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Characterization of wild bee communities in apple and blueberry orchards

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- **Abstract** 1 Wild bees provide invaluable ecosystem services in agricultural landscapes such as pollination. However, in recent decades, pollinator biodiversity, especially in wild bees, is declining on a global scale, with potentially far-reaching consequences for crop production. Thus, there is an urgent need to determine whether wild bees are present in agricultural systems, such as fruit orchards.
 - 2 In the present study, we examined the wild bee fauna at species and community levels during the period of bee activity (May to August) in apple and high-bush blueberry orchards in New England.
 - 3 Bee communities are crop-specific and dominated by very few species, which fluctuate according to crop and season. The blueberry associated bee fauna was more diverse. In apple, communities were phylogenetically clustered at the genus level and dominated by solitary ground nesting bees within the genus *Andrena*. Species fluctuated widely in presence and abundance throughout the season, leading to differences in community composition and functional trait structure.
 - 4 The results obtained in the present study show that apple and blueberry harbour a distinct and diverse bee fauna that performs vital pollination services in orchards. Our results provide essential baseline data for wild bees in blueberry and apple orchards and this can be used to improve management and conservation strategies for wild bee preservation in these crops.

Keywords Community composition, functional traits, native bees, network, phenology, phylogenetic diversity.

Introduction

Pollinators perform vital ecosystem services for native and agricultural plants (Klein *et al.*, 2007; Kremen *et al.*, 2007; Ollerton *et al.*, 2011). In agricultural systems, crop production is greatly enhanced by pollination services worth \$200 billion dollars worldwide annually (Klein *et al.*, 2007; Kleijn *et al.*, 2015). With the rise of agricultural intensification, services provided by managed bees, such as the domesticated honey bee (*Apis mellifera*) and, to a lesser degree, bumble or mason bees (e.g. *Bombus, Megachile* and *Osmia*) are most heavily relied upon because these can be readily deployed in the agricultural landscape to accommodate pollination during crop flowering time (Klein *et al.*, 2007; Potts *et al.*, 2010). Because domesticated bee colonies have shown drastic reductions in

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numbers and performance in recent decades, as a result of stress, diseases and parasites (van Engelsdorp *et al.*, 2008; Potts *et al.*, 2010; Goulson *et al.*, 2015; Brown *et al.*, 2016), they cannot solely be relied upon for these vital crop pollination services. This sparked increased interest in assessing the crop-associated wild pollinator fauna in farms and orchards.

Wild insects, especially bees, perform pollination services for a multitude of crops, ranging from sunflower and rapeseed to multiple vegetable and fruit crops (Klein *et al.*, 2007; Winfree *et al.*, 2008; Garibaldi *et al.*, 2013). A diverse and locally distinct wild bee fauna is associated with apple orchards throughout north-eastern U.S.A. and Europe (Gardner & Ascher, 2006; Sheffield *et al.*, 2013; Russo *et al.*, 2015; Gibbs *et al.*, 2017) and with blueberry farms (Tuell *et al.*, 2009; Bushmann & Drummond, 2015). In orchards, flower visitations by wild bees are beneficial because wild bees can pollinate some crops (e.g. berries and almonds) more efficiently than domesticated bees (Garibaldi *et al.*, 2013). Crop productivity, measured as fruit size and/or seed set, has been linked to the presence of a diverse wild bee fauna, in terms of species richness (Klein et al., 2012; Rogers et al., 2014; Campbell et al., 2017), abundance (Isaacs & Kirk, 2010), phylogenetic diversity (Grab et al., 2019) and functional group diversity based on traits, such as body size, nesting habits and/or sociality (Blitzer et al., 2016; Woodcock et al., 2019); but see Ratti et al. (2008). However, positive relationships of biodiversity and ecosystem services might not be generalizable across all agricultural systems because the abundance of a few dominant wild bee species in the community deliver the majority of the pollination services in a variety of crops, including watermelon, cranberry and blueberry (Winfree et al., 2015). This suggests that wild bee surveys describing common and rare species are invaluable for crop-associated pollinator assessments. Based on these multifaceted ecological relationships and the difficulties in discerning generalizable patterns, the diversity and function of wild bees in many agricultural systems and geographical regions remains elusive. Although some regions are well documented (e.g. New York, Michigan, California), less information exists about the crop-associated wild bee fauna in fruit orchards in New Hampshire.

In New Hampshire, apple (Malus domestica Borkh.) and high-bush blueberry (Vaccinium corymbosum L.) are locally important crops (USDA NASS, 2011). Apple belongs to the plant family Rosacea; five white petals shape a relatively flat or shallowly cup-shaped flower, with conspicuous stigma and whorls of stamens (Pratt, 1988). They are self-incompatible and insect mediated pollination services are essential for successful fruit production (Free, 1964; Garratt et al., 2014). As such, apple orchards associated with a diverse wild bee fauna show greatly enhanced fruit productivity (Garratt et al., 2014; Blitzer et al., 2016; Grab et al., 2019). Recently, wild bee surveys across several apple orchards in the eastern U.S.A. have shown that dominant bees in the community vary among orchards; they included species within the genera Andrena, Lasioglossum and Ceratina (Sheffield et al., 2013; Russo et al., 2015; Kammerer et al., 2016) and perhaps apple orchards in New Hampshire show a similar pattern.

Blueberry is part of the Ericaceae; its flowers comprise a bell-shaped whitish-pink corolla, with stamen and anthers inside and the stigma protruding through the opening of the corolla (Arrington & DeVetter, 2018). They are mainly bee pollinated and require sonication (i.e. buzz pollination) for adequate release and transfer of pollen between flowers (Javorek et al., 2002; Benjamin & Winfree, 2014). Because domesticated bees are not able to buzz pollinate, this crop is particularly dependent on the presence of buzz pollination capable native bees, which include species in the genera Bombus, Andrena, Osmia and Lasioglossum (Javorek et al., 2002; Ratti et al., 2008). Similar to apple orchards, wild bee surveys in blueberry orchards in northeastern U.S.A. revealed that dominant genera in the community varied with geographical location. These included Ceratina, Andrena, Lasioglossum and Augochlorella in Michigan (Tuell et al., 2009), Andrena in North Carolina (Rogers et al., 2014), and Bombus in Maine (Bushmann & Drummond, 2015). With New Hampshire being geograhically close to Maine, we anticipate Bombus to be abundant in the blueberry associated bee community. To date, the wild bee fauna associated with apple and blueberry orchards in New Hampshire has not been described.

Such baseline data provides invaluable information for farmers regarding orchard-based wild bee management and sustainable practices.

The present study characterizes the wild bee fauna associated with two locally dominant fruit crops in New England: apple and high-bush blueberry. Bees are compared between crops at the species level in terms of richness and diversity, as well as at the community level, including community composition, phylogenetic diversity and functional trait structure. We further compare the phenology of these communities in correspondence with crop bloom periods and throughout the period of bee activity.

Based on previous wild bee surveys, we hypothesize that the bee communities in apple and blueberry will be distinct, with the former being dominated by the genus *Andrena* and the latter *Bombus*. We further expect that bees will be most abundant during bloom period.

Materials and methods

Study area

Two replicate orchards, growing predominantly northern high-bush blueberry (*Vaccinium corymbosum*) and apple (*Malus pumila*), were chosen in Strafford County, New Hampshire, U.S.A. (43.2383°N, 71.0236°W). Orchards were located 17 km apart and similar in size with 10.4 ha (orchard 1) and 8.7 ha (orchard 2), featuring large stands of blueberry and apple crops. Both orchards grew multiple cultivars: for example, blueberry cultivars at orchard 1 were patriot and bluecrop, and blueray, nelson and liberty at orchards. To characterize the wild bee fauna in apple and blueberry crops, three replicate 100-m transects per crop were selected in each orchard ($2 \times 3 \times 2 = 12$ transects). Transects between crop types were approximately 500 m apart.

Bee sampling

Bees were collected from May to August 2018 using pan traps in accordance with procedures described in Tucker & Rehan (2016). In each transect, nine pan traps with alternating colours (blue, yellow and white) were filled with soapy water and placed on the ground from 08.00 h and 16.00 h on low wind sunny days. To retrieve the pan traps, the contents of the nine pans per transect were strained together and transferred into a jar filled with 70% ethanol. During bloom period (May to early June), bees were collected on a weekly base, after bloom, from mid-June onwards, bees were collected on a bi-weekly base. Eleven sampling events were carried out per orchard, resulting in 108 pan trap samples (n = 55 in orchard 1 and n = 53 in orchard 2). Monitoring bees in this fashion may introduce some bias, with effects being positive - affected by flower density (Wood et al., 2015), negative - collecting fewer species (Cane et al., 2000; O'Connor et al., 2019) or neutral (Rhoades et al., 2017).

During the blooming period, pan trap sampling was supplemented with sweep netting in the same transects, in accordance with the protocol described in Tucker & Rehan (2016). However this method accounted for <5% of individuals and <3% of species (see Supporting information, Table S1), yielded very few common and new species, and was therefore excluded.

Bee processing, identification and functional traits

Bees were processed in accordance with procedures described in Droege (2015); specimens were washed, dried, mounted and stored in the laboratory of Sandra M. Rehan at York University. Bees were identified to species level using the interactive guide Discover Life (www.DiscoverLife.org) and taxonomic literature (Mitchell, 1960; Mitchell, 1962; Michener *et al.*, 1994; Gibbs, 2011; Rehan & Sheffield, 2011; Gibbs *et al.*, 2013; Williams *et al.*, 2014).

Bee functional trait classification occurred on species level according to their (i) nesting habit and (ii) social behaviour based on published literature (Giles & Ascher, 2006; Cane *et al.*, 2007; Michener, 2007; Matteson *et al.*, 2008; Wolf & Ascher, 2008; Rehan & Sheffield, 2011; Ascher *et al.*, 2014; Sheffield *et al.*, 2014; Selfridge *et al.*, 2017). Bees were classified into ground or stem nesting depending on the substrate used: wood or pithy stems versus soil. We categorized bees into four behaviour types according to the degree of sociality: solitary (bees living solitary or loosely communal), subsocial bees known to have prolonged parental care and mother-offspring interaction (e.g. small carpenter bees), social were all primitively and advanced eusocial bees (*Apis, Bombus* and some Halictidae) and parasitic for those with a cleptoparasitic lifestyle.

Statistical analysis

Data from all sampling events (n = 11) were pooled to compare species richness and diversity and assess adequacy of sampling for each crop type. We calculated the Chao-1 index (Chao, 1984) as an estimator for species richness, Simpson's invert (1/D) as diversity index (Simpson, 1949; Magurran, 2004) and generated species accumulation curves (Gotelli & Colwell, 2001) in ESTIMATES, version 8.2 (Colwell, 2013).

Statistical analyses were conducted in R (R Development Core Team, 2017). To compare the bee fauna between crop type (apple versus blueberry), differences in bee species and abundance were analyzed using a mixed model design 'glmer.nb' in lme4 (Bates et al., 2015), analysing crop as fixed and orchard as random factor (Zuur et al., 2009). Relationships between bee communities and crop types were analyzed in three ways: (i) community composition; (ii) functional trait structure; and (iii) phylogenetic community structure. Community composition was compared between crops using the multivariate extension of generalized linear models 'manyglm' based on negative binomial distribution (Warton et al., 2012) in mvabund (Wang et al., 2012). The block function was used to account for the nested design of crops in farms (crops = fixed effect, farms = random effect) and the multivariate Wald χ^2 test statistic was used to evaluate compositional differences. Differences in bee functional traits in terms of nesting habit and social behaviour between crops were analyzed using the same approach as described for community composition.

Phylogenetic community structure was compared between crop types, using a published phylogenetic tree, based on protein-coding nuclear gene DNA sequence data, covering $> 13\,000$ wasp and bee species from Hedtke *et al.* (2013), as a baseline for further modification. Species collected during this study but not contained in the tree were added using 'add .species.to.genus' in Phytools (Revell, 2012). Surplus species were removed using 'drop.tip' in Ape (Paradis & Schliep, 2018). The resulting modified tree contained 78 species from 18 genera across five families. Phylogenetic diversity of each community was assessed using Picante (Kembel et al., 2010); we used 'ses.mpd' to calculate mean pairwise distance (MPD), a measure of average branch length of each species in the community; we used 'ses.mntd' for mean nearest taxon difference (MNTD), which is a measure for the mean distance that separates each species in a community from its closest relative (Webb, 2000; Webb et al., 2002). Both measures (MPD and MNTD) detect phylogenetic over-dispersion or clustering in a community. Expected MPD and MNTD were calculated by community randomization (999 permutations), and their standardized effect sizes (SES) were calculated by comparing the observed communities to the randomized ones (= null model). Negative SES values indicate phylogenetic clustering (i.e. species are closer related than expected) and positive SES values indicate evenness (i.e. species are spread randomly across the phylogeny).

To investigate phenology (i.e. seasonal variation of the bee fauna in regard to species richness, abundance and community), we categorized the sampling time into three periods in relation to the apple and blueberry bloom period. Both crops bloomed at the same time in spring for 2 weeks, from 17 to 31 May 2018. Thus, seasons were classified as 'pre-bloom' before 17 May, 'bloom' (17-31 May) and 'post-bloom' from June onwards. Differences in species numbers and abundances were analyzed using 'glmer.nb' in lme4 (Bates et al., 2015), and seasons were analyzed as fixed and orchards as random factors. Seasonal effects on species composition were analyzed using 'manyglm' (Warton et al., 2012) in mvabund (Wang et al., 2012), with season as fixed effect and orchards as random effect. Plant-pollinator network plots, reflecting crop-bee associations, were constructed using 'plotweb' with bee abundance data in the package bipartite (Dormann et al., 2008). We used 'networklevel' to calculate estimates of stability and robustness of the crop-pollinator association (Dormann et al., 2009), and 'specieslevel' for measures of individual bee contributions, as well as to identify the most influential and rare bees in the crop-pollinator association (Dormann, 2011). At bee species level, we calculated the number of floral hosts (i.e. if a bee species was associated with both or only one crop), and pollination service index (PSI) as a measure of relative importance of each bee species in the community, where values range from 0-1, with 1 indicating that the bee performs essential pollinator services (Dormann, 2011). At the community level, we calculated the absolute and relative number of bee species associated with each crop. Weighted nestedness was calculated as an estimate of association structure, with 1 being completely nested (i.e. interactions of generalists and specialists overlap) and 0 being chaotic with no overlap (Galeano et al., 2009). Connectance was calculated as an estimate for complexity and resilience of a community to species loss by calculating the proportion of achieved versus possible interactions, where 1 indicates robustness and 0 weakness to species loss (Dunne et al., 2002).

Results

In total, 1115 individual bees belonging to 76 species were collected using pan traps across all sites (see Supporting infromation, Fig. S1 and Table S1). The most abundant family was Andrenidae (n = 435; 39% of the total), followed by Halictidae (n = 306; 27%) and then Apidae (n = 247; 22%). The most species rich family was Halictidae (n = 24; 32%) then Apidae and Andrenidae (each n = 21; 28%). The most abundant genus was Andrena (n = 503; 38%), second was Lasioglossum (n = 205; 18%) and third was Ceratina (n = 137; 12%). The most species rich genera were Andrena (n = 20; 26%), Lasioglossum (n = 14; 18%) and Nomada (n = 9; 12%). The most abundant bee species collected was Andrena crataegi (n = 194; 16% of all individuals), followed by Lasioglossum tegulare (n = 120; 11%) and Ceratina calcarata (n = 109; 10%). Most frequent (i.e. collected in all 12 transects) were Andrena carlini and Halictus ligatus; in more than 90% of transects were Agapostemon virescens, C. calcarata, Lasioglossum tegu*lare* and *Osmia atriventris*. Rare species were 37% (n = 29), collected only with one individual (n = 20; 25%) or with two (n = 10; 13%).

Species level comparisons between crop types

Species richness, based on rarefied number of individuals (n = 369), was similar for both crops (n = 49) (see Supporting information, Fig. S2A). The blueberry associated bee fauna was slightly more diverse [Simpson's invert (1/D) = 15.69] than the apple associated fauna (1/D = 13.53). Sampling adequacy was comparable between the two crop types (78% in blueberry and 72% in apple) shown by the non-asymptotic behaviour of the species accumulation curves (see Supporting information, Fig. S2B), indicating that three quarters of the crop-associated species pool has been collected. Twice as many bees were collected from apple than from blueberry, whereas numbers of species were comparable (Fig. 1). Most abundant in both crops were the genera Andrena, Lasioglossum, Ceratina and Osmia, each collected with > 100 individuals, and together comprising 79% of the collected bees in this study (Table 1); particularly, many individuals from the genus Andrena were collected from apple; the most abundant species was A. crataegi, followed by L. tegulare, C. calcarata and A. carlini, comprising 44% of the collected bees (Table 1). In apple, there were also more Nomada, the only cleptoparasitic genus collected in this study, and Eucera pruinosa, A. virescens and O. atriventris (Table 1, see also Supporting information, Table S1). On average, significantly more bees were collected from apple than blueberry transects in terms of species (Wald $\chi 2_1 = 4.749$, P = 0.03, d.f. = 107,1) (Fig. 2A and Table 2) and individuals (Wald $\chi 2_1 = 16.767$, P < 0.0001, d.f. = 107,1) (Fig. 2B and Table 2).

Community level comparisons between crops

At the community level, a distinct bee fauna was associated with apple and blueberry crops. Species composition was significantly different between apple and blueberry (Wald $\chi 2 = 7.87$, P = 0.024, d.f. = 107.1). Differences were largely

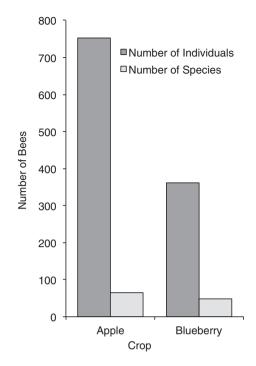


Figure 1 Number of bees (individuals and species) collected from two crop types.

driven by significantly greater abundances of A. virescens, A. carlini, E. pruinosa, Lasioglossum pectorale and L. tegulare, in apple (see Supporting information, Table S1). Phylogenetic community structure compared as MPD was not significantly different between crop types, whereas it was distinct at the tips of the phylogenetic tree: MNTD of the bee community in apple at orchard 2 was significantly more clustered than expected (MNTD SES = -1.031, P = 0.048) (Table 3). All other communities were not significantly different from expected/randomized ones (= null models). The relative distribution of functional traits was significantly different between crops for both nesting habit (Wald $\chi 2 = 4.157$, P = 0.008, d.f. = 107.1) (Fig. 3A) and social behaviour (Wald $\chi^2 = 4.528$, P = 0.02, d.f. = 107.1) (Fig. 3B). In apple, the proportion of ground nesting bees was significantly higher (Wald $\chi 2 = 4.147$, P = 0.003, d.f. = 107.1; ratio ground : stem nester 4:1) than in blueberry (ratio 2:1) (Fig. 3A). The most dominant social behaviour at both crops was solitary (n = 686; 61%), followed by social (n = 253; 23%), then subsocial (n = 137; 12%), and finally cleptoparasitic (n = 39;4%) (Fig. 3B). The proportion of solitary bees was significantly higher in apple (one-third of the community) than blueberry (one-half of the community; Wald $\chi 2 = 3.299$, P = 0.02, d.f. = 107.1).

Crop-pollinator network

The crop-pollinator network consists of 76 bee species between two crops: apple and blueberry. There were differences between crops: there were 30% more bee species associated with apple than with blueberry, resulting in a higher value for connectance (Fig. 4A and Table 4). This indicates that the apple-pollinator

	Apple	Blueberry	Overall
Genera			
Andrena	305 (40.5%)	114 (31.5%)	419 (37.6%)
Lasioglossum	149 (19.8%)	58 (16.0%)	207 (18.6%)
Ceratina	68 (9.0%)	69 (19.1%)	137 (12.3%)
Osmia	66 (8.8%)	51 (14.1%)	117 (10.5%)
Halictus	26 (3.5%)	25 (6.9%)	51 (4.6%)
Eucera	37 (4.9%)	3 0.8%)	40 (3.6%)
Agapostemon	23 (3.1%)	12 (3.3%)	35 (3.1%)
Nomada	21 (2.8%)	13 (3.6%)	34 (3.0%)
Calliopsis	14 (1.9%)	2 (0.6%)	16 (1.4%)
Apis	9 (1.2%)	6 (1.7%)	15 (1.3%)
Species			
Andrena crataegi	133 (17.7%)	46 (12.7%)	179 (16.1%)
Lasioglossum tegulare	83 (11.0%)	37 (10.2%)	120 (10.8%)
Ceratina calcarata	60 (8.0%)	49 (13.5%)	109 (9.8%)
Andrena carlini	64 (8.5%)	19 (5.2%)	83 (7.4%)
Andrena barbilabris	56 (7.4%)	10 (2.8%)	66 (5.9%)
Osmia atriventris	46 (6.1%)	16 (4.4%)	62 (5.6%)
Eucera pruinosa	37 (4.9%)	3 (0.8%)	40 (3.6%)
Agapostemon virescens	23 (3.1%)	10 (2.8%)	33 (3.0%)
Andrena vicina	24 (3.2%)	7 (0.8%)	31 (2.8%)
Halictus ligatus	15 (2.0%)	14 (3.9%)	29 (2.6%)

Percentage of site total is shown in brackets (%).

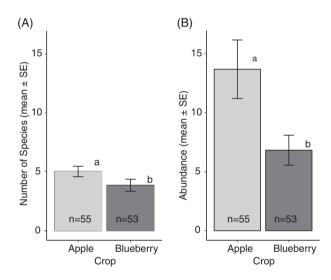


Figure 2 Bee species richness and abundance at two crops. Mean \pm SE of (A) numbers of species and (B) abundance per transect and sampling event. Small letters indicate statistical significance; *n*, sample size.

associations are more complex and robust to species loss. Weighted nestedness was close to zero for both crops, demonstrating a chaotic association with little overlap of generalist and specialist bee interactions (Table 4). Overall, 50% (n = 38) of the bee species were collected from only one crop type, of which were 35% from apple and 15% from blueberry (Fig. 4A and Table 4). These were generally low in abundance (n < 4), and some of these were singletons, occurring only once (n = 23;
 Table 2
 Summary of mixed effect negative binomial generalized linear models (glmer.Nb) for species richness and abundance of wild bees at two crops

Contrast	Estimate	SE	Z value	Pr(> Z)	Pseudo-r ²
Species richness					
Intercept	1.525	0.228	6.679	< 0.0001	0.15
Apple-blueberry	-0.300	0.138	-2.179	0.0293	
Abundance					
Intercept	2.491	0.412	5.915	< 0.0001	0.32
Apple-blueberry	-0.7807	0.191	-4.095	< 0.0001	

Shown are the model coefficient (estimate), standard error (SE), Z value, P value (Pr(>|Z|) of the chi-squared statistic and pseudo- r^2 (r^2).

 Table 3
 Summary of community phylogenetic diversity measured as mean pairwise distance (MPD) and mean nearest taxon (MNT) at two crop types and two orchards

Contrast	MPD.Obs.	P (mpd. Obs)	MNTD.Obs.	P (mntd. obs)
Apple orchard 1	-1.3915	0.297	1.1404	0.783
Apple orchard 2	1.0393	0.760	-1.0310	0.048
Blueberry orchard 1	-1.2334	0.207	1.1062	0.776
Blueberry orchard 2	-0.8219	0.371	-0.9402	0.294

Shown are standardized effect sizes based on comparison of observed versus randomized community for MPD (MPD.Obs) and MNTD (MNTD.Obs) and the *P* value *P*(*mpd.obs*) and *P*(*mntd.obs*).

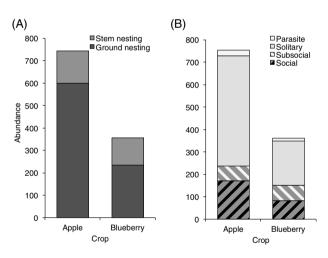


Figure 3 Bee functional trait distribution in terms of (A) nesting type and (B) social behaviour at two crop types.

30%). There were more singletons in apple (n = 17; 22%) than in blueberry (n = 6; 8%). Of particular note was *Lasioglossum pilosum*, which occurred with n = 12 individuals in apple (Fig. 4A; see also Supporting information, Table S1). PSI values for bee species were generally low, ranging from 0.0013 for singletons to 0.1635 for the most abundant species *A. crataegi* (see Supporting information, Table S1), indicating that there are no indicator/key stone species in the system and that pollination services performed by individual bee species were comparably important.

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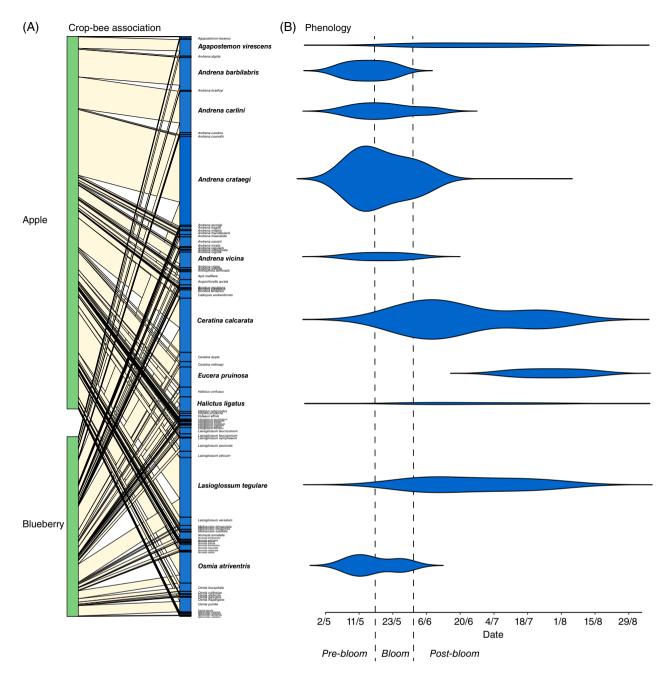


Figure 4 Plant-bee network and phenology plot over the sampling period May to August 2018. (A) Crop-bee association plot of crop (apple and blueberry) and bee species shows crop species as boxes on right and bee species as boxes on left. Box height is proportional to number of frequencies in transects, connecting lines (yellow) are abundance-weighted bee occurrences in transects. (B) Phenology plot: length of violin plots represents duration of activity throughout the season; width show relative abundance and fluctuation over time of the 10 most abundant bee species. [Colour figure can be viewed at wileyonlinelibrary.com].

Phenological comparisons of bee species and communities

Surprisingly, only 10% (n = 110) of bees were collected during bloom period (17 May to 31 May), of these, 39% were *Andrena* (n = 43), followed by 34% *Lasioglossum* (n = 17) and 5% *Osmia* (n = 10); the most abundant species were *A. crataegi* (n = 10) and *L. tegulare* (n = 9). During pre-bloom (before 17 May), a total of 56% of all bee individuals were collected

(n = 629) and post-bloom, after 31 May, 34% (n = 376) were collected. The most abundant genera during pre-bloom were *Andrena* (n = 362; 33%), *Ceratina* (n = 115; 10%) and *Osmia* (n = 106; 10%); the most abundant species were *A. crataegi* (n = 160; 14%), *C. calcarata* (n = 100; 9%) and *A. carlini* (n = 76; 7%). During post-bloom, the most abundant genera were *Lasioglossum* (n = 182; 16%), *Halictus* (n = 37; 3%); the most abundant species were *L. tegulare* (n = 120; 10%), *Eucera*

 Table 4
 Summary of crop-pollinator network level analyses for apple and blueberry

Сгор	Bee species at one crop	Number of bee species	Relative number of bee species	Weighted nestedness	Connectance
Apple	27	66	0.857	-0.2688	0.879
Blueberry	11	50	0.649	0.1499	0.720

 Table 5
 Summary of mixed effect negative binomial generalized linear models (glmer.Nb) for species richness and abundance of wild bees through the season; before blooming period (pre), during bloom (bloom) and after blooming period (post)

Contrast	Estimate	SE	Z value	Pr(> Z)	Pseudo-r ²
Species richness					
Intercept	1.199	0.243	4.944	< 0.0001	0.26
Pre-bloom	0.619	0.187	3.306	0.001	
Post-bloom	0.033	0.169	0.198	0.843	
Pre – post	0.586	0.151	-3.889	0.0001	
Abundance					
Intercept	1.456	0.372	3.913	< 0.0001	0.64
Pre-bloom	1.624	0.240	6.760	< 0.0001	
Post-bloom	0.276	0.212	1.303	0.193	
Pre – post	1.347	0.192	7.036	<0.0001	

Shown are the model coefficient (estimate), standard error (SE), Z value, P value (Pr(>|Z|)) of the chi-squared statistic and pseudo- r^2 (r^2).

pruinosa (n = 40; 4%) and A. virescens (n = 26; 2%). On average, significantly more bee species per transect and sampling event were collected before the blooming period (6.54 ± 4.14) than during bloom (3.46 ± 2.77) and afterward (3.57 ± 2.78) ; Wald $\chi 2 = 17.382$, P = 0.0002, d.f. = 106.2) (Fig. 5A and Table 5). Similarly, significantly more bee individuals were collected before the blooming period (26.21 ± 25.54) than during bloom (4.58 ± 4.04) and afterward (6.27 ± 7.24) ; Wald $\chi 2_2 = 62.072$, P < 0.0001, df 106.2) (Fig. 5B and Table 5). There were marked differences in the bee community throughout the season. Species composition changed significantly during the three periods (Wald $\chi 2 = 14.8$, P < 0.001, d.f. = 107.1). In pre-bloom, the community was composed of significantly more A. crataegi, A. carlini, Andrena barbilaris, Andrena vicina, C. calcarata and O. atriventris. During post-bloom, significantly more E. pruinosa, A. virescens, L. tegulare, H. ligatus and Lasioglossum pectrorale were present (Fig. 4B). The functional trait community structure was significantly different between seasons in terms of nesting habit (Wald $\chi^2 = 9.101$, P = 0.001, d.f. = 105.1) and social behaviour (Wald $\chi 2 = 12.3$, P = 0.001, d.f. = 105.1). Nesting habit differed significantly during the pre-bloom period because there were significantly more ground and stem nesting bees (Fig. 6A and Table 6). Similarly, social behaviour was significantly different in pre-bloom as compared with the rest of the season. These differences were mainly driven by significantly more solitary, subsocial and cleptoparasitic bees during pre-bloom and significantly more social bees during post-bloom (Fig. 6B and Table 6).

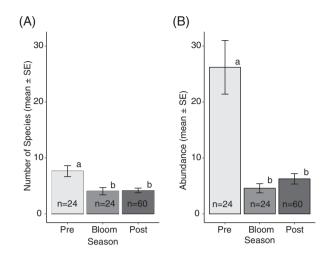


Figure 5 (A) Species richness (mean \pm SE) and (B) abundance of wild bees collected with pan traps during three seasons (pre-bloom, bloom and post-bloom). Small letters indicate statistical significance; *n*, sample size.

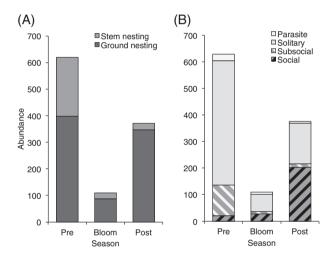


Figure 6 Bee functional trait distribution in terms of (A) nesting type and (B) social behaviour at throughout the season. Period before apple and blueberry bloom (pre), during bloom (bloom), after bloom (post).

Discussion

We evaluated the wild bee fauna at species and community level in apple and blueberry orchards in New England throughout the period of bee activity (May to August). Species richness was similar between both crops. Apple harboured numerically more bees, whereas bees in blueberry were more diverse. There were marked differences between the crop-specific bee communities. The apple associated bee community was phylogenetically more clustered at the genus level and as hypothesized dominated by solitary ground nesting bees within the genus *Andrena*. It also had a higher abundance of social bees and more unique species than blueberry. By contrast to our prediction, the community in blueberry was dominated by solitary stem nesting *Ceratina*, whereas *Bombus* was almost absent. There was a marked turnover in the bee fauna throughout the season. Bees fluctuated in species richness and abundance

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	Pre-bloom	Post-bloom	Pre – post
Nesting overall	6.784 (<i>P</i> < 0.001)	2.420 (P = 0.081)	8.467 (<i>P</i> < 0.001)
Ground nesting	4.868 (P < 0.001)	1.731 (P = 0.135)	4.168 (P < 0.001)
Stem nesting	4.725 (P < 0.001)	1.691 (P = 0.085)	7.370 (P < 0.001)
Social overall	7.736 (P < 0.001)	4.425 (P = 0.002)	11.586 (P = 0.022)
Solitary	6.261 (P < 0.001)	0.214 (P = 0.853)	7.919 (P = 0.001)
Subsocial	3.997 (P < 0.001)	0.880 (P = 0.413)	5.788 (P = 0.001)
Social	0.523 (P = 0.633)	3.656 (P = 0.003)	4.146 (P < 0.001)
Cleptoparasitic	2.097 (P < 0.043)	2.332 (P = 0.008)	4.564 (P < 0.001)

Table 6 Summary of multivariate generalized linear models (manyglm) for bee functional trait structure in terms of nesting habit and social behaviour through the season

Shown are the Wald χ^2 test statistic and *P*-value [Wald χ^2 (*P*)], for comparisons among the three periods, pre-bloom, bloom and post bloom; degrees of freedom (2,105).

throughout the season, suggesting differences in community composition and functional trait structure. Our results demonstrate that a distinct and diverse bee fauna is associated with apple and blueberry throughout the season, which may perform vital crop pollination services and enhance fruit production in orchards.

Wild bee species richness and diversity

The present study collected three quarters of the crop-associated wild bee species pool using pan traps. This compares well with previous species pool proportions collected from multiple apple orchards in New York State (Russo et al., 2015), although it is somewhat lower than the $\geq 88\%$ from high-bush blueberry in Michigan and Maine (Tuell et al., 2009; Bushmann & Drummond, 2015). Here, a larger proportion of the local species pool could have been obtained with additional collection methods (e.g. bee visitation transects, blue vein traps) (Cane et al., 2000; O'Connor et al., 2019) and/or a higher sampling effort; but see Russo et al. (2015). In the present study, bee species richness was similar for both crops – apple and blueberry (n = 53 and 51) - and numbers are comparable to other studies investigating wild bees in apple orchards (Russo et al., 2015; Blitzer et al., 2016) and low-bush blueberry fields (Vaccinium angustifolium) in Maine (Bushmann & Drummond, 2015), although it was higher than in cranberry fields (Vaccinium macrocarpon) in Massachusetts (MacKenzie & Eickwort, 1996). Here, species diversity in apple, calculated as Simpson's invert (1/D), was similar to apple orchards in Nova Scotia, Canada (Sheffield et al., 2013). We found that the blueberry associated bee fauna was more diverse than the apple associated. This is driven by large abundances of three Andrena species, A. crataegi, A. carlini and Andrena barbilabris in apple. This could also partly be associated with differences in flower volume: apple trees were generally larger and had more flowers than blueberry shrubs. Furthermore, differences in flower morphology could also have had an effect because the flat open cup-shaped apple flowers may attract more bees than the bell-shaped blueberry flowers. Similarly, species of the genus Andrena were also abundant at multiple apple orchards across the north-eastern US (Gardner & Ascher, 2006; Russo et al., 2015; Grab et al., 2019).

Bee communities in apple and blueberry crops

Three numerically dominant genera, Andrena, Lasioglossum and Ceratina, accounted for the largest proportion of bees in the community in both crops. Our results are in line with previous wild bee surveys in apple and blueberry orchards across the northeast U.S.A. (Gardner & Ascher, 2006; Tuell et al., 2009; Bushmann & Drummond, 2015; Russo et al., 2015), although they differ from previously conducted wild bee surveys in mixed produce farms in New Hampshire (Tucker & Rehan, 2017; Tucker & Rehan, 2018). Here, the apple associated bee fauna was dominated by solitary ground nesting bees of the genus Andrena, which comprised 40% of the community. One species, A. crataegi, was predominant, accounting for 18% of bees in the community. Our results support a previous study, investigating the bee fauna across multiple apple orchards in the Finger Lakes Region of western New York State, where the genus Andrena in general (Gardner & Ascher, 2006) and the species A. crataegi in particular was predominant (Russo et al., 2015). By contrast, a range of other species was dominant across northeast American apple orchards. For example, among halictid bees, Lasioglossum leucozonium was dominant in Nova Scotia, Canada (Sheffield et al., 2013), whereas Augochlora pura was dominant in Pennsylvania (Kammerer et al., 2016). We found that the bee community in blueberry was dominated by solitary ground nesting bees of the genus Andrena (32%). The subsocial stem nesting bee C. calcarata (13%) was the most dominant species. Unexpectedly, Bombus accounted for less than 1%. This stands in stark contrast to the blueberry bee community in Maine, where Bombus accounted for 30% (Bushmann & Drummond, 2015), Similar to our study, C. calcarata was most abundant in high bush blueberry in Michigan (Tuell et al., 2009). By contrast to our findings, among andrenid bees, Andrena bradlevi was dominant in North Carolina (Rogers et al., 2014), A. carlini was dominant in Michigan (Isaacs & Kirk, 2010) and the halicitd bee Lasioglossum cressonii was dominant in Maine (Bushmann & Drummond, 2015). This phenomenon of one particular species being dominant in the community might reflect the patchy distribution of insects (Gaston et al., 1997; Tscharntke & Brandl, 2004; Ewers & Didham, 2006). Turnover and differences of dominant species in fragmented, i.e. agricultural, landscapes might arise from local specifics in environmental factors, inducing climate, surrounding land use and habitat types, as well as biotic factors such as competition and parasitism (Tscharntke & Brandl, 2004; Diekötter *et al.*, 2008). This suggests that local surveys using a combination of active and passive approaches, including transect walks, sweep netting and traps (Rhoades *et al.*, 2017; O'Connor *et al.*, 2019) of crop-associated wild bees, are invaluable because broad patterns and generalizations cannot be drawn across regions or agricultural systems.

Community composition. The bee community composition differed markedly between apple and blueberry crops. Differences were driven by more abundant A. virescens, A. carlini, E. pruinosa, L. pectorale and L. tegulare in apple. Some of these species have previously been found to be abundant in the apple associated bee community, including A. virescens (Sheffield et al., 2013) and A. carlini (Russo et al., 2015). The apple associated bee community was distinct in terms of phylogenetic diversity: At orchard 2, there was more clustering at the tips of the phylogenetic tree, indicating a paucity of species representation in certain clades of the tree. This is most likely driven by fewer species within the genera Andrena, Lasioglossum and Nomada. Andrena and Lasioglossum species have previously been shown to be sensitive and responded negatively to more intensified agricultural land use types (Hendrix et al., 2018; Grab et al., 2019).

Community functional traits. The majority of the community comprised solitary ground nesting bees, some subsocial stem nesting and social ground nesting, and very few cleptoparasitic bees. Apple harboured more solitary and social ground nesting bees than blueberry, which was largely driven by more Andrena and Lasioglossum species. Our findings support previous ones in apple and blueberry orchards. Large numbers of solitary Andrena were associated with apple in New York (Russo et al., 2015; Blitzer et al., 2016), whereas large numbers of solitary and social ground nesters (Andrena and Lasioglossum) were associated with apple in Canada (Sheffield et al., 2013). Here, the majority of bees in blueberry were also solitary and ground nesting, driven by large numbers of Andrena and Agapostemon. This is in line with the wild bee fauna in low-bush blueberry in Maine (Bushmann & Drummond, 2015). We found very few (4%) cleptoparasitic bees, which belonged to only two genera, Nomada and Sphecodes. This aligns well with previous findings, where similarly few cleptoparasitic bees were collected using pan traps in apple orchards in Nova Scotia (Sheffield et al., 2013), sweep netting in apple orchards in New York State (Blitzer et al., 2016) or a combination of pan traps and hand collecting in blueberry orchards in Maine (Bushmann & Drummond, 2015). These results indicate that orchards can provide flower resources to harbour a diverse bee community in terms of species, although functional guild diversity might be diminished in homogenized agricultural landscapes (Woodcock et al., 2019).

Bee phenology

There was a marked turnover in the bee community throughout the season for both crops. Surprisingly, only a tenth of the bee fauna was collected during the 2-week bloom period, whereas more than half of the fauna was collected during the 2 weeks before bloom in early May. This suggests that the resident bee fauna depends on early spring flower resources in the vicinity, which could have been provided by herbaceous lanes between the fruit crops and along nearby roadsides. Alternatively, when the crop is in bloom the bees might be collecting nectar and pollen from the flowers and not visiting the pan traps. During both pre-bloom and bloom, solitary ground nesting Andrena species were predominant in the bee community, comprising more than one third of the individuals. The pre-bloom community was dominated by the solitary ground nesting species A. crataegi and the subsocial stem nesting bee C. calcarata. During bloom period solitary ground nesting A. crataegi and social ground nesting L. tegulare were predominant. The latter of which was also most abundant in the post-bloom period. Unlike our study, a survey in highbush blueberry in Michigan (Tuell et al., 2009) collected almost one half of the individuals and more than a third of the bee species during bloom period. Differences could arise from collection methods used, as Tuell et al. (2009) mounted pan traps on poles, whereas here the traps were placed on the ground. It is conceivable that pole mounted pan traps would have yielded a higher proportion of sampled bees during bloom period. However, similar trends emerged for both studies, as to which genera were dominant during the three periods. Similar to our findings, Andrena was dominant during pre- and bloom period, whereas Ceratina was abundant before, and Lasioglossum during bloom (Tuell et al., 2009).

We conclude that fruit orchards in New Hampshire harbour a species and trait diverse wild bee fauna, fluctuating through time. Bee communities in apple and blueberry are crop-specific and dominated by very few species, which vary depending on season and crop. Our results provide baseline survey data, the first of its kind, in blueberry and apple orchards in New Hampshire, which informs us about the resident bee community in and around these crop environments. These can be used to inform farmers about wild bee pollination services in their orchards and to implement improved management and conservation strategies. Important considerations include available nesting habitat and alternate flower resources for wild bees in agricultural landscapes. Future studies should incorporate crop-flower visitations and fruit quality/quantity to address pollination services by wild bees in more detail.

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Supporting information

Additional supporting information may be found online in the Supporting Information section at the end of the article.

Fig. S1. Abundance of bee species collected from two crop types (apple and blueberry) at two orchards in New Hampshire (May to August 2018).

Fig. S2. (A) Coleman's rarefaction and (B) species accumulation curves for bees. Species richness for two crop types based on the number of (A) individuals (mean \pm SD) and (B) samples (mean \pm SD).

Table S1. Bee species collected from apple and blueberry crops at two orchards in New Hampshire (U.S.A.) in May to August 2018. Overall abundance (pan) and abundance at each crop type and orchard, including social behaviour and nesting habit, number of associated crops (No. of links) and pollination service index (PSI). *Species also collected with sweep netting.

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