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

Ignasi Bartomeus[1,*] Daniel P. Cariveau [2,3], Tina Harrison[2], Rachael Winfree[2]

[1] Estación Biológica de Doñana (EBD-CSIC), Sevilla, Spain.

[2] Rutgers University, The State University of New Jersey, New Brunswick, NJ 08901, USA

[3] Department of Entomology, University of Minnesota, Saint Paul, MN 55113, USA

[*] Correspondence author: nacho.bartomeus@gmail.com

**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

147 change variable, as it is the dominant anthropogenic habitat type in all three
148 study systems. Percent open natural/semi-natural habitat makes up a small
149 proportion of the total land cover (mean 6.8% cover at 1500 m radius) but is
150 likely to be disproportionately important as forage and nesting habitat for bees
151 (Kleijn *et al*. 2006). Forest edge length may represent important habitat for
152 bees that nest in woods but forage in open areas (Kells & Goulson 2003).
153 Diverse patchy landscapes may be beneficial to bees as they may nest and
154 forage in different habitats (Kremen *et al.* 2007); thus we include Shannon H
155 diversity of the seven cover categories as a measure of habitat heterogeneity.
156 We calculated values for all four land cover variables at both a small scale
157 (300 m radius) and a large scale (1500 m radius), which correspond to typical
158 flight distances of small- and large-bodied bees, respectively (Greenleaf et al.
159 2007).

160 *Pollinator function*

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

167 To measure the pollination efficiency we quantified single-visit pollen
168 deposition by presenting virgin flowers to individual bees foraging on the
169 target crop. After visitation, we counted the number of pollen grains deposited

170 per flower visit (watermelon) or the number of pollen tetrads with pollen tubes
171 per flower visit (cranberry and blueberry). Because species identification in the
172 field is not possible for most bees and net collecting immediately after visits is
173 generally not possible, for the measurement of pollination efficiency we
174 grouped bees in species groups. Each group consisted of between one and
175 27 species, with the median number of species per group being 4 species
176 (Supporting Information, Table S1). Control flowers were left bagged until the
177 end of the field day, and contained few pollen grains (watermelon mean = 3
178 grains, N = 40 stigmas; cranberry mean = 0 tetrads, N = 82 stigmas; blueberry
179 mean = 2 tetrads, N= 734 stigmas). For detailed methods see Benjamin *et al.*
180 *(*2014), Winfree *et al*. (2015), Cariveau *et al.* (2013).

181 *Species traits*

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

190 We obtained the trait data as follows. Species sociality level, nesting behavior
191 and brood parasite status were extracted from the literature (Bartomeus *et al.*
192 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

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

263 **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

310 traits we studied here are not suitable for predictive purposes.

311 Being able to identify strong response traits would be a key tool for
312 understanding extinction risk, and an asset for conservation planning.
313 However, characterizing extinction risk based on traits is challenging. Despite
314 some generalities that emerge across taxa, with rare species, big species,
315 specialists, and higher trophic levels being in general more sensitive to
316 disturbances (Fisher & Owens 2004), there is a large variation in the response
317 of the species with those traits (Fritz, Bininda-Emonds & Purvis 2009; Seguin
318 *et al*. 2014). Work specifically on native bees has found that traits such as
319 specialization, body size, and sociality may predict responses to land use
320 (Winfree *et al.* 2009; Bommarco *et al*. 2010; Williams *et al*. 2010; Bartomeus
321 *et al*. 2013b; De Palma *et al*. 2015). However, studies often find contrasting
322 results. For example, De Palma et al. (2015) analyzed over 70,000 wild bee
323 records and found that small species were most sensitive to agricultural land
324 use, while others have found that larger species are more sensitive to
325 agricultural land use and/or environmental change generally (Larsen, Williams
326 & Kremen 2005; Bartomeus *et al.* 2013b; Rader *et al*. 2014), and some have
327 found little effect of body size (Williams et al. 2010). Here, we only found a
328 weak trend for big species to be more abundant in locally intense agricultural
329 areas in watermelon, but this trend disappears when land use is measured at
330 larger scales. Another trait, dietary specialization, is one of the few traits that
331 has been generally linked to increased species sensitivity to environmental
332 change (Williams *et al.* 2010; Scheper *et al*. 2014; De Palma *et al*. 2015), but
333 here we found that floral specialist bees did not decline with intensifying

334 agriculture. If anything, specialization is positively associated with agricultural
335 intensification in the blueberry system (Table S3), largely because the most
336 abundant bee species in this system (*Andrena bradleyi*) is a specialist on the
337 blueberry genus *Vaccinium*. Specialist bees observed in crop systems are
338 likely to be specialized on the crop plant family as was the case in our data
339 (e.g. *Habropoda sp.* , *Andrena bradleyi* in blueberry, but also *Peoponapis sp.*
340 in watermelon and *Mellita americana* in cranberry). We would expect different
341 responses from study designs that include natural habitat and a larger range
342 of specialist host plants (Forrest et al. 2015, Bartomeus & Winfree 2013).

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

357 If generalizable response and effect traits can be found, the final step will be
358 to link response and effects to predict changes in ecosystem services. A
359 positive association between the response and effect traits (Naeem & Wright
360 2003) such that species with the strongest response to environmental change
361 also had the strongest effect on function, indicates the land-use change has
362 the potential for dramatic effects on ecosystem function. Whether response
363 and effect traits are in general positively, negatively, or uncorrelated is an
364 important question that has not yet been answered (Larsen, Williams &
365 Kremen 2005). Despite the conceptual elegance of the response-effect trait
366 framework, it is only effective if it is predictive, and strong evidence for the
367 generality of traits has not yet been found. For example, even the very
368 thorough and rigorously analyzed study of response-effect relationships by
369 Larsen, Williams & Kremen (2005) is based on a non-significant weak
370 relationship between pollinator per visit efficiency and body size. In our study,
371 even the strongest correlations find for watermelon, where big species are
372 less sensitive to local agricultural intensification and more efficient per visit,
373 but not more frequent flower visitors than smaller species are too weak to be
374 useful for predictive purposes.

375 Predictive response and/or effect traits are often assumed in the larger
376 literature as well. For example, recent re-evaluations of community stability in
377 food webs shows that using body size as proxy of extinction risk changes the
378 outcome of the stability simulations (Brose *et al.* 2016). However, the
379 assumption that body size is a good predictor of extinction risk is not directly
380 validated. Given the correlation showing that bigger species are more

381 sensitive is usually weak (Fisher & Owens 2004), these kind of approaches
382 could produce misleading outcomes.

383 Currently trait data may be too coarse to reveal ubiquitous response and
384 effect traits for four reasons. First, some traits may simply reflect identity of
385 genera or higher taxonomic groups. For example, some bumble bee species
386 in our three systems (especially *B. impatiens*) are common, functionally
387 dominant, and robust to extinction (Cariveau *et al.* 2013, Winfree *et al.* 2015).
388 Some of the important response and effect traits that we found, such as cavity
389 nesting and body size, may simply be proxies for bumble bees. Bumble bee
390 species also share other traits (e.g. sociality) that are commonly used in trait
391 analyses. Therefore, studies that don't include phylogenetic correlations may
392 be simply characterizing the general relationship between disturbance and the
393 functionally dominant bumble bees, or other dominant taxa. As there is a great
394 variability in the responses to disturbance among bumble bee species
395 (Cameron *et al*. 2011; Bartomeus *et al.* 2013b, Persson *et al.* 2015) this may
396 also explain why some studies find big species to be more sensitive to land
397 use change (Larsen, Williams & Kremen 2005) and other studies find the
398 opposite (Rader *et al*. 2014, this study). Second, traits may interact in complex
399 ways and single traits may be not able to capture responses and functional
400 contributions across species (e.g. Bommarco *et al.* 2010, De Palma *et al.*
401 2015). Third, phenotypical variability within species, usually ignored in trait-
402 based approaches, may play a more important role than previously though
403 (Bolnik et al. 2011). Finally, the most important traits may not have been
404 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.

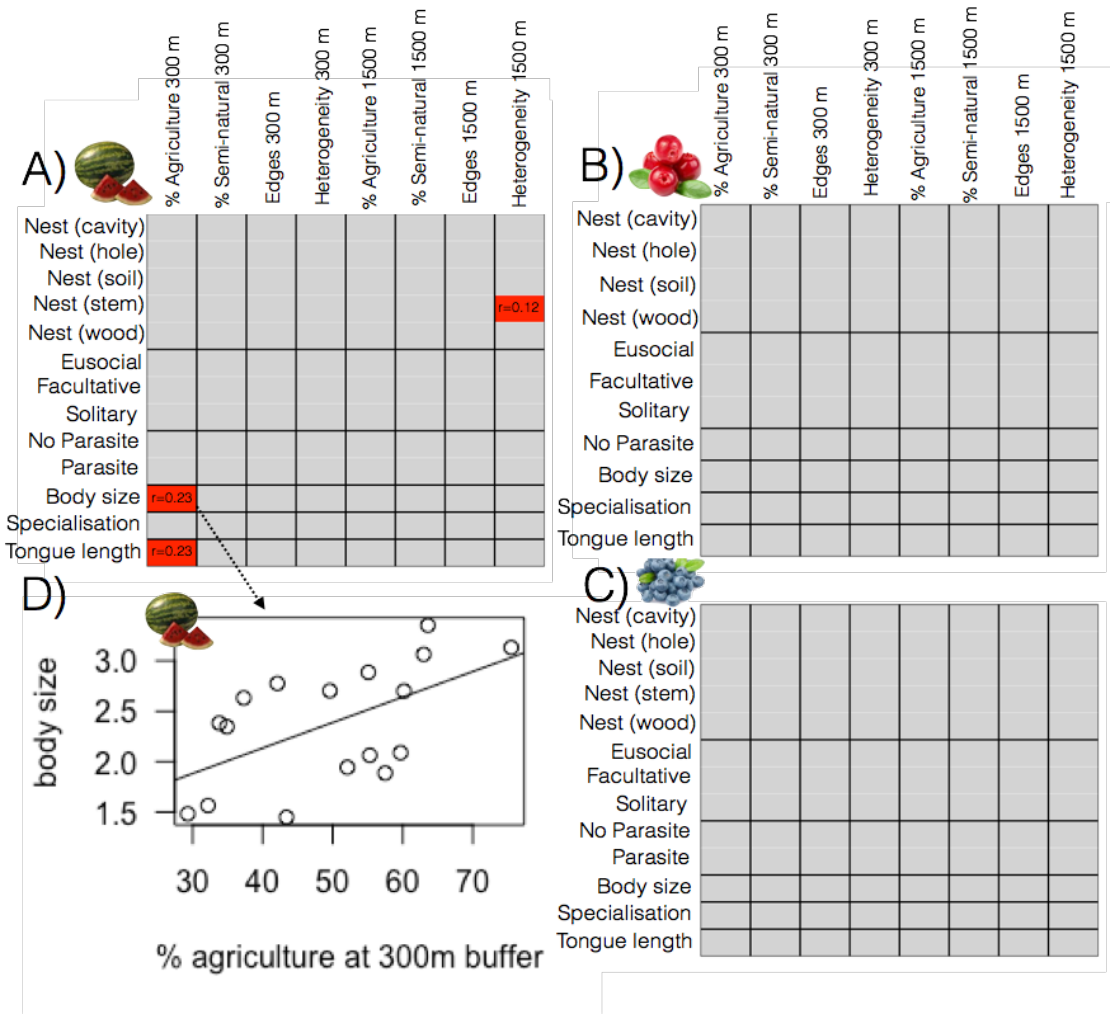
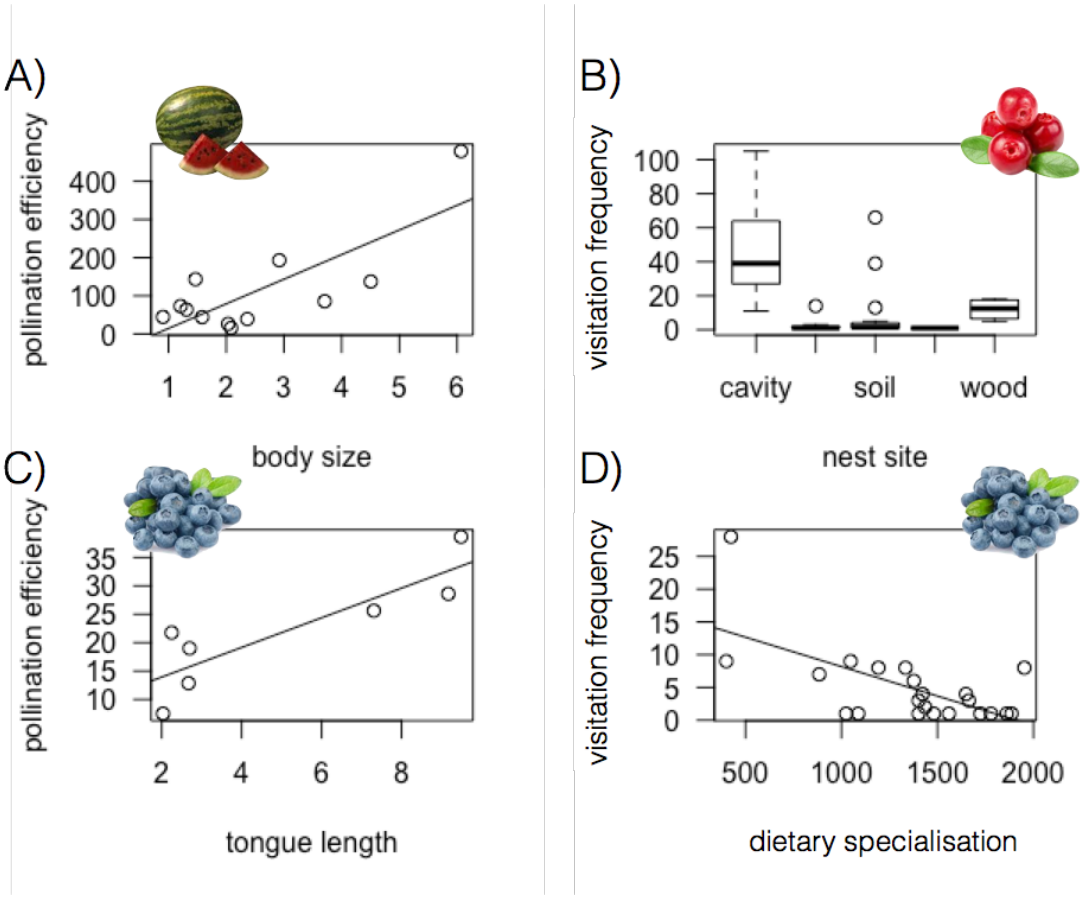


**Fig. 2: Multipanel plot showing the relationships between species traits and pollination function**, which is decomposed into efficiency (pollen deposited per flower visit) and frequency of flower visits. A) watermelon, B) cranberry, C-D) blueberry.



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

671 in sampling rounds between April and early June. 5) CIG 4600 bee x plant
672 interactions. Site were comprised of old fields as well as pollinator
673 enhancement sites. Bees using were collected using a hand net from a total of
674 a total 18 sites in 2011-2013. For each bee specimen, the plant species was
675 recorded. 6) Cape May 5858 bee x plant interactions. This study included only
676 one site. The habitat was an old field that had been planted in 20 species of
677 native perennial plants. Sampling took place over 3 years in sampling rounds
678 that occurred in May through September.

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

681 Table S3: Fourth corner results showing correlations and p-values for each
682 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 |

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|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|
| 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 |