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Investigating the Potential Effect of Pollinators on the Alpine Plant Diversity of the Southern Rocky Mountains: A Community Phylogenetic Approach

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Investigating the Potential Effect of Pollinators on the Alpine Plant Diversity of the Southern Rocky Mountains: A Community Phylogenetic Approach

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Advised by Dr. Hannah Marx

Abstract

The alpine plant community can be surprisingly diverse when compared to surrounding lowland areas, however, the drivers of this diversity remain understudied. In this study, the floral morphology of alpine plant species was used to determine their pollination syndrome and identify their major pollinator group. Given the pollination syndromes and a phylogeny containing the members of the alpine plant community, a phylogenetic community analysis was used to assess patterns of overdispersion or clustering in alpine plant communities of eight mountain summits across the southern Rocky Mountains. Across all summits bee pollination was the most common assigned syndrome for sampled species, followed by a combination of wind and fly. For all of the summits, there was no significant pattern of overdispersion or clustering in the phylogenetic community structure with respect to pollination syndromes. Therefore, it is likely that the major pollinator groups, identified through pollination syndromes, are not driving the diversity of the alpine plant community. Further study is necessary to determine what biotic or abiotic factors may or may not be driving the diversity of the alpine plant community. To better understand all possible factors contributing to the diversity of alpine plants in the southern Rocky Mountains, future studies should consider the effects of a wider range of ecological and environmental factors on the alpine plant community, and also the geologic and glacial history of a region, and should perform direct observation of floral visitors to remove the possible ambiguity inherent to pollination syndromes.

Introduction

The alpine life zone consists of high elevation land mass that occurs above the treeline in mountainous regions and is characterized by its extreme abiotic conditions and short growing season (Körner, 2023). Despite its extreme environment, the alpine is host to an astoundingly diverse plant community, whose members vary greatly in their floral morphology, including flower color, shape, size, and structure (Körner, 2023; Peng et al., 2012). Such diversity in floral morphology would imply the importance of animal pollinators (Peng et al., 2012) rather than wind pollination, which would be characterized by a high number of small, discrete flowers arranged in a spike or panicle (Culley et al., 2002). However, in high-alpine ecosystems defined by extreme abiotic conditions the role of diverse animal pollinators for structuring plant biodiversity has not been thoroughly investigated.

Previous detailed studies on pollinator visitation have established the effects of pollinator fauna on floral traits at both the species level and community level in alpine environments. Studies focused on the effects of pollinators on floral traits of individual alpine plant species from different geographic regions concluded that pollinator mediated selection can impose directional selection on floral traits (Galen, 1989; G. Zhang et al., 2017). Specifically, in the Rocky Mountain region one study found that bumblebees exerted a positive selective pressure on multiple floral traits in *Polemonium viscosum*, including the length and diameter of the corolla as well as the stem height *(Galen, 1989)*. At the community level, a study in the Rocky Mountains found that flower color shifted across an elevation gradient suggesting the influence of biotic drivers behind this trend (Gray et al., 2018). Across geographic regions, a study comparing differences in dominant flower color between alpine plant communities in Japan and New Zealand found that the alpine plant communities found in New Zealand, which were dominated by fly pollination had an increased occurrence of white flower, while the alpine plant communities found in Japan, which were dominated by bee pollination, had an increased occurrence of yellow flowers (Ishii et al., 2019a). Beyond these studies, we have much to learn about how pollinators influence the assemblance and maintenance of plant diversity across alpine summits, despite the importance of pollinators for ecosystem services (Ollerton, 2017).

Pollinators could affect the biodiversity of alpine plant communities through different mechanisms. Alpine plants with floral traits that are unable to attract available pollinators will be at a competitive disadvantage to other plant species that have floral traits that can attract the available pollinators. Therefore, pollinators can influence the presence of a species in a community depending on their floral traits (C. A. Johnson et al., 2022). This is particularly important as climate change is already causing mismatches between plant-pollinator networks (Gérard et al., 2020). As these mismatches occur, it is likely that alpine plant species will experience shifts in pollinator availability. The acquisition of these new pollinators would exert a novel selective pressure on alpine plants, which could lead to rapid evolutionary change (Mackin et al., 2021). It is important then to understand which pollinators are commonly found across alpine summits in the southern Rocky Mountains and how these pollinators have and are shaping the alpine plant community, to provide a baseline for comparison as the communities love in response to a warming climate.

In the absence of detailed observational data on pollinator visits, pollination syndromes offer a method to identify the major pollinator group of a flowering plant species (Willmer, 2011). Since angiosperms (flowering plants) rely on their flowers for reproduction, floral morphology is highly susceptible to selective pressures imposed by any biotic or abiotic factor that influences reproductive success. Flowering plants are particularly dependent on animal pollinators and therefore floral morphology is largely governed by what does or does not attract a specific animal pollinator (Ollerton et al., 2011). This reliance on animal pollinators has led many flowering plants to coevolve with their pollinators and develop distinct floral morphologies that are specialized to attract a distinct pollinator or group of pollinators (Willmer, 2011). Given that related groups of animal pollinators share similar evolutionary biases, distantly related plant groups have converged on similar floral morphologies to target the same pollinator group (Willmer, 2011). These convergent morphologies are classified as pollination syndromes and can be used to predict a plant species' major pollinator group based on its shared set of floral traits (Willmer, 2011).

Recent studies have tested the validity of pollination syndromes and have determined that syndromes are capable of predicting a plant's major pollinator group, with a couple of limiting caveats. First, syndromes can not account for multiple pollinators and/or a pollinator network. Second, the traits included in the syndrome definition greatly affects the syndrome's accuracy (Dellinger, 2020; Rosas-Guerrero et al., 2014). However, given the difficulty of conducting comprehensive direct observational study of floral visitors across multiple alpine peaks, pollination syndromes can be used as a proxy for pollinators, if their limitations are accounted for.

In this study, we used floral trait morphology to identify pollination syndromes and assessed how the diversity of pollination syndromes relates to the diversity of alpine plant communities on mountain summits. To do so, we ask two main questions. First, do we observe specific pollination syndromes on different alpine summits? If so, is the diversity of plant communities on alpine summits driven by certain pollination syndromes, which might indicate the importance of specific major pollinator groups in the structuring of floral diversity? We addressed these questions using a community phylogenetic approach. If there is no association with pollination syndromes in alpine communities, we expect species-specific pollination syndromes to be randomly distributed across the alpine plant community phylogeny. Alternatively, if pollination syndromes structure alpine summit communities, we expect to see significant patterns of phylogenetic structure in these traits (pollination syndromes will be clustered or overdispersed in alpine summit communities).

Methods

Study System

This study focused on alpine summit communities across the southern Rocky Mountains, United States. Alpine habitat was defined as all land mass that occurred above treeline on mountain summits (Körner, 2023; Testolin et al., 2020). Alpine summits share a harsh abiotic environment that hosts a diversity of micro-habitats with varying vegetation density. Habitats range from grassy meadow-like areas dominated by graminoids and forbs, to rocky talus slopes with sparse vegetation constricted to isolated pockets on the rock face. Alpine summit communities were selected based on the number of previous vouchered plant collections, and precedence was given to sites that had little to no former collections. Summits sampled were located in both southern Colorado and northern New Mexico, including sites in the San Juan Mountains (Cumberland Mountain, UN12334 - SJ1, Gibbs Peak), Latir Wilderness (Venado Peak, Baldy Mountain), Taos Ski Valley (Kachina Peak, Lake Fork Peak), and the Northern Sangre de Cristo Mountains (Simmons Peak). A map of collection sites is provided in Figure 1.

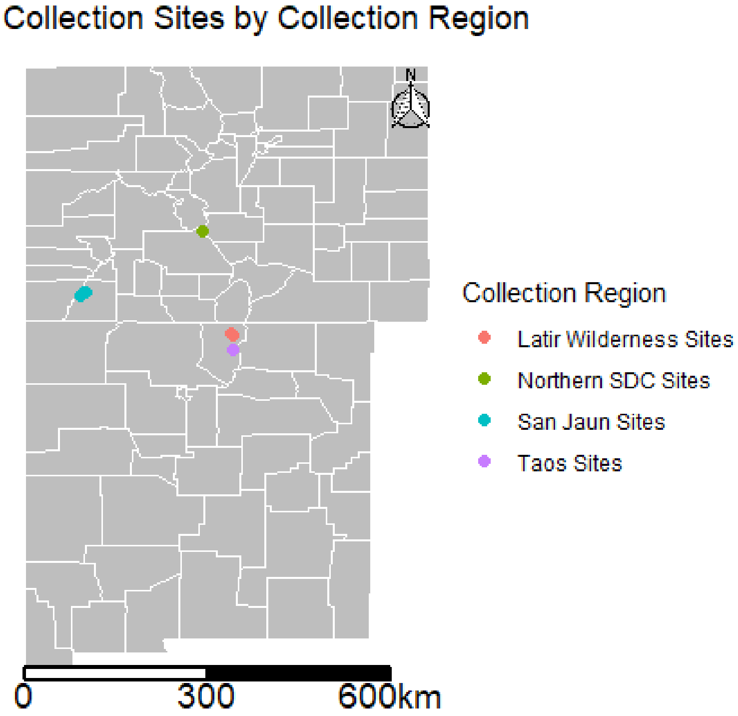

Figure 1: Map of 2022 collection sites across New Mexico and Colorado, organized by collection region.

Specimen Collection & Identification

On each alpine summit community all vascular plants were surveyed and collected to record present biodiversity. Voucher specimens were collected during multiple trips throughout the alpine growing season in 2022, from the beginning of July to the middle of August. Surveying was only conducted above treeline and when safe all aspects of the peak were sampled to provide the most representative sampling possible. Surveying started at the peak, and after the aspects were observed, one voucher specimen representing each species was collected along a spiral path from peak to treeline. Vouchers were collected in flower following best collection practices for herbarium preservation (G. M. Johnson, 2019; Marx et al., 2019). The identity of each specimen was determined using regional floras (Allred, et al., 2020, Ackerfield et al., 2015).

Syndrome Identification

The pollination syndrome for each unique vascular plant species collected across all alpine summits (alpine plant species pool) was defined using specific combinations of floral traits determined by previous studies (Rosas-Guerrero et al., 2014; Willmer, 2011). Pollination syndromes that were considered included bee, fly, butterfly, moth, beetle, bird, and bat. The specific trait combinations used to determine each pollination syndrome are given in Table S2. Traits considered included floral color, floral base color, floral symmetry, showiness of the blossom, fusion of petals, shape of the corolla, structural blossom class, length of the corolla tube, width of the corolla, flower size, presence or absence of spur, presence or absence of nectar guide, orientation of the blossom, and inflorescence type. These traits include those associated directly with the defined pollination syndromes, traits included in an attempt to improve subsequent statistical analyses, and discrete traits used to define categorical traits. floral color, showiness of the blossom, fusion of the petals, shape of the corolla, structural blossom class, presence or absence or spur, orientation of the blossom, and inflorescence type were determined through visual observation. Ccorolla tube length was measured in millimeters from the mouth of the corolla to its most distal point. corolla width was measured in millimeters across the maximum width of the corolla. Bbase flower color was determined as the more general form of the floral color to limit the potential values that floral color produced. presence or absence of nectar guides was determined using UV imaging following the protocol defined by Koski and Ashman (2013).

To test the accuracy of the considered traits for sorting species into pollination syndromes, a Multiple Correspondence Analysis (MCA) was performed on the floral characteristics identified using the R package FactoMineR (Version 2.9; Husson et al., 2017). Before being input into the MCA, the effect of missing values was accounted for and negated by developing a disjunct table produced by the estim_ncpMCA function included in the R package MissMDA (Version 1.19; Josse and Husson, 2016). This analysis groups individuals by similarity of input values. In the context of floral traits, MCA analysis attempts to group traits that commonly occur together and determine which traits best explain the variance in the data. With this analysis a relatively unbiased grouping of the plant species can be performed based on their floral traits. MCA plots were developed in ggplot2 (Version 3.44; Wickman 2016) using the coordinate information for each species output by the function MCA. Each point representing a species was grouped by the assigned pollination syndrome of that species and 0.95 confidence level stat ellipses were drawn. The groups built by MCA analysis can then be compared to the assigned pollination syndromes to determine the sorting accuracy of the assigned pollination syndromes.

Community Phylogeny , Phylogenetic Metrics, and Statistical Analyses

To understand the evolutionary relationships among plants collected across all alpine summits (alpine plant species pool) , we used a supertree approach to obtain phylogenetic relationships. A phylogeny that includes all collected species was obtained using the V.PhyloMaker2 package (Version 0.1.0; (Jin & Qian, 2022). The V.PhyloMaker2 package pulls from the GBOTB phylogeny (Smith and Brown 2018), a mega tree that is a conglomerate of phylogenies built in prior studies. The package allows you to select only species of interest and outputs a phylogeny including only those species. Species that were not included in the GBOTB phylogeny the new tip associated with the missing species was bound to a randomly selected node at and below the genus or family level basal node.

To address our questions about the influence of pollinators on community structure, we measured the phylogenetic structure of pollinator syndromes assigned to each species collected on every summit community using Mean Phylogenetic Distance (MPD). MPD is a measure of the average pairwise distance between all member taxa of a phylogeny. and Iin this study both the phylogenetic and trait distances were taken into consideration (Cadotte et al., 2013). To calculate MPD we first developed a community matrix that recorded the presence or absence of each species on all sampled summits. For each summit this produced a string of 0s and 1s, where 0 indicates the absence of a particular species and 1 indicates the presence of a particular species. The function pez.dispersion that is included in the R package pez (Version 1.2-4; Pearse, et al., 2015) was used to calculate the standard effect size of MPD for each summit. The standard effect size of MPD for each summit was calculated by comparing the observed MPD for each summit to a randomly generated community assemblage whose members were pulled from the total species pool. This process was repeated for 1000 iterations. The relative contribution of pollination syndromes on phylogenetic structure was assessed using different weighting values for the traitigram argument, ranging from 1 to 0, where 1 only considers phylogenetic contribution and 0 only considers trait contribution (Cadotte, et al. 2013). To visualize how the standard effect size of MPD for each summit varied over the different weighting coefficients (0, 0.25, 0.5, 0.75, 1.0), the standard effect size of MPD was plotted against the weighting coefficients.

Calculating species turnover allowed us to understand the relative similarity between the plant communities on different summits, and if this matched the expectations set out in previous studies, regarding geographic distance. We incorporated geographic distance to test whether nearby summits hosted more similar plant communities than distant summits. Similarity of the plant species across different summits was assessed using the Sorensen similarity coefficient calculated by the function phylosor provided in the R package pez (Version 1.2-4; Pearse, et al., 2015) and the effect of Euclidean geographic distance between peaks on the metric was determined using a line plot developed in ggplot2 (Version 3.44; Wickman 2016).

Figures were made with ggplot2 (Version 3.44; Wickman, 2016) and ggtree (Yu et al., 2017). All statistical analyses were performed using the R software (Version 4.3.1; R Core Team, 2022)**.**

Results

Specimen Collection & Identification

A total of 553 voucher specimens were surveyed and collected across all eight summits representing 162 unique vascular plant species. To assess the species richness across the sampled summits the species total taxa for each summit was compiled in Table S5. The total number of taxa sampled across the summits ranged from 48 taxa on Gibbs Peak to 87 taxa on Baldy Mountain. A community indicating the presence and absence of specific species for each summit pulled from the total species pool is given in Table S6. Collection vouchers were submitted to the UNM Herbarium and a list of voucher specimens with associated detailed collection information is provided in Table S1.

Syndrome Identification

To assess the diversity of pollination syndromes across the sampled summits we assigned pollination syndromes to all 162 vascular plant species, and summarized the number of species assigned to each syndrome across each eight alpine summit communities sampled. A table containing the floral characteristics and syndrome determinations assigned to each species in this alpine plant community for the collected specimens is provided in Table S3**.** In cases where there was a conflict between assigning syndromes, the literature was consulted and also noted in Table S3. The syndrome totals for all sampled species are given is Table S4. Across all of the summits the number of species assigned to animal pollinated syndromes was greater than the number of species assigned to wind pollination syndrome. Additionally, across all summits the bee pollination syndrome was the most common syndrome identified, followed by either the fly or wind syndrome. Butterfly, moth, beetle, bird, and bat syndromes were not found to be supported by the traits investigated. Results are summarized in Figure 2.

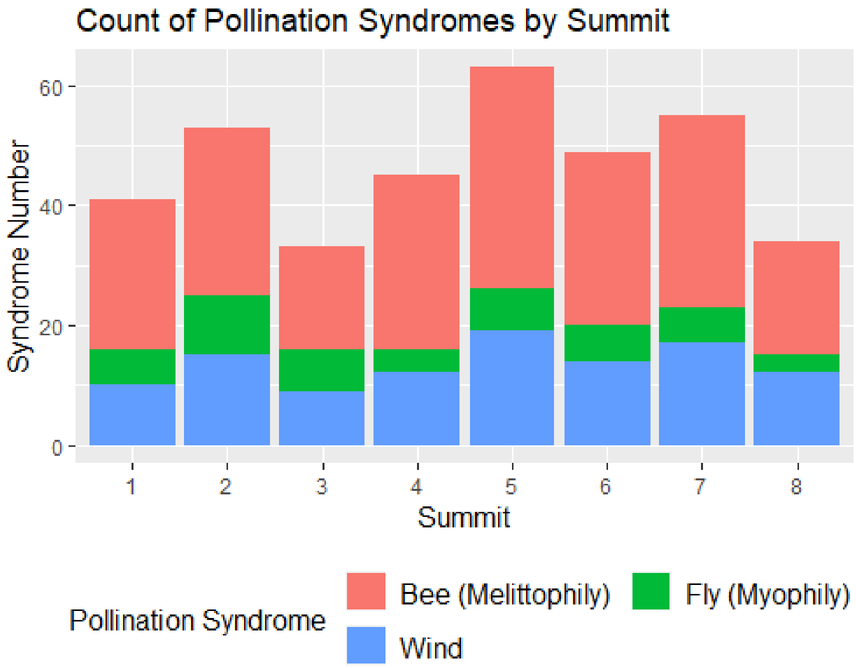

Figure 2: The number of species on each peak grouped by their assigned pollination syndrome. From left to right peaks are numbered by the temporal order in which they were sampled (1. Cumberland Mountain, 2. UN12334 - SJ1, 3. Gibbs Peak, 4. Venado Peak, 5. Baldy Mountain, 6. Lake Fork Peak, 7. Kachina Peak, 8. Simmons Peak).

Multiple Correspondence Analysis

None of the three pollination syndromes present after trait scoring are completely independent of each other (Figure S2). The wind pollinated species are most discretely defined with the majority of the species assigned the wind pollination syndrome clustering together. The species assigned either the bee or fly pollination syndrome have significant overlap. The 0.95 significance level stat ellipse for the species assigned fly pollination falls entirely within the 0.95 confidence level stat ellipse for the species assigned fly pollination.

Community Phylogeny, Phylogenetic Metrics, and Statistical Analyses

92 alpine plant species were present in the GBOTB phylogeny, and 70 species were added to the tips/branches. Figure 3 shows inferred phylogenetic relationships among our study species pool and corresponding assigned pollination syndromes.

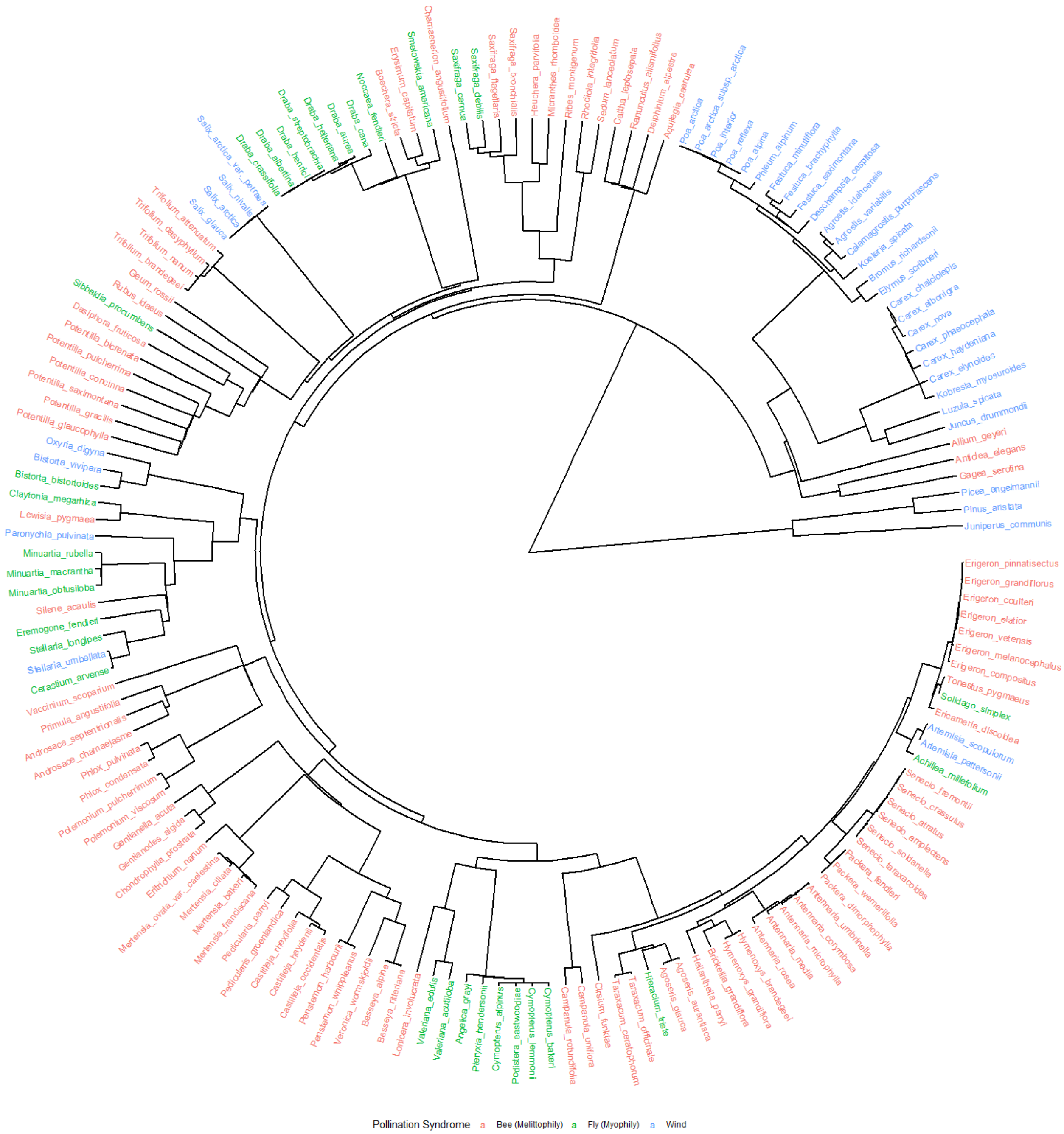

Figure 3: Phylogeny of whose members include all alpine plants sampled from all eight summits throughout the south Rocky Mountains. Phylogenetic relationships were inferred using the GBOTB phylogeny included in the R package V.PhyloMaker2. Species not represented in the GBOTB phylogeny were added to the phylogeny using scenario.2, as described in the methods.

Phylogenetic Metrics: Mean Phylogenetic Distance

None of the eight sampled summits showed a significant pattern of phylogenetic structure represented by the standard effect size of MPD with respect to pollination syndromes ($|z| < 1.96$, $p > 0.05$).

Therefore, for all of the sampled summits the distribution of plant species paired with their pollination syndromes is not significantly different from a phylogeny with members randomly selected from the overall species pool, suggesting that pollinators are not structuring the community. The results for all of the communities are summarized in Figure 4.

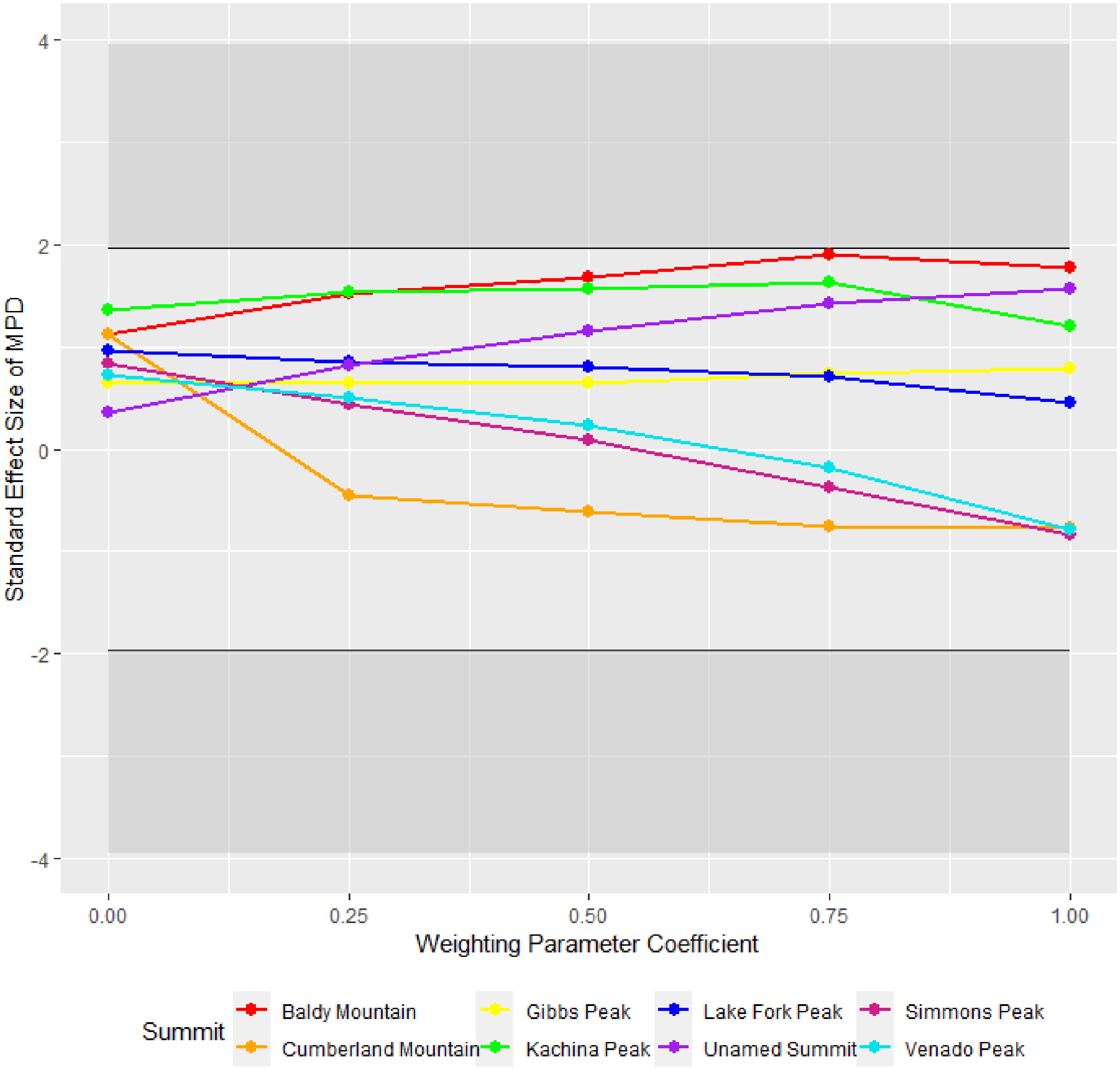

Figure 4: Standardized effect size of MPD for each summit considering different phylogenetic and trait contributions (traitigram weighting coefficients of 0, 0.25, 0.5, 0.75, 1). Weighting coefficients closer to 1 return metrics with a higher phylogenetic contribution than trait contribution, while weighting coefficient values closer to 0 return metrics with a higher trait contribution than phylogenetic. None of the summits across any of the weighting coefficients had significant deviation in MPD from a randomized null ($|z| < 1.96$, $p > 0.05$). The range of the standardized effect size of MPD across all the summits becomes greater with increasing phylogenetic contribution.

Phylogenetic Metrics: Sorenson Metric

The relationship between the Sorensen Metric, which is a measure of the beta diversity between two individual summit communities and the distance between the peaks is shown in Figure 5. Although the results are not significant ($p > 0.05$) There is a slight negative trend in the Sorenson Metric with increasing distance between peaks ($m = -1.527$), meaning that as the distance between peaks increases the similarity of the alpine plant community between the peaks decreases. This trend supports the expectation that the species richness of plant communities on nearby summits are more similar to one another than plant communities of distant summits.

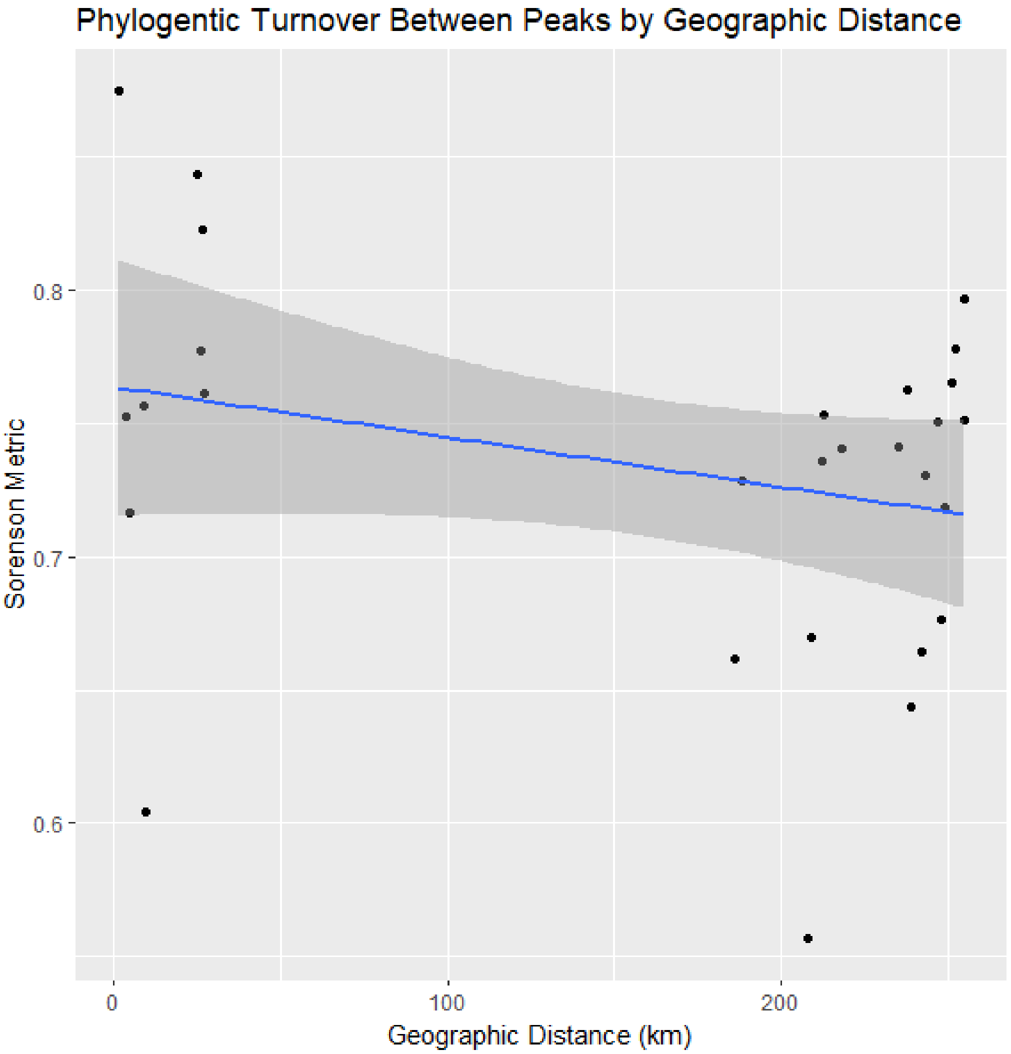

Figure 5: Plot showing the relationship between the Sorenson Metric between peaks and the euclidean geographic distance between peaks with a regression line included ($y= 0.764 - 1.53x$, $R^2 = 0.082$, $p = 0.139$).

Discussion

In this study we aimed to understand how the diversity of pollination syndromes affects the alpine plant community of mountain summits across the southern Rocky Mountains. We approached this question through a community phylogenetics approach by quantifying patterns of phylogenetic community structure with respect to pollination syndromes using MPD. To determine the phylogenetic and trait contributions to MPD, MPD was calculated across various weighting values. Finally, the similarity in plant communities across the eight peaks was assessed with respect to geographic distance, to determine if plant communities of nearby summits are more or less similar than distant summits.

In the absence of detailed observations of pollinator visits across our study area, we assigned major pollination syndromes to each alpine plant species. According to the MCA run using the floral traits of all sampled seed plant species, there is some form of overlap for all three of the observed syndromes (Figure S2). The majority of graminoids assigned to wind pollination syndromes cluster together independent from the non graminoid species assigned wind pollination syndromes due to the distinct floral morphology of this lineage. The non graminoid wind pollinated species appear to cluster more closely with species assigned to fly pollination, most likely due to the fact that both wind and fly pollinated species were defined by small and relatively inconspicuous flowers (Table S2). Additionally, the fly pollination syndrome had complete overlap with the bee pollination syndrome. There are several possible explanations for this degree of overlap. One possible reason is that the bee pollination syndrome, as defined in the literature, has the broadest set of defining floral traits, and when compared to the fly pollination syndrome, the majority of traits that define the fly pollination syndrome also define the bee pollination syndrome.. This overlap in syndromes represents one of the major restrictions for using broadly defined pollination syndromes, in that they attempt to assign only a single major pollinator group to a plant species. However, plant reproductive strategies exist along a spectrum, ranging from specialists that target a single pollinator to a more relaxed generalist approach to attract a multitude of potential pollinators (Willmer, 2011). Therefore, pollination syndromes can not easily predict the pollinators of generalist species that use floral traits easily recognized by multiple major pollinator groups and the corresponding pollinator networks produced by the visitation of multiple potential pollinator groups. To resolve this ambiguity, future studies should prioritize the use of observational study to determine the identity and frequency of insect visitors to each sampled species. In the absence of direct observational study, increasing the breadth of floral traits used to define the pollination syndromes could improve their predictive capabilities (Dellinger, 2020).

Based on floral trait assignments and consulted literature for plant species with known pollinators, the bee pollination syndrome was the most common pollination syndrome observed across all the sampled summits. This suggests that bee pollination could be the most utilized pollination method for alpine plants in the study region of the southern Rocky Mountains. Being able to determine the dominant major pollinator group of alpine plants occurring in the southern Rocky Mountains would further our understanding of the global trends in alpine pollinators. Prior research conducted in the French Alps (Lefebvre et al., 2018), the Remarkables Range of New Zealand (Ishii et al., 2019b), and the Tateyama Range of Japan (Ishii et al., 2019b), has shown that alpine pollinators are not universal, and the prevalence of specific alpine pollinators varies geographically, altitudinally, and temporally. To fully understand the pollinator community of the southern Rocky Mountains, future studies should focus on determining any additional patterns of geographical, altitudinal, temporal, or trophic partitioning of pollinators in alpine communities.

The results of the phylogenetic metrics analysis show that there is no significant pattern of phylogenetic structure across any of the eight summits with respect to pollinator syndromes. This lack of pattern indicates that pollinators are not playing a major role in driving the diversity of the alpine plant community. Instead, it is possible that other biotic or abiotic driver besides pollinators is responsible for the diversity of alpine plant communities in the southern Rocky Mountains, or that the diversity of alpine plants is due to neutral processes. Other climatic and non-climatic factors have already been shown to have significant effects on the diversity of plant communities in montane regions (Liang et al., 2023). Additionally niche and neutral processes can have significant effects on the diversity of plant communities and that plant communities dominated by different growth forms are driven by different processes, specifically that the aggregation of herb and shrub dominated communities were strongly affected by niche processes (Jiang et al., 2022). To better understand the degree to which other ecological or environmental drivers may be driving alpine plant diversity in the southern Rocky Mountains and whether niche or neutral processes are having more of an effect on the aggregation of the alpine plant community, future study should consider the effects of additional ecological and environmental factors on community diversity.

Even though none of the standard effect sizes of MPD reaches a significant level of clustering or overdispersion, it appears that with increasing phylogenetic contribution, the range of MPD standard effect sizes increases. When only the diversity of trait values is considered, with a weighting coefficient of 0, all of the summits have communities that trend towards similar levels of overdispersion, indicating that the diversity of pollination syndromes alone across the summits are similar. The increased range of the standard effect sizes of MPD when only phylogenetic diversity is considered in the calculation of MPD standard effect size, indicates that summits are not taxonomically homogenous and that individual summits have their own unique trends of phylogenetic structure. With no overarching patterns of overdispersion or clustering, it is possible that local factors are having a more significant impact on the plant communities of individual summits than regional factors.

The increase in the turnover of plant species across the eight summits with increasing geographic distance, supports the findings of prior studies that found that biological similarity typically decreased with geographic distance (Soininen et al., 2007). This relationship is more ambiguous in montane regions, with studies finding that species turnover does increase with increasing geographic distance (Lenoir et al., 2010; W. Zhang et al., 2016), but that the glacial and geological history of a particular mountain range can influence the rate of turnover between plant communities (Lenoir et al., 2010). These studies highlight the need to not only consider the effects of a wider range of ecological and environmental factors on the alpine plant community, but also how the geologic and glacial history of a region may leave lasting impressions on patterns of community diversity.

By using assigned pollination syndromes as a proxy for pollinators, we have found that pollinators are not having a significant impact on the diversity of the alpine plant community, since there are no significant levels of overdispersion or clustering in the standard effects size of MPD across any of the eight summits. We found that overall, that the bee pollination syndrome was the most common assigned pollination syndrome for the southern Rocky Mountains, followed by the wind pollination syndrome and by the fly pollination syndrome. According to the MCA all three observed syndromes had some degree of overlap, indicating the need to include additional floral traits to achieve the accurate sorting of species. Future studies should prioritize the direct observation of floral visitors to remove any possible ambiguity introduced by pollination syndromes. Future studies should also account for the effect of additional ecological and environmental variables on community diversity, while also considering the geological and glacial history of the region.

Supplemental Data

Link to Google Sheet with Tables: Collected Supplemental Tables
Link Google Doc with Figures: Collected Supplemental Figures

Table S1: Table containing the information for voucher specimens deposited at the University of New Mexico Herbarium, a division of the Museum of Southwestern Biology. The catalog number, family, scientific name, taxon ID, and locality information of the specimen are included.

Table S2: Table representing the trait combinations used to define each pollination syndrome considered in this study. Syndrome definitions were retrieved from the literature (Rosas- Guerro et al., 2014; Willmer, 2011). In total 10 syndromes were defined.

Table S3: Table containing the scored trait values for all measured species and the corresponding assigned pollination syndrome.

Table S4: Table containing syndrome totals for all measured specimens.

Table S5: Species totals across the sampled summits.

Table S6: Table containing the presence or absence of each sampled species by summit.

Table S7: Table containing the MPD values calculated across all weighting coefficients for all sampled summits.

Table S8: Table containing the euclidean geographic distance between each summit sampled and the Sorensen Metric for each peak pair.

Figure S1: MCA results run on the floral traits of all present seed plant species. Individual points represent individual species. Species have been grouped by assigned pollination syndrome and stat ellipses with a 0.95 confidence level have been drawn.

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