Floral colour versus phylogeny in structuring subalpine flowering communities

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The relative number of seeds produced by competing species can influence the community structure; yet, traits that influence seed production, such as pollinator attraction and floral colour, have received little attention in community ecology. Here, we analyse floral colour using reflectance spectra that include near-UV and examined the phylogenetic signal of floral colour. We found that coflowering species within communities tended to be more divergent in floral colour than expected by chance. However, coflowering species were not phylogenetically dispersed, in part due to our finding that floral colour is a labile trait with a weak phylogenetic signal. Furthermore, while we found that locally rare and common species exhibited equivalent floral colour distances from their coflowering neighbours, frequent species (those found in more communities) exhibited higher colour distances from their coflowering neighbours. Our findings support recent studies, which have found that (i) plant lineages exhibit frequent floral colour transitions; and (ii) traits that influence local population dynamics contribute to community structure.

**Keywords:** ecological character displacement; floral colour; phylogenetic community structure; pollinator competition

1. **INTRODUCTION**

Floral colour is thought to play an important role in the attraction of pollinators to patches and may mediate competition or facilitation for pollinators within patches (Levin & Anderson 1970; Ghazoul 2006). Indeed, colour is among the most recognizable signals in the identification of ‘pollination syndromes’ relating to the perception and preference of pollinators (Faegri & van der Pijl 1979; Gumbert 2004; Lazaro et al. 2008). For example, blue is typically associated with bee pollination, while red floral colour is related to hummingbird pollination (Faegri & van der Pijl 1979). Whether coflowering species exhibit similar or divergent pollination syndromes has received little attention (but see Armbruster 2002). While a disproportionate number of species with a similar pollination syndrome may indicate the prevalence of a certain pollinator guild (Sargent & Vamosi 2008; Arnald et al. 2009), it may also lead to pollinator competition (Caruso 2000; Botes et al. 2008). Therefore, if pollinators do not exhibit fidelity to a particular species (i.e. are generalist), the neighbouring coflowering community influences the fitness associated with a particular floral trait and can thus potentially influence the evolution of floral traits and pollination syndromes.

Plant species that do not adhere closely to any particular syndrome (i.e. generalists that employ a variety of pollinators) can still be effectively pollinated if pollinators are relatively constant in their attentions to a particular species within a single foraging bout (i.e. they exhibit floral constancy). While floral constancy has been observed to break down when coexisting species have similar floral colours (Chittka et al. 1999), more attention has been paid in community-level studies to traits such as inflorescence height, nectar production, corolla length, corolla width and flower number (Waddington 1979; Peti & Freeman 1995; Caruso 2000; Jordan & Harder 2006; Rodriguez-Girones & Santamaria 2007). The relative neglect of the role of floral colour may arise due to complexities in including the entire perceptual range of pollinators (300–660 nm, Altshuler 2003). Many previous studies investigating floral colour in natural communities (Weiss 1991; Wilson & Stine 1996; Bosch et al. 1997; Jones & Reithel 2001; Schemske & Bierzychudek 2001; Ishii 2006) have measured colour exclusively with the human perception of colour (e.g. chroma/hue metrics, wavelength range: 420–600 nm) and thus may be categorizing some species as similar when, from a pollinators perspective, they are quite different.

While many plant competition studies examine processes of competition in terms of growth rates (Cahill et al. 2008), the outcome of competition is often determined in subsequent generations by the relative number of viable seeds produced by competing species, which depends on pollination (Heilbut et al. 2001; Wilson & Harder 2003; Vamosi et al. 2007). Scaling up from these local community dynamics are examinations of how local communities are assembled from regional species pools (Chave 2004; Tilman 2004), which depend upon rates of dispersal and ecological filtering (Myers & Harms 2009) as well as competition (Inouye et al. 1980; Crawley & May 1987; Tilman 1994; Coomes & Grubb 2003). If local assemblages are non-random collections of species from the regional species

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phyladontology (Webb 2000; Cavender-Bares et al. 2004), we may infer that species coexistence depends upon traits that are evolving at varying rates upon the phyladontology. Because these community phylogenetic analyses typically examine larger time scales (Swenson et al. 2006), many previous studies have operated under the implicit assumption that immigration events of every generation are effectively summed and species are not dispersal-limited (i.e. some seeds of every species should arrive at every local site over periods of thousands of years). Over ecological time scales however, several generations of competition can occur within a local neighbourhood—for instance, most meadow herbs disperse the majority (99%) of their seeds less than or equal to 15 m from the parental plant (Vittoz & Engler 2007). Therefore, community assemblies are the net result of processes happening at different time scales, composed of species exhibiting inherited traits that were locally successful in previous generations (Kembel 2009).

Despite the reduction in seed set that may occur from interspecific pollen transfer, many coexisting species benefit from pollinator sharing by increasing the visitation rate of pollinators (Feldman et al. 2004; Moellner 2004; Ghazoul 2006; Sargent & Ackerly 2008). If increasing the visitation rate outweighs the costs of any interference from interspecific pollen transfer (Morales & Traveset 2008), then floral traits within communities should be, on average, more similar than chance would predict. Furthermore, whether floral characters are important determinants of competition or facilitation of pollination may be affected by the local abundance of a population (Spigler & Chang 2008). The abundance or density of a species within a community directly determines the amount of conspecific pollen that is available for pollination (Spigler & Chang 2008). Rare species will receive more interspecific pollen owing to the relative abundance of coflowering species and therefore may only persist in a community if they exhibit increased divergence in floral traits than do common species (Ishihama et al. 2006).

Recent models (Sargent & Otto 2006) and field studies (Gumbert et al. 1999; Spigler & Chang 2008) indicate that rare species are under more pressure to have divergent floral traits and to evolve specialist pollination than are common species. Conversely, plant–gent floral traits and to evolve specialist pollination that rare species are under more pressure to have divergent floral traits and to evolve specialist pollination than are common species. Conversely, plant–

2. MATERIAL AND METHODS

(a) Study areas, sampling and reflectance readings

Five subalpine meadows in the Kananaskis Region near Calgary, Alberta, Canada were selected for survey and sampling during the months of July and August 2008. Each study site was an open dry meadow habitat dominated by grasses and surrounded by mixed Picea spp., Pinus spp., Pseudotsuga menziesii, and Populus spp. forest. Each meadow was situated on a south-facing slope. The approximate area of the open habitats ranged from 1.3 to 4 km², and the elevations between sites ranged from 1500 to 1700 metres. Within each study site, a sampling area of approximately 75 m² in size was set up for identification and collection of specimens. All coflowering species within the sampling area were identified and their relative abundance measured. For species with less than 30 individuals in the study area, individual plants were numbered and five randomly selected plants had single flowers removed. For species with greater than or equal to 30 individuals in the study area, single flowers were haphazardly sampled from separate individuals. Variation in floral colour spectra within species and between habitats was low.

Per cent transmission of flower petals was obtained with an Ocean Optics USB 2000 spectrometer, an Ocean Optics DH-2000 Deuterium Tungsten Halogen light source and a BaSO₄ white standard for every 0.22 nm between 300 and 700 nm wavelengths. The light source, spectrometer probe and petals were covered prior to readings to prevent ambient
light from entering the readings. Reflectance readings were obtained from the dominant colour pattern of flower petals (or showy bracts) after a scan of the petals with the spectrometer for differing petal colour patterns undetectable by the human eye from 300 to 700 nm wavelength. When flowers were too small to obtain a reading, multiple flowers from the same individual were placed overlapping each other to facilitate measurement of reflectance. The mean per cent reflectance from 300 to 700 nm for the flowers of each species was subtracted from the raw per cent reflectance values to correct for brightness and allow for a comparison of spectral quality differences (colour) between species (Cuthill et al. 1999).

**Statistical analyses**
The analysis of divergence or convergence of colour traits within communities was assessed in a similar manner as an assessment of phylogenetic community structure (Webb 2000) to compare whether phylogenetic distance generates a good approximation of traits perceived to be important in competition. Statistical analyses were conducted using the general functions from R Statistical Software (R Development Core Team 2008) along with specialized functions of the picante package (Kembel et al. 2010). The raw reflectance values from all 44 species found flowering in the five communities were used to generate a Euclidean distance matrix between species, which was then used in hierarchical cluster analysis to generate a cluster dendrogram representing the regional colour distribution (similar to the functional diversity (FD) dendrogram used in other studies (Petchey & Gaston 2007; Cadotte et al. 2009)). We then compared the mean pair-wise distance within each community to the colour distribution of 10,000 randomly assembled communities from the regional species pool (using the ‘phylogeny shuffle’ option). Fisher’s combined probability test was applied to these results to test for an overall tendency of divergence or convergence of floral colour within communities. We then performed the same technique to assess the Community-wide MPD values, we also tested for a relationship between mean overall tree balance and frequency.

To test the hypothesis that floral colour is an evolutionarily labile trait, the first and second principal component score (PC1, PC2) for each species was analysed by calculating the maximum-likelihood estimated λ (Pagel 1999; Freckleton et al. 2002) and examining whether it was significantly different from 0 or 1 using a phylogenetic glm procedure kindly provided by R. Freckleton for R Statistical Software (R Development Core Team 2008). We also examined whether local abundance and frequency exhibited a phylogenetic signal by the same method and performed phylogeny-corrected GLM of rarity versus PC1.

### 3. RESULTS
Communities consisted of 11–21 coflowering species. In total, we found 44 species flowering in our five subalpine meadows of Kananaskis, Alberta in July and August 2008 (figure 1), with floral colour ranging from greenish white to bright purple (according to human perceptive abilities). Principal component analysis on floral colour revealed that colour could be adequately described with the first two principal components (PC1: 69.3% of the variance; PC2: 19.6% of the variance). Within each study site, the variance that the first principal component explained ranged from 70.2 to 90.1 per cent.

**Trait structuring in subalpine meadow communities**
Coflowering species had divergent reflectance floral colour spectra in four of five communities, and divergent reflectance spectra in one community (table 1) when compared with random colour distributions drawn...
from the regional colour pool (figure 1). One community had species with significantly divergent reflectance spectra, while other communities exhibited marginally significant divergence or no significant divergence from randomly assembled communities (table 1). However, the combined probability of floral colour distributions within communities was significantly more divergent than randomly assembled communities (Fisher's combined probability test: $\chi^2 = 24.67$, d.f. = 10, $p = 0.006$).

(b) Phylogenetic structuring in subalpine meadow communities

There were trends towards phylogenetic clustering of coflowering communities in four of five communities, and phylogenetic dispersion in one community (table 2). Phylogenetic clustering was significant in one community, while the other four coflowering communities were not significantly different from random. Overall, there was significant phylogenetic clustering of coflowering communities (Fisher’s combined probability test: $\chi^2 = 23.54$, d.f. = 10, $p = 0.009$). The opposite patterns found in community structure between floral colour traits and phylogeny can occur because of the frequent phylogenetic transitions observed in floral colour (no phylogenetic signal for either PC1 or PC2, electronic supplementary material, table S1).

(c) Floral colour and abundance

There was a significant relationship between local abundance and floral colour in three of five study sites, with

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Table 1. Summary statistics for the standard effect size of the mean pair-wise distance between species to test for divergence (high p-value) or clustering (low p-value) of colour within communities when compared with the regional colour distribution (using the 'phylogeny shuffle' randomization technique).

<table>
<thead>
<tr>
<th>study site</th>
<th>species richness</th>
<th>mean pair-wise distance (MPD)</th>
<th>random MPD</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bighorn Meadows</td>
<td>13</td>
<td>1.528</td>
<td>1.547 ± 0.076</td>
<td>0.316</td>
</tr>
<tr>
<td>Highwood Junction</td>
<td>11</td>
<td>1.666</td>
<td>1.546 ± 0.089</td>
<td>0.985</td>
</tr>
<tr>
<td>Mist Creek</td>
<td>21</td>
<td>1.603</td>
<td>1.547 ± 0.046</td>
<td>0.935</td>
</tr>
<tr>
<td>Mt. Allan</td>
<td>14</td>
<td>1.617</td>
<td>1.548 ± 0.070</td>
<td>0.878</td>
</tr>
<tr>
<td>Sibbald Meadows</td>
<td>15</td>
<td>1.624</td>
<td>1.547 ± 0.065</td>
<td>0.946</td>
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</table>

Figure 1. Hierarchical cluster dendrogram based on the reflectance spectra for all 44 flowering species found in the five communities representing the regional colour distribution used in the analysis, showing general clustering according to the human visual spectrum. Coloured squares represent the PC1 scores of the species, matched approximately to our human perception of colour. PC1 separates white/yellow flowers from those reflecting increasing amounts of purple–UV wavelengths and represented approximately 72% of the variance in colour reflectance. PC1 scores matched approximately to our human perception of colour unless the species reflected UV wavelengths. Black squares represent the community presence matrix for all sites 1–5 (order key for squares: 1st = BHM, 2nd = HJN, 3rd = MCA, 4th = MTA and 5th = SBM).
rare species exhibiting higher PC1 scores for floral colour (i.e. they were more purple) than common species (electronic supplementary material, table S2). Overall, rare species had significantly higher PC1 scores for floral colour than common ones (Fisher’s combined probability test: \( \chi^2 = 29.36, \text{d.f.} = 10, p = 0.001 \)). Examining the relationship between rarity and PC1 in all communities combined in a phylogenetically corrected analysis, we still find that rare species have higher PC1 scores (\( F_{1,42} = 7.26; p = 0.01 \); figure 2).

Rare species exhibited no significant difference from common species in floral colour divergence from coflowering neighbours (electronic supplementary material, figure S1; all communities pooled; \( F_{1,42} = 0.41; p = 0.52 \)). However, the more frequent a species was, the more it was consistently divergent in colour from its neighbours (\( F_{2,42} = 7.78, p = 0.008 \); figure 3b), although there was no relationship between frequency and phylogenetic distance to neighbours (\( F_{2,42} = 0.98, p = 0.33 \); figure 3a). We found no evidence to suggest that frequent species were drawn from more imbalanced local phylogenies than infrequent species (mean phylodistances of the communities did not change with increasing frequency; \( F_{2,42} = 0.2882; p = 0.60 \)).

Removing the four species (Achillea millefolium, Astragalus alpinus, Campanula rotundifolia and Solidago multiradiata) that were not consistently rare or common, we found a

![Figure 2. Regional phylogeny of species found in the five subalpine meadows. Boxes show values for PC1 of floral colour (exhibiting little phylogenetic signal (see electronic supplementary material, table S1)), displayed with the best match possible with human perception (as in figure 1). Note that PC1 separated UV, purple, blue, yellow and white colours very well but did not separate pink or red from blue or yellow (as PC2 did). Species that were rare (dark squares) tended to have higher PC1 scores than other species in the community (i.e. had spectral reflectance tending towards the purple/UV end of the spectrum versus the white/yellow end). Grey squares indicate species that were observed to be locally rare in some communities and abundant in others.](http://rspb.royalsocietypublishing.org/)

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been made for phenological changes (Gleeson 1981), a strain the null distributions to maintain species ‘independent swap’ (Gotelli & Entsminger 2003) or ‘trial swap’ (Miklos & Podani 2004) routines that constrain the null distributions to maintain species frequencies to be the same as observed communities, we found that the degree of colour divergence decreased (data not shown). Species that were very frequently observed in meadow communities (e.g. Castilleja miniata) were, on average, more colour dispersed from their neighbours than are less frequently observed species. This provides some evidence for the ‘Narcissus effect’ that arguably makes controlling for frequencies statistically overconservative when a trait (such as floral colour) plays roles in determining frequency and community structure (Colwell & Winkler 1984; Kembel & Hubbell 2006). We venture that the evolution into ‘rare colour space’ may be advantageous and contributes to the success of species such as Castilleja miniata (Webb & Pitman 2002). Admittedly, the unusual coloration of some of the alpine’s more widespread species could be circumstantial and more research into this pattern is warranted.

Another avenue of colour divergence variation comes from the degree of phylogenetic divergence. Our communities exhibited slight tendencies for phylogenetic clustering much like other studies in plants and animals (Webb 2000; Cavender-Bares et al. 2009; Vamosi et al. 2009). While we were not expecting to find evidence of ecological sorting in our communities because all species in our study were tolerant of subalpine environments, we find a tendency for an inverse relationship between floral colour pattern and coflowering phylogenetic community structure (tables 1 and 2). The divergence of floral colour between closely related species may provide an explanation for how closely related angiosperms coexist in phylogenetically clustered communities (Kraft et al. 2007; Vamosi et al. 2009) and is similar to the chemical defence overdispersion observed in previous studies (Becerra 2007). The converse may also be true: processes that affect phylogenetic community structure will undoubtedly affect selection on floral colour from local pollinator competition. It may be that floral colour divergence is selected only when communities are phylogenetically clustered, thus the processes that affect phylogenetic community structure may alter the context of floral colour evolution.

The lack of any phylogenetic signal in floral colour when considering the whole spectrum supports the notion that floral colour is an evolutionarily labile trait, consistent with previous studies that have found frequent colour changes with flowering plant clades (Bearnsley et al. 2003; Smith et al. 2008). Furthermore, the absence

4. DISCUSSION
While alpine meadow communities are noted for their vibrant displays of disparate colours, the colours are only moderately more divergent than expected by chance, even when the spectra are examined without the limitations of human perception. We find a consistent general tendency for floral colour dispersion, although it was weak in all but one community, lending some support for the hypothesis that communities are structured to some degree by floral colour. The divergence of floral colour suggests that visual cues have a role in distinguishing flowers in the community, functioning to attract broad categories of dominant pollinators (e.g. bird versus bee) as well as eliciting constancy within pollinator classes (Wilson & Stine 1996; Gegear 2005). Floral colour diversity may thus provide a good approximate representation of the FD in pollinator resources of the community (Petchey & Gaston 2007). Furthermore, our alpine meadows maintained colour dispersion despite showing an opposing tendency for phylogenetic clustering (close relatives coexisting more often by chance). The lack of concordance between trait and phylogenetic community structuring is due to the remarkable evolutionary flexibility in floral colour (little to no phylogenetic signal). Admittedly, our phylogeny was not completely resolved (e.g. a large polytomy remains among Asteraceae), which may have decreased our ability to detect a phylogenetic signal. Nevertheless, the lability of floral colour may represent a ‘line of least evolutionary resistance’ for character displacement compared with morphological changes, such as evolution of differing floral shape or symmetry (Whittal et al. 2006). Similar arguments have been made for phenological changes (Gleeson 1981), a transition that may be more common in areas with longer flowering seasons.

We observed substantial variation in the degree of floral colour dispersion. One contribution to this variation can be attributed to the differences in results between frequent and infrequent species. When using either the ‘independent swap’ (Gotelli & Entsminger 2003) or ‘trial swap’ (Miklos & Podani 2004) routines that constrain the null distributions to maintain species weak positive relationship between local abundance and frequency of occurrence ($F_{1,38} = 3.79; p = 0.047$), but no phylogenetic signal for either trait (electronic supplementary material, table S1).

Figure 3. Relationship between frequency of occurrence (measured as the number of communities a species was found in) and (a) standardized mean phylogenetic distance mean or (b) standardized colour distance from coflowering neighbours.
of phylogenetic signal suggests that colour cues of various pollination syndromes (e.g. bee-, bird-, fly-pollinated) are generally not as well conserved as the pollinator syndromes themselves (Sargent & Vamosi 2008). While floral colour has been associated with pollination syndromes (Faegri & van der Pijl 1979), we should note that all our species were insect-visited to some degree. While some red–orange species were present (Castillejo minita, Lilium philadelphicum) and this colour is associated with bird pollination, evidence suggests that insects regularly visit these species. We posit that divergent colours within communities do not simply divide the community among the various pollinating orders (bees, flies, moths, birds) but rather operate more commonly to elicit pollinator constancy within pollinator classes. The lack of phylogenetic signal in floral colour may be similar to behavioural traits that have been observed to be labile in animal lineages (Blomberg et al. 2003) and would be designated as an alpha-trait (a trait (Levin 1985) and further study performing detailed examinations of the fitness of a variable plant species flowering in different flowering communities would help decipher the relative frequencies of character displacement versus competitive exclusion. Furthermore, our observations on abundance appear to indicate that rare species may tolerate poor-quality visits (those with a high-proportion of heterospecific pollen) in exchange for increased total number of visits. While such a facilitating relationship may be stable, we envision that character displacement away from common colours may be associated with increases in abundance, a process that would result in correlations between abundance and species richness (Webb & Pitman 2002). Rapid transitions in traits such as rarity and floral colour are indicative of how abundance and traits are central to our understanding of the importance of phylogeny in community ecology and should be important components of future studies aimed at investigating the interaction between community assembly and adaptation.

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