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1 **Running title:** Dimensions of intraspecific diversity

2 **Multiple dimensions of intraspecific diversity affect biomass of eelgrass and its associated**
3 **community**

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24 **Abstract**

25 Genetic diversity within key species can play an important role in the functioning of entire
26 communities. However, the extent to which different dimensions of diversity (e.g., the number
27 of genotypes vs. the extent of genetic differentiation among those genotypes) best predicts
28 functioning is unknown and may yield clues into the different mechanisms underlying diversity
29 effects. We explicitly test the relative influence of genotypic richness and genetic relatedness on
30 eelgrass productivity, biomass, and the diversity of associated invertebrate grazers in a factorial
31 field experiment using the seagrass species, *Zostera marina* (eelgrass). Genotypic richness had
32 the strongest effect on eelgrass biomass accumulation, such that plots with more genotypes at the
33 end of the experiment attained a higher biomass. Genotypic diversity (richness + evenness) was a
34 stronger predictor of biomass than richness alone, and both genotype richness and diversity were
35 positively correlated with trait diversity. The relatedness of genotypes in a plot reduced eelgrass
36 biomass independently of richness. Plots containing eelgrass with greater trait diversity also had
37 a higher abundance of invertebrate grazers, while the diversity and relatedness of eelgrass
38 genotypes had little effect on invertebrate abundance or richness. Our work extends previous
39 findings by explicitly relating genotypic diversity to trait diversity, thus mechanistically
40 connecting genotypic diversity to plot-level yields. We also show that other dimensions of
41 diversity, namely relatedness, influence eelgrass performance independent of trait differentiation.
42 Ultimately, richness and relatedness captured fundamentally different components of
43 intraspecific variation and should be treated as complementary rather than competing dimensions
44 of biodiversity affecting ecosystem functioning.

45 **Key words:** genetic relatedness, trait diversity, genetic diversity, genotypic richness, community
46 functioning

47 **Introduction**

48 The number of genotypes in an assemblage (genotypic richness) can influence community
49 productivity, resistance to disturbance, colonization and invasion success, and richness and
50 abundance of associated species (Hughes and Stachowicz 2004; Reusch et al. 2005; Crutsinger et
51 al. 2006, 2008; Johnson et al. 2006; De Meester et al. 2007; Crawford and Whitney 2010;
52 Kotowska et al 2010). Genetic diversity within key species may be equally, or in some cases
53 more important, than species diversity in determining ecosystem functioning (Cook-Patton et al.
54 2011, Latta et al. 2011). However, genotypic richness is just one measure of intraspecific
55 diversity and more direct measures of genetic differentiation or functional diversity may be more
56 mechanistically related to ecological outcomes. Yet, few studies have directly compared the
57 influence of different intraspecific diversity metrics on community function.

58 Although the genotypic or species richness of an assemblage is often assumed to be a
59 rough proxy for trait diversity, with greater trait diversity promoting resource partitioning and
60 increased production, it is unlikely that each species or genotype is equally distinct. Direct
61 measurements of functional trait dissimilarity can be a better predictor of diversity effects than
62 species richness (Heemsbergen et al. 2004; Wojdak and Mittelbach 2007). However, measuring
63 traits can be labor intensive, traits may be plastic, and choosing which traits matter to ecological
64 processes *a priori* is often challenging and context dependent (Naeem and Wright 2003).
65 Consequently, interest in using measures of genetic distance as proxies for functional diversity
66 has increased (Felsenstein 1985; Harvey and Pagel 1991). Phylogenetic diversity of multispecies
67 assemblages (e.g., total branch length in a phylogeny) is often a better predictor of assemblage
68 productivity than the number of species or functional groups (Cadotte et al. 2008; Cadotte et al.
69 2009; Flynn et al. 2011). However, because not all traits that might influence ecosystem

70 functions are evolutionarily conserved (Cavender-Bares 2004, 2006; Moles et al. 2005; Silvertown
71 et al. 2006; Best and Stachowicz 2013; Best et al. 2013), the relationship between overall
72 phylogenetic distance and ecological processes can vary (Burns and Strauss 2011; Narwani et al.
73 2013; Godoy et al. 2014).

74 Analogously, genetic relatedness or allelic diversity within species could be more closely
75 linked to trait diversity and assemblage performance than genotype richness (Stachowicz et al.
76 2013, Massa et al. 2013, Fischer et al. 2017). However there is considerable uncertainty in this
77 relationship. For example, under strong selection trait differentiation can exceed (McKay and
78 Latta 2002) or be less than (Petit et al. 2001) the amount predicted by overall genetic relatedness,
79 resulting in little correlation between trait and genetic distance (Reed and Frankham 2001;
80 McKay and Latta 2002; Abbott et al. in review). Genetic relatedness among individuals within a
81 species could also have direct effects (independent of traits) on assemblage or individual
82 performance due to inbreeding or outbreeding depression (e.g. Charlesworth and Charlesworth
83 1987; Ralls et al. 1988; Crnokrak and Roff 1999; Keller and Waller 2002) or kin recognition
84 (Dudley and File 2011). Thus, the number of genotypes (richness) and their relatedness may
85 have unique effects on performance such that the question is not as simple as, “which metric best
86 captures overall trait diversity and predicts functioning?”

87 To assess the independent and interactive effects of these different dimensions of
88 diversity, we factorially manipulated the genotypic richness and genetic relatedness of
89 assemblages of the seagrass *Zostera marina* (eelgrass) in the field. Eelgrass provides critical
90 habitat for fishes and invertebrates, while buffering shorelines from erosion and playing a key
91 role in nutrient and carbon cycling (Williams and Heck 2001). Because many of these functions
92 are correlated with standing plant biomass, we measured plant growth and biomass as response

93 variables, as well as the abundance and diversity of epifaunal invertebrates. Eelgrass reproduces
94 sexually and vegetatively, forming extensive monospecific meadows where genotypic richness
95 varies at scales of meters (1-15 genotypes m⁻² in northern California, Hughes and Stachowicz
96 2009). Eelgrass genotypes differ in traits such as growth rate, nutrient uptake, photosynthetic
97 efficiency, phenolic content, susceptibility to herbivores, and detrital production (Ehlers et al.
98 2008; Hughes et al. 2009; Tomas et al. 2011; Abbott et al. in review) that are thought to underlie
99 the effects of genotypic richness (Hughes and Stachowicz 2004, 2011; Reusch et al. 2005; Massa
100 et al. 2013). We previously measured these traits for all the genotypes used in our experiment,
101 allowing us to explore the influence of trait diversity as an underlying mechanism relating the
102 different dimensions of genetic diversity on assemblage performance.

103

104 **Methods**

105 We used 41 unique genotypes to create a factorial field experiment, crossing genotypic richness
106 (2 or 6 genotypes) and relatedness (low, medium, and high, defined below). We used a large
107 number of genotypes to minimize identity effects and create assemblages that cover a wide range
108 of relatedness. We collected the 41 genotypes across three tidal heights at five sites in Bodega
109 Harbor, CA in May 2012 (Abbott et al. in review) and propagated them in outdoor tanks at the
110 UC Davis Bodega Marine Laboratory to produce enough shoots for deployment in a field
111 experiment in the summer of 2013. We estimated the relatedness of the 41 genotypes using 11
112 microsatellite loci selected from a pool of >30 loci designed specifically for *Zostera marina*
113 (Reusch et al. 1999; Reusch 2000; Oetjen and Reusch 2007; Oetjen et al. 2010; Abbott and
114 Stachowicz 2016). We determined the relatedness of all possible genotype pairs using a
115 regression-based measure of the number of shared alleles, calibrated by the frequency of those

116 alleles in the population (estimated using 220 unique genotypes collected at the same time as the
117 41) using the program STORM (Frasier 2008). We calculated the relatedness of eelgrass in the
118 six-genotype treatments as the average relatedness of all pairwise combinations of the six
119 genotypes.

120

121 *Selecting assemblages*

122 Our treatments consisted of two levels of genotype richness, two or six genotypes, and three
123 levels of relatedness within each richness level: less related than expected by chance (low), as
124 related as expected by chance (mid), and more related than expected by chance (high). “By
125 chance” here refers to expected values based on a random draw from the 41 genotypes. We
126 selected genotype combinations for these treatments to minimize genotypic identity effects and
127 standardize variation in relatedness among replicates within treatment (Table 1, see appendix A
128 for a list of all genotype combinations used).

129 We wanted to test explicitly the role of richness and relatedness in general, while
130 minimizing identity effects, thus each replicate of a given treatment contained a different
131 assemblage of genotypes. This required using a large number of genotypes, and as a result, our
132 experiment did not contain monocultures of each genotype. We avoided confounding our
133 richness and relatedness treatments with genotypic identity effects by minimizing the number of
134 replicate genotypes within a treatment and maximizing the number of genotypes shared across
135 treatments. For example, for the assemblages of six genotypes, within each relatedness level no
136 genotype was present in more than six of the 12 plots and each assemblage differed by at least
137 two genotypes. For the two-genotype plots no genotype was present in more than two pairs for
138 each relatedness level. Genotypes from different sites and tidal heights were represented in all

139 treatments: all assemblages of six genotypes had genotypes from at least three different sites and
140 two different tidal heights.

141

142 *Field Experiment*

143 In July 2013 we planted 12 replicates of each of the six treatments (two levels of richness
144 crossed with three levels of relatedness) in a randomized block design, with plots in a grid with
145 12 rows (each row is a block) and six columns, for a total of 72 plots. Although the slope of the
146 shore was gradual at our location (< 0.5 m difference between any plots) and the entire
147 experiment was > 20 m from the edge of a bed, these blocks paralleled the shore to account for
148 effects of elevation/depth (Abbott and Stachowicz 2016). We randomly assigned each treatment
149 to one of the six columns for each of the 12 rows. We established this grid within an existing
150 eelgrass bed in Bodega Harbor, CA by clearing seventy-two 70 cm by 60 cm plots of seagrass.
151 We then inserted plastic containers (40.4 cm long x 32.7 cm wide x 15.2 cm deep) lined with 2
152 mm diameter mesh into the center of each plot and filled them within 3 cm of the top with
153 homogenized, sieved, field-collected sediment. We planted 12 shoots in each plot: six of each
154 genotype for the two-genotype plots and two of each genotype for the six-genotype plots. Prior
155 to planting, we removed all epibionts from each shoot and standardized them to 30 cm of shoot
156 and 2.5 cm of rhizome. We harvested the experiment 16 months later in October 2014 (after two
157 growing seasons).

158 Prior to harvest, we assessed plant growth and mobile invertebrate community
159 composition. Two weeks prior to the breakdown of the experiment we marked ten randomly
160 selected shoots in each plot using the hole-punch method (Williams and Ruckelshaus 1993).
161 After harvesting, growth was measured as leaf area produced (length that the hole-punch mark

162 traveled from the base of the sheath x shoot width). We estimated epifaunal community
163 composition in each plot by collecting three eelgrass shoots from each plot and quickly
164 depositing all three shoots directly into a plastic bag. In the lab, we removed all invertebrate
165 grazers from the eelgrass and preserved them in 70% ethanol for later enumeration and
166 identification to the lowest taxonomic level possible. For analyses we used two measures of
167 invertebrate abundance: (1) we standardized abundance by the dry weight of the shoots of
168 eelgrass from which the invertebrates were collected, and (2) we estimated the total plot-level
169 abundance of invertebrates by multiplying the abundance per gram of eelgrass sampled by the
170 total mass of aboveground biomass from each plot at the end of the experiment. Because it is
171 unlikely that richness scales linearly with the mass of eelgrass either sampled or in the plot as a
172 whole, we used cumulative richness from all three sampled shoots in analyses.

173 We next harvested all of the eelgrass from each container. Each physically connected
174 section of eelgrass (group of ramets) was placed into individually labeled Ziploc bags and
175 transported a short distance (~2.5 km) back to the laboratory, where they were stored in a
176 refrigerator or frozen until processing. For each group of connected ramets we took a single leaf
177 tissue sample for genetic analysis so that we could attribute biomass unambiguously to a
178 genotype. We divided the final biomass of each ramet into shoots, roots, and rhizome, and
179 weighed each after drying at 60°C for at least 48 hours.

180

181 *Trait diversity*

182 We previously measured significant variation among these 41 genotypes for 17 traits when
183 grown in a common garden (Abbott et al. in review). The 17 traits included: traits related to
184 biomass accumulation (aboveground, belowground, and ratio of above to belowground), growth

185 rate (new shoots produced, and leaf and rhizome growth rate), morphology (maximum root
186 length, maximum leaf width and length, number of leaves, and rhizome diameter), nutrient
187 uptake rate (nitrate uptake by the shoots and ammonium uptake by the roots), leaf phenolic
188 content, and photosynthetic parameters based on rapid light curves measured using a Diving-
189 PAM® (Pulse Amplitude Modulated) fluorometer (Hughes et al. 2009; Reynolds et al. 2016).
190 Multivariate trait distance was uncorrelated with estimates of pairwise relatedness for these
191 genotypes (Abbott et al. in review), allowing us to evaluate the effects of trait diversity on
192 eelgrass performance, independent of relatedness. We measured trait diversity using
193 standardized trait values both as the Euclidean distance between all possible genotype pairs, and
194 as the distance among genotypes using the first two Principal Components from a Principal
195 Components Analysis to account for correlations among traits; both indices were strongly
196 correlated ($r = 0.92$, $P = <0.0001$) and the choice of index did not affect our results.

197 We quantified trait diversity for each assemblage of genotypes using Rao's quadratic
198 entropy Q (Rao 1982; Champely and Chessel 2002; Ricotta 2005), which is a measure of the
199 sum of the pairwise trait differences among genotypes weighted by their relative abundance. We
200 chose this metric because it represents the average divergence in traits among taxa (in this case
201 genotypes), and is therefore analogous to our measure of relatedness among eelgrass genotypes
202 in each assemblage (Tucker et al. 2017). It also provides a measure of functional diversity that is
203 not strongly influenced by the number of taxa present (richness), unlike other measures of
204 functional diversity (e.g. Petchey and Gaston 2002), which sum differences among taxa (Botta-
205 Dukát 2005; Mouchet et al. 2010; Clark et al. 2012; Schleuter et al. 2010). This allowed us to
206 include trait diversity as a predictor in models of biomass accumulation along with genotypic
207 richness and relatedness.

208

209 *Re-genotyping*

210 In addition to the genotype samples we took at harvest, in November 2013 and May 2014 we
211 collected 2 cm long pieces of leaf from each group of shoots we estimated to be part of the same
212 physiologically connected ramet in the field in each plot in order to assess genotypic composition
213 of the plots and how it changed over time. The tissue samples collected for genotyping were
214 processed in the same manner as in the original genetic analysis. Each sample was identified as
215 one the original 41 genotypes or a new unique genotype. By the end of the experiment new
216 “invader” genotypes established in 16 of the 72 plots, but overall they composed less than 3% of
217 the total eelgrass biomass. Within plots where invaders established, on average they composed
218 less than 10% of total plot biomass. There were no effects of richness, relatedness, or trait
219 diversity of eelgrass in a plot on the likelihood of an invader establishing (Appendix B).

220

221 *Statistical analysis*

222 Not all genotypes survived in plots in which they were planted, so we assessed whether
223 there was any effect of the initial planted diversity (richness, relatedness, and trait diversity) on
224 patterns of mortality and survival of genotypes. Because we detected no such effects (see
225 Appendix C), and because nearly two-thirds (44/68) of the genotypes that were lost during the
226 experiment had already been lost from the plots by November 2013 (four months into the
227 experiment), whereas all performance/functioning response variables were measured at the end
228 of the experiment (October 2014), we used the final genotypic composition rather than initial
229 composition to calculate plot-level realized diversity metrics. In addition to richness, relatedness,
230 and trait diversity, we also included genotypic evenness as a realized diversity metric in our

231 models to account for the differences in the relative abundance of genotypes in each plot at the
232 end of the experiment. Because we included genotypic evenness separately in the model, we
233 assumed an equal abundance of all genotypes in each plot at the end of the experiment for our
234 calculation of trait diversity. We did this to avoid systematic correlations between trait diversity
235 and other parameters in the model. Some of the plots only had one genotype left at the end of the
236 experiment; these plots all have a trait diversity and evenness of zero and richness and
237 relatedness of one. We repeated our analyses with planted diversity metrics, but none of these
238 was ever correlated with final performance (see Results).

239 We performed analyses using R 3.0.3 or R 3.3.3 (R Core Team 2014, 2017). We used
240 logistic regression (glm function from the stats package in R; R Core Team 2014) to test the
241 effects of planted genotypic richness, relatedness, and trait diversity, on the likelihood that no
242 shoots survive at the end of the experiment. For plots in which at least one genotype survived,
243 we performed separate analyses of genotype survival for those planted with two genotypes and
244 six genotypes. In two- genotype plots, we performed a logistic regression, testing the effects of
245 planted genotypic richness, relatedness, and trait diversity on whether both genotypes survived.
246 For the six-genotype plots we used the proportion of surviving genotypes as a continuous
247 response variable and used a generalized linear mixed model with the richness, relatedness, and
248 trait diversity of planted genotypes as fixed effects, and block as a random effect, using a
249 Bayesian approach in the MCMCglmm package in R (Hadfield 2010).

250 We used the same type of generalized linear mixed models (MCMCglmm package in R)
251 to assess the effects of our realized diversity metrics on the performance and functioning of the
252 eelgrass plots (eelgrass above and belowground biomass and leaf growth rate, and invertebrate
253 grazer abundance and richness). For these models we specified a Gaussian distribution for the

254 response variables and used priors that corresponded to an inverse-Gamma distribution, with
255 shape and scale parameters equal to 0.001. We evaluated relative performance of our models
256 using the model deviance information criterion (DIC). DIC is a Bayesian generalization of the
257 Akaike information criterion (AIC) that is particularly suited to comparing models that
258 use Markov chain Monte Carlo (MCMC) to obtain posterior distributions (Spiegelhalter et al.
259 2002). Similar to AIC, DIC measures model accuracy while penalizing excessive model
260 complexity (additional parameters), with a lower DIC score indicating a preferred model. We
261 tested univariate models for each diversity metric (realized richness, relatedness, trait diversity,
262 and evenness), a full model that included all four metrics, and all possible two and three variable
263 models. For simplicity only the best performing two and three variable models are presented in
264 the results.

265

266 **Results**

267 *Survivorship*

268 Eelgrass failed to establish permanently (complete mortality) in 22 of 72 plots. We found no
269 effect of the initial planted genotypic richness, average relatedness, or trait diversity of the
270 genotypes in a plot on the likelihood of complete mortality (Appendix C). Most of these plots
271 never produced any new shoots and died within a few months of the initial planting, suggesting
272 that complete mortality resulted from the failure of the transplants to establish, likely due to
273 dislodgement by currents, burrowing organisms or floating algal mats, rather than interactions
274 among shoots. Because complete mortality was independent of treatment, we excluded these
275 plots from the rest of the analyses.

276 Within the plots in which eelgrass remained at the end of the experiment, neither the
277 richness, relatedness, and trait diversity of planted genotypes, nor their interactions affected the
278 proportion of genotypes surviving or any of our measures of plant performance or animal
279 community diversity (Appendices C and D). The lack of effect of planted diversity is probably
280 because most (65%) of the genotypes that were lost from a plot in which they were planted were
281 lost within the first 4 months of the experiment. Thus, for the vast majority of the duration of the
282 experiment the genotypic composition in each plot was similar to that measured at the end of the
283 experiment.

284

285 *Plant biomass and growth*

286 Realized richness and relatedness (calculated using observed genotypic composition at the end of
287 the experiment) independently influenced several measures of plant biomass. For example, the
288 model that best explained variation in final belowground biomass included both richness, which
289 was positively correlated with biomass, and relatedness, which was negatively correlated with
290 biomass (Table 2, Fig. 1). A model that also included evenness with richness and relatedness
291 performed similarly (Δ DIC = 0.56, Table 2), suggesting that evenness also positively influenced
292 belowground biomass (as seen in univariate analyses), but not enough to improve model
293 performance while adding an additional variable. For aboveground biomass the best performing
294 model included richness and evenness having a positive affect on biomass and relatedness
295 having a negative affect, although a model that did not include relatedness performed essentially
296 the same (Δ DIC = 0.12, Table 2).

297 We included richness and evenness separately in our models to see how each contributed
298 independently to eelgrass performance, and we found that both were included in our top models

299 for explaining eelgrass biomass, although richness had a greater effect. In practice, richness and
300 evenness are often combined to calculate the diversity (e.g., Shannon index) of an assemblage.
301 Because genotypic Shannon diversity combines two measures of diversity that we found to be
302 important, and it is a ubiquitous metric used to characterize the diversity of natural communities,
303 we decided to run models that replaced the richness and evenness of eelgrass plots with their
304 genotypic diversity. Unsurprisingly, by combining information about richness and evenness into
305 a single metric and reducing the number of parameters, model performance increased when using
306 genotypic diversity (Δ DIC = 1.46 for below and 2.84 for aboveground biomass when comparing
307 the best performing models, Tables 2 and 4). Genotypic diversity proved to be the strongest
308 predictor of eelgrass biomass, however relatedness was also included in the best performing
309 models for both below and aboveground biomass (Table 2).

310 A consistent positive correlation between trait diversity and diversity of genotypes, both
311 for single traits and multivariate trait indices, suggests that trait diversity may mechanistically
312 account for the effect of genotypic diversity on plant performance (Fig. 3). Trait diversity was
313 not included in the best performing models for explaining eelgrass biomass, precisely because
314 trait diversity was strongly correlated with richness ($R^2 = 0.60$, Fig. 3), and richness was a
315 stronger predictor. Trait diversity was positively correlated with belowground and aboveground
316 biomass in univariate analyses (Table 2, Fig. 1), and the performance of the full model, which
317 included trait diversity, was not greatly reduced compared to the best performing model (Δ DIC
318 = 2.36 for below and 1.57 for aboveground biomass).

319 In addition to using multivariate trait differentiation, we assessed the effect of each trait
320 separately to see if the mean, variance, range, or extremes of trait values for genotypes in each
321 plot had any influence on plant biomass or leaf growth. The range and variance of many traits

322 were positively correlated with biomass; however, as with our multivariate trait diversity metric,
323 the strong correlation between trait and genotypic diversity meant that these factors dropped out
324 of multi-factor models once Shannon genotypic diversity was included (Appendix E).

325 Leaf growth over the last two weeks of the experiments was weakly positively affected
326 by relatedness, but not by any other dimension of diversity (Appendix F). The association of
327 high relatedness with low biomass (Fig. 1) likely reduced self-shading and contributed to higher
328 leaf growth rates in high-relatedness plots. Despite high leaf growth rates, standing biomass was
329 lower in these plots, suggesting that turnover rates, leaf number, or herbivory rates vary with
330 relatedness in such a way to reduce standing stock. The low belowground biomass in realized
331 monocultures, combined with the high aboveground growth, resulted in a higher ratio of above to
332 belowground biomass in plots with one genotype compared to plots with multiple genotypes (Fig.
333 4). By definition, realized monocultures have zero trait diversity or genotypic diversity, and a
334 richness and relatedness of one. Therefore, we also ran models excluding all realized
335 monocultures to determine whether this drove the effects we observed, which it did not
336 (Appendix G).

337

338 *Invertebrate Community Response*

339 The best performing model of invertebrate abundance contained only trait diversity (Table 3).
340 Total estimated invertebrate abundance in an entire plot increased with eelgrass trait diversity
341 (Table 3, Fig. 5), even when only considering plots with > 1 genotype (Appendix G). The
342 abundance of invertebrate grazers per unit mass of eelgrass sampled decreased with increasing
343 relatedness, the only predictor showing any effect in univariate analyses (Table 3, Fig. 5).
344 However, adding trait diversity to the model including relatedness modestly improved model fit

345 (delta AIC = 1.5) largely due to the difference between single and multi-genotype plots
346 (Appendix G). The species richness of invertebrate grazers in the eelgrass samples from each
347 plot was uncorrelated with any of the realized eelgrass diversity metrics Appendix G and H).

348

349 **Discussion**

350 Considerable current research examines the utility of different diversity measures for describing
351 the species diversity - ecosystem functioning relationship (Cadotte et al. 2008; Cadotte et al.
352 2009; Flynn et al. 2011; Fischer et al. 2017). However, we show that different metrics of
353 intraspecific diversity capture fundamentally different components of biodiversity and should be
354 treated as complementary rather than competing dimensions of biodiversity that influence
355 assemblage performance. Eelgrass assemblages with more genotypes and greater evenness of
356 genotypes (genotypic diversity) attained higher plot-level biomass, whereas relatedness
357 decreased biomass independently of genotypic and trait diversity. Furthermore, our use of
358 multiple metrics clarified particular mechanisms underlying this relationship, as more
359 genotypically diverse plots had higher trait diversity (Fig. 3), suggesting that niche
360 differentiation among genotypes and more efficient use of available resources (e.g. Loreau 2001)
361 at the plot level leads to greater eelgrass biomass accumulation. Although our study focuses on
362 intraspecific diversity in a key habitat-forming species, the same principles should apply to
363 diversity at any level of biological organization.

364 Genotypic richness showed a strong positive relationship with eelgrass biomass,
365 consistent with previous studies (Hughes and Stachowicz 2004, 2011; Reusch et al. 2005). By
366 statistically partitioning diversity effects, these studies highlighted the importance of
367 complementarity (Reusch et al. 2005; Hughes and Stachowicz 2011), but never clearly revealed

368 a trait-based mechanism. our study showed that the evenness of eelgrass assemblages also
369 positively influenced eelgrass biomass. Species evenness can affect community function (e.g.
370 Wilsey and Potvin 2000, Polley et al. 2003, Mulder et al. 2004), but the influence of intraspecific
371 genotypic evenness on function is less clear. Our finding that genotypic Shannon diversity, a
372 measure that includes both richness and evenness, best predicted biomass accumulation implies
373 that resource partitioning among genotypes promotes both coexistence at similar relative
374 abundances (Chesson 2000) and higher assemblage performance (Tilman 1999).

375 Although eelgrass genotypic diversity explained greater variation in biomass than trait
376 diversity, without knowing which traits are most important to intraspecific interactions, a
377 multivariate measure of trait differentiation may not provide the best measure for how trait
378 differences influence assemblage performance. Our multivariate trait index could be less
379 correlated with eelgrass biomass than simple genotypic richness either because we failed to
380 measure some relevant traits or because our index contains some irrelevant traits that weaken the
381 correlation between differentiation and performance. Because we measured 17 different traits
382 related to light and nutrient acquisition, biomass production above and below ground, rates of
383 clonal spread, and resistance to herbivores, the failure to measure an unidentified trait seems an
384 unlikely explanation. Unfortunately the links between trait combinations and performance are
385 likely to be complex, and different traits may be most relevant to predicting performance of
386 different sets of genotypes. Furthermore, differentiation in some traits can lead to either
387 complementarity or dominance, depending on heterogeneity in environmental conditions and the
388 nature and magnitude of tradeoffs among traits (Mayfield and Levine 2010). Without tradeoffs,
389 for example, genotypes with lower requirements for some limiting resource would likely
390 outcompete others, and the greater the variation in traits, the greater the difference in competitive

391 ability and the more likely competitive exclusion will occur (Abbott and Stachowicz 2016).
392 Differences in certain traits and environmental conditions may be more likely to lead to trade-
393 offs and thus only some subset of traits may influence how well trait diversity predicts
394 performance (Kraft 2015).

395 In contrast to the strong positive effects of genotypic richness and diversity, the
396 relatedness of eelgrass genotypes reduced eelgrass biomass. Because relatedness and trait
397 differences for the genotypes used in this study were uncorrelated (Abbott et al. in review), this
398 effect cannot be attributed to low trait diversity in high relatedness plots. Relatedness could have
399 direct effects on performance as some plants allocate fewer resources to root competition when
400 in the presence of individuals of the same species (Mahall and Callaway 1991, 1996), genotype
401 (Gersani et al. 2001; Falik et al. 2003; Gruntman and Novoplansky 2004), or close kin (Dudley
402 and File 2011). Our finding that the ratio of above to belowground biomass was higher for plots
403 that only had one genotype left at the end of experiment (realized monocultures) than those with
404 multiple genotypes (Fig. 4) could be evidence of self vs. non-self recognition, with reduced
405 allocation to intense belowground competition in the presence of closely related individuals.

406 Eelgrass trait diversity increased invertebrate grazer abundance at the plot scale, either
407 because trait diversity leads to higher plant biomass and greater habitat volume (Borer et al.
408 2012; Best et al. 2014), or because different grazer taxa prefer different genotypes as food or
409 habitat (Reynolds et al. in press *Oikos*). Trait diversity did affect eelgrass biomass, although not
410 as strongly as other variables that were uncorrelated with invertebrate abundance, suggesting that
411 higher aboveground biomass is not the only mechanism involved. Several amphipods and
412 isopods prefer different microhabitats within eelgrass beds at this site (Lürig et al. 2016), and the

413 presence of genotypes with different heights, widths, or leaf traits may have influenced
414 invertebrate biomass.

415 Our results, combined with those of previous studies, show a consistent pattern of
416 genotypic richness/diversity enhancing the productivity of eelgrass assemblages (Hughes and
417 Stachowicz 2004, 2011; Reusch et al. 2005; Stachowicz et al. 2013). Our study indicates that
418 trait diversity among genotypes contributes to these effects and also influences the eelgrass-
419 associated invertebrate community. The influence of relatedness on performance is more
420 enigmatic. Previous studies of relatedness were confounded by a spurious positive correlation
421 between relatedness and trait differentiation in a small sample of genotypes (Stachowicz et al.
422 2013). In the present study trait diversity and relatedness were uncorrelated, making the negative
423 relationship between relatedness and biomass, and the positive relationship between relatedness
424 and invertebrate grazer density more difficult to interpret. It is clear that the diversity metrics we
425 tested influenced eelgrass performance in distinct ways; however, it remains unclear why
426 relatedness influenced eelgrass and invertebrate grazers the way it did.

427 Understanding the relationship between biodiversity and ecosystem functioning is a
428 major focus of modern ecology (e.g. Tilman 1999; Schmid 2002), and one of the main lines of
429 inquiry has been the aspects of biodiversity (richness, genetic distance, functional diversity) that
430 best predict ecosystem functioning (e.g. Flynn et al. 2011, Venail et al. 2015). While many
431 studies have asked these questions about diversity among species, few have extended the
432 approach to multiple dimensions of intraspecific variation, particularly within the marine realm.
433 Each of our diversity metrics affected some community function, but the lack of correlation
434 among certain metrics suggests they represent independent dimensions of biodiversity with
435 unique effects on the eelgrass ecosystem. Genotypic diversity was the strongest predictor of

436 eelgrass performance, likely driven by the strong relationship between genotypic and trait
437 diversity. In contrast, relatedness had an independent negative effect on eelgrass biomass, and
438 trait diversity alone best predicted invertebrate abundance. Thus three different dimensions of
439 diversity influenced functioning in distinct ways (see also Cadotte et al. 2013). Considering
440 potential complementarity among different aspects of diversity improves our understanding of
441 diversity-function relationships and their underlying mechanisms.

442

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453

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For Review Only

685 **Tables:**

686 Table 1. Range and variance of relatedness values for each level of richness x relatedness. For
 687 the two-genotype plots we give the range of pairwise relatedness, mean relatedness, and variance
 688 in relatedness for the 12 pairs of genotypes at each relatedness level. For the six-genotype plots
 689 we give the range of mean pairwise relatedness and maximum variance in relatedness of all
 690 genotypes in the 12 replicate plots at each relatedness level.

	Distantly related	Intermediate relatedness	Closely related
2 genotype plots			
<i>Range</i>	-0.69 to -0.38	-0.17 to 0.06	0.31 to 0.87
<i>Mean</i>	-0.51	-0.02	0.48
<i>Variance</i>	0.01	0.004	0.02
6 genotype plots			
<i>Range of means</i>	-0.49 to -0.42	-0.045 to 0.071	0.38 to 0.45
<i>Variance</i>	<0.038	<0.032	<0.024

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698 Table 2. Summary of generalized linear mixed model results for the effects of realized diversity
 699 metrics on below and aboveground biomass of eelgrass. Block was included as a random effect
 700 in all models; but block effect results are omitted for brevity. Models are presented with posterior
 701 means (Bayes estimates), 95% credible intervals (equivalent to 95% confidence intervals), and
 702 pMCMC values (probability of the estimate overlapping zero). Section A shows results for
 703 models including genotypic richness and evenness separately and section B shows results
 704 including genotypic (Shannon) diversity in the place of richness and evenness. Results for the
 705 best performing models are in bold.
 706

<i>Models using final diversity metrics</i>	Belowground biomass					Aboveground biomass				
	<i>Post mean</i>	<i>Lower CI</i>	<i>Upper CI</i>	<i>pMC-MC</i>	<i>DIC</i>	<i>Post mean</i>	<i>Lower CI</i>	<i>Upper CI</i>	<i>pMC-MC</i>	<i>DIC</i>
A <i>Richness+relatedness+trait diversity+evenness</i>					305.41					321.72
Richness	1.95	0.32	3.37	0.01		1.51	-0.28	3.42	0.11	
Relatedness	-3.01	-6.36	0.54	0.09		-3.06	-6.87	0.73	0.12	
Trait diversity	-0.06	-0.43	0.33	0.78		-0.12	-0.61	0.33	0.62	
Evenness	3.31	-2.24	8.10	0.19		5.47	-0.71	11.35	0.07	
<i>Richness+Relatedness+evenness</i>					303.61					320.15
Richness	1.78	0.73	2.93	0.007		1.18	-0.15	2.46	0.08	
Relatedness	-2.94	-6.34	0.20	0.07		-2.89	-6.67	0.96	0.14	
Evenness	3.10	-1.97	7.78	0.23		5.04	-1.06	10.65	0.10	
<i>Richness+relatedness</i>					303.05					-
Richness	1.89	0.97	3.05	<0.001		-	-	-	-	
Relatedness	-4.11	-6.43	-1.05	0.006		-	-	-	-	
<i>Richness+evenness</i>					-					320.27

Richness	-	-	-	-	1.50	0.27	2.78	0.02
Evenness	-	-	-	-	7.50	2.74	12.33	0.001
<i>Richness</i>					310.40			327.61
Richness	2.69	1.67	3.68	<0.001	2.25	1.03	3.49	<0.001
<i>Relatedness</i>					311.89			323.72
Relatedness	-6.52	-9.21	-4.03	<0.001	-6.43	-9.79	-3.71	<0.001
<i>Trait diversity</i>					316.71			330.96
Trait diversity	0.56	0.27	0.81	<0.001	0.48	0.21	0.84	0.004
<i>Evenness</i>					317.19			324.01
Evenness	9.10	5.18	13.97	<0.001	10.06	5.56	15.03	<0.001
B <i>Genotypic diversity + relatedness + trait diversity</i>					303.38			319.18
Genotypic diversity	6.69	2.25	11.86	0.009	7.06	1.84	12.55	0.01
Relatedness	-3.19	-6.18	-0.19	0.05	-3.81	-7.34	-0.27	0.03
Trait diversity	0.07	-0.25	0.38	0.66	-0.06	-0.42	0.37	0.74
<i>Genotypic diversity + relatedness</i>					301.59			317.31
Genotypic diversity	7.20	3.24	10.91	0.001	6.55	1.73	10.74	0.003
Relatedness	-3.37	-6.30	-0.34	0.03	-3.64	-6.87	-0.015	0.04
<i>Genotypic diversity</i>					305.15			319.78
Genotypic diversity	9.79	6.20	12.78	<0.001	9.36	5.42	13.16	<0.001

707 Table 3. Summary of generalized linear mixed model results for the effects of realized diversity
 708 metrics on invertebrate grazer abundance at the plot level and per unit eelgrass biomass.
 709 Predictors and statistical testing as in Table 2. One point for invertebrate abundance (per gram
 710 eelgrass) was determined to be an outlier using the Grubbs test for single outliers ($P = 0.002$;
 711 Grubbs 1950) and was removed from analyses. Results for the best performing models are in
 712 bold.
 713

<i>Models using final diversity metrics</i>	Invertebrate abundance (/plot)					Invertebrate abundance (/g eelgrass)				
	<i>Post mean</i>	<i>Lower CI</i>	<i>Upper CI</i>	<i>pMC-MC</i>	<i>DIC</i>	<i>Post mean</i>	<i>Lower CI</i>	<i>Upper CI</i>	<i>pMC-MC</i>	<i>DIC</i>
<i>Relatedness+richness+evenness+trait diversity</i>					663.36					356.48
Richness	-12.74	-69.49	39.80	0.67		-2.25	-4.97	0.47	0.13	
Relatedness	-17.10	-134.9	109.3	0.79		5.79	-0.46	11.54	0.06	
Trait diversity	12.84	-1.78	25.53	0.07		0.87	0.22	1.58	0.01	
Evenness	-7.43	-193.1	169.9	0.95		-5.25	-13.78	4.69	0.26	
<i>Richness+relatedness+trait diversity</i>					661.32					355.01
Richness	-12.48	-63.90	45.41	0.66		-2.07	-4.64	0.83	0.15	
Relatedness	-13.18	-114.9	85.04	0.77		7.48	2.41	12.27	<0.001	
Trait diversity	12.64	-0.88	26.57	0.08		0.75	0.14	1.54	0.04	
<i>Relatedness+trait diversity</i>					-					355.23
Relatedness	-	-	-	-		8.03	2.85	13.26	<0.001	
Trait diversity	-	-	-	-		0.38	-0.08	0.89	0.11	
<i>Richness+trait diversity</i>					659.24					-
Richness	-11.24	-64.76	40.30	0.66		-	-	-	-	
Trait diversity	13.26	1.01	26.22	0.03		-	-	-	-	

<i>Richness</i>					661.64					364.20
Richness	31.23	-3.47	65.50	0.08		-1.01	-2.92	0.83	0.30	
<i>Relatedness</i>					662.18					356.71
Relatedness	-73.12	-160.5	13.06	0.11		6.12	1.55	10.70	0.01	
<i>Trait diversity</i>					657.48					364.27
Trait diversity	11.11	2.78	19.04	0.01		-0.01	-0.46	0.47	0.94	
<i>Evenness</i>					662.98					361.03
Evenness	95.01	-34.53	244.2	0.18		-7.55	-14.38	-0.31	0.04	

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714 **Figures legends:**

715 Figure 1. Effects of realized genotypic richness (A), relatedness (B), trait diversity (C), evenness
716 (D), and Shannon diversity (E) on aboveground biomass. See Table 2 for statistical analysis.

717 Different symbols are used to denote the richness of genotypes in each plot; the legend is in the
718 bottom right corner of plot E.

719

720 Figure 2. Same as figure 1 but with belowground biomass as the response variable.

721

722 Figure 3. Relationship between genotypic richness and trait diversity.

723

724 Figure 4. Relationship between the ratio of above to belowground eelgrass biomass and the
725 relatedness of eelgrass in each plot (A) and the mean ratio of above to belowground biomass in
726 plots with only one genotype (realized monoculture) compared to plots with multiple genotypes
727 (realized polycultures) at the end of the experiment (B). Different symbols in plot A are used to
728 denote the richness of genotypes in each plot. The error bars in plot B are 95% confidence
729 intervals.

730

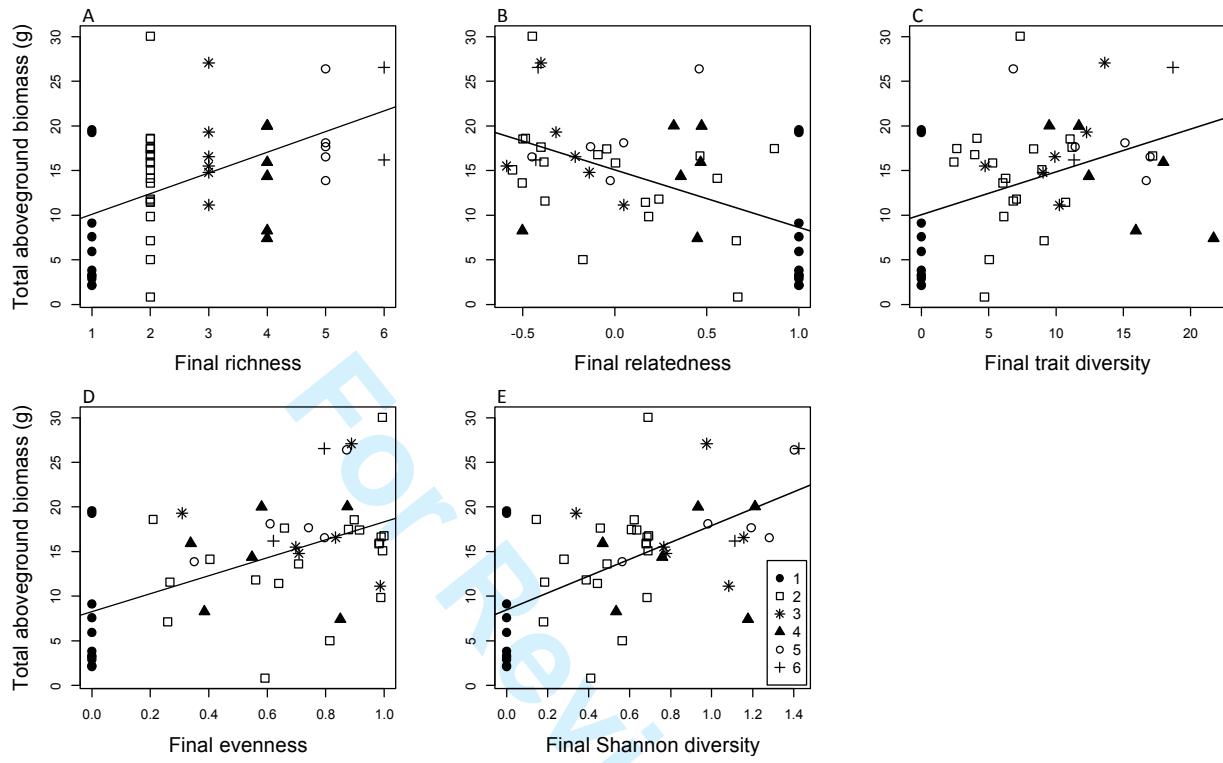
731 Figure 5. Effects of trait diversity on the abundance of invertebrate grazers per plot (A) and of
732 relatedness on invertebrate abundance per gram of eelgrass sampled (B). See Table 3 for

733 analyses. Different symbols are used to denote the richness of genotypes in each plot and the
734 legend is in the upper left corner of plot B.

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737 Figure 1



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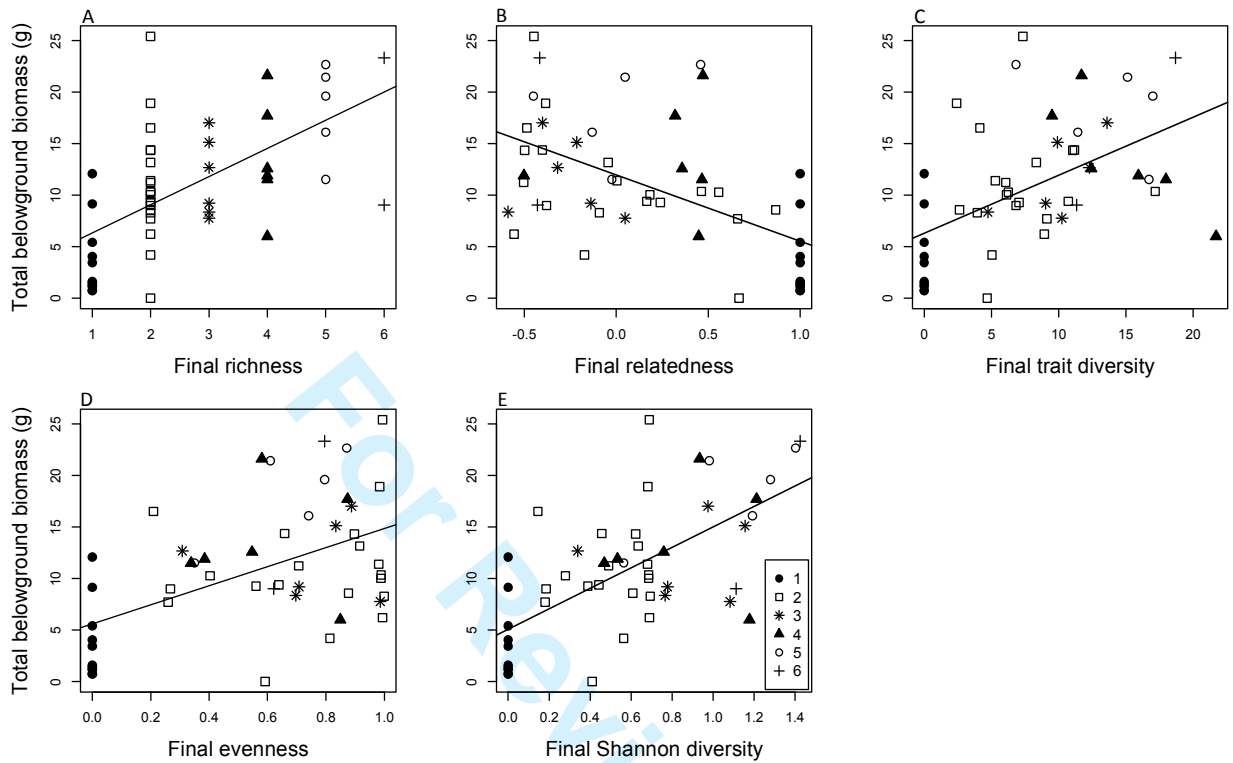
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751 Figure 2



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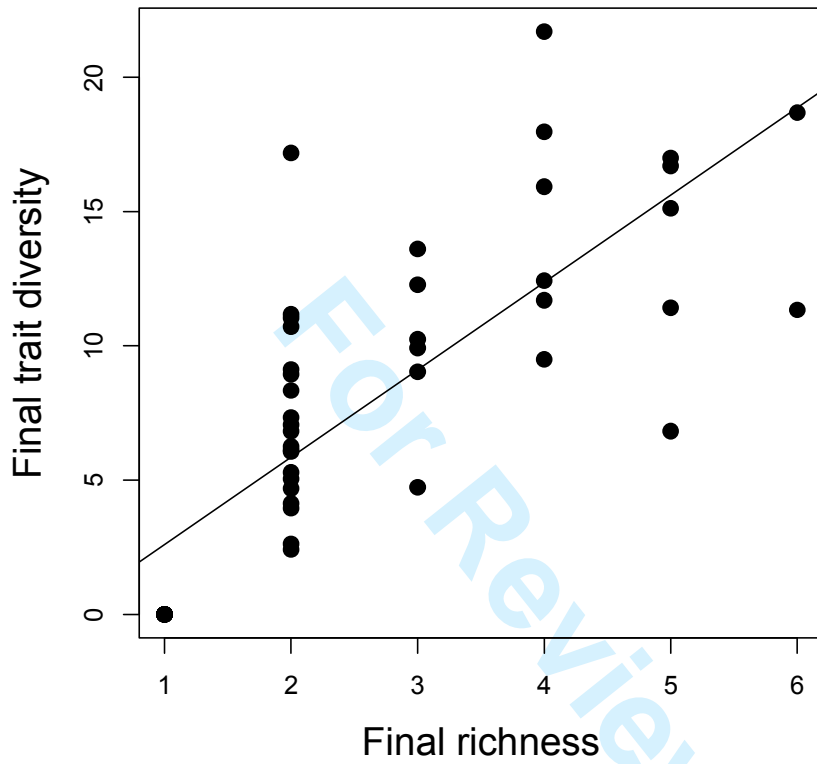
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765 Figure 3



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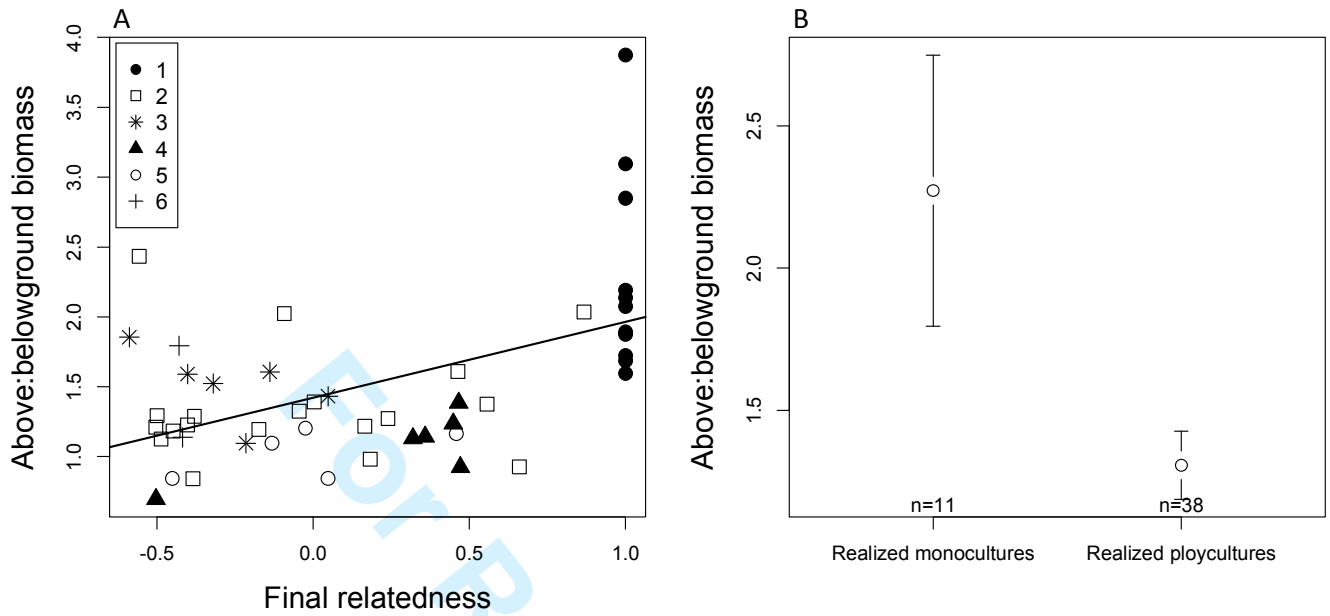
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777 Figure 4



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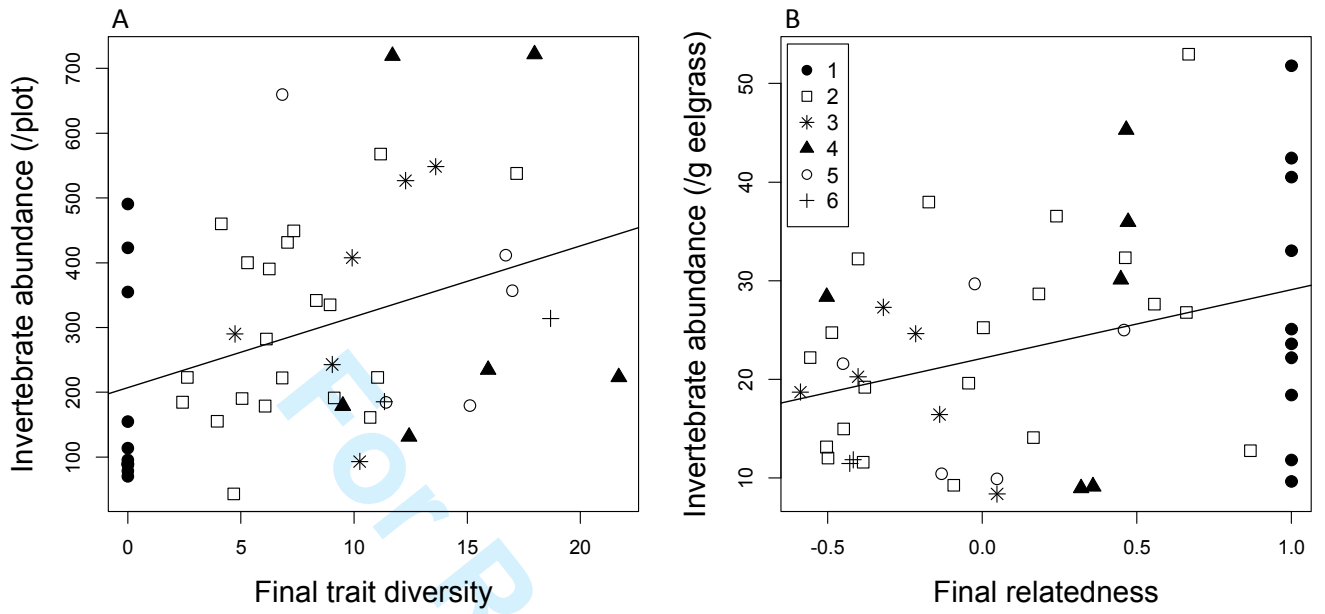
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792 Figure 5



1 **Appendix A:** Genotypic composition of all plots

2 Table A1. Genotypic composition of each plot for the field experiment. Plots were arranged in a
3 grid with 12 blocks along a slight tidal gradient and 6 plots (one of each treatment) in a row
4 (position) in each block. The table gives the block and position of each plot and lists the
5 genotypes that were planted in it. It also gives the pairwise relatedness of genotypes in the two-
6 genotype plots and average pairwise relatedness in the 6 genotype plots. A range of the
7 relatedness of all pairwise combinations of the 6 genotypes is included for the six-genotype
8 plots.

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Block	Position	Treatment	Genotype 1	Genotype 2	Genotype 3	Genotype 4	Genotype 5	Genotype 6	Relatedness (pairwise or average)	Range of pairwise relatedness
A	1	2-high	CCS9	DPHI4	-	-	-	-	0.46	-
B	4	2-high	DPS19	MMS10	-	-	-	-	0.31	-
C	3	2-high	MMH11	MMH17	-	-	-	-	0.87	-
D	6	2-high	DPHI2	WPHI4	-	-	-	-	0.52	-
E	5	2-high	WPHI3	MMH115	-	-	-	-	0.66	-
F	3	2-high	CCS14	MMLI15	-	-	-	-	0.41	-
G	1	2-high	J4	WPLI5	-	-	-	-	0.33	-
H	2	2-high	DPHI14	WPS20	-	-	-	-	0.36	-
I	6	2-high	MMS8	WPS3	-	-	-	-	0.56	-
J	3	2-high	CCHI12	J14	-	-	-	-	0.41	-
K	6	2-high	CCHI12	WPHI12	-	-	-	-	0.41	-
L	6	2-high	CCLI6	CCLI2	-	-	-	-	0.41	-
A	4	2-mid	CCHI1	WPLI12	-	-	-	-	0.02	-
B	5	2-mid	CCHI17	CCLI6	-	-	-	-	-0.04	-
C	4	2-mid	CCS14	DPLI18	-	-	-	-	0.06	-
D	2	2-mid	DPS9	WPHI4	-	-	-	-	-0.02	-
E	2	2-mid	CCS17	MMLI12	-	-	-	-	-0.01	-
F	6	2-mid	DPHI10	MMLI15	-	-	-	-	0.03	-
G	3	2-mid	DPHI14	DPLI18	-	-	-	-	0.00	-
H	5	2-mid	DPHI6	MMH18	-	-	-	-	-0.09	-
I	5	2-mid	WPLI15	WPS9	-	-	-	-	0.00	-
J	5	2-mid	DPLI7	J6	-	-	-	-	0.01	-
K	1	2-mid	DPS14	MMLI17	-	-	-	-	-0.17	-
L	5	2-mid	MMS17	WPHI3	-	-	-	-	-0.03	-
A	6	2-low	CCS17	DPHI6	-	-	-	-	-0.61	-
B	3	2-low	J6	WPLI15	-	-	-	-	-0.38	-
C	2	2-low	DPHI14	J4	-	-	-	-	-0.45	-
D	4	2-low	CCLI2	DPHI6	-	-	-	-	-0.56	-
E	1	2-low	CCS9	WPS9	-	-	-	-	-0.40	-
F	2	2-low	DPHI2	MMLI12	-	-	-	-	-0.69	-
G	2	2-low	DPHI4	DPS9	-	-	-	-	-0.50	-
H	6	2-low	DPLI10	WPLI5	-	-	-	-	-0.50	-
I	2	2-low	MMH11	WPS20	-	-	-	-	-0.43	-
J	6	2-low	J4	WPHI12	-	-	-	-	-0.44	-
K	5	2-low	DPLI7	MMH115	-	-	-	-	-0.49	-
L	1	2-low	MMLI17	WPS3	-	-	-	-	-0.66	-
A	3	6-high	CCHI12	CCLI2	CCS17	J14	WPHI3	WPHI12	0.39	0.25 to 0.45
B	1	6-high	CCS14	CCS9	DPHI14	J6	MMLI15	MMS10	0.41	0.07 to 0.65
C	1	6-high	CCS17	CCS9	DPHI14	J6	MMS8	WPLI12	0.41	0.11 to 0.65
D	5	6-high	CCS9	DPHI14	DPHI4	J14	J6	MMS10	0.41	0.18 to 0.64
E	6	6-high	CCHI12	CCLI6	CCS9	DPHI10	J14	MMS10	0.38	0.004 to 0.56
F	4	6-high	CCS14	DPS14	J6	MMS10	MMS8	WPLI12	0.45	0.24 to 0.71
G	4	6-high	CCLI6	CCLI2	CCS17	J14	MMH11	WPHI12	0.39	0.20 to 0.80
H	1	6-high	CCLI2	CCS14	DPHI14	DPLI10	WPHI3	MMH115	0.39	0.20 to 0.70
I	4	6-high	CCLI2	DPHI10	DPHI14	DPHI2	J6	MMH115	0.43	0.21 to 0.67
J	4	6-high	CCLI2	CCS17	DPLI10	MMH11	WPHI12	WPHI3	0.40	0.20 to 0.80
K	2	6-high	CCS17	DPHI10	DPHI2	J6	MMH11	WPHI4	0.42	0.09 to 0.66
L	4	6-high	CCS17	DPHI10	MMH11	MMH17	WPHI3	WPHI4	0.41	0.11 to 0.87
A	5	6-mid	CCHI17	CCLI6	CCS14	J6	MMH17	WPS3	0.02	-0.21 to 0.4
B	6	6-mid	DPS9	MMS10	WPHI4	WPLI15	WPS3	WPS3	0.04	-0.21 to 0.29
C	6	6-mid	DPS14	MMLI15	MMLI17	WPHI3	WPHI4	WPS9	-0.11	-0.53 to 0.15
D	3	6-mid	DPLI10	DPS14	MMLI17	MMS17	MMH115	WPS9	-0.02	-0.15 to 0.24
E	4	6-mid	CCHI1	DPLI10	J14	MMS8	WPLI15	WPHI4	0.04	-0.17 to 0.25
F	1	6-mid	CCLI6	CCS14	DPS9	MMLI12	WPLI5	WPS3	0.05	-0.32 to 0.16
G	6	6-mid	CCHI12	CCLI6	DPHI14	DPLI10	DPS19	MMS8	0.03	-0.18 to 0.22
H	3	6-mid	DPHI10	DPHI4	DPS14	MMLI17	WPHI12	WPS20	0.06	-0.21 to 0.31
I	3	6-mid	CCHI1	CCLI2	DPHI2	DPS9	WPLI12	WPLI5	0.04	-0.13 to 0.40
J	1	6-mid	CCHI17	CCLI6	CCS17	DPHI4	DPS14	WPLI15	0.05	-0.24 to 0.28
K	4	6-mid	CCHI1	DPHI4	DPS19	J6	MMH11	MMS8	0.03	-0.15 to 0.29
L	2	6-mid	CCHI17	CCS9	J6	J4	WPHI3	WPHI4	0.07	-0.25 to 0.35
A	2	6-low	DPS19	J4	MMH17	MMH18	WPLI15	WPS20	-0.42	-0.79 to -0.12
B	2	6-low	CCHI12	CCHI17	DPLI18	DPLI7	WPLI5	MMS17	-0.42	-0.74 to -0.07
C	5	6-low	DPS19	DPS9	MMH17	MMLI12	MMS17	WPLI15	-0.44	-0.68 to -0.07
D	1	6-low	CCHI12	CCLI6	DPLI18	DPS9	MMH18	MMLI17	-0.41	-0.76 to 0.004
E	3	6-low	DPLI18	DPS19	MMLI12	MMS17	WPLI15	WPHI4	-0.45	-0.76 to -0.12
F	5	6-low	CCHI1	CCHI12	DPLI7	MMLI15	MMH18	WPLI5	-0.49	-0.76 to -0.12
G	5	6-low	DPHI6	DPS19	DPS9	MMLI15	MMS17	WPLI15	-0.47	-0.78 to -0.14
H	4	6-low	CCLI6	DPHI6	DPLI7	MMH18	MMLI15	WPS9	-0.43	-0.66 to -0.09
I	1	6-low	DPHI10	DPLI18	DPLI7	MMLI12	MMS17	WPLI15	-0.43	-0.81 to -0.14
J	2	6-low	CCHI12	DPLI7	MMLI12	MMLI15	WPLI15	WPLI5	-0.45	-0.80 to -0.13
K	3	6-low	CCLI6	MMLI12	DPLI18	DPLI7	MMS17	WPHI4	-0.44	-0.81 to -0.14
L	3	6-low	CCHI12	DPLI18	DPS9	MMH18	MMLI17	WPS9	-0.43	-0.76 to -0.18

10 Table A2. The number of plots in which each genotype was planted for each of the treatment
 11 combinations (2 or 6 genotypes and distantly related (low), intermediately related (mid), or
 12 closely related (high). No genotype occurred in more than half of the replicates for a particular
 13 treatment combination (6/12 replicates), and all genotypes occurred in both 2 and 6 genotype
 14 treatments and at least two levels of relatedness.

Genotype	6 genotypes			2 genotypes		
	High	Mid	Low	High	mid	low
CCHI1	0	3	1	0	1	0
CCHI12	2	1	5	2	0	0
CCHI17	0	4	1	0	1	0
CCLI6	2	4	3	1	1	0
CCLI2	5	1	0	1	1	0
CCS14	3	2	0	1	0	1
CCS17	6	1	0	0	1	1
CCS9	4	1	0	1	0	1
DPHI10	4	1	1	0	1	0
DPHI14	5	1	0	1	1	1
DPHI2	2	1	0	1	0	1
DPHI4	1	3	0	1	0	1
DPHI6	0	0	2	0	1	2
DPLI10	2	3	0	0	0	1
DPLI18	0	0	6	0	2	0
DPLI7	0	0	6	0	1	1
DPS14	1	4	0	0	1	0
DPS19	0	2	4	1	0	0
DPS9	0	3	5	0	1	1
J14	4	1	0	1	0	0
J4	0	1	1	1	0	2
J6	6	3	0	0	1	1
MMHI1	4	2	0	1	0	1
MMHI7	1	1	2	1	0	0
MMHI8	0	0	5	0	1	0
MMLI12	0	1	4	0	1	1
MMLI15	1	1	4	1	1	0
MMLI7	0	3	2	0	1	1
MMS10	4	1	0	1	0	0
MMS17	0	1	6	0	1	0
MMS8	2	3	0	1	0	0
WPHI12	3	1	0	1	0	1
WPHI3	4	2	0	1	1	0
WPHI4	2	3	2	1	1	0
MMHI15	2	1	0	1	0	1
WPLI12	2	1	0	0	1	0
WPLI15	0	2	6	0	1	1
WPLI5	0	3	3	1	0	1
WPS20	0	1	1	1	0	1
WPS3	0	3	0	1	0	1
WPS9	0	2	2	0	1	1

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19 **Appendix B:** Results from analyses of the likelihood of an invading genotype establishing in a
 20 plot. We considered the establishment of invading genotypes as a binomial response and used
 21 logistic regression (glm function from the stats package in R) to test the effects of the
 22 relatedness, richness, and trait diversity of the genotypes in the plot on establishment. Because
 23 we do not know when the invading genotypes established we used both the planted (based on
 24 initial genotype composition, table B1) and realized (based on final genotype composition, table
 25 B2) diversity metrics. Tables show the coefficients, their standard error, the Wald Z-statistic, and
 26 associated p-values (at $\alpha=0.05$). Neither planted or realized diversity metrics had any effect on
 27 the establishment of new genotypes.

28 Table B1.

<i>Models using initial diversity metrics</i>	Invasion of new genotypes			
	<i>Coeff.</i>	<i>SE</i>	<i>Wald Z</i>	<i>P</i>
<i>Relatedness*richness +trait diversity</i>				
Relatedness*richness	0.47	0.41	1.15	0.25
Relatedness	-2.21	1.70	-1.30	0.19
Richness	-0.11	0.19	-0.59	0.56
Trait diversity	0.04	0.07	0.61	0.55
<i>Relatedness+richness +trait diversity</i>				
Relatedness	-0.53	0.77	-0.69	0.50
Richness	-0.13	0.18	-0.71	0.48
Trait diversity	0.03	0.06	0.52	0.61
<i>Relatedness</i>				
Relatedness	-0.50	0.76	-0.66	0.51
Richness	-0.07	0.15	-0.51	0.61
<i>Relatedness</i>				
Relatedness	-0.50	0.77	-0.65	0.52

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30 Table B2.

<i>Models using final diversity metrics</i>	Invasion of new genotypes			
	<i>Coeff.</i>	<i>SE</i>	<i>Wald Z</i>	<i>P</i>
<i>Relatedness+richness</i>				
<i>+evenness +trait diversity</i>				
Relatedness	0.41	0.77	0.53	0.60
Richness	0.28	0.34	0.81	0.42
Evenness	-1.98	3.29	-0.60	0.55
Trait diversity	-0.02	0.09	-0.18	0.86
<i>Relatedness+richness+trait diversity</i>				
Relatedness	0.43	0.76	0.66	0.57
Richness	0.23	0.24	0.96	0.34
evenness	-2.10	3.22	-0.65	0.52
<i>Richness+evenness</i>				
Richness	0.18	0.23	0.81	0.42
Evenness	-3.10	2.70	-1.15	0.25
<i>Evenness</i>				
Evenness	-2.21	2.39	-0.92	0.36

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42 **Appendix C:** Results from analyses of the likelihood that a plot will experience complete
 43 mortality across all plots (table C1) and the likelihood of exclusion in the two and six genotype
 44 plots separately (tables C2 and C3).

45

46 Table C1. Table shows the coefficients, their standard error, the Wald Z-statistic, and associated
 47 p-values (at $\alpha=0.05$).

<i>Models using initial diversity metrics</i>	Complete Mortality			
	<i>Coeff.</i>	<i>SE</i>	<i>Wald Z</i>	<i>P</i>
<i>Relatedness*richness +trait diversity</i>				
Relatedness*richness	-0.30	0.36	-0.83	0.41
Relatedness	0.26	1.41	0.19	0.85
Richness	0.14	0.16	0.89	0.37
Trait diversity	-0.04	0.05	-0.68	0.49
<i>Relatedness+richness +trait diversity</i>				
Relatedness	-0.78	0.68	-1.14	0.25
Richness	.14	0.16	0.86	0.39
Trait diversity	-0.04	0.05	-0.75	0.45
<i>Relatedness</i>				
Relatedness	-0.81	0.68	-1.19	0.23
Richness	0.07	0.13	0.53	0.60
<i>Relatedness</i>				
Relatedness	-0.81	0.68	-1.19	0.23

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50 Table C2. Model results for the effects of the relatedness and trait diversity of the initially
 51 planted genotypes on the likelihood that one genotype would be excluded from the plot in the

52 two-genotype plots. Table shows the coefficients, their standard error, the Wald Z-statistic, and
 53 associated p-values (at $\alpha=0.05$).

54

<i>Models using initial diversity metrics</i>	Coexistence in 2-genotype plots			
	<i>Coeff.</i>	<i>SE</i>	<i>Wald Z</i>	<i>P</i>
<i>Relatedness+trait diversity</i>				
Relatedness	0.25	0.97	0.26	0.38
Trait Diversity	-0.07	0.08	-0.87	0.38
<i>Relatedness</i>				
Relatedness	0.14	0.94	0.15	0.88
<i>Trait diversity</i>				
Trait diversity	-0.07	0.08	-0.85	0.39

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56

57 Table C3. Model results for the effects of the relatedness and trait diversity of the initially
 58 planted genotypes on the survivorship of genotypes in the six-genotype plots. Block was
 59 included as a random effect; however, to save space results for block are not included in the
 60 table. Models are presented with posterior means (Bayes estimates), 95% credible intervals
 61 (equivalent to 95% confidence intervals), and pMCMC values (probability of the estimate
 62 overlapping zero).

<i>Models using initial diversity metrics</i>	Survivorship in 6 genotype plots			
	<i>Post mean</i>	<i>Lower CI</i>	<i>Upper CI</i>	<i>pMCMC</i>
<i>Relatedness+trait diversity</i>				
Relatedness	0.005	-0.26	0.32	0.98
Trait diversity	0.009	-0.02	0.04	0.48
<i>Trait diversity</i>				
Trait diversity	0.009	-0.02	0.03	0.48

63

64 **Appendix D:** Summary of generalized linear mixed model results for diversity metrics based on

65 initial eelgrass composition on belowground biomass, leaf growth rate, invertebrate grazer

66 richness (raw counts from eelgrass sampled), and invertebrate grazer abundance (per gram of

67 eelgrass sampled). Results for aboveground biomass were qualitatively similar to belowground

68 biomass and results invertebrate grazer abundance per plot were qualitatively similar to

69 invertebrate grazer abundance per gram of eelgrass sampled, and thus are not presented.

70 Predictor variables evaluated are based on the composition of genotypes at the beginning of the

71 experiment and include average genetic relatedness, genotypic richness, and trait diversity

72 (Rao's Q). Block was included as a random effect; however, to save space results for block are

73 not included in the table. Models are presented with posterior means (Bayes estimates), 95%

74 credible intervals (equivalent to 95% confidence intervals), and pMCMC values (probability of

75 the estimate overlapping zero). Initially, we found a significant negative correlation between trait

76 diversity and invertebrate abundance per gram of eelgrass sampled, but this relationship was

77 driven by one extreme point, which we determined to be an outlier using the Grubbs test for

78 single outliers ($P = 0.004$; Grubbs 1950).

79

83 **Appendix E:** Table of pMCMC values (tests if the parameter is significantly different from zero,
84 analogous to p-values at $\alpha=0.05$) from analyses of the effects of individual traits of eelgrass
85 genotypes in assemblages on belowground biomass, leaf growth rate, and invertebrate grazer
86 richness. We analyzed the mean, variance, range, and maximum and minimum values of each
87 trait for each plot. We looked at the effects of each trait individually in the model (A) and
88 including any significant factors from our analyses with relatedness and genotypic diversity (B).
89 Block was included as a random effect in all models.

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Table of pMCMC values

Trait	Belowground biomass					Leaf Growth					Invertebrate richness				
	Mean	Variation	Range	Max	Min	Mean	Variation	Range	Max	Min	Mean	Variation	Range	Max	Min
A)	<i>model: trait alone</i>														
Alpha	0.71	0.09	0.004**	0.1	0.034*	0.63	0.34	0.21	0.21	0.83	0.99	0.94	0.62	0.76	0.94
Phenolic content	0.93	0.63	0.01*	0.18	0.16	0.16	0.88	0.66	0.25	0.08	0.48	0.89	0.31	0.58	0.99
Ammonium uptake	0.69	0.2	0.002**	0.02*	0.11	0.29	0.48	0.43	0.39	0.89	0.57	0.69	0.42	0.9	0.22
Nitrate uptake	0.75	0.22	<0.001***	0.07	0.03*	0.56	0.38	0.39	0.37	0.89	0.42	0.29	0.59	0.94	0.22
Terminal shoot biomass	0.47	0.18	0.006**	0.23	0.002**	0.87	0.012*	0.03*	0.09	0.2	0.72	0.49	0.43	0.82	0.69
Rhizome biomass	0.56	<0.001***	<0.001***	0.03*	0.002**	0.46	0.432	0.38	0.87	0.24	0.67	0.31	0.41	0.98	0.51
Root biomass	0.56	0.02*	<0.001***	0.1	0.01*	0.08	0.07	0.63	0.12	0.24	0.36	0.11	0.13	0.14	0.88
New shoot biomass	0.81	0.06	<0.001***	0.07	0.03*	0.19	0.06	0.29	0.13	0.45	0.67	0.27	0.41	0.76	0.45
Leaf growth biomass	0.7	0.12	<0.001***	0.16	0.01**	0.62	0.14	0.16	0.6	0.19	0.91	0.99	0.7	0.81	0.87
Leaf growth CM ²	0.88	0.12	<0.001***	0.05*	0.02*	0.36	0.12	0.1	0.75	0.11	0.92	0.45	0.34	0.39	0.74
Number of new shoots	0.45	0.002**	<0.001***	0.002**	0.06	0.67	0.93	0.84	0.78	0.47	0.15	0.85	0.96	0.23	0.25
Max shoot length	0.55	0.03*	<0.001***	0.08	0.008**	0.31	0.04*	0.07	0.63	0.07	0.19	0.77	0.45	0.13	0.33
Shoot width	0.34	0.12	<0.001***	0.004**	0.24	0.81	0.01*	0.01*	0.1	0.22	0.54	0.26	0.38	0.93	0.35
Rhizome diameter	0.58	0.16	0.004**	0.02*	0.16	0.45	0.11	0.09	0.05*	0.48	0.25	0.53	0.76	0.48	0.48
Max root length	0.29	<0.001***	<0.001***	0.04*	<0.001***	0.62	0.74	0.54	0.6	0.12	0.69	0.78	0.88	0.93	0.9
Total rhizome length	0.46	<0.001***	<0.001***	0.03*	<0.001***	0.39	0.7	0.87	0.81	0.59	0.87	0.26	0.21	0.58	0.49
above:belowground biomass	0.8	0.02*	<0.001***	0.006**	0.02*	0.43	0.03*	0.01*	0.04*	0.23	0.33	0.4	0.84	0.33	0.49
B)	<i>model: trait + relatedness</i>														
Alpha	0.6	0.71	0.75	0.73	0.32	0.25	0.94	0.74	0.26	0.26	0.53	0.31	0.43	0.99	0.16
Phenolic content	0.92	0.22	0.24	0.69	0.49	0.16	0.62	0.63	0.1	0.2	0.63	0.7	0.79	0.97	0.75
Ammonium uptake	0.74	0.18	0.25	0.9	0.14	0.27	0.89	0.78	0.77	0.41	0.59	0.7	0.75	0.42	0.73
Nitrate uptake	0.47	0.84	0.88	0.77	0.49	0.59	0.7	0.93	0.75	0.68	0.54	0.1	0.12	0.62	0.07
Terminal shoot biomass	0.56	0.84	0.68	0.84	0.49	0.92	0.03*	0.47	0.16	0.15	0.93	0.94	0.92	0.78	0.66
Rhizome biomass	0.91	0.03*	0.19	0.58	0.43	0.76	0.81	0.87	0.7	0.74	0.88	0.86	0.62	0.76	0.73
Root biomass	0.51	0.77	0.39	0.41	0.93	0.29	0.01*	0.02*	0.06	0.5	0.13	0.23	0.52	0.14	0.19
New shoot biomass	0.78	0.99	0.77	0.66	0.74	0.33	0.004**	0.01*	0.04*	0.83	0.89	0.65	0.91	0.95	0.76
Leaf growth biomass	0.98	0.86	0.5	0.96	0.56	0.89	0.39	0.5	0.88	0.48	0.71	0.41	0.56	0.88	0.32
Leaf growth CM ²	0.49	0.42	0.24	0.34	0.76	0.7	0.27	0.37	0.39	0.89	0.69	0.92	0.9	0.7	0.61
Number of new shoots	0.41	0.26	0.13	0.17	0.89	0.78	0.28	0.36	0.48	0.98	0.23	0.2	0.24	0.06	0.58
Max shoot length	0.87	0.71	0.47	0.81	0.69	0.31	0.15	0.34	0.95	0.25	0.19	0.24	0.72	0.43	0.06
Shoot width	0.99	0.75	0.7	0.96	0.79	0.96	0.02*	0.06	0.25	0.3	0.41	0.65	0.95	0.38	0.5
Rhizome diameter	0.6	0.94	0.77	0.85	0.69	0.53	0.27	0.34	0.19	0.92	0.16	0.19	0.53	0.12	0.76
Max root length	0.76	0.14	0.11	0.64	0.23	0.34	0.95	0.95	0.47	0.41	0.41	0.43	0.51	0.94	0.25
Total rhizome length	0.98	0.11	0.11	0.49	0.42	0.87	0.15	0.31	0.64	0.64	0.57	0.83	0.74	0.8	0.54
above:belowground biomass	0.76	0.65	0.47	0.71	0.64	0.76	0.07	0.11	0.14	0.41	0.11	0.1	0.44	0.03*	0.81
	<i>model: trait + relatedness</i>														
Alpha	0.6	0.71	0.75	0.73	0.32	0.25	0.94	0.74	0.26	0.26	0.53	0.31	0.43	0.99	0.16
Phenolic content	0.92	0.22	0.24	0.69	0.49	0.16	0.62	0.63	0.1	0.2	0.63	0.7	0.79	0.97	0.75
Ammonium uptake	0.74	0.18	0.25	0.9	0.14	0.27	0.89	0.78	0.77	0.41	0.59	0.7	0.75	0.42	0.73
Nitrate uptake	0.47	0.84	0.88	0.77	0.49	0.59	0.7	0.93	0.75	0.68	0.54	0.1	0.12	0.62	0.07
Terminal shoot biomass	0.56	0.84	0.68	0.84	0.49	0.92	0.03*	0.47	0.16	0.15	0.93	0.94	0.92	0.78	0.66
Rhizome biomass	0.91	0.03*	0.19	0.58	0.43	0.76	0.81	0.87	0.7	0.74	0.88	0.86	0.62	0.76	0.73
Root biomass	0.51	0.77	0.39	0.41	0.93	0.29	0.01*	0.02*	0.06	0.5	0.13	0.23	0.52	0.14	0.19
New shoot biomass	0.78	0.99	0.77	0.66	0.74	0.33	0.004**	0.01*	0.04*	0.83	0.89	0.65	0.91	0.95	0.76
Leaf growth biomass	0.98	0.86	0.5	0.96	0.56	0.89	0.39	0.5	0.88	0.48	0.71	0.41	0.56	0.88	0.32
Leaf growth CM ²	0.49	0.42	0.24	0.34	0.76	0.7	0.27	0.37	0.39	0.89	0.69	0.92	0.9	0.7	0.61
Number of new shoots	0.41	0.26	0.13	0.17	0.89	0.78	0.28	0.36	0.48	0.98	0.23	0.2	0.24	0.06	0.58
Max shoot length	0.87	0.71	0.47	0.81	0.69	0.31	0.15	0.34	0.95	0.25	0.19	0.24	0.72	0.43	0.06
Shoot width	0.99	0.75	0.7	0.96	0.79	0.96	0.02*	0.06	0.25	0.3	0.41	0.65	0.95	0.38	0.5
Rhizome diameter	0.6	0.94	0.77	0.85	0.69	0.53	0.27	0.34	0.19	0.92	0.16	0.19	0.53	0.12	0.76
Max root length	0.76	0.14	0.11	0.64	0.23	0.34	0.95	0.95	0.47	0.41	0.41	0.43	0.51	0.94	0.25
Total rhizome length	0.98	0.11	0.11	0.49	0.42	0.87	0.15	0.31	0.64	0.64	0.57	0.83	0.74	0.8	0.54
above:belowground biomass	0.76	0.65	0.47	0.71	0.64	0.76	0.07	0.11	0.14	0.41	0.11	0.1	0.44	0.03*	0.81

91 **Appendix F:** Summary of generalized linear mixed model results for the effects of realized
92 diversity metrics on the leaf growth in each plot. We only present results from analyses using all
93 plots with eelgrass at the end of the experiment because there were no significant results when
94 plots with only one genotype were excluded. The predictor variables evaluated are based on the
95 realized composition of genotypes at the end of the experiment and include for average genetic
96 relatedness, genotypic richness, genotypic evenness, and trait diversity (Rao's Q). Block was
97 included as a random effect; however, to save space results for block are not included in the
98 table. Models are presented with posterior means (Bayes estimates), 95% credible intervals
99 (equivalent to 95% confidence intervals), and pMCMC values (probability of the estimate
100 overlapping zero).

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<i>Models using final diversity metrics</i>	Leaf growth all plots with eelgrass				
	<i>Post mean</i>	<i>Lower CI</i>	<i>Upper CI</i>	<i>pMCMC</i>	<i>DIC</i>
<i>Relatedness+richness+evenness+trait diversity</i>					368.24
Relatedness	6.26	-1.15	13.66	0.10	
Richness	0.21	-3.36	3.43	0.90	
Evenness	3.06	-7.40	15.43	0.59	
Trait diversity	-0.10	-1.01	0.70	0.83	
<i>Relatedness+evenness+trait diversity</i>					366.20
Relatedness	6.33	-0.54	14.71	0.10	
Evenness	3.14	-8.47	14.17	0.59	
Trait diversity	-0.06	-0.60	0.61	0.82	
<i>Relatedness+richness</i>					364.11
Relatedness	6.27	-0.81	13.80	0.09	
Evenness	2.72	-9.82	13.12	0.60	
<i>Relatedness</i>					362.14
Relatedness	5.05	0.25	10.51	0.06	
<i>Richness</i>					365.15
Richness	-0.95	-3.15	0.92	0.35	
<i>Evenness</i>					364.94
Evenness	-3.80	-11.45	4.25	0.35	
<i>Trait diversity</i>					364.97
Trait diversity	-0.27	-0.79	0.24	0.30	

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103 **Appendix G:** Summary of generalized linear mixed model results for the effects of realized
104 diversity metrics on below and aboveground biomass (Table H1) and invertebrate richness and
105 abundance (Table H2) when plots with one genotype remaining at the end of the experiment
106 (realized monocultures) are excluded. Predictor variables evaluated are based on the composition
107 of genotypes at the end of the experiment and include average genetic relatedness, eelgrass
108 genotypic richness, genotypic evenness, and trait diversity (Rao's Q). Block was included as a
109 random effect; however, to save space results for block are not included in the table. Models are
110 presented with posterior means (Bayes estimates), 95% credible intervals (equivalent to 95%
111 confidence intervals), and pMCMC values (probability of the estimate overlapping zero).

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113 **Table G1.** Effects of various realized diversity metrics on below and aboveground biomass
 114 accumulation in plots where more than genotype remains at the end of the experiment (realized
 115 monocultures excluded).

<i>Models using final unweighted diversity metrics</i>	Only plots with more than one genotype at the end of the experiment									
	Belowground biomass					Aboveground biomass				
	<i>Post mean</i>	<i>Lower CI</i>	<i>Upper CI</i>	<i>pMC-MC</i>	<i>DIC</i>	<i>Post mean</i>	<i>Lower CI</i>	<i>Upper CI</i>	<i>pMC-MC</i>	<i>DIC</i>
<i>Relatedness+richness+evenness+trait diversity</i>					243.51					248.26
Relatedness	-3.31	-7.59	0.62	0.12		-3.80	-7.84	0.66	0.09	
Richness	1.79	0.12	3.63	0.05		1.35	-0.44	3.27	0.15	
Evenness	2.57	-4.50	10.13	0.50		5.74	-2.55	13.07	0.14	
Trait diversity	-0.02	-0.47	0.41	0.97		-0.03	-0.48	0.49	0.90	
<i>Relatedness+richness+evenness</i>					241.65					246.71
Relatedness	-3.27	-7.16	0.79	0.11		-3.77	-7.89	0.64	0.07	
Richness	1.74	0.45	2.97	0.007		1.33	-0.05	2.56	0.04	
Evenness	2.80	-4.15	10.20	0.42		5.99	-1.76	13.14	0.12	
<i>Relatedness+richness</i>					239.40					245.82
Relatedness	-3.5	-7.18	0.54	0.07		-4.45	-9.07	-0.43	0.04	
Richness	1.65	0.44	2.81	0.002		1.05	-0.17	2.45	0.11	
<i>Richness+evenness</i>					-					-
Richness	-	-	-	-		-	-	-	-	
Evenness	-	-	-	-		-	-	-	-	
<i>Relatedness</i>					243.95					245.90
Relatedness	-3.84	-8.01	0.12	0.07		-4.59	-8.80	-0.31	0.04	
<i>Richness</i>					242.18					249.93
Richness	1.71	0.41	2.93	0.01		1.19	-0.29	2.51	0.10	
<i>Evenness</i>					248.78					250.58
Evenness	1.83	-5.80	9.65	0.63		5.89	-2.07	13.15	0.14	
<i>Trait diversity</i>										251.52
Trait diversity	0.36	-0.17	0.82	0.15	245.88	0.15	-0.23	0.53	0.45	

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123 **Table G2.** Effects of realized diversity metrics on invertebrate grazer a) richness (raw counts

124 from eelgrass sampled) and b) abundance (per gram of eelgrass sampled and scaled to plot) in

125 plots where more than genotype remains at the end of the experiment (realized monocultures

126 excluded).

127

128 Table G1a:

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Only plots with more than one genotype at the end of the experiment

Invertebrate richness					
<i>Models using final diversity metrics</i>	<i>Post mean</i>	<i>Lower CI</i>	<i>Upper CI</i>	<i>pMC-MC</i>	<i>DIC</i>
<i>Relatedness+richness+evenness+trait diversity</i>					168.45
Relatedness	0.25	-1.22	1.79	0.75	
Richness	0.16	-0.47	0.79	0.62	
Evenness	-0.74	-3.45	1.81	0.56	
Trait diversity	-0.01	-0.19	0.15	0.91	
<i>Relatedness+richness+evenness</i>					166.34
Relatedness	0.23	-1.37	1.58	0.74	
Richness	0.15	-0.29	0.65	0.55	
Evenness	-0.79	-3.54	1.68	0.54	
<i>Richness+evenness</i>					164.45
Richness	0.14	-0.30	0.62	0.56	
Evenness	-0.84	-3.52	1.75	0.52	
<i>Relatedness</i>					163.07
Relatedness	0.25	-1.26	1.65	0.74	
<i>Richness</i>					162.81
Richness	-0.15	-0.29	0.67	0.53	
<i>Evenness</i>					162.65
Evenness	-0.92	-3.39	1.64	0.47	
<i>Trait diversity</i>					163.06
Trait diversity	-0.02	-0.11	0.14	0.70	

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131 Table G2b:

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<i>Models using final diversity metrics</i>	Only plots with more than one genotype at the end of the experiment									
	Invertebrate abundance (/g eelgrass)					Invertebrate abundance (/plot)				
	<i>Post mean</i>	<i>Lower CI</i>	<i>Upper CI</i>	<i>pMC-MC</i>	<i>DIC</i>	<i>Post mean</i>	<i>Lower CI</i>	<i>Upper CI</i>	<i>pMC-MC</i>	<i>DIC</i>
<i>Relatedness+richness+evenness+trait diversity</i>					286.25					520.92
Relatedness	7.39	0.72	14.26	0.04		5.53	-141.7	140.7	0.91	
Richness	-2.54	-5.54	0.33	0.08		-15.55	-72.38	39.71	0.59	
Evenness	-10.98	-23.46	1.80	0.09		-80.12	-314.8	168.8	0.50	
Trait diversity	0.56	-0.18	1.34	0.15		10.52	-5.43	25.65	0.18	
<i>Relatedness+richness+evenness</i>					286.89					-
Relatedness	7.71	0.72	14.37	0.03		-	-	-	-	
Richness	-1.25	-3.76	1.16	0.32		-	-	-	-	
Evenness	-11.01	-24.93	2.28	0.11		-	-	-	-	
<i>Richness+evenness+trait diversity</i>					-					518.84
Richness	-	-	-	-		-16.19	-71.49	43.13	0.55	
Evenness	-	-	-	-		-73.36	-305.6	151.1	0.53	
Trait diversity	-	-	-	-		10.88	-4.65	26.31	0.18	
<i>Relatedness+evenness</i>					283.58					-
Relatedness	7.99	0.71	14.25	0.02		-	-	-	-	
Evenness	-8.79	-21.75	4.01	0.16		-	-	-	-	
<i>Evenness+trait diversity</i>					-					517.08
Evenness	-	-	-	-		-70.59	-291.6	168.6	0.56	
Trait diversity	-	-	-	-		7.81	-4.77	18.77	0.19	
<i>Relatedness</i>					280.44					517.78
Relatedness	8.60	2.00	15.53	0.008		15.11	-127.5	145.8	0.81	
<i>Richness</i>					290.51					517.51
Richness	-0.81	-3.12	1.71	0.52		10.68	-31.27	56.59	0.64	
<i>Evenness</i>					288.83					517.03
Evenness	-10.75	-24.27	1.92	0.10		-95.22	-324.4	140.2	0.42	
<i>Trait diversity</i>					287.77					515.54
Trait diversity	0.23	-0.37	0.84	0.45		8.62	-3.58	20.24	0.16	

134 **Appendix H:** Summary of generalized linear mixed model results for the effects of realized
 135 diversity metrics on invertebrate grazer richness (raw counts from eelgrass sampled). Predictor
 136 variables evaluated are based on the composition of genotypes at the end of the experiment and
 137 include average genetic relatedness, eelgrass genotypic richness, genotypic evenness, and trait
 138 diversity (Rao's Q). Block was included as a random effect; however, to save space results for
 139 block are not included in the table. Models are presented with posterior means (Bayes estimates),
 140 95% credible intervals (equivalent to 95% confidence intervals), and pMCMC values
 141 (probability of the estimate overlapping zero).

<i>Models using final diversity metrics</i>	Invertebrate richness				<i>DIC</i>
	<i>Post mean</i>	<i>Lower CI</i>	<i>Upper CI</i>	<i>pMC-MC</i>	
<i>Relatedness+richness+evenness+trait diversity</i>					209.65
Relatedness	0.35	-0.94	1.51	0.580	
Richness	0.15	-0.46	0.75	0.61	
Evenness	-1.11	-3.02	0.93	0.28	
Trait diversity	-0.02	-0.17	0.14	0.82	
<i>Relatedness+richness+evenness</i>					207.78
Relatedness	0.35	-0.98	1.58	0.59	
Richness	0.08	-0.32	0.52	0.68	
Evenness	-1.15	-2.91	0.85	0.23	
<i>Relatedness+evenness</i>					205.94
Relatedness	0.27	-0.98	1.50	0.64	
Evenness	-1.10	-2.93	0.83	0.26	
<i>Relatedness</i>					205.43
Relatedness	0.72	-0.29	1.59	0.12	
<i>Richness</i>					207.68
Richness	-0.10	-0.49	0.27	0.62	
<i>Evenness</i>					204.16
Evenness	-1.32	-2.66	0.15	0.07	
<i>Trait diversity</i>					206.93
Trait diversity	-0.04	-0.13	0.05	0.31	

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