

# Processes structuring macrophyte metacommunities in Mediterranean ponds: combining novel methods to disentangle the role of dispersal limitation, species sorting and spatial scales

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1 **Processes structuring macrophyte metacommunities in Mediterranean ponds: combining**  
2 **novel methods to disentangle the role of dispersal limitation, species sorting and spatial**  
3 **scales**

4

5 **Running title:** Drivers of macrophyte metacommunities

6

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30 **ABSTRACT**

31 **Aim:** Metacommunity ecology is a vibrant area of research that has received increased  
32 attention in recent years, since it provides a framework to assess the underlying dispersal- and  
33 niche- based processes that create non-random and ecologically meaningful patterns in  
34 species assemblages across the landscape. Here we set out to test for the role of dispersal  
35 limitation, species sorting and shared effects in the assembly of pond macrophyte  
36 metacommunities across an extensive area within the Iberian Plateau, and to identify which  
37 traits, environmental variables and spatial scales are driving local community structure.

38 **Location:** Northwestern Spain (Iberian Plateau).

39 **Taxon:** Pond macrophytes.

40 **Methods:** We established a novel combination of robust methods capable of identifying the  
41 processes and most important landscape scales involved in the assembly of communities. We  
42 used metacommunity assembly modelling and multivariate multiscale codependence analysis  
43 to first estimate the relative importance of spatial and environmental effects on community  
44 structure, and then to identify significant trait-environment relationships and spatial scales.

45 **Results:** Analyses showed that the greatest effects were seen for the spatial and mixed spatial  
46 and niche-based scenarios, particularly among wind-dispersed species. Thus, dispersal  
47 limitation interfered with species sorting in determining assemblage structure by hindering  
48 species' tracking of local environmental conditions. After accounting for this, the  
49 metacommunity assembly model revealed that species' traits were involved in determining  
50 abundance structure. Multiscale codependence analysis identified the main trait-environment  
51 relationships (and spatial scales) as fruit size-nutrient status (~300 km) and growth form-mean  
52 pond depth (~250 km).

53 **Main conclusions:** Our study suggests that dispersal limitation acted in concert with species  
54 sorting to influence the community assembly processes underlying selection for particular  
55 traits in functional niche space. Accordingly, we emphasize the need to go beyond the  
56 traditional taxonomic-based analyses of community composition and the predominant  
57 thinking of considering spatial and environmental processes as two alternative and mutually  
58 exclusive scenarios of community assembly.

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61 **Keywords:** aquatic plants, ecological modelling, functional traits, MAM, mMCA, patch  
62 dynamics

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64

## 65 1. INTRODUCTION

66 Metacommunity ecology provides a framework to assess the underlying processes that create  
67 non-random and ecologically meaningful patterns in species distribution across the landscape  
68 (Capers, Selsky, & Bugbee, 2010; Heino et al., 2015a). The metacommunity concept (i.e. a set  
69 of sites connected through dispersal) has attracted much interest over the last two decades  
70 (e.g. Leibold et al., 2004; Logue, Mouquet, Peter, & Hillebrand, 2011) since it integrates the  
71 interplay between spatial processes and local niche-based forces as drivers of community  
72 assembly (Holyoak, Leibold, & Holt, 2005). Regional variation in the environment may  
73 influence community assembly when dispersal rates allow species to reach suitable habitat  
74 patches, resulting in communities controlled by species sorting and niche differentiation  
75 (Capers et al., 2010). Conversely, spatial processes may hinder species from tracking  
76 environmental variation when dispersal rates are low, constraining species to fewer habitat  
77 patches and producing a close relationship between geographic isolation and community  
78 structure (Alahuhta, 2015). However, recent theoretical and empirical research (reviewed in  
79 Brown, Sokol, Skelton, & Tornwall, 2017) recognizes that the mechanisms represented by  
80 metacommunity theory must go beyond the historically predominant thinking of considering  
81 dispersal limitation and environmental filtering as two alternative and mutually exclusive  
82 scenarios of community assembly (Meynard et al., 2013). Rather, Leibold et al. (2004) and  
83 Cottenie (2005) emphasized that metacommunity theory embraces a multidimensional  
84 continuum of community assembly dynamics spanning from scenarios dominated by spatial  
85 processes to scenarios influenced primarily by species sorting.

86 In the freshwater realm, studies focusing on a variety of biological groups, from protists to  
87 vertebrate metazoans (e.g. Landeiro, Bini, Melo, Pes, & Magnusson, 2012; Heino & Tolonen,  
88 2017), suggest that metacommunities are often structured by a combination of dispersal  
89 limitation and species sorting, yet their relative importance varies among different organisms,  
90 regions and spatial scales (Heino et al., 2015b). However, the role of niche- and dispersal-  
91 based dynamics on aquatic macrophytes of lentic waterbodies is still largely unknown (see  
92 Capers et al., 2010; Alahuhta & Heino, 2013; Alahuhta, Johnson, Olker, & Heino, 2014), and  
93 most available data come from temperate and boreal deep lakes (e.g. Alahuhta & Heino, 2013;  
94 Alahuhta et al., 2014; Alahuhta, Hellsten, Kuoppala, & Riihimäki, 2018). To our knowledge,  
95 most previous studies in Mediterranean pond environments have addressed compositional  
96 variation in macrophyte assemblages from a local perspective (e.g. Fernández-Aláez,  
97 Fernández-Aláez, García-Criado, & García-Girón, 2018; García-Girón, Fernández-Aláez,  
98 Fernández-Aláez, & Nistal-García, 2018), thus overlooking the role of dispersal limitation and  
99 species sorting in metacommunity dynamics at regional scales. Consequently, there is clearly a  
100 need to identify community assembly processes underlying macrophyte biodiversity patterns  
101 in Mediterranean landscapes, where habitat fragmentation may modify the dominance of  
102 niche- and dispersal- based mechanisms in explaining species distribution (Gallego et al.,  
103 2014). Since extensive Mediterranean environments are found in several locations worldwide

104 and are relatively sensitive to climate and land-use change (Peña-Ortiz, Barriopedro, & García-  
105 Herrera, 2015), addressing this knowledge gap has important, widespread implications.

106 An exciting challenge for metacommunity ecology is to refine statistical tools to identify if  
107 community structure along environmental and spatial gradients is consistently associated with  
108 selection for particular traits in functional niche space (e.g. De Bie et al., 2012; Brown et al.,  
109 2018). A related issue is how best to assess the common assumption that the species making  
110 up the assemblage are equivalent in their dispersal biology (Heino et al., 2015b). In this vein,  
111 an increasingly promising deconstructive approach is to divide species based on dispersal  
112 mode groups (e.g. Cottenie, 2005; Heino, 2013). Although the mechanisms of mobility in  
113 aquatic plants (i.e. anemochory, hydrochory, zoochory and autochory) are not clearly defined  
114 (Soomers et al., 2013), the premise is that spatial effects are likely to be of major concern for  
115 those species that strongly rely on hydrological connections between habitat patches (De Bie  
116 et al., 2012). Progress in this area of research may help in elucidating patterns of species  
117 diversity that would otherwise be missed in the traditional taxonomic-based analyses of  
118 community composition (Heino, 2011).

119 The standard strategy to investigating metacommunity processes is to perform community  
120 variation partitioning using constrained ordination to evaluate the unique and shared effects  
121 of spatial and environmental sets of variables (Borcard, Legendre, & Drapeau, 1992). Such an  
122 approach is highly correlative and was recently shown to result in greatly inflated estimates of  
123 the role of species sorting in common cases where the environment and species distributions  
124 are spatially structured (Clappe, Dray, & Peres-Neto, 2018). An alternative technique, which  
125 models the process of trait-based community selection from probabilistic species pools,  
126 represents a more mechanistic approach. The recent application of such an approach to  
127 stream macroinvertebrates has been promising (Brown et al., 2018). This metacommunity  
128 assembly model (MAM) is built upon on the well-established theory that sees local community  
129 composition as the result of filters acting on species' traits (Poff, 1997), requiring no  
130 assumptions about which environmental variables to include. MAM produces information on  
131 the influence of dispersal limitation, species sorting, and both in combination, as compared to  
132 a null model that excludes deterministic processes (Brown et al., 2018).

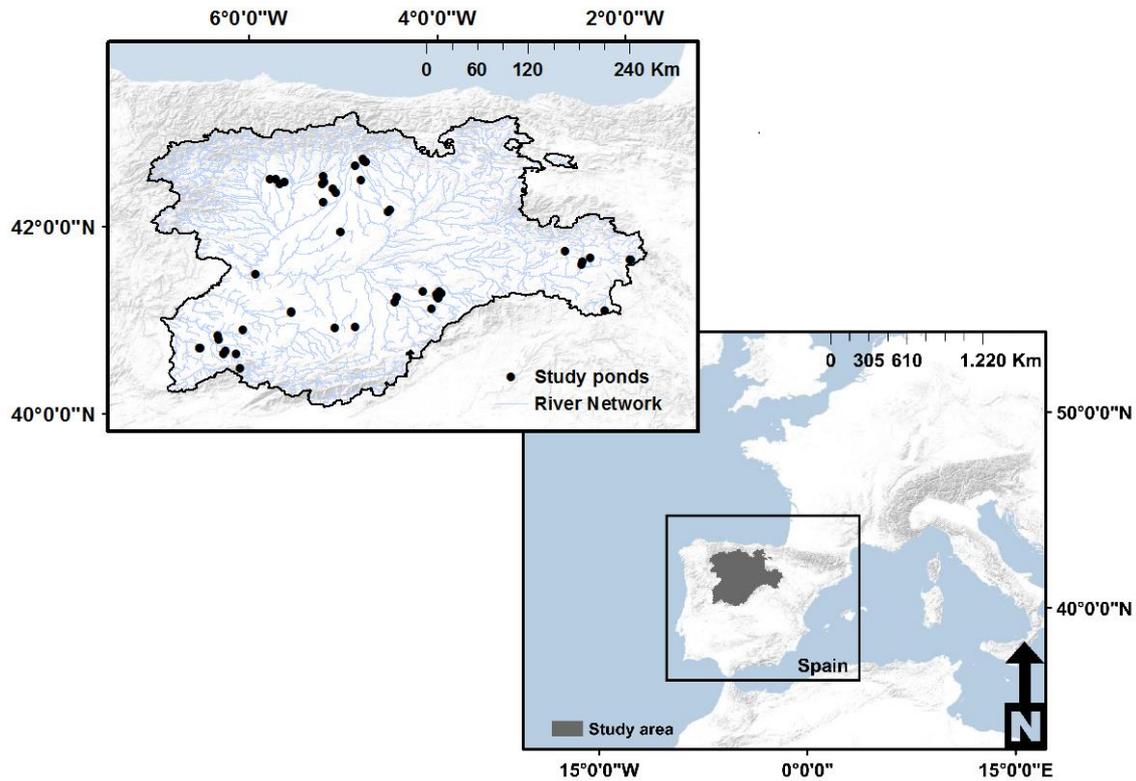
133 A further issue with variation partitioning is that, whilst information on the shared effects of  
134 spatial and environmental variables is produced, the outputs give no explicit information about  
135 the scales at which niche-based processes are likely to act, and which species or traits are  
136 involved. Recent advances in multivariate multiscale codependence analysis (mMCA) now  
137 allow for the detection of the scales at which environmental drivers influence multi-species  
138 communities (Guénard & Legendre, 2018), i.e. the scales associated with environmental filters  
139 (*sensu* Poff, 1997). Such information would be highly complementary to MAM by providing  
140 explanations for any combined effects of space and the environment.

141 Using this novel combination of techniques (MAM and mMCA), we aimed to evaluate the role  
142 of dispersal limitation, species sorting and combined effects in the assembly of pond  
143 macrophyte communities in a vast area (94,226 km<sup>2</sup>) from the northern part of the Iberian  
144 Plateau. We stratified the analyses by dispersal group (i.e. anemochory, hydrochory, zoochory  
145 and autochory) to test whether certain dispersal modes were more likely to confer dispersal  
146 limitation. We hypothesized that: (i) species sorting would be interrupted due to the isolation  
147 of ponds within the landscape; (ii) hydrochorous and autochorous taxa would be the most  
148 limited by dispersal since both mechanisms strongly rely on hydrological connections; and (iii)  
149 environmental drivers of community structure would act at relatively large spatial scales as a  
150 result of habitat fragmentation in Mediterranean environments.

## 151 **2. METHODS**

### 152 **2.1 Study area**

153 A total of 51 permanent ponds were selected for study within a heterogeneous and lowland  
154 (700-1100 m above sea level) area of approximately 94,000 km<sup>2</sup> in the Duero drainage basin in  
155 northwestern Spain (Figure 1). This region has a Mediterranean climate with a wide seasonal  
156 variation in temperature and precipitation, since winters are typically cold and wet (average  
157 winter temperature of 3.2 °C and mean winter precipitation of 173 mm) and summers are  
158 primarily hot and dry (average summer temperature of 18 °C and mean summer precipitation  
159 of 84.5 mm; 1976-2015, data provided by the Spanish Met Agency; AEMET -  
160 <http://www.aemet.es>). The predominant land uses in the study area are arable (46.3%),  
161 pasture (28.8%) and woodland (20.5%), as well as pine plantations and scrubland (4.4%;  
162 García-Girón, Fernández-Aláez, Fernández-Aláez, & Luis, 2018). The majority of ponds studied  
163 are fed mostly by groundwater and rainfall and experience a strong reduction in water volume  
164 during the summer, ranging between 0.1 and 23 ha in aerial extent and 0.2 and 6.3 m in depth.  
165 The study ponds display considerable variability in environmental conditions, including  
166 morphometry, nutrient content and mineralization (Table 1).



167

168 Figure 1. Map of the study area showing the location of the 51 study ponds.

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	Minimum	Maximum	Median	Mean
Pond area	0.1	23	2.6	4.3
Mean depth	0.2	6.3	0.7	0.9
pH	6.6	10.3	8.3	8.4
Conductivity	12	1068	215	293
Turbidity	1.4	83.3	9.2	15.7
TN	0.13	5.21	1.49	1.7
NO <sub>3</sub> <sup>-</sup> -N	0	0.25	0.05	0.06
NH <sub>4</sub> <sup>+</sup> -N	0	0.15	0.01	0.01
TP	19.6	7089.6	118.6	578.8
PO <sub>4</sub> <sup>3-</sup> -P	0.9	6633.8	18.8	578.8
Chla	0.7	362.7	13.9	38.8

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Table 1. Summary of the environmental conditions of the 51 study ponds. Pond area (ha), mean depth (m), pH, conductivity ( $\mu\text{S cm}^{-1}$ ), turbidity (NTU), total nitrogen (TN;  $\text{mg l}^{-1}$ ), nitrate ( $\text{NO}_3^-$ -N;  $\text{mg l}^{-1}$ ), ammonium ( $\text{NH}_4^+$ -N;  $\text{mg l}^{-1}$ ), total phosphorous (TP;  $\mu\text{g l}^{-1}$ ), soluble reactive phosphorous ( $\text{PO}_4^{3-}$ -P;  $\mu\text{g l}^{-1}$ ) and chlorophyll "a" (Chla;  $\text{mg l}^{-1}$ ).

## 184 2.2 Field data collection

185 Each pond was exhaustively surveyed for aquatic macrophytes (emergent, floating-leaved and  
186 submerged forms) using profiles in June and July of either 2004 or 2005; hence each pond was  
187 sampled once. A profile is defined as a line from one shore to the opposite shore at a right  
188 angle to the shoreline with the longest length. The number of profiles for each pond was  
189 determined according to the pond area and shoreline complexity (Jensén, 1977), although  
190 some corrections were implemented *in-situ* in order to account for the spatial heterogeneity of  
191 macrophyte assemblages and the accessibility to the sampling point. Quadrats (0.5 m x 0.5 m)  
192 were placed at varying intervals of 0-5 m depending on the homogeneity of the aquatic flora.  
193 The total number of profiles and quadrats for each pond was increased regularly with pond  
194 area, ranging between 1 and 3 and 5 and 83, respectively (mean density of quadrats per  
195 hectare = 5). Percentage coverage of each macrophyte species was estimated in each quadrat  
196 as the visual projection of each species in the water column onto the pond surface. Finally,  
197 mean coverage of each taxa in a pond was determined as the sum of percent coverages of that  
198 species in all quadrats divided by the number of quadrats used in the pond. Nomenclature  
199 followed Flora Ibérica (Castroviejo 1986-2012), Fernández-Aláez, Fernández-Aláez, Santiago,  
200 Núñez, & Aboal (2012), and Cirujano, Meco, García-Murillo, & Chirino (2014).

201 Pond area (ha) was measured on images available in SIGPAC (the Spanish Geographical  
202 Information System for Agricultural Parcels - <http://www.sigpac.jcyl.es/visor/>), whereas mean  
203 depth (m) was determined by measuring depth with calibrated sticks at several sites along  
204 profiles within each pond. Several water samples were randomly collected at different depths  
205 along a shore-centre transect using a cylindrical corer (diameter = 60 mm, length = 1 m). The  
206 number of samples ranged between 3 and 15 depending on the pond area. All samples from  
207 each pond were subsequently combined and mixed to form a single composite water sample.  
208 A range of environmental variables including pH, conductivity ( $\mu\text{S cm}^{-1}$ ) and turbidity (FTU)  
209 were measured *in-situ* from the composite sample using WTW field probes (Model LF 323) and  
210 a portable turbidimeter (Model HACH 2100P). The integrated water samples were preserved at  
211 4 °C and then analysed in laboratory to determine total nitrogen (TN;  $\text{mg l}^{-1}$ ), nitrate ( $\text{NO}_3^-$ -N;  
212  $\text{mg l}^{-1}$ ), ammonium ( $\text{NH}_4^+$ -N;  $\text{mg l}^{-1}$ ), total phosphorous (TP;  $\mu\text{g l}^{-1}$ ), orthophosphate ( $\text{PO}_4^{3-}$ -P;  $\mu\text{g}$   
213  $\text{l}^{-1}$ ) and chlorophyll "a" (Chla;  $\text{mg l}^{-1}$ ). Nutrient samples were previously fixed with mercuric  
214 chloride ( $\text{HgCl}_2$ ) and all analyses followed standard methods (APHA, 1989).

## 215 2.3 Data analysis

216 Using information available in Willby, Abernethy, & Demars (2000), functional traits were  
217 selected to provide information on attributes for each macrophyte species that could  
218 potentially come under selection by environmental filters. We included fuzzy scores (0 =  
219 absence of an attribute, 1 = weak affinity and 2 = strong affinity) for a total of 31 trait  
220 modalities subdivided into seven trait categories (Table 2). When no information was available  
221 in Willby et al. (2000) (e.g. *Eleocharis palustris* (L.) Roem. & Schult., *Eleocharis multicaulis* (Sm.)

222 Desv. and *Juncus articulatus* L.), traits were inferred from Castroviejo (1986-2012) and Cirujano  
 223 et al. (2014). We transformed fuzzy scores according to the established method of Chevenet,  
 224 Dolédec, & Chessel (1994), whereby trait modalities are expressed as proportions within  
 225 categories (e.g. growth form) and centred to ensure that the species × trait matrix had equal  
 226 row and column weights.

227

Traits	Attributes
Growth forms	Free floating (surface and submerged) and anchored (floating leaved, submerged leaved and emergent leaved)
Mode of reproduction	Rhizomes, fragmentation, budding, turions, stolons, tubers and seeds
Number of reproductive organs per year and individual	Low (<10), medium (10-100), high (100-1000) and very high (>1000)
Perennation	Annual, biennial and perennial
Dispersal vector	Wind, water and animals
Period of production of reproductive organ	Early (March-May), mid (June-July), late (August-September) and very late (post-September)
Fruit size	Small (<1 mm), medium (1-3 mm), large (>3 mm)

228

229 Table 2. Choice of traits and their subdivisions into attributes according to Willby et al. (2000).

230

231 To analyse the processes structuring pond macrophyte communities, we applied the MAM  
 232 approach of Brown et al. (2018). In brief, MAM mimics the selection of organisms from the  
 233 species pool through four alternative components. First, the null component selects taxa from  
 234 the species pool at random and assigns each taxon its mean abundance across the whole  
 235 landscape (metacommunity abundance). Second, the dispersal component selects species  
 236 based on a vector of probability weightings unique to each site, again assigning selected taxa  
 237 their mean metacommunity abundance. The probability weightings are given by a distance  
 238 decay function describing the proximity of each species to the site of interest. Third, the trait  
 239 selection component involves the calculation of community weighted means (CWMs) of sites  
 240 on the first two axes from a principal coordinate analysis (Laliberté & Legendre, 2010). Taxa  
 241 are selected from the species pool and assigned abundances iteratively until the CWM of the  
 242 synthetic community matches that of the observed community within a threshold ( $\pm 2.5\%$  in  
 243 our case); another pick of taxa is then taken from the species pool and the process repeated.  
 244 Finally, the mixed component combines occurrence probabilities from the dispersal  
 245 component with abundances from the trait selection component. In all cases, the number of  
 246 taxa selected from the species pool is fixed at the observed species richness for each site. The  
 247 process is repeated a number of times ( $k=500$  in our case) and the performance of each  
 248 component reported as the mean and standard deviation of the Bray-Curtis similarity. Using  
 249 these metrics, we calculated the standardized effect size (SES) as:

250 
$$SES = (\mu_{mod} - \mu_{null})/\sigma_{null}$$

251 where  $\mu_{mod}$  is the mean Bray-Curtis similarity from the alternative model components  
252 (dispersal, trait selection, mixed), and  $\mu_{null}$  and  $\sigma_{null}$  the mean and standard deviation of the  
253 Bray-Curtis similarity from the null component, respectively. See Brown et al. (2018) for full  
254 details of the method. For the purposes of fitting the trait selection component, prior to the  
255 analysis we combined functionally identical species. We also stratified the model by dispersal  
256 group (i.e. anemochory, hydrochory, zoochory and autochory) to test whether the relative role  
257 of habitat isolation and trait filtering in structuring local communities differed by dispersal  
258 vector. A species was considered a member of a dispersal group if its fuzzy trait score  
259 corresponding to that dispersal group was non-zero.

260 Finally, we performed mMCA on community (relative abundance) weighted means of  
261 transformed trait scores (Guénard & Legendre, 2018). This statistical method estimates spatial  
262 structures generated by the joint variation of environment and community composition that  
263 are described by an orthonormal set of spatial variables (spatial eigenvectors, also known as  
264 Moran's eigenvector maps, MEMs; Dray, Legendre, & Peres-Neto, 2006). We calculated the  
265 spatial variables from the irregularly spaced pond locations using the eigenmap function from  
266 the 'codep' package in R (Guénard, Legendre, & Pages, 2018). The significance of spatial  
267 codependence between macrophyte communities and environmental variables was assessed  
268 through a permutation test using the permute.cdp function of the same package. A principal  
269 component analysis (PCA) was performed to visualize the relationships between sites, traits  
270 and environmental descriptors in niche space. All environmental variables were centred and  
271 standardized to unit variance prior to conducting the PCA.

272 All analyses were performed in R version 3.4.4 (R Core Team, 2018).

### 273 **3. RESULTS**

274 We identified a total of 58 macrophyte species from 22 different families. A complete list of  
275 species and families is provided in Supporting Information Appendix S1. *Eleocharis palustris* (L.)  
276 Roem. & Schult. was the most frequent macrophyte species, occurring in 35 ponds (68%). The  
277 second and third most frequent species were *Schoenoplectus lacustris* (L.) Palla and  
278 *Potamogeton trichoides* Cham. & Schltldl., occurring in 32 (63%) and 25 (49%) ponds,  
279 respectively. Species richness among pond communities range from one to 17 ( $7\pm 4$  species per  
280 pond). The trait-based analysis showed that the majority of plant species in the study ponds  
281 produced a medium (63.8%) to high (70.7%) number of reproductive organs from mid to late  
282 summer (~100%), were submerged leaved, perennial and anemochorous (87.9%, 91.4% and  
283 70.1%, respectively), and had medium (62%) to large (29.3%) propagule size (see Table 3).

284

285

Traits	Attributes	Short names	Frequency (%)
Growth forms	Free floating	FreeFloatingSurface	10.3
	Floating leaved (anchored)	AnchoredFloatingLeaves	27.6
	Submerged leaved (anchored)	AnchoredSubmergedLeaves	87.9
	Emergent leaved (anchored)	AnchoredEmergentLeaves	63.7
Mode of reproduction	Rhizomes	Rhizome	50
	Fragmentation	Fragmentation	48.3
	Budding	Budding	13.8
	Turions	Turions	15.5
	Stolons	Stolons	46.6
	Tubers	Tubers	3.4
	Seeds	Seeds	100
Number of reproductive organs per year and individual	Low (<10)	LowRepro	10.3
	Medium (10-100)	MediumRepro	63.8
	High (100-1000)	HighRepro	70.7
	Very high (>1000)	VHighRepro	18.9
Perennation	Annual	Annual	25.9
	Biennial or short-lived perennial	BiennialShortPeren	17.2
	Perennial	Perennial	91.4
Dispersal vector	Wind	Anemochory	70.1
	Water	Hydrochory	29.3
	Animals	Zoochory	39.7
	Self	Autochory	64
Period of production of reproductive organ	Early (March-May)	EarlyRepro	32.8
	Mid (June-July)	MidRepro	100
	Late (August-September)	LateRepro	96.6
	Very late (post-September)	VLateRepro	17.2
Fruit size	Small (<1 mm)	SmallFruit	19
	Medium (1-3 mm)	MediumFruit	62
	Large (>3mm)	LargeFruit	29.3

286

287 Table 3. Relative frequencies (%) of the morphological and life history traits for the 58  
288 macrophyte species studied. Short names are used in Figure 3.

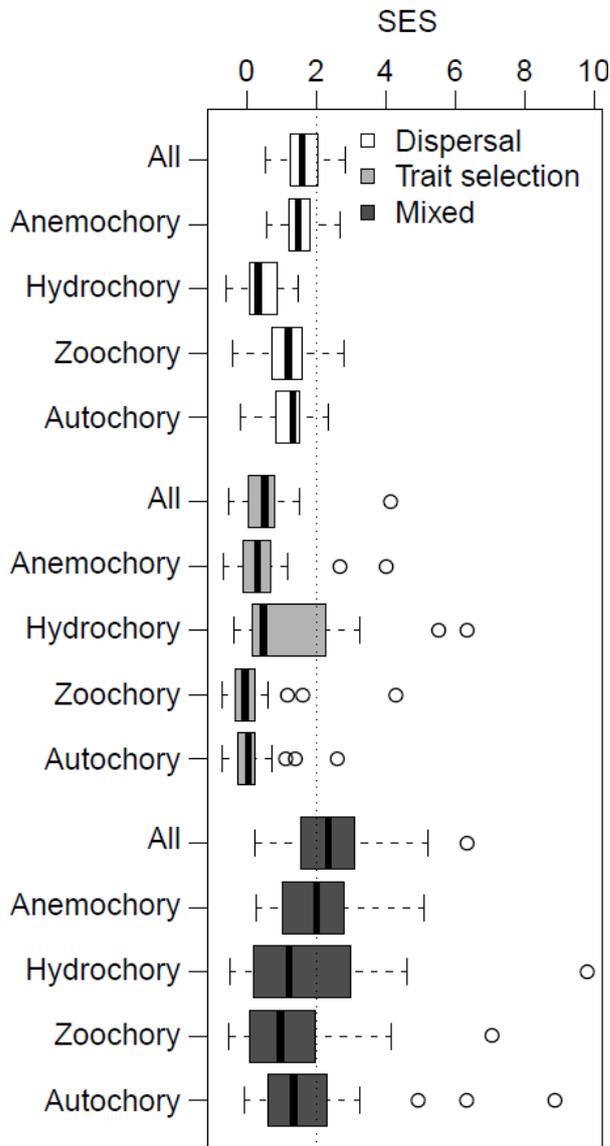
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293 Under the community assembly model, combining predictions of species' occurrences and  
 294 abundances from the dispersal and trait selection components (mixed scenario) improved  
 295 predictions relative to the pure trait and pure spatial scenarios. The greatest effects were seen  
 296 for the mixed and pure spatial scenarios when all species were considered together, closely  
 297 followed by anemochorous, autochorous and zoochorous species (Figure 2). With the  
 298 exception of water-dispersing macrophytes, the lowest SES values were seen for the pure trait  
 299 selection model. Hence, weighting each pick from the species pool on the basis of the  
 300 geographic distance between sites where each species occurred made predicted and observed  
 301 communities more similar than under the trait selection scenario, in which the composition of  
 302 artificial communities was constrained by observed CWMs on the first two synthetic trait axes.



303

304 Figure 2. Standardized effect size (SES) for each component of the community assembly model  
 305 for all species and for species grouped by dispersal mode. The greater the SES values, the  
 306 better each model component (dispersal, trait selection and mixed) performed compared to

307 the uniform model. Boxplot bold lines = median; box = interquartile range (IQR); whiskers =  
 308 maximum and minimum up to 1.5×IQR.

309

310 We obtained 48 spatial eigenvectors ranging from the largest potential spatial structures  
 311 (MEM1) to the smallest (MEM48; Supporting Information Appendix S2). The mMCA application  
 312 revealed two significant components of the spatial codependence between macrophyte trait  
 313 structure and environmental variables (Table 4). The strongest component associated total  
 314 phosphorous with macrophyte trait structure at the scale of the third spatial eigenvector  
 315 (MEM3). The next strongest component revealed the association of mean depth with trait  
 316 structure at the scale of MEM11. MEM3 and MEM11 were associated with spatial extents of  
 317 approximately 300 km and 250 km, respectively (Supporting Information Appendix S2). The  
 318 first principal component (PCA1) of the macrophyte trait structure (Figure 3) was related to  
 319 fruit size and total phosphorous. Communities with positive PCA1 loadings tended to be found  
 320 in P-poor ponds and were dominated by taxa with small and medium fruit sizes and a medium  
 321 number of reproductive organs per year, whereas negative PCA1 loadings were associated  
 322 with larger fruit and higher total phosphorous concentrations (Figure 3). PCA2 was related to  
 323 growth forms and mean depth. Taxa with submerged growth forms had negative loadings and  
 324 were generally found in shallower ponds, whereas emergent types had positive loadings  
 325 associated with deeper ponds. The mMCA results indicated a pattern varying radially from a  
 326 central-south location (MEM3) which linked total phosphorous with trait variation. A more  
 327 complex pattern was detected linking mean depth with trait structure (MEM11), which  
 328 separated north-east and southwest zones from a central band (Figure 4). Importantly, the  
 329 scales identified by mMCA suggest that artefacts arising from the clustered distribution of  
 330 sampling sites were absent or minimal.

Scale	Environmental variable	$\Phi_{v_1, v_2}$	$v_1$	$v_2$	$\rho$
<b>MEM3</b>	<b>TP</b>	<b>61.53</b>	<b>32</b>	<b>47</b>	<b>.005</b>
<b>MEM11</b>	<b>Mean depth</b>	<b>43.49</b>	<b>32</b>	<b>46</b>	<b>.015</b>
MEM7	NH <sub>4</sub> <sup>+</sup> -N	17.62	32	45	0.3

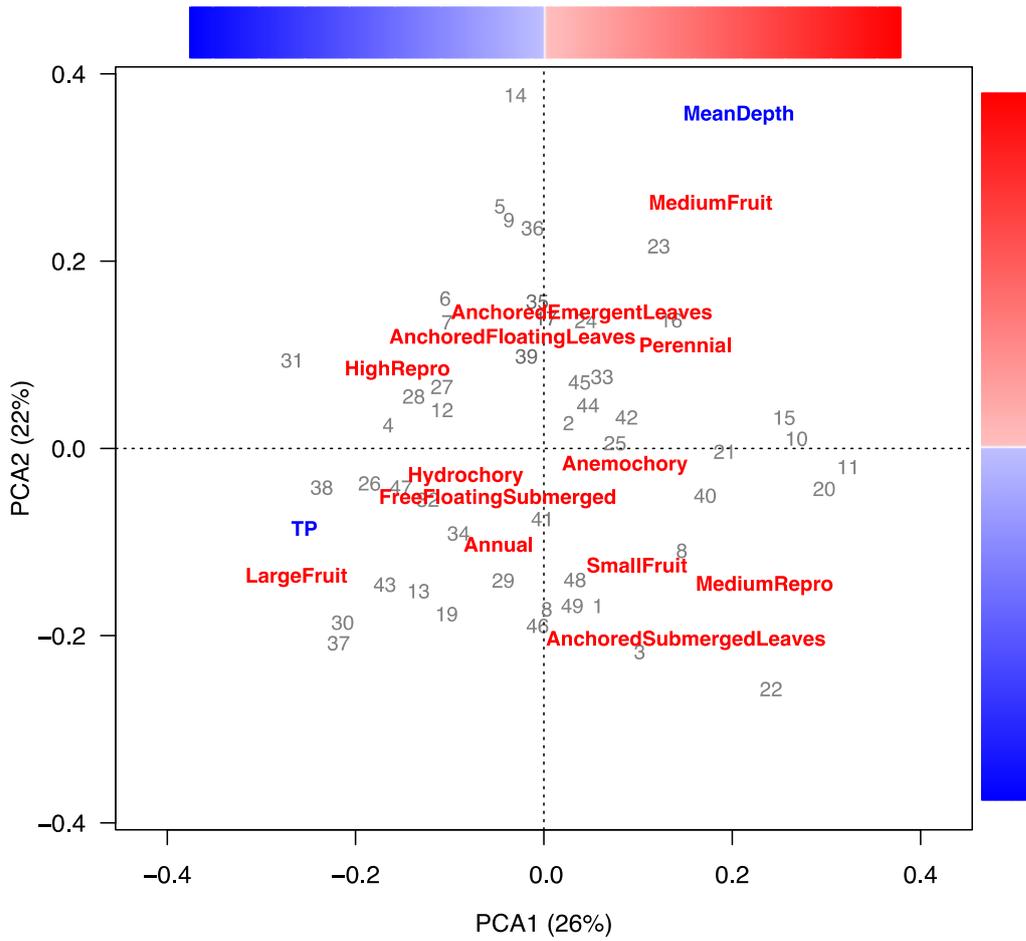
331

332 Table 4. Components of the spatial codependence between macrophyte community weighted  
 333 mean traits and environmental variables assessed by permutation tests. Note that the  
 334 permutation test adds components until adding further variables does not result in a  
 335 significant improvement in model fit. Significant components are presented in bold.

336

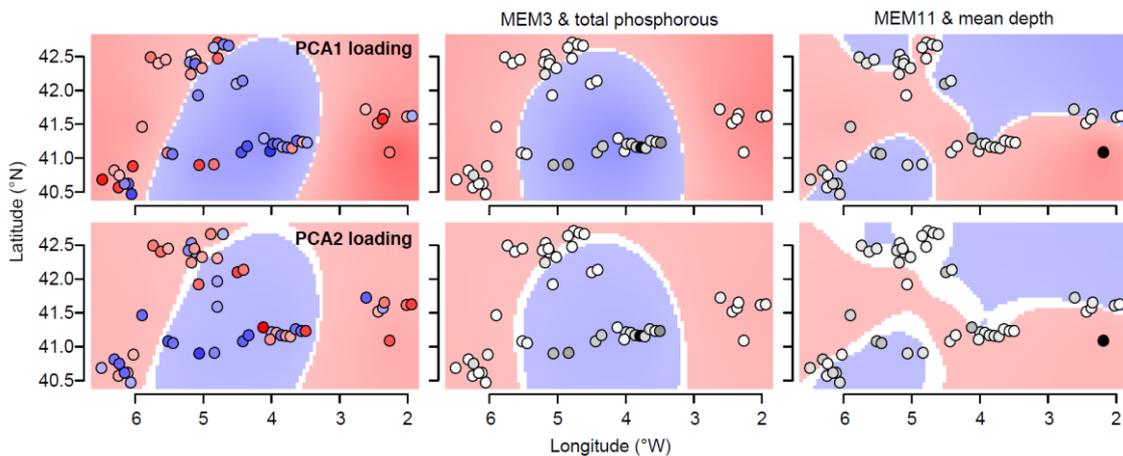
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340

341 Figure 3. The first two principal components of the macrophyte trait structure. Sites are  
 342 labelled using grey numbers, traits (community weighted means) are labelled in red, and  
 343 environmental variables identified in significant trait-environment relationships by mMCA are  
 344 labelled in blue (Table 4). To aid interpretation, only those traits with the highest loadings are  
 345 shown (top 10 on each axis). The colour scales represent values along each principal  
 346 component as represented in Figure 4.



347 Figure 4. Statistically significant spatial components of codependence between macrophyte  
348 trait structure and environmental variables from mMCA. The left panels show sites shaded  
349 with colours representing scores from the corresponding principal component (PCA1 and  
350 PCA2; Figure 3). Other panels show sites with symbols shaded in greyscale according to the  
351 site's value of the environmental variable stated above the map, with background colours  
352 corresponding to the spatial structuring variable (MEM) stated above the map (positive values  
353 red, negative values blue – see Figure 3). For all panels, background values between sites were  
354 obtained from predicted scores of the MEM(s) for single species, which were then projected  
355 on the PCA.

356

#### 357 **4. DISCUSSION**

358 Assessing the relative importance of environmental and spatial processes on community  
359 assembly is one of the key approaches for enhancing our basic understanding of  
360 metacommunity dynamics (Heino, 2011; Tonkin, Stoll, Jähnig, & Haase, 2016). Importantly, a  
361 major appeal of the theory of metacommunity organization is that it potentially offers a  
362 predictive framework with which to disentangle systematic relationships between different  
363 community assembly scenarios and species' traits (De Bie et al., 2012; Meynard et al., 2013).  
364 Using a combination of data on species' traits and a robust, probabilistic approach (MAM and  
365 mMCA), we assessed the role of dispersal limitation, species sorting and shared effects in the  
366 assembly of pond macrophyte metacommunities across an extensive area within the Iberian  
367 Plateau, and identified which traits, environmental variables and spatial scales were driving  
368 local community structure. We found that the mixed scenario had the greatest standardized  
369 effect size, suggesting that dispersal limitation acted in concert with species sorting to  
370 influence the structure of local communities. Similarly, our results revealed that nutrient status  
371 (total phosphorous) selected for fruit size at the largest extents (~300 km) and mean pond  
372 depth selected predominantly for growth forms (submerged and emergent) at a slightly  
373 smaller extent (~250 km).

##### 374 **4.1 Drivers of metacommunity structure**

375 Consistent with our first hypothesis and in agreement with a growing number of studies (e.g.  
376 Cottenie & De Meester, 2004; Capers et al., 2010; Akasaka & Takamura, 2012; De Bie et al.,  
377 2012; Padial et al., 2014), we found that dispersal limitation interfered with species sorting in  
378 determining macrophyte community assembly patterns. However, caution should be exercised  
379 when comparing the influence of species sorting and dispersal constraints on freshwater  
380 macrophytes from one study to another (Shurin, Cottenie, & Hillebrand, 2009). This is because  
381 the degree to which dispersal limitation interacts with environmental filtering is likely to vary  
382 among different spatial extents of observation (e.g. regional vs continental – Alahuhta,  
383 Rääpysjärvi, Hellsten, Kuoppala, & Aroviita, 2015 vs Viana et al., 2014) and geographic regions

384 (e.g. Temperate vs Mediterranean – Alahuhta, 2015 vs this study), with generally stronger  
385 dispersal limitation at long rather than short distances (Heino, 2011).

386 Our results are broadly in line with several studies encompassing a wide variety of organisms  
387 (i.e. benthic diatoms, rotifers, cladocerans, macroinvertebrates, molluscs, fish and  
388 amphibians), study systems (i.e. wetlands, lakes and streams), and spatial scales (i.e. regional  
389 to continental), suggesting that these communities are jointly structured by dispersal  
390 limitation and species niche differences (e.g. Pinel-Alloul, Niyonsenga, & Legendre, 1995;  
391 Soinen, Lennon, & Hillebrand, 2007; Shurin, Cottenie, & Hillebrand, 2009). Furthermore, our  
392 findings agree with Capers et al. (2010), O’Hare, Gunn, Chapman, Dudley, & Purse (2012) and  
393 Grimaldo et al. (2016), who recently found that spatial structuring and environmental control  
394 together accounted for much of the variation in aquatic plant communities across Connecticut  
395 (northeastern US), Scotland and Zambia. By contrast, our results deviate slightly from those  
396 found by Alahuhta & Heino (2013) and Alahuhta et al. (2015) in the US state of Minnesota and  
397 southern Finland, respectively, suggesting that the relative influence of dispersal- and niche-  
398 based processes on macrophyte community assembly is likely to vary rather unpredictably at  
399 continental scales.

400 Our study is the first to illustrate the interaction between spatial and environmental gradients  
401 in determining the functional structure of pond macrophytes in Mediterranean landscapes.  
402 These findings suggest that there is no strong dichotomy between community assembly  
403 scenarios – dispersal limitation and species sorting are extremes along a spectrum of processes  
404 underlying observed biodiversity patterns (Heino et al., 2015b). Our results re-emphasize the  
405 need to go beyond the traditional view of understanding spatial and environmental processes  
406 as two alternative and mutually exclusive scenarios of community assembly and embrace the  
407 full power of metacommunity theory (Leibold et al., 2004; Logue et al., 2011; Brown et al.,  
408 2017).

#### 409 **4.2 Comparison between dispersal mode groups**

410 Freshwater organisms exhibit a range of dispersal modes and capacities that should be  
411 considered when developing a predictive framework for metacommunity dynamics (Heino,  
412 2011). Modern molecular and biogeographical studies (e.g. Capers et al., 2010; Wu, Yu, Wang,  
413 Li, & Xu, 2015; Cao, Mei, & Wang, 2017) suggest that some aquatic plants may disperse more  
414 or less uniformly at distances up to ~ 200 km, beyond which habitat isolation usually becomes  
415 limiting. Our study ponds were largely isolated from each other within a terrestrial matrix  
416 (maximum pairwise distance ~ 400 km), so the further apart ponds were, the less likely they  
417 were to share a similar species composition. In these kinds of fragmented Mediterranean  
418 environments, wind usually plays the primary role for passive dispersers (Coughlan, Kelly, &  
419 Jansen, 2017), transporting propagules to other ponds over the landscape. However, contrary  
420 to expectations, our results suggest that hydrochorous taxa were the least limited by  
421 geographical distances between ponds. This finding is likely to be linked to the existence of

422 intermittent corridors between ponds via drainage ditches (Junta de Castilla y León, 2001), and  
423 agrees with the observation of Soomers et al. (2013), who found that dispersal distances of  
424 propagules in fragmented landscapes were many times longer due to hydrochorous dispersal  
425 compared to wind dispersal. Since dispersal distances by water are likely to surpass those by  
426 wind alone even for typical wind-dispersing macrophyte species (Soomers et al., 2013),  
427 anemochorous dispersal might further hinder aquatic plants from reaching new habitat  
428 patches when little or no physical connection via flowing water exists between ponds  
429 (Boedeltje, Bakker, Ten Brinke, van Groenendael, & Soesbergen, 2004). Given that the majority  
430 of plant species in our study ponds were anemochorous and autochorous (see Table 3), it  
431 seems reasonable to suppose that macrophyte dispersal may be dependent on dispersal traits,  
432 such as propagule size, and the success of dispersal vectors, particularly wind, at overcoming  
433 geographic distances and habitat isolation. However, we cannot rule out the degree to which  
434 networks of stepping-stone ponds may function as habitat connectivity providers and their  
435 implications for species movement among otherwise isolated habitat patches (Saura, Bodin, &  
436 Fortin, 2014).

#### 437 **4.3 Species' traits, environmental drivers and spatial scales**

438 We found evidence for relationships between species' traits and the spatial scales at which  
439 environmental drivers influence community assembly. Based on the mMCA results, we were  
440 able to confirm our expectations that macrophyte community trait structure (i.e. fruit size and  
441 growth forms) can be affected by environmental variation (i.e. total phosphorous and mean  
442 pond depth) via different processes that operate at relatively large spatial scales. Specifically,  
443 the role of phosphorous may be interpreted as a relationship between energy-allocation  
444 strategies and the availability of a limiting resource (Daoust & Childers, 2004), so that  
445 adaptation to increased nutrient levels generally leads to the development of larger vegetative  
446 and reproductive structures, particularly fruit size, and a decrease in the biomass of resource-  
447 acquiring structures (Li, Werger, de Kroon, During, & Zhong, 2000). The spatial codependence  
448 between fruit size and phosphorous at the largest extent is likely to be related to the well-  
449 known impact of intensive agriculture on water quality at regional spatial extents (Declerck et  
450 al., 2006). Similarly, the relationships between macrophyte growth forms and pond depth in  
451 shallow lakes and ponds has already been discussed elsewhere (e.g. Scheffer, 1998),  
452 suggesting that this effect is largely due to the attenuation of light at increasing depths which  
453 is unfavourable for macrophytes with submerged leaves. Conversely, the potential for  
454 phenotypic plasticity in morphological traits (e.g. elongation of stems and increased above-  
455 ground biomass) may facilitate the survival of emergent vegetation in deeper, turbid ponds  
456 (Coops, van den Brink, & van der Velde, 1996).

#### 457 **4.4 Implications for further studies**

458 Recent recognition of the limitations affecting the traditional approach to assessing  
459 community assembly processes called for the development of more sophisticated methods.

460 Specifically, an analysis of real and simulated community data by Clappe et al. (2018)  
461 highlighted the risk of obtaining inflated estimates of species sorting effects from application  
462 of the classic variation partitioning framework. They proposed a method whereby estimates of  
463 the shared contribution of environmental and spatial effects are adjusted to account for  
464 spatial autocorrelation. Whilst this is clearly an advance over the standard variation  
465 partitioning approach, we have chosen to apply a combination of methods that are less reliant  
466 on correlations between environmental variables and the community matrix. Our approach  
467 instead relies on well-established ecological theory (Poff, 1997) that sees local community  
468 structure as the result of trait-based filtering of species (i.e. MAM) at different spatial scales  
469 (i.e. mMCA). A particular advantage of our approach for future studies in metacommunity  
470 ecology is that it simultaneously provides estimates of the relative contributions of spatial and  
471 niche-based processes whilst explicitly identifying the traits, environmental variables and  
472 spatial scales involved. Such a mechanistic approach may help in elucidating patterns of  
473 community assembly that would otherwise be missed, or even misrepresented, under the  
474 standard variation partitioning framework.

## 475 **5. CONCLUSIONS**

476 Our results suggest that dispersal limitation acted in concert with species sorting to influence  
477 the community assembly processes underlying observed macrophyte biodiversity patterns.  
478 The novel combination of recently developed statistical models, MAM and mMCA, revealed  
479 that species' traits were involved in determining abundance structure via two major trait-  
480 environment relationships (fruit size-nutrient status and growth form-mean pond depth) that  
481 operated over relatively large spatial extents (250-300 km). These results emphasize the need  
482 to go beyond the traditional taxonomic-based analyses of community composition and the  
483 predominant thinking of considering spatial and environmental processes as two alternative  
484 and mutually exclusive scenarios of community assembly. Accordingly, the combination of  
485 data on species' traits and community structure underlies the most promising predictive  
486 framework to embrace the full scope of metacommunity theory. Our results support calls for  
487 conservation and environmental management to assess community assembly patterns and  
488 processes operating at multiple scales across the landscape.

489

## 490 **CONFLICT OF INTEREST**

491 The authors declare no conflicts of interest.

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662 **BIOSKETCH**

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