Pollinator species traits do not predict either response to agricultural intensification or functional contribution

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Running headline: Pollinator traits are not predictive

Summary:

1. The response and effect trait framework, if supported empirically, would provide for powerful and general predictions about how biodiversity loss will lead to loss in ecosystem function.

2. This framework proposes that species traits will explain how different species respond to disturbance (i.e. response traits) as well as their contribution to ecosystem function (i.e. effect traits). However, predictive response and effect traits remain elusive for most systems.

3. Here, we present detailed data on crop pollination services provided by native, wild bees to explore the role of six commonly used species traits in determining how crop pollination is affected by increasing agricultural intensification. Analyses were conducted in parallel for three crop systems (watermelon, cranberry, and blueberry) located within the same geographical region (mid-Atlantic USA).

4. Bee species traits did not strongly predict species' response to any agricultural intensification process, and the few traits that were weakly predictive were not consistent across crops. Similarly, no trait predicted species' overall functional contribution in any of the three crop systems, although body size was a good predictor of per capita efficiency in two systems.

5. Pollinator traits may be useful for understanding ecological processes in some systems, but thus far we are unable to make generalizable predictions regarding species responses to land-use change and its effect on the delivery

of ecosystem services.

Keywords: Biodiversity, bees, ecosystem services, ecosystem function, response traits, effect traits, body size, diet specialism.

Introduction

Land-use change, along with other human-induced global change drivers, is accelerating the rates of extinction of most taxa (Ellis et al. 2010). At the same time, humanity relies on ecosystem services that wild species deliver, such as pollination and pest control by insects, and nutrient cycling by microorganisms (Cardinale *et al.* 2012). Thus, it is important to understand the relationship between biodiversity loss and ecosystem service delivery (Schwartz et al. 2000). In particular, making generalizable predictions regarding how the decline or local extinction of taxa will affect ecosystem services will allow for targeted conservation actions to ameliorate negative impacts of land-use change.

One avenue for predicting the functional consequences of biodiversity loss is the response and effect trait framework (Lavorel & Garnier 2002, Naeem & Wright 2003, McGill et al. 2006). Local extinction does not occur at random because extinction risk is dependent on the species' characteristics. Identifying which traits govern species responses to particular threats ('response traits') would provide the first step for predicting future species loss. Furthermore, the magnitude by which ecosystem function declines when a species is lost depends on that species' functional contribution. This, too, is likely to be mediated by the species' traits ('effect traits'). Therefore, the relationship between response and effect traits will mediate the magnitude of the impact of human disturbance on ecosystem services (Schleuning, Fründ & García 2015). For example, if the same species traits that are associated with high function are also most sensitive to disturbance, ecosystem function would be predicted to decline rapidly (Larsen, Williams & Kremen 2005).

However, for the response-effect trait framework to be generalizable, it is first necessary to identify response and effect traits that are both explanatory and possible to measure in the field (Cadotte, Carscadden & Mirotchnick 2011). While a few generalities have emerged as to which traits make animal species at greater risk of local decline, including dietary or habitat specialization and body size (Fisher & Owens 2004; Ockinger *et al.* 2010), the correlation between these response traits and extinction risk has been found to be weak, variable, or context-dependent (Devictor, Julliard & Jiguet 2008; Powney *et al.* 2014; Fritz, Bininda-Emonds & Purviis 2009). Similarly, although some effect traits have been identified, they are often weakly predictive, and their identity varies by function and taxonomic group (Gagic *et al.* 2015). Lastly, within the functional trait field as a whole, most progress has been made in identifying functional traits for plants (Diaz *et al.* 2016), while little is known for animals (Didham et al. 2016).

Here, we seek to identify response and effect traits for wild bee species providing a key ecosystem service, crop pollination. The yield of most crop plants increases with animal pollination (Klein *et al.* 2007). While managed honey bees are a leading crop pollinator, wild insects contribute more than half of pollinator visits to crop flowers across more than 40 crop systems worldwide (Rader *et al.* 2016). A major threat to pollinators is habitat destruction, primarily conversion to agriculture (Garibaldi *et al.* 2011), which is also a leading cause of species loss worldwide (Pereira *et al.* 2010). Thus agricultural land use has the potential to affect the ecosystem service upon which agriculture itself depends (Deguines et al. 2014).

Our data sets were collected and analyzed in parallel and come from three crop systems (watermelon, cranberry and blueberry) located within the same geographical region (mid-Atlantic USA), but pollinated by distinct bee communities. We determined whether six commonly-used species traits can predict 1) species' responses to agricultural intensification (response traits) and/or 2) species' contributions to crop pollination (effect traits).

Material and methods:

Study system

We selected 49 sites across three study systems that were located throughout New Jersey and eastern Pennsylvania (USA). Watermelon sites (N = 17) were located in 90 x 60 km region central New Jersey and Eastern Pennsylvania, where the main types of land use are agriculture and suburban development, interspersed with highly fragmented deciduous forest. Cranberry and blueberry sites (N = 16 each) were both located within a 35 x

55 km area in southern New Jersey, where the main land cover types are pine-oak ericaceous heath and agriculture. All sites in all systems were separated by at least 1 km (range, watermelon: 2-90 km, cranberry: 1-32 km, blueberry 1-38 km).

All three of crops are highly dependent upon bee pollination for marketable fruit production (Klein *et al.* 2007). Commercial honey bees are used in most of our study fields. However, honey bees are primarily managed hives, moved throughout the region, and only found on sites during bloom. Therefore, honey bees are not influenced by land cover in the same manner as wild bees and are not used in our analyses. Wild bees are important pollinators in all three systems (mean percentage of wild bee visits: 73% watermelon, 25% cranberry, and 14% blueberry).

Data collection:

At all sites on all three crops, we used hand-netting to measure overall bee abundance and species richness. To collect bees, we walked along fixed transects at standard times of day and collected all bees observed to be visiting flowers. In watermelon and blueberry, bees were netted three times throughout the day for 20 minutes per transect (60 minutes per date per site) and twice each day in cranberry for 30 minutes per transect (120 minutes per date per site). Data were collected during the peak bloom in 2010 (watermelon: July, cranberry: late-May-early July, blueberry: April-early May). Data were collected on three days per site for watermelon and blueberry and two days per site for cranberry. Detailed methods can be found in Benjamin

Reilly & Winfree (2014), Winfree *et al.* (2015), Cariveau *et al.* (2013).

Land cover characteristics of sites

To relate pollinator response traits to land use, we required high-quality land cover data for each pollinator collection site. For the cranberry and blueberry sites in New Jersey, we used a continuous polygon layer classified by visual photograph interpretation into 60 categories, at a minimum mapping unit of 4047 m^2 (1 acre; GIS Data provided by the New Jersey Department of Environmental Protection). For watermelon sites that extend from central New Jersey into Pennsylvania, we created a similar land cover data layer by manually digitizing Google Earth imagery and visually classifying 15 categories, at a minimum mapping unit of 5,000 m^2 (1.24 acres). As each crop was analyzed separately, our results are robust to using different land cover data. However, to simplify the interpretation of results for the three crops, we reclassified all land cover data into the following 7 broad categories: agriculture, open managed (for example, mowed grass), open natural or semi-natural (for example, old fields), semi-urban (<30% impervious surface), urban (>30% impervious surface), wooded, and open water.

Prior to doing our spatial analyses, we explored several different landscape characteristics, because agricultural land-use change can occur at multiple scales and affect multiple landscape attributes. For each data collection site we calculated four land cover variables: a) percent agriculture, b) percent natural and semi-natural open habitat, c) forest edge length, and d) habitat heterogeneity. We used agricultural land cover as our primary land use change variable, as it is the dominant anthropogenic habitat type in all three study systems. Percent open natural/semi-natural habitat makes up a small proportion of the total land cover (mean 6.8% cover at 1500 m radius) but is likely to be disproportionately important as forage and nesting habitat for bees (Kleijn *et al*. 2006). Forest edge length may represent important habitat for bees that nest in woods but forage in open areas (Kells & Goulson 2003). Diverse patchy landscapes may be beneficial to bees as they may nest and forage in different habitats (Kremen *et al.* 2007); thus we include Shannon H diversity of the seven cover categories as a measure of habitat heterogeneity. We calculated values for all four land cover variables at both a small scale (300 m radius) and a large scale (1500 m radius), which correspond to typical flight distances of small- and large-bodied bees, respectively (Greenleaf et al. 2007).

Pollinator function

To estimate the pollination services provided per bee species, we measured two variables in the field, flower visitation frequency and per visit efficiency. As variation in visitation frequency may be a function of land use at individual farms, we use species abundances for each species at the site with its highest abundance for each crop. Hence, we assess visitation frequency at its maximum, which represents the optimal visitation frequency for each species.

To measure the pollination efficiency we quantified single-visit pollen deposition by presenting virgin flowers to individual bees foraging on the target crop. After visitation, we counted the number of pollen grains deposited per flower visit (watermelon) or the number of pollen tetrads with pollen tubes per flower visit (cranberry and blueberry). Because species identification in the field is not possible for most bees and net collecting immediately after visits is generally not possible, for the measurement of pollination efficiency we grouped bees in species groups. Each group consisted of between one and 27 species, with the median number of species per group being 4 species (Supporting Information, Table S1). Control flowers were left bagged until the end of the field day, and contained few pollen grains (watermelon mean = 3 grains, N = 40 stigmas; cranberry mean = 0 tetrads, N = 82 stigmas; blueberry mean = 2 tetrads, N= 734 stigmas). For detailed methods see Benjamin *et al.* (2014), Winfree *et al*. (2015), Cariveau *et al.* (2013).

Species traits

Bee species vary in a number of traits that are associated with their response to land-use change (Williams et al. 2010). Moreover, these traits will likely affect the pollinator contribution to function, either by modifying its abundance or because they are related to its per capita effectiveness. We obtained detailed natural history data on 6 traits for the 90 bee species in our study: a) sociality (solitary, facultative social, eusocial), b) nesting placement (hole, cavity, stem, wood, ground), c) brood parasite (yes, no), d) body size, e) diet breadth (level of specialization) and f) tongue length.

We obtained the trait data as follows. Species sociality level, nesting behavior and brood parasite status were extracted from the literature (Bartomeus *et al.* 2013a). Body size (estimated from intertegular span, IT; Cane 1987) was measured in the lab using collected specimens that had been identified to the species level by professional taxonomists. Multiple specimens were measured per species (mean = 6.6 specimens ± 3 S.E.) and the mean across the measured specimens was used as the value for the species. Bee body size also correlates strongly with foraging distance (Greenleaf *et al.* 2007), and thus is ecologically related to mobility. Tongue length was measured in the lab for 7.7 ± 1.2 SE specimens per species, and the mean across the measured specimens is used. For the 40 specimens for which we cannot obtain a tongue measure, we estimated tongue length from the species' body size and phylogeny using an allometric equation (Cariveau et al. 2016).

Diet breadth was calculated using six independent datasets previously collected at 139 sites throughout the study region by the Winfree laboratory group. Each data set consists of individual pollinator specimens that were net-collected while foraging on a flowering plant species; both pollinator and plant were then identified to the species level. Those datasets comprise overall 393 pollinator species, and 392 plant species, with 3890 plant-pollinator interactions (Supporting Information. Text S2). Prior to calculating diet breadth, we rarefied the data to 20 visitation records per bee species, to avoid confounding rarity with specialization (Blüthgen *et al.* 2008; Winfree *et al.* 2014). Nine species had fewer than 20 records and we were unable to estimate diet breadth in the manner described above. Five of these species are known to be specialized and we simulated the diet breadth index of 20 individuals visiting the known host plants. The four other species are known to be generalists and we therefore used the mean diet breadth of its genus.

These four species were extremely rare (< 5 records each) in our analyzed dataset.

To calculate diet breadth for each bee species, we considered the number of plants species as well as the phylogenetic breadth that the bees fed upon by using a rarefied phylogenetic diversity index(Nipperess & Matsen 2013). To determine phylogenetic distances among plants, we first constructed a general phylogenetic tree using the PHYLOMATIC "megatree" (version R201120829, Chamberlain & Szocs 2013) which defines relationships between higher plants (Webb, Ackerly & Kembel 2008). We then dated nodes across this tree according to Wikström et al. (2001) and used the branch-length adjustment algorithm BLADJ to estimate the age of all remaining, undated nodes. Though this procedure implies that ages within our phylogenies should be treated as approximations (Beaulieu *et al*. 2007), previous analysis indicates marked improvements of phylogenetic analyses when even a limited number of nodes are properly dated (Webb 2000).

Statistical analysis

Response traits: In order to investigate which traits are associated with environmental variables related to agricultural intensification, we used fourth-corner analysis (Legendre Galzin & Harmelin-Vivien 1997). This analysis is specifically designed to directly analyze the relationship between the biological characteristics of species and the characteristics of the habitat where they are found.

The fourth-corner approach links an R matrix of environmental variables to a

Q matrix of species traits through an L matrix of species abundance (Dray & Legendre 2008). A correlation coefficient is computed for each pair of species traits and environmental variables. We tested the significance of the trait-environment correlation by combining two permutation models (Dray & Legendre 2008). The first permutation randomizes site rows (or equivalently, environmental variables across sites) to test if communities in different environments have different trait values. The second permutation randomizes species columns (or equivalently, trait values across species) to test if trait-environment relationships are independent of community composition (Dray & Legendre 2008). Under the second null model, a consistent trait-environment relationship will not be significant if communities in similar environments have similar species composition. Thus even if the first permutation is significant but the second is not, we cannot know if the observed trait-environment correlation simply reflects random changes in trait values due to the shift in species composition. Hence, as recommended by Dray & Legendre (2008), we report the highest p-value of the two models. We the ran the fourth-corner analysis for each crop independently using 9999 permutations for each null model (R package "ade4"; Dray & Dufour 2007). No adjustments for p-values were made, but due to the high number of tests performed in the analyses, the possibility of significance by chance increases. Therefore, we mainly discuss effect sizes and only highlight results with significance level ≤ 0.01, while we consider $0.01 > \alpha \leq 0.05$ to be relatively weakly supported associations.

Effect trait analysis: To determine which traits influenced functional contribution of each species we ran separate generalized linear models with either visitation or per capita efficiency as response variables. Species traits were predictors. The best model based on AICc was selected. When differences between the best models were less than 2 we selected the simpler model. The analysis for efficiency was done at the species group level (see above: pollination function section). In order to obtain traits at the species group level we calculated the mean values over species belonging to the same group, weighted by the species mean abundance within the group. For categorical variables we chose the dominant level.

All statistical analyses were performed in R software, version 3.0.3 (R Core Team 2014).

Results

Response traits: Overall, we did not find a strong correlation between any ecological traits and the environmental variables analyzed. Some traits exhibited weak responses but they were not consistent across crops. For watermelon, small bees and those with short tongues tended to decline with increasing percentage of agriculture at 300m radius (Body size: $r = 0.23$, $p = 0.03$, Tongue length: $r = 0.23$, $p = 0.03$). Species nesting in stems were positively associated with heterogeneous landscapes at 1500m radius (Stem nesters: $r = 0.12$, $p = 0.04$). For cranberry and blueberry, we did not find any trait significantly associated with any of the landscape characteristics. A complete list of all comparisons is presented in Supporting Information (Table S3).

Effect traits: As for response traits, no traits were highly predictive of either visitation frequency or per visit efficiency across crops. For watermelon, no trait was selected on the best model for visitation frequency. However, pollination efficiency was positively correlated with body size and tongue length ($R2 = 0.75$, $F2,9 = 17.07$, $p < 0.001$, Fig 2A). For cranberry, visitation frequency was positively related to cavity nesters ($R2 = 0.38$, $F4,36 = 7.1$, $p < 0.0001$, Fig 2B). This result was driven by *Bombus* species, which are the only cavity nesters in this data set. In contrast, efficiency per visit was not related to any trait. For blueberry, visitation frequency was positively related to diet specialism ($R2 = 0.37$, $F1,20 = 13.5$, $p = 0.001$, Fig 2C), while efficiency per visit is positively related to tongue length ($R2 = 0.70$, $F1,5 = 14.9$, $p = 0.01$, Fig 2D). Model selection, can be found in Supporting Information (Table S4).

Discussion:

Identifying traits that characterize which species are more sensitive to land-use change or those that are functionally important is complex. We found evidence for response and effect traits but they differed among crop species as well as landscape variable used. Therefore, while some traits may be important in some contexts, no traits were generalizable enough to be used to predict how land-use change will influence the delivery of pollination services in other systems. Further, the relationships identified were weak, especially for response traits. This does not negate the importance of traits for understanding which mechanisms underlie species responses to land use change or pollination effectiveness, but it does suggest the commonly used traits we studied here are not suitable for predictive purposes.

Being able to identify strong response traits would be a key tool for understanding extinction risk, and an asset for conservation planning. However, characterizing extinction risk based on traits is challenging. Despite some generalities that emerge across taxa, with rare species, big species, specialists, and higher trophic levels being in general more sensitive to disturbances (Fisher & Owens 2004), there is a large variation in the response of the species with those traits (Fritz, Bininda-Emonds & Purvis 2009; Seguin *et al*. 2014). Work specifically on native bees has found that traits such as specialization, body size, and sociality may predict responses to land use (Winfree *et al.* 2009; Bommarco *et al*. 2010; Williams *et al*. 2010; Bartomeus *et al*. 2013b; De Palma *et al*. 2015). However, studies often find contrasting results. For example, De Palma et al. (2015) analyzed over 70,000 wild bee records and found that small species were most sensitive to agricultural land use, while others have found that larger species are more sensitive to agricultural land use and/or environmental change generally (Larsen, Williams & Kremen 2005; Bartomeus *et al.* 2013b; Rader *et al*. 2014), and some have found little effect of body size (Williams et al. 2010). Here, we only found a weak trend for big species to be more abundant in locally intense agricultural areas in watermelon, but this trend disappears when land use is measured at larger scales. Another trait, dietary specialization, is one of the few traits that has been generally linked to increased species sensitivity to environmental change (Williams *et al.* 2010; Scheper *et al*. 2014; De Palma *et al*. 2015), but here we found that floral specialist bees did not decline with intensifying agriculture. If anything, specialization is positively associated with agricultural intensification in the blueberry system (Table S3), largely because the most abundant bee species in this system (*Andrena bradleyi*) is a specialist on the blueberry genus *Vaccinium*. Specialist bees observed in crop systems are likely to be specialized on the crop plant family as was the case in our data (e.g. *Habropoda sp.* , *Andrena bradleyi* in blueberry, but also *Peoponapis sp.* in watermelon and *Mellita americana* in cranberry). We would expect different responses from study designs that include natural habitat and a larger range of specialist host plants (Forrest et al. 2015, Bartomeus & Winfree 2013).

Effect traits have been even harder to identify for pollinators. The limited data published on particular plants suggests insects with larger bodies tend to deposit more pollen per flower visit, but this pollen was not well distributed on the stigma (Hoehn *et al.* 2008), or that the correlation between body size and per visit pollination function is low (Larsen, Williams & Kremen 2005). Our study supports the positive correlation between body size and per-visit pollen deposition in both watermelon and blueberry (although note that tongue length is correlated with body size in blueberry r = 0.76), but not for cranberry. Hence, generality is difficult to achieve because a single pollinator trait, like big body size, may not lead to high pollination function in all contexts. Rather it seems likely that the most efficient trait will depend on the crop (Garibaldi *et al.* 2015). Moreover, the total pollination provided by a pollinator species is the product of visitation frequency and per capita efficiency (Kremen *et al.* 2005), two processes that may be governed by different traits.

If generalizable response and effect traits can be found, the final step will be to link response and effects to predict changes in ecosystem services. A positive association between the response and effect traits (Naeem & Wright 2003) such that species with the strongest response to environmental change also had the strongest effect on function, indicates the land-use change has the potential for dramatic effects on ecosystem function. Whether response and effect traits are in general positively, negatively, or uncorrelated is an important question that has not yet been answered (Larsen, Williams & Kremen 2005). Despite the conceptual elegance of the response-effect trait framework, it is only effective if it is predictive, and strong evidence for the generality of traits has not yet been found. For example, even the very thorough and rigorously analyzed study of response-effect relationships by Larsen, Williams & Kremen (2005) is based on a non-significant weak relationship between pollinator per visit efficiency and body size. In our study, even the strongest correlations find for watermelon, where big species are less sensitive to local agricultural intensification and more efficient per visit, but not more frequent flower visitors than smaller species are too weak to be useful for predictive purposes.

Predictive response and/or effect traits are often assumed in the larger literature as well. For example, recent re-evaluations of community stability in food webs shows that using body size as proxy of extinction risk changes the outcome of the stability simulations (Brose *et al.* 2016). However, the assumption that body size is a good predictor of extinction risk is not directly validated. Given the correlation showing that bigger species are more sensitive is usually weak (Fisher & Owens 2004), these kind of approaches could produce misleading outcomes.

Currently trait data may be too coarse to reveal ubiquitous response and effect traits for four reasons. First, some traits may simply reflect identity of genera or higher taxonomic groups. For example, some bumble bee species in our three systems (especially *B. impatiens*) are common, functionally dominant, and robust to extinction (Cariveau *et al.* 2013, Winfree *et al.* 2015). Some of the important response and effect traits that we found, such as cavity nesting and body size, may simply be proxies for bumble bees. Bumble bee species also share other traits (e.g. sociality) that are commonly used in trait analyses. Therefore, studies that don't include phylogenetic correlations may be simply characterizing the general relationship between disturbance and the functionally dominant bumble bees, or other dominant taxa. As there is a great variability in the responses to disturbance among bumble bee species (Cameron *et al*. 2011; Bartomeus *et al.* 2013b, Persson *et al.* 2015) this may also explain why some studies find big species to be more sensitive to land use change (Larsen, Williams & Kremen 2005) and other studies find the opposite (Rader *et al*. 2014, this study). Second, traits may interact in complex ways and single traits may be not able to capture responses and functional contributions across species (e.g. Bommarco *et al.* 2010, De Palma *et al.* 2015). Third, phenotypical variability within species, usually ignored in trait-based approaches, may play a more important role than previously though (Bolnik et al. 2011). Finally, the most important traits may not have been studied. Response traits such as dispersal ability, fecundity, and nest microclimate/soil type, and effect traits like floral visitation behavior or hairiness may be better predictors than the traits we have now. However, if these traits are not easy to measure across bee species, they may be of little use. Traits databases that include an increasing number of traits and agreed-upon measurement techniques similar to those used in plant ecology (Kattge *et al.* 2011) but that are also open-access may lead to significant advancements in functional trait ecology in wild bees.

There is a call to be more predictive in ecology (Petchey *et al.* 2015). The use of traits to predict species responses and subsequent changes in ecosystem services is a potentially powerful approach. This is especially the case for organisms such as insects where species identification is challenging and detailed species-level natural history information is lacking. The ability to effectively use a trait framework is becoming controversial because studies thus far have not clearly related specific traits to specific threats or functions (Didham et al. 2016; Shipley et al. 2016). A growing number of studies are working to address the complexity and increase the predictability of this framework (e.g. Laughlin & Messier 2015). However, until these approaches yield consistent patterns across systems, site-specific species identity and monitoring may at present be the best measure for predicting changes in ecosystem services as a result of land-use change. A few dominant species often drive ecosystem functioning (Kleijn *et al.* 2015; Winfree *et al.* 2015). Identifying the sensitivity of the functionally dominant species may be the best proxy thus far for predicting effects of species loss in ecosystem function.

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Data Accessibility: All data and code used in this manuscript is accessible in github (https://github.com/ibartomeus/RE_traits) and will be archived on acceptance in figshare.

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Tables and Figures

Fig. 1: Relationships between traits and environmental variables for A) watermelon, B) blueberry and c) cranberry. Positive significant correlations are in red ($p < 0.05$). Note no correlation is significant despite all the combinations tested for both blueberry and cranberry. D) Detail of the relationship between body size (visualized as the community weighted means for each community) and percentage of agriculture at 300 meter radii.

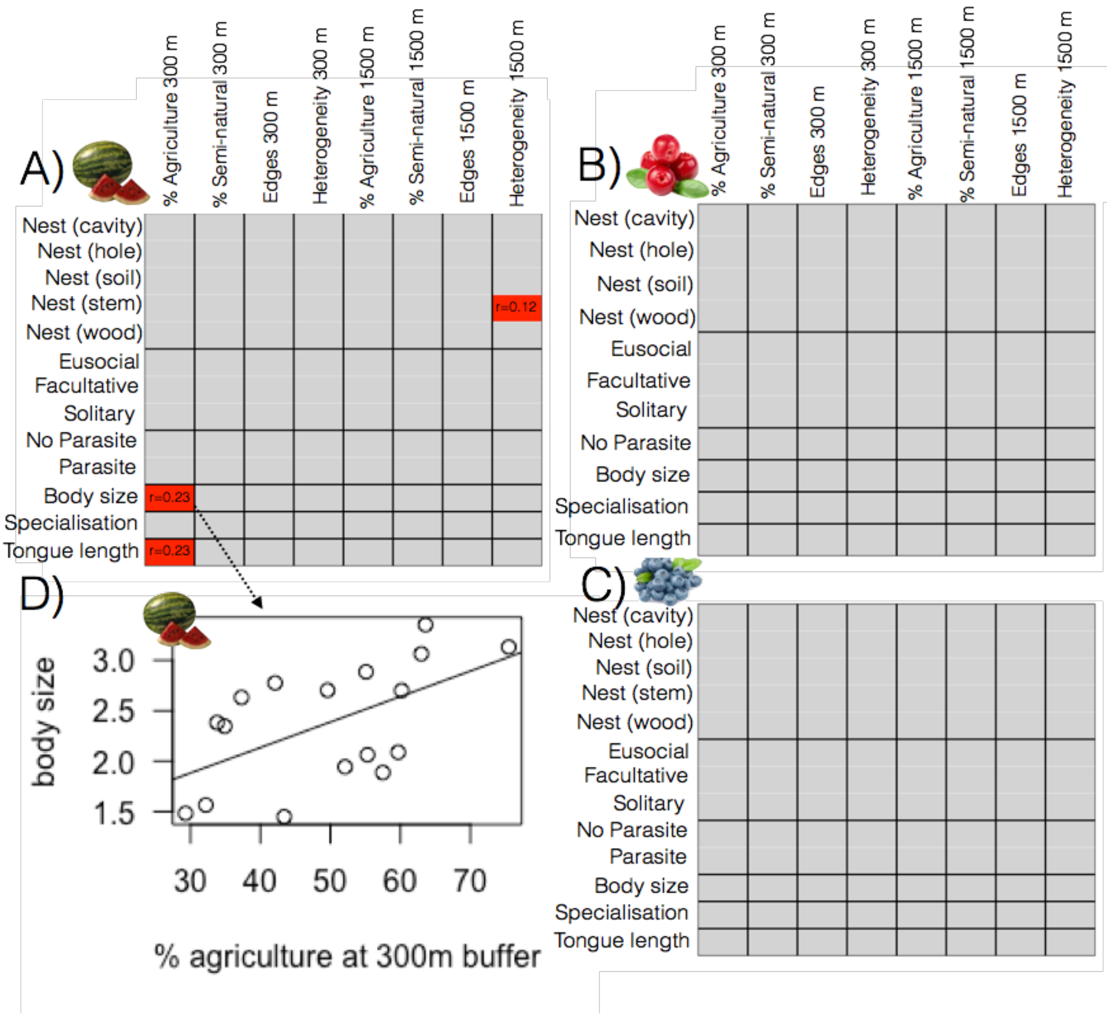
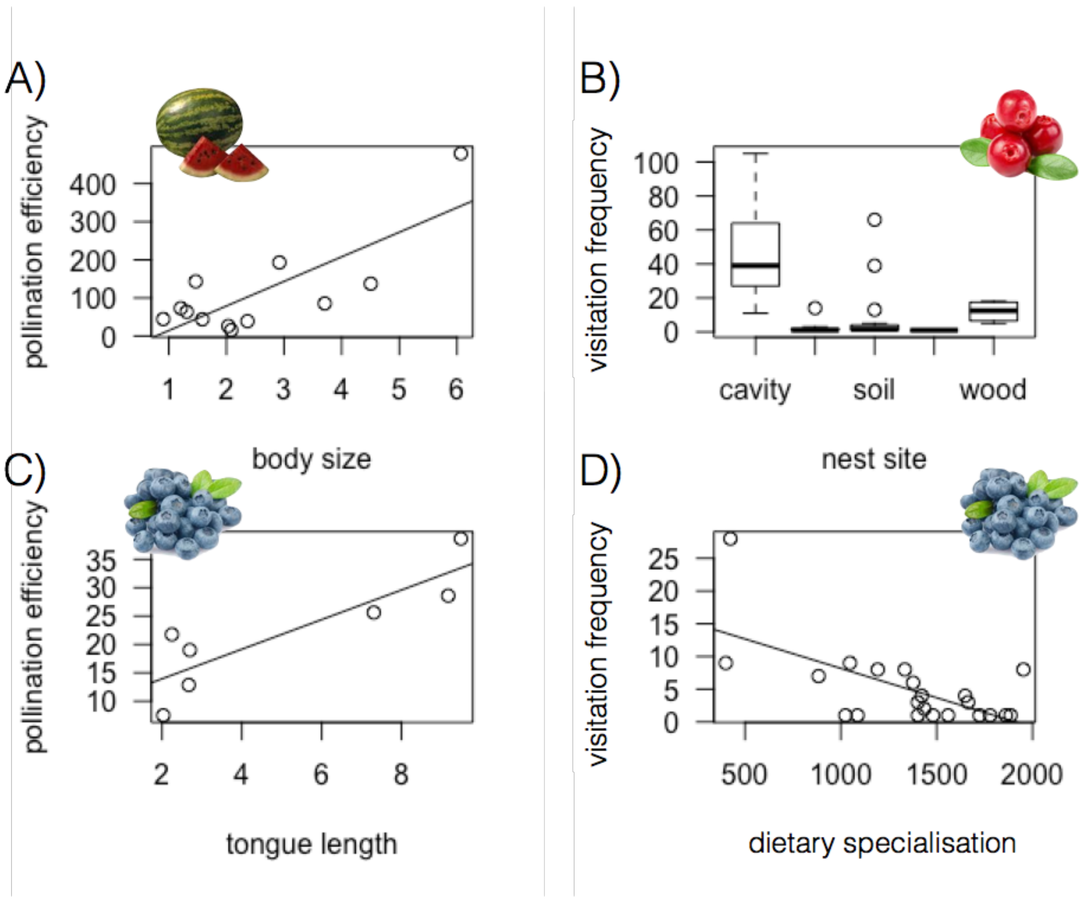


Fig. 2: Multipanel plot showing the relationships between species traits and pollination function, which is decomposed into efficiency (pollen deposited per flower visit) and frequency of flower visits. A) watermelon, B) cranberry, C-D) blueberry.



646 **Supporting Information**

647 Table S1: Equivalencies between species and groups used for single visit
648 data.

Crop	Species	Single Visit Group	Percentage within group
Blueberry	Andrena_banksi	MED_AND	0.00
Blueberry	Andrena_barbara	MED_AND	0.00
Blueberry	Andrena_bradleyi	MED_AND	0.93
Blueberry	Andrena_carlini	LG_AND	0.12
Blueberry	Andrena_carolina	LG_AND	0.01
Blueberry	Andrena_cressonii	LG_AND	0.01
Blueberry	Andrena_fenningeri	MED_AND	0.01
Blueberry	Andrena_hilaris	MED_AND	0.00
Blueberry	Andrena_ilicis	MED_AND	0.00
Blueberry	Andrena_imitatrix	MED_AND	0.01
Blueberry	Andrena_mandibularis	MED_AND	0.00
Blueberry	Andrena_morrisonella	MED_AND	0.01
Blueberry	Andrena_screpteropsis	MED_AND	0.00
Blueberry	Andrena_vicina	LG_AND	0.86
Blueberry	Augochlora_pura	Green	0.56
Blueberry	Augochlorella_aurata	Green	0.44
Blueberry	Bombus_bimaculatus	Bom_Q	0.24
Blueberry	Bombus_griseocollis	Bom_Q	0.49
Blueberry	Bombus_impatiens	Bom_Q	0.18
Blueberry	Bombus_perplexus	Bom_Q	0.08
Blueberry	Ceratina_calcarata/dupla	Dialictus	0.22
Blueberry	Colletes_inaequalis	Coll	0.26
Blueberry	Colletes_thoracicus	Coll	0.09
Blueberry	Colletes_validus	Coll	0.65
Blueberry	Habropoda_laboriosa	HAB	1.00
Blueberry	Lasioglossum_acuminatum	Dialictus	0.02
Blueberry	Lasioglossum_coeruleum	Dialictus	0.02
Blueberry	Lasioglossum_fuscipenne	Dialictus	0.02
Blueberry	Lasioglossum_leucocomum	Dialictus	0.02
Blueberry	Lasioglossum_oblongum	Dialictus	0.10
Blueberry	Lasioglossum_pilosum	Dialictus	0.15
Blueberry	Lasioglossum_versatum	Dialictus	0.02
Blueberry	Lasioglossum_weemsi	Dialictus	0.07
Blueberry	Lasioglossum_zephyrum	Dialictus	0.05

Blueberry	Nomada_luteola	Dialictus	0.02
Blueberry	Osmia_taurus	Dialictus	0.02
Blueberry	Osmia_cornifrons	Dialictus	0.02
Blueberry	Osmia_pumila	Dialictus	0.07
Blueberry	Sphecodes_aroniae	Dialictus	0.02
Blueberry	Sphecodes_stygius	Dialictus	0.02
Blueberry	Xylocopa_virginica	XYL	1.00
Cranberry	Agapostemon_splendens	Green	0.02
Cranberry	Andrena_cressonii	Melitta	0.01
Cranberry	Andrena_imitatrix	Melitta	0.01
Cranberry	Andrena_morrisonella	Melitta	0.01
Cranberry	Andrena_spiraeana	Melitta	0.01
Cranberry	Andrena_vicina	Melitta	0.02
Cranberry	Augochlora_pura	Green	0.16
Cranberry	Augochlorella_aurata	Green	0.63
Cranberry	Augochloropsis_metallica	Green	0.16
Cranberry	Augochloropsis_sumptuosa	Green	0.03
Cranberry	Bombus_bimaculatus	Bombus_bimaculatus	1.00
Cranberry	Bombus_citrinus	Bombus_spp	0.50
Cranberry	Bombus_griseocollis	Bombus_griseocollis	1.00
Cranberry	Bombus_impatiens	Bombus_impatiens	1.00
Cranberry	Bombus_perplexus	Bom_pervag	0.85
Cranberry	Bombus_sandersoni	Bombus_spp	0.50
Cranberry	Bombus_vagans	Bom_pervag	0.15
Cranberry	Ceratina_calcarata/dupla	Small_black	0.12
Cranberry	Coelioxys_immaculata	Megachile	0.02
Cranberry	Coelioxys_porterae	Megachile	0.04
Cranberry	Coelioxys_sayi	Megachile	0.02
Cranberry	Colletes_consors	Megachile	0.02
Cranberry	Halictus_rubicundus	Small_black	0.02
Cranberry	Heriades_carinatus	Osmia	0.08
Cranberry	Hoplitis_truncata	Osmia	0.12
Cranberry	Hylaeus_affinis	Small_black	0.08
Cranberry	Lasioglossum_apopkense	Small_black	0.01
Cranberry	Lasioglossum_coeruleum	Small_black	0.01
Cranberry	Lasioglossum_creberrimum	Small_black	0.02
Cranberry	Lasioglossum_fuscipenne	Small_black	0.05
Cranberry	Lasioglossum_georgeickworti	Small_black	0.05
Cranberry	Lasioglossum_lineatulum	Small_black	0.01
Cranberry	Lasioglossum_oblongum	Small_black	0.15
Cranberry	Lasioglossum_pilosum	Small_black	0.02
Cranberry	Lasioglossum_planatum	Small_black	0.02
Cranberry	Lasioglossum_subviridatum	Small_black	0.17
Cranberry	Lasioglossum_trigeminum	Small_black	0.02

Cranberry	Lasioglossum_versatum	Small_black	0.04
Cranberry	Megachile_addenda	Megachile	0.22
Cranberry	Megachile_gemula	Megachile	0.32
Cranberry	Megachile_mendica	Megachile	0.28
Cranberry	Megachile_texana	Megachile	0.08
Cranberry	Melitta_americana	Melitta	0.95
Cranberry	Nomada_bella/lepida	Small_black	0.01
Cranberry	Nomada_pygmaea	Small_black	0.01
Cranberry	Nomada_rodecki	Small_black	0.07
Cranberry	Osmia_inspergens	Osmia	0.07
Cranberry	Osmia_pumila	Osmia	0.13
Cranberry	Osmia_virga	Osmia	0.60
Cranberry	Panurginus_atramontensis	Small_black	0.09
Cranberry	Sphecodes_aroniae	Small_black	0.03
Cranberry	Sphecodes_fattigi	Small_black	0.01
Cranberry	Xylocopa_virginica	XYL	1.00
Watermelon	Agapostemon_sericeus	LG	0.25
Watermelon	Agapostemon_texanus	LG	0.11
Watermelon	Agapostemon_virescens	LG	0.52
Watermelon	Anthidium_oblongatum	LDS	0.03
Watermelon	Augochlora_pura	SG	0.80
Watermelon	Augochlorella_aurata	SG	0.20
Watermelon	Augochloropsis_metallica	LG	0.11
Watermelon	Bombus_bimaculatus	BOM	0.01
Watermelon	Bombus_fervidus	BOM	0.00
Watermelon	Bombus_griseocollis	BOM	0.01
Watermelon	Bombus_impatiens	BOM	0.98
Watermelon	Bombus_perplexus	BOM	0.00
Watermelon	Bombus_vagans	BOM	0.00
Watermelon	Calliopsis_andreniformis	SD	0.03
Watermelon	Ceratina_calcarata/dupla	CER	0.81
Watermelon	Ceratina_strenua	CER	0.19
Watermelon	Halictus_confusus	HAL_MDS	0.83
Watermelon	Halictus_ligatus	HAL_MDS	0.16
Watermelon	Halictus_parallelus	LDS	0.03
Watermelon	Halictus_rubicundus	LDS	0.56
Watermelon	Hoplitis_pilosifrons	HAL_MDS	0.00
Watermelon	Hoplitis_producta	HAL_MDS	0.00
Watermelon	Hylaeus_affinis	TD	0.01
Watermelon	Lasioglossum_admirandum	SD	0.01
Watermelon	Lasioglossum_albipenne	SD	0.00
Watermelon	Lasioglossum_atwoodi	SD	0.00
Watermelon	Lasioglossum_bruneri	SD	0.01
Watermelon	Lasioglossum_callidum	SD	0.01

Watermelon	Lasioglossum_cattellae	TD	0.00
Watermelon	Lasioglossum_cinctipes	SD	0.00
Watermelon	Lasioglossum_coreopsis	TD	0.00
Watermelon	Lasioglossum_coriaceum	SD	0.00
Watermelon	Lasioglossum_cressonii	SD	0.01
Watermelon	Lasioglossum_ellisiae	TD	0.01
Watermelon	Lasioglossum_ephialtum	SD	0.02
Watermelon	Lasioglossum_georgeickworti	SD	0.00
Watermelon	Lasioglossum_gotham	SD	0.00
Watermelon	Lasioglossum_illinoense	TD	0.05
Watermelon	Lasioglossum_imitatum	TD	0.59
Watermelon	Lasioglossum_laevissimum	SD	0.00
Watermelon	Lasioglossum_leucocomum	SD	0.02
Watermelon	Lasioglossum_leucozonium	LDS	0.09
Watermelon	Lasioglossum_lineatulum	SD	0.00
Watermelon	Lasioglossum_mitchelli	TD	0.17
Watermelon	Lasioglossum_nymphaearum	SD	0.04
Watermelon	Lasioglossum_oblongum	SD	0.01
Watermelon	Lasioglossum_obscurum	SD	0.01
Watermelon	Lasioglossum_paradmirandum	TD	0.04
Watermelon	Lasioglossum_pectinatum	SD	0.00
Watermelon	Lasioglossum_pectorale	SD	0.02
Watermelon	Lasioglossum_pilosum	SD	0.28
Watermelon	Lasioglossum_planatum	SD	0.00
Watermelon	Lasioglossum_platyparium	SD	0.00
Watermelon	Lasioglossum_rozeni	SD	0.00
Watermelon	Lasioglossum_smilacinae	SD	0.00
Watermelon	Lasioglossum_subviridatum	SD	0.00
Watermelon	Lasioglossum_tegulare	TD	0.07
Watermelon	Lasioglossum_trigeminum	SD	0.02
Watermelon	Lasioglossum_truncatum	SD	0.01
Watermelon	Lasioglossum_versatum	SD	0.44
Watermelon	Lasioglossum_viridatum	SD	0.01
Watermelon	Lasioglossum_weemsi	TD	0.05
Watermelon	Lasioglossum_zephyrum	SD	0.04
Watermelon	Megachile_brevis	LDS	0.06
Watermelon	Megachile_mendica	LDS	0.18
Watermelon	Megachile_rotundata	LDS	0.03
Watermelon	Megachile_sculpturalis	LDS	0.03
Watermelon	Melissodes_bimaculata	MEL	0.99
Watermelon	Melissodes_trinodis	MEL	0.00
Watermelon	Nomada_articulata	TRI	0.01
Watermelon	Peponapis_pruinosa	PEP	1.00
Watermelon	Ptilothrix_bombiformis	MEL	0.01

Watermelon	Triepeolus_lunatus	TRI	0.01
Watermelon	Triepeolus_remigatus	TRI	0.98
Watermelon	Xylocopa_virginica	XYL	1.00

Text S2: Datasets used for calculating dietary specialization: Six datasets were used to create the phylogenetic distance index. All data were collected in the region of the crop study. Specimens were collected using a hand net and the bee species and plant species were recorded. This resulted in a total of 18,733 bee x plant interactions for species that were also in the crop dataset. The number of species, sites, and years of collection are as follows: 1) Pine barrens in 2003: 280 bee x plant interactions. Habitat types were extensive pine-oak forest (14 sites), forest fragments (14 sites), suburban back yards (7 sites), and agricultural field borders (5 sites) in New Jersey (Winfree et al. 2007). Bees were collected in temporally stratified sampling rounds between April and September. 2) NJPA: 3906 bee x plant interactions. Data collected on watermelon field margins at a total of 20 sites. Farm types included small-scale mixed farming, both crops and field margins, both organic and low-pesticide-input conventional. All bees were collected in three temporally stratified sampling rounds in July, in each of 3 years. 3) NFWF 3906 bee x plant interactions. Habitat types were old fields. Bees were collected in May through Sept at 25 sites for two years. *Lasioglossum* species where not included for this dataset due to recent changes in its taxonomy. 4) NSF 2006 666 bee x plant interactions. Habitat types were deciduous forest fragments (13 sites), and suburban / urban yards (3 sites) and sites with extensive forests with diverse wildflower communities (4 sites). All bees were collected in sampling rounds between April and early June. 5) CIG 4600 bee x plant interactions. Site were comprised of old fields as well as pollinator enhancement sites. Bees using were collected using a hand net from a total of a total 18 sites in 2011-2013. For each bee specimen, the plant species was recorded. 6) Cape May 5858 bee x plant interactions. This study included only one site. The habitat was an old field that had been planted in 20 species of native perennial plants. Sampling took place over 3 years in sampling rounds that occurred in May through September.

Winfree, R. Griswold, T. & Kremen, C. (2007). Effect of human disturbance on bee communities in a forested ecosystem. *Conservation Biology*. 21: 213-223.

Table S3: Fourth corner results showing correlations and p-values for each trait. Significant values in bold.

Crop	Test	r	Standard deviation	P-value
watermelon	ag_300 / Nest_.cavity	0.19	1.92	0.05
watermelon	open_300 / Nest_.cavity	-0.09	-0.83	0.43
watermelon	forest_edge_300 / Nest_.cavity	-0.05	-0.31	0.71
watermelon	shannonH_300 / Nest_.cavity	-0.09	-0.88	0.4
watermelon	ag_1500 / Nest_.cavity	-0.11	-1	0.33
watermelon	open_1500 / Nest_.cavity	-0.15	-1.4	0.18
watermelon	forest_edge_1500 / Nest_.cavity	-0.02	-0.2	0.86
watermelon	shannonH_1500 / Nest_.cavity	-0.06	-0.54	0.62
watermelon	ag_300 / Nest_.hole	0	0.07	0.93
watermelon	open_300 / Nest_.hole	-0.03	-0.85	0.32
watermelon	forest_edge_300 / Nest_.hole	-0.06	-0.76	0.34
watermelon	shannonH_300 / Nest_.hole	-0.03	-0.63	0.41
watermelon	ag_1500 / Nest_.hole	-0.03	-0.54	0.41
watermelon	open_1500 / Nest_.hole	-0.05	-0.94	0.22
watermelon	forest_edge_1500 / Nest_.hole	-0.03	-0.65	0.36
watermelon	shannonH_1500 / Nest_.hole	-0.08	-1.61	0.09
watermelon	ag_300 / Nest_.soil	-0.12	-1.2	0.27
watermelon	open_300 / Nest_.soil	0.11	1.16	0.27

watermelon	forest_edge_300 / Nest_.soil	0.01	-0.07	0.95
watermelon	shannonH_300 / Nest_.soil	0.07	0.81	0.45
watermelon	ag_1500 / Nest_.soil	0.04	0.46	0.66
watermelon	open_1500 / Nest_.soil	0.07	0.73	0.5
watermelon	forest_edge_1500 / Nest_.soil	-0.05	-0.53	0.63
watermelon	shannonH_1500 / Nest_.soil	0.02	0.23	0.85
watermelon	ag_300 / Nest_.stem	-0.08	-1	0.26
watermelon	open_300 / Nest_.stem	0.03	0.44	0.66
watermelon	forest_edge_300 / Nest_.stem	0.01	0.11	0.93
watermelon	shannonH_300 / Nest_.stem	0.09	1.38	0.18
watermelon	ag_1500 / Nest_.stem	0	0.05	0.96
watermelon	open_1500 / Nest_.stem	0.07	0.87	0.27
watermelon	forest_edge_1500 / Nest_.stem	0.01	0.25	0.78
watermelon	**shannonH_1500 / Nest_.stem**	**0.12**	**2.01**	**0.04**
watermelon	ag_300 / Nest_.wood	-0.03	-0.22	0.76
watermelon	open_300 / Nest_.wood	-0.06	-0.84	0.43
watermelon	forest_edge_300 / Nest_.wood	0.05	0.66	0.52
watermelon	shannonH_300 / Nest_.wood	-0.05	-0.66	0.54
watermelon	ag_1500 / Nest_.wood	0.08	1.04	0.3
watermelon	open_1500 / Nest_.wood	0.04	0.51	0.59
watermelon	forest_edge_1500 / Nest_.wood	0.09	1.37	0.17
watermelon	shannonH_1500 / Nest_.wood	-0.04	-0.58	0.57
watermelon	ag_300 / Socia.Eusocial	0.02	0.18	0.91
watermelon	open_300 / Socia.Eusocial	-0.01	-0.09	0.93
watermelon	forest_edge_300 / Socia.Eusocial	0.04	0.27	0.86
watermelon	shannonH_300 / Socia.Eusocial	0.08	0.79	0.48
watermelon	ag_1500 / Socia.Eusocial	-0.04	-0.36	0.74
watermelon	open_1500 / Socia.Eusocial	-0.16	-1.61	0.11
watermelon	forest_edge_1500 / Socia.Eusocial	-0.06	-0.61	0.56
watermelon	shannonH_1500 / Socia.Eusocial	0.01	0.12	0.92
watermelon	ag_300 / Socia.fac_social	-0.07	-0.64	0.54
watermelon	open_300 / Socia.fac_social	0.03	0.45	0.72
watermelon	forest_edge_300 / Socia.fac_social	-0.01	0.02	0.99
watermelon	shannonH_300 / Socia.fac_social	0.06	0.86	0.47
watermelon	ag_1500 / Socia.fac_social	-0.01	-0.15	0.86
watermelon	open_1500 / Socia.fac_social	0.07	0.73	0.47
watermelon	forest_edge_1500 / Socia.fac_social	0	-0.02	0.99
watermelon	shannonH_1500 / Socia.fac_social	0.09	1.52	0.13
watermelon	ag_300 / Socia.Solitary	0.03	0.31	0.79
watermelon	open_300 / Socia.Solitary	-0.01	-0.15	0.89
watermelon	forest_edge_300 / Socia.Solitary	-0.03	-0.16	0.86

watermelon	shannonH_300 / Socia.Solitary	-0.14	-1.46	0.14
watermelon	ag_1500 / Socia.Solitary	0.05	0.54	0.61
watermelon	open_1500 / Socia.Solitary	0.13	1.33	0.2
watermelon	forest_edge_1500 / Socia.Solitary	0.07	0.74	0.48
watermelon	shannonH_1500 / Socia.Solitary	-0.08	-0.83	0.44
watermelon	ag_300 / Paras.No	-0.1	-0.85	0.48
watermelon	open_300 / Paras.No	-0.02	-0.24	0.88
watermelon	forest_edge_300 / Paras.No	-0.02	-0.22	0.82
watermelon	shannonH_300 / Paras.No	0.18	1.67	0.08
watermelon	ag_1500 / Paras.No	0	0	1
watermelon	open_1500 / Paras.No	-0.22	-2.07	0.05
watermelon	forest_edge_1500 / Paras.No	-0.12	-1.13	0.23
watermelon	shannonH_1500 / Paras.No	0.06	0.57	0.59
watermelon	ag_300 / Paras.Yes	0.1	0.85	0.48
watermelon	open_300 / Paras.Yes	0.02	0.24	0.88
watermelon	forest_edge_300 / Paras.Yes	0.02	0.22	0.82
watermelon	shannonH_300 / Paras.Yes	-0.18	-1.67	0.08
watermelon	ag_1500 / Paras.Yes	0	0	1
watermelon	open_1500 / Paras.Yes	0.22	2.07	0.05
watermelon	forest_edge_1500 / Paras.Yes	0.12	1.13	0.23
watermelon	shannonH_1500 / Paras.Yes	-0.06	-0.57	0.59
watermelon	**ag_300 / ITfam**	**0.23**	**2.19**	**0.02**
watermelon	open_300 / ITfam	-0.07	-0.61	0.56
watermelon	forest_edge_300 / ITfam	-0.1	-0.82	0.41
watermelon	shannonH_300 / ITfam	-0.15	-1.39	0.18
watermelon	ag_1500 / ITfam	-0.13	-1.15	0.27
watermelon	open_1500 / ITfam	-0.1	-0.94	0.36
watermelon	forest_edge_1500 / ITfam	-0.03	-0.29	0.79
watermelon	shannonH_1500 / ITfam	-0.09	-0.78	0.45
watermelon	ag_300 / PDrar20	-0.08	-0.76	0.52
watermelon	open_300 / PDrar20	-0.04	-0.53	0.63
watermelon	forest_edge_300 / PDrar20	0.02	0.18	0.88
watermelon	shannonH_300 / PDrar20	0.08	1	0.35
watermelon	ag_1500 / PDrar20	0.05	0.51	0.7
watermelon	open_1500 / PDrar20	-0.13	-1.56	0.12
watermelon	forest_edge_1500 / PDrar20	-0.06	-0.7	0.52
watermelon	shannonH_1500 / PDrar20	0.02	0.22	0.86
watermelon	**ag_300 / tongue**	**0.23**	**2.18**	**0.02**
watermelon	open_300 / tongue	-0.07	-0.64	0.55
watermelon	forest_edge_300 / tongue	-0.09	-0.76	0.45
watermelon	shannonH_300 / tongue	-0.14	-1.38	0.19
watermelon	ag_1500 / tongue	-0.12	-1.11	0.29
watermelon	open_1500 / tongue	-0.1	-0.92	0.37
watermelon	forest_edge_1500 / tongue	-0.03	-0.26	0.82

watermelon	shannonH_1500 / tongue	-0.08	-0.73	0.48
cranberry	ag_300 / Nest_.cavity	0.1	1.09	0.3
cranberry	open_300 / Nest_.cavity	-0.15	-1.62	0.11
cranberry	forest_edge_300 / Nest_.cavity	0	0.05	0.97
cranberry	shannonH_300 / Nest_.cavity	-0.07	-0.71	0.51
cranberry	ag_1500 / Nest_.cavity	0.05	0.48	0.65
cranberry	open_1500 / Nest_.cavity	-0.08	-0.69	0.5
cranberry	forest_edge_1500 / Nest_.cavity	-0.07	-0.75	0.47
cranberry	shannonH_1500 / Nest_.cavity	0.04	0.38	0.72
cranberry	ag_300 / Nest_.hole	0.01	0.12	0.91
cranberry	open_300 / Nest_.hole	-0.05	-0.56	0.58
cranberry	forest_edge_300 / Nest_.hole	0.01	0.18	0.88
cranberry	shannonH_300 / Nest_.hole	-0.03	-0.56	0.58
cranberry	ag_1500 / Nest_.hole	-0.04	-0.43	0.68
cranberry	open_1500 / Nest_.hole	-0.08	-0.64	0.56
cranberry	forest_edge_1500 / Nest_.hole	-0.02	-0.22	0.87
cranberry	shannonH_1500 / Nest_.hole	-0.05	-0.51	0.61
cranberry	ag_300 / Nest_.soil	-0.09	-0.89	0.41
cranberry	open_300 / Nest_.soil	0.09	0.97	0.36
cranberry	forest_edge_300 / Nest_.soil	0	0.01	1
cranberry	shannonH_300 / Nest_.soil	0.09	0.81	0.45
cranberry	ag_1500 / Nest_.soil	-0.04	-0.33	0.76
cranberry	open_1500 / Nest_.soil	0.13	1.08	0.3
cranberry	forest_edge_1500 / Nest_.soil	0.09	0.87	0.41
cranberry	shannonH_1500 / Nest_.soil	-0.02	-0.17	0.91
cranberry	ag_300 / Nest_.stem	-0.03	-0.52	0.36
cranberry	open_300 / Nest_.stem	0.02	0.21	0.84
cranberry	forest_edge_300 / Nest_.stem	0	0.07	0.94
cranberry	shannonH_300 / Nest_.stem	0.02	0.32	0.56
cranberry	ag_1500 / Nest_.stem	-0.01	-0.11	0.9
cranberry	open_1500 / Nest_.stem	0.03	0.51	0.44
cranberry	forest_edge_1500 / Nest_.stem	0.02	0.36	0.61
cranberry	shannonH_1500 / Nest_.stem	0	0.05	0.92
cranberry	ag_300 / Nest_.wood	-0.05	-0.55	0.6
cranberry	open_300 / Nest_.wood	0.17	1.77	0.07
cranberry	forest_edge_300 / Nest_.wood	-0.02	-0.3	0.76
cranberry	shannonH_300 / Nest_.wood	0.01	0.1	0.93
cranberry	ag_1500 / Nest_.wood	0	0.05	0.96
cranberry	open_1500 / Nest_.wood	0	-0.04	0.97
cranberry	forest_edge_1500 / Nest_.wood	0	0	1
cranberry	shannonH_1500 / Nest_.wood	-0.01	-0.07	0.94
cranberry	ag_300 / Socia.Eusocial	0.02	0.28	0.82
cranberry	open_300 / Socia.Eusocial	0.03	0.19	0.88
cranberry	forest_edge_300 / Socia.Eusocial	0.01	0.09	0.93

cranberry	shannonH_300 / Socia.Eusocial	0.02	0.28	0.8
cranberry	ag_1500 / Socia.Eusocial	-0.01	-0.08	0.95
cranberry	open_1500 / Socia.Eusocial	0.02	0.18	0.88
cranberry	forest_edge_1500 / Socia.Eusocial	-0.01	-0.14	0.92
cranberry	shannonH_1500 / Socia.Eusocial	0.01	0.12	0.91
cranberry	ag_300 / Socia.fac_social	0.03	0.75	0.47
cranberry	open_300 / Socia.fac_social	0.04	0.29	0.77
cranberry	forest_edge_300 / Socia.fac_social	-0.05	-1.15	0.29
cranberry	shannonH_300 / Socia.fac_social	-0.04	-0.71	0.32
cranberry	ag_1500 / Socia.fac_social	0.04	0.71	0.47
cranberry	open_1500 / Socia.fac_social	0.01	0.23	0.77
cranberry	forest_edge_1500 / Socia.fac_social	0.01	0.22	0.81
cranberry	shannonH_1500 / Socia.fac_social	0.03	0.56	0.5
cranberry	ag_300 / Socia.Solitary	-0.03	-0.41	0.74
cranberry	open_300 / Socia.Solitary	-0.04	-0.37	0.72
cranberry	forest_edge_300 / Socia.Solitary	0.01	0.15	0.9
cranberry	shannonH_300 / Socia.Solitary	-0.01	-0.09	0.94
cranberry	ag_1500 / Socia.Solitary	0	-0.03	0.97
cranberry	open_1500 / Socia.Solitary	-0.03	-0.23	0.86
cranberry	forest_edge_1500 / Socia.Solitary	0.01	0.07	0.96
cranberry	shannonH_1500 / Socia.Solitary	-0.02	-0.32	0.79
cranberry	ag_300 / Paras.No	0	-0.01	1
cranberry	open_300 / Paras.No	0.01	0.16	0.87
cranberry	forest_edge_300 / Paras.No	0	-0.05	0.96
cranberry	shannonH_300 / Paras.No	0	0.01	0.97
cranberry	ag_1500 / Paras.No	0	0.04	0.97
cranberry	open_1500 / Paras.No	0.01	-0.05	0.96
cranberry	forest_edge_1500 / Paras.No	0.02	0.14	0.88
cranberry	shannonH_1500 / Paras.No	0.03	0.24	0.74
cranberry	ag_300 / Paras.Yes	0	0.01	1
cranberry	open_300 / Paras.Yes	-0.01	-0.16	0.87
cranberry	forest_edge_300 / Paras.Yes	0	0.05	0.96
cranberry	shannonH_300 / Paras.Yes	0	-0.01	0.97
cranberry	ag_1500 / Paras.Yes	0	-0.04	0.97
cranberry	open_1500 / Paras.Yes	-0.01	0.05	0.96
cranberry	forest_edge_1500 / Paras.Yes	-0.02	-0.14	0.88
cranberry	shannonH_1500 / Paras.Yes	-0.03	-0.24	0.74
cranberry	ag_300 / ITfam	0.13	1.37	0.19
cranberry	open_300 / ITfam	-0.13	-1.36	0.18
cranberry	forest_edge_300 / ITfam	-0.05	-0.54	0.62

cranberry	shannonH_300 / ITfam	-0.12	-1.31	0.2
cranberry	ag_1500 / ITfam	0.14	1.45	0.15
cranberry	open_1500 / ITfam	0.01	0.02	0.99
cranberry	forest_edge_1500 / ITfam	0	-0.08	0.93
cranberry	shannonH_1500 / ITfam	0.11	1.18	0.27
cranberry	ag_300 / PDrar20	-0.05	-0.47	0.68
cranberry	open_300 / PDrar20	0.18	1.87	0.08
cranberry	forest_edge_300 / PDrar20	0.02	0.16	0.88
cranberry	shannonH_300 / PDrar20	0.09	0.87	0.42
cranberry	ag_1500 / PDrar20	-0.06	-0.66	0.55
cranberry	open_1500 / PDrar20	0.06	0.46	0.71
cranberry	forest_edge_1500 / PDrar20	0.03	0.27	0.82
cranberry	shannonH_1500 / PDrar20	-0.01	-0.08	0.95
cranberry	ag_300 / tongue	0.11	1.19	0.25
cranberry	open_300 / tongue	-0.15	-1.54	0.13
cranberry	forest_edge_300 / tongue	-0.01	-0.13	0.91
cranberry	shannonH_300 / tongue	-0.09	-0.9	0.39
cranberry	ag_1500 / tongue	0.07	0.72	0.5
cranberry	open_1500 / tongue	-0.06	-0.5	0.66
cranberry	forest_edge_1500 / tongue	-0.06	-0.64	0.58
cranberry	shannonH_1500 / tongue	0.06	0.6	0.6
blueberry	ag_300 / Nest_.cavity	-0.14	-0.76	0.52
blueberry	open_300 / Nest_.cavity	0.11	0.68	0.52
blueberry	forest_edge_300 / Nest_.cavity	0.1	0.61	0.64
blueberry	shannonH_300 / Nest_.cavity	0.09	0.53	0.69
blueberry	ag_1500 / Nest_.cavity	-0.34	-1.13	0.21
blueberry	open_1500 / Nest_.cavity	0.2	1.33	0.19
blueberry	forest_edge_1500 / Nest_.cavity	0.24	0.94	0.31
blueberry	shannonH_1500 / Nest_.cavity	-0.04	-0.25	0.82
blueberry	ag_300 / Nest_.hole	-0.03	-0.02	0.93
blueberry	open_300 / Nest_.hole	-0.02	-0.35	0.82
blueberry	forest_edge_300 / Nest_.hole	0.05	0.23	0.81
blueberry	shannonH_300 / Nest_.hole	0.07	0.4	0.72
blueberry	ag_1500 / Nest_.hole	0.08	0.52	0.44
blueberry	open_1500 / Nest_.hole	-0.05	-0.55	0.6
blueberry	forest_edge_1500 / Nest_.hole	0.01	0	1
blueberry	shannonH_1500 / Nest_.hole	0.05	0.29	0.71
blueberry	ag_300 / Nest_.soil	0.12	0.75	0.5
blueberry	open_300 / Nest_.soil	-0.12	-0.78	0.51
blueberry	forest_edge_300 / Nest_.soil	-0.05	-0.3	0.77
blueberry	shannonH_300 / Nest_.soil	-0.08	-0.47	0.67
blueberry	ag_1500 / Nest_.soil	0.41	1.28	0.14
blueberry	open_1500 / Nest_.soil	-0.09	-0.55	0.65
blueberry	forest_edge_1500 / Nest_.soil	-0.4	-1.48	0.08

blueberry	shannonH_1500 / Nest_.soil	-0.08	-0.48	0.72
blueberry	ag_300 / Nest_.wood	0.01	0.07	0.95
blueberry	open_300 / Nest_.wood	0.03	0.09	0.92
blueberry	forest_edge_300 / Nest_.wood	-0.07	-0.54	0.74
blueberry	shannonH_300 / Nest_.wood	-0.02	-0.19	0.92
blueberry	ag_1500 / Nest_.wood	-0.15	-0.48	0.52
blueberry	open_1500 / Nest_.wood	-0.12	-0.93	0.4
blueberry	forest_edge_1500 / Nest_.wood	0.25	1.07	0.18
blueberry	shannonH_1500 / Nest_.wood	0.15	0.85	0.33
blueberry	ag_300 / Socia.Eusocial	-0.17	-1.03	0.36
blueberry	open_300 / Socia.Eusocial	0.13	0.83	0.47
blueberry	forest_edge_300 / Socia.Eusocial	0.16	1.1	0.29
blueberry	shannonH_300 / Socia.Eusocial	0.13	0.84	0.42
blueberry	ag_1500 / Socia.Eusocial	-0.32	-1.04	0.38
blueberry	open_1500 / Socia.Eusocial	0.21	1.38	0.17
blueberry	forest_edge_1500 / Socia.Eusocial	0.2	0.77	0.67
blueberry	shannonH_1500 / Socia.Eusocial	-0.01	-0.02	0.98
blueberry	ag_300 / Socia.fac_social	0.08	0.7	0.5
blueberry	open_300 / Socia.fac_social	-0.06	-0.48	0.66
blueberry	forest_edge_300 / Socia.fac_social	-0.12	-1.09	0.29
blueberry	shannonH_300 / Socia.fac_social	-0.09	-0.76	0.46
blueberry	ag_1500 / Socia.fac_social	-0.12	-0.59	0.31
blueberry	open_1500 / Socia.fac_social	-0.18	-1.52	0.12
blueberry	forest_edge_1500 / Socia.fac_social	0.22	1.36	0.09
blueberry	shannonH_1500 / Socia.fac_social	0.13	1.19	0.26
blueberry	ag_300 / Socia.Solitary	0.11	0.67	0.55
blueberry	open_300 / Socia.Solitary	-0.08	-0.55	0.63
blueberry	forest_edge_300 / Socia.Solitary	-0.07	-0.44	0.67
blueberry	shannonH_300 / Socia.Solitary	-0.06	-0.38	0.74
blueberry	ag_1500 / Socia.Solitary	0.39	1.27	0.13
blueberry	open_1500 / Socia.Solitary	-0.08	-0.52	0.66
blueberry	forest_edge_1500 / Socia.Solitary	-0.34	-1.3	0.17
blueberry	shannonH_1500 / Socia.Solitary	-0.08	-0.51	0.73
blueberry	ag_300 / Paras.No	0	-0.71	1
blueberry	open_300 / Paras.No	0	0.65	1
blueberry	forest_edge_300 / Paras.No	0	-0.69	0.91
blueberry	shannonH_300 / Paras.No	0	0.43	0.88
blueberry	ag_1500 / Paras.No	0	0.69	0.99
blueberry	open_1500 / Paras.No	0	-0.7	0.97
blueberry	forest_edge_1500 / Paras.No	0	0.96	0.34

blueberry	shannonH_1500 / Paras.No	0	-0.72	0.88
blueberry	ag_300 / ITfam	-0.03	-0.13	0.9
blueberry	open_300 / ITfam	0.01	0.02	0.99
blueberry	forest_edge_300 / ITfam	-0.05	-0.33	0.78
blueberry	shannonH_300 / ITfam	-0.02	-0.16	0.88
blueberry	ag_1500 / ITfam	-0.42	-1.33	0.16
blueberry	open_1500 / ITfam	-0.02	-0.09	0.95
blueberry	forest_edge_1500 / ITfam	0.42	1.59	0.08
blueberry	shannonH_1500 / ITfam	0.12	0.73	0.52
blueberry	ag_300 / PDrar20	-0.08	-0.4	0.73
blueberry	open_300 / PDrar20	0.13	0.66	0.53
blueberry	forest_edge_300 / PDrar20	0	-0.02	0.98
blueberry	shannonH_300 / PDrar20	0.03	0.15	0.89
blueberry	ag_1500 / PDrar20	-0.42	-1.39	0.17
blueberry	open_1500 / PDrar20	-0.04	-0.19	0.87
blueberry	forest_edge_1500 / PDrar20	0.35	1.37	0.17
blueberry	shannonH_1500 / PDrar20	0.32	1.59	0.11
blueberry	ag_300 / tongue	-0.17	-0.91	0.41
blueberry	open_300 / tongue	0.05	0.29	0.82
blueberry	forest_edge_300 / tongue	0.08	0.41	0.72
blueberry	shannonH_300 / tongue	0.08	0.41	0.71
blueberry	ag_1500 / tongue	-0.48	-1.51	0.12
blueberry	open_1500 / tongue	0.07	0.35	0.73
blueberry	forest_edge_1500 / tongue	0.36	1.39	0.18
blueberry	shannonH_1500 / tongue	-0.02	-0.08	0.95

Table S4: Model selection procedure showing all models within 2 AICc values.

Crop	Measure	Model	Delta AICc
Watermelon	Visitation Frequency	~ body size + tongue	0
Watermelon	Visitation Frequency	~ tongue	0.06
Watermelon	Visitation Frequency	~ .	0.28
Watermelon	Visitation Frequency	~ body size	1.99
Watermelon	Pollen deposition	~ body size + tongue	0
Cranberry	Visitation Frequency	~ sociality + tongue	0
Cranberry	Visitation Frequency	~ nest place	1.43
Cranberry	Visitation Frequency	~ sociality	1.56
Cranberry	Pollen deposition	~ .	0
Blueberry	Visitation Frequency	~ specialization	0
Blueberry	Pollen deposition	~ tongue	0