

1 **The winners and losers of land-use intensification: pollinator community**
2 **disassembly is non-random and alters functional diversity**

3

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25

26 **(A)Abstract**

27 **Aim:** Pollination services are at risk from land-use change and intensification, but
28 responses of individual pollinator species are often variable, making it difficult to
29 detect and understand community-level impacts on pollination. We investigated
30 changes in community composition and functional diversity of insect pollinator
31 communities under land-use change in a highly-modified landscape.

32 **Location:** Canterbury region, South Island, New Zealand.

33 **Methods:** We trapped insect pollinators every month for one year at 24 sites across
34 four land-use types of increasing intensity in New Zealand: gardens with native
35 vegetation, blackcurrant orchards, dairy farms, and rotational cropping farms. We
36 investigated changes in pollinator species and functional richness and differences in
37 species and functional composition.

38 **Results:** Under increasing land-use intensity, both species and functional richness
39 declined markedly. Changes in functional richness, however, were overall not
40 significantly different than expected based on the observed declines in species
41 richness. Nevertheless, there was a significant trend towards greater-than-expected
42 functional richness within less intensive land-use types, and lower-than-expected
43 functional richness within intensive land-use types. The order of species loss under
44 increasing land-use intensity was non-random, as pollinators with a narrow diet
45 breadth, large body size, solitary behaviour and a preference for non-floral larval
46 food resources were lost first.

47 **Main conclusions:** Our study shows that pollinator species bearing particular trait
48 attributes are susceptible to differences in land use. Our study suggests that
49 pollination services may be more vulnerable to environmental changes and
50 disturbances in more intensive land-use types as a result of lower pollinator

51 functional richness.

52

53 Key words: agriculture, agro-ecosystem, bees, biodiversity, crop, ecosystem

54 function, functional richness, functional traits, land-use change, pollination.

55

56 **(A) Introduction**

57 Land-use change is frequently associated with biodiversity loss and altered species
58 composition (Tylianakis *et al.*, 2005; Kremen *et al.*, 2007). This has functional
59 consequences, because species with particular functional traits appear to be
60 especially vulnerable to decline (Henle *et al.*, 2004; Bartomeus *et al.*, 2013b;
61 Newbold *et al.*, 2013). As species' traits determine their contribution to ecosystem
62 processes, loss of particular traits may translate to changes in ecosystem functioning
63 and services (Kleijn *et al.*, 2004; Larsen *et al.*, 2005).

64

65 The consequences of land-use change are particularly important for insect
66 pollinators, which provide pollination services for between 78 and 94% of all
67 flowering plants and 75% of the leading global food crops (Klein *et al.*, 2007; Ollerton
68 *et al.*, 2011; Winfree *et al.*, 2011). Yet, while the benefits of pollinator biodiversity are
69 known to depend on functional trait diversity (Hoehn *et al.*, 2008; Albrecht *et al.*,
70 2012), studies on pollinator responses to land use have largely focused on metrics
71 relating to species richness and/or abundance (e.g. Hatfield, 2007; reviewed in
72 Winfree *et al.*, 2011). The full impact of disturbance (e.g., land-use intensity) on
73 communities includes changes to the identity and functional roles of species (e.g.
74 Bracken & Low, 2012). For example, social bee species have been shown to be
75 more strongly affected by isolation from natural habitat and pesticides than are
76 solitary bee species (Williams *et al.*, 2010), and small-bodied generalists tend to be
77 more strongly affected by habitat loss, compared with small-bodied specialists
78 (Bommarco *et al.*, 2010).

79

80 Non-random species losses occur because of specific trait-environment
81 relationships, and may reflect differential extinction or colonisation rates, differences
82 in dispersal ability and/or differential habitat quality (Loo *et al.*, 2002; Hylander *et al.*,
83 2005). These factors may result in communities that show a nested composition
84 pattern, whereby species in disturbed habitats are a subset of those present in less
85 disturbed habitats (Ulrich, 2009; Aizen *et al.*, 2012; Sasaki *et al.*, 2012). Nestedness
86 has thus been used as a tool to identify the functional and compositional
87 consequences of land-use change and non-random patterns of species loss
88 (Patterson & Atmar, 1986; Ulrich *et al.*, 2009; Selmants *et al.*, 2012).

89

90 In this study, we use a novel approach to investigate pollinator community response
91 to changes in land-use type by investigating functional diversity and community
92 nestedness in four anthropogenic habitats with differing land-use intensity. We base
93 our analyses on 10 pollinator morphological, behavioural and life-history traits that
94 contribute to pollination functions and are likely to influence responses to
95 disturbance.

96

97 Specifically, we ask the following questions:

- 98 1. How do pollinator richness and composition differ among land-use types and
99 do these changes translate to altered functional diversity among land-use
100 types?
- 101 2. Are losses of functional diversity predictable from losses of species diversity?
- 102 3. Which functional traits are favoured in different land-use types?

103

104 **(A) Methods**

105 (B) *Land-use types*

106 Six replicates of each of four land-use types (i.e. 24 sites) were sampled in the
107 Canterbury plains region, on the South Island of New Zealand. The sites were
108 positioned within four different land-use types (named in decreasing order of
109 intensity): rotational cropping, dairy farms, blackcurrant orchards and New Zealand
110 native gardens (Fig. S1; see Appendix S1 and S2 in Supporting Information for
111 details about site selection). The order of intensity was based on qualitative
112 information gained from farmer consultation concerning the frequency and depth of
113 soil disturbance, biomass removal, and use of external inputs (i.e. fertilizer,
114 herbicide), which, in turn, impacted vegetation complexity and the proportion of
115 exotic species (Table S1; see Appendix S1). All land-use types were embedded
116 within a highly modified agricultural landscape in the Canterbury region of New
117 Zealand.

118 (B) *Insect pollinator sampling*

119 We selected a focal sampling area (5 m x 5 m) at each replicate site, in which to trap
120 insect pollinators. Pollinators were trapped for five days each month from November
121 2008 to 2009 using flight intercept and pan traps. Insect traps were placed within a
122 field boundary nearest to the centre of a given farm of a given land-use type. At each
123 site, four yellow flight intercept/pan traps (Howlett *et al.*, 2009) were positioned 2 m
124 apart on stakes at a height of 1.2 m. Each trap consisted of a pan trap measuring 22
125 cm x 35 cm x 6 cm attached to two vertical panes (flight intercept) that were
126 arranged perpendicular to each other (Fig. S2; see Appendix S1 for more details on
127 sampling). Two traps contained a mixture of water and detergent and two traps
128 contained clear acetate sheets (22 cm x 30 cm) lined with Tanglefoot paste (The

129 Tanglefoot Company, Minnesota, USA). Tanglefoot was applied as a thin film to the
130 entire surface area of each acetate sheet to ensure maximum insect capture. We
131 applied Tanglefoot as a thin film such that pollen was retained on insect bodies and
132 not lost in drops of excess Tanglefoot; preliminary trials were conducted in
133 commercial *Brassica rapa* fields to perfect this method. The two trapping methods
134 were used to maximize the diversity and sample size of insects captured. All traps
135 were replaced daily. All insects captured were transported back to the laboratory and
136 stored in a freezer (-80 °C) until further processing. Insects were sorted to species
137 using existing collections, identification keys (Donovan, 2007; Landcare Research,
138 2013) and assistance from expert taxonomists. Potential pollinators were separated
139 from non-pollinators on the basis of the proportion of individuals carrying pollen and
140 the mean amount of pollen carried. In this dataset, some taxa comprised numerous
141 individuals that carried no pollen at all and a few that carried 1 or 2 pollen grains,
142 arriving at a mean of 0 or 1 pollen grain/s. We did not consider these to be
143 pollinators. The remaining species carried a minimum mean pollen load of five or
144 more pollen grains. These were considered potential pollinators. Although we did
145 not measure viability of pollen, the transfer and adherence of pollen to the pollinator
146 was deemed a potential pollination event. The number of pollen species carried by
147 pollinators was identified using a pollen library of plant specimens collected at each
148 site at the time of sampling. Voucher specimens are located at the New Zealand
149 Institute for Plant and Food Research in Lincoln, New Zealand.

150

151 (B) *Pollinator traits*

152 Pollinator traits were compiled using field observations and existing published and
153 unpublished datasets (Table S2; See Appendix S1) from the Canterbury region. For

154 each pollinator species, we compiled information for the following 10 traits: (1) body
155 width, measured as distance between the base of the wings in mm (i.e. inter-tegula
156 span in bees); (2) body depth (mm); (3) body length (mm); (4) pollen carrying
157 structure: scopa, corbicula, none; (5) larval feeding type: decaying vegetation;
158 parasite; predator of other insect; dung; carrion; nectar or pollen (6) behaviour:
159 social; solitary (7) foraging preference: nectar or pollen (8) mean duration of flower
160 visitation (9) richness of pollen carried (i.e. the number of plant species carried by
161 the pollinator species) (10) nesting behaviour: central nest (i.e. foraging is focused
162 around nest location); no nest (foraging is not centered around a nest location).
163 Morphological trait values (e.g. body length, width and depth) were derived by
164 obtaining the mean dimensions of ten representative specimens (Table S2,
165 Appendix S1). Traits related to foraging preferences and flower visitation were
166 measured in mass flowering *Brassica rapa* fields as part of another study (Rader *et*
167 *al.*, 2009). All species were scored for all traits, hence all species have the same
168 number of traits recorded and each trait has a number of values for continuous traits
169 and a number of levels for categorical traits. See Appendix S1 for summary
170 statistics of traits.

171

172 The traits selected were intended to capture characteristics known to be important
173 for the quantity and quality of pollination services. For example, body size correlates
174 with pollination efficiency (Larsen *et al.*, 2005), foraging duration (Stone & Willmer,
175 1989; Stone, 1994), foraging distance in some bees (Greenleaf *et al.*, 2007) and
176 susceptibility to land-use change (Larsen *et al.*, 2005; Winfree *et al.*, 2009; Williams
177 *et al.*, 2010). Although the response-effect functional trait framework suggests
178 assignment of traits to two groups (i.e. "effect" traits influence ecosystem functioning

179 while "response" traits influence how species respond to disturbance Naeem &
180 Wright, 2003; Hooper *et al.*, 2005; Violle & Jiang, 2009), most traits in our dataset
181 not only contribute to pollination functions, but are also likely to influence responses
182 to disturbance (Lavorel & Garnier, 2002; Larsen *et al.*, 2005).

183

184 *(B) Richness analyses*

185 We tested how species richness responded to our land-use intensity gradient in
186 order to provide baseline information against which to compare changes in functional
187 diversity. Data were pooled across trap types (sticky and flight intercept traps) and
188 time (i.e. monthly trap collections for 1 year). Even though sampling effort was
189 standardized, species abundances differed among sites, which can strongly
190 influence species richness estimates (Gotelli & Colwell 2001). We therefore
191 calculated rarefied richness to the lowest sample size (n=193 individuals) to test
192 whether observed richness was affected by differences in abundances among sites
193 (Gotelli & Colwell, 2001). We tested for spatial autocorrelation of both data and
194 model residuals using the Moran index in the "spdep" package (Bivand *et al.*, 2012)
195 in the R environment (R Development Core Team 2012). Spatial autocorrelation was
196 not significant, as indicated by low and non-significant Moran values (range -0.05 to
197 0.03; $P > 0.2$) and hence was not taken into account in further analysis. We used
198 linear models to compare species richness among land-use types, with species
199 richness as the response variable and land-use type as the predictor.

200

201 *(B) Nestedness and functional diversity analyses*

202 To test whether pollinator communities were nested among land-use types (i.e. if
203 species from sites with lower species richness were a subset of the species found at

204 sites with higher richness), nestedness was calculated using NODF (Almeida-Neto *et*
205 *al.*, 2008) and tested for significance against 100 null matrices using the null model
206 described in Patterson & Atmar (1986). This analysis determines the order in which
207 species are lost or colonize a system and calculates the rank of sites by taking into
208 account the percentage overlap of presences for each pair of columns (i.e. species)
209 and for each pair of rows (i.e. sites) in a matrix ordered to maximize nestedness,
210 hence both columns and rows are included in the analyses (Ulrich & Gotelli, 2007;
211 Almeida-Neto *et al.*, 2008; Ulrich *et al.*, 2009). To determine which traits were lost
212 first, we used the rank of each species on the nested configuration as a measure of
213 species loss order (Ulrich & Gotelli, 2007; Ulrich, 2009; Sasaki *et al.*, 2012) using the
214 'vegan' package in R (Oksanen *et al.*, 2011). A more nested system indicates that
215 species loss is non-random.

216

217 This rank was then used as a response variable in a linear model with species
218 abundance and individual species traits as predictors. We performed stepwise model
219 selection using AIC in the 'MASS' package (Venables & Ripley, 2002) in R to select
220 the best model. As five species were represented at all sites, their rank was
221 considered to be the same; hence we attributed the rank value of one to all five
222 species. Body depth was excluded as it was highly correlated with body width.

223

224 Just as diversity is different to composition in taxonomic diversity studies, we
225 explored both functional diversity and functional community composition to better
226 understand community response to different land-use types. Functional diversity
227 indices (functional richness and functional dispersion) were calculated using the 'FD'
228 package in R (Laliberté & Legendre, 2010). Functional richness and dispersion are

229 important metrics to understand the impacts of land-use change upon functional
230 diversity as they can be used to indicate if species within a given habitat are
231 performing similar (i.e. redundant) or different (i.e. complementary) roles for a given
232 function or service (Walker, 1992; Elmqvist *et al.*, 2003; Laliberté *et al.*, 2010). We
233 used linear models to compare each of the two functional diversity metrics among
234 land-use types, with functional richness and functional dispersion indices as
235 response variables. Details of the methods used to calculate these metrics are
236 described in Appendix S2 of the Supporting Information. We used a null model to
237 distinguish whether the observed change in functional richness was higher or lower
238 than expected given the species richness observed (Petchey, 2004). We used a
239 simulation approach to create a random (null) distribution of functional richness
240 values for a given number of species. Holding species richness constant for each
241 land-use type, we randomly selected species from the species pool (the total number
242 of species in the study) to calculate a null functional richness for each richness level.
243 We repeated this 1000 times to produce a distribution of null values and tested
244 whether the actual functional richness for each community was significantly higher or
245 lower than the mean of the null functional richness distribution, at $\alpha = 0.05$.
246 This approach permitted us to determine if changes in functional richness simply
247 reflected changes in species richness, or if species loss and trait diversity responded
248 differently to land-use management. As sites within each land-use type showed
249 different patterns in relation to the null model, we also calculated standardised
250 deviations of functional richness in each site from the null expectation and compared
251 these deviations among land-use types using linear models (Ingram & Shurin, 2009;
252 Mason *et al.*, 2012; Laliberté *et al.*, 2013).
253

254 *(B) Community-weighted mean and functional trait composition*

255 To further explore which particular traits drive the changes observed in functional
256 diversity, we obtained the community-weighted trait means (CWM) of all traits for
257 each site (Garnier *et al.*, 2004) as measures of functional composition. We used
258 permutational analysis of variance (PERMANOVA) and permutational analysis of
259 dispersion tests (PERMDISP) based on Gower distance (to enable inclusion of
260 discrete variables) to compare CWMs among land-use types, and non-parametric
261 multidimensional scaling (NMDS) to visualize functional composition of the CWM
262 indices. We used a Procrustes test (Peres-Neto & Jackson, 2001) to test whether
263 sites with similar species composition exhibited similar functional composition. This
264 method compares two distance matrices using permutation tests to calculate the
265 statistical significance of matrix resemblance (Alarcón *et al.*, 2008; Burkle and Irwin,
266 2009; Alarcón, 2010), and has been shown to be more robust than the classic
267 Mantel test (Peres-Neto & Jackson, 2001).

268

269 To test for differences in community composition among land-use types, we used
270 PERMANOVA on a Bray-Curtis distance matrix between sites using the 'vegan'
271 package in R (Oksanen *et al.*, 2011). Differences in beta diversity among land uses
272 were assessed using the PERMDISP test. To visualize patterns in species
273 composition, we used NMDS.

274 All statistical analyses in this study were conducted using R software (R
275 Development Core Team 2012).

276

277 **(A) Results**

278 We collected 23,509 pollinator individuals over one year (mean: 2439

279 individuals/month) and recorded 25 different pollinator species, the most abundant of
280 which were bees and flies (Table S3; See Appendix S1). All taxa in this study were
281 unmanaged and assemblages comprised both native (14 species) and introduced
282 (11 species) taxa. Even though we recorded *Apis mellifera* at study sites, it is likely
283 this taxon was unmanaged, as managed hives were >1.2 km away from our study
284 sites and feral honey bees existed in this region at the time of this study.

285

286 Observed species richness in gardens was significantly higher than in crops (Fig. 1
287 and 2; Table S4; See Appendix S1) and this pattern matched that of rarefied species
288 richness (Fig. 2; Table S4; See Appendix S1). Less species-rich communities
289 contained a subset of the species found in more species-rich communities (Fig. 1,
290 NODF Nestedness = 79.01, compared to 100 simulations of the null model: Mean =
291 59.81, $Z = 13.12$, $P = 0.01$). The core pollinator species present at most sites
292 included two introduced social (*Apis mellifera* and *Bombus terrestris*, Apidae) and
293 one native solitary bee (*Lasioglossum sordidum*, Halictidae) and two common flies
294 (*Delia platura*, Anthomyiidae and *Pollenia pseudorudis*, Calliphoridae, Fig. 1).

295

296 The species that were less common, with a large body size, solitary behavior, larval
297 feeding preferences other than nectar/pollen (i.e. decaying vegetation, parasitic etc.)
298 and foragers of few plant species were lost first with increasing land-use intensity
299 (Fig. 3). These species were present in less-intensive, species-rich sites,
300 representative of garden and blackcurrant land uses (Fig. 3). In contrast, common
301 species with a small body size, social behavior, preference for nectar/pollen and
302 generalist foragers of many plant species were associated with less diverse sites,
303 including cropping and dairy land uses (Fig. 3; Table S7; See Appendix S1).

304

305 Functional richness declined by 83% from the least intensive gardens to the most
306 intensive rotational cropping. Although functional richness of gardens was
307 significantly higher than that of dairy and cropping (Table S4; See Appendix S1),
308 overall, this decline was not significantly different from that expected according to a
309 random loss of species at most sites as determined by the null model (Fig. S3; see
310 Appendix S1). However, sites within each land use showed different patterns in
311 relation to the null model, as evidenced by significant differences ($P = 0.03$) in
312 standardised deviations among land-use types. Standardised deviations of observed
313 functional richness from the null expectation were positive (i.e. greater-than-
314 expected) for the less intensive land-use types (blackcurrant: 0.36; native garden:
315 0.41) and negative (i.e. lower-than-expected) for the more intensive land-use types
316 (crop: -0.11; dairy: -0.64). Functional dispersion, however, did not differ significantly
317 among land-use types (Fig. 2; Table S4; See Appendix S1).

318

319 Abundance-weighted community composition differed significantly among land-use
320 types (PERMANOVA, $R^2 = 0.23$; $P = 0.041$; Fig. S6). For example, among the
321 common species, *L. sordidum* comprised 58% and 53% of the individuals in
322 blackcurrant and rotational cropping, while only 35% and 17% in garden and dairy,
323 respectively (Table S6; See Appendix S1). The community-level weighted trait
324 means showed that communities in different land uses were characterized by
325 different traits (Figs. S4, S5; Table S5; See Appendix S1). For example, pollinators in
326 rotational cropping had a greater proportion of species that foraged on many plant
327 species than those in gardens, such as *A. mellifera* and *B. terrestris*, (Table S4; Fig.
328 S4; see Appendix S1). All land uses (with the exception of two sites) were dominated

329 by solitary species and pollinator body size did not differ among land-use types ($F_{3,20}$
330 = 1.25, $P = 0.31$; Table S5; see Appendix S1).

331

332 Congruent with the species composition results, mean trait composition differed
333 significantly among land-use types (PERMANOVA, $R^2 = 0.37$, $P = 0.005$; Fig. S7).

334 However, functional dispersion among land-uses was not significantly different
335 (PERMDISP, $F_{3,20} = 1.60$, $P = 0.22$). Not surprisingly, though, communities that
336 were more similar in species composition tended to be more functionally similar, but
337 this pattern was not statistically significant (Procrustes test; correlation: 0.42, P -value
338 = 0.09 ; based on 1000 permutations).

339

340 (A) Discussion

341 (B) Land-use change and the preferential loss of particular species

342 Land-use change is driving rapid declines in global species diversity (Sala *et al.*,
343 2000), but taxa do not all respond in the same way. Differences in sensitivity to land-
344 use intensity are largely a result of the traits species possess and species responses
345 to landscape change and associated changes in environmental factors (Kleijn *et al.*,
346 2004; Larsen *et al.*, 2005).

347

348 Vegetation loss and fragmentation in anthropogenic habitats is frequently associated
349 with declines in pollinator species richness (Garibaldi *et al.*, 2011; Winfree *et al.*,
350 2011) , yet few studies have determined the extent to which changes in composition
351 accompany changes in species richness. For example, the identification of
352 compositional shifts will enable detection of whether specialist species are being
353 replaced with more common generalist species (Tylianakis *et al.*, 2005; Aizen *et al.*,

354 2012). In our study, large-bodied taxa, solitary bees and taxa with non-floral larval
355 food requirements were the most likely to be lost with increasing land-use intensity.
356 Solitary taxa commonly nest in the ground resulting in sensitivity to changes in
357 agricultural management associated with intensification (Williams *et al.*, 2010; Jauker
358 *et al.*, 2013). The loss of large-bodied taxa concurs with larger-scale trends reported
359 for pollinators (Bartomeus *et al.*, 2013a), and the preferential loss of specialist,
360 parasitic, and cavity-nesting pollinators (Williams *et al.*, 2010; Burkle *et al.*, 2013).

361

362 Sociality and diet alone do not, however, mitigate a negative response to land-use
363 intensification. Other traits, such as body size, may mediate or exacerbate land-use
364 change impacts. For example, Jauker *et al.* (2013) demonstrated that although
365 solitary reproduction resulted in species being particularly vulnerable to habitat loss,
366 this response was mediated by body size. Small-bodied social bees within the family
367 Halictidae, were susceptible to land-use change whereas large-bodied bumblebees
368 were not. Furthermore, Bommarco *et al.* (2010) demonstrated that large-bodied
369 generalist pollinators were less affected by land-use change than were small-bodied
370 generalists. In our study, the two generalist, social bee species, *Apis mellifera* and
371 *Bombus terrestris*, were present across all study sites and hence were not sensitive
372 to changes in land use. Declines in large-bodied taxa in this dataset are thus largely
373 represented by Diptera, solitary bees (*Leioproctus sp.*) and non-bee hymenopteran
374 taxa.

375

376 (B) *The implications of pollinator loss*

377 The dominance of common species, most often exotic in our dataset, is a common
378 feature of modified or disturbed habitats (Dukes & Mooney, 1999; Tylianakis *et al.*,

379 2005; Didham *et al.*, 2007), yet its functional consequences are less obvious. This is
380 because the non-dominant functional groups that appear to be susceptible to
381 differences in land-use management (e.g. solitary taxa with non-floral larval food
382 requirements) are important pollination service providers to many New Zealand
383 native plants and some commercial mass flowering crops (Primack, 1983; Newstrom
384 & Robertson, 2005; Rader *et al.*, 2009; Howlett, 2012; Rader *et al.*, 2013b).

385

386 Determination of the full magnitude of impact of these losses would thus require an
387 assessment of the changes in pollination function associated with land-use
388 intensification. Irrespective of this knowledge gap, the losses of particular functional
389 groups will likely reduce the insurance value provided by functionally-dissimilar
390 communities (Loreau *et al.*, 2001; Bartomeus *et al.*, 2013a), as resilience is
391 conferred to diverse assemblages by the provision of a range of ecological
392 responses to environmental change (Elmqvist *et al.*, 2003; Norberg, 2004; Laliberté
393 *et al.*, 2010; Rader *et al.*, 2013a).

394

395 In conclusion, our study shows that species bearing particular trait attributes (i.e.
396 large body size, solitary behaviour and non-floral larval food resources) are more
397 susceptible to changes in land use than species without. While particular trait
398 attributes are being selected in response to intensification, intensification is not
399 currently affecting the breadth of functional diversity (i.e. functional dispersion
400 showed little difference across land-use types). Nonetheless, the capacity to cope
401 with future change may be reduced as a result of lower functional richness in more
402 intensive land-use types.

403

404

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414

415

416 **(A) References**

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619

620 **Biosketch**

621 Romina Rader is interested in plant–animal interactions. Her current research
622 focuses on the potential impacts of land-use change upon pollinator communities
623 and the provision of ecosystem services by unmanaged pollinator taxa.

624

625 **Supporting Information**

626 Additional Supporting Information may be found in the online version of this article:

627 Appendix S1 { Supplementary information relating to site selection and results }

628 Appendix S2 { Supplementary information relating to methods and analyses }

629 Appendix S3 { Supplementary information concerning trait correlation matrix }
630 Figure S1 { Location of study sites }
631 Figure S2 { Flight-intercept trap design and measurements }
632 Figure S3 { Results of null model analyses}
633 Figure S4 { Changes in continuous functional traits with land-use type }
634 Figure S5 { Changes in discrete functional traits with land-use type }
635 Figure S6 { Differences in taxonomic composition with land-use type }
636 Figure S7 { Differences in functional composition with land-use type }
637 Table S1 { Features of land-use types}
638 Table S2 { Insect functional traits used in this study }
639 Table S3 { Species list }
640 Table S4 { Model estimates for diversity indices }
641 Table S5 { Model estimates for Community Weighted Means }
642 Table S6 { Dominance of common species }
643
644 Figure captions:
645
646 Fig. 1: Matrix of species composition and land-use intensity showing nested pattern
647 (sites with fewer species contain a subset of the species in more diverse sites)
648 derived from the analyses of nestedness. Grey-shaded squares represent species
649 presence and un-shaded represents species absence at each site. Note that garden
650 and blackcurrant sites predominately occupy upper matrix, indicating higher
651 richness. Crop and dairy sites contain a subset of the species found in richer sites.
652 The curve delineates the condition in which perfect nestedness would occur, i.e.
653 whereby species on the far right of the figure are only found at few sites and those

654 species on the far left are found at all sites. A perfectly nested community would
655 thus be represented by grey shading of all cells above the line and empty white cells
656 below the line.

657

658 Fig. 2: Species and functional diversity metrics across different land-use types in the
659 Canterbury region, New Zealand: A. Species richness, B. Functional richness, C.
660 Rarefied richness, D. Functional dispersion. Significant differences indicated by
661 letters that relate to garden as the baseline habitat for comparison to other habitats;
662 see table S4 for further details.

663

664 Fig. 3: The relationship between species nestedness rank and pollinator abundance
665 and traits retained in the best model. Nestedness rank was obtained using the order
666 in which each site is listed in the nestedness matrix illustrated in Fig. 1. A higher
667 ranking represents species that are present in most sites. This ranking was used as
668 a response variable in analyses to determine if rarer species are lost first, and which
669 traits are lost first with increasing intensification. For simplicity, the slopes of the
670 univariate relationships were plotted for the predictors that were retained in the full
671 multivariate model. Significance indicated by asterisk (all $P \Rightarrow 0.01$): A. abundance
672 (log transformed), B. body length, C. sociality, D. larval feeding behaviour, E.
673 visitation duration, F. diversity of pollen carried. Refer to Table S7 in Appendix S1
674 for further details.

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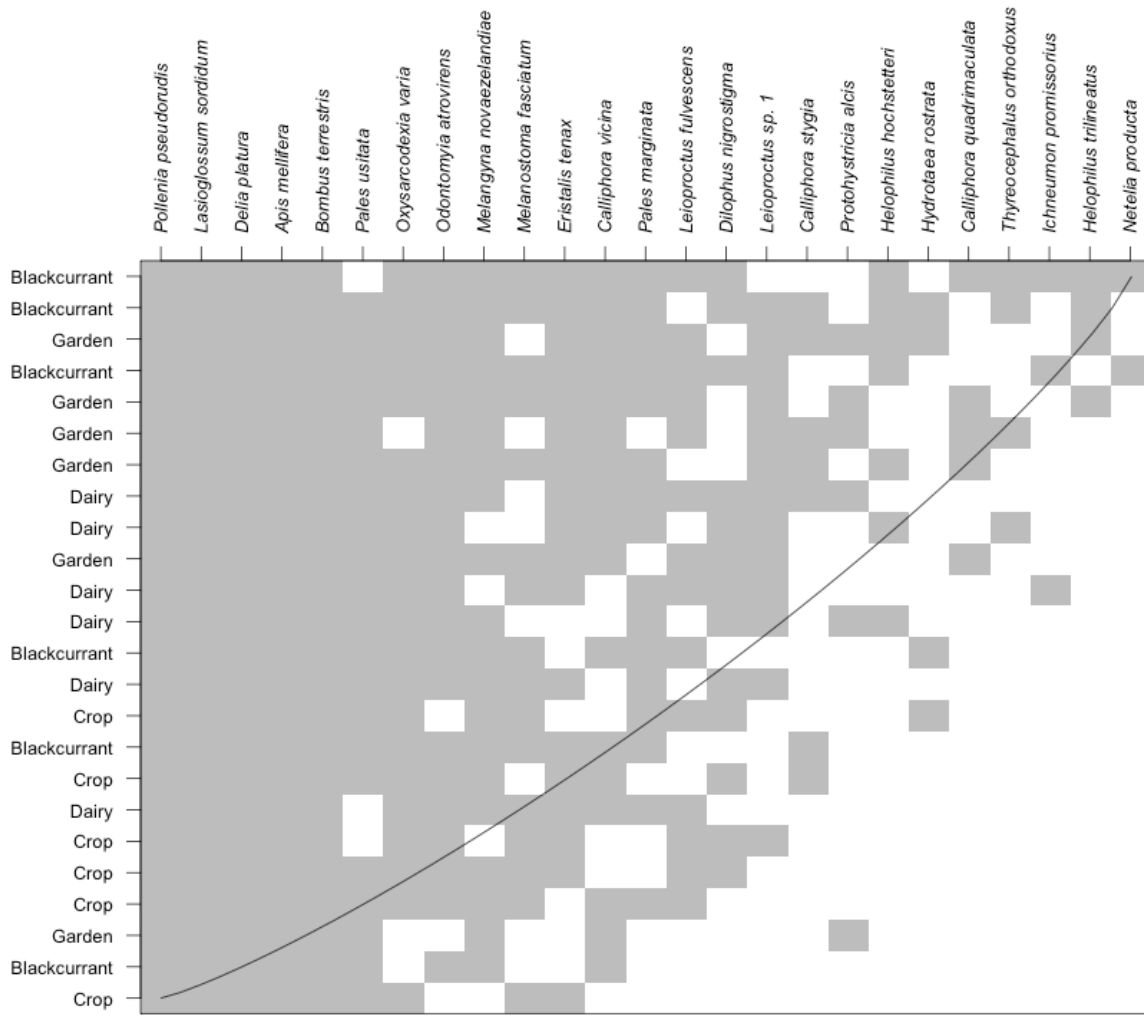
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695 Fig. 1



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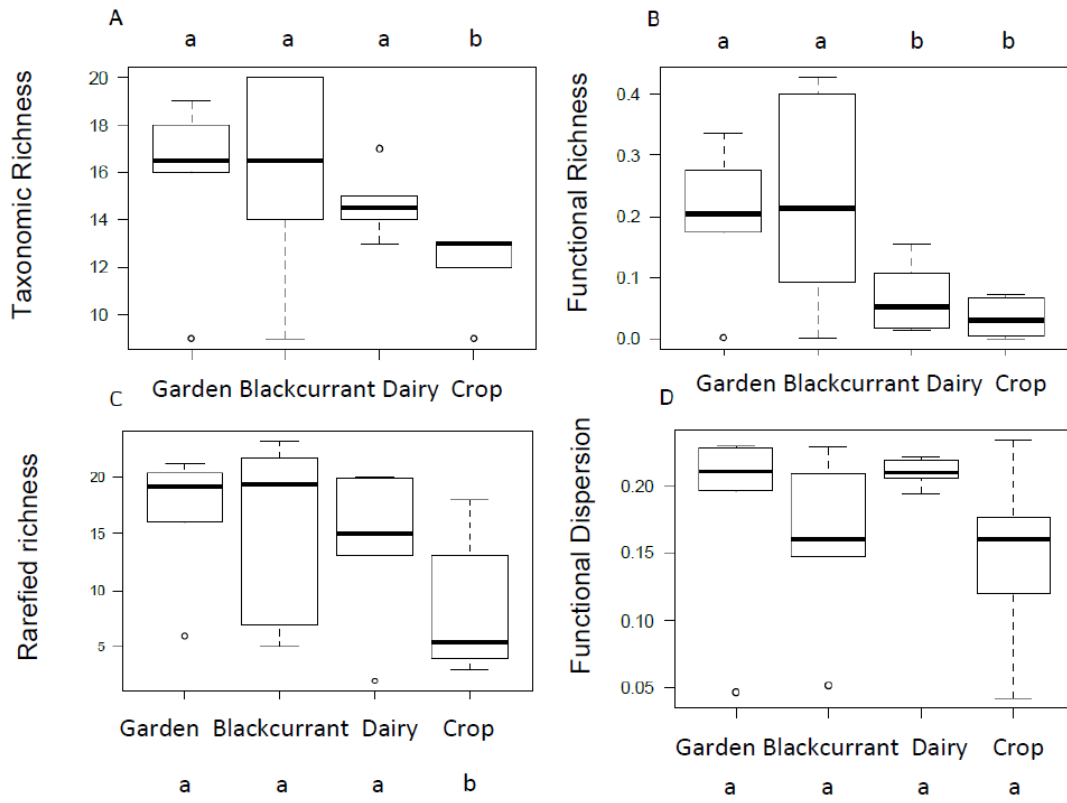
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700 Fig. 2

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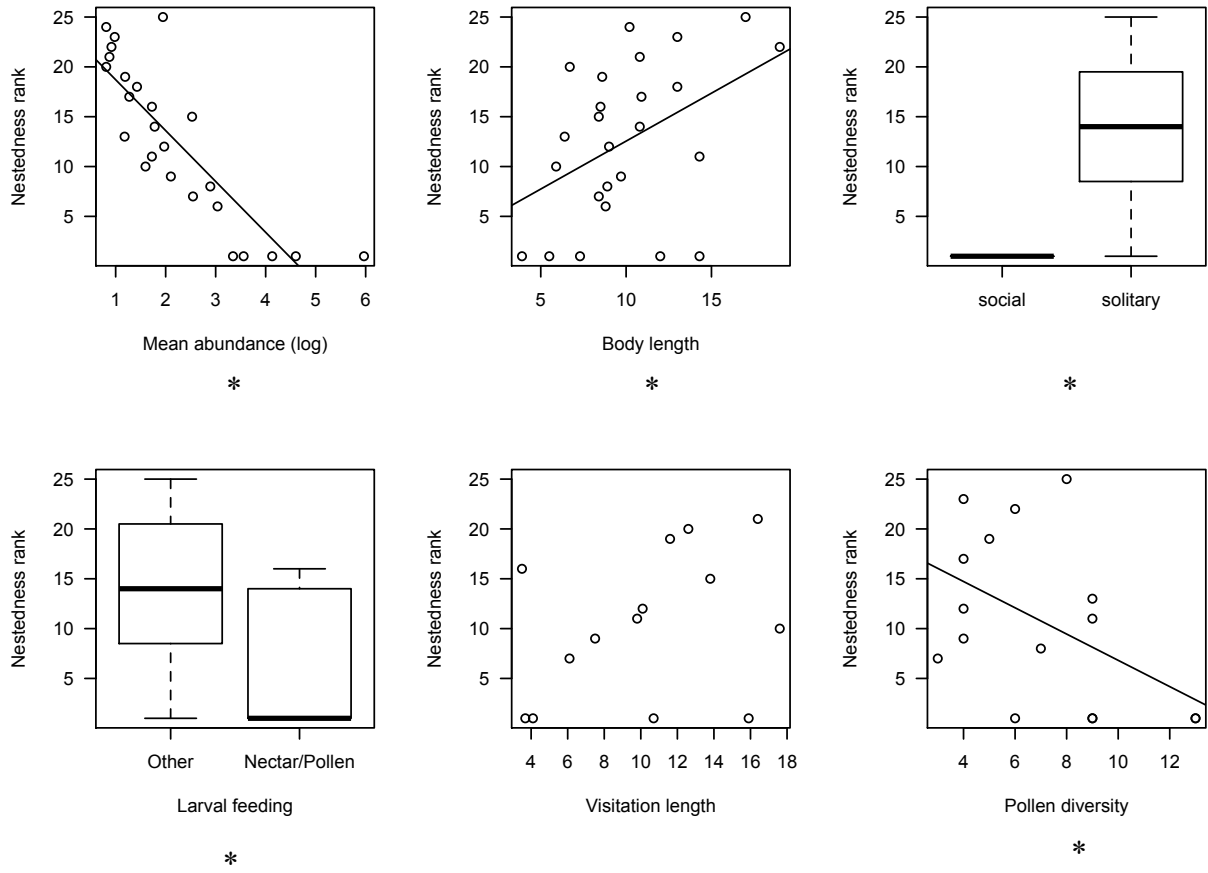
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710 Fig. 3



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