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Revisiting the Holy Grail: using plant functional traits to understand ecological processes

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26 Running head: Plant functional traits

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30

31 ABSTRACT

32   One of ecology's grand challenges is developing general rules to

33 explain and predict highly complex systems. Understanding and predicting

34 ecological processes from species' traits has been considered a 'Holy Grail'

35 in ecology. Plant functional traits are increasingly being used to develop

36 mechanistic models that can predict how ecological communities will

37 respond to abiotic and biotic perturbations and how species will affect

38 ecosystem function and services in a rapidly changing world; however,

39 significant challenges remain. In this review, we highlight recent work and

40 outstanding questions in three areas: (*i*) selecting relevant traits, (*ii*)

41 describing intraspecific trait variation and incorporating this variation into

42 models, and (*iii*) scaling trait data to community- and ecosystem-level

43 processes. Over the past decade, there have been significant advances in

44 the characterization of plant strategies based on traits and trait

45 relationships, and the integration of traits into multivariate indices and

46 models of community and ecosystem function. However, the utility of trait-

47 based approaches in ecology will benefit from efforts that demonstrate how

48 these traits and indices influence organismal, community, and ecosystem

49 processes across vegetation types, which may be achieved through meta-

50 analysis and enhancement of trait databases. Additionally, intraspecific trait

51 variation and species interactions need to be incorporated into predictive

52 models using tools such as Bayesian hierarchical modelling. Finally, existing

53 models linking traits to community and ecosystem processes need to be

54 empirically tested for their applicability to be realized.

55

56 *Key words*: community assembly, ecological modelling, intraspecific

57 variation, leaf economics spectrum, functional diversity, response traits,

58 effect traits.

59

60 CONTENTS

80

81   **I. INTRODUCTION**

82   Ecologists have a long tradition of grouping organisms based on

83   function (Grime, 1974; Raunkiaer, 1934; Root, 1967). A renewed interest in

84   this approach came in the late 1990s when a number of ecologists sought to

85   understand how the functional traits of species could predict community

86   response to environmental change and the effects of changes in community

87   composition on ecosystem processes (Chapin *et al.*, 2000; Díaz & Cabido,

88   1997; Lavorel *et al.*, 1997). Lavorel & Garnier (2002) developed a conceptual

89   framework by distinguishing traits that predict how species respond to

4

90   environmental factors (response traits) from traits that affect ecosystem

91   processes (effect traits). They argued that understanding and predicting

92   community processes from species traits, rather than species identity, was a

93   'Holy Grail' in ecology. While empirical tests of this framework were slow to

94   appear (Suding & Goldstein, 2008), the formalization of the leaf economic

95   spectrum (LES) spurred an increased focus on trait-based methodological

96   approaches. The LES shows that relationships exist among several key traits

97   across a broad range of species and different climates (Reich, Walters &

98   Ellsworth, 1997; Wright *et al.*, 2004), and that simple predictors (specific leaf

99   area, SLA) may link to hard-to-measure ecological processes (e.g. growth

100   rate).

101   Whether or not traits matter to community ecology is closely related to

102   whether or not the niche matters, as niche differentiation can be defined as

103   differential performance along environmental gradients with respect to

104   organismal traits (Chase & Leibold, 2003). Opinions regarding the relative

105   importance of the niche, and hence traits, to community dynamics fall

106   loosely into three camps. The first argues that trait differences among

107   individuals are largely irrelevant at the community level compared to factors

108   such as demographic stochasticity (e.g. Neutral Theory: Hubbell, 2001). The

109   second argues that traits are relevant to individuals, but the complexity of

110   biotic and abiotic interactions precludes us from scaling individual processes

111   to the community level (e.g. Lawton, 1999). The final camp argues that traits

112   provide a path forward to a unified theory of community ecology by

113 providing a taxon-independent means for generalizing the structure and/or

114 functioning of communities that is based on functional traits rather than

115 species identity (e.g. McGill *et al.*, 2006*a*; Westoby & Wright, 2006). While

116 the impact of stochasticity on community structure is largely undisputed, it

117 has been shown that Neutral Theory cannot, by itself, explain observed

118 species distributions in many systems (McGill, 2003; McGill, Maurer &

119 Weiser, 2006*b*). Furthermore, many recent studies have demonstrated that

120 traits within communities and regional species pools explain a large amount

121 of variance in community structure (e.g. de Bello *et al.*, 2012; Edwards,

122 Lichtman & Klausmeier, 2013) and function (e.g. Sutton-Grier & Megonigal,

123 2011). These studies demonstrate that traits can scale up to influence

124 community structure and, thus, provide optimism that it will be possible to

125 develop general, predictive rules in community ecology as we refine our

126 understanding of which traits are important in a given environment, how

127 traits are distributed within and among species, and how those traits relate

128 to mechanisms driving community dynamics and function (Fig. 1).

129 While trait-based ecology (TBE) has made significant strides over the

130 past decade, a number of critical issues must be addressed before we can

131 have confidence in the framework's ability to deliver on its significant

132 promise. This review highlights recent work and outstanding questions in

133 three areas: (*i*) selecting relevant traits, (*ii*) describing intraspecific trait

134 variation and incorporating this variation into models, and (*iii*) scaling trait

135 data to community- and ecosystem-level processes. While this review

136 focuses on plants, similar TBE movements are occurring in animal and

137 microbial ecology (e.g. Bokhorst *et al.*, 2012; Fierer, Barberán & Laughlin,

138 2014; Haddad *et al.*, 2008; Litchman *et al.*, 2007; Pedley & Dolman, 2014).

139

140 **II. SELECTING RELEVANT TRAITS**

141 **(1) Simplifying plant communities: functional groups *versus***

142 **functional traits**

143   Over time, there have been major shifts in how trait variation is

144 measured and utilized, particularly with respect to applications in community

145 ecology. Shortcomings in the predictive power of TBE have ironically

146 stemmed from one of its fundamental tenets—species can be grouped

147 according to their responses to and effects on abiotic and biotic conditions

148 (Lavorel & Garnier, 2002). Historically, ecologists have attempted to capture

149 ecological processes within communities (e.g. assembly, response to abiotic

150 factors) by measuring the distribution and responses of species groups

151 based on characteristics such as life history, life form, photosynthetic

152 pathways or other functional traits (Lavorel *et al.*, 2007; Lavorel & Garnier,

153 2002; Lavorel *et al.*, 1997). If such groups are assumed to function similarly,

154 community- to global-scale processes could be modelled without the

155 collection of detailed trait data for many species.

156   While numerous studies have found significant relationships between

157 ecosystem functions and traditional plant functional group classifications like

158 the grass–forb–legume approach (reviewed in Díaz & Cabido, 2001),

159   categorical groups mask variability, and may underestimate the important

160   role that functional diversity plays in maintaining key ecosystem functions

161   like productivity and nutrient cycling (Wright *et al.*, 2006). For example,

162   studies have shown that not all C_4 perennial grasses or C_3 annual forbs

163   respond similarly to disturbance or resource fluctuations (Badgery *et al.*,

164   2005; Firn *et al.*, 2010; Firn, Prober & Buckley, 2012; Han, Buckley & Firn,

165   2012). Further evidence of the inability of categorical functional groups to

166   predict species responses to environmental change are emerging from the

167   field of invasion ecology, as native and invasive species from similar

168   functional groups respond differently to environmental variation (Firn *et al.*,

169   2010, 2012; Funk, 2008; Han *et al.*, 2012). Simple categorical functional

170   groups can also be low in number in ecosystems like grasslands, meaning

171   that correlative relationships between simple functional groups and changes

172   in ecosystem function may be statistically significant because variability is

173   reduced and not necessarily because groups are responding in a common

174   way to perturbations.

175   Given limited abilities of traditional functional groups to capture and

176   represent trait variation, there has been a shift away from describing and

177   predicting community and ecosystem dynamics with functional categories of

178   species and towards the use of continuous trait distributions (Lavorel *et al.*,

179   2007; Westoby & Wright, 2006). Interspecific differences in continuous traits

180   have been linked to environmental gradients (e.g. Wright *et al.*, 2005; Wright

181   & Westoby, 1999), demographic responses (Poorter & Markesteijn, 2008),

182 and 'major axes of variation' describing suites of co-varying traits indicative

183 of broader ecological strategies (e.g. Díaz *et al.*, 2004; Wright *et al.*, 2004).

184 Still, trait effects on ecosystem-, landscape- and global-scale processes

185 depend on the combined traits of co-occurring species, and are likely to be

186 driven disproportionately by traits of the most abundant species (Grime,

187 1998). These realizations have led to the quantification and use of

188 aggregated trait attributes of the community [e.g. community-weighted

189 mean (CWM)] and indices of community diversity to reveal broad patterns

190 and explain more of the variation in trait–environment relationships (see

191 Section IV.1, Díaz *et al.*, 2007*a*; Villeger, Mason & Mouillot, 2008). Meanwhile,

192 alternative methods of classifying species into ecologically relevant

193 functional groups based on numerous functional traits have continued to

194 develop, often utilizing methods in cluster analysis (e.g. Aubin *et al.*, 2009;

195 Fry, Power & Manning, 2014; Grime *et al.*, 1997; Pillar & Sosinski, 2003);

196 however, identification of consistent groups and demonstrations of their

197 utility in predictive models remain sparse and equivocal (e.g. Larson *et al.*,

198 2015; Louault *et al.*, 2005; Müller *et al.*, 2007).

199

200 **(2) Trait selection**

201   Deciding which traits to measure is one of the most difficult aspects of

202 TBE. It is often difficult to know, *a priori*, the mechanism(s) responsible for

203 driving a particular community- or ecosystem-level process, much less the

204 organismal trait(s) most closely linked to the mechanism. Compounding the

205   problem is that many traits relevant to a particular mechanism are difficult or

206   expensive to measure, especially for enough individuals to accurately

207   characterize the trait distributions of a community, or even populations

208   within the community. Fortunately, these 'hard' traits are often strongly

209   correlated with more easily or cheaply measured 'soft' traits (Hodgson *et al.*,

210   1999). If certain traits are relevant to multiple plant responses and effects, it

211   may be possible to identify a set of soft but multifaceted traits which predict

212   a substantial portion of the variation in plant function and ecological

213   processes (Fig. 1). Soft traits for many species can now be acquired from

214   global databases like TRY (Kattge *et al.,* 2011) and BiolFlor (www.biolflor.de).

215   A recent study of 222 plant species found that soft traits sourced from the

216   TRY database (i.e. seed mass, wood density, and leaf traits) were strong

217   predictors of a range of life-history strategies (Adler *et al.*, 2013). Despite

218   these advances, our understanding of which traits most strongly influence

219   plant and ecosystem function reflects a bias towards leaf traits and

220   databases like TRY generally do not account for site-level differences

221   including species interactions, trait variation, and environmental variation.

222

223   (*a*) *Response traits*

224   Plant traits reflect adaptations to abiotic and biotic factors and, thus,

225   can be used to describe and predict species responses to changes in these

226   factors. In this framework, trait variation is assumed to be linked to variation

227   in organismal responses to different factors (e.g. abiotic stress or

228   competition), which scales up to influence demographic responses and

229   species abundances (Suding, Goldberg & Hartman, 2003). The particular

230   response traits of interest will depend on the specific combination of abiotic

231   and biotic factors in a vegetation community. Which traits are linked to

232   specific environmental changes has been the subject of previous reviews

233   (Lavorel *et al.*, 2007), although empircal demonstrations of trait–response

234   linkages remain relatively rare. Here, we briefly review key aspects of

235   functional variation across species and their potential relevance to species

236   responses in light of abiotic and biotic factors.

237   Plant growth rate is considered a key trait differentiating ecological

238   strategies within communities (e.g. Grime, 1977; Reich, 2014). In general,

239   growth rate has been shown to be positively associated with shade tolerance

240   and negatively associated with drought tolerance (Suding *et al.*, 2003). Rapid

241   growth has also been shown to be more prevalent in productive (e.g. Grime

242   & Hunt, 1975), high-nutrient communities (Wright & Westoby, 1999),

243   suggesting that it provides some fitness advantage when resources are not

244   limiting. In some cases, however, rapid growth can allow plants to escape

245   resource limitation in low, pulse-resource systems (e.g. among invasive

246   species; Funk, 2013). Plant relative growth rate (RGR, the rate of dry mass

247   addition per unit dry mass) has been recognized as a strong predictor of

248   species' potential for success and the most useful measure of plant growth

249   (Grime, 1977; Grime & Hunt, 1975; Hunt & Cornelissen, 1997).

250   Unfortunately, it is also difficult and time-consuming to measure. However,

251 RGR is a 'synthetic' trait summarizing the outcome of several processes (e.g.

252 photosynthesis, respiration, nutrient allocation, life-history strategies) that

253 are tied to other measurable traits, such as leaf nitrogen (N) concentration,

254 photosynthetic rate, tissue density, and SLA. A small number of soft traits,

255 such as SLA or wood density, can explain a large portion of the variation in

256 RGR across a large range of herbaceous and woody plant species (Hunt &

257 Cornelissen, 1997; Nguyen *et al.*, 2014; Poorter *et al.*, 2008; Walker &

258 Langridge, 2002).

259   In addition, terrestrial plants exhibit a consistent trade-off among these

260 growth-related traits within the LES, such that high SLA is often linked to

261 higher leaf N concentration and photosynthetic rate at the expense of tissue

262 density and longevity. Consequently, soft traits like SLA or plant tissue

263 density may also serve to represent functional strategies of nutrient

264 acquisition and conservation, across a wide range of taxa and ecosystem

265 types (Díaz *et al.*, 2004; Walker & Langridge, 2002; Wright *et al.*, 2004).

266 While these trade-offs may not be exhibited in all species or plant systems

267 (e.g. wetlands and grasslands: Funk & Cornwell, 2013; Wright & Sutton-Grier,

268 2012), the ubiquity of these trade-offs across many environmental and

269 disturbance gradients, coupled with their strong relationship to important

270 demographic rates (Donohue *et al.*, 2010), suggests that these traits are

271 associated with mechanisms determining plant success in response to

272 different abiotic and biotic factors (reviewed in Reich, 2014). As such, LES

273   traits present a good starting point in the selection of traits for plant

274   systems.

275   While great progress has been made in understanding the function of

276   LES traits, our understanding of how other traits relate to plant and

277   community responses is limited. Root traits are notoriously difficult to

278   measure, although there is some evidence that an economic axis for roots

279   exists as well, with slow-growing species having low root elongation rates,

280   specific root length (SRL), high root diameter, and low nutrient concentration

281   (Freschet *et al.*, 2010; Liu *et al.*, 2010; Larson & Funk, 2016). In arid and

282   semi-arid ecosystems, responses to changes in water availability may be

283   better predicted from root traits such as root depth or elongation rate than

284   from leaf traits (Nicotra, Babicka & Westoby, 2002; Padilla & Pugnaire, 2007).

285   However, the traits most closely linked to plant performance may change

286   depending on the environment. For example, a study of the annual species

287   *Polygonum persicaria* found that leaf-level water-use efficiency was

288   correlated with plant fitness in water-limited habitats while root biomass

289   allocation was more closely linked to fitness in moist environments (e.g.,

290   Heschel *et al.*, 2004). Recent work also suggests that leaf and stem hydraulic

291   traits (e.g. wood density; Cornwell & Ackerly, 2010) are correlated with traits

292   from the LES (reviewed in Reich, 2014), but these traits are rarely

293   incorporated into empirical tests and additional data are needed to

294   determine if the LES can adequately capture plant response to changes in

295   water availability. Lastly, traits influencing regeneration processes (i.e.

296 dispersal/colonization, resprouting, germination, emergence) also have

297 significant implications for population dynamics and community composition

298 (Aicher, Larios & Suding, 2011; Donohue *et al.*, 2010; Flores-Moreno & Moles,

299 2013; Pakeman & Eastwood, 2013; Zeiter, Stampfli & Newbery, 2006), but

300 are not well represented in trait-based theoretical frameworks.

301   Although mean trait values for organisms and species are typically

302 used in predictive models, there is growing evidence that species vary in

303 their phenotypic responses to changing abiotic and biotic factors (i.e.

304 phenotypic plasticity, see Section III), which contributes to functional

305 variation within communities (e.g. Ashton *et al.*, 2010; Firn *et al*., 2012; Funk,

306 2008; Larson & Funk, 2016; Siebenkäs, Schumacher & Roscher, 2015).

307 Although empirical links between phenotypic plasticity and performance or

308 fitness are still rare across species (Van Kleunen & Fischer, 2005; Firn *et al.*,

309 2012), if plasticity is adaptive it could be an important metric related to

310 population, species, and community responses to environmental change

311 (reviewed in Berg & Ellers, 2010; Nicotra *et al.*, 2010; Valladares *et al.*,

312 2014). For example, leaf trait plasticity has been linked to productivity and

313 plant growth in response to both nitrogen availability and cutting (da Silveira

314 Pontes *et al.*, 2010) as well as temperature and water availability (Liancourt

315 *et al.*, 2015). Ultimately, while belowground traits, regenerative traits, and

316 intraspecific trait variation have long been recognized as key (albeit difficult)

317 components to incorporate into models (Weiher *et al.*, 1999), their inclusion

318   in empirical tests is still relatively rare, and represents an important area for

319   future research.

320   Through their influence on plant response to abiotic and biotic factors,

321   response traits can be used to identify ecological processes structuring plant

322   populations and communities (Fig. 1; Dorrough, Ash & McIntyre, 2004;

323   McIntyre, 2008; Mayfield & Levine, 2010; Butterfield & Callaway, 2013; Gross

324   *et al.*, 2015). For example, Gross *et al.* (2009) used patterns of SLA to

325   determine that community structure in a subalpine grassland was influenced

326   by facilitation in water-limited areas and competition in more mesic areas. In

327   a study of soil disturbance in a lake-plain prairie, Suding *et al*. (2003) found

328   that traits conferring tolerance to shade, drought, and defoliation were better

329   predictors of abundance patterns following disturbance than was competitive

330   ability, a frequently measured response. Other studies have shown that

331   multiple traits can interact to influence community patterns. For example,

332   Maire *et al.* (2012) found that, despite differences in nutrient strategy among

333   species (niche differences), traits associated with competitive ability (e.g.

334   height) were better predictors of abundance across grazing and nutrient

335   treatments in a grassland community. Gross *et al.* (2015) found that while

336   native and invasive species differed in traits (SLA and height), they had

337   similar responses to grazing and competition because different trait

338   combinations generated similar success to these factors. These last two

339   examples demonstrate that using a diverse set of traits may be important to

340   differentiate ecological processes acting on community assembly. Selection

341 of the performance metric is also important because growth, survival, and

342 reproductive measures will have different relationships with community-level

343 processes (e.g. abundance) as environmental conditions change (Gross *et*

344 *al.*, 2007, 2009). More studies are needed that examine how traits relate to

345 plant performance across different environments; this will be critical if we are

346 to predict plant and community responses in a changing world (Meinzer,

347 2003).

348

349 (*b*) *Effect traits*

350   For functional traits to provide a comprehensive theoretical framework

351 in ecology, we must also understand how trait composition and diversity

352 influence ecosystem functioning (Fig. 1; Lavorel & Garnier, 2002). Effect

353 traits alter abiotic and biotic processes corresponding to a wide range of

354 ecosystem functions, and have been the subject of recent review (de Bello *et*

355 *al.*, 2010; Eviner & Chapin, 2003; Garnier & Navas, 2012). However, while

356 our understanding of effect traits has improved in the wake of the framework

357 laid out by Lavorel & Garnier (2002), predictive models have lagged behind

358 those incorporating response traits (Suding *et al.*, 2008). In addition to their

359 predictive role in species and community responses to environmental

360 variation, links between LES traits and ecosystem function have been best

361 characterized. The effects of RGR, SLA, and leaf N are particularly well

362 studied, with evidence suggesting positive relationships between these traits

363 and primary productivity, litter decomposition rates (see below), plant-

364 available soil N, N turnover rates, and palatability to herbivores, and

365 negative relationships with soil C and N retention (e.g. De Deyn, Cornelissen

366 & Bardgett, 2008; Grigulis *et al.*, 2013; Lavorel & Grigulis, 2012; Loranger *et*

367 *al.*, 2012). When community-scale analogues of LES traits are considered,

368 similar patterns emerge. Canopy N and leaf area index (LAI) tend to scale

369 positively with SLA and leaf N values, and have also been tied to

370 aboveground net primary productivity (ANPP; Reich, 2012).

371   The influence of leaf tissue chemistry and structure on decomposition

372 rate is among the most studied aspects of trait influence (de Bello *et al.*,

373 2010), and traits associated with the LES have been shown to influence

374 decomposition rates in several studies (Bakker, Carreño-Rocabado & Poorter,

375 2011; Cornwell *et al.*, 2008; see for example Santiago, 2007). Species on the

376 'fast return' end of the LES (rapid growth, thin leaves, high nutrient

377 concentrations, and high rates of photosynthesis) decompose more quickly

378 than species on the 'slow return' end of the LES (slow growth, thicker,

379 tougher, more recalcitrant leaves with more defences and lower rates of

380 photosynthesis), suggesting that the suite of coordinated structural and

381 chemical leaf traits maximizing photosynthesis also has important

382 implications for nutrient cycling (Santiago, 2007) and the global carbon cycle

383 (Cornwell *et al.*, 2008). However, the effects of the plant community on

384 biogeochemical cycles will likely require more than singular LES traits. For

385 example, Sutton-Grier, Wright & Richardson (2012) determined that different

386 plant traits had strong effects on plant biomass N (water-use efficiency)

387   *versus* denitrification (e.g. belowground biomass, root porosity), and the

388   traits that maximized one N removal pathway were largely orthogonal to

389   traits that maximized the other. This suggests that multiple species,

390   exhibiting a diversity of traits, may have complex effects on ecosystem

391   functions.

392   Although plant traits are an important predictor of decomposition,

393   biotic and abiotic factors are also important drivers. For example, in a

394   restored riparian wetland, Sutton-Grier *et al.* (2012) determined that

395   environmental factors including soil organic matter and soil N had

396   approximately the same amount of explanatory power as plant traits.

397   Variation in external factors such as precipitation, grazing, or land use can

398   also exert strong indirect influences on ecosystem function by driving shifts

399   in plant community composition and community-weighted trait means which

400   result in indirect effects on decomposition (Bakker *et al.* 2011; Garibaldi,

401   Semmartin & Chaneton, 2007; Santiago, Schuur & Silvera, 2005). Similarly,

402   the net influence of plant traits on soil chemistry not only depends on direct

403   effects via the quality and quantity of plant litter and exudates, but on

404   indirect effects of these inputs on soil biota (e.g. de Vries *et al.*, 2012; Orwin

405   *et al.*, 2010), whose properties may explain >70% of the variation in N

406   cycling processes (Grigulis *et al.*, 2013). Consequently, models of

407   decomposition will need to identify and incorporate traits as well as critical

408   feedback mechanisms through which biotic and abiotic factors will influence

409   decomposition.

410   Given the association of LES traits with gas and water exchange, it is

411   likely that these attributes also drive climatic and hydrologic processes

412   (Reich *et al.*, 2014). However, despite their potential utility in earth–

413   atmospheric models (e.g. Van Bodegom *et al.*, 2012; Verheijen *et al.*, 2015)

414   and the understanding that vegetation drastically influences water cycles

415   (e.g. Huxman *et al.*, 2005), demonstrations of theorized trait–effect links are

416   still relatively sparse. High leaf hydraulic conductance and leaf vein density,

417   which are often linked to rapid carbon assimilation, have been predicted to

418   increase evapotranspiration, canopy vapour flux, and precipitation dynamics

419   in historic and current climate models (Boyce *et al.*, 2009; Brodribb, Feild &

420   Sack, 2010; Lee & Boyce, 2010). Ollinger *et al.* (2008) also found that high

421   canopy N was associated with greater shortwave surface albedo and CO_2

422   uptake capacity, suggesting LES implications for surface temperatures and

423   atmospheric CO_2 concentrations, respectively. However, the effect of

424   vegetation on carbon budgets will depend not only on the assimilation of

425   carbon, but its subsequent fate in plant–soil interactions, and more work is

426   needed to map the net influence of functional traits on earth–atmosphere

427   fluxes (perhaps using tools such as structural equation modelling, see

428   Section IV.2).

429   Beyond the LES, plant height is another important axis of plant trait

430   variation (Díaz *et al.*, 2004, 2016; Westoby *et al.*, 2002). Despite its potential

431   to influence a range of ecosystem functions *via* effects on abiotic properties

432   such as moisture (e.g. Gross *et al.*, 2008), light (e.g. Violle *et al.*, 2009) and

433   standing/litter/microbial biomass (Grigulis *et al.*, 2013), demonstrations are

434   far less frequent than for LES traits (Chapin, 2003; Garnier & Navas, 2012;

435   Lavorel & Grigulis, 2012). Particularly as canopy height becomes easily

436   estimable with improvements in remote-sensing data and techniques,

437   demonstrated effects of height on ecosystem processes could prove highly

438   valuable in models of ecosystem function at larger scales, making this a key

439   area for interdisciplinary development (Turner, Ollinger & Kimball, 2004).

440   Our understanding of how root and wood traits influence ecosystem

441   function is less clear compared to other traits (e.g. LES traits), although (as

442   mentioned above) recent studies have suggested that some water-related

443   root and stem traits may align with 'fast return' and 'slow return' strategies

444   represented by the LES (Chave *et al.*, 2009). For example, lower sapwood

445   density and higher sap flux—which has been positively associated with SLA

446   (O'Grady *et al.*, 2009)—may explain higher evapotranspiration rates

447   observed in an invasive tree species relative to coexisting natives (Swaffer &

448   Holland, 2015). Independent of the LES, root morphological and architectural

449   traits have been shown to influence soil moisture (Gross *et al.*, 2008), soil

450   stability, and erosion (Stokes *et al.*, 2009), with possible impacts on soil

451   structure (Six *et al.*, 2004), leaching and infiltration (De Deyn *et al.*, 2008),

452   and evapotranspiration and climate cycles (Lee *et al.*, 2005). Like foliar

453   traits, there have been relatively few direct tests linking root and wood traits

454   to hydrologic or atmospheric processes, representing a substantial

455   opportunity for research on belowground trait influence. As in leaves, higher

456 density, lignin or dry matter content in roots and wood should slow

457 decomposition and increase soil C storage (Chambers *et al.*, 2000; De Deyn

458 *et al.*, 2008; Freschet, Aerts & Cornelissen, 2012; Klumpp & Soussana, 2009).

459 Unlike foliar tissue, however, root N is not necessarily related to root

460 decomposition rates, which may be complicated by co-occurring effects of

461 substrate chemistry, litter secondary chemistry, or mycorrhizae on root

462 decomposition (Freschet *et al.*, 2012; Langley, Chapman & Hungate, 2006).

463 Quantity and quality of root exudation could also affect soil C and N

464 dynamics, as higher quantities may increase labile C and microbial

465 stimulation (Dijkstra, Hobbie & Reich, 2006; Kaštovská *et al.*, 2015), although

466 the nature of microbial effects may depend on the type of exudate, which is

467 only just beginning to be explored (De Deyn *et al.*, 2008).

468   Relationships between plant roots and mycorrhizae or N-fixing bacteria

469 should also affect biogeochemical processes. As symbiotic relationships

470 make N and P more available, primary productivity and soil C inputs should

471 generally increase. Furthermore, increased longevity and slower

472 decomposition of colonized roots, along with C immobilization by symbionts,

473 may also increase soil C and N retention (De Deyn *et al.*, 2008; Langley *et*

474 *al.*, 2006). It is still unclear whether these trends are generalizable, as effects

475 may vary across species of plants, fungi and/or microbes (Rillig & Mummey,

476 2006). For example, Cornelissen *et al.* (2001) found plant litter of species

477 associating with ericoid mycorrhizae, ectomycorrhizae, and arbuscular

478 mycorrhizae to correspond to poor, intermediate, and rapid decomposition

479 rates, respectively. Ecologists are just beginning to understand the wide

480 functional diversity of soil microbial and fungal communities (McCormack,

481 Lavely & Ma, 2014; Van Der Heijden & Scheublin, 2007); thus, a critical

482 avenue for future research should focus on how traits, plant community

483 composition, and soil biota interact to impact soil carbon dynamics and

484 ecosystem function (e.g. Grigulis *et al.*, 2013).

485

486 (*c*) *Trait selection: future directions*

487   Moving forward, a main challenge will be identifying which of many

488 traits are likely to be most useful in predicting community and ecosystem

489 dynamics. The initial pool of traits in an analysis will strongly constrain

490 detectable patterns, but including multiple correlated traits in a given model

491 leads to diminishing returns and defeats the purpose of developing a simple

492 way to characterize community and ecosystem function (Laughlin, 2014*b*).

493 Fortunately, many emerging methods can aid trait selection when many

494 traits or environmental factors may influence species responses. For

495 example, RLQ and fourth corner analyses are ordination and bivariate

496 analyses, respectively, in a multivariate framework which reveal patterns

497 between three data tables containing environmental variables (R), species

498 abundances (L), and species traits (Q) across a range of samples (e.g. plots,

499 sites). Recently, variations in RLQ and fourth corner analyses have been

500 applied to identify objectively the most informative traits as well as their

501 relatedness to environmental variables in multivariate space (e.g. Bernhardt-

502   Römermann *et al.,* 2008; Dray *et al.*, 2014). Using the same type of data,

503   Jamil *et al.* (2013) developed a generalized linear mixed model (GLMM)

504   approach to identify more directly links between traits, environmental

505   variables, and abundances.

506   Other models have simultaneously identified traits linked to ecosystem

507   function as well as species responses (Suding *et al.*, 2008). For example,

508   working across a range of sites (e.g. pasture, agricultural, woodland) on the

509   west coast of Scotland, Pakeman (2011) extended RLQ analysis for this

510   purpose, identifying four traits which predicted species distributions across

511   sites based on their relationships with soil/management attributes and

512   ecosystem function parameters. This shortlist included SLA and leaf size,

513   which aligned positively with more fertile, disturbed sites and led to higher

514   rates of decomposition and nutrient cycling, as well as leaf dry matter

515   content (LDMC) and canopy height, which showed opposite associations. This

516   type of multivariate approach could be extended to other types of systems

517   broadly to identify traits linked to both species responses and ecosystem

518   effects. These efforts should also extend beyond the LES to begin identifying

519   traits which may capture less-understood responses and functions (e.g. root

520   architectural traits related to water availability, germination response traits

521   related to regeneration).

522   A further challenge is that traits, abiotic factors, and species

523   interactions (e.g. competition, facilitation) may interact in non-additive ways

524   to influence community and ecosystem processes (Suding *et al.*, 2008). For

525   example, while 'fast return' LES traits are generally associated with greater

526   herbivore palatability (e.g. Díaz *et al.*, 2004), Loranger *et al.* (2012) found

527   that influences from surrounding plants obscured the predicted trait

528   influence on herbivore damage. Similarly, litter decomposition rates and

529   effects on N cycling may result from non-additive effects of plant traits and

530   soil biota diversity (Hättenschwiler, Tiunov & Scheu, 2005). Consequently,

531   efforts which seek to expand upon our understanding of critical traits must

532   consider abiotic and biotic context as fully as possible and seek to develop

533   models which account for these interactions in a given system, especially

534   across trophic levels (e.g. Deraison *et al.*, 2015; Lavorel *et al.*, 2013;

535   Pakeman & Stockan, 2014). Once key traits are identified and specific

536   hypotheses are generated regarding their links to responses and effects,

537   other statistical approaches such as structural equation modelling can be

538   applied to capture and test how multiple traits ultimately drive community

539   structure (see Section IV.2).

540

541   **III. INTRASPECIFIC TRAIT VARIATION**

542   Because traits vary across biological, spatial, and temporal scales in a

543   context-dependent manner (e.g. patterns differ for individual traits and

544   species: Siefert *et al.*, 2015), traits need to be accurately characterized

545   within a species or population. Most plant traits are defined and measured on

546   individual plants (e.g. height), on organs within a plant (e.g. leaves), or on

547   populations (e.g. demography; Violle *et al.*, 2007). Ecological studies

548   commonly assign mean trait values to species, justified on the assumption

549   and frequent evidence that more variation occurs between than within

550   species (e.g. Hulshof & Swenson, 2010; Koehler, Center & Cavender-Bares,

551   2012). However, variation within species can be substantial and both

552   ecologically (e.g. Clark, 2010) and evolutionarily important (e.g. Etterson &

553   Shaw, 2001). For example, Albert *et al.* (2010) measured three traits

554   (maximum vegetative height, LDMC, leaf nitrogen concentration) on 16 co-

555   occurring alpine species with diverse life histories and found approximately

556   70% of trait variation to occur among species, leaving variation among

557   individuals of a species to account for 30% of trait variation. These values

558   correspond well to a recent global meta-analysis (Siefert *et al.*, 2015). This

559   intraspecific trait variability in natural populations may impact competitive

560   interactions and ultimately community composition (Bolnick *et al.*, 2011),

561   and can influence key ecosystem functions like productivity (Enquist *et al.*,

562   2015), nutrient cycles (Lecerf & Chauvet, 2008; Madritch & Lindroth, 2015),

563   litter decomposition (Sundqvist, Giesler & Wardle, 2011; Schweitzer *et al.*,

564   2012), and response to herbivory (Boege & Dirzo, 2004). For example,

565   Madritch & Lindroth (2015) showed using carefully controlled conditions that

566   condensed tannin concentrations varied among aspen genotypes and

567   decreased with increasing nutrient availability. Genotypic variation in leaf

568   chemistry could be directly linked to nutrient cycling *via* herbivore frass and

569   leaf litter N concentrations. The 'after-life' consequences of intraspecific

570   variation in tannin concentrations, a result of both genetic variation and

571   nutrient treatment, influenced the subsequent availability of N to plants.

572   Population-level studies illustrate the magnitude of intraspecific

573   variation that may be observed as well as the range of functional traits that

574   may vary. For example, studies of species with very large geographic ranges

575   – such as *Pinus sylvestris* and *Quercus virginiana* – have shown substantial

576   between-population variation in leaf nutrient traits (Oleksyn *et al.*, 2003),

577   needle longevity (Reich *et al.*, 2014), seed mass and growth rate/height

578   increment (Reich *et al.*, 2003), hydraulic traits (Martínez-Vilalta *et al.*, 2009),

579   freezing tolerance (Koehler *et al.*, 2012), and leaf morphology (Cavender-

580   Bares *et al.*, 2011). Studies of plant populations have also assessed the

581   degree to which intraspecific trait variation is shaped by genetic variation

582   and phenotypic plasticity, broadly defined as the capacity of an individual to

583   alter their growth in response to disturbance and fluctuating environmental

584   conditions (Valladares, Gianoli & Gomez, 2007). Common garden studies

585   indicate that the substantial intraspecific variation in needle longevity

586   observed with latitude or elevation in *P. sylvestris* and *Picea abies* is more

587   strongly influenced by phenotypic plasticity than genetic variation (Reich *et*

588   *al.*, 1996). Likewise, studies of foliar phenology in provenance trials of two

589   common European tree species (*Fagus sylvatica* and *Quercus petraea*)

590   suggest that temperature-mediated plasticity is greater than population-

591   based genetic differences or genotypic differences in plasticity (Vitasse *et*

592 *al.*, 2010). This distinction could have implications for how traits are sampled

593 and used in modelling efforts (see Section III.2).

594

595 **(1) How is variation in traits distributed across different scales of**

596 **organization?**

597   Trait variation among repeated organs within a species may be

598 separated into three components (Albert *et al.*, 2011): variation within an

599 individual plant, variation among individuals within a population, and

600 variation among populations. First, at a given point in time, the trait values

601 of organs within a plant might reflect differences in age, environmental

602 conditions, or disturbance history (e.g. herbivory). For example, differences

603 in the sun exposure and age of leaves can lead to marked differences in SLA,

604 δ^{13}C, and N concentration within a tree crown (Cavender-Bares, Keen &

605 Miles, 2006; Legner, Fleck & Leuschner, 2014; Mediavilla & Escudero, 2003;

606 Yan *et al.*, 2012). Trait values of an individual plant vary across the season

607 due to environmental tracking (*sensu* Bazzaz, 1996) including predictable

608 shifts with phenology (Donohue *et al.*, 2007; McKown *et al.*, 2013) and

609 acclimation to cold temperatures (Cavender-Bares *et al.*, 2005; Wisniewski *et*

610 *al.*, 1996). Traits also vary with ontogeny from seedlings to adults as plants

611 reach reproductive maturity (Cavender-Bares & Bazzaz, 2000; Lusk &

612 Warton, 2007). Such shifts may reflect, in part, adaptive shifts in traits that

613 accompany changing environments with life stage (Donohue *et al.*, 2010).

614 Second, trait values may vary among individuals within a population because

615 of both genetic differences among individuals and phenotypic plasticity

616 reflecting environmental conditions, ontogeny, and competition from

617 neighbouring plants (Le Bagousse-Pinguet *et al.*, 2015). Third, trait values

618 may vary among populations of a species, again reflecting both genetic

619 variation and phenotypic plasticity (e.g. Donohue *et al.*, 2005; Sultan, 2001;

620 Sultan *et al.*, 1998).

621   In addition, patterns of intraspecific variation differ among traits. For

622 instance, Albert *et al.* (2010) found that differences among populations in

623 maximum height (H_{max}) were nearly equal to differences among individuals

624 within populations across several alpine plant species, whereas more

625 variation was observed among individuals within a population than among

626 populations for LDMC. In addition, both the magnitude and patterns of

627 intraspecific variation differed among species, with individuals sampled

628 within a single plot showing two-thirds to less than one third of site-wide

629 variation in LDMC and H_{max}. For organ-level traits, sometimes more variation

630 occurs within individuals than among individuals within populations or

631 between populations. Messier, McGill & Lechowicz (2010) found LDMC to

632 vary more on average within the crown of a tree than among conspecific

633 trees within plots. In the same study, variation in SLA was near equivalent

634 within and among conspecifics within plots.

635   While interspecific trait variation is typically captured by differences in

636 mean trait values across species, there are also opportunities to integrate

637 metrics of intraspecific variation described above into our understanding of

638   how species differ functionally. For example, phenotypic plasticity can be a

639   critical component of responses to environmental change that differs

640   substantially across species (see Section II.2*a*). As such, phenotypic plasticity

641   has been explored for its potential to explain differences in ecological

642   strategy and performance between invasive and native species with mixed

643   results (e.g. Davidson, Jennions & Nicotra, 2011; Funk, 2008; Palacio-López &

644   Gianoli, 2011), as well as competitively dominant species and non-dominant

645   species (e.g. Ashton *et al.*, 2010; Grassein, Till-Bottraud & Lavorel, 2010).

646   However, while plasticity is often an independent focus of empirical efforts,

647   some evidence suggests that plasticity may tie into our broader

648   understanding of ecological strategies based on mean trait values (Grime &

649   Mackey, 2002). For example, mean plant height represents a major axis of

650   functional variation across species which has also been linked to the extent

651   of aboveground trait plasticity in response to nitrogen or light across several

652   grass and forb species (e.g. Maire *et al.*, 2013, Siebenkäs *et al.*, 2015).

653   Patterns of below-ground trait plasticity across species are less clear

654   (Siebenkäs *et al.*, 2015; Larson & Funk, 2016). There is thus a need for

655   broader testing of the mechanisms underlying interspecific variation in

656   phenotypic plasticity across traits and environmental variables (e.g. Weiner,

657   2004) and how this variation ultimately informs species and community

658   responses to environmental change. Incorporating metrics of trait plasticity

659   (reviewed in Valladares, Sanchez-Gomez & Zavala, 2006) into trait

660   databases, alongside trait data that correlate with ecological strategies,

661 would allow us to assess if trait plasticity is an inherent component of

662 ecological strategies across plant community types.

663   Beyond species, trait variation might be expected to increase

664 hierarchically among clades. However, early opinions were that ecologically

665 important traits are likely to be very labile through evolutionary time

666 (Donoghue, 2008). Empirical studies have begun to determine the extent to

667 which trait values are phylogenetically conserved; for example, seed mass

668 (Moles *et al.*, 2005), wood density (Chave *et al.*, 2006; Kerkhoff *et al.*, 2006),

669 leaf traits (Ackerly & Reich, 1999; Cavender-Bares *et al.*, 2006), xylem traits

670 (Zanne *et al.*, 2010), and disease resistance (Gilbert & Webb, 2007).

671 Additional studies have begun to assess the degree to which phylogeny and

672 functional traits influence community and ecosystem-level processes

673 (Cadotte, Cardinale & Oakley, 2008; Cadotte *et al.*, 2009; Cadotte, Dinnage &

674 Tilman, 2012; Flynn *et al.*, 2011). The early evidence suggests that

675 integrating both metrics can yield highly predictive models (e.g. community

676 assembly; Cadotte, Albert & Walker, 2013).

677

678 **(2) How does significant variability within species affect our**

679 **predictions?**

680   How variation is arranged within species influences how we design

681 sampling efforts to capture relevant trait values. How carefully a trait is

682 defined in relation to its environment becomes especially important in

683 standardizing the measurement of traits that are plastic; for example,

684   defining SLA in relation to sun exposure. If high levels of trait differentiation

685   are observed among populations within a study area, sampling methods will

686   need to reflect such differentiation to capture one or more trait values

687   pertinent to the study question.

688   The nature and scale of the questions being asked is critical. If we are

689   interested in mechanisms of coexistence (internal community dynamics),

690   sampling to capture intraspecific variation is likely to be important. Recent

691   work increasingly supports the importance of individual-level variation for

692   understanding trade-offs among species that enable coexistence of species

693   (Clark *et al.*, 2010). By contrast, if we are interested in ecosystem

694   consequences of plant community composition, capturing the mean and

695   variance of trait values at the species level may provide sufficient resolution

696   for predictive models. Still, intraspecific variation could indirectly influence

697   our ability to model ecosystem effects of plant communities. A critical and

698   timely example is forecasting changes in species distributions in response to

699   climate change. Studies of genetic diversity and local adaptation repeatedly

700   reveal that genotypes and populations within species differ in their

701   sensitivity to climate (e.g. Shaw & Etterson, 2012; Alberto *et al.*, 2013;

702   Ramirez-Valiente, Koehler & Cavender-Bares, 2015). Shifts in species

703   distributions with climate are thus unlikely to be reasonably well predicted

704   without taking this variation into account, making the ecosystem-level

705   consequences (e.g. carbon uptake) difficult to model.

706   Most traditional approaches used to model collections of species, such

707   as dynamical systems models (e.g. Tilman, 2004; Warner & Chesson, 1985),

708   can be modified to handle some degree of intraspecific variation by including

709   separate classes for each discrete phenotype within a species. Individual-

710   based models (Grimm & Railsback, 2005) go further by tracking every

711   individual in a community. Both of these methods can potentially become

712   cumbersome for speciose communities that include highly variable species.

713   Some studies simplify these issues by incorporating intraspecific variability

714   into standard statistical analyses by using different mean trait values for

715   populations at different locations along a gradient of interest (e.g. Ackerly &

716   Cornwell, 2007; Jung *et al.*, 2010; Violle *et al.*, 2012). These methods can still

717   be somewhat limiting as focusing on the mean trait, even within

718   subpopulations, neglects the effect of extreme values in the tails of the trait

719   distributions, which may have a profound impact on community response to

720   the environment (Bolnick *et al.*, 2011). Ames, Anderson & Wright (2015)

721   found that statistical inference regarding the environmental drivers of trait

722   variation was greatly altered when using regional species means rather than

723   locally measured trait values. There are several modelling approaches that

724   are better suited for incorporating intraspecific variation into models of

725   community dynamics and function.

726   Bayesian hierarchical models (BHMs, Gelman *et al.*, 2004; Gelman &

727   Hill, 2007) incorporate the hierarchical relationships inherent in scaling from

728   the traits of individuals up to the structure/function of the community in

729 which they are embedded (Clark, 2005). In a BHM, a species' trait

730 distributions are explicitly incorporated into one of the levels of the

731 hierarchy, and uncertainty around trait distributions are considered by

732 including prior distributions on the parameters of the trait distributions.

733 Further, the parameters of the trait distribution can be functions of biotic

734 and/or abiotic environmental factors in order to capture changes to the trait

735 distribution that are driven by changing environmental conditions. A major

736 advantage of BHMs is that they allow the user to explore relationships

737 among traits, the environment, and organismal performance without

738 knowing, *a priori*, the mechanisms that relate them (Webb *et al.*, 2010).

739 However, these models are limited to forecasting within the range of the

740 data used to fit them. Thus, BHMs are beneficial in identifying the traits and

741 environmental drivers that are most important in driving the dynamics of a

742 community. Because the trait distributions and their parameters are

743 described explicitly, it is also possible to explore directly the impact of

744 changes in intraspecific trait variation on the dynamics of the species and

745 the community as a whole.

746 Dynamical systems models have been developed that explicitly

747 describe the temporal dynamics of the community trait distribution in

748 response to environmental forcing for either a single trait (Norberg *et al.*,

749 2001) or multiple, correlated traits (Savage, Webb & Norberg, 2007). These

750 models use moment closure, a technique that approximates complete

751 distributions using only low-order moments such as means and variances, to

752 describe the whole community trait distribution as a function of biotic or

753 abiotic environmental factors. A drawback to this approach is that it requires

754 an explicit, known functional relationship between traits, environment, and

755 organismal performance. However, this allows these models to predict

756 changes in the trait distribution that result from environmental forcing

757 outside of the observed range, such as that expected from climate change.

758 An interesting feature of these models is that they aggregate inter- and

759 intraspecific variation into a single community trait distribution. This results

760 in a loss of information about species identity and changes in relative

761 abundances. On the other hand, for cases where the trait(s) are strongly

762 related to an ecosystem function of interest, these models may allow robust

763 prediction of function while ignoring extraneous details of species

764 composition. A more integrative approach incorporates the predictive power

765 of deterministic, dynamical systems models with the ability of Bayesian

766 models to incorporate empirical data and generate measures of uncertainty

767 associated with the model output. These 'first principles Bayesian multilevel

768 models' (Webb *et al.*, 2010) embed known mechanistic relationships into a

769 BHM and thereby allow prediction outside of the observed range of data

770 while simultaneously estimating uncertainty (Bayesian credible intervals)

771 associated with those predictions.

772

773 **IV. SCALING TRAIT–ENVIRONMENT RELATIONSHIPS TO COMMUNITY**

774 **AND ECOSYSTEM LEVELS**

775   Nearly all traits vary systematically along broad environmental

776   gradients. At the same time, nearly half of the global variation of many traits

777   can be found within individual communities (Wright *et al.*, 2004). Variation in

778   trait values among communities can be used to predict changes in

779   ecosystem functioning under persistent changes in the environment (Klumpp

780   & Soussana, 2009; Suding *et al.*, 2008), while variation within communities

781   can predict the resilience of ecosystem functioning to disturbance (Mori,

782   Furukawa & Sasaki, 2013). Systematic variation in trait distributions along

783   environmental gradients can also reveal environmentally dependent

784   assembly rules (Ackerly & Cornwell, 2007; Keddy, 1992), thereby linking

785   community assembly theory to models of biodiversity–ecosystem functioning

786   (Naeem & Wright, 2003). Trait–environment relationships are becoming

787   increasingly well described with 'global' trait–environment relationships

788   assessed for many traits (Moles *et al.*, 2007, 2009; Wright *et al.*, 2004; Zanne

789   *et al.*, 2010), although the current state of knowledge in this area is hugely

790   variable, with some traits, functional indices, and environmental gradients

791   much more intensively studied than others.

792

793   **(1) Community-level metrics of plant function**

794   Perhaps the simplest measure of community-level functional

795   composition is the community-weighted mean (CWM) trait value, which uses

796   the relative abundances of species and their trait values to calculate a

797   community aggregated trait value (Violle *et al.*, 2007). Not only does

798   variation in CWM trait values identify shifts in assembly filters along

799   environmental gradients (Ackerly & Cornwell, 2007), it is also perhaps the

800   strongest determinant of biotic effects on ecosystem functioning (Fortunel *et*

801   *al.*, 2009; Laliberté & Tylianakis, 2012; Lavorel *et al.*, 2011) as more

802   abundant species have a disproportionate influence on ecosystem processes

803   (mass ratio hypothesis; Grime, 1998). A simple null hypothesis is that CWM–

804   environment relationships are identical to interspecific trait–environment

805   relationships, at least qualitatively speaking. At the resolution of 1° of

806   latitude and longitude, Swenson *et al.* (2012) found that CWM values of leaf

807   traits, height, seed mass, and wood density based on species occurrences

808   (although species may not co-occur within 1° grid cells) were relatively

809   strongly correlated with annual mean and seasonality of temperature and

810   precipitation in ways that were consistent with expectations based on

811   species trait–environment patterns across much of the Western Hemisphere.

812   However, trait–environment relationships do not always scale linearly from

813   the species to community levels due to interactions between multiple

814   environmental factors (Rosbakh, Römermann & Poschlod, 2015) and

815   assembly processes that may not favour species with intermediate trait

816   values. For example, in one set of woody plant communities, over 80% of

817   traits were found to have linear or context-dependent abundance

818   distributions within communities while only one was unimodal (Cornwell &

819   Ackerly, 2010), thereby producing CWM–environment relationships that differ

820   from expectations based on interspecific patterns. This difference was likely

821 due to coordinated ecological selection on multiple traits that differed from

822 the evolutionary and biogeographic factors that determined trait correlations

823 among species in the regional pool. Research aimed at identifying these

824 processes and the trait–abundance distributions that they generate is

825 essential for improving predictive models of CWM–environment relationships.

826 　　　　Functional diversity indices capture the distribution of trait values

827 within communities and can also demonstrate systematic variation along

828 environmental gradients. Functional diversity can be broken down into three

829 orthogonal components – richness, evenness, and divergence (Mason *et al.*,

830 2005) – that are represented in various ways by different indices. The range,

831 or functional richness (Villeger *et al*., 2008), of trait values within a

832 community can be indicative of the intensity of environmental assembly

833 filters (Cornwell, Schwilk & Ackerly, 2006), and can have significant effects

834 on ecosystem functioning (Butterfield & Suding, 2013; Clark *et al.*, 2012).

835 The range of trait values is expected to decrease with increasing

836 environmental severity (i.e. environmental filtering), a hypothesis that has

837 been supported for a variety of traits at fine (Cornwell & Ackerly, 2009; Jung

838 *et al.*, 2010; Kooyman, Cornwell & Westoby, 2010) and coarse (Swenson *et*

839 *al.*, 2012) spatial scales, but not in all cases (Coyle *et al.*, 2014). Species

840 may, for example, use contrasting strategies to deal with stress (e.g. stress

841 avoidance *versus* tolerance; Ludlow, 1989), resulting in divergent traits and

842 greater functional richness. The distribution of trait values within a

843 community, as described by functional evenness may also vary

844   systematically along environmental gradients, although indirectly: even

845   spacing of trait values may reflect competition (which may be expected to

846   increase with productivity; Grime, 1977) and, consequently, niche

847   partitioning – although this pattern is not consistently supported (Cornwell &

848   Ackerly, 2009; Jung *et al.*, 2010). Which traits exhibit systematic variation in

849   functional richness or evenness along environmental gradients should

850   depend on their roles in community assembly. Traits related to

851   environmental filtering ought to influence functional richness, while those

852   related to competition ought to influence functional evenness.

853   The trait–environment predictions outlined above follow from relatively

854   simple models of community assembly, although several studies have

855   demonstrated that biotic interactions can strongly alter trait–environment

856   predictions. Trait-based community assembly studies have typically focused

857   on the convergence–divergence paradox which states that species with

858   similar environmental tolerances and requirements – reflected in the

859   similarity of their functional trait values – may experience simultaneous,

860   competing forces: similar species are more likely to co-occur (converge), and

861   thus to compete more strongly (diverge; Weiher, Clarke & Keddy, 1998;

862   Adler *et al.,* 2013). However, there is increasing evidence that using

863   functional divergence (i.e. degree of niche differentiation; Mason *et al*., 2005;

864   Villeger *et al*., 2008) to infer whether environmental filtering or competition

865   mechanisms are operating most strongly in communities may be narrow-

866   sighted. This framework overlooks the fact that plants often compete *via*

867   hierarchical differences in traits (fitness differences) rather than *via* limiting

868   similarity (niche differences; Kunstler *et al.*, 2012, 2016). A consequence of

869   competitive hierarchies is a reduction in the range of trait values observed

870   within a community, where species at one end of a trait spectrum are

871   competitively excluded, and functional divergence is not observed.

872   Furthermore, high divergence could result from the success of different

873   strategies dealing with stress (as described above) rather than from

874   competition. This pattern could also be enabled by facilitation, which has

875   been shown to increase the range of trait values in a community through the

876   creation of favourable microenvironments allowing species with otherwise

877   unsuitable trait values to persist (Gross *et al.*, 2009; Butterfield & Briggs,

878   2011). In a study of alpine plant communities, Schöb, Butterfield & Pugnaire

879   (2012) found that the magnitude of the net effects of competition and

880   facilitation on the CWM, richness, and evenness of trait distributions was

881   proportional to the effects of broad environmental gradients, and that the

882   biotic effects on trait distributions often countered those of the environment.

883   In short, biotic interactions can substantially alter trait–environment

884   relationships in a variety of ways, and a better understanding of the

885   functional trait basis of interaction outcomes is essential for integrating

886   these effects into predictive models of trait–environment relationships

887   (Butterfield & Callaway, 2013).

888   In addition to single-trait indices, multi-trait indices of functional

889   composition can be used to represent the multidimensional nature of the

890   'niche' (Villeger *et al.*, 2008), while other metrics such as dendrogram-based

891   indices (Petchey & Gaston, 2002) combine richness and evenness. However,

892   functional richness—the key indicator of functional spread within

893   communities—could be heavily influenced by rare, outlying species.

894   Abundance-weighted measures of spread, such as functional dispersion

895   (Laliberté & Legendre, 2010) and Rao's quadratic entropy (Botta-Dukat,

896   2005) may more accurately predict some ecosystem functions as the traits

897   of dominant species have stronger effects (i.e. mass ratio hypothesis; Grime,

898   1998). A great deal of research has gone into the mathematical properties

899   and ecological justifications of these different indices (Petchey & Gaston,

900   2006; Mouchet *et al.*, 2010); however, their relative performance in

901   identifying biotic responses to a wide variety of environmental gradients, as

902   well as biotic effects on various ecosystem processes, are only just beginning

903   to be addressed (McGill, Sutton-Grier & Wright, 2010; Sutton-Grier *et al.*,

904   2011).

905   Deciding which indices to apply to a given trait-based question is not a

906   simple task given the potential relevance of many traits and diversity

907   metrics. Single-trait indices may retain more information, as opposed to

908   combining their variation into composite indices. This may mirror the issue of

909   inter- *versus* intraspecific trait variation discussed above, where the variance

910   in trait values may be reduced through aggregation. Single-trait indices may

911   also provide a better understanding of the complexity of responses to

912   environmental gradients, as well as effects on ecosystem processes, and

40

913 may in fact be necessary for elucidating response–effect patterns in complex

914 landscapes (Butterfield & Suding, 2013) and identifying multiple assembly

915 processes that act simultaneously along environmental gradients (Spasojevic

916 & Suding, 2012). On the other hand, there are examples of patterns that can

917 only be revealed through multi-trait indices, both for community assembly

918 (Villeger, Novack-Gottshall & Mouillot, 2011) and effects on ecosystem

919 processes (Mouillot *et al.*, 2011). Additionally, while most studies have linked

920 functional diversity to single ecosystem processes (e.g. productivity), there is

921 also mounting evidence that multi-trait metrics (e.g. functional divergence

922 and dispersion) may be useful in predicting multiple processes

923 simultaneously (i.e. multifunctionality; Mouillot *et al.*, 2011; Valencia *et al.*,

924 2015). At this stage in our understanding, it is important to use both single-

925 and multi-trait indices to examine individual and multifunctional responses or

926 effects in ecosystems, since no generalization is yet available as to which

927 indices may be superior for specific questions. However, useful prescriptions

928 for trait selection and aggregation exist (Villeger *et al.*, 2008) that can aid in

929 comparing and contrasting index performance as we move forward.

930

931 **(2) Applying community-level metrics at global scales**

932   For TBE to be predictive, relationships between response traits and

933 environmental conditions and disturbance regimes need to be globally

934 consistent. It is currently unknown whether statistical models that link

935 response traits to environmental conditions in one ecosystem can be easily

936 transferred and applied to another ecosystem on another continent. This lack

937 of generality is partly hindered by the lack of a global-scale database of

938 vegetation composition and associated environmental data. Efforts are

939 underway to develop such a database (sPlot, http://www.idiv-biodiversity.de/

940 sdiv/workshops/workshops-2013/splot), which will link directly to a global-

941 scale trait database (Kattge, 2011). This research will be instrumental for

942 advancing our understanding of how traits vary along the full range of

943 environmental conditions throughout the planet. In the meantime, however,

944 there is a wealth of published trait–environment relationships that can be

945 synthesized through meta-analysis (Gurevitch & Hedges, 2001). Meta-

946 analysis can be used to determine the consistency of trait responses to

947 environmental conditions and disturbance regimes across multiple studies,

948 and can also be used to rank the importance of traits based on their effect

949 sizes and their consistency of response (e.g. Cornwell *et al.*, 2008; Díaz *et al.,*

950 2007*b*).

951   To predict the response of communities to environmental conditions in

952 new sites or times, it will be necessary to identify the critical predictor

953 variables for those new sites and times. The best-resolved trait–environment

954 relationships demonstrate the influence of temperature and precipitation

955 gradients on interspecific variation in trait values. A recent study found that

956 temperature is a stronger predictor of trait variation than is precipitation

957 across a variety of traits (Moles *et al.*, 2014), likely due to the direct effects

958 of temperature on plant function relative to the less proximate relationship

959   between precipitation and soil moisture dynamics. Predictors of water stress

960   that integrate temperature, precipitation, and other factors that influence

961   soil moisture supply are typically better predictors of plant trait spectra than

962   temperature or precipitation alone (Wright *et al.*, 2004). Soil data are

963   becoming better each year, but the quality of soil data varies among

964   countries, and often within countries. Current climate data and future climate

965   projections are available at a global scale as data layers in Geographical

966   Information Systems (Hijmans *et al.*, 2005). The tools for predicting future

967   responses are increasing rapidly, but the accuracy of our predictions will

968   depend heavily on the precision of these future projections. As access to

969   accurate, consistent environmental data improves, predicting changes in

970   community composition can be accomplished using trait-based models that

971   yield a predicted relative abundance for every species in the local pool based

972   on the traits of the species and the relationships between traits and the

973   environment (Laughlin & Laughlin, 2013).

974   Our ability to predict ecosystem processes under changing

975   environmental conditions is also contingent on our understanding of the

976   relative importance of both abiotic conditions and the effect traits of the

977   community (Díaz *et al.*, 2007*a*), and how simultaneously to test and account

978   for multiple important factors in predictive models. For example, litter

979   decomposition rate has been shown to be a function of the local climate, the

980   composition of the microbial community, and the physical and chemical

981   traits of the litter (see Section II.2*b*). Structural equation modelling (SEM) is a

982   useful tool to quantify the unique effects that are attributable to multiple

983   abiotic *versus* biotic components of the ecosystem (Mokany, Ash &

984   Roxburgh, 2008). SEM permits the specification of a network of relationships

985   that are characteristic of complex systems (Grace, 2006). The standardized

986   path coefficients that describe the statistical relationships among variables

987   are similar to partial regression coefficients, and the absolute values of these

988   coefficients can be ranked to compare their impact on an ecosystem

989   process. For example, nitrification potential was shown to be most strongly

990   driven by the direct effects of abiotic soil properties such as pH,

991   temperature, and nitrogen availability, and only weakly driven by the LES

992   traits in the understorey plant community (Laughlin, 2011). In other words,

993   altering the functional composition of leaf traits in this pine forest

994   understorey plant community would have less effect on internal nitrogen

995   cycling than if we altered the abiotic properties of the soil. In another

996   example, SEM was used to discover that ecosystem multifunctionality was

997   driven equally by both the average and the diversity of traits in a dryland

998   community (Valencia *et al.*, 2015). The ability of SEM to parse out the

999   influence of many factors and feedbacks is proving it to be an extremely

1000   useful tool for TBE as seen in several recent studies (Mokany *et al.*, 2008;

1001   Laughlin, 2011; Laliberté & Tylianakis, 2012; Lavorel *et al.*, 2013; Valencia *et*

1002   *al.*, 2015); multivariate tools such as these will have a critical role in realistic

1003   predictions of ecosystem dynamics moving forward.

1004   Finally, in addition to forecasting the future, TBE can also be used to

1005   back-cast previous palaeoecological transitions, a very useful approach to

1006   predicting changes in the future. For example, the end-Cretaceous mass

1007   extinction of plants resulted in a shift towards dominance of plants with

1008   lower LMA and higher vein density, which is consistent with a faster growth

1009   strategy in the cold and dark impact winter that followed the Chicxulub

1010   bolide impact (Blonder *et al.*, 2014). Changes in leaf vein density have also

1011   been observed over much longer timescales throughout the Cretaceous

1012   (Feild *et al.*, 2011), with the emergence of high vein densities in angiosperms

1013   likely corresponding to major shifts in climatic and hydrological processes *via*

1014   increased evapotranspiration rates and associated feedbacks (Boyce *et al.*,

1015   2009). Combining information about how traits have responded to previous

1016   climate changes with current trait–environment relationships will enhance

1017   our ability to predict how traits will respond to future environmental change.

1018

1019   **V. CONCLUSIONS**

1020   (1) Trait-based ecology can be a powerful approach to explain and predict

1021   highly complex systems. While our understanding of key components of TBE

1022   (e.g. response traits, effect traits, functional diversity) has developed

1023   continuously since Lavorel & Garnier (2002) introduced their trait-based

1024   conceptual framework, many challenges remain.

1025   (2) We have highlighted several exciting areas for future research. The

1026   usefulness of traits in predictive models hinges on deepening our

1027   understanding of which traits drive ecological processes at organismal,

1028   community, and ecosystem scales. While soft traits, such as SLA or wood

1029   density, show much promise in explaining some metrics of plant function

1030   (e.g. RGR) and species distributions, it remains to be seen if these traits can

1031   simultaneously predict multiple ecological processes across diverse

1032   community types. We demonstrated that genetic variation and phenotypic

1033   plasticity can strongly influence a range of plant functions, but how these

1034   two components contribute to intraspecific trait variation and ecological

1035   strategies across a range of species needs to be addressed. Furthermore,

1036   future work needs to identify how intraspecific trait variation should be

1037   quantified and incorporated into models. Our review also highlighted the

1038   need to understand how non-additive effects of traits, species interactions,

1039   and abiotic factors influence community- and ecosystem-level processes,

1040   and how these separate components may be incorporated into cohesive and

1041   predictive frameworks. While TBE has seen many recent advances in

1042   modelling approaches, we still do not know if algorithms developed in one

1043   community can be applied at larger spatial and temporal scales. Progress on

1044   all of these questions will be facilitated by improvements in the quality and

1045   availability of trait and environmental data.

1046   (3) While this review has focused on how TBE informs our understanding of

1047   basic ecological processes, work is underway to apply this framework to

1048   conservation and restoration programs (e.g. Funk *et al.*, 2008; Laughlin,

1049   2014*a*). For example, traits have been used to identify native species from

1050 regional species pools that can tolerate certain abiotic conditions or compete

1051 with invasive species (Funk & McDaniel, 2010; Kimball *et al.*, 2014), and

1052 traits that may be useful in re-establishing critical ecosystem services (e.g.

1053 pollination services: Lavorel *et al.*, 2011).

1054 (4) The potential for TBE to improve our understanding of basic and applied

1055 ecological processes makes the need for empirical tests of this framework a

1056 priority in ecology.

1057

1058 **VI. ACKNOWLEDGEMENTS**

1065

1066 **VII. REFERENCES**

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1919 **Figure legend**

1920

1921 **Fig. 1.** Functional traits can be used to understand a wide range of

1922 ecological processes occuring at organismal, community, and ecosystem

1923 scales. Examples are given here of how leaf, stem, and fine root traits

1924 influence a variety of ecological processes.

1925   Figure 1

Example traits	Organismal processes	Community processes	Ecosystem processes
Leaf chemistry and longevity	Carbon balance Disease resistance Growth rate	Competition Herbivory Succession	Decomposition Nutrient cycling Productivity
Leaf and stem hydraulic traits	Drought tolerance	Competition and facilitation	Hydrology Precipitation patterns
Fine root traits	Soil resource uptake Growth rate	Competition and facilitation Community invasibility	Decomposition Soil development

1926