Key-words: Apidae, Amplicon sequencing, Interaction, Metabarcoding, Network, Pollinator, Plant-pollinator interaction, Gut microbiome

Abstract

Our understanding of plant-pollinator interaction networks hinges on the methods used to describe their nodes and links. Most networks are built from field observations that may overlook many consumer–resource links, and these networks lack descriptive links that characterize interaction types and outcomes. Towards a more complete approach for building interaction networks, we compare plant interactions from the wild pollinator species, *Bombus pascuorum*, recorded by three methodologies with different implications for interaction outcomes. We compare floral visitation interactions obtained from field observations, plant consumption interactions revealed by metabarcoding of gut contents, and pollen transport interactions detected by metabarcoding of corbicular pollen loads. Our approach adds functional context to plant–pollinator network links and reveals new interactions. We show that both metabarcoding approaches increase the number of interactions and reveal links that were overlooked by field observations of visitation, highlighting plant taxa that are not pollinator-dependent, yet constitute important dietary resources. Paired with floral diversity surveys, gut-content results also reveal seasonal patterns in the spatial extent and functional diversity included in forage, which other methodologies fail to demonstrate. Metabarcoding data analyzed at the individual specimen level further contribute heterogeneity in plant resource use between pollen transport and consumption. Metabarcoding methodologies capture greater spatial, temporal, and taxonomic ranges, while field observations provide validating datasets with higher taxonomic precision. Our results show that integrating visitation, transport, and consumption data changes network topology and the roles of plant nodes, offering

a more nuanced and complete map of interactions with clearer priorities for management. We advocate for defining links explicitly by their functions and combining methods to account for hidden structure in ecological networks.

Data and Code for peer-review

All data and code used for the analyses in this manuscript are provided on an Anonymous GitHub repository (https://anonymous.4open.science/r/B_pascuorum_interaction_networks). All raw amplicon sequencing data will be deposited in a project in the European Nucleotide Archive upon final manuscript acceptance.

1. Introduction

Pollination is a critical ecosystem service that is currently threatened by global anthropogenic change, including habitat loss, intensifying agriculture, pathogens, and invasive species (Klein et al., 2006). Pollinators crucially support the reproduction of 94% of wild flowering plants and 75% of crop species (Vanbergen & Insect Pollinators Initiative, 2013), contributing to 35% of global food production (Klein et al., 2006). Despite the clear importance of understanding plant-pollinator interactions, our knowledge of interaction diversity remains incomplete, as the methodological approach to studying plant-pollinator interactions has historically been biased towards the plants (Bosch et al., 2009; Evans & Kitson, 2020). As a consequence, the well-established relationship between pollinator diversity and the productivity of plant communities (Artamendi et al., 2025; Katumo et al., 2022; Woodcock et al., 2019) lacks an equally developed mirrored perspective, describing the floral diversity that supports pollinator populations.

Network theory provides a useful framework to summarize patterns of plant–pollinator interaction

(Burkle & Alarcón, 2011), but most studies under this framework have yet to account for how the scope of networks is influenced by the interaction types that define links. Existing methodologies for reconstructing interaction networks tend to emphasize structural patterns, while overlooking the functional outcomes of interactions that are critical for understanding how plant communities support pollinators (Quintero et al., 2022). In *Apidae* species, for example, plant interactions may have several outcomes. Bees consume plant material, including pollen, nectar, or even plant tissue (Pashalidou et al., 2020; Vaudo, 2015). They also collect pollen on their corbicula for transport to the nest for feeding drones and larvae (Leach & Drummond, 2018; Vaudo, 2015). Finally, visitation of the reproductive parts of flowers can have various outcomes for both the plant and pollinator, including pollen transfer (Emer & Memmott, 2023) and pathogen transfer (Lignon et al., 2024) . Interaction networks generally represent only one of these outcomes, although each is important to understanding how plant taxa support pollinators.

The importance of different outcomes in plant-pollinator interactions becomes clear when considering the biodiversity necessary to support pollinators across life stages. Because the resources needed for a foraging adult pollinator are different from those needed at the larval stage, or by other colony members (Leach & Drummond, 2018; Vaudo, 2015), transported pollen may not completely represent the interactions necessary to sustain adult pollinators. This is especially true for bumblebees (*Bombus spp.*), which are able to evaluate pollen resource quality to discern foraging choices (Leonhardt & Blüthgen, 2012; Timberlake, de Vere, et al., 2024). Bumblebees make trial-and-error floral visits in order to find adequate forage (Selva et al., 2024), which may result in pollen transport without consumption. Conversely, consumption, or simply visitation, may occur without resulting in transport (Popic et al.,

2012). Accounting for different interaction outcomes, such as visitation, transport, and consumption, is a critical next step in representing the network of plant diversity used by pollinators.

Incorporating the pollinator-perspective by leveraging complimentary methodologies can produce a comprehensive understanding of the contexts within which plant-pollinator interactions occur. Microscopy and molecular analyses of pollen load samples sourced from insect specimens often identify greater plant species diversity within interaction networks compared to only field observations of floral visitation (Baksay et al., 2022; Bosch et al., 2009). Additionally, studies adopting a pollinator-centeric view have revealed greater detail in forage preference trends, such as how pollinators use forage quality or quantity-based strategies (Selva et al., 2024; Timberlake, de Vere, et al., 2024), seasonal changes (Leponiemi et al., 2023), life cycle timing, and metabolic specialization (Vaudo, 2015)

Genetic tools can detect plant-pollinator interactions that may be unobserved in pollen microscopy and traditional field surveys (Arstingstall et al., 2021; Bell et al., 2016; Lowe et al., 2022; Pornon et al., 2017), and target specific interaction types. Metabarcoding of conserved gene regions from pollen samples can complement field observations of visitation (Arstingstall et al., 2021; Bell et al., 2017), increasing species detection by 9 - 144% (Baksay et al., 2022; Milla et al., 2022; Smart et al., 2017) and network sampling completeness up to 30%, while reducing exaggeration of specialization (Arstingstall et al., 2021) and revealing interactions beyond the traditionally surveyed floral community (de Vere et al., 2017; Milla et al., 2022). Advances in the reliability and accessibility of sequencing technologies have made these approaches more feasible for studying plant-pollinator interactions.

Most pollinator interaction network studies that apply metabarcoding focus on the external pollen loads of bees or pollen stored in nest reserves of honey and beebread (Baksay et al., 2022; Devriese et al.,

2024; Leontidou et al., 2021; Leponiemi et al., 2023; Selva et al., 2024), despite limitations of these sampling targets. Pollen in these samples can come from the environment, even including accumulation of windborne material (Negri et al., 2015). To account for this, past studies have ignored detections of wind-pollinated taxa (Pornon et al., 2017; Tanaka et al., 2020), although this may introduce bias to results, given that many plant taxa are both wind- and insect-pollinated (Saunders, 2018). A more fundamental issue with externally carried pollen and nest reserves is their restricted ability to represent interaction types. Corbicular pollen provides an easily obtained sample, containing pollen from one or more plant species collected for transport to the nest for brood feeding (Leach & Drummond, 2018; Vaudo, 2015), only directly representing pollen transport interactions (Arstingstall et al., 2021). Given the role of this pollen in bees' life cycles, it is often suggested as the central sample type reflecting diet, thus used to represent foraging networks (Shi et al., 2025), and considered synonymous with successful pollination interactions. This may overstate the function of corbicular pollen.

Pollinator intestinal tracts (hereafter: guts) represent an additional source for observing dietary interactions, specifically consumption of pollen and other plant material (Haag et al., 2023; Li et al., 2025; Mayr et al., 2021). Plant DNA detected in gut contents can reveal interactions with consumption as the exclusive outcome, which, in addition to flower visits, can include nectar robbing (Popic et al., 2012) and occasional herbivory (Pashalidou et al., 2020). The gut-content approach can also account for environmental contamination in external pollen and nest stores by highlighting oversights resulting from the exclusion of interactions with the anemophilous and partially-anemophilous plant taxa in external pollen studies. There is an accumulating body of evidence supporting the idea that pollinators regularly search across functional groups of the plant community to meet their nutritional needs (de Vere et al.,

2017; Ibiyemi et al., 2025; Milla et al., 2022; Pojar, 1973; Selva et al., 2024; Tanaka et al., 2020; Terrell & Batra, 1984; Timberlake, de Vere, et al., 2024; Wood et al., 2022), although little attention has been given to these observations as a potentially important part of plant-pollinator networks (Saunders, 2018). This understudied component of pollinator foraging together with the surprising lack of genetic analyses of pollinator gut contents, represents a clear knowledge gap and an opportunity to uncover finer detail in plant-pollinator interaction networks.

Our objective is to determine whether a combined methodological approach can provide further insights into pollinator forage ecology and plant-pollinator interaction networks by expanding interaction detections and providing context to network links. We assess how metabarcoding of pollinator gut contents can complement or challenge the characterization of plant-pollinator interaction networks described by more common methodologies, including field surveys of plant-pollinator interactions and external pollen load metabarcoding. To this end, we compare interaction networks constructed from each of these methodologies for a single model pollinator, *Bombus pascuorum*, an easily identified bumblebee common to most of Europe (Lecocq et al., 2015). Our focus on a single pollinator species holds pollinator identity constant and attributes differences in network structure to methodology, rather than to variation among pollinator species. We hypothesize that the consumption interactions detected in gut metabarcoding will include a network of plant taxa distinct from those detected by other methodologies. Although we expect overlap between networks constructed by different methodologies, we expect to observe previously overlooked interaction network structure, including new links and significance of network links. Ideally, the resulting combination of observations will generate a network that will elevate our capacity to detect meaningful plant-pollinator interactions, and learn more about interaction

types and implications for pollinator health.

2. Methods

Our sample collection was conducted in Gorbeia Natural Park (coord: 43.068, -2.796) , a protected area in northern Spain, under permission from local authorities (Bizkaiko foru aldundia, Reference: 2023AM36). Within Gorbeia, we selected 16 sampling sites located within the mixed zones of meadows and shrublands found at higher elevations. We conducted fieldwork from early April to the end of July, 2023 covering the main flowering period and peak annual pollinator activity in Gorbeia. On each sampling day during this timeframe, we visited field sites in pairs. Sampling days were organized into six periods, in which we sampled each site pair once per period. We conducted three types of surveys during daily peaks of pollinator activity, including floral diversity surveys ("flower counts"), interaction transect surveys, and *Bombus pascuorum* specimen collection for amplicon sequencing analyses.

Interaction transects and floral resource availability surveys

We used one 250 m transect at each site for both interaction transect and flower count surveys, recording observations within a ~2 m wide transect line. Interaction surveys were conducted three times per day, each lasting 1 h. All insects observed contacting the reproductive parts of herbaceous flowers within the transect were recorded; for this study, we retained only *Bombus pascuorum* interaction data. Surveys were spaced by ~2 hours (~11:00, ~13:00, ~15:00), and transects were walked at a constant pace to cover the full length within an hour. For each site and sampling period, one flower count was conducted by recording all of the flowering herbaceous species within the transect.

Bombus pascuorum specimens

For every period visit at each site, we collected up to five *B. pascuorum* specimens for molecular analyses (N = 126). We brought specimens back from the field and froze them at -20°C until processed. In the lab, we extracted the entire gut and honey stomach of *B. pascuorum* individuals. Additionally, if present, we collected pollen from the corbicula of specimens into sterile 1.5 mL centrifuge tubes. Pollen samples were stored individually by specimen sample at -20°C.

Gut-content DNA extraction

Genomic DNA was extracted from *B. pascuorum* guts using the NucleoSpin® 96 Soil kit (Macherey-Nagel, Düren, Germany) and amplified in duplicate using the DFD forward and ASDFAS reverse primers. To avoid site and period bias, all samples were randomized before the DNA extraction. We followed the kit manufacturer protocol, only adjusting centrifuge spin duration to account for differing maxiumum velocity available within our centrifuge (See Supporting Information). Nanodrop spectrophotometry was used to quantify DNA concentration and purity of the extracts by measuring reflectance at 260/230 nm wavelengths.

DNA extraction from corbicular pollen pellets

DNA was extracted from pollen pellets (N = 25) using the Machery-Nagel NucleoSpin® 8 Food kit, including additional initial steps recommended by the kit's supplementary protocol for pollen DNA extraction (See Supporting Information). The Qubit high sensitivity dsDNA kit (Thermo Fisher Scientific) was used to quantify DNA extract concentrations for randomly selected samples.

Amplicon sequencing

We used a dual-indexed amplicon multiplexing approach to generate our metabarcoding library, as

described previously by Donald et al. (2022). Briefly, we performed a first step amplification using the Nex-F & Nex-R tagged internal transcribed spacer 2 primer pair, ITS-S2F (Chen et al., 2010) and ITS4R (White et al., 1990), with the following modifications: (1) 3-6 N-mers to increase sequence base diversity and (2) linker sequences that complement index linker. Amplified products were checked on a 1% agarose gel for successful amplification. The resulting amplicons were used as template in the second-step PCR where unique 8-mer indices and illumina p5/p7 sequencing primers were attached. Amplicons were checked for successful amplification as above, purified, normalised and size selected using SPRI-beads, and pooled equi-volume to generate the amplicon library. The resulting library was quantified using Qubit HS kit and functional library was estimated using Colibri qPCR assay. Final library was sequenced on the illumina MiSeq 3000 instrument for 300 cycles in paired-end mode at the Ecological Genetics laboratory, Bioeconomy Science Institute, Auckland, New Zealand (Detailed methods provided in Supporting Information).

Bioinformatics: taxonomic assignment and contaminant analysis

Raw base call files (BCL) were converted to fastq using bcl2fastq2 (v2.20) tool. Demultiplexing was performed on the raw fastq files using index combinations and primer pair sequence simultaneously to minimize non-target data, resulting in paired raw reads per sample. Raw reads were processed using the DADA2 bioinformatics pipeline (Callahan et al., 2016). Reference ASVs were used to call taxonomic identities using the assign taxonomy method in dada2 in conjunction with the published ITS2 reference database of Bell (2021). We selected the database due to high species coverage for our study area. All but 21 species were identified to species level, with the remaining 21 identified to genus level. Taxonomy data were combined with sample x ASV matrix and sample metadata in phyloseq R package

(add citation) and downstream quality control and statistical analyses were performed in the R analysis environment. For contaminant and misidentified ASV removal, we used a three-step screening process. First, ASVs were analyzed for contaminants using the R package, decontam (Davis et al., 2018). Second, we conducted a BLAST search using ITS2 Database (Ankenbrand et al., 2015) to verify taxa that were identified by singleton ASVs within our results. Finally, the remaining list of taxa was screened against a locally specific herbarium (Agut & Hermosilla, 2025).

Statistical analysis

We compared the results of each methodology across methodology, time, and individual specimens. As an initial broad test of whether the methodologies detected interactions with different plant communities, we used binary presence-absence matrices to compare the communities detected by each methodology on each sampling day. Data were aggregated by sampling day for all sets of observations. Community composition was contrasted using the Raup-Crick dissimilarity index in a PERMANOVA test within the R package, vegan (Oksanen et al., 2024) with methodology as the independent variable. Further pairwise comparisons of these data were made by subsetting the dissimilarity matrix used in the first test by each unique methodology pair and using multiple pairwise PERMANOVAs. We also used vegan to observe beta dispersal of our data as a further means of testing the assumptions of PERMANOVA analysis.

From the 126 *B. pascuorum* specimens, we obtained both gut-content and pollen sequence data for 23 individuals. Using this subset of paired samples, we compared the plant communities detected by the two metabarcoding methodologies at the individual sample level without aggregation. As before, Raup-Crick dissimilarity matrices were calculated using binary detection data from pollen and gut detections.

PERMANOVA compared both methodologies' detected communities in strata defined by specimens of sample origin.

B. pascuorum-plant interaction network metrics

We used interaction frequencies from the three methodologies to build *B. pascuorum*–plant interaction networks and calculate species-level metrics for plant importance and specialization. Plant importance was defined as the proportion of all *B. pascuorum* interactions involving a given plant genus. For metabarcoding and pollen-load data, interactions were counted as the number of individual bee samples in which a plant genus was detected; for observational data, interactions corresponded to recorded visits. Species-level specialization (*d'*) was calculated following Blüthgen et al. (2006), as implemented in the R package bipartite (Dormann et al., 2009).

We created a composite interaction network for *B. pascuorum*, incorporating the data of each methodology and the interaction outcome types as network metadata. Network nodes included *B. pascuorum* and the list of plant genera detected across the three interaction datasets. Single plant genera were assigned between one and three links corresponding to interaction type, depending on their detection across methodologies.

3. Results

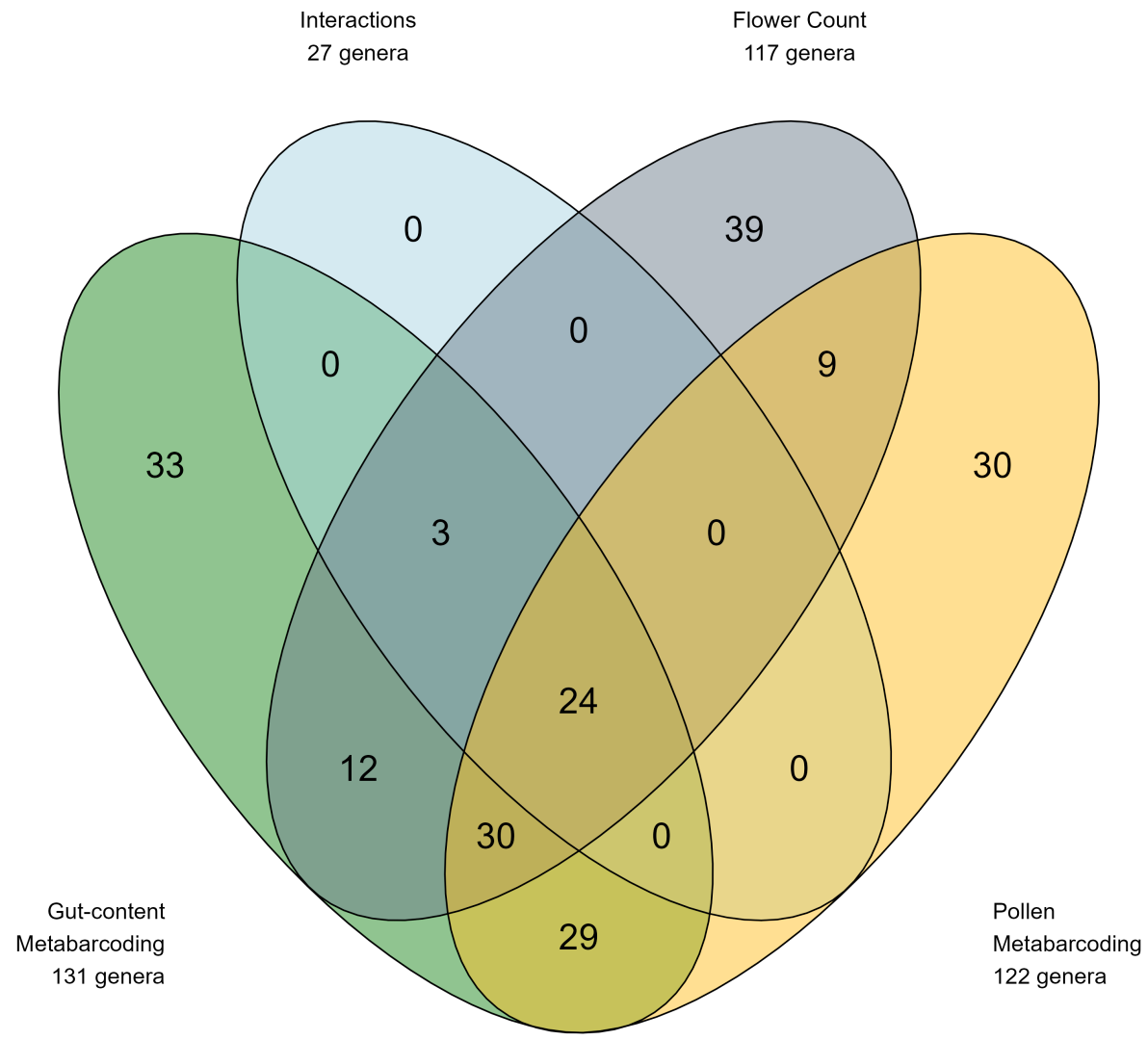
Assessment of floral resource use relative to availability

Within our flower count surveys we registered a total of 117 flowering herbaceous plant genera across the sampling season, representing the pool of floral resources available to *B. pascuorum*, which interacted with only a subset of this diversity (Fig. 1). In fact, 39 genera recorded in flower counts

were absent from the interaction networks generated by any of the methodologies. Interaction transects revealed interactions with 27 genera (23% of total floral diversity), while gut-content and corbicular pollen metabarcoding revealed interactions with 58% and 53% of available taxa, respectively.

Comparison of interaction detection by methodology

Between all pollen metabarcoding samples, we obtained 5,160 ASVs within 2,506,925 reads, while in 122 of the gut-content metabarcoding samples, we identified 2,302 ASVs from 2,973,224 reads (See Supporting Information). Before quality screening of results, 251 taxa were identified by both metabarcoding methodologies in total. After screening, 170 total taxa remained identified within our data. Both metabarcoding methodologies detected multiple unique taxa (33 taxa for gut contents and 30 for corbicular pollen), while interaction transects did not detect any unique interactions (Fig. 1). The two metabarcoding methodologies shared 83 common plant genera, representing 68% of the total corbicular pollen diversity and 63% of the gut content diversity.



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241 ***Figure 1****: Total diversity and overlap of plant genera observed by four observation methodologies:*
242 *transect surveys of floral diversity ("flower counts") and Bombus pascuorum - flower interactions,*
243 *and metabarcoding of plant DNA in corbicular pollen and gut contents of B. pascuorum.*

244 Taxonomic diversity varied across sampling periods, revealing distinct temporal patterns in flower-
245 ing taxa and interactions (Fig. 2). Although floral and interaction diversity increased overall from

the first to the last period, flowering taxa peaked in period four, whereas interactions peaked in period six. Metabarcoding consistently detected more taxa than interaction transects, with gut-content metabarcoding outperforming all other methods. In periods one, two, and six—before and after peak flowering—gut metabarcoding detected 59% more taxa than were recorded in flower counts on average, while in periods three to five floral diversity exceeded gut-content diversity.

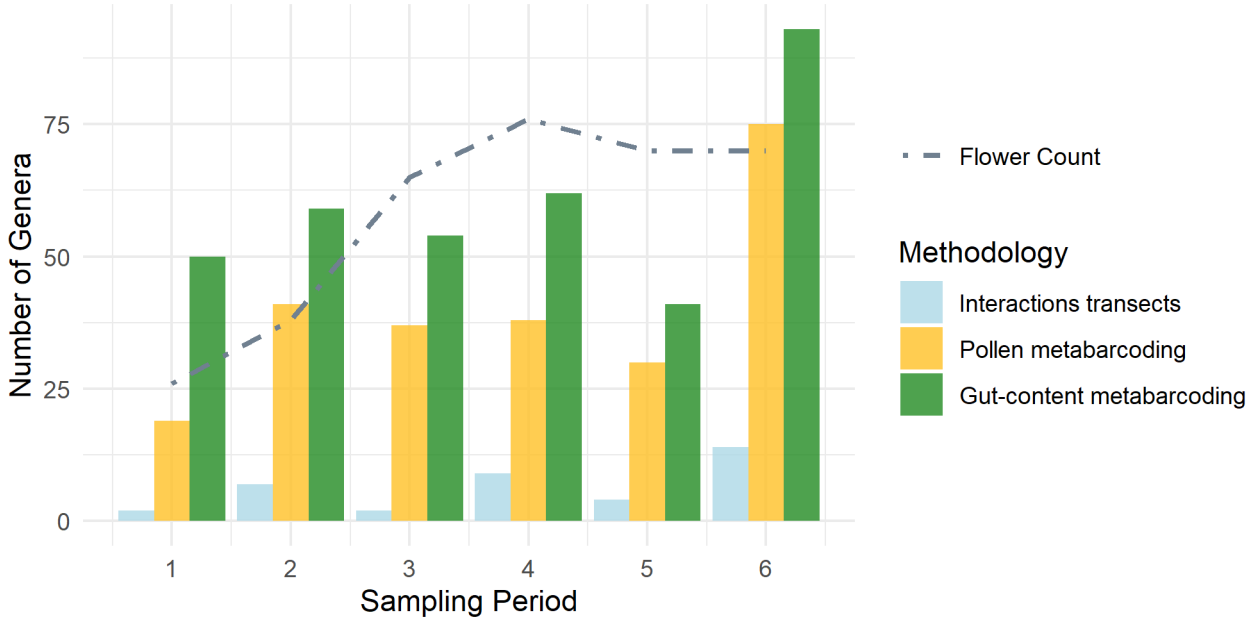


Figure 2: *Taxonomic diversity in Bombus pascuorum interaction networks over six sampling periods (April - August, 2023) observed through floral visitation surveys and ITS2 metabarcoding of DNA extracted from bumblebee gut contents and corbicular pollen loads. The results of each methodology correspond to samples or surveys taken across the same 48 sampling days. The number of plant genera indicated is a cumulative raw value for each methodology and period, with no standardization for sampling effort. Interaction diversity for transects is represented by the total number of plant taxa observed over each transect and sampling day, for each period. For metabarcoding methodologies,*

interaction diversity is the total number of plant genera observed across all samples collected during the given period.

Functional diversity observations

The design of interaction transects only included taxa from the entomophilous community, while both metabarcoding methodologies detected taxa from the anemophilous community as well, representing 28% (N = 41) of the total identified plant genera between the two methodologies. Among these were 20 genera from *Poaceae*, nine tree or woody plant genera, and 12 other herbaceous genera (See Supporting Information Fig. S3). During periods one, two, and six—when gut-content metabarcoding detected more taxa than the entomophilous community recorded in transects—an average of 13% of those taxa were anemophilous or partially anemophilous (See Supporting Information, Fig. S4).

Plant community composition across methodologies

A PERMANOVA test comparing taxonomic composition of interaction plant communities between methodologies indicated a significant effect of methodology on the observed community ($P < 0.001$, $R = 0.28$). In this analysis, interaction transects showed high beta-dispersal (distance to centroid = 0.62) compared to the more centered metabarcoding and flower count results (distance to centroid ≤ 0.10), and an ANOVA test of mean dispersal by methodology indicated different levels of dispersal ($P < 0.001$) for each methodology. The communities detected by each of the methodologies were also visualized using non-metric Multidimensional Scaling (nMDS, stress = 0.17, Fig. 3). Pairwise comparisons (Table 1) showed that the plant communities detected by flower counts were different from those of all other methodologies ($P < 0.001$, Holm-Bonferroni), although between pairs of interaction methodologies, no differences were observed.

Table 1. *Pairwise tests comparing the community composition of plant taxa detected by four methodologies. Detected communities were compared by repeating PERMANOVA tests for each methodology pair. Tests applied the Raup-Crick dissimilarity index with 9999 permutations, and adjusted p-values were calculated using the Holm–Bonferroni method. The summarized test statistics include degrees of freedom for each methodology (DF), R^2, test F-statistics (F) and associated p-value (p), as well as the adjusted p-value.*

Methodology 1	Methodology 2	DF1	DF2	R^2	F	p	Adjusted p
flower count	gut metabarcoding	1	1	0.534	161.69	<0.001	<0.001
flower count	pollen metabarcoding	1	1	0.376	64.95	<0.001	<0.001
flower count	interaction	1	1	0.230	37.64	<0.001	<0.001
gut metabarcoding	pollen metabarcoding	1	1	0.130	9.38	0.0369	0.111
gut metabarcoding	interaction	1	1	0.010	0.80	0.55	1
pollen metabarcoding	interaction	1	1	-0.024	-1.13	0.997	1

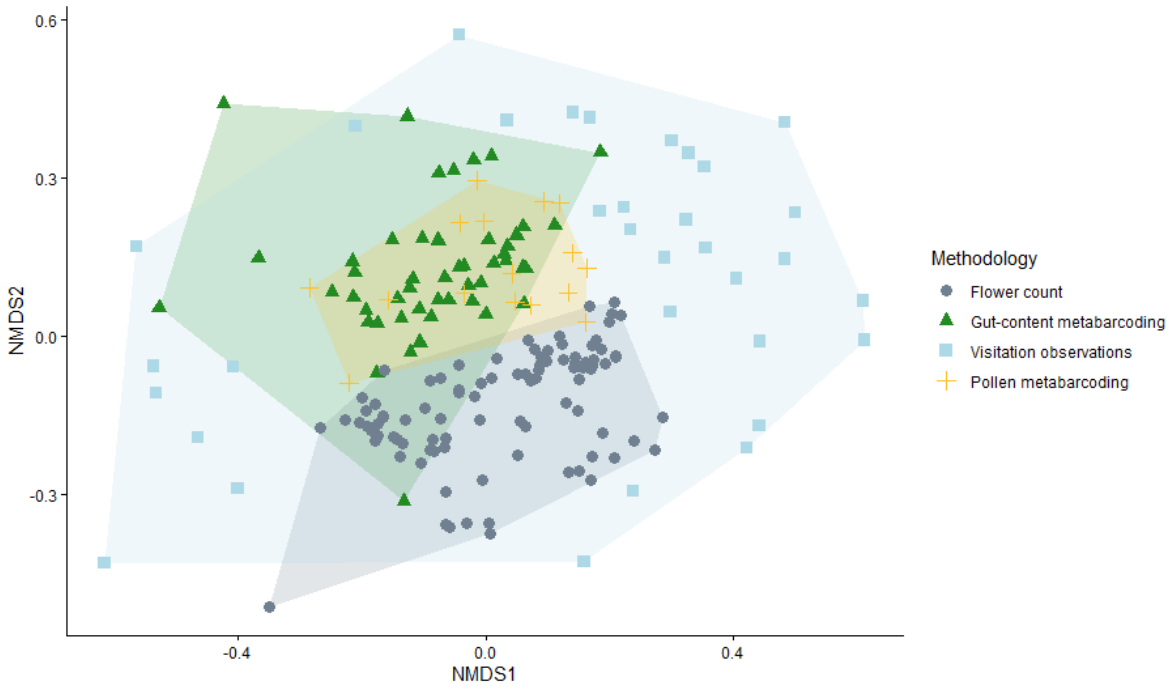


Figure 3: *Non-metric multi-dimensional scaling plot of plant communities detected by three methodologies for observing Bombus pascuorum floral interactions and a flower diversity survey. Observations from each methodology are aggregated by sampling day, reduced to binary presence/absence data, and compared in ordination using the Raup-Crick dissimilarity index (ordination stress = 0.17).*

Gut-content vs. pollen-derived plant communities from paired samples

Comparing metabarcoding results from the same specimens, gut contents yielded fewer taxa (mean = 13 genera, sd = 9) than pollen samples (mean = 19 genera, sd = 7). On average, only 21% of taxa (mean = 7 genera, sd = 3) were shared between the two sample types. A PERMANOVA with specimen as a blocking factor indicated a difference in the plant community observed by both sample types (See Supporting Information Table S2) explaining 18% of the variation between gut- and pollen-based detections. Data used in this comparison were similarly dispersed (distance to centroid = 0.08), with no

difference between the two groups observed by a permutest.

Species level interaction network

We calculated interaction specialization of *B. pascuorum* and an importance metric for the plant taxa within interaction networks. Specialization [*d'*; Blüthgen et al. (2006)] declined over the season for transect and pollen-metabarcoding data but remained relatively stable for gut-content metabarcoding (Fig. 4), with transects indicating complete specialization in the first period. Across all methods, *Lotus* emerged as the most important plant genus, though the structure of importance differed: the two metabarcoding networks showed more evenly distributed importance values (Fig. 5b-c), whereas the transect network was dominated by a few top taxa (Fig. 5a).

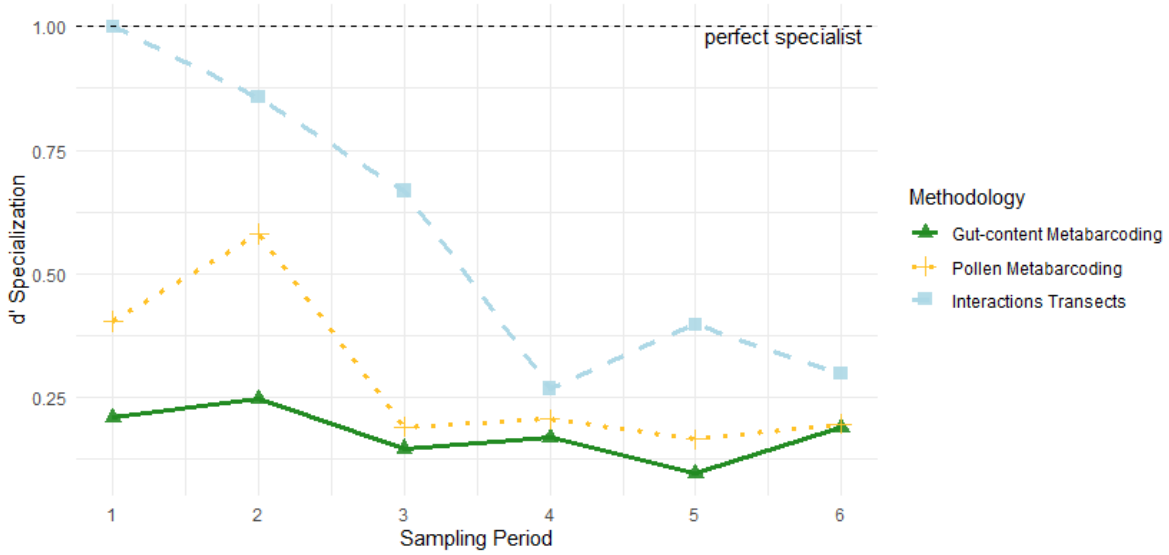
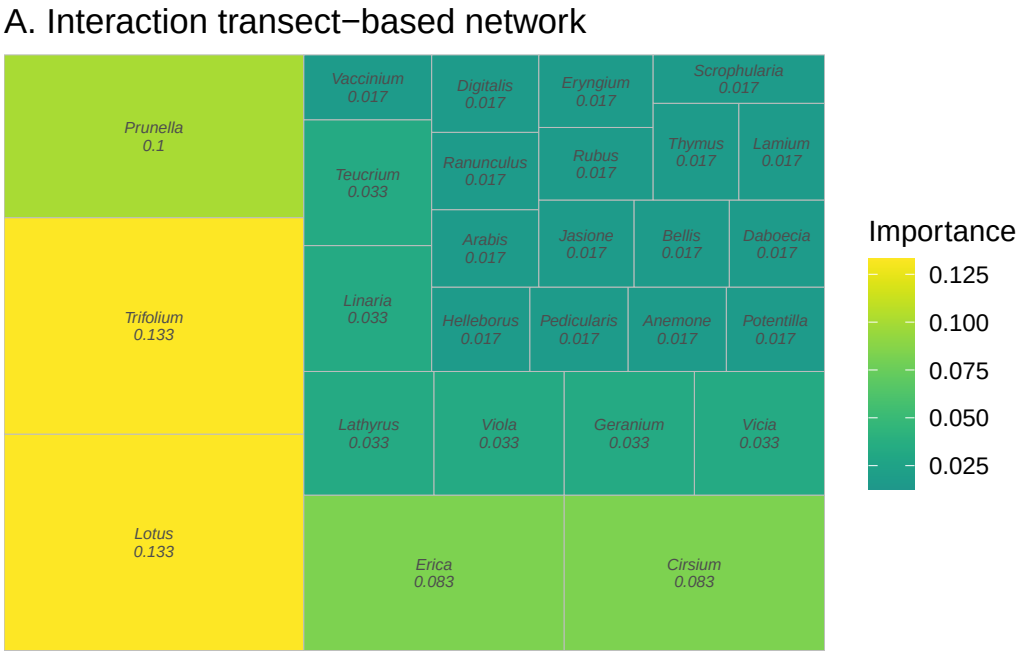
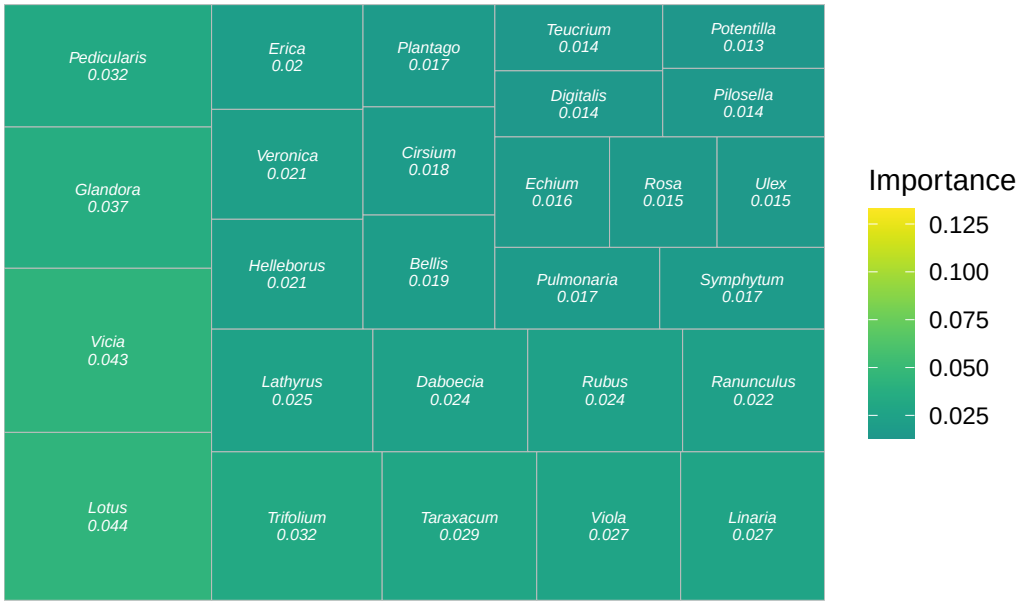
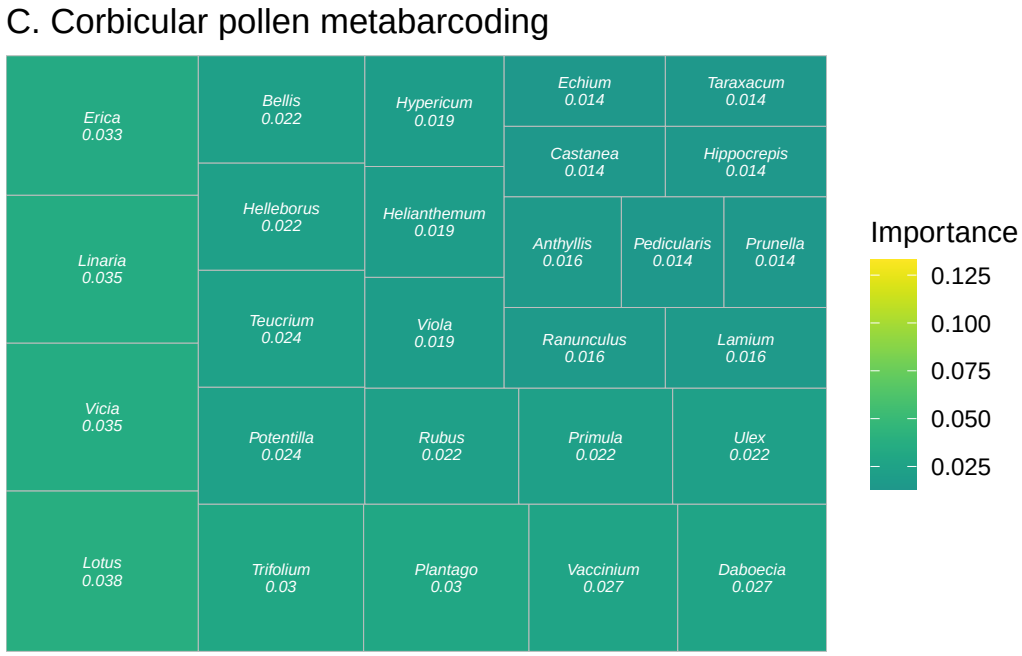


Figure 4: *Specialization of plant interactions for Bombus pascuorum as indicated by networks constructed from three interaction observation methodologies. Specialization was calculated as d' using the methodology of Blüthgen et al. (2006), with d' = 1 representing perfect specialist behavior. Specialization of B. pascuorum for each period was calculated relative to interaction data from the same*

species in other periods, rather than other pollinator species.







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316 ***Figure 5.*** *Plant "importance" within Bombus pascuorum interaction networks constructed from three*
317 *interaction observation methodologies: (**A**) interaction transects, (**B**) gut-content metabarcoding, and*
318 *(**C**) corbicular pollen metabarcoding. Importance was calculated as the proportion of total plant inter-*
319 *actions observed by the given methodology represented by interactions with the specific plant genus.*
320 *Importance is visualized with block size proportional to importance, and color scaled to minimum and*
321 *maximum values observed by each methodology.*

322 *Combined interaction network*

323 We combined the results from each interaction methodology to create an interaction network for *B.*
324 *pascuorum* with links defined by interaction outcomes, including consumption, transport, and visitation
325 (Fig. 6). This single species network included 170 nodes, increasing the number of taxa included in
326 the network compared to individual methodology constructed networks. Additionally, each plant taxa

received up to three links, including link metadata for interaction outcomes in the network. In total, the network contained 281 descriptive links.

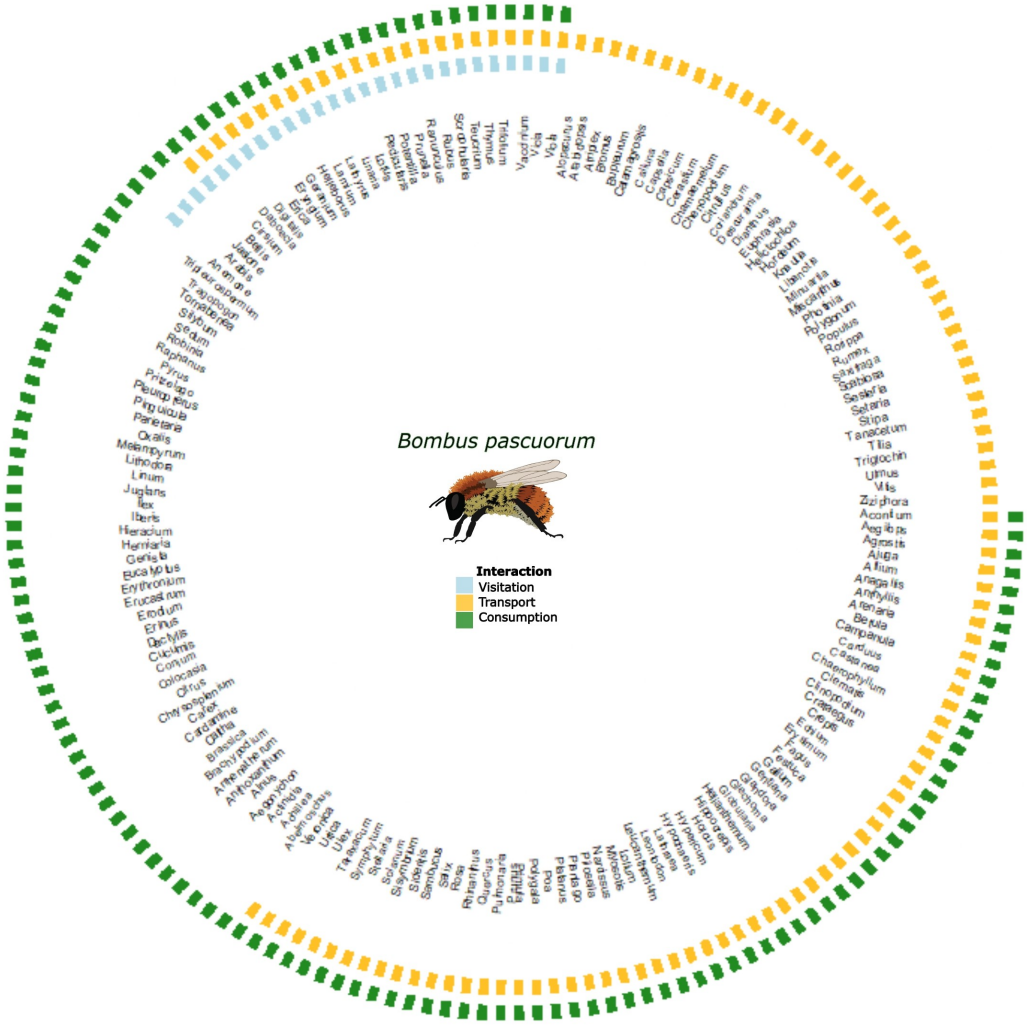

Figure 6. *Combined interaction network for Bombus pascuorum including all interaction plant taxa detected by three methodologies. Interaction transect observations are represented by visitation, corbicular pollen metabarcoding observation by transport, and gut-content metabarcoding observations*

by consumption. The network includes 170 plant genera, each with up to three links describing the outcomes of interactions with the single pollinator species. Interactions providing links represent the presence or absence of any interaction observation within the dataset of a given methodology.

4. Discussion

Plant-pollinator interaction networks are complex. We show that using functionally informative network links and combining methodologies yields a comprehensive and strongly validated plant-pollinator interaction network. Notably, the two metabarcoding approaches revealed shared interactions with anemophilous and partially anemophilous plants for pollen consumption and transport, highlighting the complementarity of their data. Although each interaction methodology overlapped statistically at the aggregated level, the combined network resulting from each methodology increased the total nodes, and each methodology provided context to network links. Metabarcoding alone also proved effective at capturing a broad range of links and providing detailed, specimen-level data. Important information from the function of links is missing under the current approach to characterizing interaction networks, but using multiple methodologies helps to fill these gaps.

We compared each methodology in terms of the diversity of detected interactions, assignment of relative importance of plant taxa and specialization of *B. pascuorum* within the resulting network, and observed plant community composition. Consistent with previous comparisons between field and metabarcoding observation of plant-pollinator interactions, metabarcoding increased observed interaction diversity (Baksay et al., 2022; Milla et al., 2022; Smart et al., 2017), in our case by more than six-fold compared to interaction transect results. Considering this, and the time dedicated to data collection for both types of methodologies, metabarcoding was a more efficient approach. Interaction transects did provide the

advantage of greater taxonomic resolution, as we were able to detect interactions at the species-species level, whereas metabarcoding provided species-genus level interactions. Beyond taxonomic detection capabilities, the results from each methodology allowed for network-level cross-validation.

Network topology and specialization patterns differed markedly across methodologies. Interaction transects tended to overstate both the degree of specialization and the dominance of the most frequently visited plant taxa. Although *B. pascuorum* is known to form strong early-season associations with certain plant species (Artamendi et al., unpublished dataset), the metabarcoding approaches indicated much lower specialization and produced more evenly distributed network structures. These results mirrored previous interaction networks constructed for individual pollinator species, which also have shown a tendency towards representing pollinators as specialists when using field observation data versus the generalist behavior indicated by metabarcoding data (Arstingstall et al., 2021). Overall, the combined datasets across methodologies suggested a more diverse foraging niche than visitation data alone would have implied.

The three methodologies showed complementary patterns in network composition. Flower counts and interaction transects overlapped as expected from the study design, yet differed statistically, likely due to the much larger number of taxa detected by the former. No statistical differences were found among the three interaction-focused methods, although their dispersion differed, reflecting variation in spatial and taxonomic coverage. Interaction transects are shaped by local habitat and plant-community differences, whereas metabarcoding integrates interactions across the broader landscape, producing more consistent results. Metabarcoding approaches overlapped minimally with the floral community detected by flower counts, indicating that interaction networks include taxa not captured within tran-

sects. This is unsurprising given that flower counts reflect potential, not actual, interactions and are constrained by spatial and temporal limits that do not restrict metabarcoding.

Between the two metabarcoding approaches, gut-content metabarcoding captured greater overall taxonomic diversity and was more efficient, given that every specimen provided a gut sample, but not necessarily a pollen sample. Pollen samples detected more taxa per individual, however, and hypothetically offered an advantage as a non-lethal sampling option. The combination of both methodologies' results broadened the interaction network greatly, and incorporated contextualized interaction links. These links showed which plant genera were consumed for adult bee nutrition, and which provided pollen for transport to the nest. In our case, gut-content metabarcoding was particularly informative for revealing seasonal foraging patterns, detecting more consumed taxa than were flowering in the early and late parts of the season, and showing relatively stable specialization over time. Together, these results indicated that the plant community represented in consumption-based interactions differs from the floral community captured by field- and pollen-based surveys.

Metabarcoding observes forage across functional groups

The diversity of plant groups observed within our metabarcoding data, especially the temporal changes in diversity observed by gut-content metabarcoding, indicated that *B. pascuorum* forages on different plant taxa than previously expected. Through metabarcoding, we observed interactions with a variety of taxa outside of the entomophilous meadow and shrubland plant community, including trees and shrubs, grasses, and other herbaceous plants. Our observations of anemophilous plant interactions are supported by previously documented records for *Bombus* species (de Vere et al., 2017; Ibiyemi et al., 2025; Milla et al., 2022; Pojar, 1973; Selva et al., 2024; Tanaka et al., 2020; Terrell & Batra, 1984;

Timberlake, de Vere, et al., 2024; Wood et al., 2022), and have especially intriguing implications for bumblebee forage behavior. Previous studies using external pollen metabarcoding have removed wind-pollinated taxa from their analyses under the argument that wind-borne pollen in samples may represent false positive interactions (Negri et al., 2015; Pornon et al., 2017; Tanaka et al., 2020). Our gut-content results, however, caution against the practice of removing these taxa as contaminants, especially if using external pollen loads as standalone proxies for forage networks.

The presence of DNA from anemophilous taxa within gut samples suggests that interactions with these taxa may be more than coincidental interactions with pollen in the environment. Indeed, beyond consumption for adult nutrition, there are previous indications that pollen from flowering trees supports colony establishment success and low larval mortality (Wood et al., 2022). Our results support the hypothesis that most bumblebees forage selectively for consumption and transport of high quality pollen (Ruedenauer et al., 2016; Timberlake, de Vere, et al., 2024), adapting their forage to take advantage of the best available resources as they change with environmental variability (Selva et al., 2024). While it is possible that some plant material may be transported or consumed incidentally (Arstingstall et al., 2021), the taxa detected within *B. pascuorum* gut contents and corbicular pollen form part of the web of biodiversity that supports the species and possibly other pollinators. Our detection of anemophilous plant DNA in both metabarcoding methodologies indicates that *B. pascuorum,* and perhaps other bumblebee species, may intentionally forage on these taxa to meet nutritional needs at various life stages.

Existing hypotheses for pollinator forage adaptations in response to environmental changes have suggested that bees expand forage diversity beyond the flowering community and across habitats in order to survive annual "hunger gaps" (Becher et al., 2024; Timberlake, Tew, et al., 2024), when blooming

floral species are limited (Morozumi et al., 2022; Wood et al., 2022). Our observation of high forage diversity in gut contents before and after the floral peak, distinct interaction and flowering taxa network topologies, and consumption of taxa across functional groups, all together support these hypotheses. While the floral community beyond the immediate area of our transects likely played a large role in these observations, the detection of anemophilous taxa in gut contents during the periods where forage diversity was higher than flowering diversity provide evidence for a community driven component as well. These observations show how the broader taxonomic detection capacity of metabarcoding allows for detection of interactions that otherwise would go unobserved by flower visitation surveys. This advantage is extended when working with metabarcoding data at the individual sample level, where greater resolution for interactions is obtainable.

Metabarcoding offers individual level analysis

Our comparative analyses understate the resolution of the metabarcoding derived data. We aggregated detections by sampling day to balance effort across methods, overlooking the individual-level detail that metabarcoding can provide. When we compared taxa detected from paired pollen and gut samples at the individual level, overlap was low, revealing a difference between sample sources that was not apparent in comparisons of aggregated data. This difference likely reflects the different roles of corbicular pollen and immediately consumed pollen in the nutrition needed for different life-cycle stages (Vaudo, 2015). Taxa repeatedly detected by both methods increased confidence in their importance. For instance, the consistent appearance of *Vicia* in both sample types early in the season supports field observations of a strong association between *B. pascuorum* and *Vicia* species (Artamendi et al., unpublished data), again underscoring the value of integrating field surveys with laboratory-based methods.

Despite the greater depth and resolution that metabarcoding provides to network characterization, it must be acknowledged that the methodology is imperfect. Primer and marker biases result in preferential amplification of certain sequences, making some taxa more or less likely to appear in final results. We also chose to use the ITS2 region as a target for amplicon sequencing, while other viable marker genes provided competitive options for targeting plant taxa (Espinosa Prieto et al., 2024), and could have yielded different results. Finally our reference database was inevitably likely to have been incomplete or unbalanced in terms of available sequences for matching our data to ASVs and taxa. In response to these limitations, we further suggest that combination with other interaction methodologies is likely to be the most effective way to overcome inherent methodological oversights.

Conclusions

The similarities between interaction data suggest robustness between each methodology, and the inherent implications of the sample sources of each provide varied means of interpreting different interactions. Interaction transects provide a valuable field-based perspective, although given their lower sampling efficiency, incorporating them as a validation of other surveys may be the best way to integrate this methodology into future studies. Field observations can fill gaps left by metabarcoding methodologies, such as confirmation of pollination efficacy, interaction frequency, and species-level resolution. As a direct observation of the pollen transported to the nest, corbicular pollen may also be a good starting point for identifying plants that may provide pollen with optimal macronutrients for larval development. Similarly, gut-content metabarcoding provides an important perspective on the nutritional needs of actively foraging pollinators, identifying taxa that provide pollen as food for supporting this activity (Li et al., 2025). Knowing which taxa are actually ingested by pollinators is

especially useful for identifying taxa that facilitate microbiota exchange and acquisition during plant interactions (Cullen et al., 2021; Keller et al., 2021), including parasite and disease transfer (Lignon et al., 2024). Although they are not equal, our research highlights overall that each methodology offers advantages and disadvantages in terms of sensitivity, sampling effort, and perspective.

While most of the methodologies we applied, aside from gut-content metabarcoding, have previously been used independently to characterize plant–pollinator networks (e.g., Devriese et al., 2024; Magrach et al., 2023), our findings highlight the synergistic value of integrating them. Gut-content metabarcoding emerges as a promising approach, but its greatest potential is realized when combined with established approaches. A key next step is improving our ability to quantify interaction frequencies at the individual level using metabarcoding, whether from gut contents or pollen. Overall, methodological advances are likely to come from linking complementary data sources to fill the informational gaps left by any single approach.

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