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Evolutionary assembly of flowering plants into sky islands

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Although they experience cold climates, particularly in temperate mountains during winter, alpine floras (plants in the vegetation belts above the climatic treelines) are generally species-rich. Yet, whether these floras represent evolutionarily independent, but convergent, assemblages drawn from their regional floras, or they originated from particular clades pre-adapted to harsh conditions, has not been determined. Here, we analyze the evolutionary relationships of angiosperm (flowering plant) species in 63 alpine floras worldwide (~7,000 species) in comparison with their regional floras (~94,000 species) and to the entire global flora. We find that each of the alpine floras represents an assemblage of more closely related species in comparison to their respective regional floras. The degree of phylogenetic clustering of species in alpine floras in tropical mountains exceeds that in temperate mountains. However, in relation to the global flora, temperate alpine floras are phylogenetically closely-related subsets of floras that colonized cold temperate areas during inter-glacial periods. We conclude that alpine floras include a few dominant families that have evolved tolerance to low temperature, and that evolutionary niche conservatism explains their phylogenetic clustering, compared to species in their regional species pools.

The local assembly of species from a pool of regionally available species (i.e., the regional species pool) reflects an interplay between evolutionary and ecological processes¹⁻². Under strong environmental filtering, the tendency of lineages to retain ancestral ecological traits over time (phylogenetic niche conservatism³) will leave a signature in the phylogenetic structure of local assemblages⁴.

Because most plant taxonomic orders (or higher-level taxa) originated tens of millions of years ago, when Earth experienced predominately tropical conditions⁵⁻⁶, ancestral traits are likely to emphasize adaptation to warm and wet environments. Steep gradients of decreasing temperature from tropical to temperate latitudes emerged following global climate cooling since the late Eocene⁷. These more recent conditions promoted adaptation to cold climates, particularly to withstanding freezing temperatures⁸. However, many lineages have not adapted to cold climates^{7,9-10}, and those that did might be more closely related to each other than expected by chance due to phylogenetic niche

conservatism. This would likely result in phylogenetic clustering (i.e., species being more closely related than expected) in areas with cold climates. That plant assemblages in cold climates include phylogenetically more closely related species than those in warm climates supports this argument (e.g., ref. 11). Because vegetation zonation from low to high elevations parallels zonation from low to high latitudes¹², we expect plant species at high elevations to be more closely related (i.e., more phylogenetically clustered) than those at low elevations. However, unlike strong latitudinal gradients of temperature, which originated only since the late Eocene (~34 million years ago) and thus are relatively young, strong elevational gradients of temperature have existed since plants have grown on mountains, well before the origin of angiosperms (flowering plants)¹³. Elevational gradients also occupy smaller geographical areas than latitudinal gradients, and thus may structure local floras. Altogether, changes in species assemblages across elevational gradients, and notably their phylogenetic structure, might thus differ from variation across latitudinal gradients. Understanding those differences is essential to gather a better understanding of the history of plant assembly.

Several studies (e.g., refs. 14-15) have shown that the phylogenetic relatedness of high-elevation tree species decreases with elevation, which contrasts with the increase in phylogenetic relatedness within tree assemblages with increasing latitude¹⁶⁻¹⁷. This pattern suggests that niche convergence, rather than niche conservatism, has characterized the assembly of tree species along tropical elevational gradients¹⁸. Whether niche convergence is restricted to tropical mountains, and whether it characterizes assemblages of both lowland and alpine vegetation (i.e., the entire regional flora), and for both woody and herbaceous plants, remain open questions.

Here, we describe the phylogenetic structure of alpine floras across the world in comparison to their regional floras and to the global flora. Specifically, we analyzed a dataset of 63 alpine angiosperm floras (i.e., flowering plants occurring above the tree line) compared to their regional angiosperm floras (i.e., all flowering plants present in a mountain system from the lowlands to the alpine belt), from all continents except Antarctica (Figure 1; Supplementary Table 1).

Results and Discussion

We constructed a phylogeny for the 94,161 species of angiosperms (more than one quarter of all angiosperm species) occurring in the regional floras utilized in this study. We did so by using an updated version of the largest dated phylogeny of seed plants¹⁹ as a backbone and V.PhyloMaker²⁰ as a tool to attach additional species to the backbone phylogeny (see Methods). To capture the phylogenetic structure of the floras, we used two complementary metrics²¹, namely phylogenetic diversity (PD) and mean pairwise distance (MPD). PD represents the sum of the branch lengths of the phylogenetic tree linking all species of a particular assemblage. MPD represents the mean phylogenetic distance between all pairs of species in an assemblage, the phylogenetic distance between a pair of species being defined as the total branch length of the shortest path between the two species. A species assemblage with a large PD or MPD represents an assemblage with species from different clades far apart in the phylogeny. In contrast, a species assemblage with low PD or MPD might represent an assemblage from a single clade, or a few clades that recently diversified. However, because these metrics are influenced by species richness, they need to be standardized to be comparable between sites. Each

metric was thus standardized using a set of null models to compare the phylogenetic structure of each alpine flora with its regional flora, with significant differences indicating elevational gradient effects. Expanding the breadth of the compared flora, up to the global flora, allows comparison of the phylogenetic structure of each alpine flora with that of the global pool of species. By varying the scale of the pool of species considered in null models, one can test hypotheses about mechanisms that have generated the phylogenetic structure of alpine assemblages²².

Once corrected by these tailor-made null models (Methods), the resulting standardized effect size (ses) metrics quantify the relative excess (e.g., several clades far apart in the phylogeny, old and unique species) or a deficit (e.g., a single highly diversified clade) in phylogenetic diversity for a given assemblage relative to the overall species pool. More specifically, the standardized effect size of PD (PD_{ses}) reveals the phylogenetic structure that predominates at the tips of the phylogenetic tree (recent divergences), while standardized effect size of MPD (MPD_{ses}) reflects deep-branching (i.e., ancient) divergences²¹. We used these two complementary metrics because different processes may act over different evolutionary time scales, which would not be detectable using a single metric²¹.

Using these metrics, we test whether angiosperm species in alpine floras are phylogenetically clustered (as predicted by the niche conservatism hypothesis) or phylogenetically over-dispersed (as predicted by the niche convergence hypothesis) in comparison to their respective regional species pools (including species in alpine belts and below). We also investigate whether this phylogenetic structure differs between continents and climate regions of the world. Finally, we test whether the phylogenetic clustering of alpine floras differs across latitude (and thus temperature) gradients and in relation to the species pool considered.

All 63 alpine floras analyzed here comprise groups of phylogenetically more closely related species (i.e., MPD_{ses} and $PD_{ses} < 0$), compared to groups of species randomly drawn from their regional species pools (Supplementary Figure 1). This result was significant for 50 (79%) and 59 (94%) of the 63 alpine floras for MPD_{ses} and PD_{ses} , respectively (i.e., MPD_{ses} and $PD_{ses} < -1.96$) (Figure 1, Supplementary Figure 2). Thus, most alpine floras represent specific phylogenetic subsets of the regional floras of the mountain systems in which they occur. Interestingly, clustering due to shallow-branching divergences (i.e., PD_{ses}) near the tips of the phylogenetic tree was stronger than clustering due to deep-time divergences (i.e., MPD_{ses} , Supplementary Figure 2), with the exception of the alpine floras in South America (Supplementary Figure 2). Thus, phylogenetic clustering is rather recent for most alpine floras and characterizes shallow-branching divergences within the regional phylogenies. Conversely, evolutionary divergence between alpine and lowland floras in South America involves primarily deep-time splits within the regional floras. This pattern might originate from ancient mountain uplifts in South America that early on induced deep-time divergence of floras. We tested whether phylogenetic clustering holds even when alpine floras and their respective regional species pools are aggregated at continental scales. Here again, alpine floras represented closely-related assemblages compared to their respective continental species pools, irrespective of the metric used (Figure 2). This result was confirmed when the combinations of species in all alpine floras were compared to the combinations of the species in all regional species pools. In this case, values for MPD_{ses} and PD_{ses} were

extremely negative ($MPD_{ses} = -38.6$ and $PD_{ses} = -35.0$), demonstrating very strong phylogenetic clustering for the global alpine flora examined in this study.

Strikingly, the strength of phylogenetic clustering of each alpine flora varies with latitude (Figure 1, Figure 3), irrespective of the metric used. When each alpine flora was compared to its regional flora, clustering was stronger at low latitudes than at high latitudes (Figure 3a). Thus, the alpine floras of tropical mountains form distinct phylogenetic groupings of species, compared to their regional floras. In contrast, species in alpine floras at high latitudes, such as those in North America and Europe, are only loosely clustered assemblages of species drawn from their regional floras (Figure 3a). This difference might reflect the fact that high latitude floras are already a non-random set of the global flora, primarily with clades adapted to cold conditions¹¹, with an arctic-alpine affiliation. To test this hypothesis, we first compared each alpine flora to a global pool of the 313,855 angiosperm species in the combination of our regional floras and The Plant List (see Methods), and then compared each associated regional flora (alpine and lowland species combined) to the same global angiosperm species pool. Interestingly, high latitude alpine floras were still less clustered than low latitude ones when extending the species pool of each alpine flora to the global species pool of angiosperms (Figure 3b). However, in agreement with the hypothesis that high latitude regional floras (i.e., the species in alpine belts plus lowlands) are already clustered phylogenetically compared to low latitude floras, the strength of the phylogenetic clustering is strongly linked to latitude but with a negative slope (Figure 3d). This clustering of the entire regional mountain floras at high latitudes partly explains the lower phylogenetic clustering of their individual alpine floras in contrast to that in low latitude alpine floras. When each alpine flora was compared to the combination of all angiosperm species in the 63 alpine floras, species in alpine floras at low latitudes tended to be more strongly clustered than those at high latitudes (Figure 3c). This implies that species in each of the alpine floras at high latitudes are more phylogenetically related to each other than those at low latitudes when species in each alpine flora are compared to the species pool that included all species of the 63 alpine floras. When latitude was substituted with growing degree days in these analyses, the results were generally consistent with those based on latitude (Supplementary Figure 3).

Overall, our analyses, based on two complementary metrics and tailored definitions of the species pool, confirmed that alpine floras represent phylogenetically closely-related species assemblages and that the origin of this clustering varies with latitude. These observations do not reflect sampling bias since our study includes the majority (~70%) of all alpine angiosperm species in the world (based on the global estimate reported in ref. 23). Instead, the phylogenetic clustering appears to reflect strong environmental filtering in combination with phylogenetic niche conservatism. That is, owing to shared evolutionary adaptations to low temperature, species in alpine environments are likely more closely related to each other, on average, than are species in lowlands.

Biotic interactions may further increase this pattern¹¹. For instance, both asymmetric competition²⁴ and facilitation between similar species²⁵ can increase phylogenetic clustering. However, these processes probably do not drive the observed pattern for alpine plants because competitive interactions are usually reduced, and plant-plant interactions are thought to be more positive due to facilitation (mutual benefits of

shelter) in alpine environments²⁶. For example, plant species with a cushion habit (e.g., an androsace, or rock jasmine) can facilitate the establishment of individuals of species that would otherwise be less successful at such locations²⁷. Such a mechanism should lead to phylogenetic overdispersion (androsace and grass are far apart on the phylogeny of angiosperms), rather than phylogenetic clustering. It is also unlikely that, within each mountain system, dispersal limitation has caused phylogenetic clustering of alpine species compared to the whole flora of the mountain system. This is because geographical distances across elevational gradients are relatively small, and major dispersal barriers are unlikely across such small geographical extents²⁸. However, dispersal limitation might explain, to some degree, the stronger phylogenetic clustering observed when an alpine flora is compared to the global species pool. This is because defining the global species pool to include species from different biogeographic realms, i.e., on different continents, would likely over-extend the breadth of the phylogenetic tree used to standardize the phylogenetic metrics of a given alpine flora. In other words, the global species pool includes some lineages (e.g., families or even orders) that are absent from the biogeographic realm of any particular focal alpine flora, which tend to ‘artificially’ increase the relative phylogenetic clustering of the alpine flora, compared to the global species pool. This is supported by our major result, i.e., the average MPD_{ses} of the 63 alpine floras was less negative when their respective regional floras were used as species pools, compared to that when the global species pool was used as species pools for each alpine flora (-4.76 and -5.91, respectively). In other words, the larger the reference species pool, the more deficient in phylogenetic diversity the alpine flora becomes. This pattern reflects the dominance of few clades in the alpine flora of the world compared to the global angiosperm flora.

Interestingly, while the phylogenetic clustering of alpine floras presents a general pattern, its strength varies with latitude, with temperate alpine floras less clustered than tropical alpine floras compared to their respective lowland regional floras. This difference might result, at least in part, from the fact that ecological gradients (particularly temperature) are shorter in high latitude mountains with fewer altitudinal life belts than in low latitude mountains²⁸ (e.g., a tropical mountain has a tropical vegetation belt at low elevations, but this belt is lacking in temperate mountains). However, this general pattern is reversed when the overall angiosperm flora of a mountain area (including both alpine and lowland elevations) is compared to the global species pool of angiosperms. This simply confirms that species in temperate floras are already a clustered, rather than random, subset of the entire angiosperm flora of the world¹¹. In other words, tropical alpine floras represent primarily clades that have diverged early in flowering plant evolution, while temperate alpine floras are recent clustered assemblages of temperate floras (i.e., mostly herbaceous species), which are particular, closely-related species groups of the global angiosperm flora.

Nonetheless, these relationships cannot fully explain the overall patterns. Indeed, when comparing each alpine flora to the angiosperm flora of the world, low latitude alpine floras remained more clustered than high latitude ones (Figure 3b). A complementary hypothesis is that ecological gradients are shorter in high latitude mountains with fewer life belts than in low latitude mountains, as noted above. Because genera and families are generally similar among all alpine floras of the world (e.g., 88% of angiosperm families in tropical-latitude alpine floras examined in this study also occur

in temperate-latitude alpine floras), including more tropical taxa (families, genera, and species) in regional species pools of low latitude regions would necessarily cause stronger phylogenetic clustering for their alpine floras, compared to their regional species pools.

Interestingly, when each alpine flora is compared to the species pool that includes only the species of the 63 alpine floras, species in low latitude alpine floras remain more strongly clustered than those in high latitude alpine floras (Figure 3c). The following hypothesis might account for this pattern. Angiosperms originated in, and spread from, the tropics²⁹. Some early tropical lineages became adapted to tropical montane climates, forming clustered assemblages compared to lowland tropical floras. While species in tropical alpine belts, as a whole, might be clustered compared to the global species pool, species adapted to tropical alpine belts within different continents or major mountain systems might belong to different major lineages, and thus might be further clustered, because dispersal among mountains within and between continents is particularly limited within tropical latitudes³⁰. This would cause ‘double-clustering’ for tropical alpine floras. In contrast, although species in temperate alpine floras are also clustered compared to the global species pool, glacial-interglacial cycles during the Pleistocene repeatedly mixed species of alpine floras at low elevation among different regions and continents, particularly in the Northern Hemisphere. This would have tended to homogenize alpine floras across continental regions. Overall, these processes would have resulted in stronger phylogenetic clustering in tropical than in temperate alpine floras, in comparison with the global alpine species pool.

Methods

Alpine belt

We defined the alpine belt in a mountain system as the area located above the natural climatic limit of trees (alpine treeline). Because alpine belts of different mountains are commonly separated by extensive forested or rangeland areas below alpine treelines, alpine belts are often considered as ‘sky islands’³¹⁻³². Alpine vegetation represents the only terrestrial biogeographic unit that occurs at all latitudes worldwide²³, a remarkable fact first documented by Alexander von Humbolt³³. Vegetation above the alpine (elevational) treeline resembles that north of the arctic (latitudinal) treeline^{23,34}. Although the total area of alpine vegetation represents only 2.6 % of the Earth’s terrestrial surface outside Antarctica^{23,35}, and only half as much area as arctic vegetation (c. 5% of the land area), global species diversity of vascular plants in alpine vegetation is ca. six-fold higher than that in arctic vegetation (ca. 10,000 species in alpine vegetation; vs. ca. 1,500 arctic species; ref. 36). Alpine belts present severe environmental challenges to plant life, including low temperatures and high ultraviolet radiation²¹.

Floras

The latitudinal range of this study was confined between 50°N and 50°S. We did not include higher latitudes because elevational gradients below alpine treelines at these latitudes are generally short, with few vegetation belts, which would have weakened comparisons with other alpine belts. We assembled 63 alpine floras worldwide (Figure 1). Of these 63 alpine floras, 62 are typical alpine floras located above climate treelines. No true alpine flora exists in southeastern North America; to represent this broad region in

our study, we included one plant assemblage from the highest mountain peaks for this region (maximum elevation 2037 m) (we call it an “alpine” flora for convenience of discussion). The 63 alpine floras represent the major mountain systems across the world, including Mount Kenya and the Drakensberg Escarpment in Africa, the Himalayas in Asia, the Andes in South America, the Rocky Mountains in North America, and the European Alps. We assigned each of the 63 alpine floras to either temperate or tropical latitudes, using 23.5°N and 23.5°S as the temperate-tropical boundaries.

We then assembled a regional species pool for each alpine flora. These regional species pools included all angiosperm species along the entire elevational gradient (from the lowest to highest elevations) within the region. For example, the regional species pool for the alpine flora of Nepal included all angiosperm species recorded in Nepal from 59 to 6,400 m in elevation (i.e., the entire elevation range of Nepal over which angiosperms are distributed). Details about each alpine flora and its regional species pool are available in Supplementary Table 1. The species of the alpine floras included in this study are restricted to non-tree species. Botanical nomenclature was standardized according to The Plant List (version 1.1, www.theplantlist.org). Intraspecific taxa were combined with their respective species. Non-native species in each flora were excluded. In total, the regional species pools of the 63 alpine floras included 94,161 species in 369 families of angiosperms (more than one quarter of angiosperm species in the world). Of these, 6,918 species in 140 families) comprised the 63 alpine floras. Each species was assigned to a family recognized in APG IV³⁷, based on information on the relationships between genera and families provided by the Angiosperm Phylogeny Website (<http://www.mobot.org/MOBOT/research/APweb/>).

For the 63 alpine floras, on average, each regional species pool included 3,867 (\pm 4,709 SD) angiosperm species, and each alpine flora included 171 (\pm 124) angiosperm species; on average, 9.1% of species in a regional species pool were present in its alpine flora. When the 63 sites were considered together, 7.3% of the 94,161 species in the regional species pools occurred in the 63 alpine floras.

Phylogeny reconstruction

We used a recently generated time-calibrated megatree for vascular plants, GBOTB_extended.tre²⁰, as a backbone to generate a phylogeny for the 94,161 species. The megatree included an updated version of the phylogeny for pteridophytes (ref. 8) and an updated version of GBOTB for seed plants (ref. 19). The megatree includes all families of vascular plants worldwide, including families that are absent from the phylogenies of refs. 8 and 19. Of the 8,341 genera in our data set, 80% (6,673) were present in the megatree. We added the genera and species in our data set that were absent from the megatree to their respective families and genera using the Phylomatic and BLADJ approaches³⁸ implemented in the V.PhylMaker software²⁰. V.PhylMaker sets branch lengths of added taxa in a family by placing the nodes evenly between dated nodes and terminals within the family and placing a missing species at the mid-point of the branch length of its genus (e.g., ref. 14). A recent study (ref. 39) showed that for the two phylogenetic metrics used in our present study (see below), values of a phylogenetic metric derived from a phylogenetic tree resolved only at the genus level are nearly perfectly correlated to those derived from a phylogenetic tree resolved fully at the species level (Pearson’s correlation coefficient is 1.000 for one phylogenetic metric and 0.992 for

the other phylogenetic metric), suggesting that patterns of phylogenetic structure measured with the two phylogenetic metrics would be similar or identical regardless of whether a phylogenetic tree resolved at the species or genus level is used to calculate these phylogenetic metrics. Finally, we pruned the megatree to generate a phylogenetic tree for each of the regional species pools, retaining only the species present in the regional species pool.

We also used V.PhyloMaker, and the approach described above, to build a phylogeny for angiosperm species worldwide, which included all angiosperm species in the regional floras included in this study, plus angiosperm species in The Plant List that can be directly assigned to the families of APG IV. We considered the 313,855 species in this phylogeny as a global species pool of angiosperms for the analyses in this study.

Phylogenetic structure metrics

We analyzed the phylogenetic structure of the alpine floras using two complementary metrics, namely phylogenetic diversity (PD; ref. 40) and mean pairwise distance (MPD). Because PD and MPD are positively correlated with species richness, in order to make them comparable between sites, it is necessary to standardize their values by accounting for species richness. This is commonly done with the use of a null model that keeps species richness constant while randomizing the phylogenetic relationships between species. Using this null model, the standardized effect size, which gives the relative position of an observed value with respect to the null distribution, can be calculated as:

$$\text{Metric}_{\text{ses}} = [\text{Metric}_{\text{obs}} - \text{mean}(\text{Metric}_{\text{null}})]/\text{sd}(\text{Metric}_{\text{null}}),$$

where $\text{Metric}_{\text{ses}}$ is the standardized effect size of PD or MPD (i.e., PD_{ses} or MPD_{ses} , respectively), $\text{Metric}_{\text{obs}}$ is the observed phylogenetic structure metric in a given alpine flora, and $\text{Metric}_{\text{null}}$ is the same metric calculated n times with n randomized assemblages drawn from a species pool (see below for the definition of the species pool). Both PD_{ses} and MPD_{ses} quantify the relative excess (overdispersion) or deficit (clustering) in phylogenetic structure for a given alpine flora relatively to the species pool. In other words, a negative PD_{ses} or MPD_{ses} reflects relative phylogenetic clustering of species while a positive PD_{ses} or MPD_{ses} reflects relative phylogenetic overdispersion of species.

PD_{ses} and MPD_{ses} measure the phylogenetic structure of assemblages at different evolutionary depths: MPD_{ses} is linked to the more basal structure of the phylogenetic tree, whereas PD_{ses} describes the more terminal structure of the phylogenetic tree⁴¹. It is important to use metrics that can assess phylogenetic structure at both basal and shallow depths of evolutionary history across a phylogeny because some processes produce basal clustering while others create terminal overdispersion, generating ‘clusters of overdispersion’²¹.

The two metrics were calculated using computationally efficient algorithms⁴²⁻⁴³ based on exact solutions given a particular phylogenetic tree and species richness (rather than being based on a resampling approximation of the mean and variance), using a null model that considers all possible combinations of S species from the species pool (where S is the number of species in a sample under investigation) to be equally likely⁴⁴. To determine whether MPD_{ses} and PD_{ses} values for a particular alpine flora were significantly smaller (i.e., more clustering and lower phylogenetic diversity) or larger (i.e., more

overdispersion and higher phylogenetic diversity) compared to null assemblages randomly drawn from its species pool, we generated 999 null assemblages from the given species pool with the number of species in each null assemblage being equal to the number of species in the alpine flora. The position of the observed value relative to the null distribution was computed as the proportion of null values that are lower or higher than the observed value, which corresponds to a p -value. For normally distributed data, significance at p -value < 0.05 is equivalent to a standardized effect size > 1.96 (or < -1.96).

Phylogenetic structure and defined species pools

To depict the evolutionary structure of alpine floras around the world, we considered several ways to define the species pools and associated alpine floras. First, we used three species pools to calculate values of MPD_{ses} and PD_{ses} for each alpine flora: (1) a species pool that included all angiosperm species in the region within which the focal alpine flora was located (the ‘regional species pool’, see below for details; Supplementary Table 1), (2) a species pool that included all angiosperm species in the 63 alpine floras, and (3) a global species pool for angiosperms, which included 313,855 species (see above for details). For each alpine flora, the regional species pool was defined as all the species in the published flora of the mountain region (Supplementary Table 1). When several independent regional species pools could be retrieved from the literature, we chose the one that maximized the elevation range while minimizing the area of the region. This strategy provided a good representation of the area while minimizing the effects of dispersal limitation. On average, the geographic distance from the alpine belt of a region to the edge of the region was less than 250 km in our study. Because the distributions of most plant species exceed this distance within a region, we suggest that plant species distributions across different elevation belts within a mountain region are primarily a result of environmental sorting, rather than dispersal limitation.

Second, to test whether the phylogenetic structure of alpine floras varied significantly between climate zones across latitudes (tropical and temperate) and between continents, we combined the 63 alpine floras, and their respective regional species pools, into 12 climato-continental species pools (temperate versus tropical across continents). For each of the 12 species pools, we generated a species list of alpine plants by combining all alpine plant species in the alpine floras belonging to each pool (Supplementary Table 2). These species pools allowed us to strictly compare MPD_{ses} and PD_{ses} values across continents and climates. We also generated a global alpine flora and a single associated species pool.

Finally, to test whether species in temperate regional floras are more closely related (clustered) than species in tropical regional floras, compared to the global flora of angiosperms, we measured phylogenetic structure for each of the 63 regional floras based on the global angiosperm species pool.

Data availability

The data used in this study have been published and are accessible. Details about data sources are provided in Supplementary Table 1 or cited in the article. The data on which the analyses of this study were based are available at <https://github.com/Kifir0411/NATECOLEVOL-200610646>.

Code availability

This study used codes in published R packages, which were cited in the article.

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Competing interests

The authors declare no competing interests.

Figure Legends

Figure 1 Geographic patterns of standardized effect size of mean pairwise distance (MPD_{ses} , upper panel) and standardized effect size of phylogenetic diversity (PD_{ses} , lower panel) for the 63 alpine floras used in this study. MPD_{ses} and PD_{ses} of each alpine flora were calculated in regard to its regional flora. Filled symbols are significant ($p < 0.05$). A more negative value represents a stronger degree of phylogenetic clustering among species within an alpine flora compared to its regional flora. Note that the location of a dot represents the location of the mid-point of a region, for which its alpine flora was analyzed in this study, i.e., the center of a regional flora (species pool), not a place where an alpine flora was located.

Figure 2. Comparisons of standardized effect size of mean pairwise distance (MPD_{ses} , red triangles) and standardized effect size of phylogenetic diversity (PD_{ses} , blue triangles) with histograms for distributions of these two phylogenetic metrics derived from null assemblages (see Methods for details) for different climates (temperate versus tropical) and continents, and the globe. Each histogram represents the frequency (Freq.) of MPD_{ses} or PD_{ses} values derived from 999 null assemblages randomly drawn from the species pool defined at the climato-continental or global scale. A more negative value of MPD_{ses} or PD_{ses} (indicated by a red or blue triangle) represents a stronger degree of phylogenetic clustering among alpine species compared to the reference species pool.

Figure 3. Relationships (Pearson's correlation coefficient, r) between latitude (in absolute terms) and standardized effect size of mean pairwise distance (MPD_{ses}) for (a) species in alpine floras with MPD_{ses} being calculated using the regional species pool of each of the alpine floras, (b) species in alpine floras with MPD_{ses} being calculated using the global species pool of angiosperm species in the combination of our regional floras and The Plant List (Methods), (c) species in alpine floras with MPD_{ses} being calculated using all species in the 63 alpine floras as a species pool, and (d) species in the regional floras of the alpine sites with MPD_{ses} being calculated using the global species pool of angiosperm species in the combination of our regional floras and The Plant List. Lines are linear least squares best fits; we used them to show linear trends, not for statistical tests.

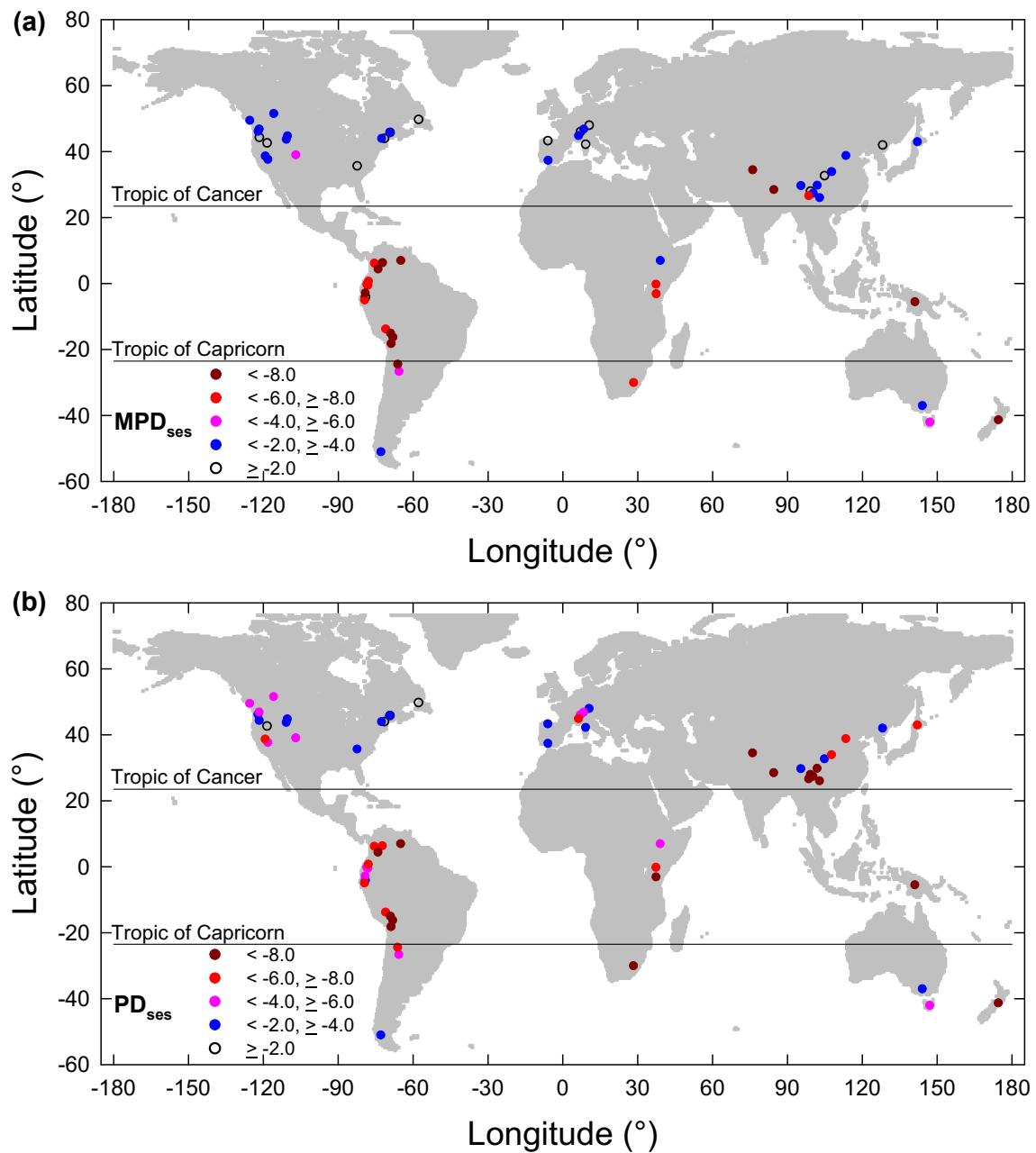


Figure 1

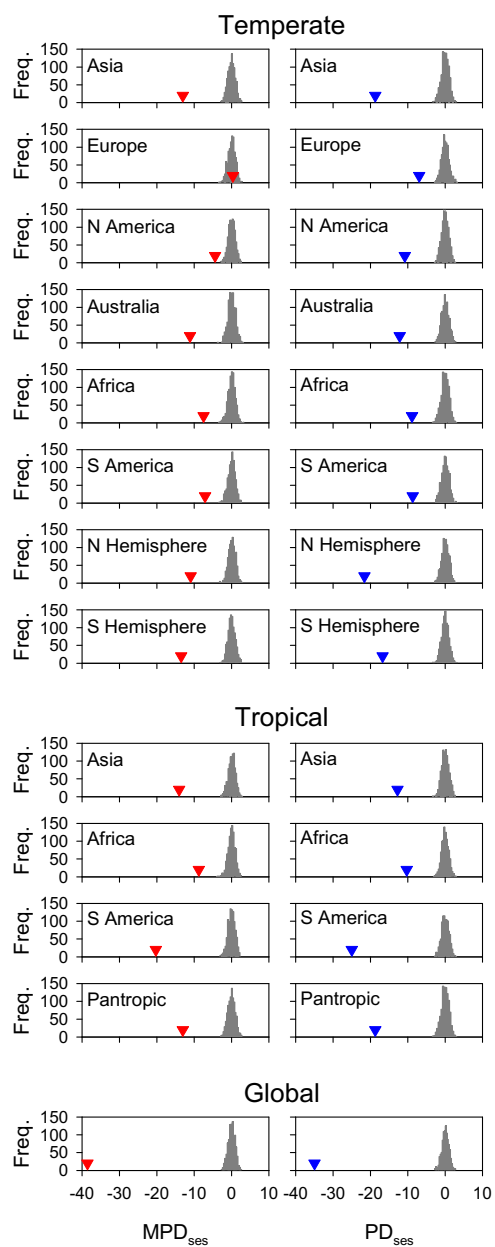


Figure 2

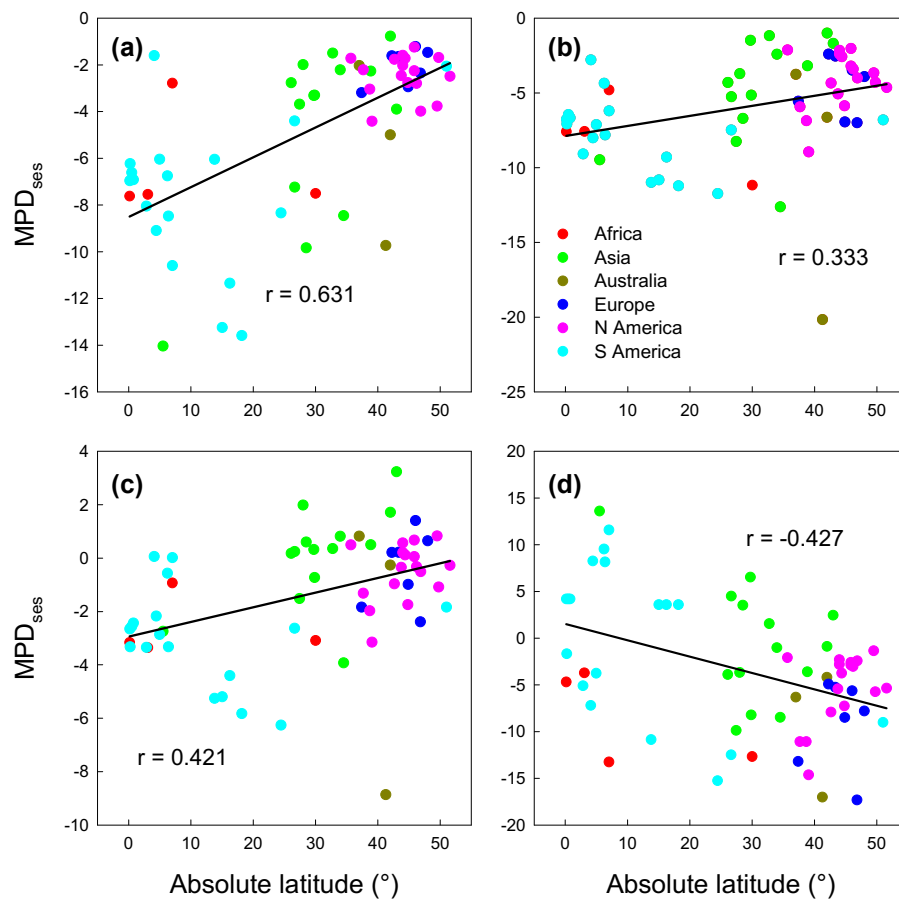


Figure 3

Supplementary Information

Supplementary Table 1. Alpine floras and their regional species pools used in this study.

Supplementary Table 2. Alpine floras and their species pools in broad geographical regions.

Supplementary Figure 1. Standardized effect size of mean pairwise distance (MPD_{ses} , red triangles) and standardized effect size of phylogenetic diversity (PD_{ses} , blue triangles) in the 63 alpine floras examined in this study.

Supplementary Figure 2. Standardized effect size of mean pairwise distance (MPD_{ses}) and the standardized effect size of phylogenetic diversity (PD_{ses}) for the 63 alpine floras examined in this study.

Supplementary Figure 3. Relationships between growing degree days and standardized effect size of mean pairwise distance (MPD_{ses}).

Supplementary Table 1 Alpine floras and their regional species pools used in this study.

Site ID	Continent	Country [region]	Alpine flora	Regional species pool	Data source
1	Africa	Ethiopia	Alpine flora of Mt Galama	Flora of Ethiopia	1, 63
2	Africa	Kenya	Alpine flora of Mt. Kenya	Flora of Kenya	2, 63
3	Africa	South Africa and Lesotho	Alpine flora of Drakensberg Mountains	Flora of KwaZulu-Natal Province of South Africa and Lesotho	3, 64, 101
4	Africa	Tanzania	Alpine flora of Mount Kilimanjaro	Flora of Tanzania	4, 53, 63
5	Asia	China	Alpine flora of Baima Snow Mountains	Flora of Baima Snow Mountains	5
6	Asia	China	Alpine flora of Big Bend Gorge of Yalu Tsangpo	Flora of Big Bend Gorge of Yalu Tsangpo	6
7	Asia	China	Alpine flora of Changbai Mountains	Flora of Changbai Mountains	7, 65
8	Asia	China	Alpine flora of Gaoligong Mountains	Flora of Gaoligong Mountains	8
9	Asia	China	Alpine flora of Gongga Mountains	Flora of grid cell #1616 in ref. 66	9, 66
10	Asia	China	Alpine flora of Jiaozi Mountains	Flora of Jiaozi Mountains	10, 54
11	Asia	China	Alpine flora of Motianling	Flora of Baishuijiang Nature Reserve	11
12	Asia	China	Alpine flora of Taibai Mountains	Flora of Taibai Mountains	12, 67
13	Asia	China	Alpine flora of Wutai Mountains	Flora of grid cell #990 in ref. 66	13, 66
14	Asia	China	Alpine flora of Yulong Snow Mountains	Flora of Yulong Snow Mountains	14, 55, 61
15	Asia	India	Alpine flora of Kashmir Himalaya	Flora of Jammu and Kashmir	15, 68
16	Asia	Japan	Alpine flora of Hokkaido	Flora of Hokkaido	16, 69
17	Asia	Nepal	Alpine flora of Nepal	Flora of Nepal	17
18	Asia	[New Guinea]	Alpine flora of New Guinea	Flora of New Guinea	18, 56, 70, 96
19	Australia	Australia	Alpine flora of Tasmania	Flora of Tasmania	19, 71
20	Australia	Australia	Alpine flora of Victoria	Flora of Victoria	20, 71
21	Australia	New Zealand	Alpine flora of New Zealand	Flora of New Zealand	21, 72
22	Europe	France	Alpine flora of Corsica	Flora of Corsica	22
23	Europe	France	Alpine flora of Écrins National Park	Flora of Écrins National Park	23
24	Europe	Germany	Alpine flora of Germany	Flora of Baden-Württemberg and Bavaria States	24, 57, 73
25	Europe	Spain	Alpine flora of Rasón and San Isidro	Flora of Asturias	25, 74
26	Europe	Spain	Alpine flora of Sierra Nevada	Flora of Andalusia	26, 74
27	Europe	Switzerland	Alpine flora of Switzerland	Flora of Switzerland	27, 75

28	Europe	Switzerland	Alpine flora of Valais (Western Alps)	Flora of Valais	28, 76
29	North America	Canada	Alpine flora of Banff National Park	Flora of Banff and Jasper National Park	29, 77, 97, 100
30	North America	Canada	Alpine flora of Gros Morne National Park	Flora of Gros Morne National Park	30, 78
31	North America	Canada	Alpine flora of Vancouver Island	Flora of Vancouver Island	31, 58, 79
32	North America	USA	Alpine flora of Adirondack Mountains	Flora of Adirondack Mountains (Adirondack Park) - 5 northeastern counties	32, 59, 62, 80
33	North America	USA	Alpine flora of Baxter State Park	Flora of Piscataquis County	33, 81, 98
34	North America	USA	Alpine flora of Elk Mountains	Flora of Colorado	34, 82
35	North America	USA	Alpine flora of Mount Hood	Flora of Clackamas and Hood River counties of Oregon State	35, 83
36	North America	USA	Alpine flora of Mount Rainier National Park	Flora of Mount Rainier National Park	36, 84
37	North America	USA	Alpine flora of Mount St. Helens	Flora of Skamania County	37, 83, 99
38	North America	USA	Alpine flora of Mount Washburn	Flora of Yellowstone National Park in Wyoming	38, 85
39	North America	USA	Alpine flora of New Hampshire State	Flora of New Hampshire State	39, 86
40	North America	USA	Alpine flora of Appalachian Mountains in North Carolina	Flora of Blue Ridge Mountains in North Carolina	40, 87
41	North America	USA	Alpine flora of Steens Mountain	Flora of Steens Mountain	41, 88
42	North America	USA	Alpine flora of Sweetwater Mountains	Flora of Mono County	42, 89
43	North America	USA	Alpine flora of Teton Range	Flora of Teton County	43, 90
44	North America	USA	Alpine flora of Vermont State	Flora of Vermont State	44, 85
45	North America	USA	Alpine flora of White Mountains	Flora of Mono County	45, 89
46	South America	Argentina	Alpine flora of Monumento Natural Abra del Acay	Flora of Salta Province	46, 91
47	South America	Argentina	Alpine flora of Parque Provincial Cumbres Calchaquies	Flora of Tucumán Province	46, 91
48	South America	Bolivia	Alpine flora of Área Natural de Manejo Integrado Apolobamba	Flora of Bolivia	46, 92
49	South America	Bolivia	Alpine flora of Parque Nacional Sajama	Flora of Bolivia	46, 92
50	South America	Bolivia	Alpine flora of Parque Nacional Tuni Condoriri	Flora of Bolivia	46, 92

51	South America	Chile	Alpine flora of Paine National Park	Flora of Region XII of Chile	47, 91
52	South America	Colombia	Alpine flora of Antioquia Department	Flora of Antioquia Department	48
53	South America	Colombia	Alpine flora of Parque Nacional Natural Cocuy	Flora of Colombia	46, 93
54	South America	Colombia	Alpine flora of Chisacá	Flora of Colombia	49, 93
55	South America	Ecuador	Alpine flora of Complejo Volcánico Pichincha	Flora of northwestern Ecuador (incl. the provinces of Esmeraldas, Carch, Imbabura, Pichincha)	46, 92
56	South America	Ecuador	Alpine flora of El Cajas	Flora of Azuay Province	50, 60, 92
57	South America	Ecuador	Alpine flora of Parque Nacional Podocarpus	Flora of Loja Province	46, 92
58	South America	Ecuador	Alpine flora of Quito	Flora of Pichincha Province	51, 92
59	South America	Ecuador	Alpine flora of Reserva Ecológica Antisana	Flora of northwestern Ecuador (incl. the provinces of Esmeraldas, Carch, Imbabura, Pichincha)	46, 92
60	South America	Ecuador	Alpine flora of Reserva Ecológica El Ángel	Flora of northwestern Ecuador (incl. the provinces of Esmeraldas, Carch, Imbabura, Pichincha)	46, 92
61	South America	Peru	Alpine flora of Cordillera de Vilcanota - Laguna de Sibinacocha	Flora of Cuzco Department (Region)	46, 94
62	South America	Peru	Alpine flora of Páramos de Pacaipampa	Flora of Piura Department (Region)	46, 94
63	South America	Venezuela	Alpine flora of Venezuela	Flora of Venezuela	52, 95

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Supplementary Table 2 Alpine floras and their species pools in broad geographical regions.

Group of alpine floras	Number of alpine species	Number of species in species pool
Temperate Asia	2314	14984
Temperate Europe	668	5318
Temperate North America	894	5996
Temperate Australia	1078	4981
Temperate Africa	435	4925
Temperate South America	331	4158
Temperate Northern Hemisphere	3665	25072
Temperate Southern Hemisphere	1839	13871
Tropical Asia	290	13347
Tropical Africa	190	8590
Tropical South America	1088	40892
Pantropic	1562	61390
Globe	6918	94161

Supplementary Table 3 The numbers of species and genera (in parentheses) for the ten largest families in the alpine floras examined in this study for each of the 12 geographic regions shown in Supplementary Table 2.

(a)

temp.Asia	temp.Europe	temp.N.America	temp.Australia
Asteraceae 305 (56)	Asteraceae 94 (40)	Asteraceae 148 (46)	Asteraceae 193 (36)
Ranunculaceae 139 (20)	Poaceae 66 (22)	Cyperaceae 77 (5)	Poaceae 133 (25)
Primulaceae 109 (6)	Caryophyllaceae 41 (13)	Poaceae 73 (23)	Plantaginaceae 78 (8)
Rosaceae 105 (23)	Rosaceae 33 (12)	Brassicaceae 51 (14)	Ericaceae 76 (19)
Brassicaceae 104 (35)	Brassicaceae 32 (20)	Rosaceae 49 (16)	Apiaceae 72 (12)
Ericaceae 103 (17)	Fabaceae 32 (10)	Ericaceae 45 (18)	Cyperaceae 64 (11)
Saxifragaceae 101 (4)	Cyperaceae 29 (4)	Fabaceae 35 (5)	Ranunculaceae 38 (4)
Gentianaceae 99 (9)	Ranunculaceae 25 (11)	Ranunculaceae 30 (12)	Juncaceae 32 (4)
Caryophyllaceae 98 (14)	Saxifragaceae 22 (1)	Orobanchaceae 29 (6)	Rubiaceae 25 (4)
Cyperaceae 97 (10)	Plantaginaceae 22 (7)	Caryophyllaceae 28 (8)	Fabaceae 21 (14)

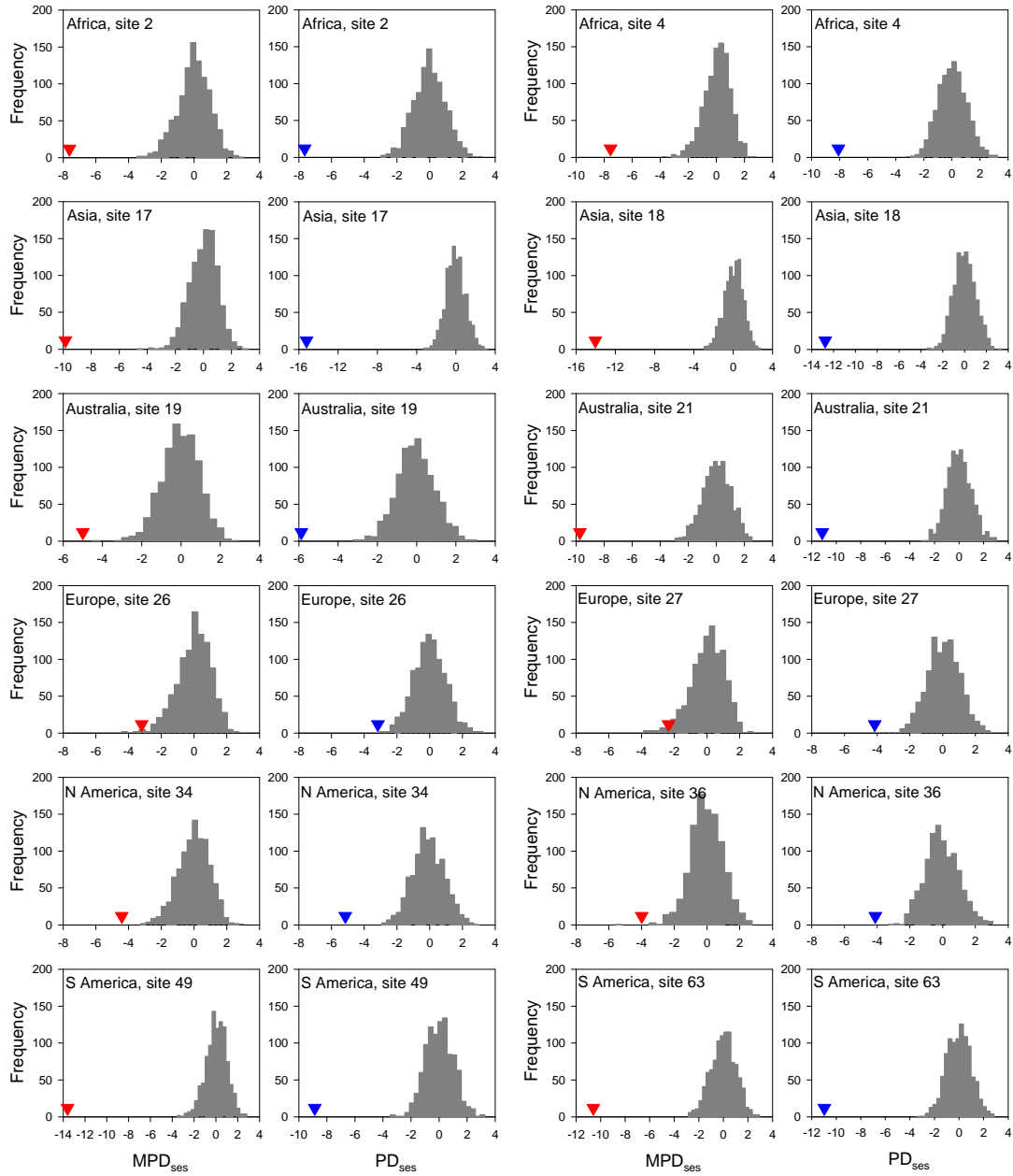
(b)

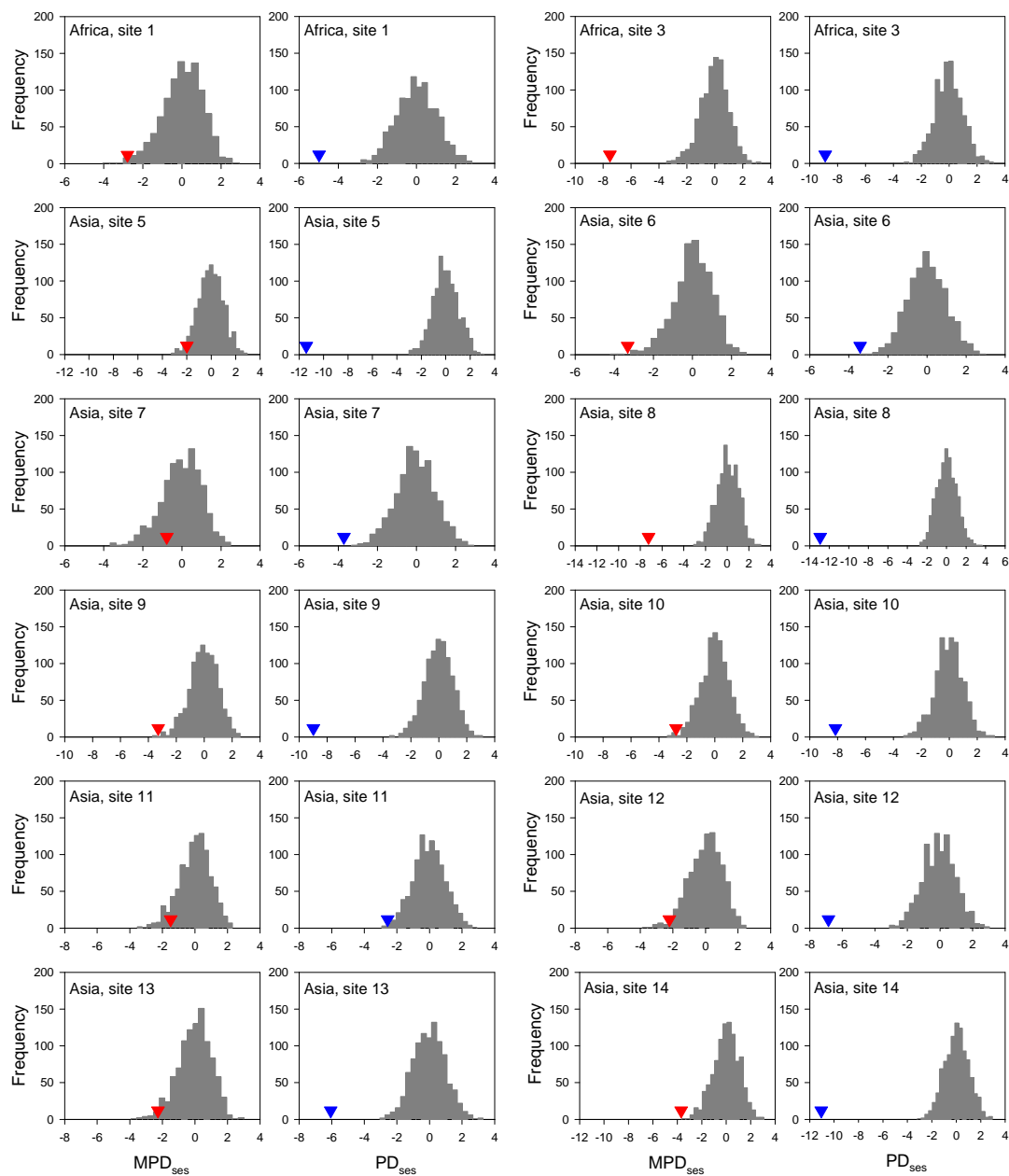
temp.Africa	temp.S.America	temp.N.hemisphere	temp.S.hemisphere
Asteraceae 107 (31)	Asteraceae 87 (29)	Asteraceae 531 (107)	Asteraceae 387 (88)
Poaceae 35 (21)	Poaceae 47 (16)	Poaceae 219 (43)	Poaceae 213 (45)
Scrophulariaceae 34 (11)	Brassicaceae 24 (15)	Ranunculaceae 186 (24)	Apiaceae 93 (22)
Iridaceae 25 (6)	Fabaceae 23 (5)	Brassicaceae 182 (52)	Ericaceae 85 (21)
Crassulaceae 24 (3)	Caryophyllaceae 18 (8)	Rosaceae 176 (28)	Plantaginaceae 83 (8)
Aizoaceae 22 (3)	Apiaceae 11 (6)	Cyperaceae 176 (10)	Cyperaceae 81 (13)
Orchidaceae 21 (10)	Rosaceae 10 (4)	Caryophyllaceae 157 (19)	Fabaceae 54 (26)
Asparagaceae 14 (8)	Ranunculaceae 10 (4)	Ericaceae 147 (28)	Ranunculaceae 52 (5)
Cyperaceae 13 (6)	Iridaceae 7 (3)	Fabaceae 143 (26)	Brassicaceae 42 (21)
Campanulaceae 13 (5)	Juncaceae 7 (3)	Saxifragaceae 141 (8)	Juncaceae 41 (4)

(c)

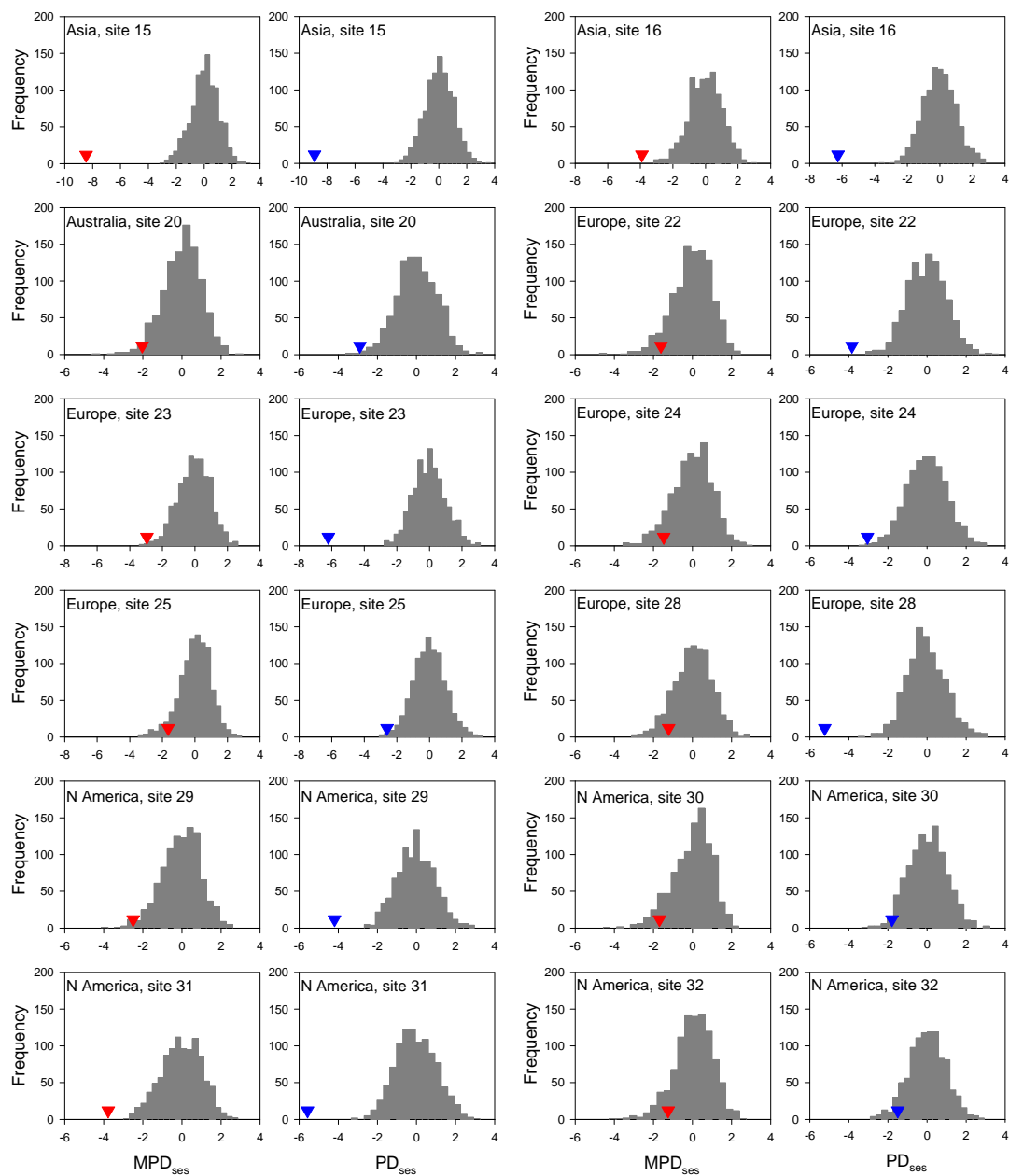
trop.Asia	trop.Africa	trop.S.America	pantropic
Asteraceae 53 (22)	Asteraceae 44 (16)	Asteraceae 244 (63)	Asteraceae 244 (93)
Poaceae 41 (13)	Poaceae 28 (13)	Poaceae 125 (32)	Poaceae 125 (43)
Ericaceae 33 (9)	Apiaceae 10 (6)	Brassicaceae 43 (12)	Ericaceae 29 (20)
Cyperaceae 19 (7)	Lamiaceae 9 (5)	Caryophyllaceae 38 (8)	Rosaceae 36 (9)
Plantaginaceae 16 (5)	Rosaceae 8 (2)	Rosaceae 36 (9)	Cyperaceae 32 (12)
Rosaceae 14 (3)	Cyperaceae 7 (2)	Orchidaceae 35 (13)	Brassicaceae 43 (15)
Ranunculaceae 12 (1)	Caryophyllaceae 7 (5)	Gentianaceae 34 (4)	Caryophyllaceae 38 (11)
Orchidaceae 11 (7)	Brassicaceae 6 (5)	Cyperaceae 32 (10)	Orchidaceae 35 (21)
Orobanchaceae 10 (1)	Iridaceae 6 (4)	Caprifoliaceae 31 (5)	Plantaginaceae 23 (10)
Urticaceae 9 (2)	Crassulaceae 6 (3)	Ericaceae 29 (12)	Apiaceae 27 (17)

Supplementary Figure 1. Standardized effect size of mean pairwise distance (MPD_{ses}, red triangles) and standardized effect size of phylogenetic diversity (PD_{ses}, blue triangles) in the 63 alpine floras examined in this study. The first twelve alpine floras included two representative alpine floras for each continent, and the remaining 51 alpine floras are shown in the rest of this appendix. Each histogram represents frequency of MPD_{ses} and PD_{ses} values derived from 999 null assemblages randomly drawn from its respective regional species pool. Details about each site are available in Supplementary Table 1.

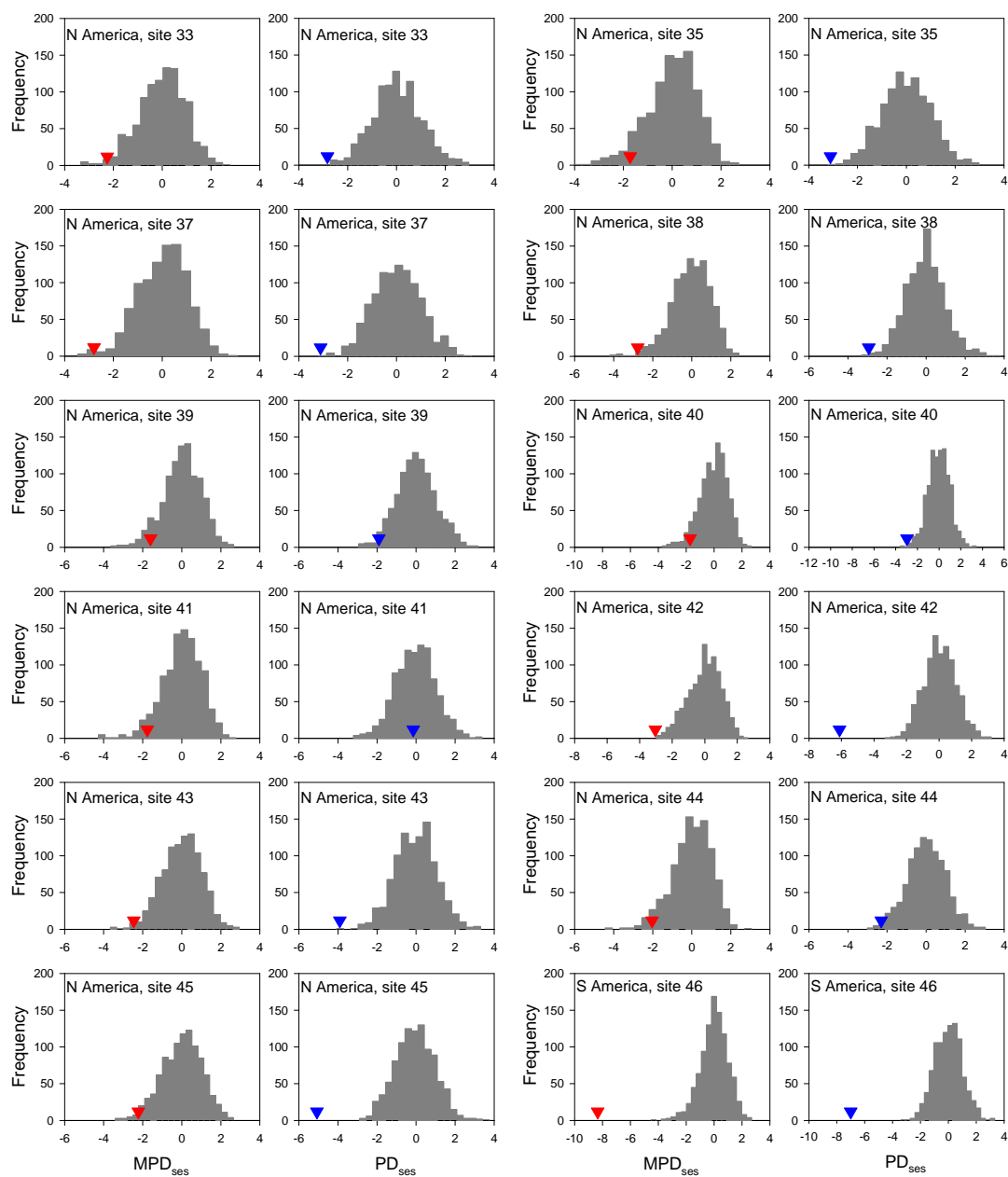




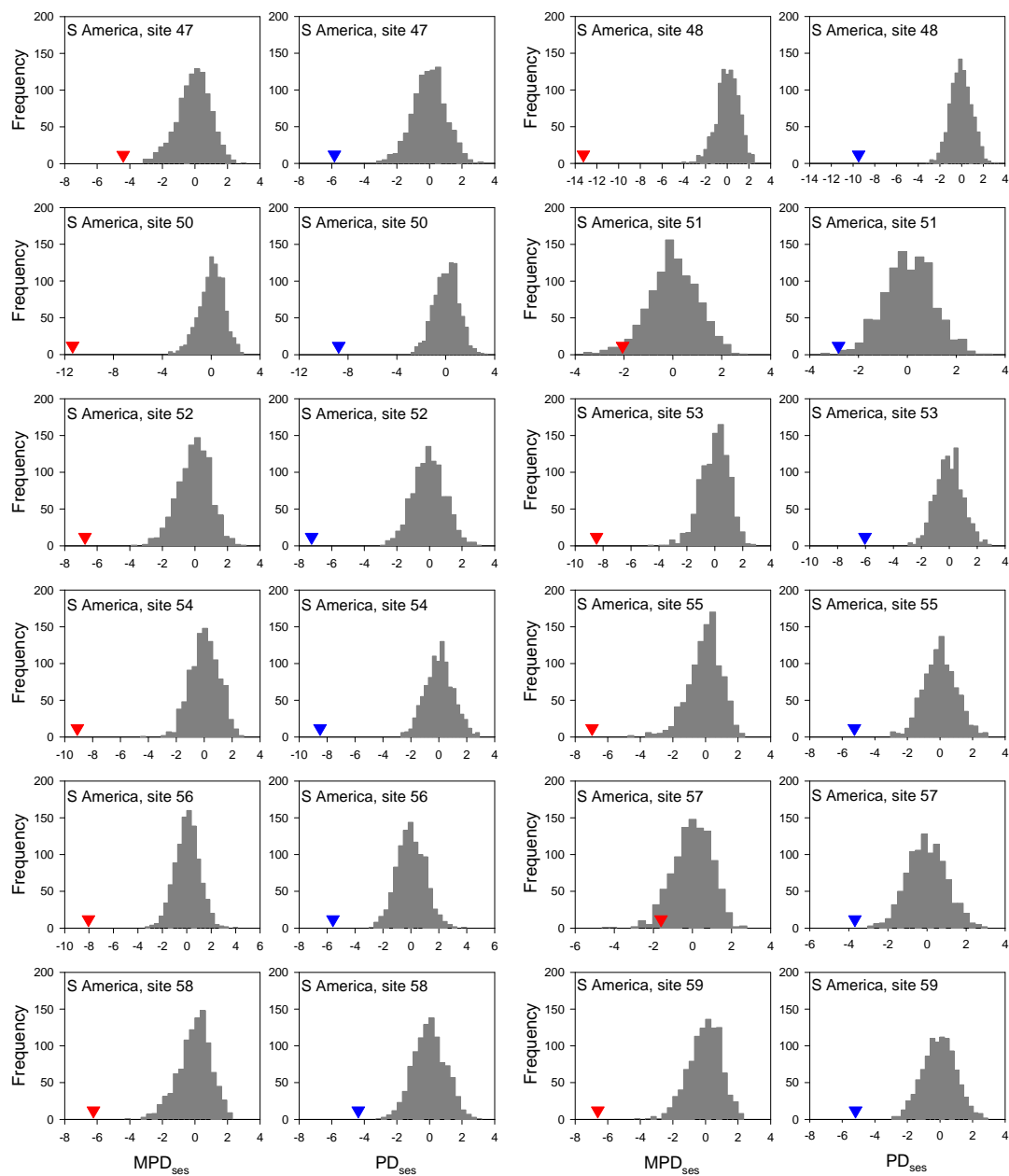
Supplementary Figure 1 (continued, 1).



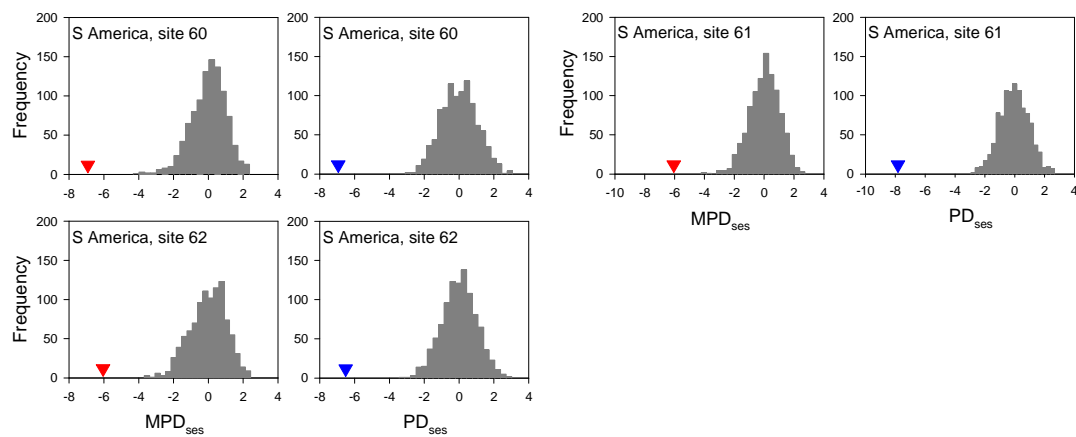
Supplementary Figure 1 (continued, 2).



Supplementary Figure 1 (continued, 3).

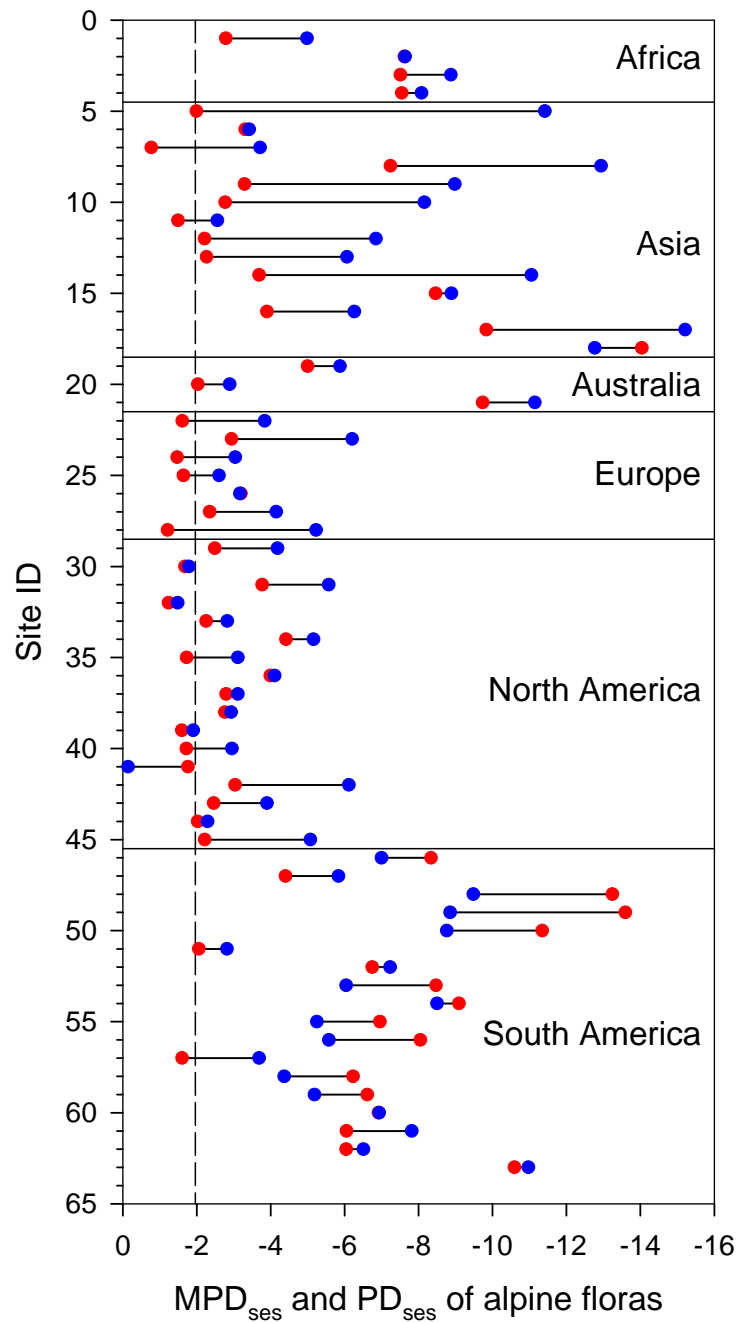


Supplementary Figure 1 (continued, 4).



Supplementary Figure 1 (continued, 5).

Supplementary Figure 2. Standardized effect size of mean pairwise distance (MPD_{ses} , red dots) and the standardized effect size of phylogenetic diversity (PD_{ses} , blue dots) for the 63 alpine floras examined in this study. Each pair of dots represents an alpine flora. The dash line represents -1.96 of MPD_{ses} and PD_{ses} .



Supplementary Figure 3. Relationships between growing degree days (GDD) and standardized effect size of mean pairwise distance (MPD_{ses}) for (a) species in alpine floras with MPD_{ses} being calculated using the regional species pool of each of the alpine floras, (b) species in alpine floras with MPD_{ses} being calculated using the global species pool of angiosperm species in The Plant List (Methods), (c) species in alpine floras with MPD_{ses} being calculated using all species in the 63 alpine floras as a species pool, and (d) species in the regional floras of the alpine floras with MPD_{ses} being calculated using the global species pool of angiosperm species in The Plant List. GDD for each site represents the average value of annual growing degree days above 5°C calculated for an area of nine squares of half-degree latitude and longitude (with the centroid of the focal site being located in the center square of the frame work of 3 by 3 squares) using climate data obtained from IIASA (<https://iiasa.ac.at>). GDD was standardized to vary from 0 to 1. Lines are linear least squares best fits; we used them to show linear trends, not for statistical tests.

