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Plant genetic diversity affects interactions among multiple trophic levels

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32

33 **Abstract:** Intraspecific diversity (genetic diversity) is an important component of biodiversity.

34 A substantial body of evidence has demonstrated positive direct or indirect effects of plant

35 genetic diversity on plant performance. However, it has remained unclear whether plant

36 genetic diversity increases plant performance by reducing the pressure of plant-damaging

37 organisms across trophic levels in different plant life forms, ecosystems and climatic zones.

38 Here, we analyse 4702 effect sizes reported in 413 studies that consider effects of plant

39 genetic diversity on trophic groups and their interactions. We found that increasing plant

40 genetic diversity decreases the performance of plant-damaging organisms including

41 invertebrate herbivores, weeds, plant-feeding nematodes and plant diseases, while increasing

42 the performance of plants and natural enemies of herbivores. We also provide evidence that

43 plant genetic diversity increases plant performance by reducing plant-damaging organism

44 pressure. These results reveal that plant genetic diversity often influences multiple trophic

45 levels in ways that enhance natural pest control in managed ecosystems and consumer control

46 of plants in natural ecosystems for sustainable plant production.

47

48

49 Plant genetic diversity has been shown to provide multiple ecosystem services (e.g.,

50 biocontrol service¹) in terrestrial¹⁻⁵ and marine ecosystems⁶. In natural ecosystems, plant

51 genetic diversity is a key component of species and ecosystem health and can also be

52 obtained by manipulating the population genetic richness of plants within or around managed

53 lands^{1,2,7} or aquatic areas⁸. In particular, increasing plant genetic diversity can increase plant

54 productivity^{9,10} and crop yields¹, reduce plant-damaging organisms such as insect herbivores¹¹,

55 weeds (i.e., harmful plants for humans in agroforestry)¹², plant diseases^{2,13} or plant-feeding

56 nematodes¹⁴, and promote pest natural enemies^{15,16}. Single genotypes in monocultures can
57 have negative effects on natural enemies of invertebrate herbivores¹⁷ and crop yields¹⁸ but
58 positive effects on herbivores¹⁹ and plant diseases (i.e., pathogenic bacteria, fungi and plant
59 virus)²⁰. Together, these results indicate a possible influence of plant genetic diversity across
60 multiple interacting trophic levels. However, the global effects of increasing plant genetic
61 diversity across trophic levels in different plant life forms, ecosystems or climatic zones have
62 not yet been explored.

63 Trophic interactions among plants, plant-damaging organisms (e.g., invertebrate
64 herbivores) and natural enemies of herbivores are universal in nature^{21,22} and their role in
65 structuring ecological communities has been extensively recognized (e.g. Underwood et al.,
66 2017)²³. For example, theory on trophic interactions predicts that natural enemies indirectly
67 increase plant performance by feeding on herbivores^{24,25}, and many studies have shown that
68 plant genetic diversity strengthens bottom-up effects on higher trophic groups^{16,26}. This is
69 realized through increases in the abundance or diversity of predators and parasitoids^{9,27},
70 decreases in the damage or abundance of herbivorous and nematode pests^{11,14}, and decreased
71 damage by plant pathogens²⁸. This generally results in increased plant growth and
72 reproduction⁹ at higher genetic diversity. However, several other studies have found results
73 different from those described above^{11,29-31}.

74 A generalized literature synthesis is therefore needed to illustrate the gaps and trends in the
75 research based on the existing literature, and to achieve generalized effect sizes^{32,33}. Previous
76 meta-analyses have concluded that plant genetic diversity promotes crop yields¹⁸ and
77 increases abundance and species richness of predators, while there were no significant effects
78 on herbivore abundance or herbivory damage¹⁷. However, these syntheses involved only
79 selected trophic levels (plants, or arthropod herbivores and their natural enemies) and

80 selected study systems (crop species), but not weeds, plant diseases or plant-feeding
81 nematodes. Meanwhile, these syntheses did not explore whether plant genetic diversity
82 increases plant performance by reducing the pressure of plant-damaging organisms or not the
83 tri-trophic interactions among plants, herbivores and their natural enemies. Furthermore,
84 these meta-analyses did not compare these diversity effects across different plant life forms,
85 ecosystems or climatic zones on a global scale.

86 Here we present a synthesis of 4702 estimates reported in 413 experimental studies that
87 measured the effects of plant genetic diversity on different trophic groups — plants,
88 plant-damaging organisms including invertebrate herbivores, weeds, plant-feeding nematodes
89 and plant diseases (i.e., plant bacteria, fungi and viruses), and natural enemies of herbivores
90 (i.e., predators and parasitoids) — from terrestrial and marine ecosystems around the world
91 (Fig. 1 and Supplementary Table 1). We defined the term “performance” of trophic groups
92 according to Wan et al.²² Specially, invertebrate herbivore performance included the
93 abundance, damage and diversity of herbivores; natural enemy performance covered the
94 abundance and diversity of predators and parasitoids, and the parasitism); weed performance
95 included the growth and diversity of weeds; plant-feeding nematode performance was only
96 involved in nematode abundance; plant disease performance included the disease spread and
97 disease damage to plants; plant performance included the growth, reproduction and quality of
98 plants; and plant-damaging organism performance includes the performance of herbivores,
99 weeds, plant-feeding nematodes and plant diseases. We calculated the standardized mean
100 difference between measures of these trophic groups in genetically diverse and monospecific
101 plant stands, used a meta-regression model to analyse responses of trophic groups to plant
102 genetic diversity, and then used piecewise structural equation to analyze trophic interactions
103 using path analysis. Through these approaches, we asked three questions: (i) How does plant

104 genetic diversity affect the performance of plants, plant-damaging organisms, herbivores,
105 weeds, plant-feeding nematodes, plant diseases, and natural enemies of herbivores? (ii) do the
106 effects differ among ecosystems, plant life forms or climatic zones? (iii) what are the direct
107 and indirect effects of plant genetic diversity across trophic interactions?

108

109 **Results and Discussion**

110 We found that increasing plant genetic diversity decreases the performance of plant-damaging
111 organisms, herbivores, weeds, plant-feeding nematodes and plant diseases, while increasing
112 the performance of plants and natural enemies (Fig. 1b). A similar pattern was found when
113 trophic groups were divided into sub-groups (e.g., plant performance into plant growth, plant
114 quality and plant reproduction, weed performance into weed growth and weed diversity, and
115 plant disease performance into disease spread and disease damage). Only for a small number
116 of sub-groups (plant-damaging organism diversity, herbivore diversity and parasitism) where
117 sample sizes were small (Supplementary Table 4), the results were inconclusive.

118 In a second step, we tested whether these effects differed among ecosystems
119 (agroecosystems, grasslands, forests, old-field ecosystems, marine ecosystems, wetlands and
120 shrublands), plant life forms (herbaceous vs. woody), experiment types (field plots vs. pot
121 experiments) or climatic zones (tropical and temperate). In agroecosystems or grasslands, the
122 overall pattern described above was confirmed (Extended Data Figs. 1a, b; Supplementary
123 Table 5). For the other ecosystems, the responses were variable (Extended Data Figs. 1c–g;
124 Supplementary Table 5). The overall pattern was also confirmed at the types of experimental
125 study (i.e., plot and pot experiments) (Extended Data Fig. 2; Supplementary Table 6), and at
126 the plant life-form level (i.e., herbaceous and woody plants) (Extended Data Fig. 3;
127 Supplementary Table 7). Across climatic zones, we found a stronger response in temperate

128 than in tropical zones (Extended Data Fig. 4; Supplementary Table 8), likely because of a
129 smaller sample size in tropical systems.

130 Interestingly, plant genetic diversity decreased herbivore performance in agroecosystems,
131 grasslands, and forests (Supplementary Table 5). This reduction might reflect resource
132 heterogeneity effects on foraging behaviour of herbivores²⁷, as well as on herbivore
133 movement³⁴. The reduction might be due to the fact that these studies were usually focused
134 on control of a single herbivore species by mixing crop or plant genotypes with known
135 differences in resistance to this herbivore, thus increasing the chances of associational
136 resistance in genotypic mixtures⁴. The ‘resource concentration hypothesis (RCH)’ proposed
137 that diverse plant communities resulted in lower herbivore abundance because of lower
138 concentrations of their host plants in diverse stands as compared to monocultures⁴. While
139 RCH was used to analyze the effects of plant species diversity on herbivores, it has been
140 recommended that it should be extended to plant genetic diversity effects mainly due to the
141 fact that herbivores are known to distinguish between plant genotypes¹⁹. Conversely, plant
142 genetic diversity increased herbivore performance in old-field systems, which potential
143 mechanisms responsible for this pattern fall into two broad categories. First, complementary
144 resource use among plant genotypes increased plant performance and consequently increased
145 herbivore abundance in this case^{9,35}. Second, high herbivore performance in genotypic
146 mixtures is simply a result of greater plant quantity³⁶.

147 We also found that plant genetic diversity reduced weeds in agroecosystems and grasslands
148 (Extended Data Figs. 1a, b), diseases in agroecosystems, grasslands, forests and old-field
149 ecosystems (Extended Data Figs. 1a–d), and plant-feeding nematodes in agroecosystems
150 (Extended Data Fig. 1a), indicating strong biocontrol services. Such biological control effects
151 may be an indication of genetic heterogeneity (i) inhibiting the growth of weeds through

152 allelopathic effects and growth competition¹², (ii) diluting the concentration of resources or
153 disrupting the movement of pathogens between host plants¹ or (iii) rhizosphere inhibition
154 zones against nematodes³⁷. Generally, physical barrier and variety resistance effects of plant
155 genetic diversity on decreased insect herbivores, nematodes and diseases (e.g., air-borne
156 pathogens, splashborne propagules and soil-borne bacteria) are important factors³⁸.

157 Plant genetic diversity also had a direct influence on higher trophic levels across
158 ecosystems. Specifically, we found that more genetically diverse plant stands support more
159 natural enemies, such as predators and parasitoids (Fig. 1b). Such effects can be direct^{15,31},
160 mediated by increases in herbivore abundance^{30,35}, driven by trait-mediated indirect
161 effects^{39,40}, or directly mediated by natural enemies through top-down effects as indicated by
162 the ‘enemy hypothesis (EH)’^{4,41}. In light of EH hypothesis, diverse plant genotypes will
163 increase abundance and diversity of natural enemies of insect herbivores by providing a
164 higher diversity of alternative food resources and refuges that allows for optimized nutrient
165 uptake or increases host or prey biomass, which will give rise to a better control of herbivore
166 densities by natural enemies in more diverse plant stands. Such top-down effects may explain
167 a positive influence of plant genetic diversity on plant performance. However, such top-down
168 effects were not significant in forests where genetically rich communities often grew more
169 slowly and suffered higher levels of herbivory than genetic monocultures⁴². The weaker
170 effects of increased tree genotypes on natural enemies and associated biocontrol services
171 resulted from the complex habitat properties because even low-diversity forests can maintain
172 a high degree of habitat heterogeneity and may provide niches for many predator and
173 parasitoid species⁴³.

174 Finally, for a subset of the data, we obtained 1606 interactive estimates derived from 163
175 studies testing the effects of plant genetic diversity across multiple trophic levels. We tested

176 the effect of plant genetic diversity on bi-trophic interactions between plants and
177 plant-damaging organisms (1484 estimates derived from 139 studies) using multilevel
178 piecewise structural equation models. In these models, different plant-damaging organisms
179 (i.e., invertebrate herbivores, weeds, plant-feeding nematodes or plant diseases) were
180 considered together. We found that plant genetic diversity affects plant performance directly
181 and indirectly by reducing plant-damaging organism performance (Fig. 2). The same pattern
182 was also verified in agroecosystems, but not in other ecosystems (Extended Data Fig. 23). In
183 these cases, plant genetic diversity mainly showed a direct effect on plant or plant-damaging
184 organism performance, but no mediating effects. No evidence of an indirect effect of plant
185 genetic diversity on plant performance through a reduction of plant-damaging organism
186 pressure was found when we tested herbivore, weed and nematode performance separately
187 (Extended Data Figs. 22a–c). However, the models confirmed a direct effect of plant genetic
188 diversity on plant and plant-damaging organism performance. It is likely that further studies
189 will be needed to validate such models. Indeed, when more data were available, as for the
190 case of disease performance (N = 969), such mediating effects were evident (Extended Data
191 Fig. 22d).

192 For a subset of studies (N = 91), where the effect of plant genetic diversity in tri-trophic
193 systems (plant-herbivore-natural enemy interactions) was quantified, we tested effects of
194 plant genetic diversity on tri-trophic interactions. The structural equation model showed a
195 direct influence of plant genetic diversity on natural enemy, invertebrate herbivore, and plant
196 performance, but no significant indirect effects mediated via trophic cascades. Specifically,
197 we found a positive effect of plant genetic diversity on natural enemy and plant performances
198 and a negative effect on herbivore performance. These findings indicate a potential effect of
199 plant genetic diversity triggering a tri-trophic cascade (Fig. 3).

200 Our synthesis comprehensively shows that plant genetic diversity promotes ecosystem
201 services by strengthening trophic interactions: benefiting natural enemies including
202 invertebrate predators and parasitoids, in turn suppressing invertebrate herbivores, and
203 enhancing plant performance; and meanwhile suppressing weeds, plant-feeding nematodes
204 and diseases, and logically enhancing plant performance. These findings contribute to
205 explaining the mechanisms by which manipulation of plant genetic diversity can affect
206 different trophic groups and their interactions. From an applied perspective, promoting plant
207 genetic diversity can be important to promote both pest control in managed ecosystems and
208 consumer control of plant production in natural ecosystems and to enhance associated
209 ecosystem functions and services. In conclusion, our results indicate that plant genetic
210 diversity can help society, decision-makers and stakeholders to take advantage of the
211 important biocontrol services provided by plant genetic diversity on Earth.

212

213

214 **Methods**

215 **Study Selection**

216 We conducted a literature search on the Web of Science and China National Knowledge
217 Internet (www.cnki.net) (last accessed in September 2021) using the Boolean search string:
218 ["plant genetic diversity" OR "plant genotypic diversity" OR "crop genetic diversity" OR
219 "crop genotypic diversity" OR "intraspecific diversity" OR "inter-genotypic" OR
220 "intervarietal" OR "resistant *susceptible cultivar*" OR "pure * mixed cultivar" OR "cultivar
221 mixture" OR "varietal mixture"] AND ["predat*" OR "herbivor*" OR "parasitoid" OR
222 "wasp*" OR "natural enem*" OR "pest management" OR "pest control" OR "biological
223 control" OR "plant disease" OR "plant virus" OR "nematode" OR "weed" OR "yield" OR

224 “productivity” OR “biomass”]. Overall, about 145000 papers were screened for relevance.
225 Additionally, references were obtained from 27 review papers identified in the original search
226 (Supplementary References). Finally, we arrived at 413 papers based on the following criteria:
227 the study included at least one comparison between plant stands with one genotype
228 (monoculture control treatment) or ≥ 2 genotypes (mixed treatment); the use of pesticides and
229 other practices (fertilizer, irrigation, etc) should be the same for the control and mixed
230 treatments; both the control and the mixed treatment had one and the same plant species; and
231 the measurements of treatment and control groups were performed at the same spatiotemporal
232 scale. When a study covered multiple levels of plant genotypes, measurements of
233 monoculture stands and different numbers of plant genotypes were recognized as independent
234 observations. We extracted the data using the “GetData Graph Digitizer” software²². We first
235 used the data for which the authors in a cited paper had listed the mean values of multiple
236 sampling dates or multiple sampling years. If the authors did not present these mean values,
237 we adopted the data of the latest sampling date²² (more details in Supplementary Methods).

238 For studies that included \geq one location, we considered these experimental observations
239 separately in each location and used the longitudes and latitudes of all locations in Fig.1,
240 respectively. When the means of observed weed performance indicators (e.g., weed growth in
241 one study), or the indicators for herbivores (e.g., herbivore damage in one study) and
242 predators (e.g., predator abundance in one study) were not given in the study, we extracted
243 these values directly from the figures (e.g. if a linear or a non-linear relationship between
244 plant genetic diversity and one of these indicators was presented in a figure in the paper, we
245 extracted the values from the fitting equations). When the treatment group was paired with
246 the control group, we excluded multiple comparisons within a single study, and we selected
247 different comparison data (observations with pure or /single plant genetic diversity were

248 considered as control group while the others as the treatment group). Thus, we tried our best
249 to diminish the possibility that some of these 4702 effect sizes might inflate the results with
250 meta-analytical replicates.

251

252 **Predictor variables**

253 We adopted six categorical variables and one continuous variable (a detailed description is
254 described in Supplementary Methods). (1) Trophic group: a categorical variable that denotes
255 whether the organisms whose responses were studied were invertebrate herbivores (i.e.,
256 arthropod herbivores, amphipod herbivores and molluscan herbivores), natural enemies of
257 invertebrate herbivores (i.e., carnivores of invertebrate herbivores and parasitic wasps),
258 weeds (harmful plants for humans in managed ecosystems dominated by other plants or
259 crops), plant-feeding nematodes, plant diseases (plant bacteria, fungi and viruses which infest
260 or infect plants and cause damage to plants), or plants; to reformulate variables, we adopted a
261 comprehensive categorical variable (i.e., plant-damaging organisms⁴⁴) which included
262 invertebrate herbivores, weeds, plant-feeding nematodes and plant diseases; (2) Response
263 variable: abundance and diversity of herbivores, herbivory damage, abundance and diversity
264 of invertebrate predators, abundance, diversity and parasitism of parasitoids, growth and
265 diversity of weeds, nematode abundance, disease spread and disease damage, and growth,
266 reproduction and quality of plants (here “diversity” includes species richness and Shannon
267 Diversity of herbivores, predators or parasitoids); (3) Ecosystem Type: agroecosystems,
268 old-field ecosystems, marine ecosystems, grasslands, forests, shrublands and wetlands (cited
269 studies for each ecosystem type included in this paper should be more than 3, presented in
270 Supplementary Table 1)²²; (4) Plant life form: herbaceous and woody plants²²; (5) climatic
271 zone type: temperate and tropical; (6) Experiment type: plot and pot experiments (specially,

272 common garden experiments with a few or several replicated plots were considered as plot
273 experiments, field plot experiments in terrestrial ecosystems were involved in plot
274 experiments, experiments in aquatic ecosystems with a few or several replicated plots were
275 also considered as plot experiment, and tray, box, tanker and container experiments were
276 considered as pot experiments); and (7) Number of added plant genotypes: a continuous
277 variable presenting the number of genotypes by which the number of plant genotypes was
278 increased over the pure plant genotype or variety (i.e., the number of genotypes added by
279 manipulated plant genetical diversity in experimental designs, such as interplanting,
280 undersowing, intercropping, mixed cropping and mixed planting). When we compared the
281 genotypes of the control (pure or mono- genotype) with the ones of the treatment (higher
282 genotypes, ≥ 2 genotypes), we confirmed that both the control and treatment were compared
283 on a single plant species.

284

285 **Effect size measures**

286 In this paper, we calculated the Standardized Mean Difference (SMD) to quantify the plant
287 genetic diversity effects on the various trophic groups as $SMD_i = (M_{ti} - M_{ci}) / sd_i, 1 \leq i \leq m,$

288 in which M_{ti} and M_{ci} were the mean values in the treatment and control groups,

289 respectively, and $sd_i = \sqrt{\frac{(n_{ti} - 1) \times sd_{ti}^2 + (n_{ci} - 1) \times sd_{ci}^2}{n_{ti} + n_{ci} - 2}}$, in which n_{ti} and n_{ci} were the

290 sample sizes and sd_{ti} and sd_{ci} were the standard deviations in the two groups,

291 respectively. The sampling variance was evaluated by the unbiased approach⁴⁵.

292

293 **Meta-regression models**

294 Meta-regression⁴⁶ was employed to assess whether the effects of plant genetic diversity
295 (measures as standardized mean difference in genetically diverse and genetically
296 monospecific plant stands; SMD plant genetic diversity) on different trophic groups could be
297 explained by ecosystem type, plant life form, climatic zone type, type of experimental study,
298 and number of added plant genotypes. This was obtained by treating the trophic groups and
299 the interactions between them as moderator variables in the model (Supplementary Methods).
300 In addition, every unique study identity was considered as a random effect factor to avoid the
301 heterogeneity in terms of study observations and overlapping samples within each study⁴⁷
302 with each effect size nested within the corresponding study ID for incorporating the
303 hierarchical error structure of multiple effects coming from the same study. Specifically, We
304 performed meta-regression analysis using the R package metafor (version 2.4-0), in which we
305 took SMD as the effect size measure (in the function “`escalc()`”, the argument “`measure`” was
306 specified as “`SMD`”). Then, unbiased sample variance estimates were constructed to evaluate
307 the variances of SMDs (in the function “`escalc()`”, the argument “`vtype`” was specified as
308 “`UB`”). Supposing there are trophic groups (herbivores, natural enemies, weeds, plant-feeding
309 nematodes, plant diseases and plants), newly integrated trophic groups (i.e., plant-damaging
310 organisms, natural enemies of herbivores and plants) and different moderators (i.e. ecosystem
311 types, types of experimental study, plant life forms, climatic zones, and number of added
312 plant genotypes), we employed a likelihood ratio test to compare the full model with the null
313 model to investigate the significance of the interactive effects between trophic groups or
314 integrated trophic groups and various moderators. Concurrently, the signs of SMDs in trophic
315 groups were converted to absolute values to facilitate interpretation of the results before
316 fitting the models. Notably, for meta-estimates, we did not transform the signs of trophic
317 values. We also analyzed subsets of the included studies to better understand the effects

318 within different subgroups (Supplementary Methods). To examine whether the mean effect
319 sizes in the different categories differed significantly from zero, we analyzed t-distributions
320 with 95% confidence intervals, which were derived from the fitted meta-regression models.

321 First, we fitted a base model by treating the trophic group (invertebrate herbivores, weeds,
322 plant-feeding nematodes, disease, plant-damaging organisms, natural enemies or plants) as
323 the only variable in a mixed-effects model. Second, the interactions between the trophic
324 group and other moderator variables (types of ecosystem, experimental study, plant life form,
325 climatic zone and \log_2 (added plant genotypes over control) were also included in the model
326 to assess whether model fit was improved, using a likelihood-ratio test (LRT). Third, the
327 trophic group response category (nested within trophic group) and the interactive effects
328 between the response category and types of ecosystem, experimental study, plant life form,
329 climatic zone were also included in the model to assess the significance of each moderator
330 variable (using a likelihood-ratio test (LRT) and comparing against the first degree interaction
331 model) (Supplementary Table 2).

332

333 **Analysis of trophic interactions**

334 To investigate the bi-trophic and tri-trophic interactions among various trophic groups, we
335 constructed a new data subset containing paired trophic observations (e.g., natural enemy
336 performance vs. invertebrate herbivore performance vs. plant performance, herbivore
337 performance vs. plant performance, weed performance vs. plant performance, plant-feeding
338 nematode performance vs. plant performance, and plant disease performance vs. plant
339 performance; Fig. 3). Then, another data subset was established which encompassed the
340 paired observations of plant-damaging organism performance vs. plant performance within
341 different ecosystems (i.e., global ecosystems, agroecosystem, grassland, forest, old-field

342 ecosystem, marine ecosystem, wetlands and shrubland; Extended Data Fig. 23). Three
343 additional data subsets were then made, comprising the paired observations of
344 plant-damaging organism performance vs. plant performance within different types of
345 experimental study, plant life form and climatic zone, respectively (Extended Data Fig. 24).
346 Subsequently, the effect sizes of the responses for each performance to SMD plant genetic
347 diversity (Extended Data Figs. 22–24) and the number of added plant genotypes (Extended
348 Data Figs. 19–21) were calculated on each data subset using meta-regression models, which
349 were also employed via the R function “factanal” for conducting the factor analyses
350 (Supplementary Table 16). Additionally, the number of added plant genotypes treated as
351 extensive predictor was also included in the factor analyses using the R function "factanal" to
352 reveal the effect of the specific value of added plant genotypes on the trophic interactions.

353 Piecewise structural equation models⁴⁷ were fitted on each of the additional data subsets to
354 test the direct and indirect effects of SMD plant genetic diversity and number of added plant
355 genotypes on all potential interactions among the trophic groups. Briefly, piecewiseSEM
356 models were fitted using series of linear mixed-effects models with random intercepts for
357 plots or sites nested within study IDs. Heteroscedasticity was accounted for by supplying
358 fixed variances based on SMD, and setting sigma to 1 in the lme call.

359 Specifically, we tested the effects of plant genetic diversity on the tri-trophic interactions of
360 herbivore, natural enemy and plant performances, and on each of the bi-trophic interactions
361 between performance values of herbivores and plants, weeds and plants, plant-feeding
362 nematodes and plants, and plant diseases and plants, respectively (Extended Data Fig. 22).
363 Structural equation models were also used to test the effects of SMD plant genetic diversity
364 on the bi-trophic interactions between the performance of all combined plant-damaging
365 organisms and plants in different ecosystems (i.e., global ecosystems, agroecosystem,

366 grassland, forest, old-field ecosystem, marine ecosystem, wetlands and shrubland) (Extended
367 Data Fig. 23), as well as the effects of SMD plant genetic diversity on the bi-trophic
368 interactions between the combined plant-damaging organism performance and plant
369 performance within different experiment types (i.e., plot and pot experiments), plant life
370 forms (herbaceous and woody plants) and climatic zones (temperate and tropical zones),
371 respectively (Extended Data Fig. 24). Concurrently, in order to explore the effects of varying
372 levels of genotype diversity, we carried out structural equation modelling to examine the
373 direct and indirect effects of the number of added plant genotypes on the bi-trophic
374 interactions among different pairs of trophic groups (Extended Data Fig. 19), on the
375 bi-trophic interactions of plant-damaging organism performance and plant performance for
376 different ecosystems (Extended Data Fig. 20), experiment types, plant life forms and climatic
377 zones, respectively (Extended Data Fig. 21). Different meta-regression models were
378 constructed to detect correlations between natural enemy performance and herbivore
379 performance, between herbivore performance and plant performance, and between natural
380 enemy performance and plant performance, respectively, in which the trophic group not being
381 tested was included as a co-variate (Supplementary Methods). Additionally, we also adopted
382 SMD plant genetic diversity compared to the control (pure or mono- genotype), which
383 indicated that when the behaviour or activity of genetic diversity planting was employed, how
384 the alteration of effect size impacted the bi-trophic (Fig. 2; Extended Data Figs. 22–24) or
385 tri-trophic (Fig. 3) interaction relationship. Furthermore, the \log_2 -transformed number of
386 added plant genotypes over the control was considered as an extra measurement of plant
387 genetic diversity to explore the magnitude of effect on the trophic interaction relationship
388 (Extended Data Figs. 19–21).

389

390 **Publication bias test**

391 Publication bias was evaluated by performing regression tests⁴⁸ on the number of fitted
392 models which encompassed different moderators (see Supplementary Table 3). In other words,
393 these models were mixed-effects models. For examining the sensitivity of the results, and
394 because the trim and fill method⁴⁹ could only be used in the context of the fixed- or
395 random-effects model (i.e., in models without moderators), the adopted models by Egger et al.
396 would not evaluate it⁴⁸. Instead, we followed the suggested approach of Nakagawa and
397 Santos⁴⁶, where residuals from different established models were used to estimate publication
398 bias in mixed-effects meta-regression analysis. In addition, the Rosenthal fail-safe number for
399 the full dataset⁵⁰ was assessed, using a fail-safe number of 101836 for the full dataset
400 (Supplementary methods).

401 R version 4.0.2⁵¹ was applied for all statistical analyses, in which meta-regression and
402 publication bias were estimated by means of the R package “metafor” (Viechtbauer...).
403 Additionally, the R packages “piecewiseSEM”⁵² and “nlme”⁵³ were used for piecewise
404 structural equation modelling. All tests used 0.05 as significance level.

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516

517 **Supplementary information**

518 Supplementary Tables 1–16, Methods and References.

519

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525

526 **Author contributions**

527 N.F.W. conceived the idea. N.F.W., L.F. and Y.Q.H. collected and analyzed the data, and
528 drafted the article. N.F.W., L.F., M.D., Y.Q.H., L.P.K., F.I., and C.S wrote the manuscript. All
529 authors prepared and edited the final drafts.

530

531 **Competing interests**

532 The authors declare no competing financial interests.

533

534 **Correspondence and requests for materials** should be addressed to N.F.W.

535

536 **Data availability**

537 All data used in this analysis are available at Zenodo ([10.5281/zenodo.5596865](https://zenodo.org/doi/10.5281/zenodo.5596865)).

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539 **Code availability**

540 All code used in this analysis is available at Zenodo ([10.5281/zenodo.5827568](https://zenodo.org/doi/10.5281/zenodo.5827568)).

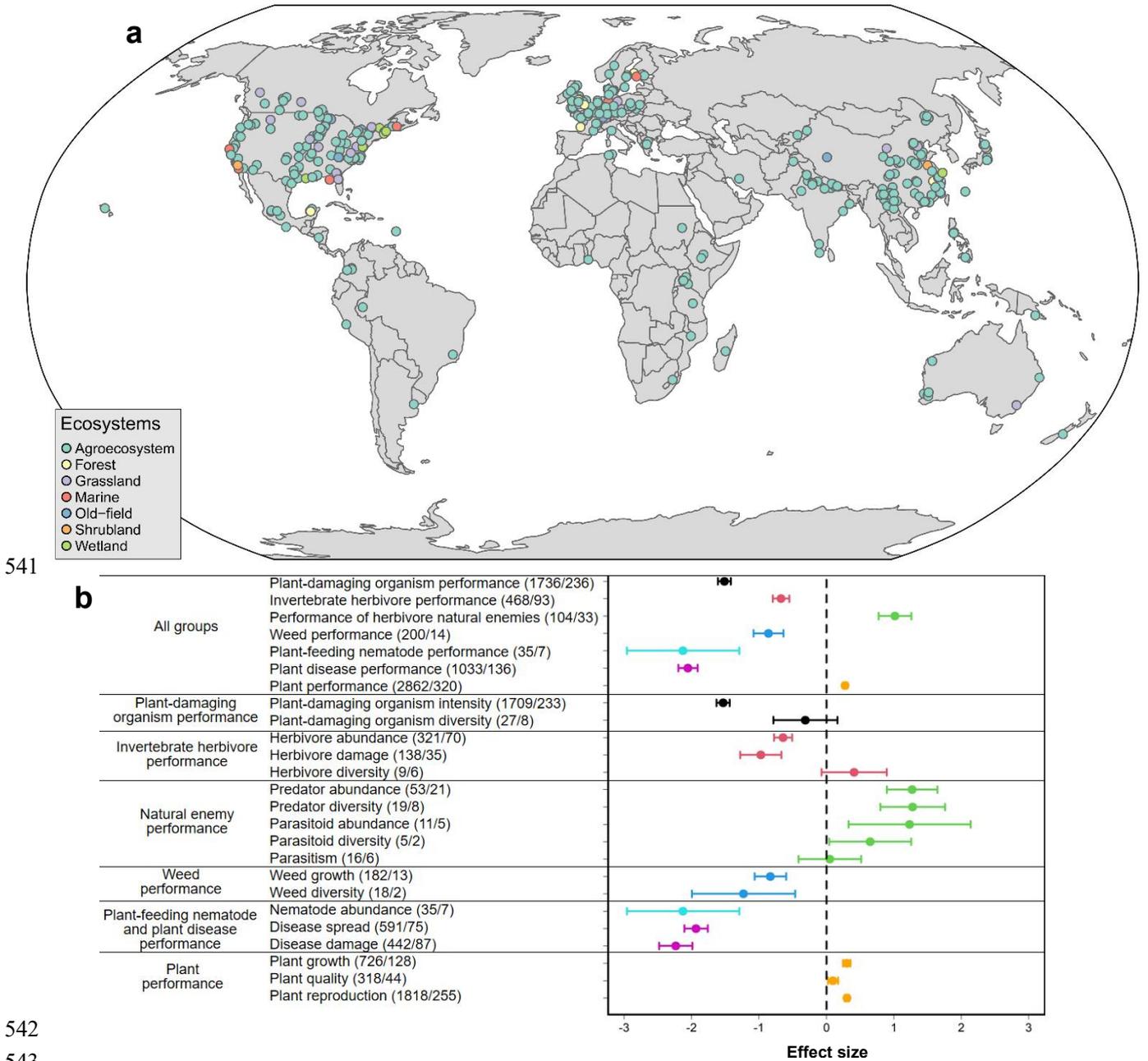


Fig. 1 | Global distribution of plant genetic diversity study locations and the responses of trophic groups to plant genetic diversity. a, Study locations across all ecosystems (world map in World Robinson projection). **b**, Responses of trophic groups across all studies. A literature search identified study locations for agroecosystems (414), forests (16), grasslands (24), old-field ecosystems (14), marine ecosystems (11), wetlands (9) and shrublands (5) respectively, from a total of 413 published articles. Forty-nine articles included more than one study location (range 2–8). In Fig. 1b, horizontal lines indicate the 95% confidence intervals around the means; numbers in brackets indicate the numbers of observations and studies; seven lines represent plant-damaging organism (black), invertebrate herbivore (red), natural enemy of invertebrate herbivores (green), weed (blue), plant-feeding nematode (turquoise), plant disease (purple) and plant (orange) performance responses, respectively; plant-damaging organisms include herbivores, weeds, nematodes and diseases; and natural enemies include predators and parasitoids. Responses of trophic groups to plant genetic diversity on seven ecosystems, in two experimental types, for two plant life forms and for two climatic zone types are presented in Extended Data Figs. 1–4.

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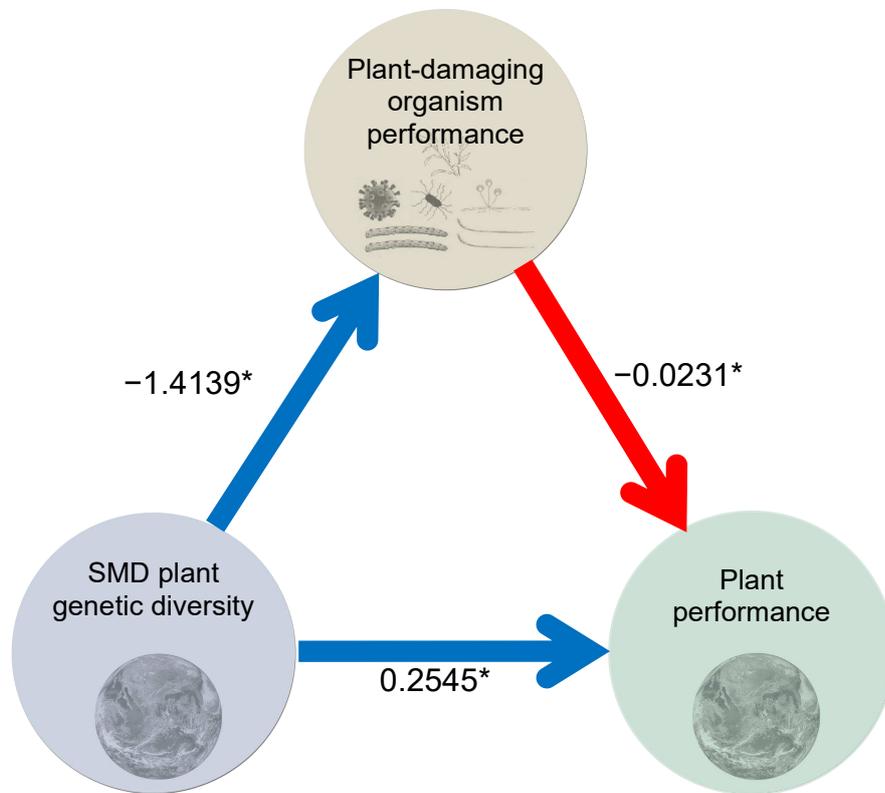


Fig. 2 | Piecewise structural equation model for the effects of SMD plant genetic diversity on bi-trophic interactions of plant-damaging organism performance and plant performance across global ecosystems. The effects of SMD plant genetic diversity (measures as standardized mean difference in genetically diverse and genetically monospecific plant stands) on bi-trophic interactions of invertebrate herbivore and plant performance, weed and plant performance, plant-feeding nematode and plant performance, and plant disease and plant performance are presented in Extended Data Figs. 22a–d, respectively. Plant genetic diversity is shown in dusty blue. plant-damaging organism performance including herbivore performance (abundance, damage and diversity of herbivores), weed performance (growth and diversity of weeds), plant-feeding nematode performance (nematode abundance) and plant disease performance (disease spread and damage) is shown in beige circles. Plant performance (growth, quality and reproduction of plants) is shown in teal color. Blue and red arrows denote positive and negative relationships, respectively, and numbers next to each arrow are the estimated coefficients from piecewise structural equation models (Supplementary Tables 11, 12).

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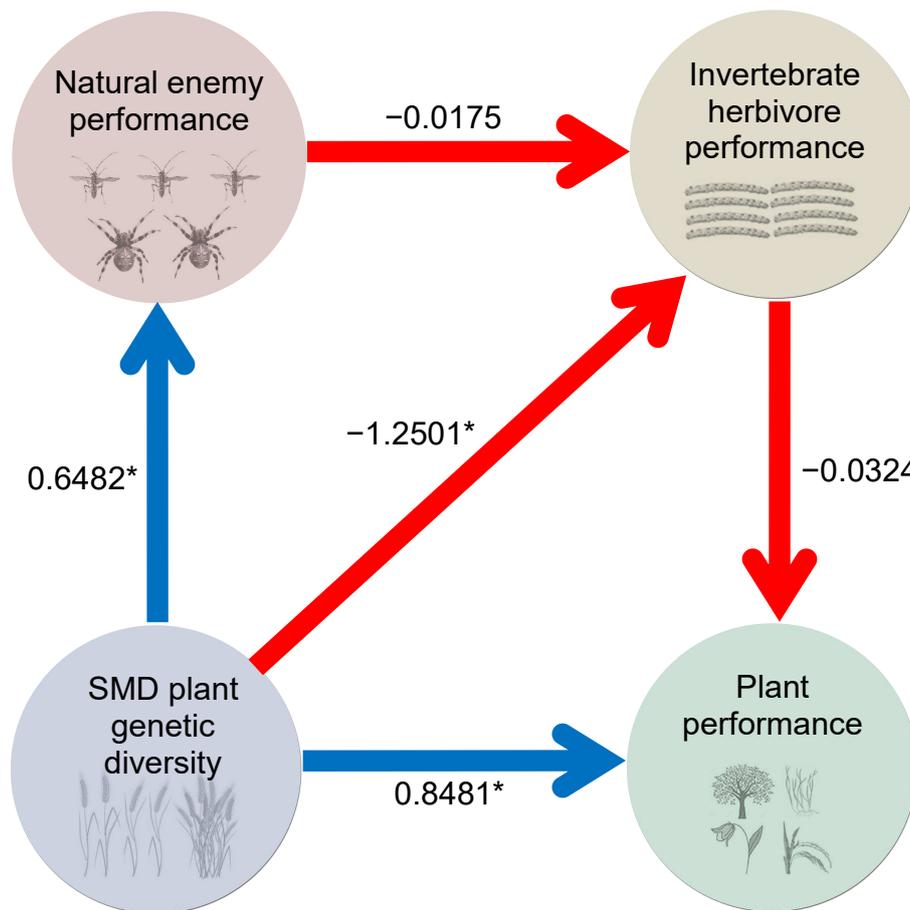
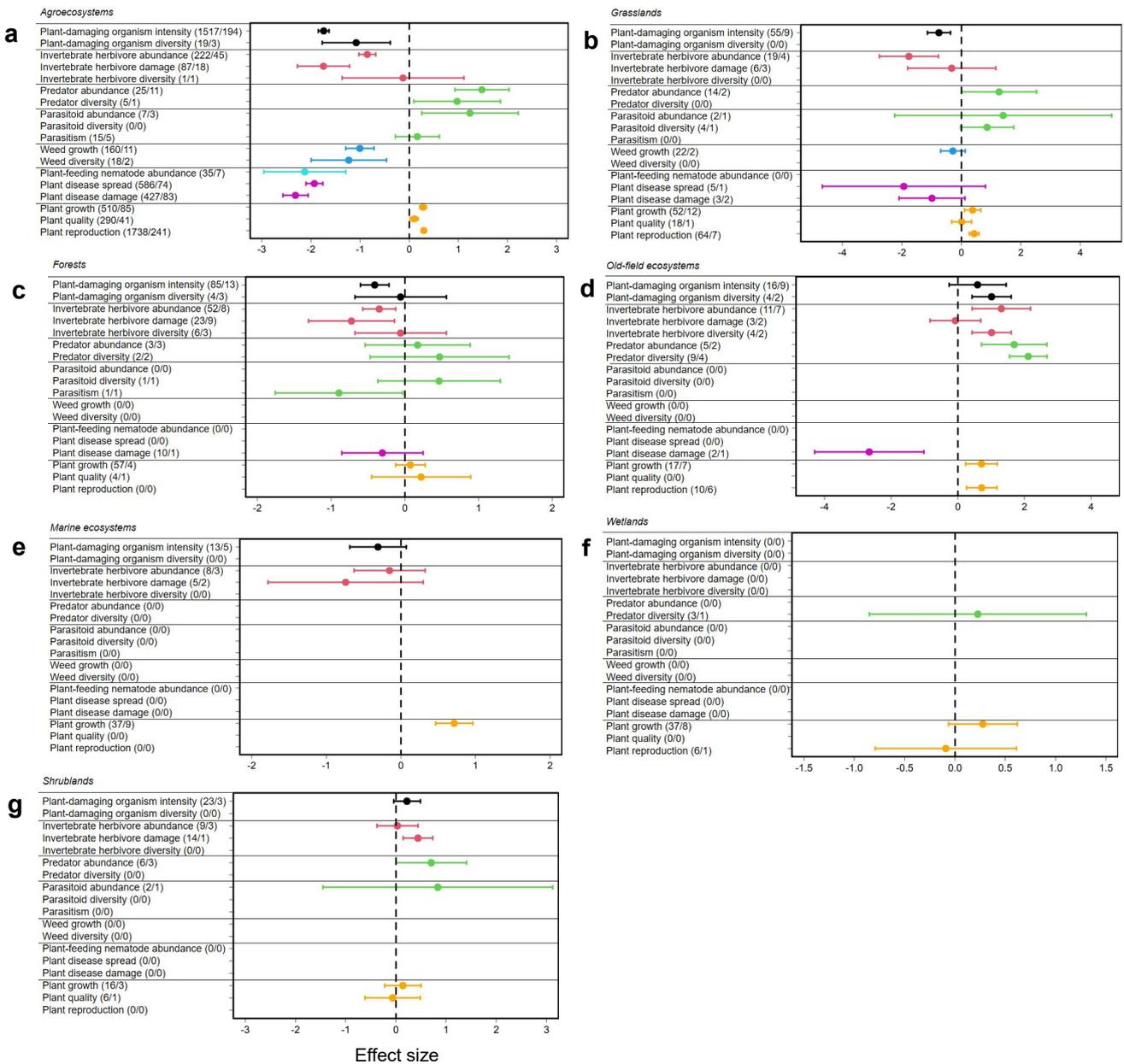
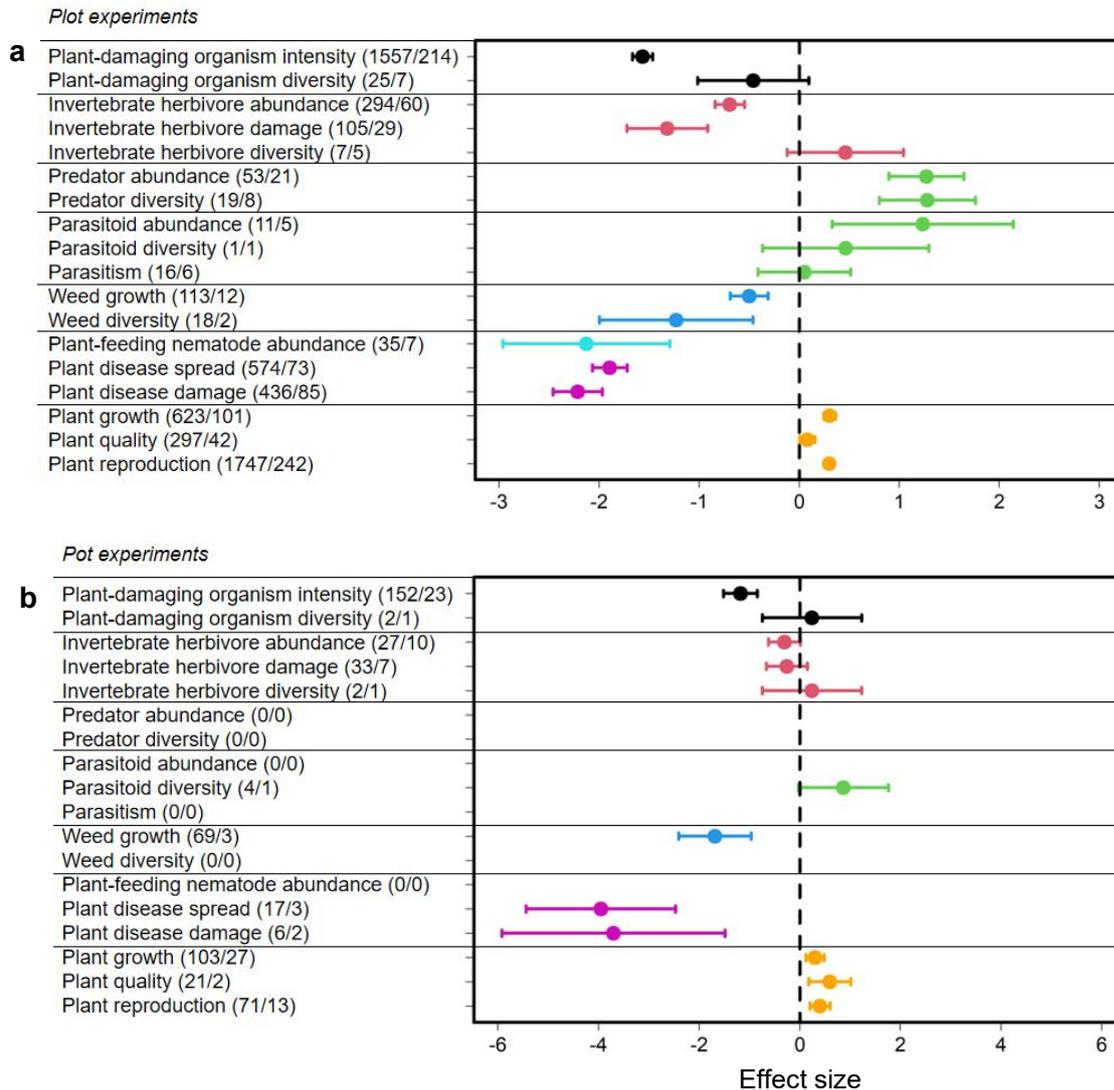


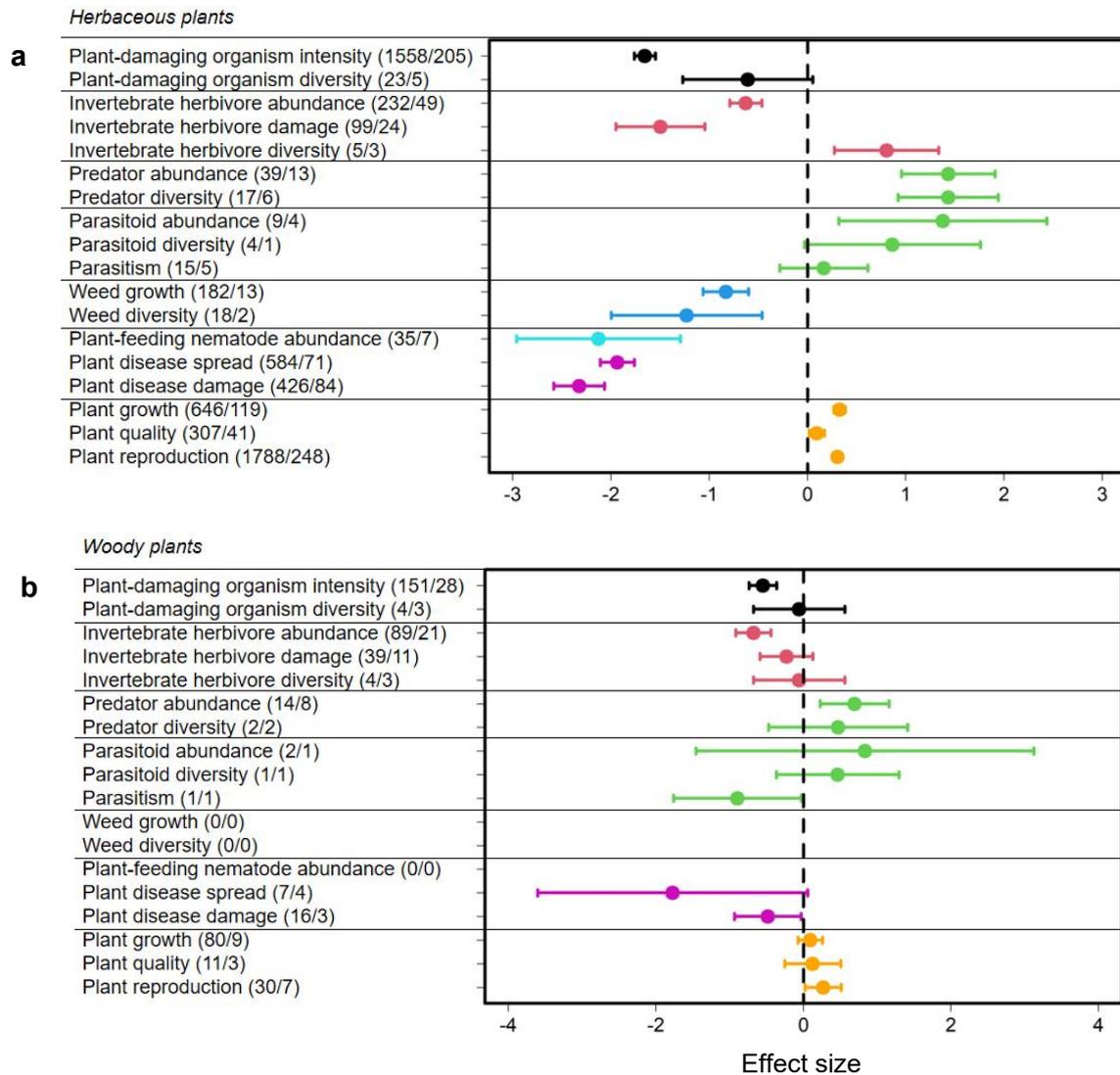
Fig. 3 | Piecemeal structural equation model for the effects of SMD plant genetic diversity on tri-trophic interactions of invertebrate herbivore, natural enemy and plant performances. Plant genetic diversity is shown in dusty blue. Natural enemy performance (predator abundance, predator diversity, parasitoid abundance, parasitoid diversity and parasitism) is shown in pink. Herbivore performance (abundance, damage and diversity of herbivores) is shown in beige circles. Plant performance (growth, quality and reproduction of plants) is shown in teal colour. The blue and red arrows denote positive and negative relationships, respectively, and numbers beside each arrow are the estimated coefficients from piecemeal structural equation models (Supplementary Tables 9, 10). The asterisks indicate the significance at 5% level.



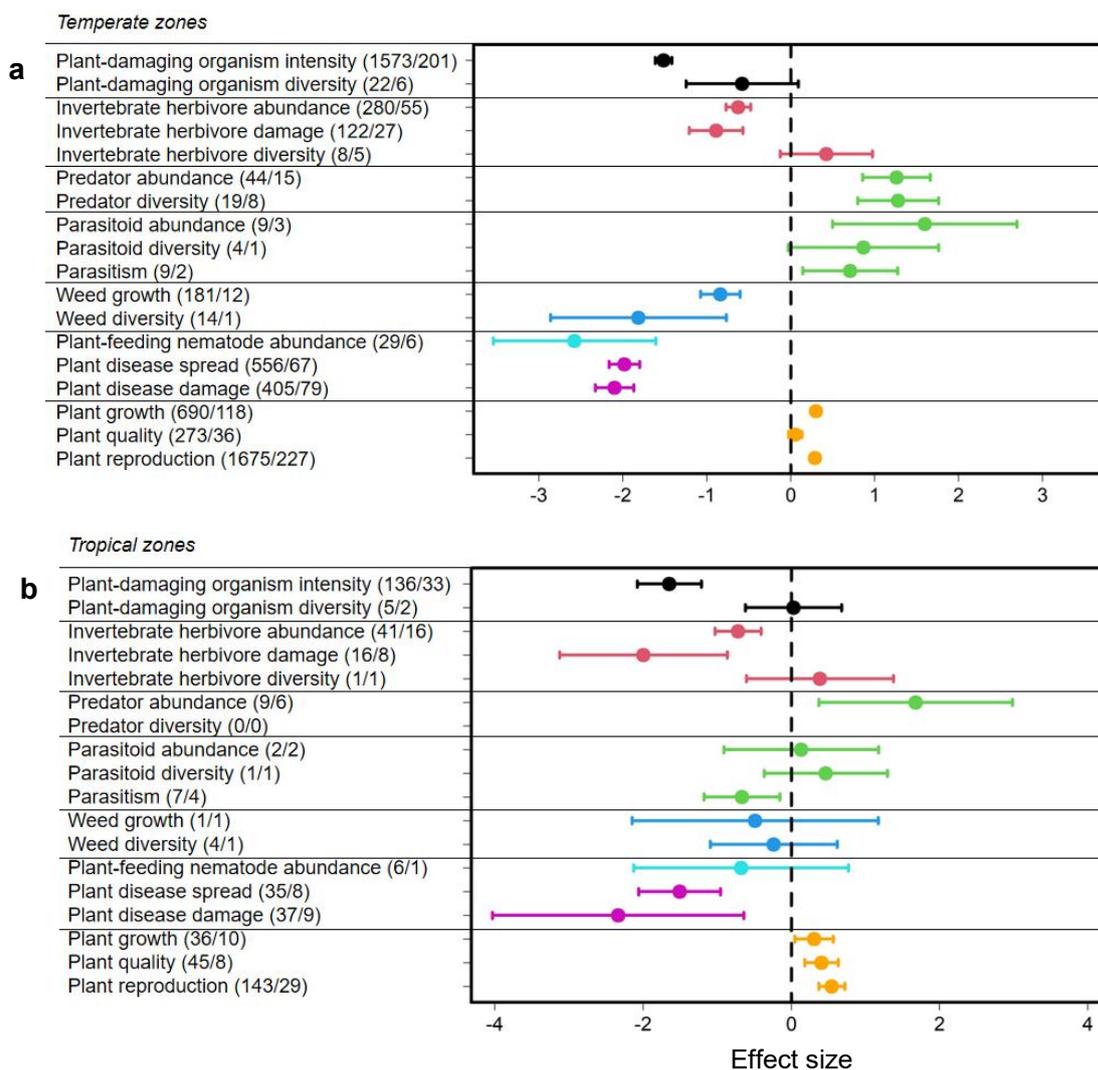
Extended Data Fig. 1 | Mean effect sizes of 18 response categories for the seven trophic groups. a, In agroecosystems. b, In grasslands. c, In forests. d, In old-field ecosystems. e, In marine ecosystems. f, In wetlands. g, In shrublands. Numbers in brackets indicate the numbers of observations and studies. Black, red, green, blue, turquoise, purple and orange lines denote plant-damaging organisms, invertebrate herbivores, natural enemies of herbivores, weeds, plant-feeding nematodes, plant diseases and plants, respectively.



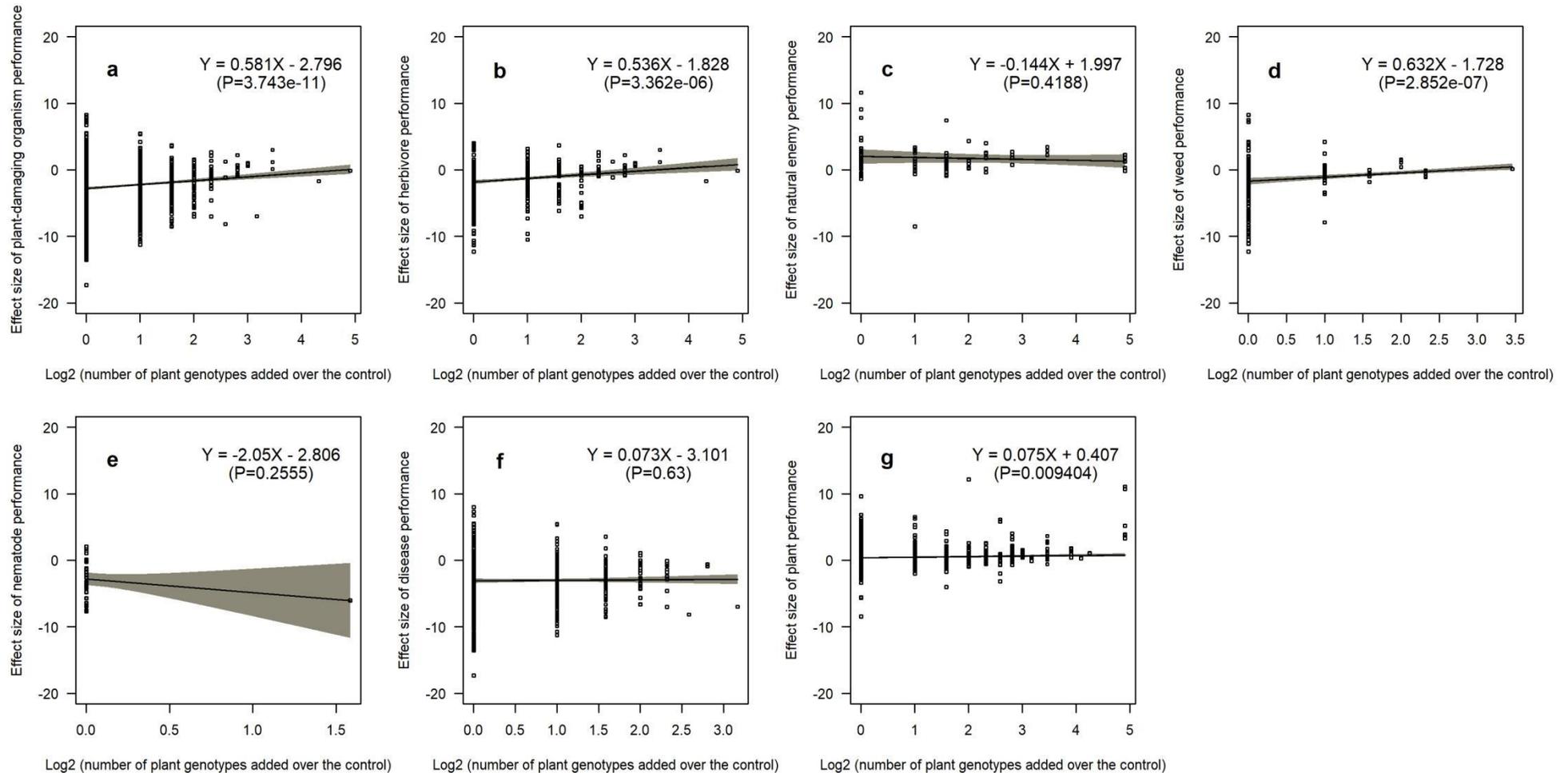
Extended Data Fig. 2 | Mean effect sizes of 18 response categories for the seven trophic groups. a, For plot experiment. **b,** For pot experiment. Numbers in brackets indicate the numbers of observations and studies. Black, red, green, blue, turquoise, purple and orange lines denote plant-damaging organisms, invertebrate herbivores, natural enemies of herbivores, weeds, plant-feeding nematodes, plant diseases and plants, respectively.



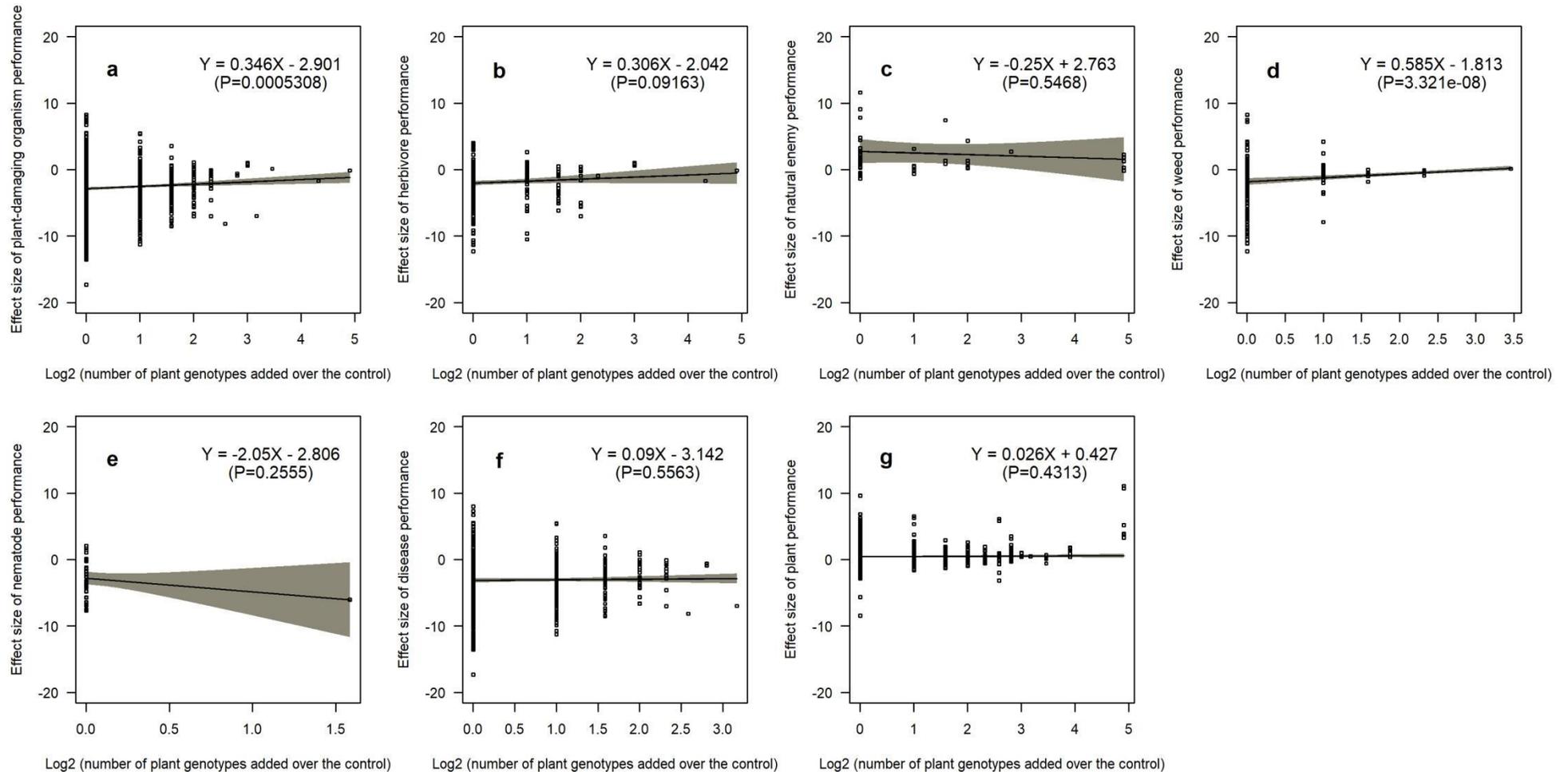
Extended Data Fig. 3 | Mean effect sizes of 18 response categories for the seven trophic groups. a, For herbaceous plants. **b,** For woody plants. Numbers in brackets indicate the numbers of observations and studies. Black, red, green, blue, turquoise, purple and orange lines denote plant-damaging organisms, invertebrate herbivores, natural enemies of herbivores, weeds, plant-feeding nematodes, plant diseases and plants, respectively.



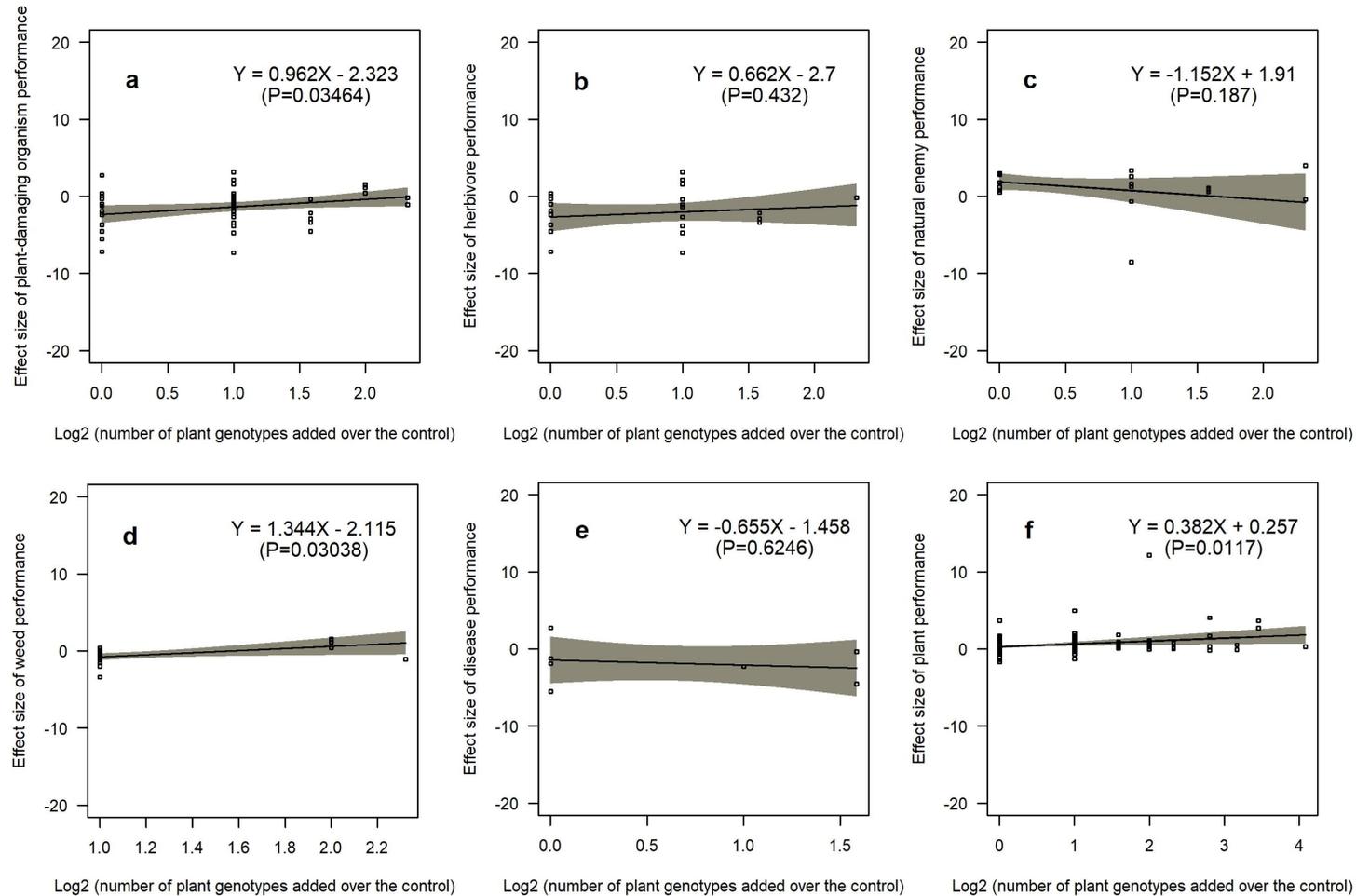
Extended Data Fig. 4 | Mean effect sizes of 18 response categories for the seven trophic groups. a, In temperate zones. **b,** In tropical zones. Numbers in brackets indicate the numbers of observations and studies. Black, red, green, blue, turquoise, purple and orange lines denote plant-damaging organisms, invertebrate herbivores, natural enemies of herbivores, weeds, plant-feeding nematodes, plant diseases and plants, respectively.



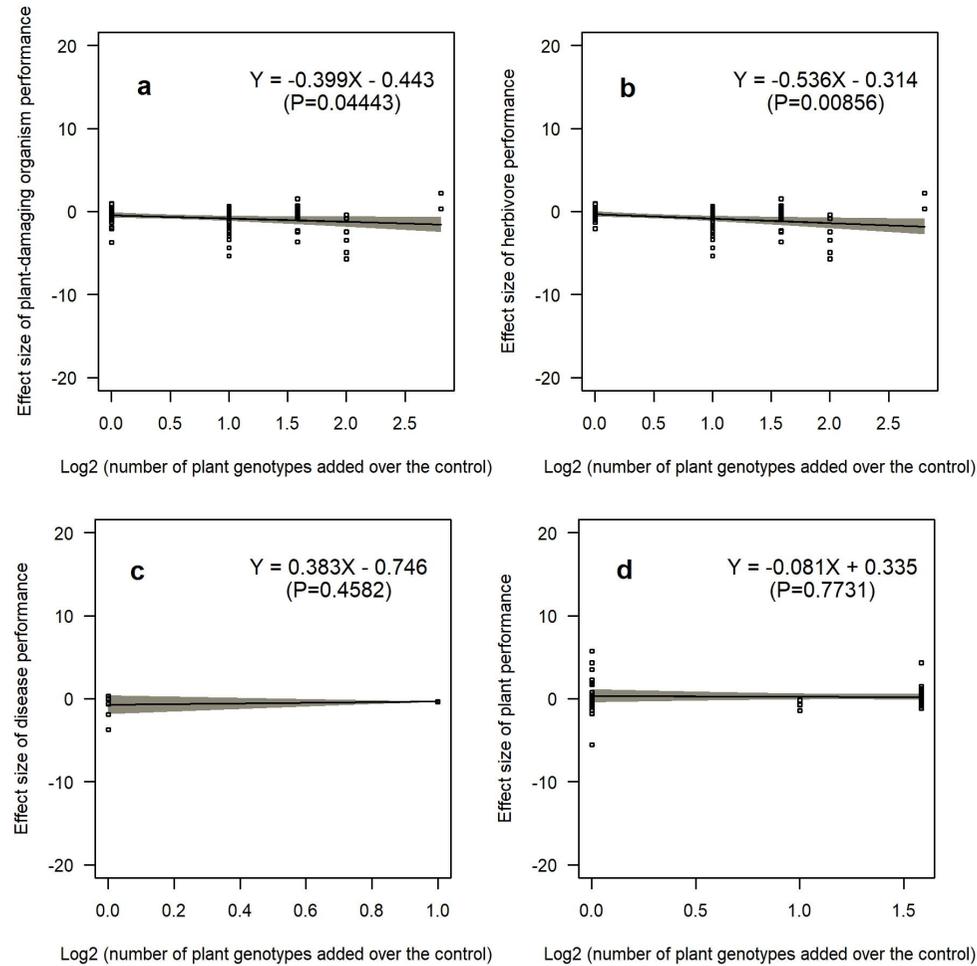
Extended Data Fig. 5 | Relationship between log-transformed number of added genotypes in the plant genetic diversity treatment over the control and the effect sizes along with the fitted meta-regression line across all the studies. Note that a value of zero on the x axis indicates that only one genotype was added (log scale). **a**, Scatter plot for plant-damaging organism performance (1736 observations / 236 studies). **b**, Scatter plot for invertebrate herbivore performance (468 observations / 93 studies). **c**, Scatter plot for natural enemy performance (104 observations / 33 studies). **d**, Scatter plot for weed performance (200 observations / 14 studies). **e**, Scatter plot for plant-feeding nematode performance (35 observations / 7 studies). **f**, Scatter plot for plant disease performance (1033 observations / 136 studies). **g**, Scatter plot for plant performance (2862 observations / 320 studies). Plant-damaging organism performance include herbivore, weed, nematode and disease performances. Herbivore performance includes herbivore abundance, herbivore damage and herbivore diversity. Natural enemy performance includes predator abundance and diversity of predators, abundance and diversity of parasitoids and parasitism. Weed performance includes weed growth and weed diversity. Nematode performance is nematode abundance. Disease performance includes spread and damage of disease. Plant performance includes growth, reproduction and quality of plants. The dark shaded region indicates the 95% confidence interval for the predicted average SMD. The regression model intercepts, slopes and the P-values for the slopes are presented.



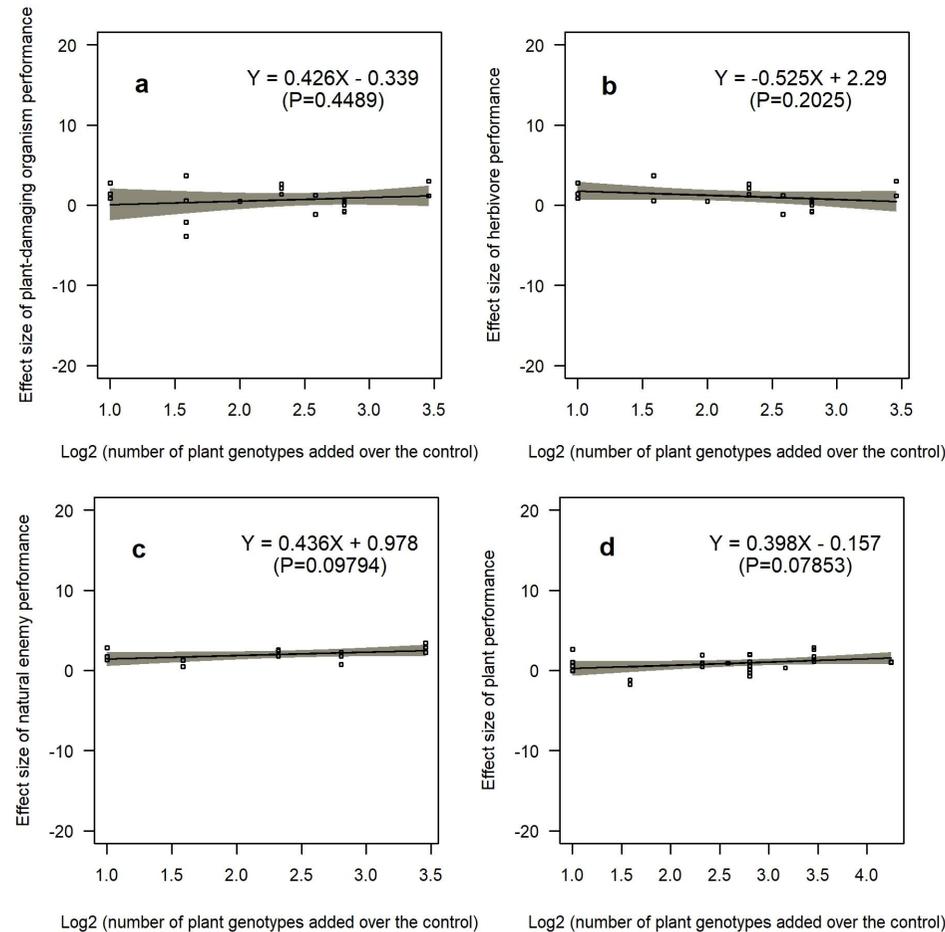
Extended Data Fig. 6 | Relationship between log-transformed number of added genotypes in the plant genetic diversity treatment over the control and the effect sizes along with the fitted meta-regression line on agroecosystems. **a**, Scatter plot for plant-damaging organism performance (1536 observations / 195 studies). **b**, Scatter plot for invertebrate herbivore performance (311 observations / 57 studies). **c**, Scatter plot for natural enemy performance (52 observations / 17 studies). **d**, Scatter plot for weed performance (178 observations / 12 studies). **e**, Scatter plot for plant-feeding nematode performance (35 observations / 7 studies). **f**, Scatter plot for plant disease performance (1013 observations / 131 studies). **g**, Scatter plot for plant performance (2538 observations / 267 studies). Plant-damaging organism performance include herbivore, weed, nematode and disease performances. Herbivore performance includes herbivore abundance, herbivore damage and herbivore diversity. Natural enemy performance includes predator abundance and diversity of predators, abundance and diversity of parasitoids and parasitism. Weed performance includes weed growth and weed diversity. Nematode performance is nematode abundance. Disease performance includes spread and damage of disease. Plant performance includes growth, reproduction and quality of plants. The dark shaded region indicates the 95% confidence interval for the predicted average SMD. The regression model intercepts, slopes and the P-values for the slopes are presented.



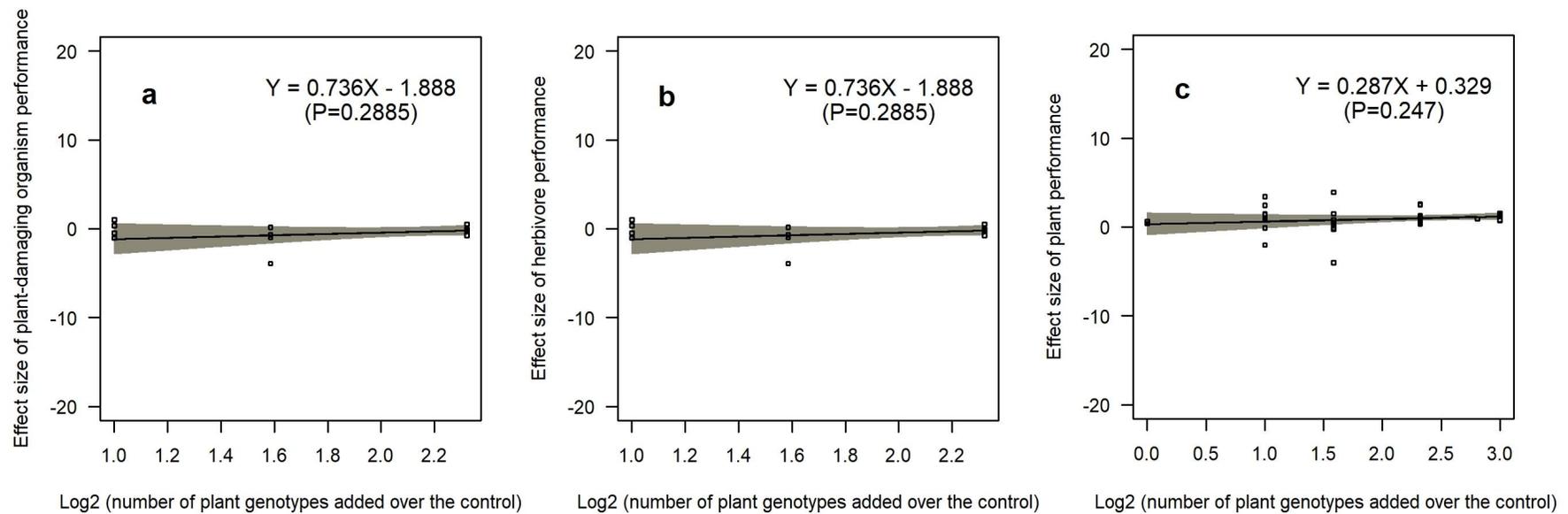
Extended Data Fig. 7 | Relationship between log-transformed number of added genotypes in the plant genetic diversity treatment over the control and the effect sizes along with the fitted meta-regression line on grasslands. **a**, Scatter plot for plant-damaging organism performance (55 observations / 9 studies). **b**, Scatter plot for invertebrate herbivore performance (25 observations / 5 studies). **c**, Scatter plot for natural enemy performance (20 observations / 3 studies). **d**, Scatter plot for weed performance (22 observations / 2 studies). **e**, Scatter plot for plant disease performance (8 observations / 3 studies). **f**, Scatter plot for plant performance (134 observations / 17 studies). Plant-damaging organism performance include herbivore, weed, nematode and disease performances. No scatter plots were found for plant-feeding nematode (i.e., 0 observations / 0 studies). Herbivore performance includes herbivore abundance, herbivore damage and herbivore diversity. Natural enemy performance includes predator abundance and diversity of predators, abundance and diversity of parasitoids and parasitism. Weed performance includes weed growth and weed diversity. Nematode performance is nematode abundance. Disease performance includes spread and damage of disease. Plant performance includes growth, reproduction and quality of plants. The dark shaded region indicates the 95% confidence interval for the predicted average SMD. The regression model intercepts, slopes and the P-values for the slopes are presented.



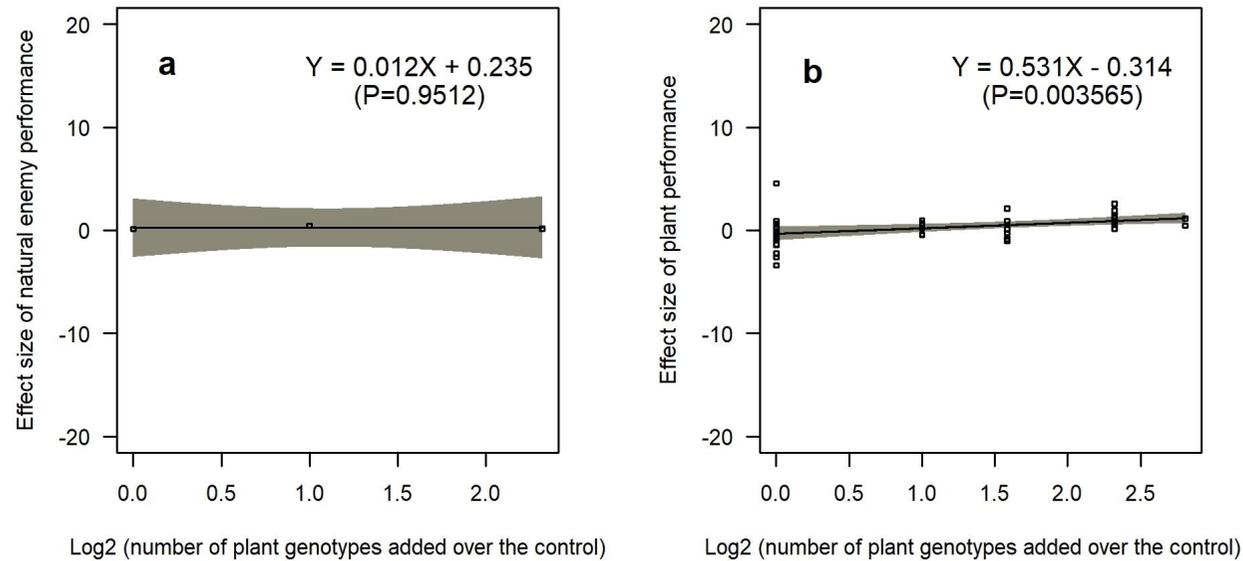
Extended Data Fig. 8 | Relationship between log-transformed number of added genotypes in the plant genetic diversity treatment over the control and the effect sizes along with the fitted meta-regression line on forests. **a**, Scatter plot for plant-damaging organism performance (89 observations / 14 studies). **b**, Scatter plot for invertebrate herbivore performance (79 observations / 14 studies). **c**, Scatter plot for plant disease performance (10 observations / 1 studies). **d**, Scatter plot for plant performance (61 observations / 4 studies). No relationship between added genotypes and natural enemy performance (7 observations / 5 studies) was found. No scatter plots were found for weed performance (0 observations / 0 studies) or plant-feeding nematode performance (0 observations / 0 studies). Plant-damaging organism performance include herbivore, weed, nematode and disease performances. Herbivore performance includes herbivore abundance, herbivore damage and herbivore diversity. Natural enemy performance includes predator abundance and diversity of predators, abundance and diversity of parasitoids and parasitism. Weed performance includes weed growth and weed diversity. Nematode performance is nematode abundance. Disease performance includes spread and damage of disease. Plant performance includes growth, reproduction and quality of plants. The dark shaded region indicates the 95% confidence interval for the predicted average SMD. The regression model intercepts, slopes and the P-values for the slopes are presented.



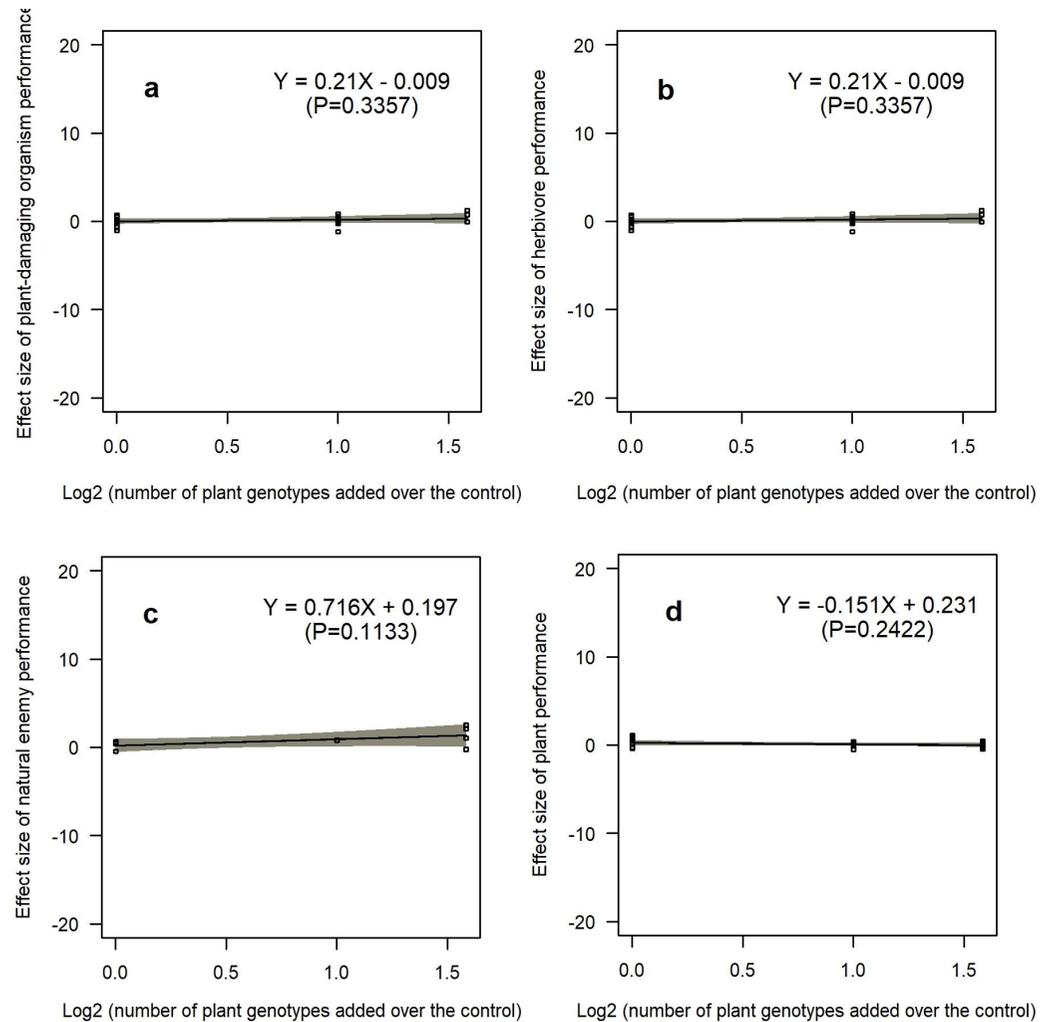
Extended Data Fig. 9 | Relationship between log-transformed number of added genotypes in the plant genetic diversity treatment over the control and the effect sizes along with the fitted meta-regression line on old-field ecosystems. **a**, Scatter plot for plant-damaging organism performance (20 observations / 10 studies). **b**, Scatter plot for invertebrate herbivore performance (18 observations / 9 studies). **c**, Scatter plot for natural enemy performance (14 observations / 4 studies). **d**, Scatter plot for plant performance (27 observations / 11 studies). No relationship between added genotypes and plant disease performance (2 observations / 1 studies) was found. No scatter plots were found for weed performance (0 observations / 0 studies) or plant-feeding nematode performance (0 observations / 0 studies). Plant-damaging organism performance include herbivore, weed, nematode and disease performances. Herbivore performance includes herbivore abundance, herbivore damage and herbivore diversity. Natural enemy performance includes predator abundance and diversity of predators, abundance and diversity of parasitoids and parasitism. Weed performance includes weed growth and weed diversity. Nematode performance is nematode abundance. Disease performance includes spread and damage of disease. Plant performance includes growth, reproduction and quality of plants. The dark shaded region indicates respectively the 95% confidence interval for the predicted average SMD. The regression model intercepts, slopes and the P-values for the slopes are presented.



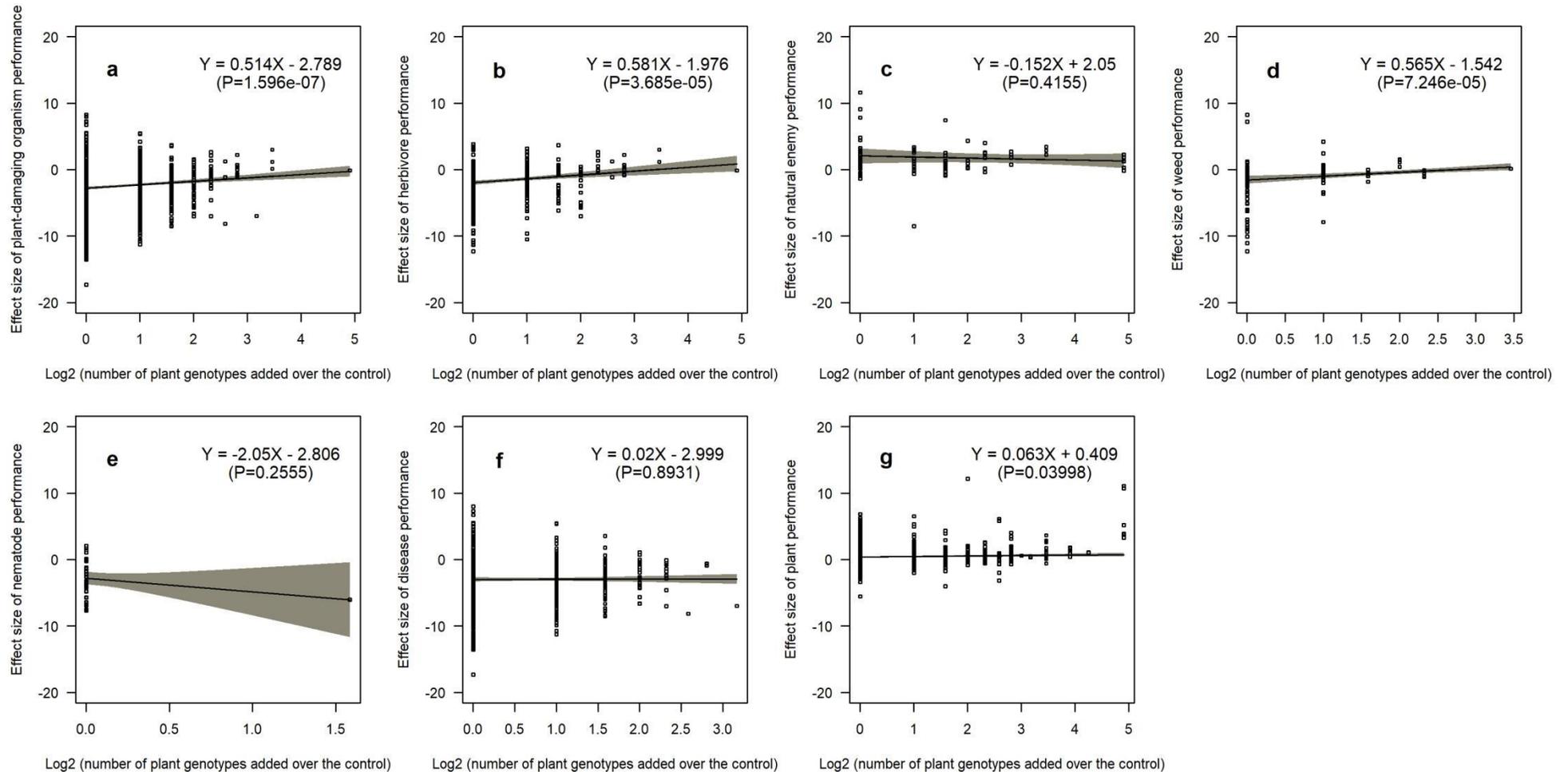
Extended Data Fig. 10 | Relationship between log-transformed number of added genotypes in the plant genetic diversity treatment over the control and the effect sizes along with the fitted meta-regression line on marine ecosystems. **a**, Scatter plot for plant-damaging organism performance (13 observations / 5 studies). **b**, Scatter plot for invertebrate herbivore performance (13 observations / 5 studies). **c**, Scatter plot for plant performance (37 observations / 9 studies). No scatter plots were found for natural enemy performance (0 observations / 0 studies), weed performance (0 observations / 0 studies), plant-feeding nematode performance (0 observations / 0 studies) or plant disease performance (0 observations / 0 studies). Plant-damaging organism performance include herbivore, weed, nematode and disease performances. Herbivore performance includes herbivore abundance, herbivore damage and herbivore diversity. Natural enemy performance includes predator abundance and diversity of predators, abundance and diversity of parasitoids and parasitism. Weed performance includes weed growth and weed diversity. Nematode performance is nematode abundance. Disease performance includes spread and damage of disease. Plant performance includes growth, reproduction and quality of plants. The dark shaded region indicates the 95% confidence interval for the predicted average SMD. The regression model intercepts, slopes and the P-values for the slopes are presented.



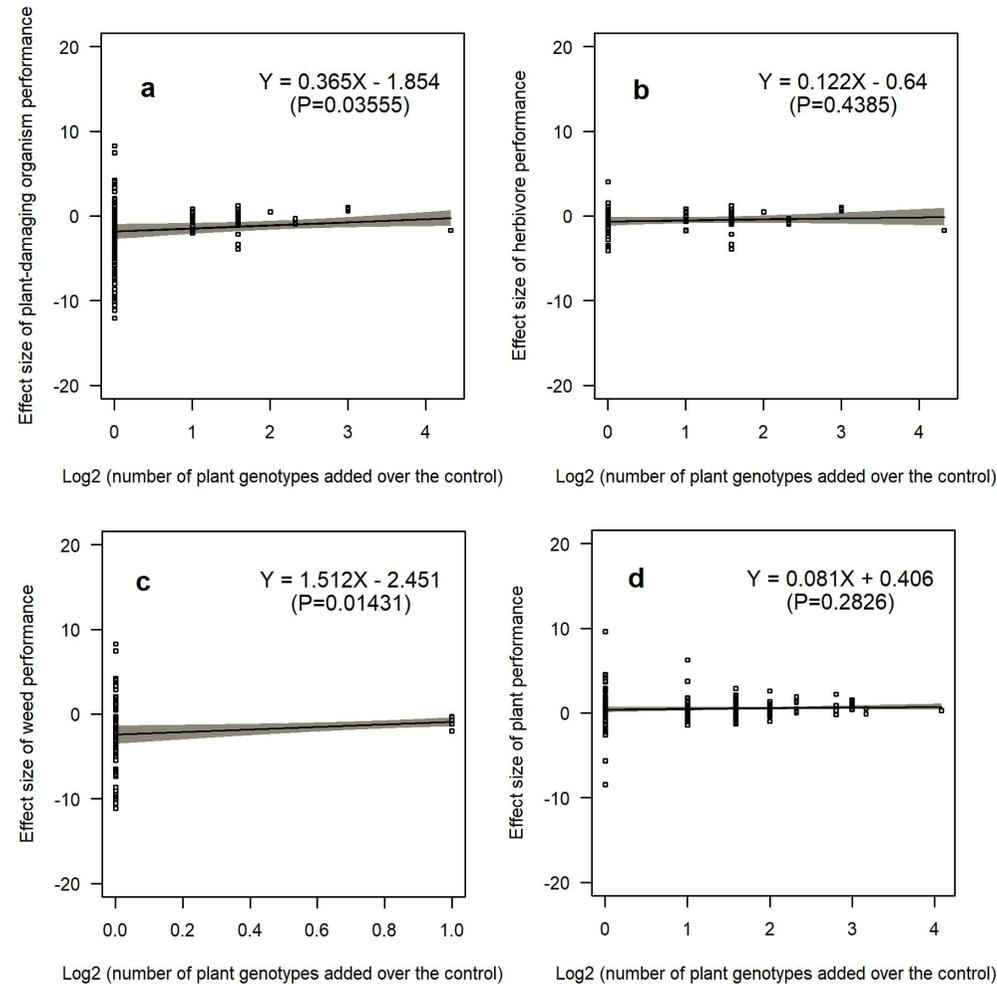
Extended Data Fig. 11 | Relationship between log-transformed number of added genotypes in the plant genetic diversity treatment over the control and the effect sizes along with the fitted meta-regression line on wetlands. **a**, Scatter plot for natural enemy performance (3 observations / 1 studies). **b**, Scatter plot for plant performance (43 observations / 9 studies). No scatter plots were found for plant-damaging organism performance (0 observations / 0 studies), invertebrate herbivore performance (0 observations / 0 studies), weed performance (0 observations / 0 studies), plant-feeding nematode performance (0 observations / 0 studies) or plant disease performance (0 observations / 0 studies). Plant-damaging organism performance include herbivore, weed, nematode and disease performances. Herbivore performance includes herbivore abundance, herbivore damage and herbivore diversity. Natural enemy performance includes predator abundance and diversity of predators, abundance and diversity of parasitoids and parasitism. Weed performance includes weed growth and weed diversity. Nematode performance is nematode abundance. Disease performance includes spread and damage of disease. Plant performance includes growth, reproduction and quality of plants. The dark shaded region indicates the 95% confidence interval for the predicted average SMD. The regression model intercepts, slopes and the P-values for the slopes are presented.



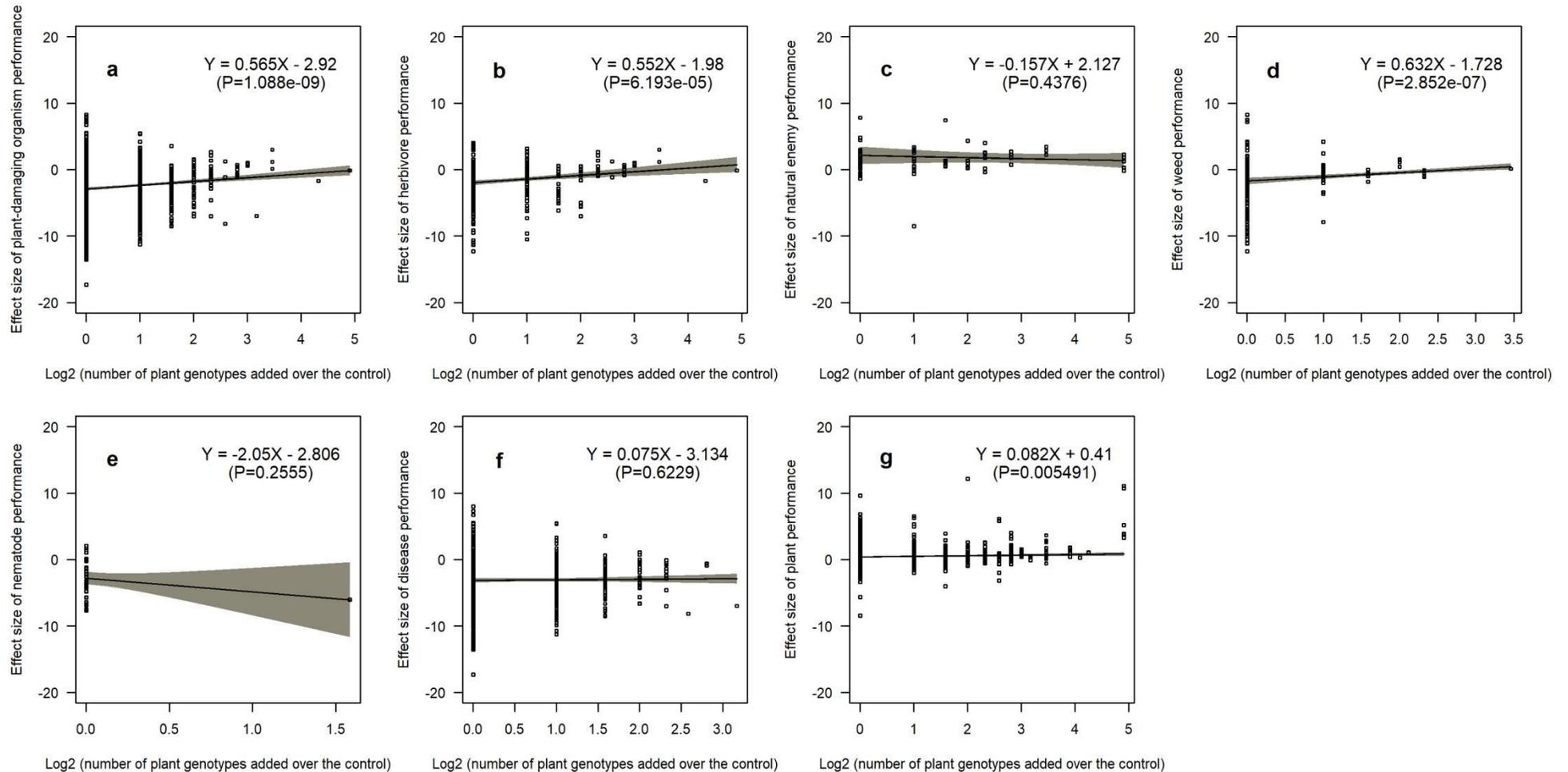
Extended Data Fig. 12 | Relationship between log-transformed number of added genotypes in the plant genetic diversity treatment over the control and the effect sizes along with the fitted meta-regression line on shrublands. **a**, Scatter plot for plant-damaging organism performance (23 observations / 3 studies). **b**, Scatter plot for invertebrate herbivore performance (23 observations / 3 studies). **c**, Scatter plot for natural enemy performance (8 observations / 3 studies). **d**, Scatter plot for plant performance (22 observations / 3 studies). No scatter plots were found for weed performance (0 observations / 0 studies), plant-feeding nematode performance (0 observations / 0 studies) or plant disease performance (0 observations / 0 studies). Plant-damaging organism performance include herbivore, weed, nematode and disease performances. Herbivore performance includes herbivore abundance, herbivore damage and herbivore diversity. Natural enemy performance includes predator abundance and diversity of predators, abundance and diversity of parasitoids and parasitism. Weed performance includes weed growth and weed diversity. Nematode performance is nematode abundance. Disease performance includes spread and damage of disease. Plant performance includes growth, reproduction and quality of plants. The dark shaded region indicates the 95% confidence interval for the predicted average SMD. The regression model intercepts, slopes and the P-values for the slopes are presented.



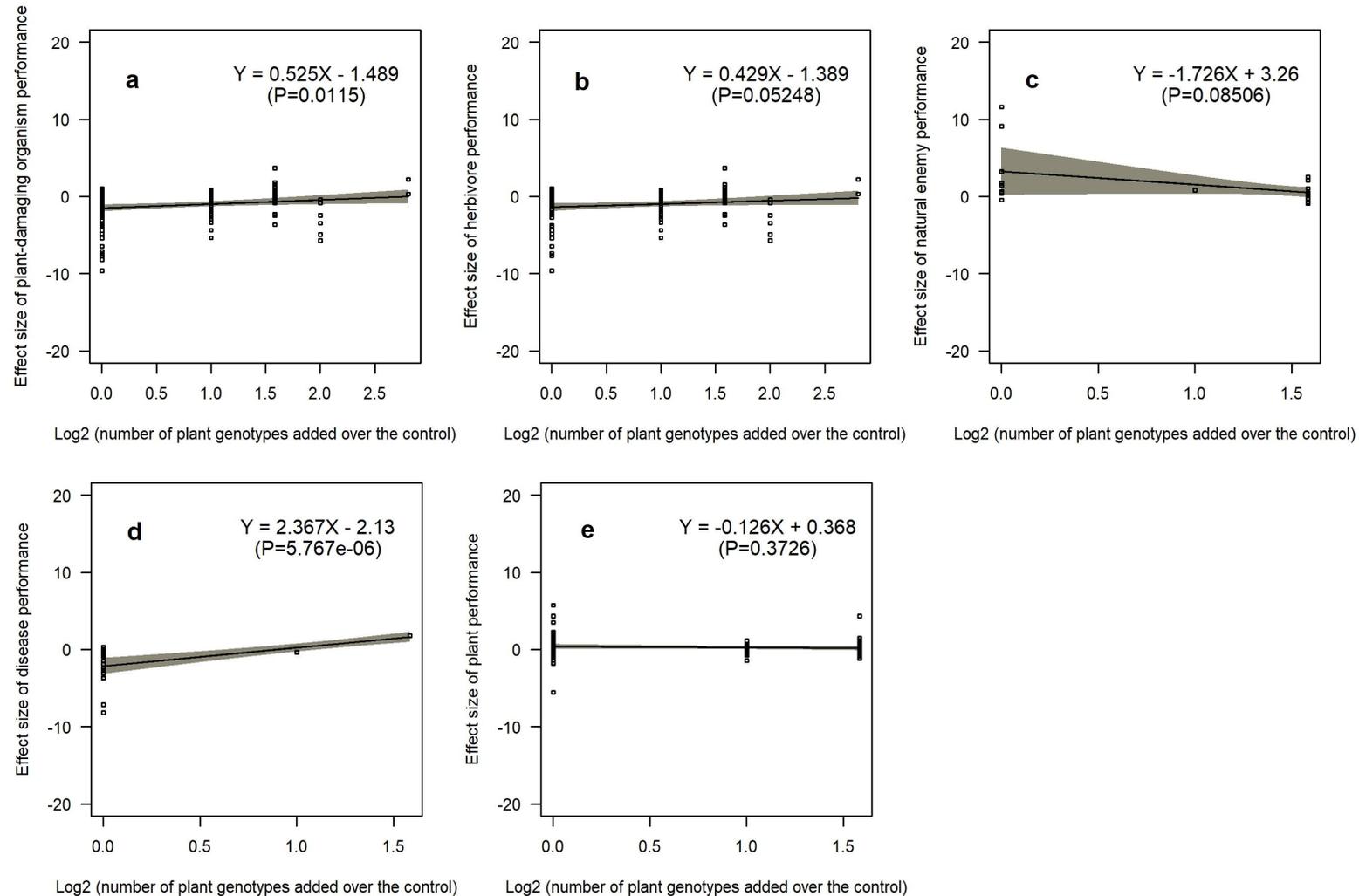
Extended Data Fig. 13 | Relationship between log-transformed number of added genotypes in the plant genetic diversity treatment over the control and the effect sizes along with the fitted meta-regression line in plot experiment. **a**, Scatter plot for plant-damaging organism performance (1582 observations / 216 studies). **b**, Scatter plot for invertebrate herbivore performance (406 observations / 78 studies). **c**, Scatter plot for natural enemy performance (100 observations / 32 studies). **d**, Scatter plot for weed performance (131 observations / 13 studies). **e**, Scatter plot for plant-feeding nematode performance (35 observations / 7 studies). **f**, Scatter plot for plant disease performance (1010 observations / 132 studies). **g**, Scatter plot for plant performance (2667 observations / 286 studies). Plant-damaging organism performance include herbivore, weed, nematode and disease performances. Herbivore performance includes herbivore abundance, herbivore damage and herbivore diversity. Natural enemy performance includes predator abundance and diversity of predators, abundance and diversity of parasitoids and parasitism. Weed performance includes weed growth and weed diversity. Nematode performance is nematode abundance. Disease performance includes spread and damage of disease. Plant performance includes growth, reproduction and quality of plants. The dark shaded region indicates the 95% confidence interval for the predicted average SMD. The regression model intercepts, slopes and the P-values for the slopes are presented.



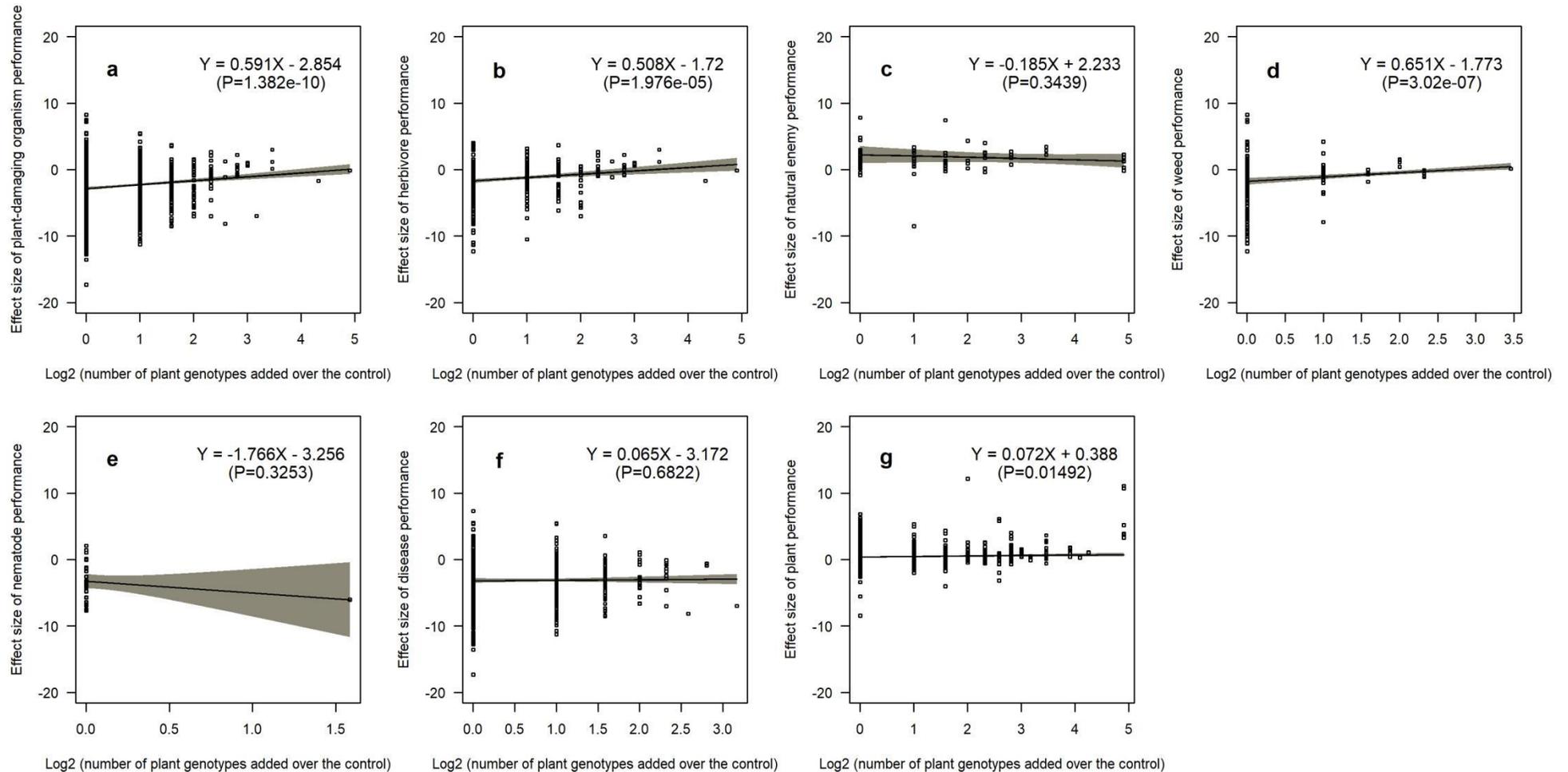
Extended Data Fig. 14 | Relationship between log-transformed number of added genotypes in the plant genetic diversity treatment over the control and the effect sizes along with the fitted meta-regression line in pot experiment. **a**, Scatter plot for plant-damaging organism performance (154 observations / 24 studies). **b**, Scatter plot for invertebrate herbivore performance (62 observations / 16 studies). **c**, Scatter plot for weed performance (69 observations / 3 studies). **d**, Scatter plot for plant performance (195 observations / 34 studies). No relationships between added genotypes and natural enemy performance (4 observations / 1 studies) and between added genotypes and plant disease performance (23 observations / 5 studies) were found. No scatter plots were found for plant-feeding nematode performance (0 observations / 0 studies). Plant-damaging organism performance include herbivore, weed, nematode and disease performances. Herbivore performance includes herbivore abundance, herbivore damage and herbivore diversity. Natural enemy performance includes predator abundance and diversity of predators, abundance and diversity of parasitoids and parasitism. Weed performance includes weed growth and weed diversity. Nematode performance is nematode abundance. Disease performance includes spread and damage of disease. Plant performance includes growth, reproduction and quality of plants. The dark shaded region indicates the 95% confidence interval for the predicted average SMD. The regression model intercepts, slopes and the P-values for the slopes are presented.



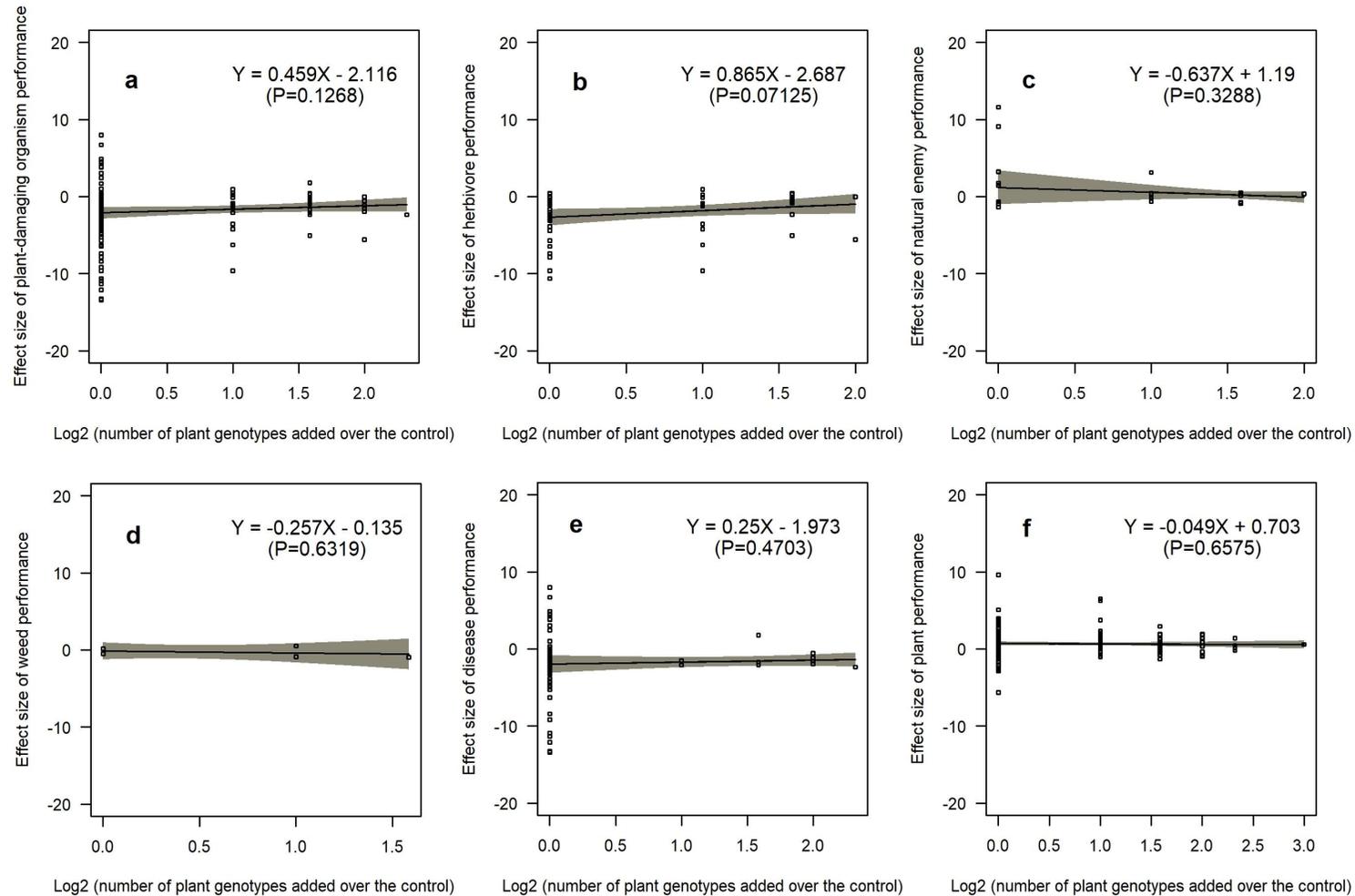
Extended Data Fig. 15 | Relationship between log-transformed number of added genotypes in the plant genetic diversity treatment over the control and the effect sizes along with the fitted meta-regression line for herbaceous plants. **a**, Scatter plot for plant-damaging organism performance (1537 observations / 207 studies). **b**, Scatter plot for invertebrate herbivore performance (340 observations / 66 studies). **c**, Scatter plot for natural enemy performance (84 observations / 23 studies). **d**, Scatter plot for weed performance (200 observations / 14 studies). **e**, Scatter plot for plant-feeding nematode performance (35 observations / 7 studies). **f**, Scatter plot for plant disease performance (1010 observations / 131 studies). **g**, Scatter plot for plant performance (2741 observations / 306 studies). Plant-damaging organism performance include herbivore, weed, nematode and disease performances. Herbivore performance includes herbivore abundance, herbivore damage and herbivore diversity. Natural enemy performance includes predator abundance and diversity of predators, abundance and diversity of parasitoids and parasitism. Weed performance includes weed growth and weed diversity. Nematode performance is nematode abundance. Disease performance includes spread and damage of disease. Plant performance includes growth, reproduction and quality of plants. The dark shaded region indicates the 95% confidence interval for the predicted average SMD. The regression model intercepts, slopes and the P-values for the slopes are presented.



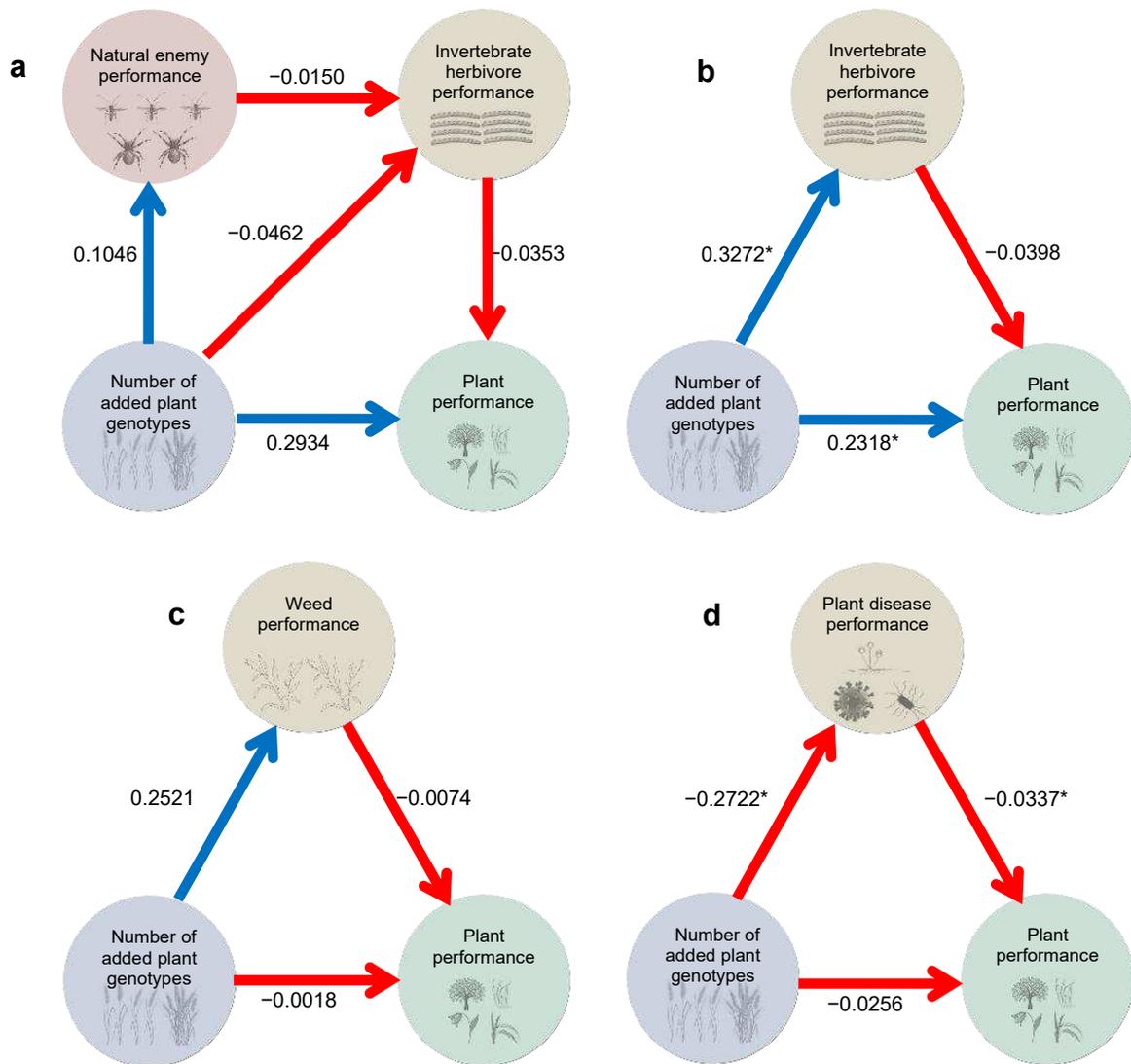
Extended Data Fig. 16 | Relationship between log-transformed number of added genotypes in the plant genetic diversity treatment over the control and the effect sizes along with the fitted meta-regression line for woody plants. a, Scatter plot for plant-damaging organism performance (157 observations / 29 studies). **b,** Scatter plot for invertebrate herbivore performance (134 observations / 28 studies). **c,** Scatter plot for natural enemy performance (20 observations / 10 studies). **d,** Scatter plot for plant disease performance (23 observations / 5 studies). **e,** Scatter plot for plant performance (121 observations / 14 studies). No scatter plots were found for weed performance (0 observations / 0 studies) or plant-feeding nematode performance (0 observations / 0 studies). Plant-damaging organism performance include herbivore, weed, nematode and disease performances. Herbivore performance includes herbivore abundance, herbivore damage and herbivore diversity. Natural enemy performance includes predator abundance and diversity of predators, abundance and diversity of parasitoids and parasitism. Weed performance includes weed growth and weed diversity. Nematode performance is nematode abundance. Disease performance includes spread and damage of disease. Plant performance includes growth, reproduction and quality of plants. The dark shaded region indicates the 95% confidence interval for the predicted average SMD. The regression model intercepts, slopes and the P-values for the slopes are presented.



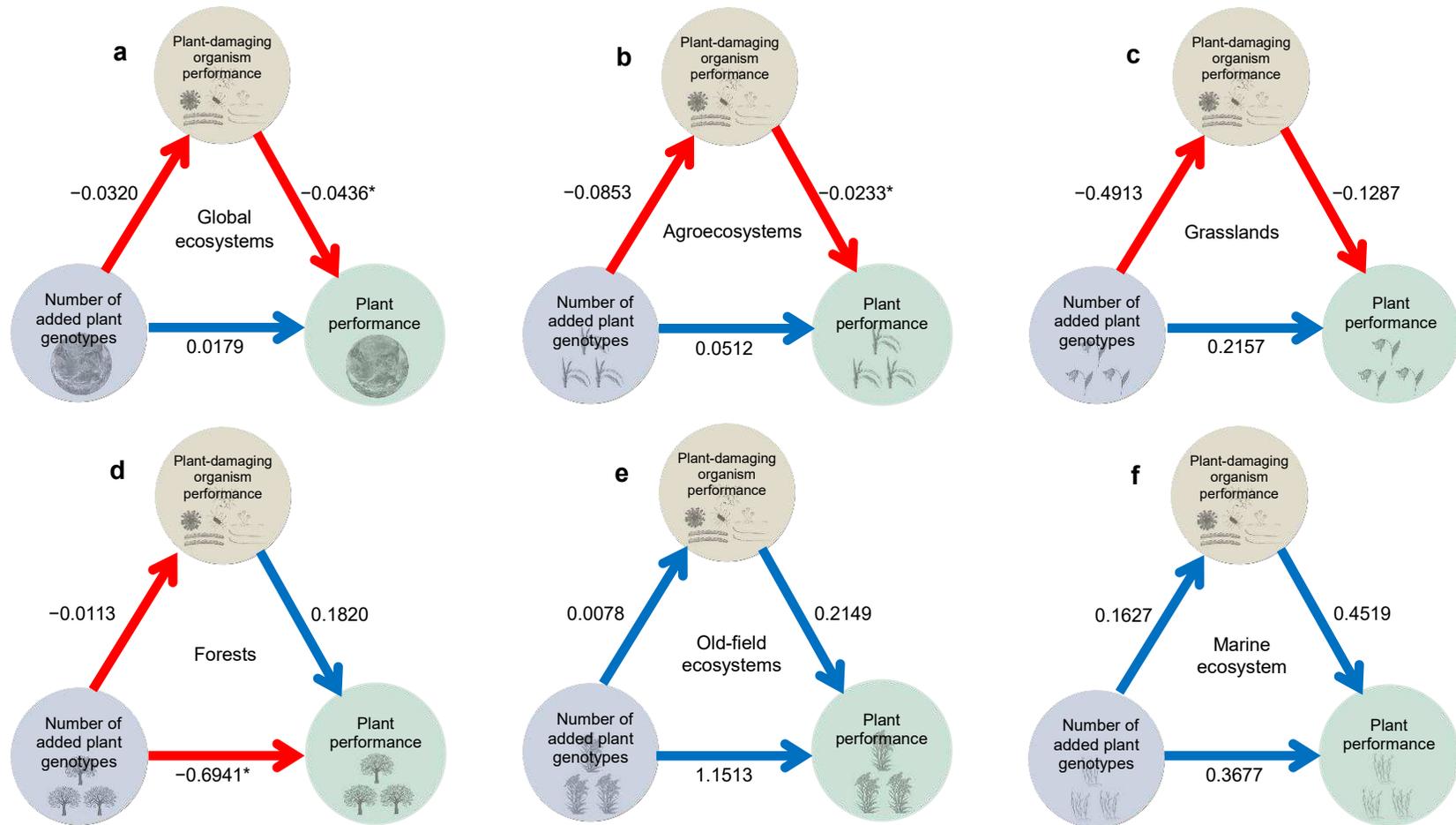
Extended Data Fig. 17 | Relationship between log-transformed number of added genotypes in the plant genetic diversity treatment over the control and the effect sizes along with the fitted meta-regression line for temperate zones. **a**, Scatter plot for plant-damaging organism performance (1559 observations / 204 studies). **b**, Scatter plot for invertebrate herbivore performance (410 observations / 74 studies). **c**, Scatter plot for natural enemy performance (85 observations / 23 studies). **d**, Scatter plot for weed performance (195 observations / 12 studies). **e**, Scatter plot for plant-feeding nematode performance (29 observations / 6 studies). **f**, Scatter plot for plant disease performance (961 observations / 122 studies). **g**, Scatter plot for plant performance (2638 observations / 289 studies). Plant-damaging organism performance include herbivore, weed, nematode and disease performances. Herbivore performance includes herbivore abundance, herbivore damage and herbivore diversity. Natural enemy performance includes predator abundance and diversity of predators, abundance and diversity of parasitoids and parasitism. Weed performance includes weed growth and weed diversity. Nematode performance is nematode abundance. Disease performance includes spread and damage of disease. Plant performance includes growth, reproduction and quality of plants. The dark shaded region indicates the 95% confidence interval for the predicted average SMD. The regression model intercepts, slopes and the P-values for the slopes are presented.



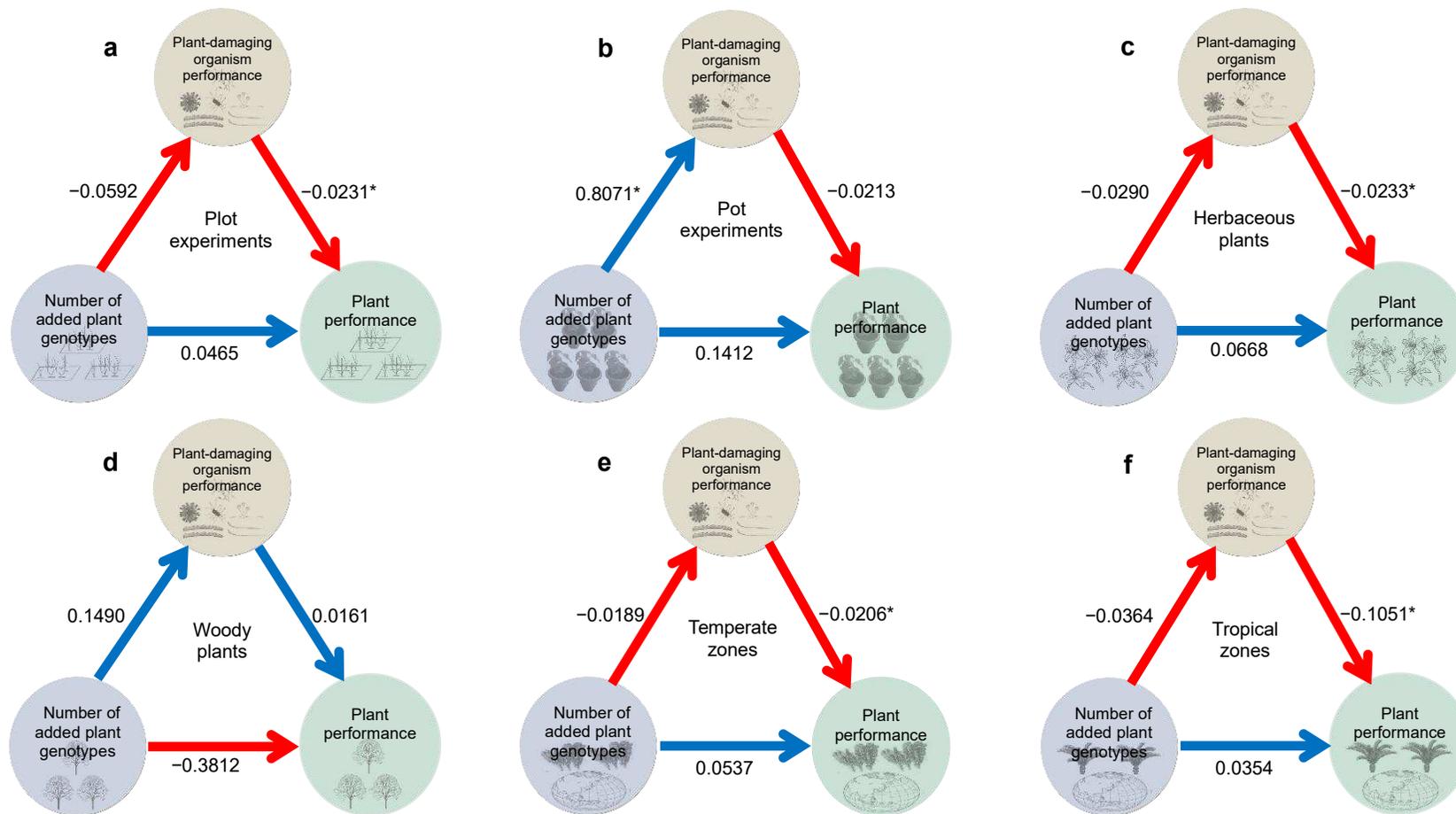
Extended Data Fig. 18 | Relationship between log-transformed number of added genotypes in the plant genetic diversity treatment over the control and the effect sizes along with the fitted meta-regression line for tropical zones. **a**, Scatter plot for plant-damaging organism performance (141 observations / 33 studies). **b**, Scatter plot for invertebrate herbivore performance (58 observations / 20 studies). **c**, Scatter plot for natural enemy performance (19 observations / 11 studies). **d**, Scatter plot for weed performance (5 observations / 2 studies). **e**, Scatter plot for plant disease performance (72 observations / 15 studies). **f**, Scatter plot for plant performance (224 observations / 33 studies). No relationship between added genotypes and plant-feeding nematode performance (6 observations / 1 studies) was found. Plant-damaging organism performance include herbivore, weed, nematode and disease performances. Herbivore performance includes herbivore abundance, herbivore damage and herbivore diversity. Natural enemy performance includes predator abundance and diversity of predators, abundance and diversity of parasitoids and parasitism. Weed performance includes weed growth and weed diversity. Nematode performance is nematode abundance. Disease performance includes spread and damage of disease. Plant performance includes growth, reproduction and quality of plants. The dark shaded region indicates the 95% confidence interval for the predicted average SMD. The regression model intercepts, slopes and the P-values for the slopes are presented.



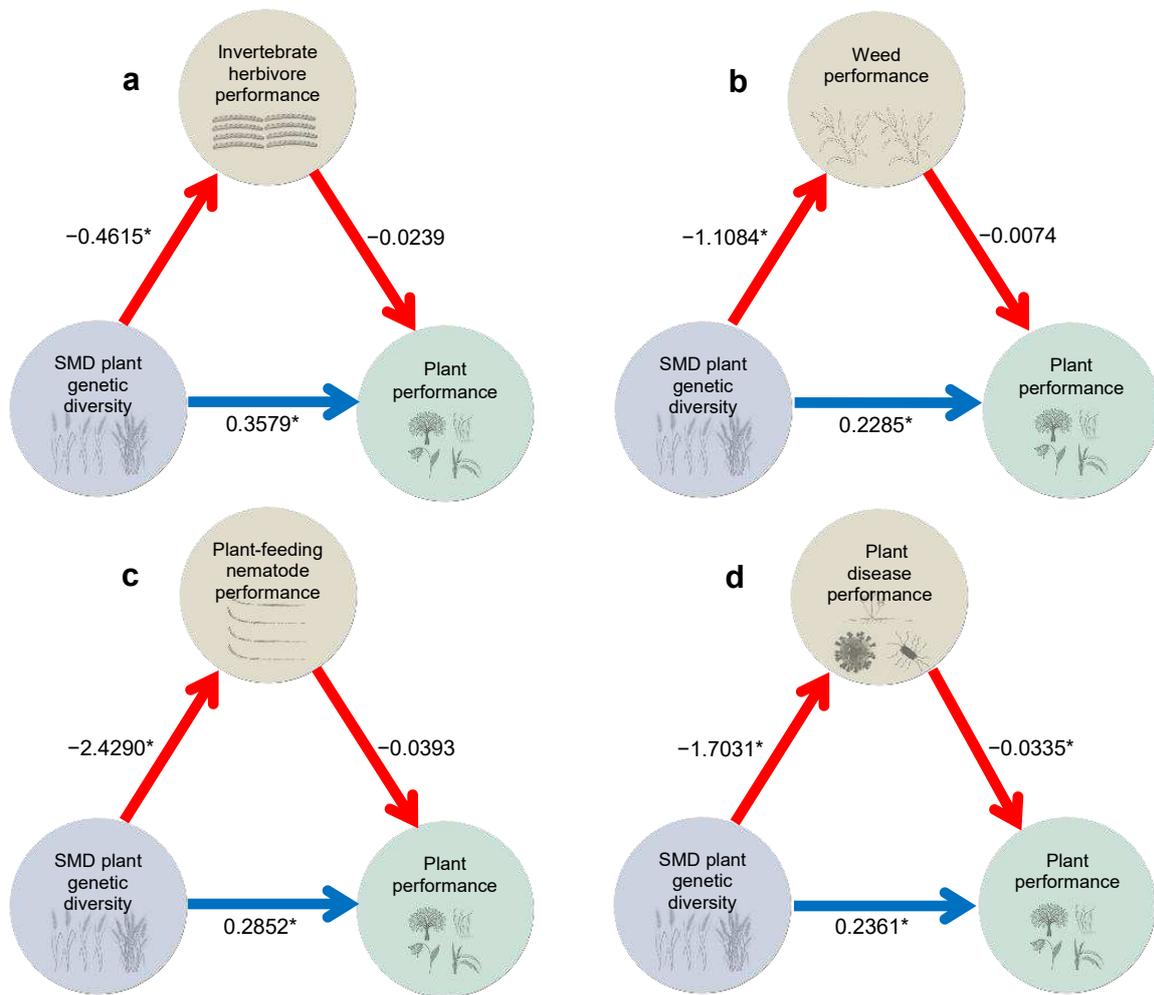
Extended Data Fig. 19 | Path analysis for the effects of number of added plant genotypes in all analyzed ecosystems. a, on tri-trophic interactions of invertebrate herbivore, natural enemy and plant performances. **b**, on bi-trophic interactions of invertebrate herbivore and plant performance. **c**, on bi-trophic interactions of weed and plant performance. **d**, on bi-trophic interactions of plant disease and plant performance. No data are found to test the effects of the number of added plant genotypes on bi-trophic interactions of plant-feeding nematode and plant performance. Herbivore performance, weed performance (growth and diversity of weeds), nematode performance (nematode abundance), and disease performance (disease spread and damage) are shown in beige circles. Plant genetic diversity is shown in dusty blue. Natural enemy performance (predator abundance, predator diversity, parasitoid abundance, parasitoid diversity and parasitism) is shown in pink. Plant performance (growth, quality and reproduction of plants) is shown in teal. The blue and red arrows denote positive and negative relationships, respectively, and numbers beside each arrow are the estimate coefficients for the fitted path-analytic models (Supplementary Tables 9, 10). The asterisks indicate the significance at 5% level.



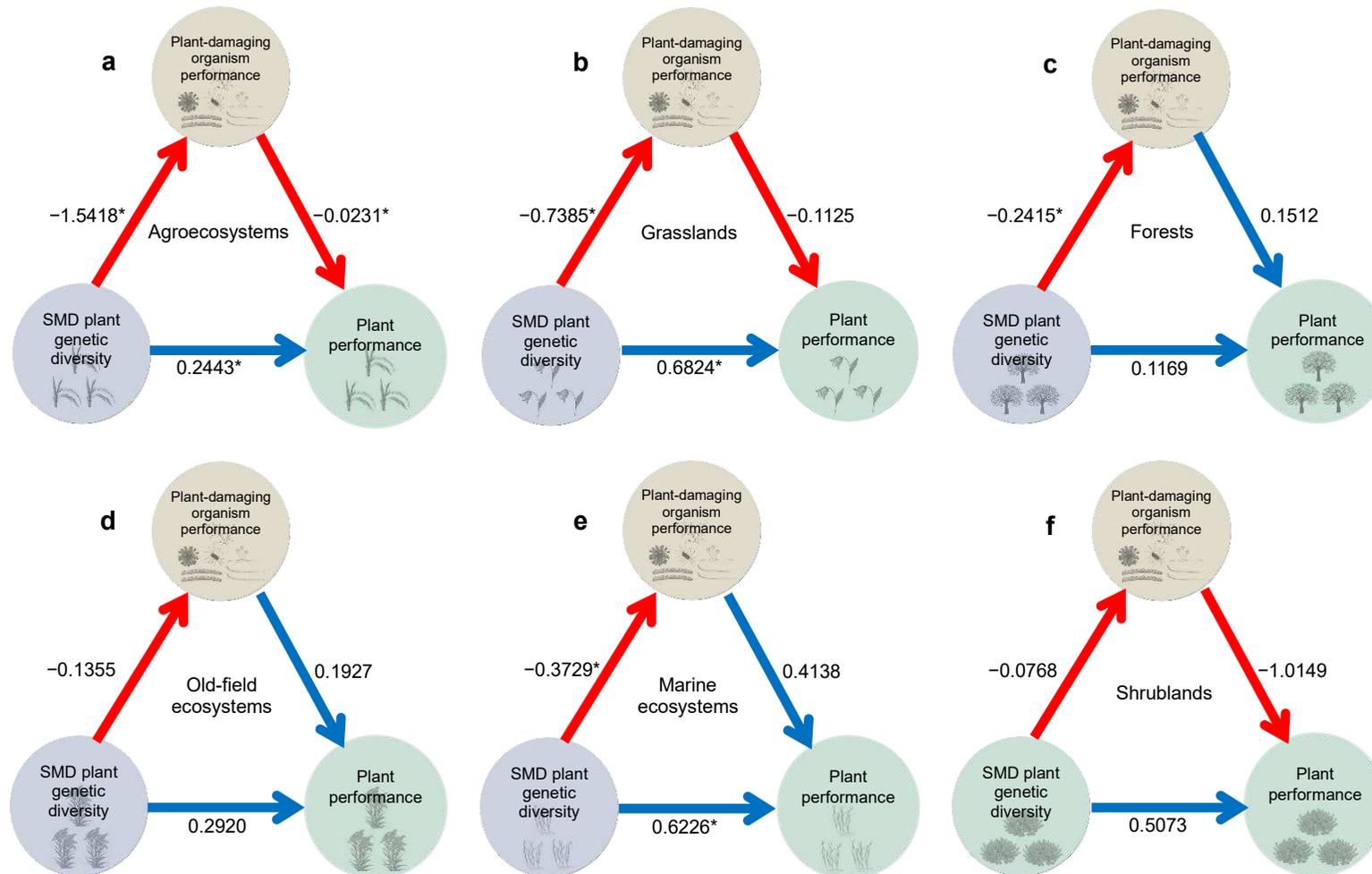
Extended Data Fig. 20 | Path analysis for the effects of number of added plant genotypes on the bi-trophic interactions of plant-damaging organism and plant performance. a, In global ecosystems. b, In agroecosystems. c, In grasslands. d, In forests. e, In old-field ecosystems. f, In marine ecosystems. No bi-trophic interactions were found in wetlands or shrublands. Plant-damaging organism performance including herbivore performance (abundance, damage and diversity of herbivores), weed performance (growth and diversity of weeds), plant-feeding nematode performance (nematode abundance) and plant disease performance (disease spread and damage) are shown in beige circles. Plant genetic diversity is shown in dusty blue. Plant performance (growth, quality and reproduction of plants) is shown in teal. The blue and red arrows denote positive and negative relationships, respectively, and numbers beside each arrow are the estimate coefficients for the fitted path-analytic models (Supplementary Tables 11, 12).



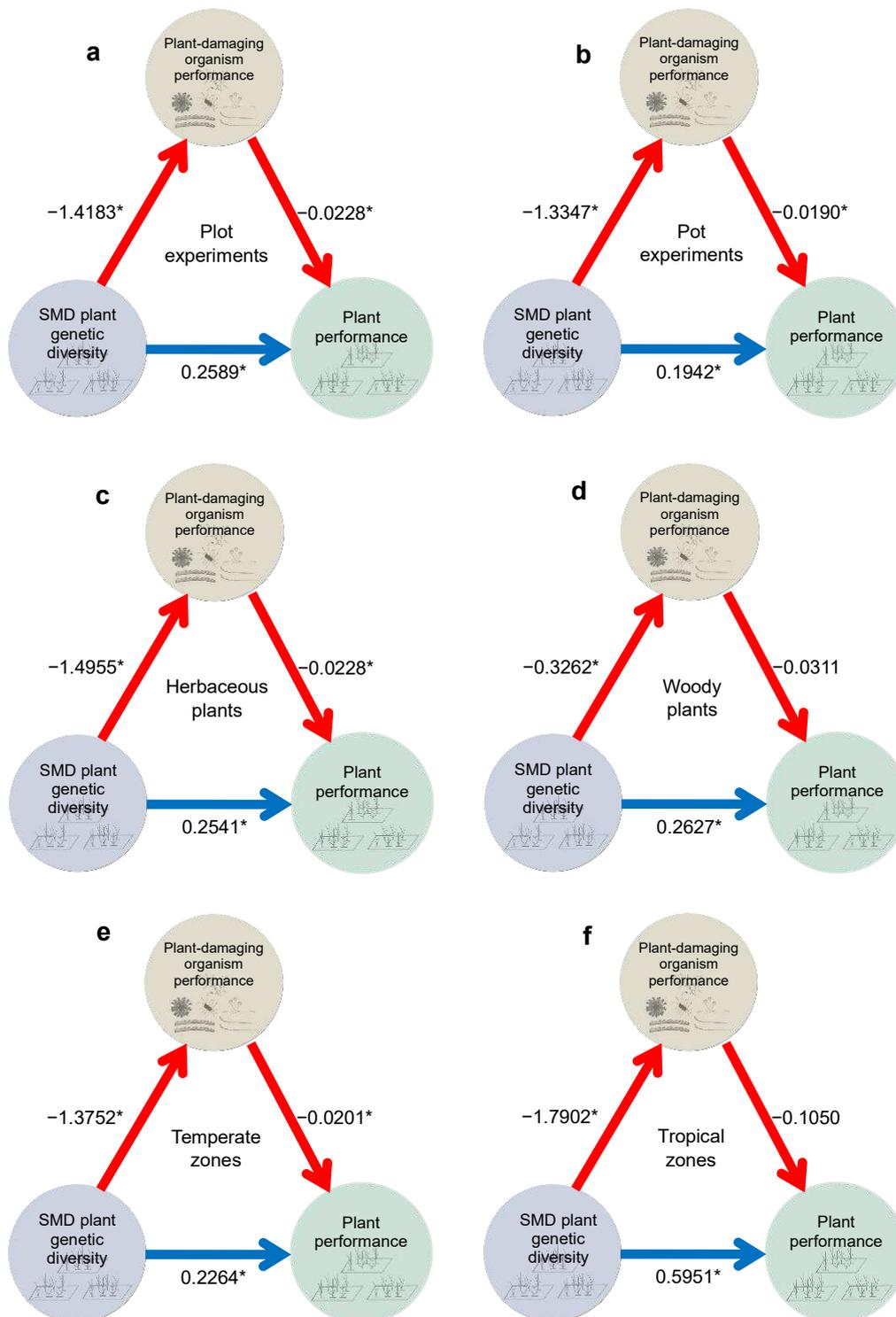
Extended Data Fig. 21 | Path analysis for the effects of number of added plant genotypes on the bi-trophic interactions of plant-damaging organism and plant performance. a, In plot experiments. b, In pot experiments. c, In herbaceous plants. d, In woody plants. e, In temperate zones. f, In tropical zones. Plant-damaging organism performance including herbivore performance (abundance, damage and diversity of herbivores), weed performance (growth and diversity of weeds), nematode performance (nematode abundance), and disease performance (disease spread and damage) are shown in beige circles. Plant genetic diversity is shown in dusty blue. Plant performance (growth, quality and reproduction of plants) is shown in teal. The blue and red arrows denote positive and negative relationships, respectively, and numbers beside each arrow are the estimate coefficients for the fitted path-analytic models (Supplementary Tables 13, 14). Arrow widths are proportional to estimate coefficients.



Extended Data Fig. 22 | Path analysis for the effects of SMD plant genetic diversity in all analyzed ecosystems. a, on bi-trophic interactions of invertebrate herbivore and plant performance. **b,** on bi-trophic interactions of weed and plant performance. **c,** on bi-trophic interactions of plant-feeding nematode and plant performance. **d,** on bi-trophic interactions of plant disease and plant performance. Herbivore performance (abundance, damage and diversity of herbivores), weed performance (growth and diversity of weeds), nematode performance (nematode abundance), and disease performance (disease spread and damage) are shown in beige circles. Plant genetic diversity is shown in dusty blue. Natural enemy performance (predator abundance, predator diversity, parasitoid abundance, parasitoid diversity and parasitism) is shown in pink. Plant performance (growth, quality and reproduction of plants) is shown in teal. The blue and red arrows denote positive and negative relationships, respectively, and numbers beside each arrow are the estimate coefficients for the fitted path-analytic models (Supplementary Tables 9, 10). The asterisks indicate the significance at 5% level.



Extended Data Fig. 23 | Path analysis for the effects of SMD plant genetic diversity on bi-trophic interactions of plant-damaging organism and plant performance on different ecosystems. a, agroecosystems. b, grasslands. c, forests. d, old-field ecosystems. e, marine ecosystems. f, shrublands. Bi-trophic interactions between plant-damaging organism and plant performance were not found in wetlands. Plant-damaging organism performance including herbivore performance (abundance, damage and diversity of herbivores), weed performance (growth and diversity of weeds), plant-feeding nematode performance (nematode abundance) and plant disease performance (disease spread and damage) are shown in beige circles. Plant genetic diversity is shown in dusty blue. Plant performance (growth, quality and reproduction of plants) is shown in teal. Blue and red arrows denote positive and negative relationships, respectively, and numbers beside each arrow are the estimated coefficients for the fitted path-analytic models (Supplementary Tables 11, 12).



Extended Data Fig. 24 | Path analysis for the effects of SMD plant genetic diversity on trophic interactions of plant-damaging organism and plant performance. a, plot experiments. b, pot experiments. c, herbaceous plants. d, woody plants. e, temperate zones. f, tropical zones. Plant-damaging organism performance including herbivore performance (abundance, damage and diversity of herbivores), weed performance (growth and diversity of weeds), nematode performance (nematode abundance), and disease performance (disease spread and damage) are shown in beige circles. Plant genetic diversity is shown in dusty blue. Plant performance (growth, quality and reproduction of plants) is shown in teal. The blue and red arrows denote positive and negative relationships, respectively, and numbers beside each arrow are the estimate coefficients for the fitted path-analytic models (Supplementary Tables 13, 14).

Supplementary Files

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