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NATURAL HISTORY NOTE

Do past and present abiotic conditions explain variation in the nutritional quality of wildflower pollens for bees?

Anthony D. Vaudo[1,2] · **Eva Lin**[1] · **Jillian A. Luthy**[1] · **Anne S. Leonard**[1] · **Eliza M. Grames**[1,3]

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Abstract
Floral traits such as color, scent, and nectar often vary substantially within plant species. However, when it comes to pollen chemistry, the scale of intraspecific variation is largely unknown, as are its potential abiotic drivers. Bees collect pollen as their primary source of protein and lipids, and interspecific variation in pollen quality influences bee foraging preferences. Understanding the scale of intraspecific spatiotemporal variation in pollen macronutrient content could further uncover the nutritional basis of many plant-pollinator interactions influenced by geographic and climatic factors. Here, we sampled pollen from 35 bee-visited wildflower species across multiple sites in Great Basin/Eastern Sierra sagebrush steppe habitat (Nevada/California, USA) and analyzed their protein and lipid concentrations. Then, using Bayesian sparse regression, we explored the relationship between 44 site-specific climate variables and variation in pollen nutritional content. In some plant species, we discovered variation in protein or lipid concentrations across sites at a scale likely meaningful to bee performance. Further, this variation was weakly but significantly related to both current season below-ground (climatic water deficit) and previous season above-ground (dewpoint) conditions, uncovering the potential for community interactions mediated by floral nutrition to be altered via multiple plant ecophysiological pathways. Identifying the causes and consequences of variation in pollen nutrition is an effort critical to understanding how climate change impacts plant fitness via interactions with pollinators as well as the health of managed and wild bees.

Keywords Climate change · Climatic water deficit · Dewpoint · Floral rewards · Intraspecific trait variation · Pollination ecology

Introduction

Floral traits that mediate interactions between plants and pollinators are rarely static across space and time (reviewed in López-Goldar and Agrawal 2021). For example, floral color and scent often vary across a landscape (Weber et al. 2019; Koski and Galloway 2020; Manincor et al. 2022), reflecting both phenotypic plasticity (Campbell

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et al. 2018) and genetic differences (Milano et al. 2016; Koski and Galloway 2020). More broadly, characterizing functional intraspecific trait variation (ITV) in plants (e.g., growth rate, phenology, size, inflorescence number) has been key to identifying patterns of local adaptation and informing restoration efforts (Brabec et al. 2017; Chaney et al. 2017; Baughman et al. 2019).

In contrast to floral display or vegetative traits, it is interesting to consider the potential for ITV in pollen given its vital roles for both plants and pollinators. Most obviously, pollen maintains viability and prevents desiccation of plants' male gametes (Bedinger 1992; Pacini and Hesse 2005). At the same time, many plants reward pollinators with pollen exclusively or alongside nectar. For pollinators such as bees, pollen serves as a primary source of macro- and micronutrients (Nicolson 2011) and interspecific variation in its composition affects both bees' foraging choices (Vaudo et al. 2016, 2024) and their resilience to disease, pesticides, and abiotic stressors (Alaux et al. 2010; Vanderplanck et al. 2019; Barraud et al. 2020; Crone and Grozinger 2021).

Pollen's role in plant reproduction implies that some of its traits may be relatively invariable within a species. For example, variation in pollen protein content between plant species has previously been explained by the length of the pistil (from stigma, through style, to ovary) that a pollen tube must germinate (Roulston et al. 2000), and thus intraspecific variation in this trait might accordingly show something of a floor effect (Vaudo et al. 2022). Additionally, pollenkitt lipids are a major fraction of pollen's external chemistry, which has a variety of functions, including mediating interactions with floral visitors, buffering against desiccation, and potentially managing microbial activity (Dobson et al. 1987, 1999; Dobson 1988; Pacini and Hesse 2005; Rivest and Forrest 2020). Thus, it is possible that this trait shows (as in nectar; Suni et al. 2020, 2023) relatively more intraspecific variation depending on environmental conditions (e.g., temperature effects on pollen lipids; Russo et al. 2020) or ecological context.

Whether such patterns play out across plant species within an ecological setting is an open question. The few manipulative experiments that consider environmental influence on pollen chemistry show the clear potential for plasticity, but hint at a potential for idiosyncratic effects across species (e.g., temperature effects on pollen protein content varied across two different species; Descamps et al. 2021a, b). Likewise, to understand climate impacts on agricultural systems, most previous work evaluating the effect of environmental conditions on pollen chemistry considers crops (including non-animal pollinated systems) under extreme conditions (Borghi et al. 2019), or involves controlled conditions without attention to population differences (Descamps et al. 2020).

As a result, we know little about the scale of standing pollen ITV within ecological communities. In our previous research, we used a phylogenetic framework to compare *interspecific* variation in pollen nutrition between plant species and how it influences bee community foraging preferences (Vaudo et al. 2024). Thus, the simplifying assumption that pollen chemistry is static across populations remains untested. This assumption could complicate efforts to understand how pollen traits shape interaction networks (Vaudo et al. 2024), to identify plants providing nutritionally diverse resources for restoration efforts (Vaudo et al. 2015; Glenny et al. 2023), and to predict how climate stressors may rewire nutritionally-based interactions between bees and plants in natural communities (Settele et al. 2016; Jamieson et al. 2017).

In this study we explore the potential for *intraspecific* variation in pollen nutrition among plant species occupying multiple sites in the same ecoregion. Here, we surveyed common, native, bee-visited wildflower species collected from different sites in the Great Basin/Eastern Sierra (Nevada/California, USA). We asked (1) if pollen protein

and lipid content exhibit biologically meaningful ITV at the site level and (2) if pollen site-level ITV could be explained by climatic variables.

Methods

Field data collection

In 2021, we collected fresh pollen one to two times within the same week from 35 common and abundant sagebrush steppe, perennial (except for the annual *Lupinus malacophyllus*) bee host-plant species, located at 2–7 sites per species (NV/CA, USA; Fig. S1, Table S1). We selected species present in patches of ~ 25 m^2 that had > 10 plants flowering. In 2020, during 10-min periods, we confirmed that foraging bees collected pollen from these plants. We collected all bees we observed contacting their anthers and identified these to the genus level (Table S2; Vaudo et al. 2024). We collected flowers in the field and harvested pollen from anthers in the laboratory. We subsequently analyzed pollen macronutrient concentrations (µg nutrient mg^{-1} pollen, Bradford assay for protein, and sulfo-phospho-vanillin for lipids; Supplementary Information 1) using methods detailed in Vaudo et al. (2024), resulting in three measurements of pooled pollen protein and lipid quality per species per site.

Climate and weather data

We downloaded daily weather data for total precipitation, minimum, mean, and maximum air temperature, mean dew point temperature, and minimum and maximum vapor pressure deficit for each plant species location from PRISM (4 km^2 quadrant encompassing host plant species coordinates; PRISM Climate Group, Oregon State University, https://prism.oregonstate.edu, data created and accessed 11 Nov 2022). PRISM models historical climate data using information from a network of thousands of weather stations, which it combines with information about elevation and other topographic features (Daly et al. 2008). PRISM is the official source of climatological data for the USDA and is one of the most widely-used spatial climate models in the United States. We downloaded a 1-arc second digital elevation model from the 3D Elevation Program (USGS 2022) for tiles encompassing the study sites and calculated slope and aspect with four neighbors (terrain function from the R package raster v3.5-11; Hijmans et al. 2021). Soil available water capacity was downloaded from the USGS Soil Properties Dataset based on the Gridded National Soil Survey (gNATSGO) and Gridded Soil Survey (gSSURGO) Geographic Databases (Boiko et al. 2021).

We calculated snowpack, potential evapotranspiration, soil moisture, and ultimately climatic water deficit (directly relevant to plant physiology and distributions; Dilts et al. 2015) using the formulas from Lutz et al. (2010) as implemented by Redmond (2022). We modified these variables for within-year values as opposed to across-year trends (Table S3). We calculated mean values for our 11 weather variables across four time periods: previous fall (October 1–December 31) to represent the periods in which plants are senescing and in dormancy; spring (April 1–June 30) for when vegetative tissue and flowers are being produced; 28 days prior to sampling each site to represent a more narrow time frame in which flowers are developing; and 7 days prior to sampling at each site to closely represent the time frame in which the floral rewards would be produced before being collected. This

combination of variables and time periods resulted in 44 potential variables. Our approach is relatively insensitive to collinearity (Lu and Lou 2021); however, many of our climatic variables were extremely highly correlated or perfectly collinear (e.g., if all snowpack and precipitation values were zero for a time period). We dropped one variable from pairs of extremely collinear predictors, resulting in 35 potential measures of climate and weather conditions across all sites and sampling dates remained (Fig. S2). This resulted in dropping soil moisture in spring and over the previous 28 days, snowpack over the previous seven and 28 days, precipitation over the previous seven days, and maximum vapor pressure deficit across all time periods.

Statistical analysis

Previous studies of pollen nutrition in response to drought and temperature have not shown predictable responses of protein or lipid content across species (Borghi et al. 2019; Descamps et al. 2020). Therefore, in the absence of a priori known mechanistic relationships linking weather and pollen nutrition, we adopted a Bayesian sparse regression approach for variable selection. In sparse modeling, few of the many possible predictors have non-zero effects, and the rest are excluded by local and global shrinkage parameters. We used a Bayesian sparse regression model with a horseshoe estimator as the prior for coefficients associated with all climate variables (Table 1). Because we had multiple replicate measurements of the same populations (i.e., sites) of species on the same dates, we treated each replicate pollen sample as arising from a distribution of pollen nutrition (lipid and protein concentration measured separately) for each population i with a mean μ_i and standard deviation σ_i estimated from uninformative gamma priors (Table 1 Eqs. 1, 10). The mean μ_i for each population was estimated as a function of a random intercept for each species β_s (Eq. 11) and the sum of the effect of environmental covariates $\boldsymbol{X}$ (Eq. 2). For each environmental covariate in $\boldsymbol{X}$, we estimated if it should be included in the model with a binary inclusion status γ drawn from a Bernoulli prior with probability 0.5 (Eqs. 2, 12) and subsequently modeled the effect β with a horseshoe estimator using half-Cauchy priors for the global shrinkage parameters and the local shrinkage parameter λ fixed to 0.1 (Eqs. 3–9), following Roberts and Zhao (2021). This model structure allowed us to estimate both the probability of inclusion for every climate variable based on γ and generate parameter estimates for selected variables.

Table 1 Bayesian sparse regression model equations

$y_i \sim N(\mu_i, \sigma_i)$	Eq. 1
$\mu_i = \beta_s + \boldsymbol{\gamma} * \boldsymbol{\beta} * \mathbf{X}$	Eq. 2
$\boldsymbol{\beta} \sim N(0, \lambda * \boldsymbol{\nu} * \omega)$	Eq. 3
$\boldsymbol{\nu} = \lvert\chi_1\rvert / \sqrt{\tau_1}$	Eq. 4
$\omega = \lvert\chi_2\rvert / \sqrt{\tau_2}$	Eq. 5
$\tau_1 \sim Gamma(0.5, 0.5)$	Eq. 6
$\tau_2 \sim Gamma(0.5, 0.5)$	Eq. 7
$\chi_1 \sim N(0, 1)$	Eq. 8
$\chi_2 \sim N(0, 1)$	Eq. 9
$\sigma \sim Gamma(0.01, 0.01)$	Eq. 10
$\beta_s \sim N(0, 0.001)$	Eq. 11
$\gamma \sim Bern(0.5)$	Eq. 12

We selected covariates with a probability of inclusion from the sparse regression model greater than 0.6 for subsequent analysis. Because coefficient estimates for the environmental covariates are biased towards zero when using a horseshoe estimator for the prior, we fit a second linear model with the selected covariates using uninformative normal priors (Eq. 11). To assess model fit, we used within-sample posterior predictive checks.

We used Markov chain Monte Carlo (MCMC) implemented in JAGS (Plummer 2003) using saveJAGS v0.0.4.9002 (Meredith 2021) and R2jags v0.6-1 (Su and Yajima 2021) to fit the models. After a burn-in of 10,000, we ran the models for 300,000 iterations and sampled the posterior every tenth iteration, resulting in a posterior sample of 90,000 from three chains. For the stage two models, we reduced burn-in to 4000 and ran the models for 6000 iterations and sampled every third iteration, resulting in a posterior sample of 2000 from three chains. We assessed model convergence with the Gelman-Rubin statistic ($\widehat{R}$) and assumed chains had converged when $\widehat{R}$ was less than or equal to 1.1 for all parameters. All data and code are provided at https://doi.org/10.6084/m9.figshare.24101226.

Results

Raw values of pollen protein and lipid concentrations among plant species (and orders) are presented in two-dimensional nutritional space and across sites (Fig. 1, S3). Pollen protein and lipid content varied differentially among species across sites, and on average, we found that the scale of site-level variation in both traits was roughly the same (Fig. 2; mean, 90% CI, range for protein coefficient of variation (CV) = 9.3%, 6.9–11.6%, 0.8–33.0%; lipid CV = 10.0%, 8.5–11.5%, 0.8–26.2%).

Environmental conditions and lipid concentration

The lipid sparse regression model converged normally after 300,000 iterations with all parameters exhibiting $\widehat{R} < 1.1$. The mean probability of inclusion (ɣ) across all variables was 0.47 (90% CI: 0.42, 0.58). Using 0.60 probability of inclusion as a cutoff for variable selection, we retained climatic water deficit over the 28 days prior to sampling (mean, 90% CI = 0.67, 0.66–0.69) and mean dew point temperature the previous fall (mean, 90% CI = 0.62, 0.60–0.64). All other potential environmental covariates had a probability of inclusion < 0.60 (Fig. 3A).

Our linear models to estimate effects on lipid concentration of climatic water deficit over 28 days and mean dew point temperature the previous fall converged normally after 6000 iterations with all monitored chains exhibiting $\widehat{R}$ values < 1.1. All observations were included in the 90% prediction interval for their respective populations suggesting a good model fit to the data. Climatic water deficit over 28 days prior to sampling (Fig. 4A) had a negative effect on lipid concentration (mean, 90% CI: −0.09, −0.14, −0.04) as did previous fall mean dew point temperature (mean, 90% CI: −0.07, −0.12, −0.02) after accounting for species-specific differences (Fig. 4B).

Environmental conditions and protein concentration

For protein concentration, sparse regression models converged normally after 300,000 iterations, with all parameters exhibiting $\hat{R} < 1.1$. The mean probability of inclusion (ɣ) across all variables was 0.48 (90% CI: 0.45, 0.52). Using 0.60 probability of inclusion as

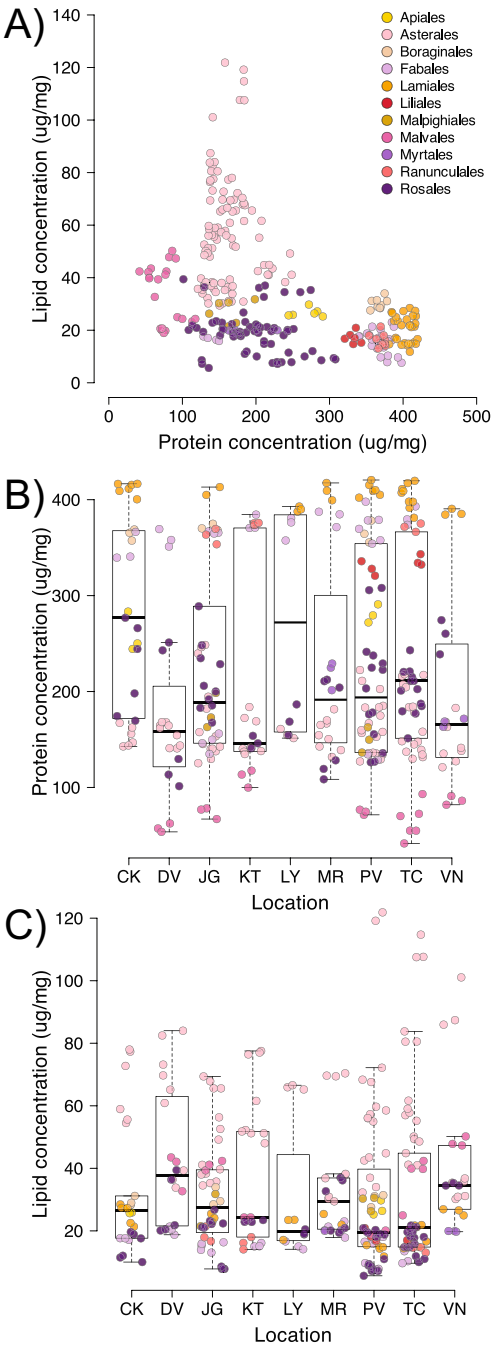

Fig. 1 Raw measures of lipid and protein concentration shown **A**) as the relationship between lipid and protein concentration within plant orders, and variation in **B**) protein and **C**) lipid concentration across sites. Points are colored by plant order; for site locations, see Figure S1. Boxes represent the interquartile range with the center line indicating the median; whiskers show the quartiles ±1.5 time the interquartile range

a cutoff for variable selection, we retained only one measure—climatic water deficit over the seven days prior to sampling (mean ɣ, 90% CI = 0.70, 0.68–0.71). All other potential environmental covariates had a probability of inclusion < 0.60 (Fig. 3B).

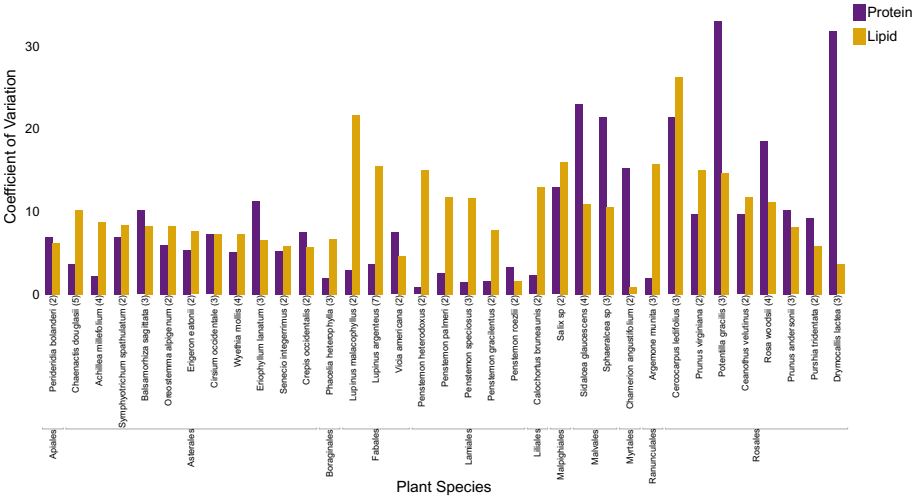

Fig. 2 Coefficient of variation (%) of protein and lipid concentrations between sites (number of sites in parentheses) for each plant species

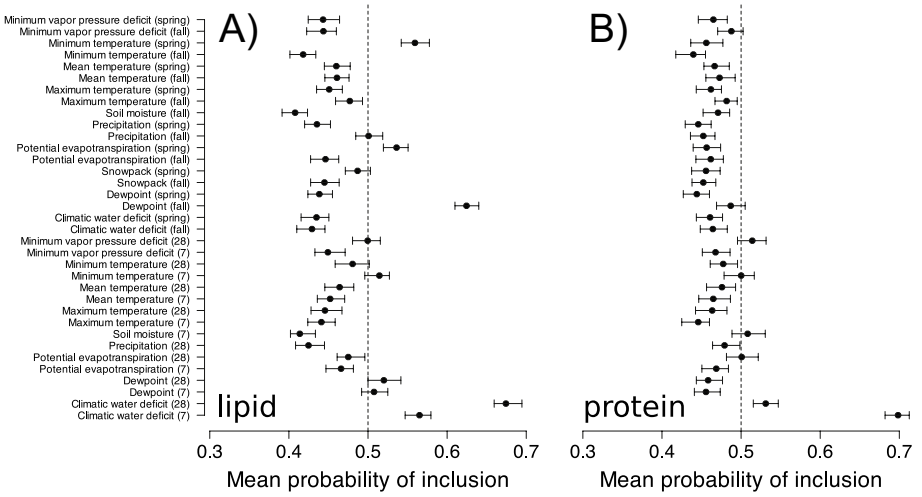

Fig. 3 Posterior probability of variables being selected as predictors of **A**) lipid and **B**) protein concentration. Points indicate mean estimate from the posterior, with 90% credible intervals generated through bootstrapping 100 mean estimates, each representing samples of 2,000 from the posterior

Our linear models to estimate effects of climatic water deficit over seven days prior to sampling on pollen protein concentration converged normally after 6000 iterations with all monitored chains exhibiting $\hat{R}$ values < 1.1. All observations were included in the 90% credible interval for their respective populations suggesting a good model fit to the data. Climatic water deficit over seven days prior to sampling had a positive effect on protein concentration (mean, 90% CI: 0.07, 0.03, 0.12) after accounting for species-specific differences (Fig. 4C).

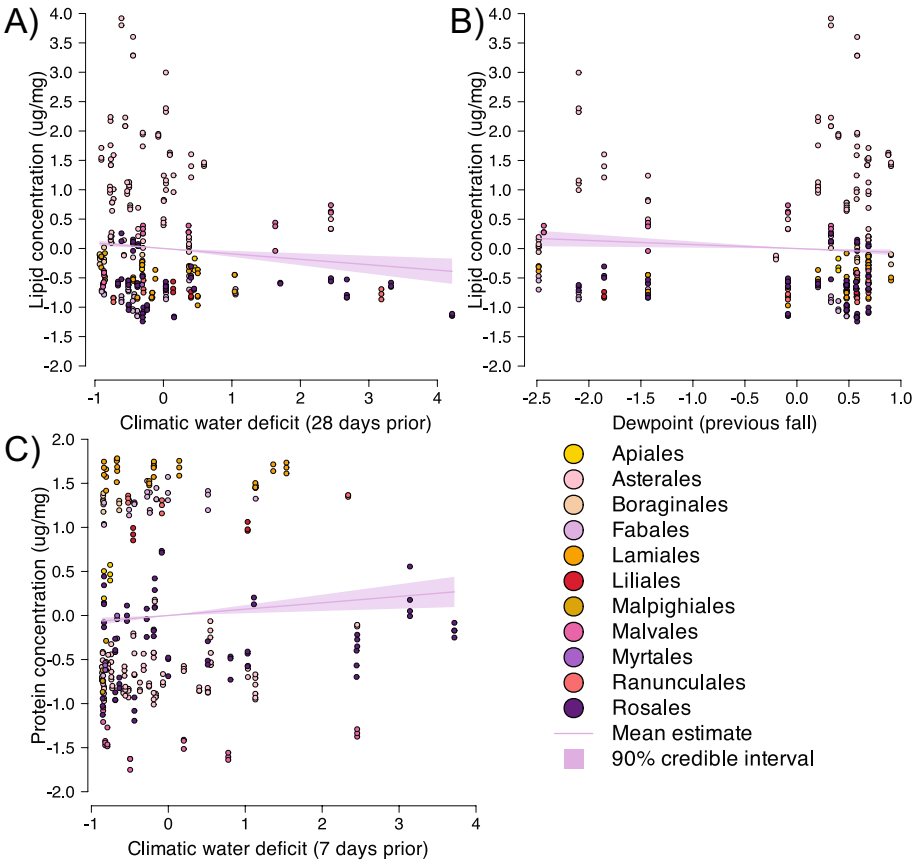

Fig. 4 Estimated effects of selected predictors on pollen nutrition, showing the relationship after accounting for species-specific differences between **A**) climatic water deficit over 28 days prior to sampling on lipid concentration, **B**) mean dewpoint temperature the previous fall on lipid concentration, and **C**) climatic water deficit over seven days prior to sampling on protein concentration. Pollen nutrition and climate variables are standard scores to show effect sizes. Points are colored by order; purple lines indicate the mean estimated effect surrounded by the 90% credible interval after accounting for species-specific differences

Discussion

Although the biotic and abiotic drivers of variation at the individual and population levels are well-studied in relation to vegetative traits and fecundity (Richardson et al. 2014, 2015; Baughman et al. 2019; Johnson et al. 2023), whether the actual rewards at the core of many plant-pollinator mutualisms show similar intraspecific trait variation (ITV) has been neglected in comparison (Parachnowitsch et al. 2018). Nectar and pollen are essential nutritional resources for many pollinator taxa, so establishing whether and why they vary could yield better predictions about climate effects on plant-pollinator communities and inform restoration practices (e.g., in the case of local adaptation; Baughman et al. 2019; Suni et al. 2020; Johnson et al. 2023). Pollen nutritional chemistry is an urgent target in this context, given its role as a primary source of nutrition for wild bees and other pollinator taxa. Here, we report the first study of geographic ITV in pollen chemical traits. Namely, pollen protein and lipid content, two essential macronutrients bees obtain

from pollen (reviewed in Vaudo et al. 2015, 2020), varied across the sagebrush steppe landscape. Further, variation in these traits across species appeared to be influenced by local environmental variables.

A key finding from our survey of pollens sampled from 35 bee-visited wildflowers is that higher climatic water deficits during floral development (within the month prior to collection), were associated with lower lipid concentrations and higher protein concentrations (Fig. 4A, C). Climatic water deficit measures below-ground drought stress, i.e., when actual evapotranspiration exceeds water availability, influenced by both soil moisture and temperature. Climatic water deficit is commonly associated with plant community distributions, and even physiological, phytochemical, and trophic responses to drought stress for plants in dryland ecosystems such as the sagebrush steppe (Stephenson 1998; Pringle et al. 2013; Dilts et al. 2015; Ahmed et al. 2017; Diethelm et al. 2022). Our findings newly suggest it may also impact pollen macronutrient content.

In the broader context of how climate affects floral rewards, it is worth noting that our results run somewhat counter to experimental research showing that heating can result in *higher* pollen lipid concentrations (e.g., *Carduus nutans* in Russo et al. 2020). This may reflect a process whereby heat stress, which may also be associated with drought stress in dryland ecosystems, leads to de-unsaturation of lipids and higher lipid deposition on pollen to prevent desiccation (Lahlali et al. 2014; Narayanan et al. 2016; Lwe et al. 2020), and/or the abortion of pollen production, potentially leading to lower protein investment (Borghi et al. 2019). Yet, the association we report between *drought* stress, *lower* lipid content, and *higher* protein may simply reflect a different suite of plant physiological responses. For example, dry below-ground conditions can lead to fewer nutrients absorbed through the roots, and above ground, the closing of stomata to prevent water loss. A resulting reduction in both photosynthesis and transport of sugars to the stamen during pollen grain development (Borghi et al. 2019) could then curtail the synthesis of pollens' sporopollenin, pollenkitt, triglycerides, and sterols (Bedinger 1992; Pacini and Hesse 2005; Vanderplanck et al. 2011). Likewise, drought coinciding with heat stress may cause upregulation of some proteins (e.g., heat shock proteins and proline; Lahlali et al. 2014; Borghi et al. 2019) leading to higher measures of total protein concentrations. Our findings thus highlight the need to consider the separate and synergistic effects of heat and drought, as well as potential taxonomic variation: indeed, in other studies, temperature stress alone caused idiosyncratic changes in pollen protein in two plant species (Descamps et al. 2021a, b).

Our second main finding is that higher dewpoints in the autumn prior to pollen collection predicted lower pollen lipid concentrations (Fig. 4B). In perennial and evergreen plants, nutrient uptake and storage in the preceding fall often predetermine growth during the current season (Montville et al. 1996; Islam et al. 2009; Shi et al. 2014), and abiotic conditions in the year prior can also influence floral phenology (Schnablová et al. 2021; Schaub et al. 2022). Higher dewpoints reflect a greater capacity for air at a given temperature to hold moisture, here experienced after most of the plants in this study seeded or senesced. Above, we reported that recent drought stress appeared to similarly predict lower pollen lipid content. Are higher fall dewpoints inducing physiological stress playing out in the same way across a different timescale? This is not clear: in the arid western U.S., higher dewpoints seem likely to represent *better* conditions for plants (i.e. higher moisture; Malek et al. 1999; Agam and Berliner 2006) but it is also worth noting that more moisture in the air may also promote fungal pathogens (Romero et al. 2022) and potentially alter dormancy dynamics (Atkinson et al. 2013). The most valuable insight from this may simply be evidence that the previous season contributes to floral resource traits. The potential for more complex

synergies with short-term environmental conditions is an open question that should be considered when predicting plant responses to climate stressors (Schaub et al. 2022), such as changes in precipitation patterns (Morecroft et al. 2004), drought, and severe heatwaves (Hemberger et al. 2022).

To date, most research charting variation in pollen traits among or within species has been done absent a community context (e.g., opportunistically sampled or experimentally grown as in Cook et al. 2003; Descamps et al. 2018, 2021b; Palmer-Young et al. 2019; Russo et al. 2019; Ruedenauer et al. 2019; Suni et al. 2020, 2023; Vaudo et al. 2020) as opposed to plants co-occurring and often co-flowering in the same communities and sharing similar pollinators (Vaudo et al. 2024). Likewise, previous work has tended to focus on species- or genus-level averages. For example, in our previous research, we demonstrated that interspecific variation in pollen nutritional quality can determine bee foraging preferences: plant species that share similar pollen nutritional qualities share similar bee visitors, while plants with different pollen nutritional values are visited by different communities of bees (Vaudo et al. 2024).

Here, our findings show that intraspecific variation in the nutritional value of rewards within ecological communities may exhibit spatiotemporal variation with fluctuating environmental conditions. We show that across sites, plant species often still occupy their relative position in nutritional space in relation to protein and lipid quality (Fig. 1A, S3), and the overall effect size of climate variables on pollen quality across all species is biologically small; but some species may shift in nutritional space enough to cross into possible other nutritional niches. For example, the scale of ITV we uncover in some species here (e.g., *Lupinus malacophyllus* or *L. argenteus* lipid content varying by 15–20%, or protein content in *Potentilla gracilis* varying by 30%; Fig. 2) aligns with the scale of variation in pollen chemistry which bees can empirically discriminate, and which may result in measurable performance differences (Vaudo et al. 2016; Treanore et al. 2019; Ruedenauer et al. 2020; Wood et al. 2021). Here, we found that the universal predicted effect size of climatic water deficit and dewpoint was significant, but small. This is perhaps not surprising given non-uniform variation in pollen quality and environmental conditions between sites. Likewise, we can imagine additional abiotic or biotic drivers of variation in pollen chemistry (e.g., soil chemistry, herbivore presence, belowground interactions, microbes, UV radiation) that may occur at any given site could explain a wider swath of the variation we have uncovered here. Whether large fluctuations in environmental conditions might cause a perturbation or even a re-wiring of relationships between host plants and pollen-foraging bees across a landscape, as certain plant species become more or less valuable as sources of lipid vs. protein specifically, is a critical open question in the face of climate change. As pollen nutrition is linked to bee resilience to climate stressors (e.g., extreme heat; Vanderplanck et al. 2019; Quinlan et al. 2023), mismatches between bee nutritional needs and the quality of pollen resources available in a hotter or drier world would be ecologically and economically significant.

Of course, our study only considers the bulk macronutrient content of pollen, and the changes in additional pollen traits linked to interactions with pollinators (e.g., amino acids, fatty acids, sterols, specialized metabolites; nectar chemistry) should be considered as well. Given the difficulty of collecting wildflower pollen across space and time, manipulative experiments would be needed to directly identify the causal drivers of our observed relationships and replicate across seasons. For example, common garden experiments comparing traits across seed zones in a restoration context might well consider including pollen (and nectar) traits (Richardson et al. 2015; Baughman et al. 2019; Suni et al. 2020, 2023). Similarly, access to museum specimens or planned

long term sample collection could facilitate complementary research into how temporal variation in abiotic variables tracks with variation in pollen chemistry.

Conclusions

Temperature and drought stress are well known to impact a suite of traits that mediate plant-pollinator interactions, including flower production, floral volatiles, and nectar production and composition (Burkle and Runyon 2016; Settele et al. 2016; Phillips et al. 2018; Descamps et al. 2020; Rering et al. 2020; Hemberger et al. 2022; Suni et al. 2023). Until now, the effect of variation in natural climatic conditions across a landscape has not been considered in relation to pollen chemistry. We demonstrate that both previous and current season above- and below-ground environments predict patterns of variation in pollen macronutrients at the site level. Pollen chemistry is at the heart of the mutualism supporting plant reproduction and pollinator community health, and in the context of climate change, if plants experience stress that disrupts the quality of these resources, there could be a loss of interactions and stability in these mutualisms. Determining the functional consequences of site-level variation in pollen nutrition, for example, whether they lead to shifts in the composition or frequency of floral visitation, is an obvious open question raised by these findings. Especially within dryland ecosystems, our findings raise many additional follow-up questions. For example, largescale studies that sample across a wider range of geographical replicates and seasons could better resolve the scale of ITV in pollen traits we have discovered here, and common garden experiments could offer complementary insight into the potential for phenotypic plasticity vs. local adaption in pollen nutritional traits. Identifying populations of plants whose floral reward quality remains resilient to abiotic stress could help inform the design of conservation efforts that support plant-pollinator communities.

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Author's contribution ADV–Conceptualization; Data curation; Investigation; Formal Analysis; Methodology; Project administration; Supervision; Validation; Visualization; Writing–original draft; Writing–review & editing. EL–Investigation; Writing–review & editing. JAL–Investigation; Writing–review & editing. ASL–Conceptualization; Funding acquisition; Project administration; Supervision; Validation; Writing–original draft; Writing–review & editing. EAG–Conceptualization; Data curation; Formal analysis; Investigation; Methodology; Software; Validation; Visualization; Writing–review & editing.

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Data availability All pollen nutrition data, climate data, map data, and code: https://doi.org/10.6084/m9.figshare.24101226.

Code availability All code: https://doi.org/10.6084/m9.figshare.24101226.

Declarations

Conflict of interest The authors declare no conflict of interests.

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Authors and Affiliations

Anthony D. Vaudo[1,2] · Eva Lin[1] · Jillian A. Luthy[1] · Anne S. Leonard[1] · Eliza M. Grames[1,3]

✉ Anthony D. Vaudo
anthony.vaudo@usda.gov

Eva Lin
evalinx4@gmail.com

Jillian A. Luthy
jillianluthy@yahoo.com

Anne S. Leonard
anneleonard@unr.edu

Eliza M. Grames
egrames@binghamton.edu

[1] Department of Biology, University of Nevada, Reno, NV 89557, USA

[2] Rocky Mountain Research Station, USDA Forest Service, Moscow, ID 83843, USA

[3] Department of Biological Sciences, Binghamton University, Binghamton, NY 13902, USA

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CORRECTION

Correction to: Do past and present abiotic conditions explain variation in the nutritional quality of wildflower pollens for bees?

Anthony D. Vaudo[1,2] · **Eva Lin**[1] · **Jillian A. Luthy**[1] · **Anne S. Leonard**[1] · **Eliza M. Grames**[1,3]

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The wrong Supplementary file was originally published with this article; it has now been replaced with the correct file.
The original article has been corrected.

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✉ Anthony D. Vaudo
anthony.vaudo@usda.gov

Eva Lin
evalinx4@gmail.com

Jillian A. Luthy
jillianluthy@yahoo.com

Anne S. Leonard
anneleonard@unr.edu

Eliza M. Grames
egrames@binghamton.edu

[1] Department of Biology, University of Nevada, Reno, NV 89557, USA

[2] Rocky Mountain Research Station, USDA Forest Service, Moscow, ID 83843, USA

[3] Department of Biological Sciences, Binghamton University, Binghamton, NY 13902, USA

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