occupied cells proportional to the loss of suitable area (b, d and f) and the under optimistic (a and b) and pessimistic scenario (c–f), and the sites available for translocation in protected areas within the distributional range. Black circles are species that have less sites available for translocation in protected areas within the distributional range than they need to compensate range loss

4.1 | Planning assisted colonisation under an optimistic climate change scenario

According to our SDMs, the optimistic scenario revealed that cell loss was maintained below the 30% threshold in all cases, with minor differences between proportional cell loss and cell loss. This can be explained by considering that the climate predicted in the Mediterranean region under this scenario falls within the climatic variability of the Holocene (Cramer et al., 2018). In the Mediterranean region, some thermophilous species might exploit a weak global warming expanding their distribution range (Casazza et al., 2014; Dagnino et al., 2020; Esteve-Selma et al., 2012). This result supports the effectiveness of policy aimed to reducing emissions. Consequently, even considering the highest loss of occupied cells, all taxa would continue to be listed in their initial threat category under Criterion A3 (AOO reduction < 30%). Thus, despite the Mediterranean basin being one of most vulnerable areas to the impacts of climate change (Giorgi, 2006), in an optimistic scenario, AC may not be a key strategy for plant conservation, especially as 175 of the 188 endemic taxa are currently least concern (LC) or near threatened (NT) and therefore do not qualify for urgent action (Orsenigo et al., 2018). Nevertheless, AC may be needed to improve the conservation status of the 13 species currently listed as VU or EN. Such species already show a restricted distribution and a further range reduction due to climate change may increase their vulnerability to other threats like habitat fragmentation and degradation (Orsenigo et al., 2018). Independently of current and future climate change, conservation introduction sensu IUCN (2013) may compensate for species range loss due to threats other than climate change. For instance, some of the species considered in this study are affected by habitat degradation as a consequence of abandonment of traditional landscape management or habitat destruction due to planned future activities (e.g. Canella et al., 2020; Draper et al., 2016; Orsenigo et al., 2021).

4.2 | Planning assisted colonisation under a pessimistic climate change scenario

Simulations under a pessimistic climate change scenario showed that most species would lose more than 30% of their range. This implies a change of status for most taxa from a low threat category to a higher one, independently from their current threat category.

In particular, eight taxa were predicted to lose more than 95% of their current suitable cells. In this scenario, AC may help avoid extinction of these taxa and contribute to maintain the current conservation status for several other taxa (Wang et al., 2019). A very critical case is represented by *Cerastium supramontanum*, for which no suitable cells at higher elevation are available. In this case, ex situ conservation measures should be immediately put in place. It is worth noting that seven of the above-mentioned eight taxa are currently assessed as LC or NT. Such cases fall in the long-lasting debate on when it is worth applying conservation measures, that is, before or after a threat has begun to produce an effect (Butt et al., 2020).

A key challenge in conservation translocation including AC is the selection of suitable release sites (Abeli & Dixon, 2016). Short-distance AC is predicted to reduce the risks connected to long-distance AC (Abeli et al., 2014; Mueller & Hellman, 2008), and avoid the need for continuous management (Gross & Mackay, 2014; Wadgymar et al., 2015), but may not be so effective in terms of species rescue potential. This is especially the case in the long term, as areas within or just outside the current distribution range may soon be made unsuitable by increasing rates of climate change (Ferrarini et al., 2016). However, SDMs suggest that all analysed Italian endemic species will have enough suitable sites to persist under future climate within their distributional range regardless of projected losses. The availability of suitable sites within the range of the species (e.g. at higher elevation) indicates that the current distribution of such species may be shaped by limited dispersal ability and/or habitat fragmentation (Hargreaves et al., 2014; Wang et al., 2019), and that short-distance AC could be planned for these species to mitigate the effect of climate change. It is worth noting that, even in the pessimistic scenario, 90% of species needing AC would be able to compensate for the forecasted range loss using suitable sites in protected areas, and only 10% of AC candidates would not have this option. Therefore, the availability of suitable within-range areas for AC that are also protected presents a favourable option for the future conservation perspectives of Italian endemic species in the context of global warming.

Our study reveals that the network of protected areas should be employed to accommodate natural or assisted range shift of species affected by climate change (Attorre et al., 2018; Fois et al., 2018) and site selection further refined with ecological and phylogenetic information to identify suitable sites within the protected landscapes (Carta et al., 2019). For example, *Cerastium utriense* would experience a dramatic range loss due to climate change, but AC must be informed by its strict association with specific substrata and ecological conditions, as it lives only on ultramafic substrates (Marsili et al., 2009). *Bellevalia webbiana* shows inter-population genetic differentiation, so that an evolutionarily significant unit (ESU) distinct from others was detected near Faenza (Peruzzi et al., 2021). However, evidence for genetic adaptation to climate change is still relatively scarce (Foden et al., 2019) and phenotypic shifts associated with contemporary climate change seem to be due to phenotypic plasticity, rather than to genetic microevolutionary responses that are much more difficult to be detected (Merilä & Hendry, 2014; Thompson et al., 2013). Nevertheless, even if evolutionary responses to climate change are far from being clarified, difference in phenotypic traits should be carefully considered in planning AC for this species.

Future suitable areas for our target species outside protected areas should be soon included in the design of new protected areas. However, although SDMs can efficiently define a range of potentially suitable areas to be protected, other considerations, including those related to socio-economic and political issues, should be taken in account (Fenu et al., 2019) and will ultimately define the potential for an expanded protected area network.

5 | CONCLUSIONS

Assisted colonisation will likely become more common in Conservation Biology. The availability of tools turning into practice the principle of theoretical decision frameworks available in the literature (Abeli et al., 2014; Hoegh-Guldberg et al., 2008; Schwartz et al., 2012) and the increasing reliability of SDMs will likely boost the applicability of this type of actions and drive experimental trials (e.g. Martín-Alcón et al., 2016). Setting AC goals to aim at is important for planning effective actions in the long term and evaluate feasibility. As suggested by our study, the IUCN red listing criteria (in particular, criterion A3) offer worldwide recognised standards that can be used as a reference to set final AC goals and objectives. As conservation often stands on a trade-off between conservation benefits and available resources, prioritisation of AC in terms of effort required is also important. The number of new populations to be created to achieve a specific conservation target proved to be a good insight into effort and feasibility of AC. Finally, although AC is often intended as long-distance movements of organisms, we highlight that AC may include short-distance movements, that would minimise biological, social, ethical and logistical risks.

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AUTHORS' CONTRIBUTIONS

G.C., T.A., S.O. conceived the idea; G.C., L.V., D.D., L.M. analysed the data; G.B., G.F., D.G., C.M., L.P., G.R. provided part of the data and wrote parts of the manuscript.

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SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section.

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Mat. Sup. Paper I

Supplementary information Evolutionary relationships in the taxonomically complex genus *Santolina* endemic to the Mediterranean Basin

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Sample*	Taxon	Country	Statut	Description material	Collector
AC-1-1-155200_S52_R1_001	Achillea millefolium	Italy	Cultivated	Plant leaves collected in Genova Botanical Garden	University of Genova
AC-1-1-155202_S36_R1_001	Argyranthemum coronopifoliu	Italy	Cultivated	Plant leaves collected in Hanbury Botanical Garden in Ventimiglia	University of Genova
AF-1-1_S59_R1_001	Santolina africana	Tunisia	Wild	Plant leaves collected in field	University of Santiago de Compostela
AF-2-1_S3_R1_001	Santolina africana	Morocco	Wild	Plant leaves collected in field	University of Santiago de Compostela
AF-3-1_S14_R1_001	Santolina africana	Tunisia	Wild	Plant leaves collected from Firenze herbarium	University of Genova
AR-1-1_S9_R1_001	Santolina rosmarinifolia	Spain	Wild	Plant leaves collected in field	University of Santiago de Compostela
BE-1-1_S67_R1_001	Santolina benthamina	France	Wild	Plant leaves collected in field	University of Pisa
BE-1-2_S43_R1_001	Santolina benthamina	France	Wild	Plant leaves collected in field	University of Pisa
CA-1-1_S91_R1_001	Santolina canescens	Spain	Wild	Plant leaves collected in field	University of Santiago de Compostela
CH-1-1_S57_R1_001	Santolina chamaecyparissus	France	Wild	Plant leaves collected in field	University of Pisa and Cagliari
CH-1-2_S29_R1_001	Santolina chamaecyparissus	France	Wild	Plant leaves collected in field	University of Pisa and Cagliari
CO-1-1_S51_R1_001	Santolina corsica	France	Wild	Plant leaves collected in field	University of Pisa and Cagliari
CO-1-2_S55_R1_001	Santolina corsica	Italy	Wild	Plant leaves collected in field	University of Pisa and Cagliari
CO-2-1_S26_R1_001	Santolina corsica	Italy	Wild	Plant leaves collected in field	University of Pisa and Cagliari
CO-2-2_S6_R1_001	Santolina corsica	Spain	Wild	Plant leaves collected in field	University of Pisa and Cagliari
CT-1-1_S89_R1_001	Santolina rosmarinifolia	France	Wild	Plant leaves collected in field	University of Santiago de Compostela
DE-1-1_S32_R1_001	Santolina decumbens	France	Wild	Plant leaves collected in field	University of Pisa
DE-1-2_S66_R1_001	Santolina decumbens	Spain	Wild	Plant leaves collected in field	University of Pisa
EL-1-1_S94_R1_001	Santolina elegans	Italy	Cultivated	Plant leaves collected in field	University of Santiago de Compostela
EP-1-1_S11_R1_001	Euryops pectinatus	France	Wild	Plant leaves collected in field	University of Pisa
ER-1-1_S73_R1_001	Santolina ericoides	Spain	Wild	Plant leaves collected in field	University of Pisa
ER-1-2_S88_R1_001	Santolina ericoides	Italy	Wild	Plant leaves collected in field	University of Pisa
ET-1-1_S50_R1_001	Santolina etrusca	Italy	Wild	Plant leaves collected in field	University of Pisa
ET-1-2_S69_R1_001	Santolina etrusca	Italy	Wild	Plant leaves collected in field	University of Pisa
ET-2-1_S16_R1_001	Santolina etrusca	Italy	Wild	Plant leaves collected in field	University of Pisa
ET-2-2_S41_R1_001	Santolina etrusca	Spain	Wild	Plant leaves collected in field	University of Pisa
FR-1-1_S27_R1_001	Santolina fructicosa	Spain	Wild	Plant leaves collected in field	University of Santiago de Compostela
IM-1-1_S87_R1_001	Santolina impressa	Italy	Wild	Plant leaves collected in field	University of Santiago de Compostela
IN-1-1_S74_R1_001	Santolina insularis	Italy	Wild	Plant leaves collected in field	University of Pisa and Cagliari
IN-2-1_S58_R1_001	Santolina insularis	Italy	Wild	Plant leaves collected in field	University of Pisa and Cagliari
IN-3-1_S13_R1_001	Santolina insularis	Italy	Wild	Plant leaves collected in field	University of Pisa and Cagliari
IN-4-1_S37_R1_001	Santolina insularis	Italy	Wild	Plant leaves collected in field	University of Pisa and Cagliari
IN-5-1_S72_R1_001	Santolina insularis	Italy	Wild	Plant leaves collected in field	University of Pisa and Cagliari
LI-1-1_S5_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-1-2_S33_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-1-3_S2_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-1-4_S92_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-2-1_S68_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-2-2_S38_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-2-3_S31_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-2-4_S25_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-2-5_S79_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-3-1_S23_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-3-2_S86_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-3-3_S12_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-3-4_S76_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-3-5_S20_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-4-1_S93_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-4-2_S75_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-4-3_S7_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-4-4_S77_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-4-5_S85_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-5-1_S44_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-5-2_S17_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-5-3_S78_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-5-4_S42_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-5-5_S90_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-6-1_S48_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-6-2_S8_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-6-3_S54_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-6-4_S70_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-6-5_S45_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-7-1_S49_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-7-2_S53_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-7-3_S15_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-7-4_S82_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
LI-7-5_S95_R1_001	Santolina ligustica	Italy	Wild	Plant leaves collected in field	University of Genova
MA-1-1_S1_R1_001	Santolina magonica	Spain	Wild	Plant leaves collected in field	University of Barcelona
MA-2-1_S56_R1_001	Santolina magonica	Spain	Wild	Plant leaves collected in field	University of Barcelona
MA-3-1_S19_R1_001	Santolina magonica	Spain	Wild	Plant leaves collected in field	University of Barcelona
ME-1-1_S22_R1_001	Santolina melidensis	Spain	Wild	Plant leaves collected in field	University of Santiago de Compostela
NE-1-1_S39_R1_001	Santolina neapolitana	Italy	Wild	Plant leaves collected in field	University of Napoli
NE-1-2_S60_R1_001	Santolina neapolitana	Italy	Wild	Plant leaves collected in field	University of Napoli
NE-1-3_S65_R1_001	Santolina neapolitana	Italy	Wild	Plant leaves collected in field	University of Napoli
OB-1-1_S34_R1_001	Santolina oblongifolia	Spain	Wild	Plant leaves collected in field	University of Santiago de Compostela
OB-2-1_S64_R1_001	Santolina oblongifolia	Spain	Wild	Plant leaves collected in field	University of Santiago de Compostela
PC-1-1_S18_R1_001	Santolina benthamina	Spain	Wild	Plant leaves collected in field	University of Santiago de Compostela
PE-1-1_S80_R1_001	Santolina pectinata	Spain	Wild	Plant leaves collected in field	University of Santiago de Compostela
PE-2-1_S35_R1_001	Santolina pectinata	Spain	Wild	Plant leaves collected in field	University of Santiago de Compostela
PI-1-1_S28_R1_001	Santolina pinnata	Italy	Wild	Plant leaves collected in field	University of Pisa
PI-2-1_S30_R1_001	Santolina pinnata	Italy	Wild	Plant leaves collected in field	University of Pisa
PI-3-1_S21_R1_001	Santolina pinnata	Italy	Wild	Plant leaves collected in field	University of Pisa
PI-4-1_S47_R1_001	Santolina pinnata	Italy	Wild	Plant leaves collected in field	University of Pisa
PI-5-1_S10_R1_001	Santolina pinnata	Italy	Wild	Plant leaves collected in field	University of Pisa
RO-1-1_S71_R1_001	Santolina rosmarinifolia	Spain	Wild	Plant leaves collected in field	University of Santiago de Compostela
RO-2-1_S83_R1_001	Santolina rosmarinifolia	Spain	Wild	Plant leaves collected in field	University of Santiago de Compostela
RO-3-1_S61_R1_001	Santolina rosmarinifolia	Spain	Wild	Plant leaves collected in field	University of Santiago de Compostela
SM-1-1_S4_R1_001	Santolina semidentata	Spain	Wild	Plant leaves collected in field	University of Santiago de Compostela
TA-1-1_S62_R1_001	Tanacetum vulgare	Italy	Cultivated	Plant leaves collected in Hanbury Botanical Garden in Ventimiglia	University of Genova
VE-1-1_S84_R1_001	Santolina vedranensis	Spain	Wild	Plant leaves collected in field	University of Barcelona
VE-2-1_S81_R1_001	Santolina vedranensis	Spain	Wild	Plant leaves collected in field	University of Barcelona
VE-3-1_S24_R1_001	Santolina vedranensis	Spain	Wild	Plant leaves collected in field	University of Barcelona
VI-1-1_S40_R1_001	Santolina villosa	Spain	Wild	Plant leaves collected in field	University of Santiago de Compostela
VI-1-2_S46_R1_001	Santolina villosa	Spain	Wild	Plant leaves collected in field	University of Pisa
VS-1-1_S63_R1_001	Santolina viscosa	Spain	Wild	Plant leaves collected in Firenze Herabrium	

The samples received were morphologically checked by University of Pisa to confirm the correct nomenclature

Table S1. Sampling of individuals from *Santolina*. Columns of the table give the code of either individuals or populations (Sample), species name (Taxon), collection place (Country), plant condition (wild or cultivated), description of the collected material (Description material), name of the collectors (Collector).

c085						
MIN SAMPLES PER LOCUS	**N° LOCI**	**HETEROZ. RATE**	**ERROR RATE**	**Nb_snps**	**NA**	**Sum_PIS**
12	27926.76087	0.02168837	0.011644413	126905	55.22%	56722
24	1827.26087	0.02168837	0.011644413	43095	35.72%	19756
32	1408.379149	0.02168837	0.011644413	15667	23.69%	7017
ds	15190.91796	4.24919E-18	4.24919E-18	57951.56588	0.159117975	25817.80491

c090						
MIN SAMPLES PER LOCUS	**N° LOCI**	**HETEROZ. RATE**	**ERROR RATE**	**Nb_snps**	**NA**	**Sum_PIS**
12	5863.369565	0.02168837	0.011644413	180913	55.86%	82870
24	2457.173913	0.02168837	0.011644413	59214	36.24%	27757
32	980.3913043	0.02168837	0.011644413	20275	23.80%	9278
ds	2504.214194	4.24919E-18	0	83796.83702	0.161634444	38285.54704

c095						
MIN SAMPLES PER LOCUS	**N° LOCI**	**HETEROZ. RATE**	**ERROR RATE**	**Nb_snps**	**NA**	**Sum_PIS**
12	4254.304348	0.02168837	0.011644413	205412	58.13%	90474
24	2512.804348	0.02168837	0.011644413	55289	36.60%	25731
32	962.3043478	0.02168837	0.011644413	18288	24.08%	8352
ds	1646.923217	4.24919E-18	0	99097.07405	0.172225327	43277.60886

Table S2. IPYRAD statistics for the nine different datasets with different clustering thresholds and minimal samples per locus containing 43 samples representing 19 Santolina species and the three outgroups.

Samples	Taxon	reads_raw	reads_passed_filter	clusters_total	clusters_hidepth	reads_consens	loci_in_assembly
AC-1-1-155200_S52001	*Achillea millefolium*	3622352	3619317	576676	74600	69213	333
AF-1-1_S59001	*Santolina africana*	727935	727045	144273	20760	19437	2721
AF-3-1_S14001	*Santolina africana*	2824517	2821357	337036	56270	52723	5985
AR-1-1_S9001	*Santolina rosmarinifolia*	654468	653619	136963	19392	18216	1812
BE-1-1_S67001	*Santolina benthamiana*	2112691	2110368	282546	46221	43357	8453
CA-1-1_S91001	*Santolina canescens*	1892655	1891014	274880	40873	38144	3540
CH-1-1_S57001	*Santolina chamaecyparissus*	2575146	2571952	385135	59313	55323	10609
CH-1-2_S29001	*Santolina chamaecyparissus*	3087360	3084001	398419	68304	63944	11338
CO-1-1_S51001	*Santolina corsica*	1435874	1434199	256007	38549	36106	7313
CO-1-2_S55001	*Santolina corsica*	2232969	2230240	343454	53402	50017	9507
CO-2-2_S6001	*Santolina corsica*	1743063	1741364	297767	45502	42551	7422
CT-1-1_S89001	*Santolina rosmarinifolia*	3814384	3811013	388846	58368	54451	4293
DE-1-1_S32001	*Santolina decumbens*	1490415	1488729	217843	38006	35880	6967
DE-1-2_S66001	*Santolina decumbens*	1238461	1237142	207709	32982	31009	6609
EP-1-1_S11001	*Euryops pectinatus*	4473224	4470716	368269	45912	43028	92
ER-1-1_S73001	*Santolina etrusca*	3430595	3426196	357871	56771	53323	9279
ER-1-2_S88001	*Santolina etrusca*	2919731	2916256	390348	58786	55039	9509
ET-1-1_S50001	*Santolina etrusca*	2878514	2875530	330234	50059	46816	10883
ET-1-2_S69001	*Santolina etrusca*	976290	975305	151050	25216	23763	6070
ET-2-1_S16001	*Santolina etrusca*	4135416	4130504	442070	71043	66822	11753
IN-1-1_S74001	*Santolina insularis*	1005430	1004015	177832	29480	27813	4121
IN-3-1_S13001	*Santolina insularis*	710598	709837	116524	22113	20940	3645
IN-4-1_S37001	*Santolina insularis*	1414072	1412773	258955	39872	37218	6472
IN-5-1_S72001	*Santolina insularis*	2161233	2159059	425989	53705	49525	8602
LI-1-1_S5001	*Santolina ligustica*	3066618	3063689	390431	55273	51351	11833
LI-6-2_S8001	*Santolina ligustica*	1674332	1672711	234626	37357	35068	8971
LI-7-5_S95001	*Santolina ligustica*	2019469	2017347	276145	43370	40595	10073
MA-1-1_S1001	*Santolina magonica*	2172478	2169929	332614	45561	42410	10100
MA-2-1_S56001	*Santolina magonica*	3016703	3013458	454324	61075	56428	10988
MA-3-1_S19001	*Santolina magonica*	2606191	2603438	377417	53853	50001	10913
ME-1-1_S22001	*Santolina melidensis*	3419471	3416021	463428	63548	58692	4675
NE-1-1_S39001	*Santolina neapolitana*	1512699	1511018	226242	37235	34996	8886
NE-1-2_S60001	*Santolina neapolitana*	1778584	1776413	229264	38373	36146	8794
NE-1-3_S65001	*Santolina neapolitana*	2010170	2008037	274625	43598	40857	9514
PE-1-1_S80001	*Santolina pectinata*	902283	900951	174854	22898	21417	2043
PE-2-1_S35001	*Santolina pectinata*	432965	432593	110714	12198	11237	1227
PI-1-1_S28001	*Santolina pinnata*	3316233	3312017	361499	56033	52706	10245
PI-3-1_S21001	*Santolina pinnata*	3611721	3608288	408875	59152	55147	10901
PI-4-1_S47001	*Santolina pinnata*	2851035	2848051	331992	51907	48651	10345
PI-5-1_S10001	*Santolina pinnata*	5123284	5116344	550486	80474	74955	11949
SM-1-1_S4001	*Santolina semidentata*	1391774	1390292	230385	32220	30016	2881
TA-1-1_S62001	*Tanacetum vulgare*	4004952	4003151	602639	87464	80517	285
VE-1-1_S84001	*Santolina vedranensis*	3709961	3705952	491950	62326	57472	9969
VE-2-1_S81001	*Santolina vedranensis*	4208489	4203567	492894	64963	60201	10435
VE-3-1_S24001	*Santolina vedranensis*	3046761	3043516	431913	52735	48615	9441
VI-1-2_S46001	*Santolina villosa*	3829181	3826155	573744	78584	72604	7478

Table S3. Final Ipyrad stats summary for the selected dataset (c095msl12).

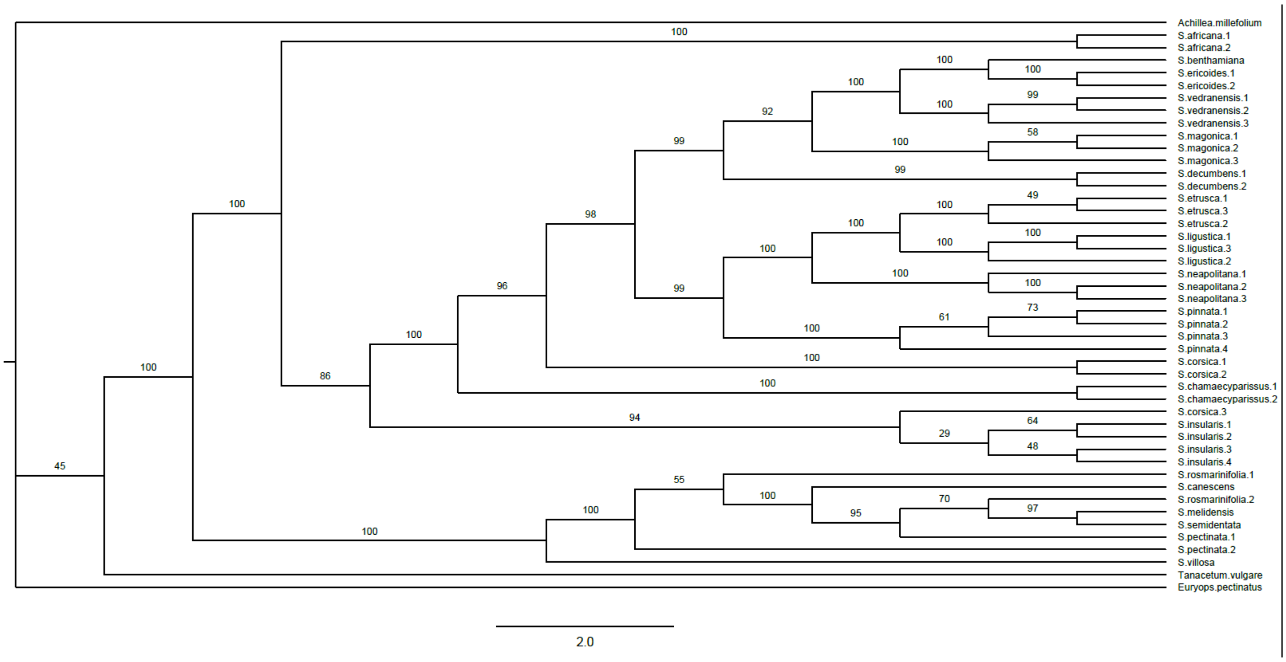

Fig. S1. Species tree constructed using SVD quartets with bootstrap values overlaid over the branches

P2-P3	*S_benthamiana*	*S_canescens*	*S_chamaecyparissus*	*S_corsica*	*S_decumbens*	*S_ericoides*	*S_etrusca*	*S_insularis*	*S_ligustica*	*S_magonica*	*S_melidensis*	*S_neapolitana*	*S_pectinata*	*S_pinnata*	*S_rosmarinifolia*	*S_semidentata*	*S_vedranensis*	*S_villosa*
S_benthamiana	0	0.505576	0	0	0	0	0	0	0	0	0	0	0.493827	0	0.405136	0	0	0.430721
S_chamaecyparissus	0	0.321722	0	0	0	0	0	0.38349	0	0	0.395216	0	0.44123	0	0.427071	0.431561	0	0.358246
S_corsica	0	0.534965	0.249929	0	0	0	0	0.48356	0	0	0.367869	0	0.385386	0	0.400137	0.401132	0	0.317526
S_decumbens	0	0	0.392985	0.377091	0	0	0.473791	0.379746	0.538039	0	0	0.486188	0	0.408279	0	0	0	0
S_ericoides	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0.309612
S_etrusca	0.242469	0	0.339314	0.467891	0.318226	0.242529	0	0.363069	0	0.363452	0	0	0	0	0	0	0.223011	0
S_insularis	0	0.667898	0	0	0	0	0	0	0	0	0.56774	0	0.579874	0	0.664899	0.625026	0	0.477598
S_ligustica	0	0	0.297165	0.471486	0.309649	0	0	0.340184	0	0.284908	0	0	0	0	0	0	0	0
S_magonica	0	0	0.319032	0.306316	0.194952	0	0.380714	0.289963	0.386388	0	0	0.341986	0	0.256439	0	0	0	0.198415
S_neapolitana	0	0	0.176741	0.426932	0.177575	0	0.347406	0.305024	0.379481	0.218207	0	0	0	0	0	0	0	0
S_pectinata	0	0	0	0	0.603604	0	0	0	0	0	0	0	0	0	0	0	0	0
S_vedranensis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.319601
S_villosa	0.396349	0	0.327778	0.315649	0.514634	0.351145	0.502907	0	0.45152	0.253156	0	0.449339	0	0.425179	0	0	0.412428	0

Table S4. ABBA/BABA test output from Dsuite showing quartets with D statistic values of 0.05 or greater. The table is arranged from highest D statistic to lowest. Introgression is always between P2 and P3 and the outgroup, *S. africana*, are not shown.

Mat. Sup. Paper III

Supporting information

Title: Dealing with disjunct populations of vascular plants: implications for assessing the effect of climate change

Authors: Varaldo Lucia[1*], Guerrina Maria[1*], Dagnino Davide[1], Minuto Luigi[1], Casazza Gabriele[1]

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Table S1. The amount of variance in current and future climates explained by the first (PC1) and the second principal axis (PC2), and the remaining variance not explained by the first two axes (NE).

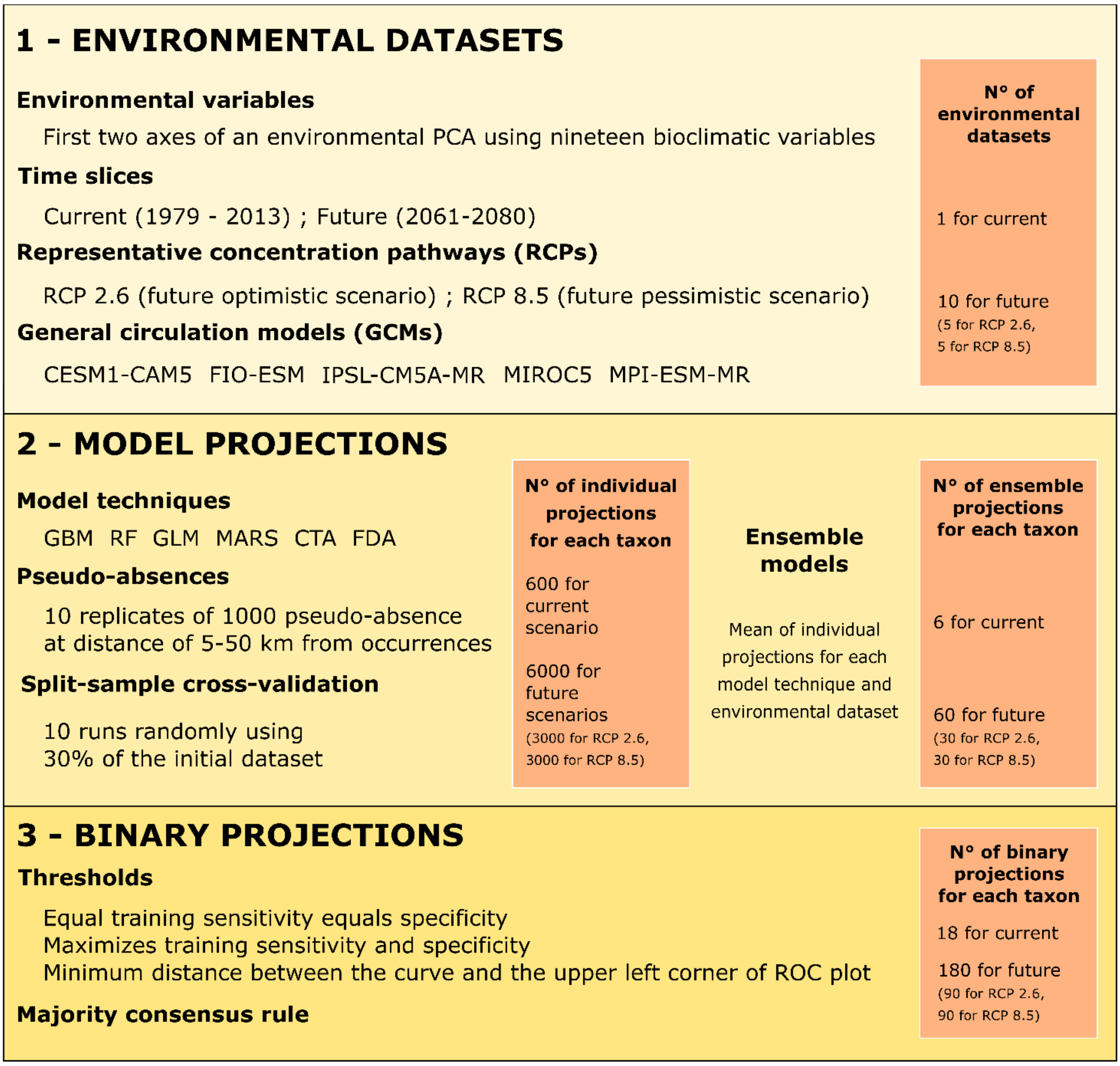
Species	PC1 (%)	PC2 (%)	NE
Adonis pyrenaica	53.64	17.85	28.51
Allium narcissiflorum	48.83	33.67	17.50
Crocus ligusticus	62.34	13.24	24.42
Cytisus ardoinii	61.50	16.94	21.56
Erysimum collisparsum	59.34	13.28	27.38
Eryngium spinalba	64.93	10.87	24.20
Gentiana alpina	52.93	13.17	33.90
Potentilla nivalis	57.54	14.20	28.26
Primula hirsuta	53.69	12.82	33.49
Thymelaea dioica	56.45	15.69	27.86
Valeriana rotundifolia	62.17	13.92	23.91
Valeriana saxatilis	49.76	16.55	33.69

Table S2. Results of niche overlap and niche similarity test between core and disjunct populations. Backgrounds are defined by applying 5, 10 and 15 km buffer zones around the occurrence points. Significant results are indicated by 'less' for significant divergence or 'more' for significant similarity between test and comparison taxa.

Species	Niche Overlap	Similarity test					
		core vs disjunct background			disjunct vs core background		
		5km	10km	15km	5km	10km	15km
Adonis pyrenaica	0.14	ns	ns	ns	more	more	more
Allium narcissiflorum	0.16	ns	more	more	ns	ns	ns
Crocus ligusticus	0.30	ns	more	more	more	ns	ns

Cytisus ardoinii	0.16	ns	ns	ns	more	more	ns
Erysimum collisparsum	0.08	ns	ns	ns	ns	ns	ns
Eryngium spinalba	0.06	ns	ns	ns	ns	ns	ns
Gentiana alpina	0.27	ns	ns	ns	more	more	ns
Potentilla nivalis	0.19	ns	ns	more	ns	ns	more
Primula hirsuta	0.39	ns	more	more	more	more	more
Thymelaea dioica	0.06	ns	more	ns	more	more	ns
Valeriana rotundifolia	0.00	ns	ns	ns	ns	ns	ns
Valeriana saxatilis	0.00	ns	ns	ns	ns	ns	ns

Mat. Sup. Paper IV



1 - ENVIRONMENTAL DATASETS

Environmental variables

First two axes of an environmental PCA using nineteen bioclimatic variables

Time slices

Current (1979 - 2013) ; Future (2061-2080)

Representative concentration pathways (RCPs)

RCP 2.6 (future optimistic scenario) ; RCP 8.5 (future pessimistic scenario)

General circulation models (GCMs)

CESM1-CAM5 FIO-ESM IPSL-CM5A-MR MIROC5 MPI-ESM-MR

N° of environmental datasets

1 for current

10 for future
(5 for RCP 2.6,
5 for RCP 8.5)

2 - MODEL PROJECTIONS

Model techniques

GBM RF GLM MARS CTA FDA

Pseudo-absences

10 replicates of 1000 pseudo-absence
at distance of 5-50 km from occurrences

Split-sample cross-validation

10 runs randomly using
30% of the initial dataset

N° of individual projections for each taxon

600 for current scenario

6000 for future scenarios
(3000 for RCP 2.6,
3000 for RCP 8.5)

Ensemble models

Mean of individual projections for each model technique and environmental dataset

N° of ensemble projections for each taxon

6 for current

60 for future
(30 for RCP 2.6,
30 for RCP 8.5)

3 - BINARY PROJECTIONS

Thresholds

Equal training sensitivity equals specificity
Maximizes training sensitivity and specificity
Minimum distance between the curve and the upper left corner of ROC plot

Majority consensus rule

N° of binary projections for each taxon

18 for current

180 for future
(90 for RCP 2.6,
90 for RCP 8.5)

Fig. S1 Environmental layers and model settings. RCP2.6 and RCP8.5 are two representative concentration pathways named according to two possible range of radiative forcing values in the year 2100 relative to preindustrial values (+2.6 and +8.5 W/m2, respectively). GCMs are general circulation models provided by National Center for Atmospheric Research (CESM1-CAM5), First Institute of Oceanography (FIO-ESM), Institut Pierre Simon Laplace (IPSL-CM5A-MR), International Centre for Earth Simulation (MIROC5), Max Planck Institute for Meteorology (MPI-ESM-MR). Optimistic and pessimistic scenarios are the mean value of the four GCMs for RCP2.6 and RCP8.5, respectively. Model techniques: GBM, Generalised Boosted Models; RF, Random Forest; GLM, Generalized Linear Models; MARS, Multivariate Adaptive Regression Splines; CTA, Classification Tree Analysis and FDA, Flexible Discriminant Analysis.

			Optimistic	Pessimistic	Optimistic	Pessimistic
Family	**Taxa**	**IUCN Category**	**Proportional cell loss (%)**	**Proportional cell loss (%)**	**Cell loss (%)**	**Cell loss (%)**
Sapindaceae	*Acer cappadocicum* Gled. subsp. *lobelii* (Ten.) A.E.Murray	LC	0.02	58	18.52	37.04
Fabaceae	*Adenocarpus complicatus* (L.) J.Gay subsp. *brutius* (Brullo, De Marco & Siracusa) Peruzzi & Bernardo	NT	1.08	63.31	10.71	53.57
Asteraceae	*Adenostyles australis* (Ten.) Iamonico & Pignatti	LC	0	55.99	3.9	53.25
Lamiaceae	*Ajuga tenorei* C.Presl	LC	0.48	70.61	16.67	47.62
Brassicaceae	*Alyssum diffusum* Ten. subsp. *diffusum*	LC	0.03	78.62	14	48
Ranunculaceae	*Anemonoides trifolia* (L.) Holub subsp. *brevidentata* (Ubaldi & Puppi) Galasso, Banfi & Soldano	LC	0	34.77	6.94	37.14
Plantaginaceae	*Antirrhinum siculum* Mill.	LC	0	25.88	6.67	44.44
Ranunculaceae	*Aquilegia lucensis* E.Nardi	NT	0	94.21	0	79.49
Brassicaceae	*Arabis collina* Ten. subsp. *rosea* (DC.) Minuto	LC	0	45.77	17.28	49.38
Caryophyllaceae	*Arenaria huteri* A.Kern.	LC	0	44.99	11.76	47.06
Plumbaginaceae	*Armeria arenaria* (Pers.) Schult. subsp. *marginata* (Levier) Arrigoni	LC	0.06	83.07	6.06	57.58
Plumbaginaceae	*Armeria brutia* Brullo, Gangale & Uzunov	LC	0	84.62	3.12	71.88
Plumbaginaceae	*Armeria denticulata* (Bertol.) DC.	LC	0	57.53	9.09	56.82
Asteraceae	*Artemisia caerulescens* L. subsp. *cretacea* (Fiori) Brilli-Catt. & Gubellini	LC	0	55.24	3.03	39.39
Asteraceae	*Artemisia campestris* L. subsp. *variabilis* (Ten.) Greuter	NT	0	26.09	15.69	33.33
Fabaceae	*Astragalus parnassi* Boiss. subsp. *calabricus* (Fisch.) Maassoumi	LC	0.04	74.43	8.33	61.11
Campanulaceae	*Asyneuma trichocalycinum* (Ten.) K.Malý	LC	0.19	72.32	9.76	60.98
Rhamnaceae	*Atadinus glaucophyllus* (Sommier) Hauenschild	LC	0	88.67	9.8	68.63
Asparagaceae	*Bellevalia webbiana* Parl.	EN	2.31	99.9	6.67	96.67
Asteraceae	*Bellium crassifolium* Moris	EN	0	11.5	8.33	38.89
Brassicaceae	*Biscutella apuana* Raffaelli	LC	0.01	88.12	10.53	68.42
Brassicaceae	*Biscutella morisiana* Raffaelli	LC	0	48.94	12.5	59.38
Poaceae	*Brachypodium genuense* (DC.) Roem. & Schult.	LC	0	68.69	13.02	34.91
Brassicaceae	*Brassica glabrescens* Poldini	LC	0	99.75	0	100
Poaceae	*Bromopsis caprina* (A.Kern. ex Hack.) Banfi & N.G.Passal.	LC	0.07	60.3	11.63	55.81

Asteraceae	*Buphthalmum salicifolium* L. subsp. *flexile* (Bertol.) Garbari	LC	0.01	90.71	10.94	71.88
Campanulaceae	*Campanula bertolae* Colla	LC	0.44	50.56	4.55	58.33
Campanulaceae	*Campanula carnica* Schiede ex Mert. & W.D.J.Koch subsp. *puberula* Podlech	LC	0	36.37	9.09	45.45
Campanulaceae	*Campanula elatines* L.	LC	0.07	35.24	5.62	40.45
Campanulaceae	*Campanula martinii* F.Fen., Pistarino, Peruzzi & Cellin.	LC	0	50.17	3.23	62.9
Campanulaceae	*Campanula micrantha* Bertol.	LC	0.09	88.42	10	55
Campanulaceae	*Campanula morettiana* Rchb.	LC	0.01	42.48	10.45	36.57
Campanulaceae	*Campanula raineri* Perp.	LC	0.24	39.51	6.58	36.84
Campanulaceae	*Campanula sabatia* De Not.	VU	0	15.4	5.13	20.51
Campanulaceae	*Campanula tanfanii* Podlech	LC	0.06	66.44	5.88	38.24
Asteraceae	*Carduus nutans* L. subsp. *perspinosus* (Fiori) Arènes	LC	0.06	69.27	5.56	61.11
Cyperaceae	*Carex macrostachys* Bertol.	LC	0.01	90.99	12.5	64.58
Asteraceae	*Carlina hispanica* Lam. subsp. *globosa* (Arcang.) Meusel & Kästner	LC	0	40.33	1.56	53.12
Asteraceae	*Centaurea aplolepa* Moretti subsp. *aplolepa*	LC	0	29.72	3.03	21.21
Asteraceae	*Centaurea aplolepa* Moretti subsp. *carueliana* (Micheletti) Dostál	LC	0.02	98.93	9.38	100
Asteraceae	*Centaurea aplolepa* Moretti subsp. *lunensis* (Fiori) Dostál	LC	0	27.59	3.77	39.62
Asteraceae	*Centaurea poeltiana* Puntillo	LC	2.44	65.22	11.76	50
Asteraceae	*Centaurea subtilis* Bertol.	NT	0	95.33	6.06	84.85
Caryophyllaceae	*Cerastium apuanum* Parl.	LC	0	85.7	10.26	69.23
Caryophyllaceae	*Cerastium scaranoi* Ten.	LC	1.03	60.66	8.77	45.61
Caryophyllaceae	*Cerastium supramontanum* Arrigoni	NT	0	96.85	8.57	97.14
Caryophyllaceae	*Cerastium tomentosum* L.	LC	0.06	42.8	15.69	41.18
Caryophyllaceae	*Cerastium utriense* Barberis	LC	0	99.75	6	96
Caryophyllaceae	*Cherleria laricifolia* (L.) Iamonico subsp. *ophiolitica* (Pignatti) Iamonico	LC	0	70.7	12.5	58.93
Asteraceae	*Cirsium bertolonii* Spreng.	LC	0.31	89.05	17.07	58.54
Asteraceae	*Cirsium tenoreanum* Petr.	LC	0.01	77.14	9.84	47.54
Asteraceae	*Cirsium vallis-demonii* Lojac.	NT	0	73.62	10	50
Colchicaceae	*Colchicum neapolitanum* (Ten.) Ten.	LC	0	30.93	14.29	52.38
Iridaceae	*Crocus biflorus* Mill.	LC	0	38.49	19.27	36.36
Iridaceae	*Crocus etruscus* Parl.	NT	0	28.04	5.41	43.24
Iridaceae	*Crocus imperati* Ten.	LC	0	40.98	0	35.71
Iridaceae	*Crocus suaveolens* Bertol.	LC	0	14.06	3.03	9.09

Apiaceae	*Cryptotaenia thomasii* (Ten.) DC.	EN	0.07	67.68	7.55	64.15
Boraginaceae	*Cynoglossum apenninum* L.	LC	0	74.47	18.92	45.95
Thymelaeaceae	*Daphne petraea* Leyb.	LC	0	58.47	10.26	38.46
Caryophyllaceae	*Dianthus carthusianorum* L. subsp. *tenorei* (Lacaita) Pignatti	LC	0.01	66.17	12.82	43.59
Caryophyllaceae	*Dianthus sardous* Bacch., Brullo, Casti & Giusso	LC	0	60.14	15.79	42.11
Caryophyllaceae	*Dianthus tarentinus* Lacaita	LC	0	73.92	2.27	61.36
Poaceae	*Drymochloa drymeja* (Mert. & W.D.J.Koch) Holub subsp. *exaltata* (C.Presl) Foggi & Signorini	LC	0	57.87	17.27	59.09
Asteraceae	*Echinops siculus* Strobl	LC	0	35.77	13.85	46.15
Orchidaceae	*Epipactis meridionalis* H.Baumann & R.Lorenz	VU	0.18	57.86	14.58	64.58
Brassicaceae	*Erysimum apenninum* Peccenini & Polatschek	LC	0.04	73.46	12	53.6
Brassicaceae	*Erysimum crassistylum* C.Presl subsp. *garganicum* Peccenini & Polatschek	LC	0.01	77.14	13.46	73.08
Brassicaceae	*Erysimum etruscum* Peccenini & Polatschek	LC	0.04	90.51	17.28	74.07
Brassicaceae	*Erysimum pseudorhaeticum* Polatschek	LC	0.04	84.89	6.19	66.37
Euphorbiaceae	*Euphorbia ceratocarpa* Ten.	NT	0	28.49	5.88	41.18
Euphorbiaceae	*Euphorbia corallioides* L.	LC	0	52.2	15.58	49.35
Euphorbiaceae	*Euphorbia nicaeensis* All. subsp. *japygica* (Ten.) Arcang.	LC	0	93.08	7.5	82.5
Euphorbiaceae	*Euphorbia variabilis* Ces.	LC	0	54.96	7.32	56.1
Orobanchaceae	*Euphrasia tricuspidata* L.	LC	0	27.81	4.1	39.43
Poaceae	*Festuca alfrediana* Foggi & Signorini subsp. *ferrariniana* Foggi, Parolo & Gr.Rossi	NT	0.02	87.17	4.26	57.45
Poaceae	*Festuca austrodolomitica* Pils & Prosser	LC	0.01	51.95	0	59.26
Poaceae	*Festuca riccerii* Foggi & Gr.Rossi	LC	0	96.49	0	83.67
Poaceae	*Festuca robustifolia* Markgr.-Dann.	LC	0	41.81	5.66	31.13
Poaceae	*Festuca violacea* Ser. ex Gaudin subsp. *italica* Foggi, Gr.Rossi & Signorini	LC	0	79.48	7.5	60
Poaceae	*Festuca violacea* Ser. ex Gaudin subsp. *puccinellii* (Parl.) Foggi, Gr.Rossi & Signorini	LC	0.14	83.14	17.86	33.93
Rubiaceae	*Galium baldense* Spreng.	LC	0	47.16	4.49	46.12
Fabaceae	*Genista etnensis* (Raf.) DC.	LC	0.12	55.88	14.29	65.71
Fabaceae	*Genista tyrrhena* Vals.	LC	0	0	8.82	8.82
Plantaginaceae	*Globularia incanescens* Viv.	LC	0	87.36	12.96	51.85

Asteraceae	*Helichrysum litoreum* Guss.	LC	0.02	67.19	22.54	78.17
Asteraceae	*Helichrysum saxatile* Moris subsp. *saxatile*	LC	0	75.38	11.43	51.43
Poaceae	*Helictochloa praetutiana* (Parl. ex Arcang.) Bartolucci, F.Conti, Peruzzi & Banfi subsp. *praetutiana*	LC	0.01	72.82	8.57	43.81
Ranunculaceae	*Helleborus viridis* L. subsp. *bocconei* (Ten.) Peruzzi	LC	0	25.48	5	35.83
Hypericaceae	*Hypericum barbatum* Jacq. subsp. *calabricum* (Spreng.) Peruzzi & N.G.Passal.	VU	0	79.65	8.2	68.85
Iridaceae	*Iris cengialti* Ambrosi ex A.Kern. subsp. *cengialti*	LC	0	38.58	0	52.11
Asteraceae	*Jacobaea maritima* (L.) Pelser & Meijden subsp. *bicolor* (Willd.) B.Nord. & Greuter	NT	0	0.19	18.52	18.52
Asteraceae	*Klasea flavescens* (L.) Holub subsp. *cichoracea* (L.) Greuter & Wagenitz	LC	0.12	58.04	0	78.57
Caprifoliaceae	*Knautia baldensis* A.Kern. ex Borbás	LC	0	36.19	5	33.75
Caprifoliaceae	*Knautia persicina* A.Kern.	LC	0	40.83	2.75	39.45
Poaceae	*Koeleria splendens* C.Presl	LC	0.04	50.35	12.68	50.7
Apiaceae	*Laserpitium nitidum* Zanted.	LC	0	38.53	5.08	44.07
Asteraceae	*Leontodon anomalus* Ball	LC	0.08	87.02	8.96	56.72
Asteraceae	*Leontodon intermedius* (Fiori) Huter, Porta & Rigo ex Rigo	LC	0	47.44	8.57	67.14
Plumbaginaceae	*Limonium acutifolium* (Rchb.) Salmon subsp. *acutifolium*	LC	0	55.75	3.45	100
Plumbaginaceae	*Limonium ilvae* Pignatti	NT	0	93.39	6.45	100
Plumbaginaceae	*Limonium merxmuelleri* Erben subsp. *sulcitanum* (Arrigoni) Arrigoni	LC	0	0	14.81	18.52
Plumbaginaceae	*Limonium multiforme* Pignatti	LC	0	93.48	26.19	100
Plumbaginaceae	*Limonium remotispiculum* (Lacaita) Pignatti	LC	0	40.32	5.88	50
Plantaginaceae	*Linaria purpurea* (L.) Mill.	LC	0	27.39	10.91	34.55
Juncaceae	*Luzula sylvatica* (Huds.) Gaudin subsp. *sicula* (Parl.) K.Richt.	LC	0	64.81	15.22	43.48
Caryophyllaceae	*Mcneillia graminifolia* (Ard.) Dillenb. & Kadereit subsp. *rosanoi* (Ten.) F.Conti, Bartolucci, Iamonico & Del Guacchio	LC	0.05	76.94	16.28	51.16
Orobanchaceae	*Melampyrum italicum* (Beauverd) Soó	LC	0.01	59.02	11.73	49.44
Lamiaceae	*Micromeria cordata* (Moris ex Bertol.) Moris	LC	0	76.05	15.15	63.64
Lamiaceae	*Micromeria graeca* (L.) Benth. ex Rchb. subsp. *tenuifolia* (Ten.) Nyman	LC	0	31.14	13.92	39.24
Caryophyllaceae	*Moehringia glaucovirens* Bertol.	LC	0	31.21	3.64	41.82
Boraginaceae	*Moltkia suffruticosa* (L.) Brand subsp. *bigazziana* Peruzzi & Soldano	LC	0	84.38	9.76	58.54
Boraginaceae	*Myosotis graui* Selvi	LC	0	77.51	8	50
Boraginaceae	*Myosotis sylvatica* Hoffm. subsp. *elongata* (Strobl) Grau	LC	0.01	61.2	12.77	53.19

Brassicaceae	*Odontarrhena argentea* (All.) Ledeb.	NT	0.65	47.68	4.88	41.46
Brassicaceae	*Odontarrhena bertolonii* (Desv.) Jord. & Fourr.	LC	0	30.31	2.7	62.16
Apiaceae	*Oenanthe lisae* Moris	LC	0	64.64	18.29	34.15
Boraginaceae	*Onosma echioides* (L.) L. subsp. *echioides*	LC	0.01	45.67	20.29	53.62
Boraginaceae	*Onosma pseudoarenaria* Schur subsp. *tridentina* (Wettst.) Br.-Bl.	VU	0	64.83	0	61.9
Orchidaceae	*Ophrys appennina* Romolini & Soca	LC	0	48.36	18.46	54.62
Orchidaceae	*Ophrys apulica* (O.Danesch & E.Danesch) O.Danesch & E.Danesch	LC	0	13.07	3.23	38.71
Orchidaceae	*Ophrys bertolonii* Moretti subsp. *bertoloniiformis* (O.Danesch & E.Danesch) H.Sund	LC	0	31.38	10.87	36.25
Orchidaceae	*Ophrys classica* Devillers-Tersch. & Devillers	LC	0	44.71	16.92	51.24
Orchidaceae	*Ophrys crabronifera* Mauri	LC	0	44.82	5.33	56
Orchidaceae	*Ophrys exaltata* Ten. subsp. *exaltata*	LC	0.12	43.31	12.82	48.72
Orchidaceae	*Ophrys exaltata* Ten. subsp. *montis-leonis* (O.Danesch & E.Danesch) Soca	LC	0	35.27	4.35	41.3
Orchidaceae	*Ophrys lucana* P.Delforge, Devillers-Tersch. & Devillers	LC	0.1	72.77	15.05	53.76
Orchidaceae	*Ophrys lunulata* Parl.	LC	0	20.43	9.8	39.22
Orchidaceae	*Ophrys minipassionis* Romolini & Soca	LC	0	64.72	10.64	53.19
Orchidaceae	*Ophrys passionis* Sennen ex Devillers-Tersch. & Devillers subsp. *majellensis* (Helga Daiss & Herm.Daiss) Romolini & Soca	LC	0.12	63.33	12.5	53.12
Orchidaceae	*Ophrys promontorii* O.Danesch & E.Danesch	LC	0.01	73.05	12.82	58.97
Orchidaceae	*Ophrys tenthredinifera* Willd. subsp. *neglecta* (Parl.) E.G.Camus	LC	0	20.23	11.11	31.94
Asparagaceae	*Ornithogalum exscapum* Ten.	LC	0	47.87	11.54	58.97
Apiaceae	*Pimpinella anisoides* V.Brig.	LC	0	41.15	2.38	33.33
Lentibulariaceae	*Pinguicula christinae* Peruzzi & Gestri	NT	0.58	94.21	5.26	65.79
Plantago	*Plantago sarda* C.Presl	LC	0	95.65	0	76.92
Polygalaceae	*Polygala alpestris* Rchb. subsp. *angelisii* (Ten.) Nyman	LC	0.05	59.83	14.63	43.9
Polygalaceae	*Polygala flavescens* DC. subsp. *maremmana* (Fiori) Arrigoni	LC	0	86.6	3.23	77.42
Polygalaceae	*Polygala sardoa* Chodat	EN	0	62.31	18.52	33.33
Rosaceae	*Potentilla rigoana* Th.Wolf	LC	0.18	71.89	7.41	42.59
Primulaceae	*Primula polliniana* Moretti	LC	0	35.96	12.16	37.84
Primulaceae	*Primula tyrolensis* Schott ex Rchb.f.	LC	0	31.11	8	34
Apiaceae	*Ptychotis sardoa* Pignatti & Metlesics	EN	0	79.22	17.86	57.14
Boraginaceae	*Pulmonaria vallarsae* A.Kern.	LC	0	34.53	4.17	36.46

Fagaceae	*Quercus ichnusae* Mossa, Bacch. & Brullo	LC	0	66.64	9.09	54.55
Brassicaceae	*Rhizobotrya alpina* Tausch	VU	0	55.89	12.5	41.67
Polygonaceae	*Rumex scutatus* L. subsp. *glaucescens* (Guss.) Brullo, Scelsi & Spamp.	LC	0	40.17	9.43	52.83
Salicaceae	*Salix arrigonii* Brullo	VU	0	97.49	10	87.5
Salicaceae	*Salix brutia* Brullo & Spamp.	LC	0	41.77	5	30
Salicaceae	*Salix purpurea* L. subsp. *eburnea* (Borzí) Cif. & Giacom. ex Pignatti	NT	0.02	63.44	17.95	69.23
Lamiaceae	*Salvia haematodes* L.	LC	0	23.85	8.11	45.95
Asteraceae	*Santolina etrusca* (Lacaita) Marchi & D'Amato	NT	0	60.79	2.22	42.22
Asteraceae	*Santolina insularis* (Gennari ex Fiori) Arrigoni	LC	0	51.86	10.64	40.43
Saxifragaceae	*Saxifraga arachnoidea* Sternb.	LC	0	48.76	9.09	54.55
Saxifragaceae	*Saxifraga depressa* Sternb.	LC	0	80.08	0	76.47
Saxifragaceae	*Saxifraga facchinii* W.D.J.Koch	NT	0	59.85	5.26	47.37
Saxifragaceae	*Saxifraga hostii* Tausch subsp. *rhaetica* (A.Kern. ex Engl.) Braun-Blanq.	LC	0.02	30.53	11.76	26.47
Saxifragaceae	*Saxifraga presolanensis* Engl.	NT	0.83	84.71	9.09	81.82
Saxifragaceae	*Saxifraga tombeanensis* Boiss. ex Engl.	EN	0	45.07	3.12	56.25
Saxifragaceae	*Saxifraga vandellii* Sternb.	LC	0	40.98	18.18	34.09
Caprifoliaceae	*Scabiosa holosericea* Bertol.	LC	0	24.09	14.29	40
Caprifoliaceae	*Scabiosa uniseta* Savi	LC	0.1	69.98	8.51	72.34
Caprifoliaceae	*Scabiosa vestina* Facchini ex W.D.J.Koch	LC	0	43.43	2	42
Asteraceae	*Scorzonera callosa* Moris	NT	0	70.26	15.15	48.48
Asteraceae	*Scorzonera villosa* Scop. subsp. *columnae* (Guss.) Nyman	LC	0.59	47.16	17.39	41.3
Crassulaceae	*Sedum alsinifolium* All.	LC	0.57	48.9	5.56	42.59
Asteraceae	*Senecio ovatus* (G.Gaertn., B.Mey. & Scherb.) Willd. subsp. *stabianus* (Lacaita) Greuter	LC	0.12	66.02	4.44	42.22
Poaceae	*Sesleria nitida* Ten.	LC	0.03	68.42	11.11	37.04
Poaceae	*Sesleria pichiana* Foggi, Gr.Rossi & Pignotti	LC	0.01	76.87	2.63	52.63
Caryophyllaceae	*Silene italica* (L.) Pers. subsp. *sicula* (Ucria) Jeanm.	LC	0.05	41.59	16	44
Caryophyllaceae	*Silene nummica* Vals.	LC	0	15.04	3.23	22.58
Apiaceae	*Siler montanum* Crantz subsp. *siculum* (Spreng.) Iamonico, Bartolucci & F.Conti	LC	0.57	72.56	7.46	50.75
Rosaceae	*Spiraea decumbens* W.D.J.Koch subsp. *tomentosa* (Poech) Dostál	LC	0	28.25	15.56	31.11
Poaceae	*Stipa etrusca* Moraldo	LC	0	21.91	7.69	41.03
Asteraceae	*Tephroseris italica* Holub	LC	0.01	83.06	7.55	58.49

Santalaceae	*Thesium sommieri* Hendrych	LC	0	85.81	13.51	59.46
Lamiaceae	*Thymus spinulosus* Ten.	LC	0.01	69.49	6.67	55.56
Asteraceae	*Tolpis virgata* (Desf.) Bertol. subsp. *grandiflora* (Ten.) Arcang.	LC	0	39.58	9.09	42.42
Fabaceae	*Trifolium pratense* L. subsp. *semipurpureum* (Strobl) Pignatti	LC	0	39.05	17.58	43.96
Poaceae	*Trisetaria villosa* (Bertol.) Banfi & Soldano	LC	0.03	86.04	9.43	50.94
Fabaceae	*Vicia ochroleuca* Ten. subsp. *ochroleuca*	LC	0	30.58	4.17	43.75
Violaceae	*Viola aethnensis* (Ging. & DC.) Strobl subsp. *splendida* (W.Becker) Merxm. & Lippert	LC	0	68.66	16.33	40.82
Violaceae	*Viola bertolonii* Pio	LC	0	96.08	6.67	76.67
Violaceae	*Viola cassinensis* Strobl subsp. *pseudogracilis* (A.Terracc.) Bartolucci, Galasso & Wagens.	LC	0.06	59.18	9.09	33.33
Violaceae	*Viola dubyana* Burnat ex Gremli	LC	0	35.54	3.03	33.33
Violaceae	*Viola etrusca* Erben	EN	0.08	86.93	9.68	87.1
Violaceae	*Viola eugeniae* Parl. subsp. *eugeniae*	LC	0	73.35	12.82	46.15
Violaceae	*Viola ferrarinii* Moraldo & Ricceri	LC	0	92.59	4.48	56.72

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Table S2. Percentage of variable contribution to the first two axes (PC1 and PC2) of the Principal Component Analysis. bio1 = Annual mean temperature; bio2 = Mean diurnal range; bio3 = Isothermality; bio4 = Temperature seasonality; bio5 = Max temperature of warmest month; bio6 = Min temperature of coldest month; bio7 = Temperature annual range; bio08 = Mean temperature of wettest quarter; bio09 = Mean temperature of driest quarter; bio10 = Mean temperature of warmest quarter; bio11 = Mean temperature of coldest quarter; bio12 = Annual precipitation; bio13 = Precipitation of wettest month; bio14 = Precipitation of driest month; bio15 = Precipitation seasonality; bio16 = Precipitation of wettest quarter; bio17 = Precipitation of driest quarter; bio18 = Precipitation of warmest quarter; bio19 = Precipitation of coldest quarter.

Bioclimatic variable	PC1	PC2
bio01	6.07	8.15
bio02	0.17	0.38
bio03	0.31	0.18
bio04	0.00	0.59
bio05	6.02	8.21
bio06	6.12	8.08
bio07	0.06	0.51
bio08	5.98	8.20
bio09	6.13	7.94
bio10	6.05	8.17
bio11	6.09	8.11
bio12	8.15	5.90
bio13	8.11	5.92
bio14	8.15	5.89
bio15	0.02	0.22
bio16	8.13	5.90
bio17	8.15	5.90
bio18	8.20	5.86
bio19	8.09	5.89

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Table S3. Evaluation of individual modelling techniques for 188 taxa endemic to Italy. Mean values of evaluation runs for each algorithm and standard deviation values (in brackets) are showed. Statistics given are the mean values for area under the curve (AUC) and the true skill statistic (TSS). Accuracy classification for AUC: 1>excellent>0.9>good>0.8>fair>0.7>poor>0.6>fail; accuracy classification for TSS: 1>excellent>0.8>good>0.6>fair>0.4>poor>0.2>fail

Taxa	Modelling techniques	ROC	TSS	KAPPA
Acer cappadocicum subsp. *lobelii*	CTA	0.84 (0.047)	0.68 (0.092)	0.68 (0.093)
Adenocarpus complicatus subsp. *brutius*	CTA	0.85 (0.06)	0.69 (0.105)	0.67 (0.105)
Adenostyles australis	CTA	0.92 (0.038)	0.84 (0.074)	0.83 (0.073)
Ajuga tenorei	CTA	0.88 (0.054)	0.75 (0.107)	0.74 (0.107)
Alyssum diffusum subsp. *diffusum*	CTA	0.85 (0.054)	0.69 (0.102)	0.68 (0.104)
Anemonoides trifolia subsp. *brevidentata*	CTA	0.9 (0.04)	0.72 (0.06)	0.72 (0.06)
Antirrhinum siculum	CTA	0.82 (0.063)	0.65 (0.112)	0.62 (0.11)
Aquilegia lucensis	CTA	0.97 (0.028)	0.94 (0.057)	0.93 (0.054)
Arabis collina subsp. *rosea*	CTA	0.83 (0.048)	0.64 (0.086)	0.65 (0.088)
Arenaria huteri	CTA	0.84 (0.074)	0.69 (0.135)	0.65 (0.15)
Armeria arenaria subsp. *marginata*	CTA	0.93 (0.044)	0.86 (0.088)	0.84 (0.088)
Armeria brutia	CTA	0.87 (0.056)	0.74 (0.102)	0.67 (0.108)
Armeria denticulata	CTA	0.84 (0.065)	0.71 (0.125)	0.73 (0.133)
Artemisia caerulescens subsp. *cretacea*	CTA	0.82 (0.078)	0.65 (0.122)	0.59 (0.125)
Artemisia campestris subsp. *variabilis*	CTA	0.83 (0.056)	0.64 (0.1)	0.62 (0.105)
Astragalus parnassi subsp. *calabricus*	CTA	0.87 (0.063)	0.74 (0.107)	0.7 (0.111)
Asyneuma trichocalycinum	CTA	0.86 (0.05)	0.72 (0.098)	0.68 (0.101)
Atadinus glaucophyllus	CTA	0.83 (0.059)	0.66 (0.112)	0.62 (0.113)
Bellevalia webbiana	CTA	0.84 (0.079)	0.68 (0.132)	0.65 (0.14)
Bellium crassifolium	CTA	0.9 (0.045)	0.8 (0.087)	0.78 (0.111)
Biscutella apuana	CTA	0.82 (0.076)	0.63 (0.128)	0.57 (0.142)
Biscutella morisiana	CTA	0.8 (0.057)	0.62 (0.099)	0.65 (0.099)
Brachypodium genuense	CTA	0.91 (0.031)	0.81 (0.055)	0.81 (0.055)
Brassica glabrescens	CTA	0.92 (0.064)	0.84 (0.128)	0.79 (0.124)
Bromopsis caprina	CTA	0.86 (0.056)	0.72 (0.106)	0.71 (0.101)
Buphthalmum salicifolium subsp. *flexile*	CTA	0.83 (0.049)	0.66 (0.09)	0.64 (0.092)
Campanula bertolae	CTA	0.87 (0.038)	0.69 (0.075)	0.69 (0.075)
Campanula carnica subsp. *puberula*	CTA	0.82 (0.076)	0.63 (0.128)	0.61 (0.133)
Campanula elatines	CTA	0.87 (0.044)	0.69 (0.085)	0.69 (0.085)
Campanula martinii	CTA	0.89 (0.044)	0.77 (0.085)	0.76 (0.086)
Campanula micrantha	CTA	0.91 (0.049)	0.82 (0.096)	0.84 (0.089)
Campanula morettiana	CTA	0.85 (0.043)	0.68 (0.075)	0.68 (0.075)
Campanula raineri	CTA	0.9 (0.058)	0.75 (0.105)	0.75 (0.106)
Campanula sabatia	CTA	0.93 (0.036)	0.86 (0.072)	0.83 (0.077)
Campanula tanfanii	CTA	0.89 (0.049)	0.79 (0.09)	0.81 (0.088)
Carduus nutans subsp. *perspinosus*	CTA	0.85 (0.058)	0.71 (0.113)	0.67 (0.118)
Carex macrostachys	CTA	0.87 (0.048)	0.73 (0.097)	0.74 (0.104)
*Carlina hispanica*subsp. *globosa*	CTA	0.81 (0.066)	0.62 (0.115)	0.62 (0.123)

Centaurea aplolepa subsp. *aplolepa*	CTA	0.97 (0.028)	0.93 (0.056)	0.88 (0.081)
Centaurea aplolepa subsp. *carueliana*	CTA	0.87 (0.076)	0.7 (0.136)	0.66 (0.141)
Centaurea aplolepa subsp. *lunensis*	CTA	0.85 (0.056)	0.69 (0.097)	0.69 (0.096)
Centaurea poeltiana	CTA	0.85 (0.056)	0.71 (0.105)	0.64 (0.114)
Centaurea subtilis	CTA	0.89 (0.054)	0.72 (0.114)	0.71 (0.123)
Cerastium apuanum	CTA	0.8 (0.067)	0.6 (0.116)	0.55 (0.125)
Cerastium scaranoi	CTA	0.88 (0.046)	0.75 (0.087)	0.75 (0.093)
Cerastium supramontanum	CTA	0.9 (0.049)	0.81 (0.097)	0.8 (0.099)
Cerastium tomentosum	CTA	0.84 (0.05)	0.68 (0.094)	0.66 (0.096)
Cerastium utriense	CTA	0.9 (0.044)	0.79 (0.08)	0.75 (0.092)
Cherleria laricifolia subsp. *ophiolitica*	CTA	0.84 (0.075)	0.67 (0.134)	0.67 (0.141)
Cirsium bertolonii	CTA	0.92 (0.049)	0.83 (0.098)	0.86 (0.081)
Cirsium tenoreanum	CTA	0.86 (0.057)	0.72 (0.099)	0.71 (0.103)
Cirsium vallis-demonii	CTA	0.84 (0.062)	0.68 (0.102)	0.65 (0.12)
Colchicum neapolitanum	CTA	0.85 (0.067)	0.66 (0.111)	0.65 (0.118)
Crocus biflorus	CTA	0.85 (0.031)	0.68 (0.051)	0.68 (0.051)
Crocus etruscus	CTA	0.85 (0.062)	0.71 (0.11)	0.69 (0.118)
Crocus imperati	CTA	0.83 (0.076)	0.63 (0.126)	0.68 (0.124)
Crocus suaveolens	CTA	0.89 (0.052)	0.79 (0.103)	0.81 (0.099)
Cryptotaenia thomasii	CTA	0.86 (0.072)	0.68 (0.129)	0.69 (0.147)
Cynoglossum apenninum	CTA	0.89 (0.049)	0.79 (0.097)	0.8 (0.091)
Daphne petraea	CTA	0.87 (0.061)	0.74 (0.115)	0.69 (0.126)
Dianthus carthusianorum subsp. *tenorei*	CTA	0.87 (0.055)	0.75 (0.108)	0.76 (0.105)
Dianthus sardous	CTA	0.89 (0.049)	0.78 (0.097)	0.78 (0.099)
Dianthus tarentinus	CTA	0.83 (0.072)	0.63 (0.132)	0.63 (0.144)
Drymochloa drymeja subsp. *exaltata*	CTA	0.84 (0.046)	0.66 (0.077)	0.66 (0.077)
Echinops siculus	CTA	0.83 (0.066)	0.64 (0.104)	0.65 (0.108)
Epipactis meridionalis	CTA	0.82 (0.061)	0.63 (0.112)	0.6 (0.121)
Erysimum apenninum	CTA	0.9 (0.034)	0.81 (0.068)	0.81 (0.068)
Erysimum crassistylum subsp. *garganicum*	CTA	0.82 (0.071)	0.64 (0.122)	0.67 (0.128)
Erysimum etruscum	CTA	0.83 (0.053)	0.65 (0.088)	0.66 (0.088)
Erysimum pseudorhaeticum	CTA	0.9 (0.027)	0.79 (0.052)	0.79 (0.052)
Euphorbia ceratocarpa	CTA	0.83 (0.068)	0.66 (0.117)	0.63 (0.131)
Euphorbia corallioides	CTA	0.83 (0.058)	0.62 (0.106)	0.64 (0.107)
Euphorbia nicaeensis subsp. *japygica*	CTA	0.81 (0.076)	0.62 (0.122)	0.61 (0.121)
Euphorbia variabilis	CTA	0.85 (0.061)	0.72 (0.112)	0.71 (0.113)
Euphrasia tricuspidata	CTA	0.89 (0.03)	0.72 (0.048)	0.72 (0.048)
Festuca alfrediana subsp. *ferrariniana*	CTA	0.94 (0.038)	0.89 (0.074)	0.87 (0.078)
Festuca austrodolomitica	CTA	0.89 (0.056)	0.74 (0.087)	0.73 (0.092)
Festuca riccerii	CTA	0.98 (0.026)	0.95 (0.052)	0.95 (0.048)
Festuca robustifolia	CTA	0.86 (0.048)	0.7 (0.084)	0.7 (0.084)
Festuca violacea subsp. *italica*	CTA	0.93 (0.042)	0.86 (0.085)	0.87 (0.075)
Festuca violacea subsp. *puccinellii*	CTA	0.92 (0.051)	0.84 (0.089)	0.85 (0.086)
Galium baldense	CTA	0.88 (0.03)	0.74 (0.041)	0.74 (0.041)
Genista etnensis	CTA	0.84 (0.059)	0.66 (0.116)	0.63 (0.134)
Genista tyrrhena	CTA	0.95 (0.041)	0.89 (0.081)	0.88 (0.09)
Globularia incanescens	CTA	0.9 (0.033)	0.79 (0.066)	0.79 (0.066)
Helichrysum litoreum	CTA	0.89 (0.04)	0.77 (0.066)	0.77 (0.066)
Helichrysum saxatile subsp. *saxatile*	CTA	0.87 (0.063)	0.74 (0.107)	0.73 (0.115)
Helictochloa praetutiana subsp. *praetutiana*	CTA	0.93 (0.041)	0.84 (0.066)	0.84 (0.066)

Helleborus viridis subsp. *bocconei*	CTA	0.84 (0.052)	0.64 (0.082)	0.64 (0.082)
Hypericum barbatum subsp. *calabricum*	CTA	0.86 (0.056)	0.7 (0.098)	0.69 (0.106)
Iris cengialti subsp. *cengialti*	CTA	0.86 (0.052)	0.69 (0.085)	0.69 (0.085)
Jacobaea maritima subsp. *bicolor*	CTA	0.9 (0.05)	0.79 (0.101)	0.75 (0.101)
Klasea flavescens subsp. *cichoracea*	CTA	0.79 (0.057)	0.6 (0.108)	0.62 (0.113)
Knautia baldensis	CTA	0.9 (0.044)	0.74 (0.081)	0.74 (0.081)
Knautia persicina	CTA	0.89 (0.041)	0.77 (0.076)	0.77 (0.076)
Koeleria splendens	CTA	0.86 (0.045)	0.68 (0.077)	0.68 (0.077)
Laserpitium nitidum	CTA	0.88 (0.052)	0.71 (0.102)	0.7 (0.105)
Leontodon anomalus	CTA	0.86 (0.064)	0.72 (0.107)	0.72 (0.109)
Leontodon intermedius	CTA	0.84 (0.067)	0.67 (0.108)	0.7 (0.105)
Limonium acutifolium subsp. *acutifolium*	CTA	0.93 (0.052)	0.85 (0.105)	0.78 (0.107)
Limonium ilvae	CTA	0.94 (0.039)	0.88 (0.077)	0.81 (0.091)
Limonium merxmuelleri subsp. *sulcitanum*	CTA	0.96 (0.034)	0.91 (0.066)	0.89 (0.07)
Limonium multiforme	CTA	0.95 (0.036)	0.9 (0.07)	0.88 (0.079)
Limonium remotispiculum	CTA	0.82 (0.085)	0.62 (0.143)	0.62 (0.159)
Linaria purpurea	CTA	0.9 (0.034)	0.79 (0.067)	0.79 (0.067)
Luzula sylvatica subsp. *sicula*	CTA	0.82 (0.067)	0.64 (0.116)	0.64 (0.121)
Mcneillia graminifolia subsp. *rosanoi*	CTA	0.91 (0.045)	0.81 (0.088)	0.83 (0.083)
Melampyrum italicum	CTA	0.89 (0.033)	0.69 (0.047)	0.69 (0.047)
Micromeria cordata	CTA	0.89 (0.047)	0.77 (0.094)	0.78 (0.087)
Micromeria graeca subsp. *tenuifolia*	CTA	0.85 (0.049)	0.65 (0.073)	0.67 (0.074)
Moehringia glaucovirens	CTA	0.85 (0.061)	0.68 (0.103)	0.66 (0.112)
Moltkia suffruticosa subsp. *bigazziana*	CTA	0.81 (0.067)	0.63 (0.113)	0.61 (0.116)
Myosotis graui	CTA	0.92 (0.043)	0.83 (0.081)	0.86 (0.072)
Myosotis sylvatica subsp. *elongata*	CTA	0.84 (0.057)	0.68 (0.104)	0.67 (0.108)
Odontarrhena argentea	CTA	0.87 (0.057)	0.68 (0.101)	0.67 (0.101)
Odontarrhena bertolonii	CTA	0.82 (0.084)	0.64 (0.145)	0.65 (0.137)
Oenanthe lisae	CTA	0.88 (0.039)	0.75 (0.078)	0.76 (0.077)
Onosma echioides subsp. *echioides*	CTA	0.84 (0.06)	0.64 (0.099)	0.67 (0.096)
Onosma pseudoarenaria subsp. *tridentina*	CTA	0.86 (0.076)	0.68 (0.131)	0.69 (0.135)
Ophrys appennina	CTA	0.84 (0.039)	0.66 (0.064)	0.66 (0.064)
Ophrys apulica	CTA	0.89 (0.056)	0.77 (0.112)	0.73 (0.101)
Ophrys bertolonii subsp. *bertoloniiformis*	CTA	0.88 (0.026)	0.68 (0.038)	0.68 (0.038)
Ophrys classica	CTA	0.82 (0.036)	0.64 (0.053)	0.64 (0.053)
Ophrys crabronifera	CTA	0.83 (0.055)	0.61 (0.098)	0.62 (0.1)
Ophrys exaltata subsp. *exaltata*	CTA	0.81 (0.078)	0.6 (0.128)	0.57 (0.143)
Ophrys exaltata subsp. *montis-leonis*	CTA	0.86 (0.061)	0.71 (0.103)	0.69 (0.117)
Ophrys lucana	CTA	0.85 (0.058)	0.64 (0.093)	0.65 (0.093)
Ophrys lunulata	CTA	0.82 (0.068)	0.63 (0.118)	0.63 (0.127)
Ophrys minipassionis	CTA	0.8 (0.084)	0.62 (0.13)	0.66 (0.127)
Ophrys passionis subsp. *majellensis*	CTA	0.85 (0.074)	0.67 (0.126)	0.66 (0.126)
Ophrys promontorii	CTA	0.77 (0.088)	0.57 (0.135)	0.6 (0.138)
Ophrys tenthredinifera subsp. *neglecta*	CTA	0.86 (0.059)	0.68 (0.107)	0.68 (0.109)
Ornithogalum exscapum	CTA	0.81 (0.051)	0.62 (0.082)	0.64 (0.081)
Pimpinella anisoides	CTA	0.82 (0.072)	0.62 (0.114)	0.67 (0.121)
Pinguicula christinae	CTA	0.95 (0.035)	0.9 (0.068)	0.87 (0.073)
Plantago sarda	CTA	0.98 (0.024)	0.95 (0.048)	0.95 (0.046)
Polygala alpestris subsp. *angelisii*	CTA	0.9 (0.055)	0.79 (0.108)	0.82 (0.095)
Polygala flavescens subsp. *maremmana*	CTA	0.9 (0.061)	0.79 (0.115)	0.72 (0.127)

Polygala sardoa	CTA	0.86 (0.051)	0.73 (0.099)	0.73 (0.096)
Potentilla rigoana	CTA	0.89 (0.056)	0.79 (0.09)	0.78 (0.095)
Primula polliniana	CTA	0.87 (0.04)	0.68 (0.069)	0.68 (0.069)
Primula tyrolensis	CTA	0.8 (0.057)	0.6 (0.1)	0.56 (0.115)
Ptychotis sardoa	CTA	0.89 (0.052)	0.79 (0.099)	0.77 (0.107)
Pulmonaria vallarsae	CTA	0.89 (0.048)	0.77 (0.084)	0.76 (0.084)
Quercus ichnusae	CTA	0.92 (0.036)	0.84 (0.069)	0.79 (0.081)
Rhizobotrya alpina	CTA	0.85 (0.054)	0.69 (0.104)	0.67 (0.111)
Rumex scutatus glaucescens	CTA	0.81 (0.059)	0.6 (0.099)	0.57 (0.104)
Salix arrigonii	CTA	0.85 (0.067)	0.66 (0.113)	0.7 (0.118)
Salix brutia	CTA	0.87 (0.066)	0.72 (0.118)	0.68 (0.116)
Salix purpurea subsp. *eburnea*	CTA	0.83 (0.071)	0.65 (0.117)	0.62 (0.131)
Salvia haematodes	CTA	0.79 (0.076)	0.6 (0.13)	0.61 (0.143)
Santolina etrusca	CTA	0.85 (0.053)	0.69 (0.092)	0.65 (0.101)
Santolina insularis	CTA	0.89 (0.046)	0.78 (0.092)	0.8 (0.089)
Saxifraga arachnoidea	CTA	0.89 (0.053)	0.77 (0.108)	0.71 (0.11)
Saxifraga depressa	CTA	0.9 (0.045)	0.79 (0.088)	0.75 (0.098)
Saxifraga facchinii	CTA	0.89 (0.049)	0.79 (0.097)	0.73 (0.098)
Saxifraga hostii subsp. *rhaetica*	CTA	0.83 (0.071)	0.66 (0.129)	0.58 (0.132)
Saxifraga presolanensis	CTA	0.88 (0.079)	0.77 (0.147)	0.72 (0.156)
Saxifraga tombeanensis	CTA	0.88 (0.062)	0.75 (0.115)	0.71 (0.112)
Saxifraga vandellii	CTA	0.82 (0.073)	0.64 (0.114)	0.61 (0.121)
Scabiosa holosericea	CTA	0.84 (0.054)	0.66 (0.093)	0.69 (0.092)
Scabiosa uniseta	CTA	0.86 (0.07)	0.7 (0.112)	0.71 (0.115)
Scabiosa vestina	CTA	0.91 (0.04)	0.79 (0.08)	0.76 (0.082)
Scorzonera callosa	CTA	0.86 (0.061)	0.71 (0.114)	0.68 (0.11)
Scorzonera villosa subsp. *columnae*	CTA	0.83 (0.065)	0.65 (0.113)	0.66 (0.11)
Sedum alsinifolium	CTA	0.88 (0.057)	0.69 (0.107)	0.67 (0.108)
Senecio ovatus subsp. *stabianus*	CTA	0.92 (0.037)	0.83 (0.073)	0.8 (0.076)
Sesleria nitida	CTA	0.92 (0.035)	0.83 (0.069)	0.84 (0.066)
Sesleria pichiana	CTA	0.81 (0.084)	0.59 (0.134)	0.58 (0.158)
Silene italica subsp. *sicula*	CTA	0.84 (0.048)	0.67 (0.086)	0.67 (0.086)
Silene nummica	CTA	0.92 (0.051)	0.84 (0.1)	0.83 (0.1)
Siler montanum subsp. *siculum*	CTA	0.91 (0.05)	0.81 (0.09)	0.8 (0.09)
Spiraea decumbens subsp. *tomentosa*	CTA	0.82 (0.073)	0.61 (0.133)	0.61 (0.134)
Stipa etrusca	CTA	0.81 (0.069)	0.61 (0.115)	0.59 (0.12)
Tephroseris italica	CTA	0.91 (0.042)	0.81 (0.085)	0.83 (0.08)
Thesium sommieri	CTA	0.87 (0.052)	0.75 (0.103)	0.76 (0.094)
Thymus spinulosus	CTA	0.84 (0.065)	0.67 (0.11)	0.71 (0.112)
Tolpis virgata subsp. *grandiflora*	CTA	0.8 (0.088)	0.61 (0.146)	0.65 (0.149)
Trifolium pratense subsp. *semipurpureum*	CTA	0.86 (0.057)	0.66 (0.09)	0.66 (0.09)
Trisetaria villosa	CTA	0.92 (0.04)	0.84 (0.078)	0.86 (0.069)
Vicia ochroleuca subsp. *ochroleuca*	CTA	0.84 (0.062)	0.65 (0.113)	0.66 (0.11)
Viola aethnensis subsp. *splendida*	CTA	0.9 (0.055)	0.78 (0.1)	0.78 (0.097)
Viola bertolonii	CTA	0.84 (0.071)	0.68 (0.125)	0.61 (0.13)
Viola cassinensis subsp. *pseudogracilis*	CTA	0.87 (0.059)	0.73 (0.118)	0.72 (0.113)
Viola dubyana	CTA	0.87 (0.064)	0.75 (0.114)	0.7 (0.115)
Viola etrusca	CTA	0.87 (0.063)	0.73 (0.124)	0.69 (0.134)
Viola eugeniae subsp. *eugeniae*	CTA	0.91 (0.059)	0.81 (0.109)	0.84 (0.093)
Viola ferrarinii	CTA	0.93 (0.036)	0.86 (0.072)	0.87 (0.068)

Acer cappadocicum subsp. *lobelii*	FDA	0.93 (0.041)	0.8 (0.089)	0.82 (0.082)
Adenocarpus complicatus subsp. *brutius*	FDA	0.93 (0.035)	0.77 (0.084)	0.78 (0.08)
Adenostyles australis	FDA	0.95 (0.025)	0.85 (0.069)	0.85 (0.068)
Ajuga tenorei	FDA	0.96 (0.034)	0.85 (0.08)	0.85 (0.08)
Alyssum diffusum subsp. *diffusum*	FDA	0.93 (0.044)	0.78 (0.089)	0.79 (0.088)
Anemonoides trifolia subsp. *brevidentata*	FDA	0.94 (0.016)	0.75 (0.048)	0.75 (0.048)
Antirrhinum siculum	FDA	0.89 (0.052)	0.72 (0.09)	0.72 (0.095)
Aquilegia lucensis	FDA	0.99 (0.018)	0.97 (0.034)	0.96 (0.041)
Arabis collina subsp. *rosea*	FDA	0.87 (0.052)	0.69 (0.096)	0.7 (0.093)
Arenaria huteri	FDA	0.9 (0.063)	0.75 (0.119)	0.73 (0.12)
Armeria arenaria subsp. m*arginata*	FDA	0.98 (0.033)	0.94 (0.064)	0.94 (0.06)
Armeria brutia	FDA	0.97 (0.026)	0.9 (0.058)	0.86 (0.078)
Armeria denticulata	FDA	0.9 (0.051)	0.77 (0.088)	0.79 (0.087)
Artemisia caerulescens subsp. *cretacea*	FDA	0.9 (0.051)	0.74 (0.117)	0.72 (0.115)
Artemisia campestris subsp. *variabilis*	FDA	0.9 (0.055)	0.74 (0.101)	0.76 (0.092)
Astragalus parnassi subsp. *calabricus*	FDA	0.94 (0.044)	0.83 (0.093)	0.81 (0.1)
Asyneuma trichocalycinum	FDA	0.94 (0.045)	0.83 (0.095)	0.83 (0.094)
Atadinus glaucophyllus	FDA	0.91 (0.045)	0.75 (0.085)	0.75 (0.082)
Bellevalia webbiana	FDA	0.96 (0.033)	0.87 (0.087)	0.84 (0.095)
Bellium crassifolium	FDA	0.95 (0.039)	0.87 (0.075)	0.88 (0.068)
Biscutella apuana	FDA	0.93 (0.044)	0.79 (0.1)	0.78 (0.096)
Biscutella morisiana	FDA	0.84 (0.052)	0.66 (0.086)	0.68 (0.082)
Brachypodium genuense	FDA	0.96 (0.019)	0.84 (0.053)	0.84 (0.053)
Brassica glabrescens	FDA	0.97 (0.021)	0.91 (0.058)	0.85 (0.081)
Bromopsis caprina	FDA	0.93 (0.044)	0.78 (0.095)	0.79 (0.093)
Buphthalmum salicifolium subsp. *flexile*	FDA	0.89 (0.048)	0.72 (0.093)	0.73 (0.088)
Campanula bertolae	FDA	0.95 (0.02)	0.8 (0.053)	0.8 (0.053)
Campanula carnica subsp. *puberula*	FDA	0.93 (0.049)	0.81 (0.098)	0.81 (0.089)
Campanula elatines	FDA	0.94 (0.027)	0.76 (0.073)	0.76 (0.073)
Campanula martinii	FDA	0.95 (0.032)	0.82 (0.074)	0.81 (0.074)
Campanula micrantha	FDA	0.96 (0.041)	0.88 (0.081)	0.9 (0.069)
Campanula morettiana	FDA	0.93 (0.025)	0.73 (0.06)	0.73 (0.06)
Campanula raineri	FDA	0.95 (0.023)	0.81 (0.068)	0.81 (0.066)
Campanula sabatia	FDA	0.96 (0.032)	0.9 (0.063)	0.89 (0.064)
Campanula tanfanii	FDA	0.95 (0.049)	0.84 (0.111)	0.84 (0.092)
Carduus nutans subsp. *perspinosus*	FDA	0.92 (0.045)	0.78 (0.089)	0.76 (0.092)
Carex macrostachys	FDA	0.9 (0.056)	0.8 (0.092)	0.8 (0.086)
*Carlina hispanica*subsp. *globosa*	FDA	0.94 (0.029)	0.77 (0.076)	0.79 (0.072)
Centaurea aplolepa subsp. *aplolepa*	FDA	0.97 (0.027)	0.92 (0.062)	0.9 (0.072)
Centaurea aplolepa subsp. *carueliana*	FDA	0.93 (0.052)	0.75 (0.12)	0.74 (0.111)
Centaurea aplolepa subsp. *lunensis*	FDA	0.93 (0.046)	0.8 (0.091)	0.81 (0.086)
Centaurea poeltiana	FDA	0.93 (0.052)	0.79 (0.107)	0.79 (0.099)
Centaurea subtilis	FDA	0.95 (0.043)	0.82 (0.111)	0.81 (0.108)
Cerastium apuanum	FDA	0.88 (0.061)	0.7 (0.104)	0.71 (0.096)
Cerastium scaranoi	FDA	0.95 (0.036)	0.84 (0.08)	0.84 (0.077)
Cerastium supramontanum	FDA	0.95 (0.038)	0.89 (0.072)	0.88 (0.072)
Cerastium tomentosum	FDA	0.89 (0.057)	0.73 (0.102)	0.74 (0.097)
Cerastium utriense	FDA	0.98 (0.022)	0.91 (0.053)	0.9 (0.061)
Cherleria laricifolia subsp. *ophiolitica*	FDA	0.94 (0.036)	0.82 (0.08)	0.82 (0.076)
Cirsium bertolonii	FDA	0.94 (0.052)	0.86 (0.099)	0.89 (0.079)

Cirsium tenoreanum	FDA	0.92 (0.042)	0.78 (0.084)	0.78 (0.08)
Cirsium vallis-demonii	FDA	0.95 (0.034)	0.81 (0.087)	0.82 (0.08)
Colchicum neapolitanum	FDA	0.85 (0.067)	0.66 (0.111)	0.69 (0.103)
Crocus biflorus	FDA	0.89 (0.023)	0.71 (0.043)	0.71 (0.043)
Crocus etruscus	FDA	0.94 (0.051)	0.81 (0.108)	0.81 (0.101)
Crocus imperati	FDA	0.86 (0.061)	0.66 (0.107)	0.69 (0.097)
Crocus suaveolens	FDA	0.95 (0.049)	0.85 (0.101)	0.86 (0.089)
Cryptotaenia thomasii	FDA	0.94 (0.035)	0.79 (0.078)	0.8 (0.07)
Cynoglossum apenninum	FDA	0.92 (0.056)	0.83 (0.096)	0.86 (0.087)
Daphne petraea	FDA	0.94 (0.045)	0.81 (0.103)	0.81 (0.1)
Dianthus carthusianorum subsp. *tenorei*	FDA	0.92 (0.051)	0.79 (0.099)	0.8 (0.088)
Dianthus sardous	FDA	0.92 (0.056)	0.81 (0.098)	0.82 (0.089)
Dianthus tarentinus	FDA	0.92 (0.046)	0.76 (0.09)	0.77 (0.085)
Drymochloa drymeja subsp. *exaltata*	FDA	0.9 (0.033)	0.71 (0.076)	0.71 (0.076)
Echinops siculus	FDA	0.89 (0.048)	0.71 (0.09)	0.72 (0.085)
Epipactis meridionalis	FDA	0.94 (0.033)	0.79 (0.085)	0.79 (0.081)
Erysimum apenninum	FDA	0.94 (0.026)	0.82 (0.064)	0.82 (0.064)
Erysimum crassistylum subsp. *garganicum*	FDA	0.89 (0.049)	0.69 (0.094)	0.73 (0.082)
Erysimum etruscum	FDA	0.88 (0.046)	0.7 (0.084)	0.71 (0.081)
Erysimum pseudorhaeticum	FDA	0.95 (0.017)	0.81 (0.046)	0.81 (0.046)
Euphorbia ceratocarpa	FDA	0.91 (0.064)	0.76 (0.115)	0.79 (0.092)
Euphorbia corallioides	FDA	0.91 (0.043)	0.71 (0.093)	0.72 (0.089)
Euphorbia nicaeensis subsp. *japygica*	FDA	0.92 (0.044)	0.76 (0.087)	0.76 (0.081)
Euphorbia variabilis	FDA	0.93 (0.049)	0.81 (0.094)	0.8 (0.094)
Euphrasia tricuspidata	FDA	0.94 (0.015)	0.77 (0.041)	0.77 (0.041)
Festuca alfrediana subsp. *ferrariniana*	FDA	0.98 (0.018)	0.94 (0.045)	0.93 (0.046)
Festuca austrodolomitica	FDA	0.94 (0.032)	0.81 (0.075)	0.8 (0.079)
Festuca riccerii	FDA	0.98 (0.02)	0.96 (0.039)	0.96 (0.041)
Festuca robustifolia	FDA	0.94 (0.024)	0.78 (0.061)	0.78 (0.061)
Festuca violacea subsp. *italica*	FDA	0.96 (0.035)	0.91 (0.069)	0.92 (0.058)
Festuca violacea subsp. *puccinellii*	FDA	0.95 (0.038)	0.88 (0.078)	0.89 (0.068)
Galium baldense	FDA	0.96 (0.015)	0.8 (0.05)	0.8 (0.05)
Genista etnensis	FDA	0.9 (0.049)	0.74 (0.097)	0.75 (0.096)
Genista tyrrhena	FDA	0.96 (0.037)	0.92 (0.074)	0.92 (0.075)
Globularia incanescens	FDA	0.92 (0.032)	0.82 (0.057)	0.82 (0.057)
Helichrysum litoreum	FDA	0.96 (0.021)	0.81 (0.056)	0.81 (0.056)
Helichrysum saxatile subsp. *saxatile*	FDA	0.92 (0.053)	0.77 (0.1)	0.76 (0.101)
Helictochloa praetutiana subsp. *praetutiana*	FDA	0.99 (0.013)	0.92 (0.046)	0.92 (0.046)
Helleborus viridis subsp. *bocconei*	FDA	0.91 (0.028)	0.72 (0.062)	0.72 (0.062)
Hypericum barbatum subsp. *calabricum*	FDA	0.92 (0.041)	0.81 (0.075)	0.82 (0.071)
Iris cengialti subsp. *cengialti*	FDA	0.94 (0.026)	0.8 (0.068)	0.8 (0.068)
Jacobaea maritima subsp. *bicolor*	FDA	0.91 (0.063)	0.82 (0.118)	0.8 (0.111)
Klasea flavescens subsp. *cichoracea*	FDA	0.89 (0.06)	0.7 (0.096)	0.72 (0.093)
Knautia baldensis	FDA	0.95 (0.025)	0.79 (0.073)	0.79 (0.073)
Knautia persicina	FDA	0.96 (0.018)	0.84 (0.06)	0.84 (0.06)
Koeleria splendens	FDA	0.91 (0.044)	0.75 (0.092)	0.75 (0.092)
Laserpitium nitidum	FDA	0.93 (0.038)	0.76 (0.092)	0.76 (0.089)
Leontodon anomalus	FDA	0.92 (0.037)	0.75 (0.081)	0.75 (0.078)
Leontodon intermedius	FDA	0.85 (0.059)	0.69 (0.099)	0.71 (0.098)
Limonium acutifolium subsp. *acutifolium*	FDA	0.96 (0.045)	0.91 (0.086)	0.9 (0.086)

Limonium ilvae	FDA	0.98 (0.017)	0.96 (0.039)	0.93 (0.063)
Limonium merxmuelleri subsp. *sulcitanum*	FDA	0.99 (0.015)	0.97 (0.041)	0.96 (0.047)
Limonium multiforme	FDA	0.98 (0.021)	0.96 (0.046)	0.94 (0.053)
Limonium remotispiculum	FDA	0.89 (0.063)	0.71 (0.112)	0.74 (0.1)
Linaria purpurea	FDA	0.92 (0.036)	0.79 (0.072)	0.79 (0.072)
Luzula sylvatica subsp. *sicula*	FDA	0.92 (0.043)	0.76 (0.089)	0.78 (0.081)
Mcneillia graminifolia subsp. *rosanoi*	FDA	0.95 (0.045)	0.85 (0.089)	0.86 (0.08)
Melampyrum italicum	FDA	0.93 (0.014)	0.71 (0.036)	0.71 (0.036)
Micromeria cordata	FDA	0.94 (0.058)	0.84 (0.112)	0.85 (0.101)
Micromeria graeca subsp. *tenuifolia*	FDA	0.86 (0.051)	0.69 (0.079)	0.7 (0.077)
Moehringia glaucovirens	FDA	0.93 (0.032)	0.74 (0.081)	0.74 (0.083)
Moltkia suffruticosa subsp. *bigazziana*	FDA	0.91 (0.048)	0.75 (0.097)	0.76 (0.09)
Myosotis graui	FDA	0.96 (0.041)	0.87 (0.084)	0.88 (0.073)
Myosotis sylvatica subsp. *elongata*	FDA	0.91 (0.05)	0.77 (0.088)	0.78 (0.084)
Odontarrhena argentea	FDA	0.93 (0.046)	0.77 (0.093)	0.78 (0.088)
Odontarrhena bertolonii	FDA	0.91 (0.052)	0.74 (0.099)	0.74 (0.094)
Oenanthe lisae	FDA	0.92 (0.04)	0.78 (0.076)	0.79 (0.075)
Onosma echioides subsp. *echioides*	FDA	0.84 (0.054)	0.66 (0.092)	0.69 (0.089)
Onosma pseudoarenaria subsp. *tridentina*	FDA	0.94 (0.039)	0.79 (0.08)	0.79 (0.075)
Ophrys appennina	FDA	0.87 (0.035)	0.68 (0.065)	0.68 (0.065)
Ophrys apulica	FDA	0.95 (0.057)	0.84 (0.109)	0.82 (0.109)
Ophrys bertolonii subsp. *bertoloniiformis*	FDA	0.92 (0.015)	0.7 (0.037)	0.7 (0.037)
Ophrys classica	FDA	0.86 (0.035)	0.65 (0.06)	0.65 (0.06)
Ophrys crabronifera	FDA	0.86 (0.057)	0.67 (0.096)	0.68 (0.093)
Ophrys exaltata subsp. *exaltata*	FDA	0.86 (0.054)	0.66 (0.092)	0.69 (0.098)
Ophrys exaltata subsp. *montis-leonis*	FDA	0.93 (0.044)	0.79 (0.089)	0.8 (0.083)
Ophrys lucana	FDA	0.91 (0.041)	0.73 (0.086)	0.73 (0.086)
Ophrys lunulata	FDA	0.89 (0.055)	0.76 (0.09)	0.78 (0.085)
Ophrys minipassionis	FDA	0.87 (0.068)	0.69 (0.116)	0.71 (0.106)
Ophrys passionis subsp. *majellensis*	FDA	0.88 (0.067)	0.72 (0.114)	0.73 (0.103)
Ophrys promontorii	FDA	0.85 (0.083)	0.68 (0.122)	0.71 (0.108)
Ophrys tenthredinifera subsp. *neglecta*	FDA	0.9 (0.041)	0.72 (0.084)	0.72 (0.081)
Ornithogalum exscapum	FDA	0.89 (0.042)	0.68 (0.083)	0.69 (0.081)
Pimpinella anisoides	FDA	0.88 (0.061)	0.68 (0.115)	0.72 (0.104)
Pinguicula christinae	FDA	0.97 (0.047)	0.91 (0.094)	0.91 (0.09)
Plantago sarda	FDA	0.99 (0.01)	0.98 (0.028)	0.96 (0.043)
Polygala alpestris subsp. *angelisii*	FDA	0.94 (0.051)	0.84 (0.111)	0.84 (0.102)
Polygala flavescens subsp. *maremmana*	FDA	0.96 (0.043)	0.88 (0.095)	0.86 (0.101)
Polygala sardoa	FDA	0.9 (0.047)	0.75 (0.087)	0.76 (0.084)
Potentilla rigoana	FDA	0.97 (0.024)	0.89 (0.066)	0.88 (0.066)
Primula polliniana	FDA	0.94 (0.02)	0.76 (0.056)	0.76 (0.056)
Primula tyrolensis	FDA	0.93 (0.033)	0.74 (0.078)	0.74 (0.074)
Ptychotis sardoa	FDA	0.94 (0.051)	0.84 (0.103)	0.84 (0.095)
Pulmonaria vallarsae	FDA	0.95 (0.024)	0.81 (0.066)	0.81 (0.066)
Quercus ichnusae	FDA	0.98 (0.023)	0.91 (0.065)	0.89 (0.073)
Rhizobotrya alpina	FDA	0.92 (0.04)	0.77 (0.093)	0.76 (0.093)
Rumex scutatus glaucescens	FDA	0.91 (0.045)	0.74 (0.099)	0.76 (0.096)
Salix arrigonii	FDA	0.88 (0.057)	0.74 (0.096)	0.77 (0.086)
Salix brutia	FDA	0.95 (0.033)	0.84 (0.075)	0.83 (0.077)
Salix purpurea subsp. *eburnea*	FDA	0.92 (0.049)	0.76 (0.096)	0.77 (0.081)

Salvia haematodes	FDA	0.88 (0.062)	0.72 (0.11)	0.75 (0.103)
Santolina etrusca	FDA	0.92 (0.046)	0.78 (0.093)	0.78 (0.094)
Santolina insularis	FDA	0.93 (0.046)	0.81 (0.085)	0.82 (0.079)
Saxifraga arachnoidea	FDA	0.96 (0.039)	0.84 (0.086)	0.83 (0.08)
Saxifraga depressa	FDA	0.94 (0.033)	0.84 (0.071)	0.81 (0.079)
Saxifraga facchinii	FDA	0.96 (0.03)	0.88 (0.073)	0.86 (0.086)
Saxifraga hostii subsp. *rhaetica*	FDA	0.94 (0.05)	0.78 (0.1)	0.76 (0.1)
Saxifraga presolanensis	FDA	0.93 (0.058)	0.85 (0.107)	0.81 (0.124)
Saxifraga tombeanensis	FDA	0.95 (0.038)	0.85 (0.084)	0.82 (0.09)
Saxifraga vandellii	FDA	0.9 (0.055)	0.74 (0.096)	0.74 (0.093)
Scabiosa holosericea	FDA	0.88 (0.048)	0.69 (0.091)	0.71 (0.088)
Scabiosa uniseta	FDA	0.9 (0.057)	0.73 (0.102)	0.74 (0.097)
Scabiosa vestina	FDA	0.97 (0.022)	0.89 (0.062)	0.87 (0.076)
Scorzonera callosa	FDA	0.89 (0.077)	0.75 (0.129)	0.77 (0.118)
Scorzonera villosa subsp. *columnae*	FDA	0.86 (0.064)	0.7 (0.097)	0.72 (0.093)
Sedum alsinifolium	FDA	0.94 (0.03)	0.78 (0.082)	0.79 (0.086)
Senecio ovatus subsp. *stabianus*	FDA	0.95 (0.041)	0.85 (0.083)	0.84 (0.086)
Sesleria nitida	FDA	0.96 (0.029)	0.87 (0.062)	0.87 (0.06)
Sesleria pichiana	FDA	0.91 (0.055)	0.75 (0.105)	0.75 (0.109)
Silene italica subsp. *sicula*	FDA	0.92 (0.031)	0.76 (0.061)	0.76 (0.061)
Silene nummica	FDA	0.95 (0.046)	0.91 (0.091)	0.9 (0.091)
Siler montanum subsp. *siculum*	FDA	0.97 (0.028)	0.85 (0.071)	0.85 (0.07)
Spiraea decumbens subsp. *tomentosa*	FDA	0.89 (0.058)	0.69 (0.116)	0.71 (0.107)
Stipa etrusca	FDA	0.89 (0.049)	0.7 (0.09)	0.71 (0.09)
Tephroseris italica	FDA	0.94 (0.037)	0.82 (0.085)	0.83 (0.079)
Thesium sommieri	FDA	0.93 (0.047)	0.82 (0.093)	0.84 (0.077)
Thymus spinulosus	FDA	0.85 (0.066)	0.65 (0.117)	0.66 (0.116)
Tolpis virgata subsp. *grandiflora*	FDA	0.88 (0.075)	0.71 (0.135)	0.73 (0.13)
Trifolium pratense subsp. *semipurpureum*	FDA	0.92 (0.032)	0.76 (0.086)	0.76 (0.086)
Trisetaria villosa	FDA	0.95 (0.038)	0.87 (0.067)	0.88 (0.058)
Vicia ochroleuca subsp. *ochroleuca*	FDA	0.86 (0.055)	0.66 (0.103)	0.7 (0.097)
Viola aethnensis subsp. *splendida*	FDA	0.95 (0.039)	0.84 (0.086)	0.84 (0.081)
Viola bertolonii	FDA	0.96 (0.031)	0.85 (0.08)	0.82 (0.088)
Viola cassinensis subsp. *pseudogracilis*	FDA	0.97 (0.033)	0.9 (0.077)	0.89 (0.078)
Viola dubyana	FDA	0.95 (0.037)	0.85 (0.091)	0.82 (0.092)
Viola etrusca	FDA	0.92 (0.052)	0.76 (0.111)	0.75 (0.106)
Viola eugeniae subsp. *eugeniae*	FDA	0.96 (0.04)	0.91 (0.08)	0.91 (0.071)
Viola ferrarinii	FDA	0.97 (0.027)	0.91 (0.055)	0.92 (0.055)
Acer cappadocicum subsp. *lobelii*	GBM	0.9 (0.049)	0.73 (0.089)	0.75 (0.085)
Adenocarpus complicatus subsp. *brutius*	GBM	0.91 (0.046)	0.74 (0.09)	0.75 (0.086)
Adenostyles australis	GBM	0.96 (0.028)	0.86 (0.063)	0.86 (0.062)
Ajuga tenorei	GBM	0.93 (0.048)	0.8 (0.083)	0.8 (0.077)
Alyssum diffusum subsp. *diffusum*	GBM	0.91 (0.043)	0.76 (0.093)	0.77 (0.089)
Anemonoides trifolia subsp. *brevidentata*	GBM	0.94 (0.017)	0.76 (0.053)	0.76 (0.053)
Antirrhinum siculum	GBM	0.89 (0.064)	0.73 (0.101)	0.74 (0.1)
Aquilegia lucensis	GBM	0.99 (0.019)	0.98 (0.035)	0.97 (0.038)
Arabis collina subsp. *rosea*	GBM	0.88 (0.046)	0.7 (0.079)	0.71 (0.077)
Arenaria huteri	GBM	0.91 (0.05)	0.75 (0.11)	0.77 (0.096)
Armeria arenaria subsp. *marginata*	GBM	0.96 (0.041)	0.92 (0.068)	0.92 (0.065)
Armeria brutia	GBM	0.95 (0.047)	0.85 (0.085)	0.84 (0.083)

Armeria denticulata	GBM	0.87 (0.065)	0.75 (0.101)	0.79 (0.087)
Artemisia caerulescens subsp. *cretacea*	GBM	0.92 (0.061)	0.76 (0.117)	0.77 (0.122)
Artemisia campestris subsp. *variabilis*	GBM	0.91 (0.049)	0.74 (0.086)	0.76 (0.085)
Astragalus parnassi subsp. *calabricus*	GBM	0.92 (0.051)	0.82 (0.09)	0.81 (0.087)
Asyneuma trichocalycinum	GBM	0.93 (0.046)	0.81 (0.091)	0.81 (0.091)
Atadinus glaucophyllus	GBM	0.9 (0.048)	0.73 (0.085)	0.75 (0.087)
Bellevalia webbiana	GBM	0.91 (0.066)	0.8 (0.099)	0.8 (0.092)
Bellium crassifolium	GBM	0.96 (0.044)	0.86 (0.076)	0.87 (0.07)
Biscutella apuana	GBM	0.91 (0.064)	0.74 (0.104)	0.74 (0.099)
Biscutella morisiana	GBM	0.84 (0.056)	0.68 (0.094)	0.71 (0.09)
Brachypodium genuense	GBM	0.95 (0.02)	0.83 (0.051)	0.83 (0.051)
Brassica glabrescens	GBM	0.97 (0.041)	0.92 (0.073)	0.88 (0.091)
Bromopsis caprina	GBM	0.93 (0.04)	0.77 (0.093)	0.78 (0.088)
Buphthalmum salicifolium subsp. *flexile*	GBM	0.89 (0.044)	0.7 (0.089)	0.71 (0.085)
Campanula bertolae	GBM	0.93 (0.024)	0.73 (0.06)	0.73 (0.06)
Campanula carnica subsp. *puberula*	GBM	0.9 (0.076)	0.75 (0.11)	0.76 (0.104)
Campanula elatines	GBM	0.93 (0.032)	0.76 (0.072)	0.76 (0.072)
Campanula martinii	GBM	0.95 (0.03)	0.85 (0.066)	0.84 (0.067)
Campanula micrantha	GBM	0.95 (0.04)	0.86 (0.074)	0.88 (0.069)
Campanula morettiana	GBM	0.91 (0.029)	0.7 (0.064)	0.7 (0.064)
Campanula raineri	GBM	0.95 (0.024)	0.8 (0.067)	0.8 (0.066)
Campanula sabatia	GBM	0.96 (0.039)	0.89 (0.067)	0.89 (0.063)
Campanula tanfanii	GBM	0.94 (0.045)	0.82 (0.102)	0.83 (0.095)
Carduus nutans subsp. *perspinosus*	GBM	0.91 (0.054)	0.76 (0.103)	0.78 (0.094)
Carex macrostachys	GBM	0.9 (0.062)	0.79 (0.096)	0.81 (0.087)
*Carlina hispanica*subsp. *globosa*	GBM	0.9 (0.034)	0.7 (0.075)	0.72 (0.072)
Centaurea aplolepa subsp. *aplolepa*	GBM	0.98 (0.02)	0.93 (0.058)	0.9 (0.085)
Centaurea aplolepa subsp. *carueliana*	GBM	0.93 (0.076)	0.81 (0.107)	0.79 (0.096)
Centaurea aplolepa subsp. *lunensis*	GBM	0.93 (0.04)	0.76 (0.092)	0.78 (0.085)
Centaurea poeltiana	GBM	0.94 (0.054)	0.79 (0.1)	0.79 (0.095)
Centaurea subtilis	GBM	0.94 (0.065)	0.81 (0.115)	0.8 (0.111)
Cerastium apuanum	GBM	0.88 (0.055)	0.68 (0.114)	0.72 (0.107)
Cerastium scaranoi	GBM	0.94 (0.034)	0.82 (0.073)	0.83 (0.068)
Cerastium supramontanum	GBM	0.95 (0.047)	0.86 (0.084)	0.85 (0.083)
Cerastium tomentosum	GBM	0.9 (0.042)	0.72 (0.095)	0.75 (0.09)
Cerastium utriense	GBM	0.97 (0.036)	0.87 (0.067)	0.86 (0.068)
Cherleria laricifolia subsp. *ophiolitica*	GBM	0.9 (0.051)	0.73 (0.094)	0.75 (0.091)
Cirsium bertolonii	GBM	0.92 (0.052)	0.84 (0.085)	0.88 (0.067)
Cirsium tenoreanum	GBM	0.93 (0.035)	0.77 (0.075)	0.78 (0.07)
Cirsium vallis-demonii	GBM	0.94 (0.043)	0.79 (0.095)	0.81 (0.089)
Colchicum neapolitanum	GBM	0.87 (0.061)	0.69 (0.109)	0.73 (0.101)
Crocus biflorus	GBM	0.88 (0.024)	0.71 (0.045)	0.71 (0.045)
Crocus etruscus	GBM	0.89 (0.059)	0.76 (0.097)	0.78 (0.089)
Crocus imperati	GBM	0.88 (0.064)	0.7 (0.111)	0.73 (0.099)
Crocus suaveolens	GBM	0.92 (0.054)	0.82 (0.099)	0.82 (0.091)
Cryptotaenia thomasii	GBM	0.92 (0.039)	0.72 (0.087)	0.75 (0.085)
Cynoglossum apenninum	GBM	0.92 (0.057)	0.79 (0.101)	0.81 (0.095)
Daphne petraea	GBM	0.92 (0.053)	0.79 (0.091)	0.79 (0.082)
Dianthus carthusianorum subsp. *tenorei*	GBM	0.92 (0.056)	0.8 (0.086)	0.8 (0.081)
Dianthus sardous	GBM	0.94 (0.039)	0.83 (0.094)	0.84 (0.084)

Dianthus tarentinus	GBM	0.91 (0.053)	0.71 (0.104)	0.73 (0.101)
Drymochloa drymeja subsp. *exaltata*	GBM	0.88 (0.038)	0.7 (0.066)	0.7 (0.066)
Echinops siculus	GBM	0.89 (0.057)	0.71 (0.092)	0.73 (0.087)
Epipactis meridionalis	GBM	0.93 (0.033)	0.75 (0.088)	0.76 (0.08)
Erysimum apenninum	GBM	0.93 (0.028)	0.81 (0.061)	0.81 (0.061)
Erysimum crassistylum subsp. *garganicum*	GBM	0.87 (0.057)	0.7 (0.086)	0.74 (0.083)
Erysimum etruscum	GBM	0.87 (0.042)	0.7 (0.074)	0.71 (0.071)
Erysimum pseudorhaeticum	GBM	0.95 (0.012)	0.8 (0.04)	0.8 (0.04)
Euphorbia ceratocarpa	GBM	0.95 (0.036)	0.8 (0.099)	0.79 (0.098)
Euphorbia corallioides	GBM	0.86 (0.043)	0.67 (0.076)	0.69 (0.074)
Euphorbia nicaeensis subsp. *japygica*	GBM	0.9 (0.056)	0.72 (0.098)	0.74 (0.089)
Euphorbia variabilis	GBM	0.92 (0.052)	0.8 (0.085)	0.8 (0.084)
Euphrasia tricuspidata	GBM	0.94 (0.016)	0.76 (0.044)	0.76 (0.044)
Festuca alfrediana subsp. *ferrariniana*	GBM	0.98 (0.03)	0.95 (0.051)	0.94 (0.056)
Festuca austrodolomitica	GBM	0.95 (0.02)	0.79 (0.058)	0.78 (0.06)
Festuca riccerii	GBM	0.99 (0.019)	0.98 (0.035)	0.97 (0.039)
Festuca robustifolia	GBM	0.92 (0.032)	0.76 (0.078)	0.76 (0.078)
Festuca violacea subsp. *italica*	GBM	0.93 (0.055)	0.89 (0.083)	0.91 (0.067)
Festuca violacea subsp. *puccinellii*	GBM	0.95 (0.038)	0.89 (0.066)	0.9 (0.06)
Galium baldense	GBM	0.95 (0.013)	0.76 (0.043)	0.76 (0.043)
Genista etnensis	GBM	0.9 (0.058)	0.73 (0.097)	0.74 (0.101)
Genista tyrrhena	GBM	0.96 (0.046)	0.93 (0.065)	0.93 (0.065)
Globularia incanescens	GBM	0.91 (0.038)	0.84 (0.06)	0.84 (0.06)
Helichrysum litoreum	GBM	0.96 (0.017)	0.82 (0.056)	0.82 (0.056)
Helichrysum saxatile subsp. *saxatile*	GBM	0.94 (0.035)	0.78 (0.095)	0.78 (0.103)
Helictochloa praetutiana subsp. *praetutiana*	GBM	0.98 (0.015)	0.9 (0.052)	0.9 (0.052)
Helleborus viridis subsp. *bocconei*	GBM	0.9 (0.037)	0.71 (0.062)	0.71 (0.062)
Hypericum barbatum subsp. *calabricum*	GBM	0.91 (0.046)	0.77 (0.091)	0.79 (0.086)
Iris cengialti subsp. *cengialti*	GBM	0.94 (0.034)	0.79 (0.083)	0.79 (0.079)
Jacobaea maritima subsp. *bicolor*	GBM	0.94 (0.056)	0.83 (0.099)	0.81 (0.106)
Klasea flavescens subsp. *cichoracea*	GBM	0.84 (0.063)	0.65 (0.096)	0.69 (0.088)
Knautia baldensis	GBM	0.96 (0.021)	0.8 (0.071)	0.8 (0.071)
Knautia persicina	GBM	0.95 (0.021)	0.81 (0.061)	0.81 (0.061)
Koeleria splendens	GBM	0.91 (0.042)	0.73 (0.085)	0.75 (0.081)
Laserpitium nitidum	GBM	0.93 (0.041)	0.77 (0.079)	0.77 (0.076)
Leontodon anomalus	GBM	0.92 (0.034)	0.74 (0.073)	0.76 (0.074)
Leontodon intermedius	GBM	0.85 (0.056)	0.69 (0.085)	0.72 (0.081)
Limonium acutifolium subsp. *acutifolium*	GBM	0.97 (0.053)	0.92 (0.072)	0.88 (0.085)
Limonium ilvae	GBM	0.98 (0.025)	0.9 (0.072)	0.87 (0.094)
Limonium merxmuelleri subsp. *sulcitanum*	GBM	0.99 (0.019)	0.95 (0.053)	0.94 (0.06)
Limonium multiforme	GBM	0.98 (0.021)	0.93 (0.053)	0.92 (0.055)
Limonium remotispiculum	GBM	0.86 (0.071)	0.7 (0.12)	0.74 (0.108)
Linaria purpurea	GBM	0.92 (0.032)	0.81 (0.062)	0.81 (0.062)
Luzula sylvatica subsp. *sicula*	GBM	0.89 (0.05)	0.73 (0.08)	0.76 (0.074)
Mcneillia graminifolia subsp. *rosanoi*	GBM	0.96 (0.031)	0.85 (0.076)	0.87 (0.069)
Melampyrum italicum	GBM	0.93 (0.014)	0.71 (0.035)	0.71 (0.035)
Micromeria cordata	GBM	0.93 (0.061)	0.83 (0.106)	0.85 (0.088)
Micromeria graeca subsp. *tenuifolia*	GBM	0.86 (0.045)	0.7 (0.076)	0.72 (0.073)
Moehringia glaucovirens	GBM	0.94 (0.034)	0.78 (0.083)	0.78 (0.082)
Moltkia suffruticosa subsp. *bigazziana*	GBM	0.9 (0.046)	0.71 (0.101)	0.74 (0.098)

Myosotis graui	GBM	0.95 (0.038)	0.85 (0.074)	0.87 (0.064)
Myosotis sylvatica subsp. *elongata*	GBM	0.89 (0.046)	0.72 (0.09)	0.74 (0.093)
Odontarrhena argentea	GBM	0.93 (0.051)	0.77 (0.094)	0.78 (0.087)
Odontarrhena bertolonii	GBM	0.86 (0.074)	0.72 (0.116)	0.74 (0.102)
Oenanthe lisae	GBM	0.92 (0.039)	0.79 (0.07)	0.8 (0.068)
Onosma echioides subsp. *echioides*	GBM	0.83 (0.059)	0.65 (0.093)	0.68 (0.09)
Onosma pseudoarenaria subsp. *tridentina*	GBM	0.93 (0.053)	0.79 (0.109)	0.8 (0.1)
Ophrys appennina	GBM	0.89 (0.037)	0.69 (0.071)	0.69 (0.071)
Ophrys apulica	GBM	0.95 (0.045)	0.84 (0.096)	0.81 (0.097)
Ophrys bertolonii subsp. *bertoloniiformis*	GBM	0.92 (0.014)	0.7 (0.03)	0.7 (0.03)
Ophrys classica	GBM	0.88 (0.025)	0.68 (0.048)	0.68 (0.048)
Ophrys crabronifera	GBM	0.86 (0.051)	0.67 (0.086)	0.68 (0.083)
Ophrys exaltata subsp. *exaltata*	GBM	0.86 (0.062)	0.7 (0.095)	0.73 (0.092)
Ophrys exaltata subsp. *montis-leonis*	GBM	0.92 (0.05)	0.75 (0.111)	0.76 (0.108)
Ophrys lucana	GBM	0.91 (0.033)	0.73 (0.069)	0.73 (0.069)
Ophrys lunulata	GBM	0.86 (0.06)	0.73 (0.09)	0.76 (0.082)
Ophrys minipassionis	GBM	0.86 (0.068)	0.68 (0.109)	0.71 (0.098)
Ophrys passionis subsp. *majellensis*	GBM	0.85 (0.086)	0.72 (0.121)	0.76 (0.107)
Ophrys promontorii	GBM	0.86 (0.069)	0.68 (0.112)	0.71 (0.101)
Ophrys tenthredinifera subsp. *neglecta*	GBM	0.91 (0.038)	0.76 (0.082)	0.77 (0.078)
Ornithogalum exscapum	GBM	0.88 (0.049)	0.7 (0.087)	0.72 (0.084)
Pimpinella anisoides	GBM	0.83 (0.08)	0.67 (0.11)	0.73 (0.098)
Pinguicula christinae	GBM	0.99 (0.034)	0.95 (0.06)	0.94 (0.061)
Plantago sarda	GBM	1 (0.007)	0.98 (0.02)	0.97 (0.033)
Polygala alpestris subsp. *angelisii*	GBM	0.93 (0.052)	0.84 (0.091)	0.85 (0.08)
Polygala flavescens subsp. *maremmana*	GBM	0.96 (0.058)	0.87 (0.076)	0.85 (0.08)
Polygala sardoa	GBM	0.9 (0.052)	0.77 (0.095)	0.79 (0.087)
Potentilla rigoana	GBM	0.97 (0.023)	0.88 (0.076)	0.86 (0.082)
Primula polliniana	GBM	0.93 (0.022)	0.72 (0.057)	0.72 (0.057)
Primula tyrolensis	GBM	0.92 (0.037)	0.71 (0.082)	0.72 (0.084)
Ptychotis sardoa	GBM	0.91 (0.065)	0.84 (0.105)	0.86 (0.093)
Pulmonaria vallarsae	GBM	0.95 (0.023)	0.81 (0.065)	0.81 (0.065)
Quercus ichnusae	GBM	0.97 (0.037)	0.91 (0.065)	0.87 (0.076)
Rhizobotrya alpina	GBM	0.94 (0.037)	0.78 (0.096)	0.78 (0.099)
Rumex scutatus glaucescens	GBM	0.91 (0.04)	0.72 (0.084)	0.73 (0.086)
Salix arrigonii	GBM	0.85 (0.073)	0.68 (0.113)	0.72 (0.105)
Salix brutia	GBM	0.94 (0.034)	0.77 (0.089)	0.76 (0.081)
Salix purpurea subsp. *eburnea*	GBM	0.9 (0.068)	0.73 (0.109)	0.75 (0.103)
Salvia haematodes	GBM	0.81 (0.096)	0.67 (0.138)	0.72 (0.12)
Santolina etrusca	GBM	0.91 (0.04)	0.72 (0.095)	0.74 (0.085)
Santolina insularis	GBM	0.91 (0.057)	0.81 (0.09)	0.83 (0.082)
Saxifraga arachnoidea	GBM	0.95 (0.055)	0.85 (0.081)	0.82 (0.084)
Saxifraga depressa	GBM	0.95 (0.032)	0.85 (0.064)	0.83 (0.068)
Saxifraga facchinii	GBM	0.95 (0.044)	0.88 (0.069)	0.85 (0.077)
Saxifraga hostii subsp. *rhaetica*	GBM	0.92 (0.056)	0.76 (0.113)	0.74 (0.102)
Saxifraga presolanensis	GBM	0.93 (0.069)	0.84 (0.107)	0.81 (0.103)
Saxifraga tombeanensis	GBM	0.94 (0.059)	0.84 (0.097)	0.8 (0.097)
Saxifraga vandellii	GBM	0.89 (0.05)	0.71 (0.102)	0.74 (0.093)
Scabiosa holosericea	GBM	0.87 (0.054)	0.7 (0.086)	0.72 (0.083)
Scabiosa uniseta	GBM	0.91 (0.045)	0.72 (0.084)	0.73 (0.086)

Scabiosa vestina	GBM	0.96 (0.031)	0.87 (0.072)	0.84 (0.078)
Scorzonera callosa	GBM	0.92 (0.049)	0.76 (0.103)	0.77 (0.095)
Scorzonera villosa subsp. *columnae*	GBM	0.84 (0.072)	0.7 (0.111)	0.74 (0.106)
Sedum alsinifolium	GBM	0.94 (0.042)	0.77 (0.091)	0.77 (0.089)
Senecio ovatus subsp. *stabianus*	GBM	0.95 (0.036)	0.88 (0.072)	0.87 (0.077)
Sesleria nitida	GBM	0.96 (0.029)	0.86 (0.066)	0.87 (0.064)
Sesleria pichiana	GBM	0.88 (0.061)	0.68 (0.108)	0.72 (0.096)
Silene italica subsp. *sicula*	GBM	0.88 (0.042)	0.72 (0.074)	0.72 (0.074)
Silene nummica	GBM	0.97 (0.04)	0.92 (0.072)	0.89 (0.079)
Siler montanum subsp. *siculum*	GBM	0.97 (0.018)	0.86 (0.06)	0.85 (0.061)
Spiraea decumbens subsp. *tomentosa*	GBM	0.91 (0.05)	0.73 (0.101)	0.74 (0.099)
Stipa etrusca	GBM	0.88 (0.056)	0.69 (0.092)	0.72 (0.09)
Tephroseris italica	GBM	0.94 (0.042)	0.87 (0.076)	0.88 (0.067)
Thesium sommieri	GBM	0.93 (0.058)	0.83 (0.098)	0.85 (0.086)
Thymus spinulosus	GBM	0.89 (0.056)	0.73 (0.088)	0.75 (0.081)
Tolpis virgata subsp. *grandiflora*	GBM	0.85 (0.089)	0.68 (0.119)	0.71 (0.114)
Trifolium pratense subsp. *semipurpureum*	GBM	0.9 (0.033)	0.7 (0.062)	0.71 (0.061)
Trisetaria villosa	GBM	0.96 (0.029)	0.86 (0.068)	0.87 (0.067)
Vicia ochroleuca subsp. *ochroleuca*	GBM	0.89 (0.053)	0.72 (0.104)	0.75 (0.095)
Viola aethnensis subsp. *splendida*	GBM	0.95 (0.033)	0.85 (0.077)	0.85 (0.077)
Viola bertolonii	GBM	0.94 (0.048)	0.81 (0.103)	0.8 (0.113)
Viola cassinensis subsp. *pseudogracilis*	GBM	0.96 (0.038)	0.85 (0.085)	0.82 (0.093)
Viola dubyana	GBM	0.94 (0.044)	0.83 (0.086)	0.8 (0.091)
Viola etrusca	GBM	0.92 (0.062)	0.8 (0.109)	0.79 (0.105)
Viola eugeniae subsp. *eugeniae*	GBM	0.96 (0.028)	0.88 (0.081)	0.9 (0.072)
Viola ferrarinii	GBM	0.96 (0.026)	0.93 (0.043)	0.93 (0.04)
Acer cappadocicum subsp. *lobelii*	GLM	0.93 (0.034)	0.8 (0.07)	0.71 (0.078)
Adenocarpus complicatus subsp. brutius	GLM	0.93 (0.031)	0.79 (0.069)	0.67 (0.079)
Adenostyles australis	GLM	0.96 (0.016)	0.86 (0.047)	0.79 (0.058)
Ajuga tenorei	GLM	0.94 (0.028)	0.84 (0.054)	0.66 (0.094)
Alyssum diffusum subsp. *diffusum*	GLM	0.92 (0.037)	0.77 (0.084)	0.64 (0.076)
Anemonoides trifolia subsp. *brevidentata*	GLM	0.93 (0.017)	0.72 (0.05)	0.72 (0.046)
Antirrhinum siculum	GLM	0.89 (0.041)	0.68 (0.075)	0.63 (0.09)
Aquilegia lucensis	GLM	0.99 (0.012)	0.98 (0.026)	0.92 (0.053)
Arabis collina subsp. *Rosea*	GLM	0.86 (0.046)	0.64 (0.086)	0.61 (0.096)
Arenaria huteri	GLM	0.91 (0.034)	0.75 (0.093)	0.54 (0.115)
Armeria arenaria subsp. *marginata*	GLM	0.97 (0.03)	0.94 (0.051)	0.88 (0.064)
Armeria brutia	GLM	0.98 (0.017)	0.93 (0.052)	0.78 (0.069)
Armeria denticulata	GLM	0.91 (0.047)	0.75 (0.099)	0.73 (0.09)
Artemisia caerulescens subsp. *cretacea*	GLM	0.89 (0.041)	0.75 (0.086)	0.47 (0.095)
Artemisia campestris subsp. *variabilis*	GLM	0.88 (0.049)	0.68 (0.096)	0.63 (0.098)
Astragalus parnassi subsp. *calabricus*	GLM	0.93 (0.032)	0.82 (0.066)	0.63 (0.09)
Asyneuma trichocalycinum	GLM	0.93 (0.038)	0.85 (0.069)	0.68 (0.094)
Atadinus glaucophyllus	GLM	0.9 (0.038)	0.73 (0.074)	0.63 (0.095)
Bellevalia webbiana	GLM	0.95 (0.033)	0.89 (0.06)	0.71 (0.086)
Bellium crassifolium	GLM	0.97 (0.017)	0.89 (0.063)	0.81 (0.085)
Biscutella apuana	GLM	0.94 (0.033)	0.8 (0.071)	0.64 (0.09)
Biscutella morisiana	GLM	0.85 (0.035)	0.65 (0.067)	0.7 (0.075)
Brachypodium genuense	GLM	0.95 (0.015)	0.8 (0.048)	0.78 (0.049)
Brassica glabrescens	GLM	0.96 (0.028)	0.91 (0.058)	0.71 (0.093)

Bromopsis caprina	GLM	0.91 (0.037)	0.75 (0.086)	0.63 (0.091)
Buphthalmum salicifolium subsp. *flexile*	GLM	0.9 (0.038)	0.72 (0.082)	0.63 (0.081)
Campanula bertolae	GLM	0.92 (0.019)	0.75 (0.044)	0.69 (0.046)
Campanula carnica subsp. *puberula*	GLM	0.95 (0.037)	0.82 (0.098)	0.69 (0.103)
Campanula elatines	GLM	0.94 (0.019)	0.75 (0.052)	0.74 (0.061)
Campanula martinii	GLM	0.96 (0.018)	0.85 (0.05)	0.76 (0.067)
Campanula micrantha	GLM	0.96 (0.031)	0.88 (0.071)	0.88 (0.064)
Campanula morettiana	GLM	0.93 (0.02)	0.72 (0.053)	0.68 (0.062)
Campanula raineri	GLM	0.96 (0.015)	0.82 (0.045)	0.74 (0.065)
Campanula sabatia	GLM	0.98 (0.02)	0.94 (0.045)	0.83 (0.065)
Campanula tanfanii	GLM	0.97 (0.017)	0.9 (0.059)	0.67 (0.084)
Carduus nutans subsp. *perspinosus*	GLM	0.78 (0.053)	0.6 (0.088)	0.33 (0.096)
Carex macrostachys	GLM	0.9 (0.037)	0.79 (0.07)	0.67 (0.078)
*Carlina hispanica*subsp. *globosa*	GLM	0.94 (0.026)	0.76 (0.066)	0.72 (0.076)
Centaurea aplolepa subsp. *aplolepa*	GLM	0.95 (0.044)	0.9 (0.089)	0.73 (0.152)
Centaurea aplolepa subsp. *carueliana*	GLM	0.95 (0.027)	0.83 (0.071)	0.65 (0.091)
Centaurea aplolepa subsp. *lunensis*	GLM	0.95 (0.022)	0.79 (0.067)	0.73 (0.082)
Centaurea poeltiana	GLM	0.94 (0.028)	0.79 (0.082)	0.62 (0.107)
Centaurea subtilis	GLM	0.92 (0.04)	0.82 (0.067)	0.54 (0.082)
Cerastium apuanum	GLM	0.9 (0.039)	0.71 (0.09)	0.62 (0.098)
Cerastium scaranoi	GLM	0.95 (0.026)	0.81 (0.062)	0.75 (0.07)
Cerastium supramontanum	GLM	0.96 (0.028)	0.88 (0.066)	0.73 (0.088)
Cerastium tomentosum	GLM	0.89 (0.04)	0.69 (0.08)	0.57 (0.089)
Cerastium utriense	GLM	0.98 (0.008)	0.93 (0.036)	0.81 (0.064)
Cherleria laricifolia subsp. *ophiolitica*	GLM	0.92 (0.029)	0.77 (0.072)	0.68 (0.078)
Cirsium bertolonii	GLM	0.95 (0.042)	0.87 (0.078)	0.86 (0.067)
Cirsium tenoreanum	GLM	0.92 (0.031)	0.75 (0.084)	0.67 (0.073)
Cirsium vallis-demonii	GLM	0.95 (0.028)	0.85 (0.065)	0.68 (0.082)
Colchicum neapolitanum	GLM	0.81 (0.06)	0.56 (0.099)	0.45 (0.128)
Crocus biflorus	GLM	0.89 (0.025)	0.68 (0.052)	0.71 (0.05)
Crocus etruscus	GLM	0.94 (0.034)	0.82 (0.065)	0.7 (0.101)
Crocus imperati	GLM	0.87 (0.051)	0.64 (0.099)	0.56 (0.103)
Crocus suaveolens	GLM	0.96 (0.025)	0.86 (0.074)	0.65 (0.098)
Cryptotaenia thomasii	GLM	0.94 (0.024)	0.8 (0.074)	0.68 (0.089)
Cynoglossum apenninum	GLM	0.92 (0.044)	0.8 (0.09)	0.73 (0.089)
Daphne petraea	GLM	0.96 (0.023)	0.88 (0.061)	0.73 (0.083)
Dianthus carthusianorum subsp. *tenorei*	GLM	0.93 (0.032)	0.77 (0.077)	0.59 (0.081)
Dianthus sardous	GLM	0.88 (0.054)	0.77 (0.097)	0.63 (0.083)
Dianthus tarentinus	GLM	0.87 (0.037)	0.67 (0.067)	0.48 (0.095)
Drymochloa drymeja subsp. *exaltata*	GLM	0.86 (0.035)	0.66 (0.059)	0.64 (0.066)
Echinops siculus	GLM	0.87 (0.045)	0.66 (0.078)	0.66 (0.101)
Epipactis meridionalis	GLM	0.94 (0.03)	0.77 (0.09)	0.7 (0.099)
Erysimum apenninum	GLM	0.93 (0.019)	0.78 (0.046)	0.75 (0.048)
Erysimum crassistylum subsp. *garganicum*	GLM	0.87 (0.04)	0.64 (0.08)	0.55 (0.101)
Erysimum etruscum	GLM	0.87 (0.035)	0.66 (0.078)	0.64 (0.097)
Erysimum pseudorhaeticum	GLM	0.95 (0.013)	0.8 (0.035)	0.8 (0.035)
Euphorbia ceratocarpa	GLM	0.93 (0.035)	0.77 (0.094)	0.72 (0.11)
Euphorbia corallioides	GLM	0.92 (0.026)	0.73 (0.071)	0.72 (0.064)
Euphorbia nicaeensis subsp. *japygica*	GLM	0.92 (0.034)	0.78 (0.081)	0.65 (0.104)
Euphorbia variabilis	GLM	0.94 (0.031)	0.83 (0.091)	0.7 (0.087)

Euphrasia tricuspidata	GLM	0.94 (0.015)	0.75 (0.037)	0.75 (0.034)
Festuca alfrediana subsp. *ferrariniana*	GLM	0.99 (0.01)	0.97 (0.028)	0.9 (0.056)
Festuca austrodolomitica	GLM	0.96 (0.014)	0.8 (0.05)	0.73 (0.068)
Festuca riccerii	GLM	0.99 (0.019)	0.96 (0.038)	0.92 (0.048)
Festuca robustifolia	GLM	0.93 (0.021)	0.75 (0.047)	0.71 (0.054)
Festuca violacea subsp. *italica*	GLM	0.97 (0.03)	0.9 (0.063)	0.87 (0.068)
Festuca violacea subsp. *puccinellii*	GLM	0.97 (0.029)	0.9 (0.054)	0.86 (0.067)
Galium baldense	GLM	0.95 (0.013)	0.8 (0.037)	0.77 (0.041)
Genista etnensis	GLM	0.93 (0.036)	0.76 (0.093)	0.73 (0.112)
Genista tyrrhena	GLM	0.98 (0.028)	0.95 (0.056)	0.89 (0.094)
Globularia incanescens	GLM	0.92 (0.027)	0.8 (0.055)	0.8 (0.052)
Helichrysum litoreum	GLM	0.96 (0.011)	0.81 (0.036)	0.75 (0.047)
Helichrysum saxatile subsp. *saxatile*	GLM	0.94 (0.027)	0.78 (0.08)	0.65 (0.088)
Helictochloa praetutiana subsp. *praetutiana*	GLM	0.98 (0.008)	0.92 (0.036)	0.89 (0.042)
Helleborus viridis subsp. *bocconei*	GLM	0.92 (0.021)	0.72 (0.059)	0.73 (0.054)
Hypericum barbatum subsp. *calabricum*	GLM	0.91 (0.026)	0.79 (0.049)	0.59 (0.067)
Iris cengialti subsp. *cengialti*	GLM	0.94 (0.023)	0.79 (0.066)	0.7 (0.066)
Jacobaea maritima subsp. *bicolor*	GLM	0.95 (0.024)	0.86 (0.073)	0.58 (0.097)
Klasea flavescens subsp. *cichoracea*	GLM	0.83 (0.041)	0.68 (0.07)	0.46 (0.071)
Knautia baldensis	GLM	0.96 (0.011)	0.82 (0.043)	0.73 (0.059)
Knautia persicina	GLM	0.96 (0.016)	0.83 (0.043)	0.77 (0.055)
Koeleria splendens	GLM	0.92 (0.031)	0.74 (0.076)	0.68 (0.074)
Laserpitium nitidum	GLM	0.93 (0.028)	0.76 (0.059)	0.69 (0.08)
Leontodon anomalus	GLM	0.91 (0.032)	0.75 (0.068)	0.6 (0.078)
Leontodon intermedius	GLM	0.85 (0.046)	0.7 (0.07)	0.59 (0.081)
Limonium acutifolium subsp. *acutifolium*	GLM	0.98 (0.022)	0.93 (0.045)	0.77 (0.093)
Limonium ilvae	GLM	0.99 (0.021)	0.97 (0.043)	0.85 (0.071)
Limonium merxmuelleri subsp. *sulcitanum*	GLM	0.99 (0.018)	0.98 (0.034)	0.94 (0.039)
Limonium multiforme	GLM	0.96 (0.013)	0.91 (0.026)	0.75 (0.106)
Limonium remotispiculum	GLM	0.88 (0.051)	0.68 (0.109)	0.54 (0.105)
Linaria purpurea	GLM	0.93 (0.024)	0.78 (0.054)	0.79 (0.05)
Luzula sylvatica subsp. *sicula*	GLM	0.9 (0.046)	0.74 (0.092)	0.69 (0.093)
Mcneillia graminifolia subsp. *rosanoi*	GLM	0.96 (0.027)	0.86 (0.076)	0.82 (0.077)
Melampyrum italicum	GLM	0.93 (0.012)	0.71 (0.035)	0.72 (0.034)
Micromeria cordata	GLM	0.94 (0.04)	0.82 (0.094)	0.74 (0.088)
Micromeria graeca subsp. *tenuifolia*	GLM	0.86 (0.034)	0.65 (0.068)	0.68 (0.08)
Moehringia glaucovirens	GLM	0.94 (0.02)	0.77 (0.064)	0.67 (0.075)
Moltkia suffruticosa subsp. *bigazziana*	GLM	0.92 (0.032)	0.76 (0.087)	0.64 (0.086)
Myosotis graui	GLM	0.98 (0.014)	0.91 (0.053)	0.82 (0.063)
Myosotis sylvatica subsp. *elongata*	GLM	0.92 (0.033)	0.74 (0.079)	0.68 (0.092)
Odontarrhena argentea	GLM	0.95 (0.032)	0.8 (0.081)	0.72 (0.105)
Odontarrhena bertolonii	GLM	0.88 (0.048)	0.71 (0.093)	0.52 (0.107)
Oenanthe lisae	GLM	0.87 (0.039)	0.78 (0.073)	0.74 (0.068)
Onosma echioides subsp. *echioides*	GLM	0.84 (0.044)	0.64 (0.076)	0.69 (0.083)
Onosma pseudoarenaria subsp. *tridentina*	GLM	0.96 (0.035)	0.85 (0.081)	0.74 (0.088)
Ophrys appennina	GLM	0.86 (0.033)	0.66 (0.062)	0.67 (0.069)
Ophrys apulica	GLM	0.96 (0.028)	0.84 (0.071)	0.7 (0.099)
Ophrys bertolonii subsp. *bertoloniiformis*	GLM	0.88 (0.018)	0.65 (0.036)	0.65 (0.036)
Ophrys classica	GLM	0.84 (0.028)	0.63 (0.055)	0.63 (0.056)
Ophrys crabronifera	GLM	0.86 (0.041)	0.64 (0.076)	0.63 (0.087)

Ophrys exaltata subsp. *exaltata*	GLM	0.85 (0.059)	0.66 (0.101)	0.52 (0.124)
Ophrys exaltata subsp. *montis-leonis*	GLM	0.95 (0.022)	0.81 (0.066)	0.75 (0.081)
Ophrys lucana	GLM	0.9 (0.031)	0.69 (0.06)	0.71 (0.07)
Ophrys lunulata	GLM	0.89 (0.052)	0.73 (0.087)	0.69 (0.101)
Ophrys minipassionis	GLM	0.83 (0.045)	0.63 (0.083)	0.45 (0.097)
Ophrys passionis subsp. *majellensis*	GLM	0.85 (0.045)	0.66 (0.095)	0.45 (0.116)
Ophrys promontorii	GLM	0.83 (0.053)	0.6 (0.101)	0.56 (0.106)
Ophrys tenthredinifera subsp. *neglecta*	GLM	0.88 (0.035)	0.66 (0.068)	0.58 (0.072)
Ornithogalum exscapum	GLM	0.89 (0.036)	0.68 (0.064)	0.65 (0.082)
Pimpinella anisoides	GLM	0.86 (0.043)	0.65 (0.078)	0.45 (0.086)
Pinguicula christinae	GLM	0.99 (0.005)	0.96 (0.022)	0.88 (0.073)
Plantago sarda	GLM	0.99 (0.021)	0.98 (0.041)	0.94 (0.047)
Polygala alpestris subsp. *angelisii*	GLM	0.95 (0.033)	0.86 (0.065)	0.74 (0.089)
Polygala flavescens subsp. *maremmana*	GLM	0.98 (0.01)	0.93 (0.042)	0.8 (0.09)
Polygala sardoa	GLM	0.89 (0.041)	0.77 (0.081)	0.65 (0.074)
Potentilla rigoana	GLM	0.97 (0.015)	0.89 (0.053)	0.78 (0.069)
Primula polliniana	GLM	0.94 (0.015)	0.76 (0.044)	0.75 (0.047)
Primula tyrolensis	GLM	0.94 (0.023)	0.75 (0.066)	0.69 (0.081)
Ptychotis sardoa	GLM	0.95 (0.037)	0.86 (0.082)	0.76 (0.098)
Pulmonaria vallarsae	GLM	0.96 (0.015)	0.82 (0.043)	0.77 (0.047)
Quercus ichnusae	GLM	0.97 (0.03)	0.89 (0.079)	0.76 (0.085)
Rhizobotrya alpina	GLM	0.93 (0.022)	0.77 (0.068)	0.64 (0.09)
Rumex scutatus glaucescens	GLM	0.93 (0.031)	0.74 (0.078)	0.7 (0.09)
Salix arrigonii	GLM	0.86 (0.053)	0.69 (0.088)	0.55 (0.095)
Salix brutia	GLM	0.96 (0.016)	0.86 (0.059)	0.67 (0.083)
Salix purpurea subsp. *eburnea*	GLM	0.79 (0.058)	0.61 (0.097)	0.43 (0.104)
Salvia haematodes	GLM	0.88 (0.048)	0.68 (0.083)	0.61 (0.119)
Santolina etrusca	GLM	0.93 (0.032)	0.78 (0.084)	0.66 (0.087)
Santolina insularis	GLM	0.94 (0.035)	0.81 (0.082)	0.75 (0.08)
Saxifraga arachnoidea	GLM	0.98 (0.012)	0.9 (0.052)	0.74 (0.086)
Saxifraga depressa	GLM	0.94 (0.023)	0.82 (0.051)	0.63 (0.076)
Saxifraga facchinii	GLM	0.97 (0.024)	0.88 (0.067)	0.74 (0.094)
Saxifraga hostii subsp. *rhaetica*	GLM	0.94 (0.03)	0.78 (0.071)	0.66 (0.123)
Saxifraga presolanensis	GLM	0.93 (0.047)	0.85 (0.084)	0.61 (0.112)
Saxifraga tombeanensis	GLM	0.95 (0.028)	0.86 (0.06)	0.65 (0.098)
Saxifraga vandellii	GLM	0.91 (0.037)	0.73 (0.083)	0.61 (0.112)
Scabiosa holosericea	GLM	0.88 (0.029)	0.7 (0.061)	0.56 (0.069)
Scabiosa uniseta	GLM	0.78 (0.054)	0.55 (0.082)	0.34 (0.086)
Scabiosa vestina	GLM	0.98 (0.009)	0.91 (0.031)	0.78 (0.071)
Scorzonera callosa	GLM	0.85 (0.072)	0.75 (0.108)	0.57 (0.11)
Scorzonera villosa subsp. *columnae*	GLM	0.87 (0.052)	0.7 (0.088)	0.57 (0.097)
Sedum alsinifolium	GLM	0.94 (0.023)	0.79 (0.055)	0.66 (0.078)
Senecio ovatus subsp. *stabianus*	GLM	0.96 (0.024)	0.88 (0.059)	0.71 (0.076)
Sesleria nitida	GLM	0.97 (0.016)	0.88 (0.045)	0.83 (0.051)
Sesleria pichiana	GLM	0.88 (0.034)	0.69 (0.077)	0.42 (0.1)
Silene italica subsp. *sicula*	GLM	0.91 (0.027)	0.75 (0.05)	0.69 (0.056)
Silene nummica	GLM	0.97 (0.032)	0.9 (0.062)	0.71 (0.097)
Siler montanum subsp. *siculum*	GLM	0.97 (0.015)	0.87 (0.052)	0.73 (0.071)
Spiraea decumbens subsp. *tomentosa*	GLM	0.9 (0.038)	0.7 (0.088)	0.67 (0.098)
Stipa etrusca	GLM	0.91 (0.033)	0.71 (0.082)	0.71 (0.109)

Tephroseris italica	GLM	0.94 (0.025)	0.82 (0.07)	0.7 (0.082)
Thesium sommieri	GLM	0.92 (0.04)	0.79 (0.091)	0.78 (0.083)
Thymus spinulosus	GLM	0.73 (0.052)	0.47 (0.096)	0.26 (0.07)
Tolpis virgata subsp. *grandiflora*	GLM	0.81 (0.073)	0.64 (0.114)	0.49 (0.125)
Trifolium pratense subsp. *semipurpureum*	GLM	0.92 (0.032)	0.72 (0.08)	0.7 (0.072)
Trisetaria villosa	GLM	0.95 (0.026)	0.86 (0.065)	0.87 (0.062)
Vicia ochroleuca subsp. *ochroleuca*	GLM	0.87 (0.047)	0.65 (0.096)	0.73 (0.088)
Viola aethnensis subsp. *splendida*	GLM	0.96 (0.023)	0.87 (0.05)	0.77 (0.071)
Viola bertolonii	GLM	0.96 (0.025)	0.88 (0.065)	0.67 (0.092)
Viola cassinensis subsp. *pseudogracilis*	GLM	0.99 (0.013)	0.95 (0.042)	0.82 (0.081)
Viola dubyana	GLM	0.95 (0.031)	0.89 (0.056)	0.67 (0.084)
Viola etrusca	GLM	0.92 (0.041)	0.75 (0.086)	0.65 (0.124)
Viola eugeniae subsp. *eugeniae*	GLM	0.98 (0.029)	0.93 (0.068)	0.88 (0.069)
Viola ferrarinii	GLM	0.98 (0.021)	0.93 (0.046)	0.92 (0.043)
Acer cappadocicum subsp. *lobelii*	MARS	0.91 (0.052)	0.78 (0.091)	0.79 (0.089)
Adenocarpus complicatus subsp. *brutius*	MARS	0.9 (0.058)	0.75 (0.103)	0.75 (0.096)
Adenostyles australis	MARS	0.96 (0.03)	0.88 (0.071)	0.87 (0.072)
Ajuga tenorei	MARS	0.92 (0.068)	0.82 (0.103)	0.81 (0.089)
Alyssum diffusum subsp. *diffusum*	MARS	0.91 (0.063)	0.77 (0.098)	0.78 (0.096)
Anemonoides trifolia subsp. *brevidentata*	MARS	0.94 (0.017)	0.75 (0.047)	0.75 (0.047)
Antirrhinum siculum	MARS	0.86 (0.068)	0.7 (0.112)	0.72 (0.108)
Aquilegia lucensis	MARS	0.98 (0.029)	0.95 (0.057)	0.94 (0.064)
Arabis collina subsp. *rosea*	MARS	0.88 (0.05)	0.7 (0.093)	0.71 (0.093)
Arenaria huteri	MARS	0.88 (0.069)	0.73 (0.115)	0.72 (0.114)
Armeria arenaria subsp. *marginata*	MARS	0.93 (0.059)	0.86 (0.112)	0.85 (0.105)
Armeria brutia	MARS	0.94 (0.057)	0.87 (0.106)	0.85 (0.106)
Armeria denticulata	MARS	0.87 (0.061)	0.75 (0.103)	0.77 (0.095)
Artemisia caerulescens subsp. *cretacea*	MARS	0.88 (0.068)	0.72 (0.109)	0.7 (0.108)
Artemisia campestris subsp. *variabilis*	MARS	0.88 (0.069)	0.74 (0.104)	0.76 (0.097)
Astragalus parnassi subsp. *calabricus*	MARS	0.91 (0.069)	0.8 (0.118)	0.8 (0.111)
Asyneuma trichocalycinum	MARS	0.91 (0.06)	0.8 (0.099)	0.81 (0.095)
Atadinus glaucophyllus	MARS	0.9 (0.052)	0.73 (0.09)	0.74 (0.091)
Bellevalia webbiana	MARS	0.93 (0.063)	0.85 (0.114)	0.84 (0.11)
Bellium crassifolium	MARS	0.9 (0.071)	0.81 (0.102)	0.82 (0.096)
Biscutella apuana	MARS	0.9 (0.076)	0.75 (0.117)	0.73 (0.112)
Biscutella morisiana	MARS	0.83 (0.056)	0.65 (0.093)	0.67 (0.092)
Brachypodium genuense	MARS	0.96 (0.02)	0.83 (0.047)	0.83 (0.047)
Brassica glabrescens	MARS	0.95 (0.054)	0.9 (0.1)	0.86 (0.101)
Bromopsis caprina	MARS	0.92 (0.06)	0.78 (0.107)	0.78 (0.099)
Buphthalmum salicifolium subsp. *flexile*	MARS	0.89 (0.05)	0.73 (0.105)	0.74 (0.102)
Campanula bertolae	MARS	0.95 (0.025)	0.78 (0.07)	0.78 (0.07)
Campanula carnica subsp. *puberula*	MARS	0.91 (0.066)	0.78 (0.115)	0.77 (0.112)
Campanula elatines	MARS	0.93 (0.028)	0.76 (0.069)	0.76 (0.069)
Campanula martinii	MARS	0.92 (0.05)	0.81 (0.089)	0.81 (0.089)
Campanula micrantha	MARS	0.92 (0.064)	0.83 (0.108)	0.84 (0.098)
Campanula morettiana	MARS	0.93 (0.023)	0.73 (0.062)	0.73 (0.062)
Campanula raineri	MARS	0.95 (0.029)	0.84 (0.063)	0.83 (0.064)
Campanula sabatia	MARS	0.94 (0.045)	0.88 (0.078)	0.88 (0.069)
Campanula tanfanii	MARS	0.91 (0.059)	0.82 (0.107)	0.8 (0.101)
Carduus nutans subsp. *perspinosus*	MARS	0.89 (0.069)	0.75 (0.112)	0.73 (0.11)

Carex macrostachys	MARS	0.89 (0.063)	0.78 (0.108)	0.79 (0.102)
*Carlina hispanica*subsp. *globosa*	MARS	0.91 (0.049)	0.74 (0.088)	0.74 (0.086)
Centaurea aplolepa subsp. *aplolepa*	MARS	0.96 (0.043)	0.91 (0.075)	0.9 (0.069)
Centaurea aplolepa subsp. *carueliana*	MARS	0.91 (0.071)	0.79 (0.114)	0.77 (0.109)
Centaurea aplolepa subsp. *lunensis*	MARS	0.92 (0.066)	0.79 (0.118)	0.79 (0.113)
Centaurea poeltiana	MARS	0.92 (0.052)	0.78 (0.094)	0.77 (0.103)
Centaurea subtilis	MARS	0.92 (0.069)	0.83 (0.11)	0.8 (0.11)
Cerastium apuanum	MARS	0.87 (0.065)	0.68 (0.116)	0.7 (0.107)
Cerastium scaranoi	MARS	0.92 (0.061)	0.81 (0.094)	0.81 (0.089)
Cerastium supramontanum	MARS	0.91 (0.063)	0.82 (0.109)	0.8 (0.114)
Cerastium tomentosum	MARS	0.89 (0.069)	0.73 (0.102)	0.75 (0.091)
Cerastium utriense	MARS	0.95 (0.054)	0.88 (0.093)	0.86 (0.094)
Cherleria laricifolia subsp. *ophiolitica*	MARS	0.9 (0.059)	0.78 (0.097)	0.78 (0.094)
Cirsium bertolonii	MARS	0.92 (0.058)	0.83 (0.099)	0.84 (0.09)
Cirsium tenoreanum	MARS	0.9 (0.053)	0.74 (0.1)	0.74 (0.1)
Cirsium vallis-demonii	MARS	0.92 (0.059)	0.8 (0.103)	0.79 (0.108)
Colchicum neapolitanum	MARS	0.83 (0.069)	0.67 (0.101)	0.71 (0.094)
Crocus biflorus	MARS	0.88 (0.025)	0.7 (0.046)	0.7 (0.046)
Crocus etruscus	MARS	0.9 (0.059)	0.79 (0.097)	0.79 (0.094)
Crocus imperati	MARS	0.88 (0.072)	0.69 (0.122)	0.71 (0.117)
Crocus suaveolens	MARS	0.91 (0.071)	0.8 (0.122)	0.8 (0.111)
Cryptotaenia thomasii	MARS	0.93 (0.05)	0.79 (0.096)	0.79 (0.092)
Cynoglossum apenninum	MARS	0.9 (0.057)	0.78 (0.094)	0.79 (0.1)
Daphne petraea	MARS	0.93 (0.048)	0.84 (0.086)	0.82 (0.086)
Dianthus carthusianorum subsp. *tenorei*	MARS	0.89 (0.068)	0.75 (0.123)	0.76 (0.115)
Dianthus sardous	MARS	0.89 (0.069)	0.77 (0.118)	0.75 (0.115)
Dianthus tarentinus	MARS	0.92 (0.062)	0.77 (0.102)	0.76 (0.093)
Drymochloa drymeja subsp. *exaltata*	MARS	0.88 (0.038)	0.7 (0.071)	0.7 (0.071)
Echinops siculus	MARS	0.89 (0.046)	0.72 (0.084)	0.73 (0.08)
Epipactis meridionalis	MARS	0.92 (0.043)	0.76 (0.083)	0.75 (0.077)
Erysimum apenninum	MARS	0.93 (0.029)	0.79 (0.061)	0.79 (0.061)
Erysimum crassistylum subsp. *garganicum*	MARS	0.89 (0.055)	0.69 (0.095)	0.71 (0.088)
Erysimum etruscum	MARS	0.88 (0.046)	0.7 (0.08)	0.71 (0.078)
Erysimum pseudorhaeticum	MARS	0.95 (0.015)	0.81 (0.041)	0.81 (0.041)
Euphorbia ceratocarpa	MARS	0.89 (0.079)	0.76 (0.125)	0.75 (0.124)
Euphorbia corallioides	MARS	0.9 (0.04)	0.7 (0.079)	0.71 (0.078)
Euphorbia nicaeensis subsp. *japygica*	MARS	0.91 (0.05)	0.76 (0.101)	0.76 (0.1)
Euphorbia variabilis	MARS	0.91 (0.053)	0.79 (0.092)	0.78 (0.095)
Euphrasia tricuspidata	MARS	0.94 (0.015)	0.78 (0.04)	0.78 (0.04)
Festuca alfrediana subsp. *ferrariniana*	MARS	0.96 (0.037)	0.92 (0.074)	0.92 (0.074)
Festuca austrodolomitica	MARS	0.94 (0.034)	0.81 (0.071)	0.8 (0.072)
Festuca riccerii	MARS	0.98 (0.026)	0.95 (0.051)	0.95 (0.052)
Festuca robustifolia	MARS	0.93 (0.034)	0.76 (0.07)	0.76 (0.07)
Festuca violacea subsp. *italica*	MARS	0.95 (0.052)	0.88 (0.099)	0.89 (0.094)
Festuca violacea subsp. *puccinellii*	MARS	0.94 (0.051)	0.87 (0.089)	0.87 (0.089)
Galium baldense	MARS	0.96 (0.014)	0.8 (0.045)	0.8 (0.045)
Genista etnensis	MARS	0.87 (0.075)	0.71 (0.112)	0.73 (0.107)
Genista tyrrhena	MARS	0.94 (0.049)	0.89 (0.085)	0.88 (0.079)
Globularia incanescens	MARS	0.91 (0.037)	0.8 (0.063)	0.8 (0.063)
Helichrysum litoreum	MARS	0.95 (0.027)	0.82 (0.056)	0.82 (0.056)

Helichrysum saxatile subsp. *saxatile*	MARS	0.91 (0.068)	0.78 (0.119)	0.76 (0.107)
Helictochloa praetutiana subsp. *praetutiana*	MARS	0.98 (0.024)	0.91 (0.053)	0.91 (0.053)
Helleborus viridis subsp. *bocconei*	MARS	0.91 (0.034)	0.72 (0.072)	0.72 (0.072)
Hypericum barbatum subsp. *calabricum*	MARS	0.92 (0.043)	0.81 (0.075)	0.81 (0.072)
Iris cengialti subsp. *cengialti*	MARS	0.93 (0.041)	0.77 (0.072)	0.77 (0.07)
Jacobaea maritima subsp. *bicolor*	MARS	0.92 (0.082)	0.83 (0.131)	0.81 (0.122)
Klasea flavescens subsp. *cichoracea*	MARS	0.87 (0.069)	0.68 (0.099)	0.68 (0.096)
Knautia baldensis	MARS	0.96 (0.024)	0.83 (0.073)	0.83 (0.074)
Knautia persicina	MARS	0.95 (0.028)	0.85 (0.065)	0.85 (0.065)
Koeleria splendens	MARS	0.91 (0.038)	0.75 (0.087)	0.76 (0.087)
Laserpitium nitidum	MARS	0.92 (0.049)	0.77 (0.093)	0.77 (0.093)
Leontodon anomalus	MARS	0.92 (0.037)	0.75 (0.074)	0.76 (0.075)
Leontodon intermedius	MARS	0.85 (0.064)	0.69 (0.099)	0.71 (0.093)
Limonium acutifolium subsp. *acutifolium*	MARS	0.95 (0.053)	0.9 (0.107)	0.87 (0.107)
Limonium ilvae	MARS	0.97 (0.043)	0.93 (0.084)	0.9 (0.087)
Limonium merxmuelleri subsp. *sulcitanum*	MARS	0.98 (0.023)	0.96 (0.048)	0.95 (0.048)
Limonium multiforme	MARS	0.96 (0.04)	0.92 (0.073)	0.91 (0.073)
Limonium remotispiculum	MARS	0.86 (0.075)	0.69 (0.111)	0.69 (0.096)
Linaria purpurea	MARS	0.92 (0.033)	0.8 (0.07)	0.8 (0.07)
Luzula sylvatica subsp. *sicula*	MARS	0.92 (0.057)	0.77 (0.099)	0.78 (0.09)
Mcneillia graminifolia subsp. *rosanoi*	MARS	0.94 (0.046)	0.83 (0.078)	0.84 (0.074)
Melampyrum italicum	MARS	0.94 (0.015)	0.72 (0.039)	0.72 (0.039)
Micromeria cordata	MARS	0.9 (0.077)	0.8 (0.115)	0.8 (0.104)
Micromeria graeca subsp. *tenuifolia*	MARS	0.85 (0.058)	0.69 (0.09)	0.7 (0.087)
Moehringia glaucovirens	MARS	0.92 (0.053)	0.76 (0.091)	0.74 (0.089)
Moltkia suffruticosa subsp. *bigazziana*	MARS	0.9 (0.059)	0.74 (0.104)	0.75 (0.104)
Myosotis graui	MARS	0.95 (0.048)	0.89 (0.089)	0.88 (0.084)
Myosotis sylvatica subsp. *elongata*	MARS	0.89 (0.053)	0.75 (0.087)	0.77 (0.085)
Odontarrhena argentea	MARS	0.92 (0.06)	0.77 (0.111)	0.78 (0.106)
Odontarrhena bertolonii	MARS	0.89 (0.074)	0.75 (0.112)	0.74 (0.112)
Oenanthe lisae	MARS	0.92 (0.038)	0.79 (0.068)	0.79 (0.065)
Onosma echioides subsp. *echioides*	MARS	0.84 (0.055)	0.67 (0.083)	0.7 (0.079)
Onosma pseudoarenaria subsp. *tridentina*	MARS	0.92 (0.058)	0.8 (0.099)	0.79 (0.094)
Ophrys appennina	MARS	0.87 (0.04)	0.69 (0.064)	0.69 (0.064)
Ophrys apulica	MARS	0.92 (0.062)	0.83 (0.108)	0.79 (0.112)
Ophrys bertolonii subsp. *bertoloniiformis*	MARS	0.93 (0.012)	0.7 (0.035)	0.7 (0.035)
Ophrys classica	MARS	0.88 (0.035)	0.68 (0.058)	0.68 (0.058)
Ophrys crabronifera	MARS	0.85 (0.048)	0.67 (0.084)	0.68 (0.083)
Ophrys exaltata subsp. *exaltata*	MARS	0.85 (0.069)	0.69 (0.114)	0.7 (0.111)
Ophrys exaltata subsp. *montis-leonis*	MARS	0.92 (0.057)	0.8 (0.098)	0.8 (0.093)
Ophrys lucana	MARS	0.9 (0.038)	0.72 (0.078)	0.72 (0.078)
Ophrys lunulata	MARS	0.87 (0.067)	0.73 (0.105)	0.75 (0.101)
Ophrys minipassionis	MARS	0.86 (0.059)	0.68 (0.098)	0.7 (0.097)
Ophrys passionis subsp. *majellensis*	MARS	0.87 (0.07)	0.73 (0.109)	0.74 (0.097)
Ophrys promontorii	MARS	0.85 (0.064)	0.68 (0.106)	0.69 (0.101)
Ophrys tenthredinifera subsp. *neglecta*	MARS	0.91 (0.046)	0.76 (0.094)	0.76 (0.091)
Ornithogalum exscapum	MARS	0.89 (0.05)	0.71 (0.08)	0.72 (0.078)
Pimpinella anisoides	MARS	0.85 (0.074)	0.68 (0.11)	0.71 (0.105)
Pinguicula christinae	MARS	0.96 (0.052)	0.9 (0.097)	0.89 (0.083)
Plantago sarda	MARS	0.98 (0.032)	0.95 (0.064)	0.95 (0.058)

Polygala alpestris subsp. *angelisii*	MARS	0.93 (0.055)	0.83 (0.091)	0.82 (0.086)
Polygala flavescens subsp. *maremmana*	MARS	0.94 (0.069)	0.86 (0.121)	0.84 (0.115)
Polygala sardoa	MARS	0.88 (0.062)	0.74 (0.095)	0.75 (0.093)
Potentilla rigoana	MARS	0.95 (0.039)	0.89 (0.068)	0.88 (0.07)
Primula polliniana	MARS	0.94 (0.023)	0.76 (0.062)	0.76 (0.062)
Primula tyrolensis	MARS	0.91 (0.053)	0.74 (0.092)	0.72 (0.099)
Ptychotis sardoa	MARS	0.9 (0.077)	0.79 (0.133)	0.78 (0.115)
Pulmonaria vallarsae	MARS	0.94 (0.04)	0.8 (0.067)	0.8 (0.067)
Quercus ichnusae	MARS	0.94 (0.047)	0.88 (0.087)	0.87 (0.094)
Rhizobotrya alpina	MARS	0.91 (0.041)	0.75 (0.085)	0.73 (0.09)
Rumex scutatus glaucescens	MARS	0.91 (0.052)	0.75 (0.09)	0.76 (0.09)
Salix arrigonii	MARS	0.85 (0.085)	0.7 (0.124)	0.73 (0.119)
Salix brutia	MARS	0.93 (0.049)	0.82 (0.087)	0.8 (0.095)
Salix purpurea subsp. *eburnea*	MARS	0.89 (0.061)	0.72 (0.101)	0.73 (0.099)
Salvia haematodes	MARS	0.87 (0.058)	0.7 (0.093)	0.72 (0.093)
Santolina etrusca	MARS	0.9 (0.061)	0.74 (0.107)	0.74 (0.1)
Santolina insularis	MARS	0.91 (0.054)	0.79 (0.086)	0.81 (0.081)
Saxifraga arachnoidea	MARS	0.94 (0.05)	0.85 (0.094)	0.82 (0.093)
Saxifraga depressa	MARS	0.95 (0.041)	0.85 (0.081)	0.84 (0.088)
Saxifraga facchinii	MARS	0.93 (0.058)	0.84 (0.106)	0.81 (0.109)
Saxifraga hostii subsp. *rhaetica*	MARS	0.9 (0.078)	0.75 (0.121)	0.73 (0.126)
Saxifraga presolanensis	MARS	0.88 (0.083)	0.77 (0.15)	0.75 (0.149)
Saxifraga tombeanensis	MARS	0.92 (0.059)	0.82 (0.098)	0.8 (0.098)
Saxifraga vandellii	MARS	0.89 (0.065)	0.73 (0.105)	0.73 (0.105)
Scabiosa holosericea	MARS	0.89 (0.049)	0.7 (0.094)	0.71 (0.091)
Scabiosa uniseta	MARS	0.89 (0.061)	0.73 (0.106)	0.73 (0.105)
Scabiosa vestina	MARS	0.95 (0.04)	0.87 (0.076)	0.84 (0.075)
Scorzonera callosa	MARS	0.88 (0.079)	0.75 (0.134)	0.73 (0.127)
Scorzonera villosa subsp. *columnae*	MARS	0.85 (0.062)	0.71 (0.102)	0.73 (0.096)
Sedum alsinifolium	MARS	0.92 (0.04)	0.76 (0.09)	0.75 (0.085)
Senecio ovatus subsp. *stabianus*	MARS	0.94 (0.052)	0.86 (0.096)	0.85 (0.096)
Sesleria nitida	MARS	0.96 (0.024)	0.88 (0.055)	0.88 (0.055)
Sesleria pichiana	MARS	0.9 (0.075)	0.74 (0.13)	0.74 (0.122)
Silene italica subsp. *sicula*	MARS	0.92 (0.037)	0.75 (0.074)	0.75 (0.074)
Silene nummica	MARS	0.95 (0.054)	0.9 (0.097)	0.87 (0.096)
Siler montanum subsp. *siculum*	MARS	0.96 (0.037)	0.85 (0.077)	0.85 (0.077)
Spiraea decumbens subsp. *tomentosa*	MARS	0.89 (0.055)	0.71 (0.098)	0.71 (0.101)
Stipa etrusca	MARS	0.86 (0.071)	0.66 (0.108)	0.68 (0.105)
Tephroseris italica	MARS	0.93 (0.048)	0.84 (0.074)	0.83 (0.076)
Thesium sommieri	MARS	0.91 (0.055)	0.79 (0.101)	0.82 (0.1)
Thymus spinulosus	MARS	0.88 (0.06)	0.72 (0.11)	0.73 (0.11)
Tolpis virgata subsp. *grandiflora*	MARS	0.87 (0.078)	0.71 (0.124)	0.71 (0.129)
Trifolium pratense subsp. *semipurpureum*	MARS	0.92 (0.035)	0.73 (0.075)	0.74 (0.074)
Trisetaria villosa	MARS	0.94 (0.041)	0.86 (0.068)	0.86 (0.071)
Vicia ochroleuca subsp. *ochroleuca*	MARS	0.87 (0.07)	0.7 (0.121)	0.72 (0.112)
Viola aethnensis subsp. *splendida*	MARS	0.93 (0.047)	0.83 (0.082)	0.81 (0.082)
Viola bertolonii	MARS	0.92 (0.062)	0.81 (0.108)	0.77 (0.1)
Viola cassinensis subsp. *pseudogracilis*	MARS	0.93 (0.064)	0.86 (0.123)	0.84 (0.109)
Viola dubyana	MARS	0.92 (0.065)	0.83 (0.125)	0.8 (0.117)
Viola etrusca	MARS	0.9 (0.074)	0.77 (0.13)	0.75 (0.133)

Viola eugeniae subsp. *eugeniae*	MARS	0.94 (0.045)	0.87 (0.084)	0.88 (0.084)
Viola ferrarinii	MARS	0.97 (0.023)	0.92 (0.05)	0.93 (0.048)
Acer cappadocicum subsp. *lobelii*	RF	0.88 (0.054)	0.74 (0.097)	0.76 (0.088)
Adenocarpus complicatus subsp. *brutius*	RF	0.91 (0.044)	0.72 (0.098)	0.74 (0.092)
Adenostyles australis	RF	0.95 (0.028)	0.87 (0.063)	0.88 (0.061)
Ajuga tenorei	RF	0.92 (0.044)	0.79 (0.088)	0.8 (0.082)
Alyssum diffusum subsp. *diffusum*	RF	0.9 (0.04)	0.71 (0.083)	0.74 (0.078)
Anemonoides trifolia subsp. *brevidentata*	RF	0.94 (0.018)	0.75 (0.05)	0.75 (0.05)
Antirrhinum siculum	RF	0.89 (0.062)	0.74 (0.111)	0.75 (0.099)
Aquilegia lucensis	RF	1 (0.007)	0.98 (0.024)	0.97 (0.037)
Arabis collina subsp. *rosea*	RF	0.86 (0.047)	0.68 (0.079)	0.7 (0.078)
Arenaria huteri	RF	0.9 (0.057)	0.74 (0.113)	0.76 (0.101)
Armeria arenaria subsp. *marginata*	RF	0.97 (0.03)	0.91 (0.069)	0.91 (0.064)
Armeria brutia	RF	0.94 (0.035)	0.83 (0.076)	0.81 (0.081)
Armeria denticulata	RF	0.88 (0.06)	0.76 (0.097)	0.79 (0.083)
Artemisia caerulescens subsp. *cretacea*	RF	0.9 (0.069)	0.73 (0.131)	0.74 (0.123)
Artemisia campestris subsp. *variabilis*	RF	0.87 (0.056)	0.69 (0.088)	0.73 (0.083)
Astragalus parnassi subsp. *calabricus*	RF	0.91 (0.054)	0.78 (0.107)	0.78 (0.104)
Asyneuma trichocalycinum	RF	0.92 (0.043)	0.76 (0.092)	0.78 (0.091)
Atadinus glaucophyllus	RF	0.89 (0.046)	0.7 (0.086)	0.73 (0.084)
Bellevalia webbiana	RF	0.92 (0.052)	0.8 (0.097)	0.8 (0.09)
Bellium crassifolium	RF	0.95 (0.038)	0.85 (0.079)	0.87 (0.068)
Biscutella apuana	RF	0.93 (0.045)	0.77 (0.102)	0.77 (0.097)
Biscutella morisiana	RF	0.86 (0.051)	0.7 (0.084)	0.73 (0.079)
Brachypodium genuense	RF	0.93 (0.025)	0.82 (0.052)	0.82 (0.052)
Brassica glabrescens	RF	0.98 (0.02)	0.93 (0.06)	0.9 (0.091)
Bromopsis caprina	RF	0.9 (0.051)	0.77 (0.103)	0.79 (0.097)
Buphthalmum salicifolium subsp. *flexile*	RF	0.87 (0.052)	0.69 (0.095)	0.71 (0.09)
Campanula bertolae	RF	0.92 (0.026)	0.73 (0.058)	0.73 (0.058)
Campanula carnica subsp. *puberula*	RF	0.88 (0.075)	0.71 (0.124)	0.75 (0.109)
Campanula elatines	RF	0.91 (0.032)	0.72 (0.073)	0.73 (0.072)
Campanula martinii	RF	0.94 (0.031)	0.81 (0.074)	0.81 (0.073)
Campanula micrantha	RF	0.94 (0.046)	0.85 (0.083)	0.87 (0.066)
Campanula morettiana	RF	0.92 (0.026)	0.74 (0.062)	0.74 (0.062)
Campanula raineri	RF	0.95 (0.023)	0.79 (0.074)	0.79 (0.071)
Campanula sabatia	RF	0.97 (0.025)	0.89 (0.072)	0.89 (0.072)
Campanula tanfanii	RF	0.92 (0.053)	0.8 (0.097)	0.81 (0.087)
Carduus nutans subsp. *perspinosus*	RF	0.9 (0.056)	0.74 (0.113)	0.75 (0.113)
Carex macrostachys	RF	0.9 (0.049)	0.77 (0.086)	0.79 (0.077)
*Carlina hispanica*subsp. *globosa*	RF	0.91 (0.045)	0.74 (0.095)	0.76 (0.087)
Centaurea aplolepa subsp. *aplolepa*	RF	0.98 (0.016)	0.94 (0.041)	0.9 (0.062)
Centaurea aplolepa subsp. *carueliana*	RF	0.93 (0.057)	0.79 (0.11)	0.78 (0.102)
Centaurea aplolepa subsp. *lunensis*	RF	0.9 (0.046)	0.73 (0.092)	0.75 (0.086)
Centaurea poeltiana	RF	0.9 (0.051)	0.73 (0.101)	0.75 (0.094)
Centaurea subtilis	RF	0.95 (0.05)	0.81 (0.095)	0.79 (0.088)
Cerastium apuanum	RF	0.85 (0.061)	0.66 (0.113)	0.7 (0.105)
Cerastium scaranoi	RF	0.93 (0.043)	0.8 (0.086)	0.81 (0.081)
Cerastium supramontanum	RF	0.95 (0.035)	0.88 (0.073)	0.88 (0.074)
Cerastium tomentosum	RF	0.87 (0.053)	0.72 (0.094)	0.75 (0.085)
Cerastium utriense	RF	0.97 (0.026)	0.87 (0.063)	0.87 (0.062)

Cherleria laricifolia subsp. *ophiolitica*	RF	0.88 (0.056)	0.72 (0.1)	0.74 (0.091)
Cirsium bertolonii	RF	0.9 (0.049)	0.83 (0.084)	0.86 (0.068)
Cirsium tenoreanum	RF	0.92 (0.039)	0.77 (0.082)	0.79 (0.079)
Cirsium vallis-demonii	RF	0.92 (0.046)	0.77 (0.093)	0.79 (0.085)
Colchicum neapolitanum	RF	0.84 (0.073)	0.69 (0.108)	0.74 (0.096)
Crocus biflorus	RF	0.87 (0.023)	0.69 (0.042)	0.69 (0.042)
Crocus etruscus	RF	0.87 (0.06)	0.74 (0.101)	0.77 (0.092)
Crocus imperati	RF	0.84 (0.065)	0.67 (0.108)	0.71 (0.1)
Crocus suaveolens	RF	0.91 (0.061)	0.82 (0.096)	0.82 (0.087)
Cryptotaenia thomasii	RF	0.91 (0.042)	0.74 (0.086)	0.76 (0.078)
Cynoglossum apenninum	RF	0.9 (0.058)	0.78 (0.103)	0.8 (0.092)
Daphne petraea	RF	0.93 (0.044)	0.78 (0.096)	0.78 (0.097)
Dianthus carthusianorum subsp. *tenorei*	RF	0.9 (0.061)	0.76 (0.107)	0.77 (0.099)
Dianthus sardous	RF	0.91 (0.062)	0.79 (0.109)	0.8 (0.098)
Dianthus tarentinus	RF	0.9 (0.055)	0.72 (0.103)	0.74 (0.098)
Drymochloa drymeja subsp. *exaltata*	RF	0.88 (0.041)	0.7 (0.068)	0.7 (0.068)
Echinops siculus	RF	0.89 (0.052)	0.71 (0.089)	0.73 (0.083)
Epipactis meridionalis	RF	0.94 (0.034)	0.77 (0.088)	0.77 (0.089)
Erysimum apenninum	RF	0.92 (0.032)	0.81 (0.062)	0.81 (0.062)
Erysimum crassistylum subsp. *garganicum*	RF	0.84 (0.066)	0.67 (0.107)	0.71 (0.096)
Erysimum etruscum	RF	0.85 (0.057)	0.68 (0.093)	0.7 (0.089)
Erysimum pseudorhaeticum	RF	0.94 (0.015)	0.79 (0.045)	0.79 (0.045)
Euphorbia ceratocarpa	RF	0.93 (0.05)	0.8 (0.097)	0.8 (0.094)
Euphorbia corallioides	RF	0.86 (0.045)	0.67 (0.082)	0.69 (0.079)
Euphorbia nicaeensis subsp. *japygica*	RF	0.88 (0.056)	0.69 (0.112)	0.72 (0.109)
Euphorbia variabilis	RF	0.92 (0.047)	0.79 (0.089)	0.8 (0.084)
Euphrasia tricuspidata	RF	0.94 (0.015)	0.77 (0.038)	0.77 (0.038)
Festuca alfrediana subsp. *ferrariniana*	RF	0.98 (0.02)	0.93 (0.049)	0.93 (0.05)
Festuca austrodolomitica	RF	0.95 (0.024)	0.79 (0.066)	0.79 (0.063)
Festuca riccerii	RF	1 (0.007)	0.99 (0.023)	0.98 (0.032)
Festuca robustifolia	RF	0.91 (0.032)	0.74 (0.065)	0.74 (0.065)
Festuca violacea subsp. *italica*	RF	0.93 (0.045)	0.87 (0.089)	0.9 (0.073)
Festuca violacea subsp. *puccinellii*	RF	0.96 (0.029)	0.91 (0.054)	0.92 (0.051)
Galium baldense	RF	0.95 (0.015)	0.77 (0.046)	0.77 (0.046)
Genista etnensis	RF	0.88 (0.062)	0.72 (0.108)	0.75 (0.105)
Genista tyrrhena	RF	0.97 (0.029)	0.93 (0.062)	0.94 (0.06)
Globularia incanescens	RF	0.9 (0.036)	0.81 (0.063)	0.81 (0.063)
Helichrysum litoreum	RF	0.96 (0.016)	0.82 (0.05)	0.82 (0.05)
Helichrysum saxatile subsp. *saxatile*	RF	0.93 (0.051)	0.8 (0.106)	0.8 (0.1)
Helictochloa praetutiana subsp. *praetutiana*	RF	0.97 (0.017)	0.88 (0.054)	0.88 (0.054)
Helleborus viridis subsp. *bocconei*	RF	0.88 (0.037)	0.68 (0.065)	0.68 (0.065)
Hypericum barbatum subsp. *calabricum*	RF	0.88 (0.053)	0.74 (0.083)	0.77 (0.078)
Iris cengialti subsp. *cengialti*	RF	0.92 (0.037)	0.74 (0.077)	0.75 (0.076)
Jacobaea maritima subsp. *bicolor*	RF	0.92 (0.058)	0.82 (0.102)	0.82 (0.096)
Klasea flavescens subsp. *cichoracea*	RF	0.86 (0.052)	0.68 (0.079)	0.71 (0.075)
Knautia baldensis	RF	0.94 (0.029)	0.78 (0.079)	0.77 (0.079)
Knautia persicina	RF	0.95 (0.023)	0.82 (0.065)	0.82 (0.065)
Koeleria splendens	RF	0.89 (0.041)	0.73 (0.078)	0.75 (0.074)
Laserpitium nitidum	RF	0.92 (0.037)	0.75 (0.087)	0.75 (0.082)
Leontodon anomalus	RF	0.9 (0.039)	0.71 (0.091)	0.72 (0.088)

Leontodon intermedius	RF	0.84 (0.067)	0.69 (0.096)	0.72 (0.09)
Limonium acutifolium subsp. *acutifolium*	RF	0.98 (0.02)	0.94 (0.052)	0.91 (0.073)
Limonium ilvae	RF	0.98 (0.016)	0.94 (0.05)	0.9 (0.075)
Limonium merxmuelleri subsp. *sulcitanum*	RF	0.99 (0.012)	0.95 (0.043)	0.94 (0.052)
Limonium multiforme	RF	0.98 (0.023)	0.94 (0.047)	0.93 (0.05)
Limonium remotispiculum	RF	0.84 (0.078)	0.68 (0.114)	0.72 (0.104)
Linaria purpurea	RF	0.91 (0.032)	0.78 (0.068)	0.78 (0.068)
Luzula sylvatica subsp. *sicula*	RF	0.87 (0.062)	0.7 (0.112)	0.74 (0.105)
Mcneillia graminifolia subsp. *rosanoi*	RF	0.94 (0.037)	0.84 (0.083)	0.86 (0.073)
Melampyrum italicum	RF	0.93 (0.014)	0.71 (0.039)	0.71 (0.039)
Micromeria cordata	RF	0.91 (0.049)	0.8 (0.102)	0.83 (0.095)
Micromeria graeca subsp. *tenuifolia*	RF	0.85 (0.051)	0.68 (0.083)	0.7 (0.081)
Moehringia glaucovirens	RF	0.92 (0.035)	0.74 (0.083)	0.75 (0.085)
Moltkia suffruticosa subsp. *bigazziana*	RF	0.88 (0.057)	0.73 (0.111)	0.76 (0.102)
Myosotis graui	RF	0.92 (0.05)	0.83 (0.087)	0.85 (0.078)
Myosotis sylvatica subsp. *elongata*	RF	0.91 (0.045)	0.76 (0.077)	0.77 (0.075)
Odontarrhena argentea	RF	0.91 (0.046)	0.74 (0.094)	0.74 (0.098)
Odontarrhena bertolonii	RF	0.87 (0.077)	0.72 (0.126)	0.74 (0.11)
Oenanthe lisae	RF	0.91 (0.044)	0.79 (0.086)	0.8 (0.084)
Onosma echioides subsp. *echioides*	RF	0.83 (0.058)	0.66 (0.085)	0.69 (0.081)
Onosma pseudoarenaria subsp. *tridentina*	RF	0.91 (0.047)	0.74 (0.098)	0.75 (0.092)
Ophrys appennina	RF	0.88 (0.035)	0.69 (0.063)	0.69 (0.063)
Ophrys apulica	RF	0.94 (0.037)	0.81 (0.085)	0.79 (0.1)
Ophrys bertolonii subsp. *bertoloniiformis*	RF	0.92 (0.015)	0.7 (0.033)	0.7 (0.033)
Ophrys classica	RF	0.87 (0.035)	0.67 (0.061)	0.67 (0.061)
Ophrys crabronifera	RF	0.86 (0.049)	0.66 (0.085)	0.68 (0.082)
Ophrys exaltata subsp. *exaltata*	RF	0.85 (0.078)	0.67 (0.124)	0.72 (0.114)
Ophrys exaltata subsp. *montis-leonis*	RF	0.92 (0.048)	0.76 (0.102)	0.77 (0.097)
Ophrys lucana	RF	0.91 (0.033)	0.73 (0.078)	0.73 (0.078)
Ophrys lunulata	RF	0.86 (0.06)	0.71 (0.097)	0.73 (0.092)
Ophrys minipassionis	RF	0.88 (0.06)	0.7 (0.1)	0.73 (0.094)
Ophrys passionis subsp. *majellensis*	RF	0.84 (0.068)	0.68 (0.114)	0.72 (0.104)
Ophrys promontorii	RF	0.87 (0.07)	0.69 (0.124)	0.7 (0.116)
Ophrys tenthredinifera subsp. *neglecta*	RF	0.9 (0.033)	0.75 (0.064)	0.76 (0.064)
Ornithogalum exscapum	RF	0.87 (0.043)	0.69 (0.075)	0.71 (0.072)
Pimpinella anisoides	RF	0.84 (0.091)	0.67 (0.129)	0.72 (0.117)
Pinguicula christinae	RF	0.99 (0.007)	0.96 (0.04)	0.95 (0.052)
Plantago sarda	RF	1 (0.004)	0.99 (0.016)	0.99 (0.025)
Polygala alpestris subsp. *angelisii*	RF	0.9 (0.06)	0.8 (0.097)	0.84 (0.082)
Polygala flavescens subsp. *maremmana*	RF	0.97 (0.031)	0.88 (0.08)	0.87 (0.082)
Polygala sardoa	RF	0.88 (0.053)	0.73 (0.097)	0.76 (0.088)
Potentilla rigoana	RF	0.97 (0.025)	0.86 (0.077)	0.85 (0.077)
Primula polliniana	RF	0.93 (0.022)	0.74 (0.059)	0.74 (0.059)
Primula tyrolensis	RF	0.9 (0.043)	0.69 (0.086)	0.7 (0.089)
Ptychotis sardoa	RF	0.94 (0.044)	0.84 (0.093)	0.84 (0.092)
Pulmonaria vallarsae	RF	0.95 (0.026)	0.81 (0.075)	0.81 (0.075)
Quercus ichnusae	RF	0.98 (0.018)	0.9 (0.058)	0.86 (0.076)
Rhizobotrya alpina	RF	0.92 (0.041)	0.76 (0.1)	0.76 (0.098)
Rumex scutatus glaucescens	RF	0.89 (0.047)	0.7 (0.098)	0.73 (0.089)
Salix arrigonii	RF	0.84 (0.074)	0.7 (0.119)	0.74 (0.11)

Salix brutia	RF	0.93 (0.043)	0.76 (0.089)	0.75 (0.09)
Salix purpurea subsp. *eburnea*	RF	0.89 (0.072)	0.74 (0.122)	0.76 (0.107)
Salvia haematodes	RF	0.79 (0.092)	0.64 (0.137)	0.7 (0.123)
Santolina etrusca	RF	0.87 (0.053)	0.7 (0.108)	0.73 (0.098)
Santolina insularis	RF	0.91 (0.042)	0.82 (0.08)	0.83 (0.076)
Saxifraga arachnoidea	RF	0.95 (0.038)	0.83 (0.086)	0.8 (0.091)
Saxifraga depressa	RF	0.96 (0.026)	0.85 (0.064)	0.84 (0.069)
Saxifraga facchinii	RF	0.96 (0.029)	0.86 (0.064)	0.85 (0.072)
Saxifraga hostii subsp. *rhaetica*	RF	0.93 (0.042)	0.76 (0.089)	0.74 (0.1)
Saxifraga presolanensis	RF	0.93 (0.057)	0.83 (0.112)	0.81 (0.105)
Saxifraga tombeanensis	RF	0.94 (0.041)	0.82 (0.091)	0.79 (0.095)
Saxifraga vandellii	RF	0.89 (0.06)	0.7 (0.109)	0.72 (0.094)
Scabiosa holosericea	RF	0.86 (0.052)	0.69 (0.086)	0.71 (0.08)
Scabiosa uniseta	RF	0.9 (0.058)	0.74 (0.109)	0.76 (0.1)
Scabiosa vestina	RF	0.97 (0.02)	0.87 (0.072)	0.85 (0.073)
Scorzonera callosa	RF	0.92 (0.039)	0.76 (0.083)	0.76 (0.078)
Scorzonera villosa subsp. *columnae*	RF	0.86 (0.06)	0.7 (0.105)	0.73 (0.1)
Sedum alsinifolium	RF	0.93 (0.038)	0.75 (0.093)	0.76 (0.095)
Senecio ovatus subsp. *stabianus*	RF	0.94 (0.036)	0.82 (0.077)	0.81 (0.085)
Sesleria nitida	RF	0.94 (0.033)	0.85 (0.062)	0.85 (0.06)
Sesleria pichiana	RF	0.89 (0.063)	0.7 (0.101)	0.73 (0.092)
Silene italica subsp. *sicula*	RF	0.88 (0.051)	0.72 (0.077)	0.72 (0.077)
Silene nummica	RF	0.98 (0.03)	0.92 (0.07)	0.89 (0.076)
Siler montanum subsp. *siculum*	RF	0.95 (0.03)	0.82 (0.077)	0.81 (0.075)
Spiraea decumbens subsp. *tomentosa*	RF	0.91 (0.05)	0.73 (0.104)	0.75 (0.1)
Stipa etrusca	RF	0.88 (0.054)	0.7 (0.101)	0.73 (0.096)
Tephroseris italica	RF	0.92 (0.046)	0.84 (0.079)	0.84 (0.078)
Thesium sommieri	RF	0.91 (0.054)	0.82 (0.104)	0.85 (0.088)
Thymus spinulosus	RF	0.88 (0.051)	0.71 (0.103)	0.74 (0.095)
Tolpis virgata subsp. *grandiflora*	RF	0.82 (0.079)	0.65 (0.128)	0.7 (0.117)
Trifolium pratense subsp. *semipurpureum*	RF	0.91 (0.036)	0.71 (0.074)	0.72 (0.073)
Trisetaria villosa	RF	0.97 (0.024)	0.89 (0.06)	0.9 (0.054)
Vicia ochroleuca subsp. *ochroleuca*	RF	0.88 (0.058)	0.72 (0.106)	0.74 (0.095)
Viola aethnensis subsp. *splendida*	RF	0.94 (0.035)	0.82 (0.091)	0.81 (0.088)
Viola bertolonii	RF	0.92 (0.047)	0.75 (0.101)	0.75 (0.098)
Viola cassinensis subsp. *pseudogracilis*	RF	0.92 (0.054)	0.77 (0.109)	0.78 (0.1)
Viola dubyana	RF	0.95 (0.04)	0.83 (0.099)	0.82 (0.098)
Viola etrusca	RF	0.94 (0.043)	0.8 (0.099)	0.78 (0.096)
Viola eugeniae subsp. *eugeniae*	RF	0.95 (0.035)	0.87 (0.076)	0.88 (0.067)
Viola ferrarinii	RF	0.97 (0.025)	0.91 (0.054)	0.91 (0.052)

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Table S4. Species having a performance of evaluation of individual modelling techniques lower than good.

Species	Modelling techniques	Evaluation method
Thymus spinulosus	GLM	ROC, TSS
Ophrys promontorii	CTA	ROC, TSS
Carduus nutans subsp. *perspinosus*	GLM	ROC
Scabiosa uniseta	GLM	ROC, TSS
Klasea flavescens subsp. *cichoracea*	CTA	ROC
Salvia haematodes	CTA, RF	ROC
Salix purpurea subsp. *eburnea*	GLM	ROC
Sesleria pichiana	CTA	TSS
Colchicum neapolitanum	GLM	TSS