

## The community and ecosystem consequences of intraspecific diversity: a meta-analysis

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#### 1 The community and ecosystem consequences of intraspecific

#### 2 diversity: a meta-analysis

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#### 19 ABSTRACT

Understanding the relationships between biodiversity and ecosystem functioning has major implications. Biodiversity–ecosystem functioning relationships are generally investigated at the interspecific level, although intraspecific diversity (i.e. withinspecies diversity) is increasingly perceived as an important ecological facet of biodiversity. Here, we provide a quantitative and integrative synthesis testing, across

25 diverse plant and animal species, whether intraspecific diversity is a major driver of 26 community dynamics and ecosystem functioning. We specifically tested (i) whether the 27 number of genotypes/phenotypes (i.e. intraspecific *richness*) or the specific identity of 28 genotypes/phenotypes (i.e. intraspecific *variation*) in populations modulate the structure 29 of communities and the functioning of ecosystems, (ii) whether the ecological effects of 30 intraspecific richness and variation are strong in magnitude, and (iii) whether these 31 effects vary among taxonomic groups and ecological responses. We found a non-linear 32 relationship between intraspecific richness and community and ecosystem dynamics 33 that follows a saturating curve shape, as observed for biodiversity-function 34 relationships measured at the interspecific level. Importantly, intraspecific richness 35 modulated ecological dynamics with a magnitude that was equal to that previously 36 reported for interspecific richness. Our results further confirm, based on a database 37 containing more than 50 species, that intraspecific variation also has substantial effects 38 on ecological dynamics. We demonstrated that the effects of intraspecific variation are 39 twice as high as expected by chance, and that they might have been underestimated 40 previously. Finally, we found that the ecological effects of intraspecific variation are not 41 homogeneous and are actually stronger when intraspecific variation is manipulated in 42 primary producers than in consumer species, and when they are measured at the 43 ecosystem rather than at the community level. Overall, we demonstrated that the two 44 facets of intraspecific diversity (richness and variation) can both strongly affect 45 community and ecosystem dynamics, which reveals the pivotal role of within-species 46 biodiversity for understanding ecological dynamics.

47

48 Key words: ecosystem functioning, community, genotype, phenotype, meta-analysis,

49 biodiversity, eco-evolutionary dynamics.

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## 71 I. INTRODUCTION

Understanding the relationships between biodiversity and ecosystem functioning is an
intensely active field of research informing on the services provided by biodiversity

74 (Chapin et al., 2000; Loreau, 2000; Hooper et al., 2005; Cardinale et al., 2012). 75 Biodiversity is generally quantified as the taxonomic, functional and/or phylogenetic 76 diversity of a species assemblage, and most studies on biodiversity-ecosystem 77 functioning relationships have to date focused on the interspecific facet of biodiversity 78 (Naeem et al., 1994; Downing & Leibold, 2002; Hillebrand & Matthiessen, 2009). 79 However, biodiversity also includes an intraspecific facet that is defined as the 80 phenotypic, functional and genetic diversity measured within a single species (Odling-81 Smee, Laland & Feldman, 2003; Bolnick et al., 2003). During the last two decades, 82 intraspecific diversity has been demonstrated to account for a non-negligible part of the 83 total biodiversity measured in plants and animals (Fridley & Grime, 2010; de Bello et 84 al., 2011), representing in some cases up to a quarter of the total variability measured in 85 communities (Fridley & Grime, 2010; de Bello et al., 2011; Siefert et al., 2015).

86 In parallel, the hypothesis that intraspecific diversity may affect ecological 87 dynamics at levels higher than the population level (for instance the composition and 88 the dynamics of communities and/or the dynamics of ecosystem functions) has been 89 conceptualized (Bolnick et al., 2003, 2011; Hughes et al., 2008; Bailey et al., 2009; 90 Violle et al., 2012). These conceptual insights have been validated by several key 91 experiments both in plants and animals (Whitham et al., 2003; Madritch, Greene & 92 Lindroth, 2009; Matthews et al., 2016; Rudman & Schluter, 2016). For instance, the 93 experimental manipulation of fish phenotypes from several evolutionarily independent 94 fish populations has been shown to generate significant changes in both the community 95 structure of invertebrate prey and the primary productivity of the ecosystem (Harmon et 96 al., 2009; Matthews et al., 2016).

97 Intraspecific diversity can be characterized based on the *richness* of populations,
98 which corresponds to the differences in the number of genotypes and/or phenotypes

99 composing populations. For instance, populations are often characterized according to 100 their 'allelic, genotypic or phenotypic richness', which is a population parallel of 101 species richness, a common metric measured at the interspecific level and classically 102 used to investigate biodiversity-ecosystem function (BEF) relationships (Crutsinger et 103 al., 2006). Intraspecific richness can also affect ecological dynamics hence generating 104 'intraspecific BEF' (Whitham et al., 2006; Crutsinger et al., 2006). The basic 105 hypothesis for intraspecific BEF is that increasing the number of genotypes/phenotypes 106 in a population should alter (either negatively or positively) key ecological functions 107 such as the decomposition rate of organic matter or the structure of communities. For 108 instance, experiments manipulating the number of genotypes (from one to 12 109 genotypes) in plant (Solidago altissima) populations have shown that richer populations 110 contained a higher diversity of invertebrates (Crutsinger et al., 2006). Actually, the 111 ecological consequences of intraspecific richness should follow a saturating curve (i.e. a 112 rapid increase followed by a plateau) as often described for BEF observed at the 113 interspecific level (Hughes et al., 2008). Although rarely tested empirically, this 114 saturating shape could be due to the combined effects of several mechanisms. 115 Populations with different richness could have different ecological consequences 116 because of ecological complementarity among genotypes/phenotypes (i.e. niche 117 partitioning, facilitation occurring when genotypes use different resources), inhibition 118 among genotypes/phenotypes (when multiple genotypes are in competition for 119 resources), or functional redundancy among genotypes/phenotypes that can make 120 populations ecologically equivalent (Johnson, Lajeunesse & Agrawal, 2006; Hughes et 121 al., 2008). Yet, the shape of the relationship between intraspecific richness and 122 ecological dynamics has rarely been investigated empirically and to our knowledge has 123 never been quantified across species.

124 The ecological consequences of intraspecific diversity can also be investigated 125 through the lens of *variation* in genotypic or phenotypic attributes. Adaptive and non-126 adaptive evolutionary processes such as natural selection, plasticity or genetic drift can 127 generate unique phenotypic differences among populations. These differences can be 128 associated to key functional processes such as food acquisition or nutrient cycling (e.g. 129 Grant & Grant, 2006; Rudgers & Whitney, 2006; Lowe, Kovach & Allendorf, 2017), 130 resulting in both trophic and non-trophic effects of intraspecific variation on ecological 131 dynamics (Odling-Smee et al., 2003; Whitham et al., 2003; Matthews et al., 2011). For 132 instance, it has been shown experimentally that plant genotypes differing in their 133 susceptibility to herbivores harbour different communities of herbivores (Crutsinger, 134 Cadotte & Sanders, 2009a; Barbour et al., 2009b). Similarly, mesocosm experiments 135 have shown that differences in diet within predator populations can modify prey 136 community structure (Post et al., 2008; Harmon et al., 2009; Howeth et al., 2013). Non-137 trophic interactions can also have an important role. For instance, differences in the 138 chemical composition of individuals can result in differences in excretion rate or in leaf 139 chemistry that can then affect ecosystem functions such as primary production or 140 nutrient recycling (Lecerf & Chauvet, 2008; El-Sabaawi et al., 2015). Recently, Des 141 Roches et al. (2018) demonstrated that intraspecific variation can affect ecological 142 dynamics to the same extent as the removal or replacement of a species in the 143 environment. Although based on a relatively limited number of studies (25 studies on 144 15 species), their study confirmed the hypothesis that intraspecific variation might be a 145 non-negligible driver of ecological dynamics.

Here, we investigated – across various species and ecosystems – the extent to which both intraspecific richness and intraspecific variation affect the structure of communities and the functioning of ecosystems, and whether intraspecific diversity is a 149 major driver of ecological dynamics. We reviewed published studies testing the causal 150 effects of intraspecific diversity on ecological dynamics in two meta-analyses 151 synthesizing published data across taxa and ecosystems for intraspecific richness and 152 variation, respectively, and to fulfil three specific objectives. First, we tested the 153 significance and the shape of the relationship between intraspecific richness and 154 ecological dynamics. We expected to find a significant saturating relationship between 155 intraspecific richness and ecological dynamics, because of potential facilitation and 156 functional redundancy among genotypes and phenotypes (Hughes et al., 2008). Second, 157 we tested whether manipulating intraspecific richness has similar effects on ecological 158 dynamics to manipulating interspecific richness, by comparing the ecological effects of 159 intraspecific richness with those of interspecific richness obtained from experimental 160 studies manipulating species richness (Duffy, Godwin & Cardinale, 2017). Finally, we 161 provided a novel and extensive quantitative synthesis testing for the effects of 162 intraspecific variation on ecological dynamics. Des Roches et al. (2018) previously 163 focused on studies removing or replacing the target species (by which intraspecific 164 variation was manipulated) to investigate the ecological consequences of intraspecific 165 variation. This strongly restricted the number of available studies for which effects sizes 166 could be calculated, and potentially upwardly biased the resulting estimates (Des 167 Roches *et al.*, 2018). We here relax this restriction by considering all studies 168 manipulating intraspecific variation, and use a null-model approach to provide a more 169 accurate relative effect size of intraspecific variation on ecological dynamics. We also 170 built on this extended data set to partition variance in the ecological consequences of 171 intraspecific variation according to the type of organism manipulated and the type of 172 response variable measured. We tested whether the magnitude of the effects of 173 intraspecific variation on ecological dynamics vary among organism types (primary

producers *versus* consumers) and levels of biological organization (community *versus* ecosystem levels). Because primary producers form the basis of trophic chains, we expect stronger ecological effects of intraspecific variation in producers than in consumers. We also expect stronger effects of intraspecific variation on ecosystem functions than on metrics describing community structure because ecosystem functions are affected by both trophic and non-trophic effects of biodiversity (Matthews *et al.*, 2014).

181

#### 182 II. MATERIALS AND METHODS

#### 183 (1) Data collection

184 We compiled data from published articles quantifying the effects of intraspecific 185 diversity in a single species on community structure and/or ecosystem functioning. We 186 focused only on intraspecific diversity that represented the integrative phenotypic effect 187 of multiple evolutionary processes including selection, drift and/or plasticity. As a 188 result, we did not consider articles focusing on experimentally induced intraspecific 189 diversity through induced plastic responses to particular predatory or environmental 190 cues [for example see Werner & Peacor (2003) for a review]. We reviewed several 191 experimental studies manipulating intraspecific variation and/or richness within a single 192 species to test their respective ecological effects. We also reviewed some observational 193 studies with strong biological hypotheses and adequate design allowing inferring causal 194 links from intraspecific diversity to ecological dynamics (e.g. Post et al., 2008). Studies 195 varying intraspecific diversity within a set of multiple species (e.g. Booth & Grime, 196 2003) were not included in this meta-analysis. The literature search was carried out 197 using the ISI Web of Knowledge and Scopus platforms (last accessed 25th July 2018). 198 We also scrutinized the reference list of each article to obtain additional articles. The

199 following key words were used in various combinations: community genetics AND 200 intraspecific variation, eco-evolutionary dynamics AND ecosystem function, community 201 genetics AND ecosystem function, and intraspecific genetic variation AND ecosystem 202 *function*. We selected articles describing the effects of genotypic and/or phenotypic 203 richness (intraspecific richness) and/or different genotypes/phenotypes (intraspecific 204 *variation*) in a single target species on community and/or ecosystem dynamics. A total 205 of 90 studies with available statistics were selected (see online Supporting information, 206 Appendix S1 and Fig. S1). Among these, 23 studies (100% experimental studies) 207 focused on intraspecific richness and 75 studies (90% experimental studies, 10% 208 empirical studies) focused on intraspecific variation.

209 For each study, we recorded the Latin name of the target species and classified them as 210 primary producers or consumers (including primary and secondary consumers as well as 211 predators) and according to the major taxonomic categories represented in our data sets: 212 arthropods (9 species), fishes (6 species), herbaceous plants (14 species), trees (31 213 species), and fungi (5 species). Overall, this led to 52 species for studies focusing on 214 intraspecific variation, and 17 species for studies focusing on intraspecific richness. We 215 recorded seven main response variables related to community structure and ecosystem 216 functioning. A community is here defined as a group of at least two species, and we 217 focused on three types of response variables describing the structure of communities: 218 (1) species abundance: total number of individuals of all species; (2) biomass: total 219 mass of individuals of all species; (3) community structure: number of species (e.g. 220 Simpson or Shannon indices), species evenness and/or species richness.

Regarding response variables at the ecosystem level, we considered four main ecosystem functions: (1) decomposition rate: rate at which organic matter is recycled; (2) elemental cycling: quantity of organic or inorganic materials; (3) primary

productivity: measured as several proxies of primary producers: biomass of primary
producers excluding the productivity of the target species, chlorophyll *a* concentration,
daily oxygen production, and photosynthetically active radiation; (4) ecosystem
respiration: rate of oxygen consumption.

228

#### 229 (2) Meta-analysis

230 (a) The ecological consequences of intraspecific richness

231 To test for the consequences of intraspecific richness on ecological dynamics, we 232 focused only on studies investigating the consequences of genotypic richness since this 233 was the intraspecific diversity facet most commonly manipulated to test for the effects 234 of intraspecific richness on ecological dynamics. Here, we used the log-transformed response ratio (lnRR) as an effect size. lnRR was computed as: ln  $\left(\frac{XG}{1G}\right)$ , where *IG* is the 235 236 average of the response variable measured for the treatment with a single genotype (i.e. 237 monoculture), and XG is the average of the response variable measured for each 238 treatment independently including more than one genotype. For each response variable, 239 lnRR increases as the difference in the mean response variable measured in the 240 treatment with a single genotype and treatments including more than one genotype 241 increases. We also recorded the difference in the number of genotypes between the 242 single genotype treatment (monoculture) and all other treatments separately (i.e. 243 treatments including 2–12 genotypes) as the 'difference in intraspecific richness'. In our 244 data set, difference in intraspecific richness therefore varied between one and 11 245 genotypes. This approach allowed quantifying the ecological consequences of 246 increasing the number of genotypes for each target species. Since each study generally 247 assessed the effects of intraspecific richness on more than one response variable, our 248 data set included a total of 135 assays.

249 We wanted to test the shape and the significance of the relationship between 250 lnRR and the difference in intraspecific richness across all case studies. The general 251 expectation is that ecological differences between treatments increase as differences in 252 intraspecific richness increase, although this increase may be non-linear (Hughes et al., 253 2008). We therefore used non-linear mixed-effect models to test the significance and 254 shape of the relationship between absolute values of lnRR (|lnRR|) and differences in 255 intraspecific richness. More precisely, we modelled this relationship using four different 256 models to determine the most likely shape of the relationship between  $|\ln RR|$  and 257 difference in intraspecific richness: (1) a null model (one parameter) was computed for 258 the null-effect hypothesis (i.e. no significant relationship between |lnRR| and difference 259 in intraspecific richness); (2) a linear model (two parameters) suggesting a positive and 260 linear relationship between  $|\ln RR|$  and difference in intraspecific richness; (3) a 261 Michaelis-Menten model (two parameters) in which |lnRR| increases with intraspecific 262 richness, until a plateau is reached (saturating shape); (4) an asymptotic exponential 263 model (two parameters) with a shape similar to the Michaelis-Menten model, except 264 that the plateau is reached sooner.

265 All models cited above included article ID and the monoculture ID (i.e. the monoculture 266 treatment to which each other treatment of richness was compared for a given response 267 variable within each study) as random terms to account for non-independence of effect 268 sizes (Noble et al., 2017), and the inverse of the sample size as a weighting parameter 269 giving greater weight to articles including more replicates. Models were compared using 270 the Akaike information criterion (AIC) and we retained (as "best models") all models 271 that fell within a  $\triangle AIC < 4$  (Burnham & Anderson, 2002). We also calculated for each 272 model the Akaike weight that provides a conditional probability for each model to be 273 best supported by the data (Burnham & Anderson, 2002).

274 We then compared the magnitude (absolute effect size) of ecological effects of 275 intraspecific and interspecific richness. We extracted from each study and for each 276 response variable the lnRR corresponding to the most extreme levels of genotypic richness  $(x_{max})$  manipulated in each study  $(N = 63 \ln RR)$ . These values were 277 278 subsequently compared to published lnRR values calculated following a similar method 279 for experiments (N = 35) manipulating interspecific richness (Duffy *et al.*, 2017). 280 Because absolute effect sizes follow a folded-normal distribution, we used an 'analyse 281 and transform' approach (sensu Morrissey, 2016a,b) to estimate the absolute means of 282 effect sizes. This approach consists first of estimating the mean and variance of lnRR 283 (using non-absolute values), and then deriving the mean absolute value from these 284 estimates. To do so, we estimated the mean of lnRR for interspecific and intraspecific 285 richness, respectively, using two independent intercepts models with lnRR as the 286 response variable, article ID as the random effect and the inverse of the sample size as 287 the weighting parameter. These intercepts models were implemented using the 288 MCMCglmm package in R (Hadfield, 2010). Markov chain Monte Carlo (MCMC) chains were run on  $15 \times 10^5$  iterations, with a burn-in interval of  $3 \times 10^4$ , a thinning 289 interval of  $1 \times 10^3$ , and an inverse-Wishart prior (V = 1 and  $\eta = 0.002$ ). Finally, the 290 291 estimated means' lnRR values were converted into absolute-magnitude |lnRR| values 292 (following Morrissey, 2016b), and we compared the magnitudes of the ecological 293 effects of interspecific and intraspecific richness based on visual inspection of 95% 294 percentile intervals (PIs).

Finally, to compare the ecological consequences of intraspecific richness between levels of biological organization, we performed the same 'analyse and transform' approach described above. We used a linear mixed-effect model (implemented in the MCMCglmm package in R, and parameterized similarly than

above) with the ln*RR* as the dependent variable, the inverse of the sample size as the weighting parameter, article ID and monoculture ID as random factors, and with the level of biological organization (community *versus* ecosystem response variables) treated as a fixed effect. The type of organism was not included in this analysis given that studies on intraspecific richness focused almost exclusively on primary producers (with two exceptions on fungi).

305

#### 306 (b) The ecological consequences of intraspecific variation

307 Given that most studies (86%) did not include a control (i.e. a treatment without the 308 target species), we compared the strength of effects among all unique genotypes and/or 309 phenotypes that were considered in each study. Studies generally compared the 310 consequences of 2-10 different unique genotypes and/or phenotypes (i.e. 2-10 311 treatments, with each treatment corresponding to a unique genotype/phenotype) on 312 community and/or ecosystem dynamics; we gathered from each study the statistic (t, F, t)Chi-squared, Pearson's r, Spearman's r,  $R^2$  or Hedges' g) associated with the between-313 314 treatments comparison (i.e. the variation of the phenotypes/genotypes). The higher the 315 absolute value of the statistic, the higher the community and ecosystem consequences 316 due to the variation of genotypes and/or phenotypes. The value of each statistic was 317 converted into a correlation coefficient (r) ranging from 0 to 1 (see Table S1 for the 318 formulae used). We did not use the direction of the statistic (i.e. positive or negative) 319 because this depended upon the ecological response variable that was considered, which 320 complicates comparisons on the direction of effects. The Z-Fisher transformation then was used to obtain a standardized effect size using the formula:  $Zr = 0.5 \ln \frac{(1+r)}{(1-r)}$ . For 321 each Zr value, we calculated the corresponding standard error as  $se_{Zr} = \frac{1}{\sqrt{n-3}}$ 322 323 (Nakagawa & Cuthill, 2007). Since each study generally focused on more than one

response variable, we obtained a total of 502 observed Zr values, each corresponding to the effect size of intraspecific variation observed within one species on a single response variable. The mean global Zr or mean effect size observed (MES<sub>obs</sub>) and its 95% confidence interval (CI) were calculated using an intercept-only model. This intercept-only model was run as a mixed model with no fixed effect, article ID as the random effect and  $se_{Zr}$  included as a weighting parameter to give more weight to studies with a larger sample size (Koricheva, Gurevitch & Mengersen, 2013).

331 Because Zr ranged between 0 and  $+\infty$ , the CIs of the MES<sub>obs</sub> do not theoretically 332 overlap 0, which makes it difficult to assess the significance of the strength of the 333 MES<sub>obs</sub>. We therefore used a null-model approach to test if MES<sub>obs</sub> was significantly 334 different from that expected under the null hypothesis, i.e. the true effect of intraspecific 335 variation in all studies was zero. We resampled each statistic (e.g. t, F) from each 336 empirical study in their respective null distribution with the adequate degree of freedom. 337 This resampled set of statistics (N = 502) was transformed into Zr as described above to 338 create a set of resampled Zr values. We used this set of resampled Zr values to fit an 339 intercept-only model with no fixed effect, the corresponding article ID as a random term 340 and  $se_{Zr}$  included as a weighting parameter (as for MES<sub>obs</sub>). The mean global 341 resampled Zr (MES<sub>res</sub>) was extracted from the model, and we repeated this resampling 342 procedure 1000 times to obtain 1000 values of MES<sub>res</sub>. This resampled distribution of 343 1000 MES<sub>res</sub> approximates the range of possible MES values expected if the null hypothesis was true. Finally, we calculated the probability of MES<sub>obs</sub> to be larger than 344 345 expected under this null hypothesis using a one-tailed test (Manly, 1997).

We then compared the median of effect sizes (MES<sub>common</sub>) of studies that were in common between our extended data set and that used by Des Roches *et al.* (2018) (i.e. 15 studies that were used both in our meta-analysis and that of Des Roches *et al.*) to a selection of 15 studies randomly sampled from our extended data set (i.e. 75 studies in our extended data set). We calculated the median effect size for the subset of random studies (MES<sub>ran</sub>) and repeated this resampling procedure 1000 times to obtain 1000 values of MES<sub>ran</sub>. We then compared MES<sub>common</sub> to each MES<sub>ran</sub> value to calculate the probability that MES<sub>common</sub> was higher than a random subset of 15 studies taken from the whole data set (Manly, 1997).

355 We then investigated the variability in effect sizes (Zr) and the potential 356 moderators. We analysed the heterogeneity in effect sizes across articles using the  $I^2$ 357 statistic, which was calculated using an intercept model with the article ID as the 358 random effect and  $se_{Zr}$  as the weighting parameter (Higgins & Thompson, 2002; Senior 359 et al., 2016). Finally, we tested whether effect sizes (Zr) differed among organism types 360 with intraspecific variation manipulation, and among the ecological response variables 361 considered. We hence computed meta-regressions based on linear mixed-effect models 362 with Zr values (for all 75 studies and 502 measures) as the dependent variable, and 363 organism type or ecological response variable as fixed effects. The article ID was 364 included as a random effect, and  $se_{Zr}$  was included as a weighting parameter. Four 365 models were run to assess the differences of effect sizes (i) between organism types 366 classified as consumers or primary producers, and (ii) between detailed taxonomic 367 categories (arthropods, fishes, herbaceous plants and trees). We then tested whether the 368 effect sizes of intraspecific variation differed among ecological response variables (iii) 369 classified as community or ecosystem variables, and (iv) classified according to more 370 detailed categories (abundance, biomass, community structure, decomposition, nutrient 371 cycling, primary productivity and respiration of the ecosystem).

#### 373 (3) Publication bias

374 For both intraspecific variation and intraspecific richness, we assessed potential 375 publication bias by combining Egger's regressions and funnel plots (Egger et al., 1997). 376 Egger's regressions and funnel plots were computed using the residuals of meta-377 regressions related effect sizes to the main modifiers (i.e. the explanatory variables) and 378 a measure of study size (the inverse of  $se_{Zr}$  and sample size for intraspecific variation 379 and intraspecific richness, respectively; Horvathova, Nakagawa & Uller, 2012; 380 Nakagawa & Santos, 2012). Typically, for intraspecific variation we ran an Egger's 381 regression model including the residuals of the meta-regression linking intraspecific 382 variation to the modifiers as a response variable and the inverse of  $se_{Zr}$  as the 383 explanatory variable. A similar approach was used for intraspecific richness. The 384 intercept  $\alpha$  and the slope  $\beta$  of the Egger's regressions are expected not to differ 385 significantly from zero if the data sets are not biased towards significant results. Finally, 386 funnel plots were produced as a scatterplot linking the residuals described above to the 387 respective measure of the study size. An unbiased data set is expected to generate a 388 funnel plot in which articles with larger sample sizes will be close to the mean effect 389 size, whereas articles with small sample sizes will show more variance around the mean 390 effect size (Horvathova et al., 2012; Nakagawa & Santos, 2012).

391 Overall, and after accounting for important modifiers we found that there was 392 no strong visual sign of publication bias, neither for intraspecific variation nor for 393 intraspecific richness (Fig. S2). This visual inspection of funnel plots was confirmed by 394 the Egger's regressions since parameter values were not significant for intraspecific 395 variation ( $\alpha = 0.015$ , P = 0.404;  $\beta = -0.001$ , P = 0.501) or for intraspecific richness ( $\alpha =$ 396 -0.001, P = 0.914;  $\beta < 0.001$ , P = 0.961).

All statistical analyses were performed using the R environment (R core team,
2013, Appendix S2). The nlme package (Pinheiro *et al.*, 2014) was used to compute
linear and non-linear mixed-effect models, unless specified otherwise.

400

#### 401 III. RESULTS

402 All articles (N = 90) selected for investigating the effects of intraspecific richness and 403 intraspecific variation were published between 2000 and 2018, and 74% used primary 404 producers as target species (Fig. 1). The first studies focusing on consumers were 405 published in 2008, using fish (60%), arthropods (32%), and fungi (8%) as model 406 species.

407

#### 408 (1) The intraspecific richness–ecological dynamics relationship

409 As expected, we found a significant, positive and non-linear relationship between 410 intraspecific richness and ecological dynamics that approximated a saturating curve 411 (Fig. 2A). The AIC selection procedure revealed that one out of the four tested models 412 was highly likely to be supported by the data (i.e. 99% chance of being the best fitting 413 model according to the Akaike weight and  $\Delta AIC > 15.721$  for the other models, Table 414 1). The model that best supported the data was the exponential asymptotic model, 415 suggesting that the relationship between intraspecific richness and changes in 416 community structure and ecosystem functioning (i.e. effect size: lnRR) likely followed a 417 saturating shape (Fig. 2A).

We further found that the ecological effects of intraspecific richness were similar to the ecological effects induced by interspecific richness (Fig. 2B). Indeed, the two distributions largely overlapped and the estimated means were similar (intraspecific richness  $|\ln RR| = 0.132$ , PI = 0.048–0.216; interspecific richness  $|\ln RR| = 0.134$  PI =

422 0.012–0.462). The ecological effects of intraspecific richness tended to be higher, 423 although the difference was not significant, for community metrics (|lnRR| = 0.156, PI = 424 0.070–0.242) than for ecosystem metrics (|lnRR| = 0.045, PI = 0.004–0.137) (see Fig. S3 425 for details of ecological metrics).

426

#### 427 (2) The ecological consequences of intraspecific variation

We extended the meta-analysis performed by Des Roches *et al.* (2018) to 52 species (15 species were used in Des Roches *et al.*, 2018). We found that that the observed effect size of intraspecific variation on community structure and ecosystem dynamics was significant, and was twice as large as the resampled effect size expected under the null expectation (MES<sub>obs</sub> = 0.521, 95% confidence interval (CI) = 0.444–0.598; MES<sub>null</sub> = 0.259, CI = 0.258–0.259; resampled test, P < 0.001; see Figs 3 and S4).

434 We tested the extent to which the more restricted data set of Des Roches et al. 435 (2018) was representative of our extended data set, or whether it was upwardly biased 436 as expected by Des Roches et al. (2018). We found that that effect sizes for studies in 437 common with the Des Roches *et al.* (2018) data set (MES<sub>common</sub> = 0.299, 95% percentile 438 interval (PI) = 0.033-1.092) were not significantly different from the distribution of effect sizes measured in our extended data set (MES<sub>ran</sub> = 0.418, PI = 0.255-0.616; 439 440 resampling test, P = 0.118; Fig. S5), and in fact showed a tendency to be downwardly 441 biased.

Finally, a relatively low heterogeneity in effect size (*Zr*) was detected across articles ( $I^2 = 0.151$ ). The ecological effects induced by intraspecific variation were stronger when primary producers rather than consumers were manipulated (F = 3.968d.f. = 1, 425, P = 0.047; Fig. 4A). Nonetheless, the strongest ecological effects of intraspecific variation tended to be observed in arthropods and herbaceous species,

whereas the smallest effects were observed in fish and tree species (F = 2.475 d.f. = 3, 447 448 417, P = 0.061; Fig. 4A). Irrespective of organism type, the effects of intraspecific 449 variation were significantly stronger when the response variables were measured at the 450 ecosystem level rather than at the community level (F = 7.295, d.f = 1, 425, P = 0.007; 451 Fig. 4B). The strongest effects were detected when response variables concerned 452 nutrient cycling and the assembly of community, whereas the lowest effects were found 453 for general measures of abundance and density of species (F = 2.725, d.f = 6, 417, P =454 0.013; Fig. 4B).

455

#### 456 IV. DISCUSSION

457 Intraspecific diversity is increasingly recognized as an important facet of biodiversity 458 that can affect all biological levels (Bailey et al., 2009). Several studies have 459 experimentally tested the ecological effects of intraspecific diversity, and we here 460 provide the first global and quantitative estimates of the consequences of intraspecific 461 richness and variation on community structure and ecosystem functioning. We 462 demonstrated for the first time that the intraspecific BEF followed - as theoretically 463 expected – a non-linear saturating curve with a plateau at 4–6 genotypes per population. 464 Importantly, we demonstrated also for the first time that intraspecific richness affects 465 community and ecosystem dynamics with a magnitude comparable to that of 466 biodiversity measured at the species level. We further confirmed and extended the result 467 that genotypic and/or phenotypic variation observed between populations can have non-468 negligible effects on community structure and ecosystem functions, and we 469 demonstrated that previous estimates (Des Roches et al., 2018) of these ecological 470 effects of intraspecific variation actually tended to be underestimated. Finally, our 471 exhaustive quantitative survey identified that the ecological consequences of

472 intraspecific variation differ among biological level of organization, and among
473 organism types. These findings provide novel and integrative insights, as well as
474 multiple research perspectives, into the ecological role of intraspecific diversity.

475

#### 476 (1) Intraspecific diversity and the dynamics of communities and ecosystems

477 Although the form of the relationship between intraspecific richness and 478 ecological consequences has already been discussed conceptually (Hughes *et al.*, 2008), 479 our meta-analysis provides for the first time a qualitative and quantitative assessment of 480 intraspecific BEF measured experimentally. Specifically, although considering mostly 481 primary producers, our results demonstrated that an increase in intraspecific richness 482 resulted in a non-linear (saturating) increase in the magnitude of its effects on ecological 483 dynamics. This finding supports the idea that ecological divergence between an 484 environment hosting populations composed of a single genotype and an environment 485 hosting populations composed of multiple genotypes increases until a plateau is reached 486 as the number of genotypes increases. This result echoes the BEF as defined at the 487 interspecific level (Reiss et al., 2009; Cadotte, Carscadden & Mirotchnick, 2011) and 488 suggests that the saturating shape might arise from similar mechanisms occurring at the 489 intraspecific and interspecific levels (Johnson et al., 2006; Hughes et al., 2008). More 490 specifically, the initial linear increase is assumed to be due to complementarity and 491 facilitation among genotypes, whereas the plateau likely occurs due to functional 492 redundancy among genotypes (Johnson et al., 2006). Redundant genotypes probably 493 display functionally similar traits since two genotypes do not necessarily generate two 494 functionally different traits (e.g. through synonymous mutations or trait convergences). 495 Thus manipulating trait richness rather than genotypic richness, or more precisely 496 manipulating functional effect traits [i.e. traits with ecological effects (Violle et al.,

497 2007)], in future experiments should allow us to explore the mechanisms underlying the498 intraspecific biodiversity–ecological dynamics relationship.

499 We found that effect sizes for intraspecific richness were very similar to values 500 reported recently reported for experimental interspecific BEF, indicating that the 501 ecological effects of varying phenotypic/genotypic richness within populations are close 502 to those induced by varying species richness within communities. This finding raises 503 several questions regarding the general relationships among intraspecific diversity, 504 community structure, ecosystem functioning and common abiotic constraints. A large 505 body of literature has demonstrated that intraspecific genetic diversity and species 506 diversity (a measure of community structure) might co-vary because of common 507 environmental drivers and/or reciprocal causal relationships between intraspecific 508 genetic diversity and species diversity [i.e. the species-genetic diversity correlation 509 (SGDC) framework (Vellend & Geber, 2005; Vellend, 2005)]. Because most studies 510 considered in our meta-analysis are experimental, our findings confirm that intraspecific 511 diversity can directly influence the structure of communities irrespective of the abiotic 512 environments, hence adding weight to the SGDC framework. Additionally, we suggest 513 expanding the SGDC framework since intraspecific diversity can also affect ecosystem 514 functioning. This suggests that intraspecific diversity, community structure and 515 ecosystem functioning may actually be tightly linked in a tripartite relationship. A major 516 future challenge will be to tease apart the causal relationships linking these three 517 components within a common abiotic environment. These relationships might be direct 518 (e.g. intraspecific diversity directly affects community structure), indirect (e.g. 519 intraspecific diversity indirectly affects ecosystem functions through its direct effect on 520 community structure such as the trophic cascade), and/or due to the parallel effects of 521 common abiotic drivers (e.g. temperature directly affects intraspecific diversity,

522 community structure and ecosystem functions). As has been done recently for the BEF 523 (Grace *et al.*, 2016; Duffy *et al.*, 2016) and the SGDC (Fourtune *et al.*, 2016; Lamy *et al.*, 2017) frameworks, we argue that a future important step will be to combine 525 powerful statistical methods (e.g. path analysis; Shipley, 2000; Grace, 2006) with 526 appropriate experimental designs to disentangle causal relationships between 527 intraspecific diversity, community structure, ecosystem functions and their common 528 environment.

529 We further demonstrated that intraspecific variation has significant ecological 530 effects across a large set of species (52 species and 75 articles), hence confirming and 531 refining a previous estimate based on a more restricted species set (Des Roches et al., 532 2018). By more than tripling the number of species being investigated in this meta-533 analysis, we extend the conclusion to a greater taxonomic set that intraspecific variation 534 is involved in shaping ecological dynamics, and that the ecological effects of 535 intraspecific variation might be more common than expected. Moreover, we 536 demonstrated that previous estimates (Des Roches et al., 2018) were not upwardly 537 biased (as expected from their focus on a non-random species pool), but were well 538 within the range of estimates we report here and actually tended to be slight 539 underestimates. Our finding hence strongly supports the idea that adaptive and non-540 adaptive processes can lead to unique populations differentially and significantly 541 affecting ecological systems.

Although our conclusions held true for many species, the ecological effects of intraspecific variation were not homogeneous across species, and this was partly explained by their trophic level. Indeed, and according to expectations, the ecological effects of intraspecific variation were stronger when the target species was a primary producer than when it was a consumer. Several non-exclusive mechanisms might

547 explain this result. For instance, many primary producers considered here provide a 548 habitat for many invertebrate species (Southwood, Brown & Reader, 1979) (this is not 549 the case for the consumer species), and this habitat can be modulated by changes in 550 plant structure. The relative biomass of primary producers is higher than that of 551 consumers, thus primary producers could generate stronger effects on communities and 552 ecosystems than consumers simply because of this biomass effect. However, a more 553 detailed analysis showed that the effects of intraspecific variation tended to be stronger 554 for arthropod and herbaceous species than for fish (and to a lesser extent tree) species. 555 This suggests that the trophic level of a species may not be the only predictor of the 556 ecological effects of intraspecific diversity, and we argue that future work should aim to 557 test specifically why intraspecific variation matters more for some species than others.

558 Finally, the effects of intraspecific variation were globally higher for ecosystems 559 than for communities, hence generalizing across organism and ecosystem types a 560 previous conclusion for freshwater consumer species (Palkovacs et al., 2015). We can 561 speculate that this difference arises because intraspecific variation acts on community 562 dynamics through trophic mechanisms, whereas ecosystem functions can be modulated 563 through both trophic and non-trophic interactions [e.g. excretion rate or leaf chemistry (Vanni, 2002; Schmitz et al., 2014)]. For instance, a consumer species that shows 564 565 intraspecific variation in resource selectivity and/or consumption rate could affect both 566 the community structure and productivity of its resource (Harmon et al., 2009). Non-567 trophic mechanisms such as variability in organismal stoichiometry could reinforce the 568 effect of the consumer species on several ecosystem functions [e.g. primary production 569 or soil mineralization (Schmitz, Hawlena & Trussell, 2010; Hawlena et al., 2012)]. 570 Alternatively, changes in ecosystem functions might be due to both direct effects of 571 intraspecific diversity and indirect effects of intraspecific diversity mediated through

572 changes in community structure, which may overall strengthen the effects of 573 intraspecific diversity at the ecosystem level. However, a more detailed analysis 574 revealed that much variation exists between sub-categories of response variables (Fig. 575 4B), and that the dichotomy between variables measured at the community and 576 ecosystem levels is not straightforward. Although providing the first attempts to 577 separate variance in the ecological effects of intraspecific variation into its component 578 parts, our findings call for further studies on various taxa and in different ecosystems in 579 order to understand fully the ecological effects of intraspecific diversity.

580

# (2) Research perspectives on the relationships between intraspecific diversity and the dynamics of communities and ecosystems

583 We highlight several research avenues that may greatly enhance our understanding of 584 the relationships between intraspecific diversity and the dynamics of communities and 585 ecosystems.

586 Our review demonstrates that the ecological effect size of intraspecific diversity varies 587 among species and that this interspecific variance in effect size can be partly explained 588 by the type of organism (i.e. primary producer or consumer). However, species 589 composing a community also vary according to abundance, role in the ecosystem (e.g. 590 keystone species; Paine, 1969), body size (or height for plants), life-history strategy 591 (e.g. r-K strategy), recent history (e.g. whether the species is non-native), functional 592 characteristics (e.g. stoichiometry, metabolism), etc. The next challenge will be to 593 partition this interspecific variance in effect size better by determining the species 594 characteristics that best predict the strength of effect sizes; this is a pre-requisite to 595 design coherent conservation plans at the intraspecific level (Mimura et al., 2016).

596 Intraspecific diversity is often manipulated with respect to a single target 597 species. However, in nature, species are interacting and we argue that future studies 598 should manipulate intraspecific diversity within multiple interacting species to reflect 599 natural conditions, and to allow partitioning the relative importance of intraspecific 600 diversity between interacting (and potentially co-evolving) species.

Ecosystems are interconnected through cross-ecosystem fluxes of matter 601 602 (Loreau, Mouquet & Holt, 2003). For instance, freshwater ecosystems such as rivers 603 receive a large amount of material from surrounding terrestrial ecosystems [e.g. dead 604 leaves falling from trees (Bartels et al., 2012)]. A major future challenge would be to 605 assess the relative effects of intraspecific diversity on allochtonous ecosystems versus 606 autochtonous ecosystems; for example testing whether the consequences of intraspecific 607 diversity manipulation in a fish species are greater in associated aquatic ecosystems than 608 on nearby terrestrial ecosystems [see Jackrel & Wootton (2014), Crutsinger et al. 609 (2014)b and Rudman et al. (2015) for attempts to quantify across-ecosystem effects of 610 intraspecific diversity]. This is an important next step to quantify in a more integrative 611 way the importance of intraspecific diversity in natural systems.

612 Previous studies have mainly assessed the consequences of intraspecific 613 diversity by considering the genetic or the phenotypic characteristics of organisms as a 614 whole. However, some traits have been shown to be more important for ecological 615 dynamics than others; this is the case for functional effect traits that are defined as traits 616 with an ecological impact [e.g. excretion rate or leaf nutrient content (Violle et al., 617 2007; Díaz et al., 2013)]. We suggest that direct manipulation of the functional trait 618 diversity of individuals within a species, rather than their genotypic or phenotypic 619 diversity as a whole would be a powerful means to understanding the mechanisms by 620 which intraspecific diversity acts on ecological dynamics.

621 Although we emphasize that intraspecific diversity is an essential component of 622 the community and ecosystem facets of ecological dynamics, comparisons with the 623 effects of other major ecological constraints (e.g. temperature, interspecific biodiversity, 624 human disturbance) have rarely been conducted (but see Burkle et al., 2013; El-Sabaawi 625 et al., 2015). To evaluate and quantify the importance of intraspecific diversity in 626 natural systems better, it is important to assess the relative contributions of intraspecific 627 diversity and other determinants of ecosystem functioning. This will be an essential step 628 in confirming that intraspecific variation is a key determinant, and not just a random 629 signal in complex systems.

630

#### 631 V. CONCLUSIONS

(1) This study provides empirical evidence that the ecological effects of intraspecific
richness increase asymptotically, paralleling well-known patterns observed at the
interspecific level (Loreau, 2000; Hooper *et al.*, 2005) and confirming previous
hypotheses (Hughes *et al.*, 2008).

(2) We found that experimental manipulations of intraspecific richness caused
community and ecosystem differentiations as large as those generated by interspecific
richness. This suggests that variation in richness within populations can have similar
ecological consequences to variation in richness among species.

(3) We also demonstrated that variation in phenotypes or genotypes within species is an
important driver of community and ecosystem dynamics. These major ecological effects
of intraspecific diversity held true for a range of organisms including plants and
animals, although much remains to be tested.

644 (4) Overall these findings demonstrate that intraspecific diversity - beyond its645 importance for species to adapt to environmental changes - is an important facet of

biodiversity for understanding and predicting the ecological dynamics of communities and ecosystems, reinforcing the need for a better appraisal of the causes and consequences of intraspecific diversity in natural populations and for improved conservation plans.

650

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| 1138                                 |   |
| 1139                                 | VIII. SUPPORTING INFORMATION  |

- 1141 Additional supporting information may be found in the online version of this article.
- 1142 Appendix S1. Papers used in the meta-analysis.

- 1143 Fig. S1. Flow diagram of manuscript screening and eligibility for this meta-analysis.
- 1144 **Table S1.** Formulae used to convert different statistical values into an *r* correlation
- 1145 coefficient.
- 1146 Fig. S2. Funnel plots describing the residuals effect size distribution against an estimate
- 1147 of the study size for (A) intraspecific variation and (B) intraspecific richness.
- 1148 Appendix S2. R script of the principal functions used in analyses.
- 1149 **Fig, S3.** Distribution of effect sizes (ln*RR*) across ecological metrics.
- 1150 Fig. S4. Distribution of resampled mean effect size (MES) expected under the null
- 1151 hypothesis, i.e. the effect of intraspecific identity in all studies is zero.
- 1152 Fig. S5. Distribution of median effect sizes calculated for each of the 1000 sets of 15
- 1153 studies randomly selected within our extended data set of 75 studies.

1154 Figure legends

1155 Fig. 1. Publication year of the 90 selected articles used in the meta-analysis.

1156

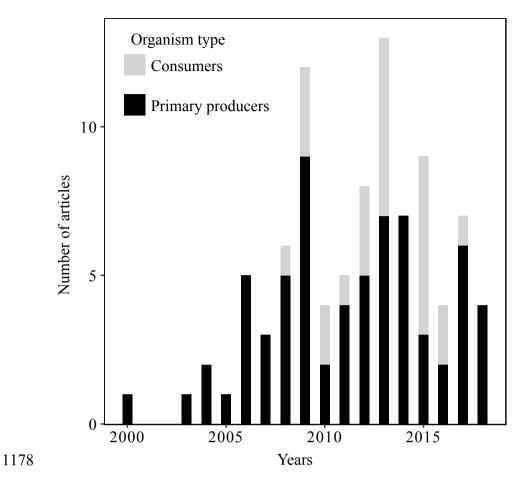
1157 Fig. 2. (A) Relationship between intraspecific richness and effect size  $(\ln RR)$  on 1158 community (points) and ecosystem (crosses) dynamics. The line represents the shape of 1159 the relationship as predicted using an exponential asymptotic non-linear mixed effect 1160 model. The blue shadow represents 95% CI. Symbol colours denote the target species: 1161 herbaceous plant (black), tree (blue) or fungus (grey). (B) Density of absolute effect size 1162 (lnRR) for intraspecific and interspecific richness on ecological dynamics. Posterior 1163 means and 95% percentile intervals (points and horizontal lines, respectively) were 1164 estimated using a model including article ID as the random effect and the inverse of 1165 sample size as a weighting parameter.

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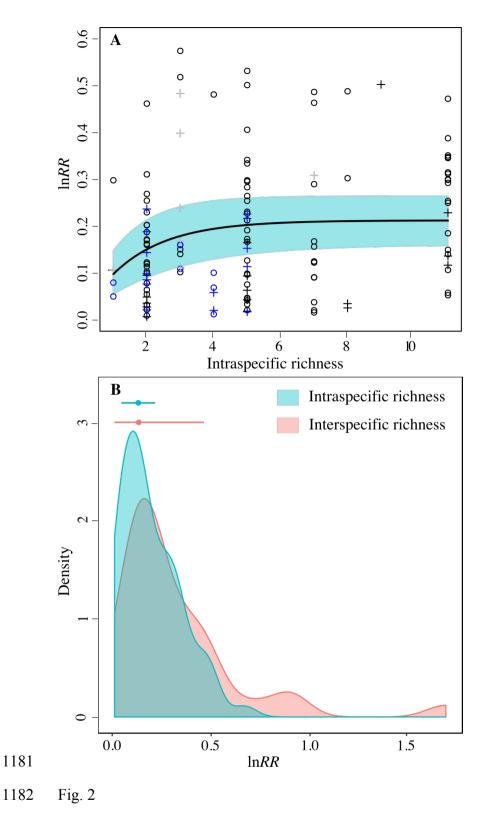
Fig. 3. Density probability of effect size Zr. The vertical broken line represents the resampled Zr mean under the null hypothesis (confidence intervals not shown because they are too narrow); the black curve shows the distribution of observed Zr and its mean (vertical black straight line) and 95% CIs (grey shading).

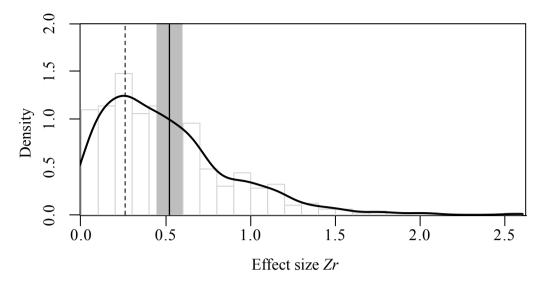
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1172 **Fig. 4.** (A) Mean effect size Zr for different species groups. The sample sizes (N) 1173 represent the number of species and the number of effect sizes, respectively. The 1174 horizontal broken line represents the mean effect size; error bars represent  $\pm 1$  SE. (B) 1175 Mean Zr for the ecological response variables. The sample sizes (N) of the number of 1176 effect sizes are given. The horizontal broken line represents the mean effect size; error 1177 bars represent  $\pm$ 1 SE.

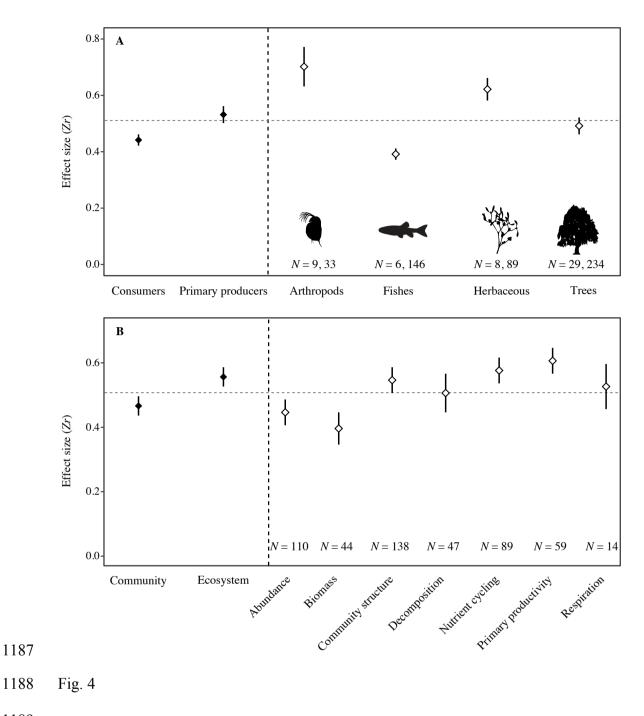












1191 Table 1. Summary table of model selection by Akaike information criterion (AIC)

1192 comparison to explain the shape of the relationship between the ecological

1193 consequences and the intraspecific richness. Models were run as non-linear mixed-

1194 effect models with the article ID as a random factor; equations and parameters estimates

are also shown. IR, intraspecific richness; lnRR, effect size of intraspecific richness on

1196 ecological dynamics.

1197

| Model                              | AIC      | ΔΑΙϹ    | AIC<br>weight | Equation                       | Parameter estimates      |
|------------------------------------|----------|---------|---------------|--------------------------------|--------------------------|
| Asymptotic<br>exponential<br>model | -176.695 | 0       | 0.999         | $lnRR = a * (1 - e^{-b * IR})$ | a = 0.221<br>b = 0.617   |
| Michaelis–<br>Menten model         | -11.873  | 164.821 | < 0.001       | $lnRR = V * \frac{IR}{k + IR}$ | V = 0.054<br>k = -2.712  |
| Linear model                       | -160.974 | 15.721  | < 0.001       | lnRR = b0 + b1 * IR            | b1 = 0.012<br>b0 = 0.122 |
| Null model                         | -144.191 | 32.503  | < 0.001       | lnRR = b0                      | <i>b0</i> = 0.183        |