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1 **Benthic diatom metacommunity across small freshwater lakes: driving mechanisms, β -**
2 **diversity and ecological uniqueness**

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13

14 **Abstract**

15

16 In this study, driving forces and diversity patterns of a benthic diatom metacommunity across
17 small freshwater lakes exhibiting environmental heterogeneity were investigated.
18 Furthermore, local (LCBD) and species (SCBD) contributions to β -diversity and their driving
19 parameters were assessed with abundance- and incidence-based analyses. Our results revealed
20 that both spatial distance and environmental heterogeneity affected the community assembly,
21 which corresponds most to the mass-effect (ME) concept. This theory was confirmed by high
22 α -diversity of sampling sites, however, high overall β -diversity enhanced mainly by turnover
23 contradicted the ME paradigm. LCBD indices were affected by environmental variables
24 furthermore, LCBD and LCBD in terms of species replacement showed a strong positive
25 correlation. The ecologically most unique sites hosted relatively low species richness, and
26 common species with intermediate-sized or broad niches contributed mostly to the regional β -
27 diversity. However, abundance- and incidence-based calculations revealed different
28 relationships of SCBD with the species' total abundance and the number of occupied sites.
29 Consequently, we favor the previous suggestions that comprehensive research focusing on
30 conservation should incorporate the investigation of LCBD, SCBD, species-rich sites and also
31 ecologically restricted species. Moreover, in assessing ecological uniqueness, both abundance
32 and binary data sets should be considered since they might shed light on distinct patterns.

33

34 **Key words:** assembly mechanisms, diversity patterns, ecological uniqueness, mass-effect,
35 species richness

36

37 **Introduction**

38 The current ecology- and conservation-oriented research tends to explore the possible causes
39 of community assembly by examining it at regional scale, rather than by only “snap-shot”
40 investigation of groups of biota within a given habitat. That is, studies focusing on
41 metacommunity processes as well as β -diversity and its components are gaining more and
42 more attention. Within the metacommunity framework (Leibold et al., 2004) four different
43 concepts can be distinguished in explaining the importance of local- (species’ competitive
44 abilities, demographic processes) and regional-scale (degree of environmental heterogeneity,
45 dispersal) processes. In the neutral theory (NT), species are assumed to be identical
46 concerning their interspecific interactions and response to any limiting factor; demographic
47 processes (birth-death rates) are stochastic; the environment is homogeneous in the region;
48 and species are limited in their dispersion. The patch dynamic (PD) archetype assumes that
49 the species’ relative competitive abilities depend on the local environmental conditions; the
50 population-level extinctions are stochastic due to the individual-level stochasticity; the
51 environment is completely homogeneous or spatial heterogeneity may occur in response to
52 the environment; dispersal is limited but interspecific differences in colonization abilities are
53 allowed. In the mass-effect (ME) concept, competitive abilities and birth-death rates are
54 assumed to be largely dependent on the local environment, which displays heterogeneous
55 patterns; species are able to persist in suboptimal localities if there is a sufficient immigration
56 from adjacent sites with high population growth. The species-sorting (SS) concept, similarly
57 to the ME, expects that the environment is heterogeneous, local conditions regulate the
58 competitive abilities of species and the demographic processes; dispersal is sufficient, thus
59 each species can persist in any habitat where it can achieve positive population growth
60 (Leibold & Chase, 2017). Processes assumed to be acting in the four metacommunity
61 archetypes is summarized in Fig. 1. However, the role of these local- and regional-scale

62 processes, and thus the interpretation of metacommunity concepts, may change with the
63 extent of the investigated area (Langenheder & Ragnarsson, 2007; Mykrä et al., 2007; Heino
64 et al., 2010; Vilmi et al., 2016) and the connectivity among sites (Göthe et al., 2013; Dong et
65 al., 2016; Vilmi et al., 2016).

66 In estimating the heterogeneity of communities and in unraveling the mechanisms
67 acting behind metacommunity patterns, β -diversity analyses play a key role (Viana et al.,
68 2016). One of the most important and most commonly applied framework for β -diversity
69 surveys was proposed by Baselga (2010). He introduced the multiple-site Sørensen
70 dissimilarity index as suitable to measure overall dissimilarity among a set of sampling sites,
71 which can be divided into turnover (species replacement) and nestedness (reflects species
72 loss) components (Baselga et al., 2007; Baselga, 2010). Its analogous method, the abundance-
73 based multiple-site Bray-Curtis dissimilarity index, has been published recently and can be
74 partitioned into abundance balanced variation and abundance gradients components (Baselga,
75 2017).

76 Total β -diversity (i.e. the total variation in community concerning binary or abundance
77 matrix) can be divided into the relative contribution of individual sampling units (Local
78 Contribution to Beta Diversity - LCB_D) and of individual species (Species Contribution to
79 Beta Diversity - SC_B_D) to the overall β -diversity, which targets the assessing of ecological
80 uniqueness of sites and species (Legendre & De Cáceres, 2013). In addition, calculations have
81 been extended to the measure of sites' uniqueness in terms of species replacement and
82 nestedness (Legendre & De Cáceres, 2013).

83 Although Baselga's (2010) incidence-based calculations are widely used in terrestrial
84 and aquatic ecology (e.g., Maloufi et al., 2016; Conradi et al., 2017; Szabó et al., 2018),
85 publications applying his abundance-based multiple-site framework have been lagging.
86 Moreover, estimation of local and species contributions to β -diversity is receiving increasing

87 scientific interest (e.g., Lopes et al., 2014; Tonkin et al., 2016; Heino & Grönroos, 2017;
88 Vilmi et al., 2017). Nevertheless, to our knowledge, diatom studies on LCBD in terms of
89 replacement and nestedness as well as the comparison of their incidence- and abundance-
90 based results are absent.

91 The first aim of this study was to investigate the driving mechanisms of benthic
92 diatom communities in small freshwater lakes of the Carpathian Basin: whether they are
93 assembled merely due to the selection forces of the local environment or spatial variables are
94 also important. Distances between our sampling sites can be considered as intermediate (2-
95 400 km) and it covers regional scale instead of continental. Furthermore, environmental
96 parameters vary reasonably across the sampled lakes (Table S1), however, none of them
97 represents such extremely stressed environments as for instance, natural shallow saline lakes
98 of the Carpathian Basin. Therefore, we assumed that both spatial distance between sites and
99 local environmental characteristics should equally affect the development of diatom
100 communities.

101 Our second goal was to estimate the regional β -diversity of diatom assemblages
102 formed by metacommunity processes and to assess whether it is enhanced mainly by species
103 turnover or nestedness related to the richness difference between sites. Similarly to the
104 findings reported for most biota at low- or mid-latitude ecosystems (e.g., Tisseuil et al., 2012;
105 Maloufi et al., 2016; Viana et al., 2016; Soininen et al., 2018; Szabó et al., 2018), we expected
106 a high β -diversity of diatom communities due to the high degree of species turnover and a
107 much smaller role of the nestedness component.

108 Furthermore, we intended to assess if sampled lakes contribute equally to β -diversity
109 or some of them plays a particularly important role with its unique community composition
110 and to determine which factors are responsible for the established patterns. Also, we wanted
111 to examine this issue in terms of species turnover and nestedness, as well. We assumed that

112 sampling sites where one or more environmental parameters deviate considerably from the
113 average, thereby resulting in unique species combinations and/or low species richness
114 (Legendre, 2014), should have the largest contribution to β -diversity.

115 Finally, we wanted to quantify to what extent the individual species contribute to β -
116 diversity in the sampled region. We hypothesized that species that are characteristic of
117 restricted environmental conditions should affect overall β -diversity to the greatest extent.

118 Legendre (2014) suggested that the spatial distance among sampling sites should be
119 taken into account when choosing a dissimilarity index. Abundance-based calculations are
120 presumed to be appropriate at small spatial scales where species more likely differ in their
121 abundances rather than in their incidences. In contrast, incidence-based calculations are more
122 preferable within large spatial extents where sampling sites probably host different species.
123 Therefore, we aimed to test each of our hypotheses both with abundance- and incidence-based
124 analyses and to compare whether they provide distinct results.

125

126 **Material and Methods**

127 *Study sites, sampling and laboratory analyses*

128 In August 2010, a total of 38 freshwater lakes were sampled in the Carpathian Basin (Fig. 2,
129 Table S2). Each of them had a surface smaller than 3 km² and their altitude varied between 73
130 and 311 m (Table S2). Altitude of sampling sites (Table S1) were measured in Google Earth
131 Pro. The geographical distance between two sampling sites ranged from 2 to 400 km.

132 Phytobenthos samples were collected in the littoral region primarily from common
133 reed (*Phragmites australis* (Cav.) Trin. ex Steud.) or from other characteristic emergent
134 macrophytes, such as sedge (*Carex* sp.) or bulrush (*Typha* sp.) (CEN, 2003; King et al.,
135 2006). In each case, five macrophyte stems of the same species were chosen and starting ca. at
136 10 cm below the water surface, their 15-cm sections were cut. In some lakes, where

137 macrophyte vegetation was not characteristic or was absent, benthic diatoms were taken from
138 permanently-submerged natural stones, boughs or in case of their absence, from mud surface
139 with pipette. In each lake, only one type of substrates was sampled. Diatom valves were
140 cleaned by hot hydrogen-peroxide method and embedded in Zrax[®] resin (CEN, 2003).
141 Species were identified at 1000× magnification using Zeiss Axio Imager A1 with
142 Planapochromat DIC lense (Zeiss, 518N) according to the standard taxonomic guides (Bey &
143 Ector, 2010; Hofmann et al., 2011; Krammer, 2000, 2002, 2003; Krammer & Lange-Bertalot,
144 1991, 1999a, b, 2000; Lange-Bertalot, 2001; Lange-Bertalot et al., 2011; Levkov, 2009;
145 Levkov et al., 2013). In each sample, a minimum of 400 diatom valves was counted. All
146 diatom taxa (identified at species or genera level) were regarded as individual species and
147 were included in each subsequent statistical analysis.

148 Furthermore, water physical and chemical characteristics were determined for each
149 sampling site. Water temperature, oxygen saturation (DO%), conductivity, pH and turbidity
150 were measured *in situ* using an HQ40d Hach Lange multimeter. In laboratory, concentration
151 of HCO₃⁻, Cl⁻, SO₄²⁻ and COD were determined titrimetrically (APHA, 1998), whereas NO₂⁻,
152 NO₃⁻, NH₄⁺, SRP, TP (APHA 1998) and SRSi (Wetzel & Likens, 2000)
153 spectrophotometrically.

154

155 *Statistical analyses*

156 Prior to the metacommunity-analyses, non-metric multidimensional scaling (NMDS) was
157 performed to visualize whether community composition of benthic diatoms was separated
158 according to the substrate types. NMDS was conducted based on the Hellinger-transformed
159 species abundance data applying Bray-Curtis distance. The NMDS projection displayed that
160 benthic diatom communities were not separated according to the substrate types and their

161 distribution was relatively homogeneous (Fig. S1). Therefore, all samples were included in
162 the subsequent statistical analyses.

163 The relative contribution of pure and shared effect of environmental heterogeneity and
164 spatial distance to variability of diatom communities was investigated with variation
165 partitioning method (Peres-Neto et al., 2006). In this analysis, two data matrices were used to
166 define the two explanatory variable groups. One of that was the group “environmental
167 heterogeneity”, which consisted of the first two principal components’ scores produced by a
168 principal component analysis (PCA) on a correlation matrix of standardized physical and
169 chemical parameters. In the group ‘spatial distance’, distance-based Moran’s eigenvectors
170 (dbMEMs) were included as explanatory variables computed by principal coordinate analysis
171 (PCoA) of a truncated geographic distance matrix among sampling locations (Borcard &
172 Legendre, 2002; Borcard et al., 2004). Variation partitioning was performed both for
173 Hellinger transformed species abundance (Legendre & Gallagher, 2001; Borcard et al., 2011)
174 and species incidence data. ANOVA (permutations = 999) of RDA models were run to assess
175 the significance of adjusted R^2 values for testable fractions (pure environmental heterogeneity
176 and spatial distance).

177 To estimate overall β -diversity of diatom communities across the 38 sampling sites,
178 first we calculated abundance-based multiple-site Bray-Curtis dissimilarity (β_{BC}), which was
179 partitioned into its two components: abundance balanced variation ($\beta_{BC.BAL}$) and abundance
180 gradients ($\beta_{BC.GRA}$) (Baselga, 2017). Then, we transformed diatom abundance data into
181 presence-absence data and performed the same estimation using incidence-based multiple-site
182 Sørensen dissimilarity index (Baselga, 2010). Sørensen index (β_{SOR}) was also divided into its
183 components: turnover (β_{SIM}) and nestedness resultant (β_{NES}) component (Baselga et al., 2007;
184 Baselga, 2010).

185 Local contribution to β -diversity was calculated for each sampling site to quantify
186 their ecological uniqueness. The computation was carried out both for abundance
187 ($\text{LCBD}_{D\%diff}$) and presence-absence (LCBD_{DS}) data based on indices from the Baselga-family,
188 Sørensen group. We used percentage different dissimilarity ($D\%_{diff}$) for quantitative (Baselga,
189 2013) and Sørensen dissimilarity (D_S) for binary data (Baselga, 2010). To stratify Euclidean
190 property, we applied square-root transformation for dissimilarity matrices ($D\%_{diff}$ and D_S)
191 (Legendre & De Cáceres, 2013). To assess how unique each site is in terms of species
192 replacement and nestedness, LCBD values were computed for replacement ($\text{LCBD}_{\text{ReplB}\%diff}$,
193 $\text{LCBD}_{\text{ReplBS}}$) and nestedness ($\text{LCBD}_{\text{NesB}\%diff}$, $\text{LCBD}_{\text{NesBS}}$) decomposing $\text{LCBD}_{D\%diff}$ and
194 LCBD_{DS} (Legendre & De Cáceres, 2013).

195 To describe the relative importance of individual species in affecting overall β -
196 diversity, we calculated species contribution to β -diversity for Hellinger-transformed
197 abundance data (SCBD_{ab}) and for species incidence data (SCBD_{pa}) (Legendre & De Cáceres,
198 2013).

199 Since LCBD and SCBD indices (response variables) exhibit relative contribution data
200 taking values between 0 and 1, generalized additive models (GAMs) using beta regression
201 family with logit link function (Wood et al., 2016) were applied to investigate the relationship
202 of $\text{LCBD}_{D\%diff}$, and LCBD_{DS} with the local species richness as well as the relationship of
203 SCBD_{ab} and SCBD_{pa} with the number of sites occupied by a given species and with the total
204 abundance of the species. We run regression tree model analyses (Breiman et al., 1984) to
205 find the most important environmental factors determining the variation in LCBD indices
206 ($\text{LCBD}_{D\%diff}$, LCBD_{DS} , $\text{LCBD}_{\text{ReplB}\%diff}$, $\text{LCBD}_{\text{ReplBS}}$, $\text{LCBD}_{\text{ReplB}\%diff}$, $\text{LCBD}_{\text{ReplBS}}$).
207 Furthermore, Pearson correlation coefficient was computed for each pair of LCBD indices to
208 estimate the correlation between them.

209 R statistical software (R. 3.4.1; R Development Core Team, 2017) was used to
210 conduct statistical analyses. We applied codep (Guenard et al., 2017) and ape (Paradis et al.,
211 2004) R packages for dbMEM analysis and PCoA, and vegan (Oksanen et al., 2017) for
212 variation partitioning. Multiple-site β -diversity indices were calculated in betapart (Baselga et
213 al., 2017), LCBD and SCBD indices in adespatial (Dray et al., 2017), ade4 (Dray & Dufour,
214 2007) R packages and with beta.div function (Legendre & De Cáceres, 2013). Regression tree
215 model analyses and GAMs were conducted and illustrated using rpart (Therneau et al., 2017),
216 rpart.plot (Milborrow, 2017), mgcv (Wood, 2011) and ggplot2 (Wickham, 2009) R packages.

217

218 **Results**

219 Physical and chemical parameters varied considerably among the 38 lakes, many of them had
220 a higher standard deviation than the mean (Table S1). According to the PCA results (Fig. 3),
221 33.7% of the variance in environmental factors is explained by PC1 axis and 17.3% by PC2
222 axis. In descending order, HCO_3^- , conductivity, TP and SRP showed the highest correlation
223 with PC1 axis (absolute values of Pearson correlation coefficients were above 0.8) and had
224 the highest PC1 loading. Variables correlated most with PC2 axis (absolute values of Pearson
225 correlation coefficients were above 0.6) and possessing the highest PC2 loading were O_2
226 saturation and pH.

227 Based on the results of variation partitioning (Fig. 4), the establishment of diatom
228 community composition was affected significantly by environmental heterogeneity and spatial
229 distance among the sampling sites as well. However, either in case of species abundance or
230 incidence data, the pure spatial distance explained a slightly higher proportion (7.3% and
231 3.4%) of community variation than environmental heterogeneity alone (2.8% and 2.1%).

232 In the 38 phytobenthos samples, 273 diatom taxa were found, of which 269 were
233 identified at species level and four at genus level. The number of species showed high

234 variability: its lowest value was 20 and the highest was 66 (average and standard deviation: 42
235 ± 12). We found high overall β -diversity of diatom communities according to the abundance-
236 based ($\beta_{BC}=0.956$) as well as the incidence-based ($\beta_{SOR}=0.934$) multiple-site framework. In
237 both cases, β -diversity patterns were enhanced mainly by the component accounting for
238 species substitution (abundance balanced variation: $\beta_{BC.BAL}=0.953$ and turnover: $\beta_{SIM}=0.914$)
239 whereas the component accounting for subsets (abundance gradients: $\beta_{BC.GRA}=0.003$ and
240 nestedness $\beta_{NES}=0.020$) was very low.

241 We found strong positive correlation between $LCBD_{D\%diff}$ and $LCBD_{ReplB\%diff}$ as well
242 as between $LCBD_{DS}$ and $LCBD_{ReplBS}$ (Pearson correlation coefficients were 0.98 and 0.94,
243 respectively) furthermore, $LCBD_{NesB\%diff}$ correlated negatively with $LCBD_{D\%diff}$ and
244 $LCBD_{ReplB\%diff}$ (Pearson correlation coefficients were -0.51 and -0.47, respectively). For any
245 other pairs of indices, no significant correlation was displayed (Table S3). GAMs and
246 regression tree model analyses revealed that distinct factors affect the LCBD indices using
247 abundance and incidence data. There was no significant relationship between $LCBD_{D\%diff}$ and
248 local species richness, but $LCBD_{DS}$ showed a significant decrease with the increase of species
249 richness (Table 1, Fig. 5a-b).

250 Sites with the highest local contribution to β -diversity were different when conducting
251 computations on species abundance and presence-absence matrix. These two types of data
252 revealed different results also during the investigation of sampling sites' uniqueness in terms
253 of species replacement and nestedness. Sites possessing the highest $LCBD_{D\%diff}$ index
254 (>0.030) were CSA, CSI, HAR, ÖRE and SZT (Fig. S2a), and according to the regression tree
255 model analyses, environmental variables driving $LCBD_{D\%diff}$ were TP and NO_3^- (Fig. 6a).
256 Similarly, sampling sites with the highest $LCBD_{ReplB\%diff}$ value (>0.034) were CSA, CSI,
257 HAR, ÖRE and SZT (Fig. S2b) where SRP and COD were the most decisive (Fig. 6b). In
258 turn, sites represented by the highest $LCBD_{NesB\%diff}$ (>0.115) were KHT, TDO, VDK and

259 MÁM (Fig. S2c) determined primarily by TP, COD and pH (Fig. 6c). In case of the
260 incidence-based data, the highest LCBD_{DS} indices (>0.031) were found at sites HÁM, KEN,
261 KFT, SÁR, VAD and PIR (Fig. S3a), where SRP, COD and SRSi had the most important
262 effect (Fig. 7a). HÁM, KEN, KFT, SÁR and VAD (Fig. S3b) achieved the highest
263 LCBD_{ReplBS} value (>0.036) affected mainly by SRP and NH₄⁺ (Fig. 7b). Sites with
264 outstanding LCBD_{NesBS} index (>0.095) were PIR, TÚR and TOL (Fig. S3c) driven by SRP
265 and TP concentration (Fig. 7c).

266 Contribution of the individual species to β -diversity depended on the type of the
267 applied data matrix (abundance- or incidence-based). According to the GAMs' results, SCBD
268 using abundance data (SCBD_{ab}) depended both on the number of sites occupied by the given
269 species and on the total abundance of the species (Table 1, Fig. 5c, e): it showed an increasing
270 trend with the increase of both explanatory variables. In turn, SCBD based on incidence data
271 (SCBD_{pa}) was significantly related only to the number of occupied sites and a unimodal
272 (hump-shaped) relationship was revealed between them (Table 1, Fig. 5d, f): SCBD_{pa}
273 increased up to 20 occupied sites and then, it started to decrease. Species with the highest
274 SCBD_{ab} value (>0.05) were *Achnanthydium minutissimum* (Kützing) Czarnecki, *Amphora*
275 *pediculus* (Kützing) Grunow and *Cocconeis placentula* Ehrenberg, all of which occupied high
276 number of samples (≥ 28) and were present with high total abundance (≥ 1060 individuals
277 counted during the study). In contrast, *Eolimna minima* (Grunow) Lange-Bertalot,
278 *Halamphora veneta* (Kützing) Levkov, *Nitzschia palea* var. *tenuirostris* Grunow, *Nitzschia*
279 *palea* var. *debilis* (Kützing) Grunow and *Nitzschia supralitorea* Lange-Bertalot had the
280 highest SCBD_{pa} (>0.01). These species occurred at intermediate proportion of sites (at 18-20
281 sites) and with moderate total abundance (110-354 individuals).

282

283 Discussion

284 *Structuring drivers and β -diversity of diatom communities*

285 In accordance with our first hypothesis, the composition of benthic diatom communities in the
286 studied small, freshwater lakes of the Carpathian Basin depended significantly on the spatial
287 variables, however, the filtering effect of the lakes' local environmental characteristics played
288 also a significant role. Studies using variation partitioning to unravel metacommunity
289 mechanisms assume, in general, i) species-sorting if solely the "environmental variables"
290 fraction explains significantly the community structures; ii) neutral theory or patch dynamics
291 if only the "spatial variables" fraction is significant and iii) mass-effect concept or the
292 combination of species-sorting and mass-effect if both fractions have significant explanatory
293 power (Cottenie, 2005; Soininen, 2014). However, instead of regarding metacommunity
294 concepts as distinct alternatives, considering them as continuum is suggested (Alonso et al.,
295 2006; Gravel et al., 2006; Leibold & McPeck, 2006; Adler et al., 2007; Chase, 2007). It is
296 impossible to firmly determine the boundaries between the types of metacommunities due to
297 several interfering factors (Leibold & Chase, 2017). The degree of environmental
298 heterogeneity within the studied area and the traits of species, such as size and dispersal rate,
299 greatly influence the response of species to habitat heterogeneity. Relatively large species
300 with low dispersal rates are assumed to be structured according to spatial variables due to
301 their limited dispersion complying with the neutral theory and patch dynamics rather than by
302 environmental characteristics. In contrast, smaller species with better dispersion abilities are
303 likely driven by habitat heterogeneity because they might be able to respond more sensitively
304 even to the minor environmental differences (Hájek et al., 2011; De Bie et al., 2012; Heino,
305 2013). In case of intermediate dispersal rates, dispersion limitation is not probable and
306 environmental heterogeneity inherent to species-sorting mechanisms is the most decisive,
307 whereas structure of the best dispersing species is slightly better explained by the spatial
308 variables and habitat heterogeneity is less important that is, mass-effect will become prevalent

309 (Leibold & Chase, 2017). Our variation partitioning results, and taking into account the small
310 size and the effective passive dispersion (Kristiansen, 1996; Finlay, 2002) of diatoms, point to
311 the fact that at intermediate spatial scale in the Carpathian Basin lake benthic diatoms were
312 assembled in conformity with the mass-effect theory. However, despite that diatoms are
313 regarded as relatively well dispersing organisms within large areas (e.g., at continental or
314 global scale), geographic separation tend to limit their ubiquitous dispersal thus showing pure
315 spatial patterns, which can be explained by the neutral theory (Heino et al., 2010).
316 Nevertheless, it would be difficult to decide exclusively for one metacommunity concept
317 without quantifying accurately the species' dispersal rate and the strength of environmental
318 gradients within the studied region (Logue et al., 2011; Lindström & Langenheder, 2012;
319 Maloufi et al., 2016). In addition, the observed high proportion of unexplained variation
320 (residuals) probably deriving from unmeasured environmental parameters, undersampling of
321 rare species and stochastic processes should not be ignored during the interpretation of the
322 observed patterns. For instance, if an originally unmeasured variable were spatially structured,
323 the importance of the “spatial variables” fraction would increase, whereas if it were not
324 spatially structured, residuals would be higher, leading to distinct conclusions regarding
325 metacommunity theories (Leibold & Chase, 2017). Moreover, unregulated ecological drifts
326 and colonization-extinction stochasticity (predicted by the neutral theory and patch dynamics,
327 respectively) might also increase residual variation (Hubbell, 2001; Vellend, 2010, 2016;
328 Leibold & Chase, 2017).

329 We experienced a high average of local diatom species richness, which confirms
330 Mouquet & Loreau's (2003) theory that consequent on mass-effect, α -diversity should
331 increase if dispersal rate slightly increases. However, this process should result in a decreased
332 β -diversity among sites. Contrary to this, but in agreement with our expectations and previous
333 findings (Tisseuil et al., 2012; Maloufi et al., 2016; Viana et al., 2016; Soininen et al., 2018;

334 Szabó et al., 2018) that at mid-latitudes (like the Carpathian Basin) driving mechanisms
335 expounded above, resulted in very high β -diversity primarily due to the high degree of species
336 turnover among the sampling sites. In turn, nestedness resulted from richness differences was
337 inconsiderable based on our analyses. In the meta-analysis by Soininen et al. (2018) species
338 turnover and total β -diversity showed strong correlation as both quantify the compositional
339 dissimilarities between samples, whereas nestedness is represented with several times smaller
340 proportion (even close to zero) than turnover and it may only measure the bias caused by
341 richness differences. They also described that β -diversity and its turnover component are
342 slightly smaller near the poles, which could be explained by the more homogeneous
343 environment, less limited species dispersion (Mouquet & Loreau, 2003; Leibold et al., 2004)
344 and less pronounced biotic interactions (Willig et al., 2003; Schemske et al., 2009). Towards
345 higher latitudes, where glaciation might have played an important role in the local and
346 regional extinction and recolonization processes, the increase of nestedness was found
347 (Soininen et al., 2018). Either species abundance or presence-absence data were applied
348 during the analyses, we were able to draw the same conclusion that both the local
349 environment and the spatial distance influenced the benthic diatom assemblages and high β -
350 diversity was enhanced by species turnover. However, similarly to previous studies (Heino et
351 al., 2010; Vilmi et al., 2016; Szabó et al., 2018), the unexplained variation in community
352 structure was higher when only the incidence of diatom species was considered.

353

354 *Local contribution of sampling sites to β -diversity*

355 Calculation of LCBD is suitable for quantifying which sites contribute more (or less) to β -
356 diversity than the mean and thereby for evaluating the ecological uniqueness of communities
357 at each sites (Legendre & De Cáceres, 2013). Local contribution to β -diversity and local
358 contribution in terms of species replacement showed a strong positive relationship applying

359 either abundance- or incidence-based data. However, in case of using abundance data, LCBD
360 for nestedness decreased significantly with increasing LCBD and LCBD for replacement.
361 Accordingly, sites with highest uniqueness in terms of replacement contributed to the greatest
362 extent to total β -diversity of diatom communities, as well. This may be related to the fact that
363 in general, total β -diversity also correlates positively with its turnover component and
364 negatively with its nestedness component (Soininen et al., 2018). It is supposed that species-
365 rich sites exhibit low LCBD due to the greater chance of sharing species with other
366 communities (Maloufi et al., 2016). Nevertheless, our assumption that sites with low diatom
367 species richness have greater contribution to the regional β -diversity than sites with higher
368 richness, was only partly confirmed by the results. The declining trend in LCBD with
369 increasing local richness was observed both for abundance and presence-absence data, but the
370 relationship was significant only for species incidences. A part of former studies confirms,
371 whereas some of them contradicts our findings depending on the organisms and the habitat
372 type targeted. Applying abundance data for stream (Vilmi et al., 2017) and pond (Teittinen et
373 al., 2017) diatom communities, negative correlation between LCBD and species richness was
374 reported, however, this relationship was not evident for lake benthic diatoms (Vilmi et al.,
375 2017). In case of dung beetles (Da Silva & Hernández, 2014) and stream insect assemblages
376 (Heino & Grönroos, 2017), LCBD decreased significantly with increasing local species
377 richness if calculations were conducted on presence-absence data, which is in line with our
378 findings. Consequently, we concluded that sites sustaining less diverse communities have
379 greater ecological uniqueness, however, this coherence varies among different groups of
380 organisms and ecosystems, furthermore also depends largely on the data type applied.

381 Our results revealed that local environmental variables affected sampling sites'
382 contribution to β -diversity, including its extension to replacement and nestedness, as well.
383 Although sites with highest LCBD indices were different based on abundance- and incidence-

384 based community data, we did not find explicit contrast in their main driving variables. Most
385 decisive factors were phosphorus forms for each LCBD index, which corroborates our
386 hypothesis, since these parameters displayed relatively high variance among the sites.
387 Additionally, nitrogen forms, pH, COD and SRSi were also crucial in evolving sites'
388 ecological uniqueness for diatom communities. These findings are not surprising, since
389 nutrient supply plays a key role in establishment of autotrophic algal assemblages and trophic
390 status is also related, for instance, to oxygen conditions and pH. Thereby, it affects indirectly
391 the physiological processes of aquatic organisms (Soininen, 2007). The above chemical
392 parameters have already been emphasized as master variables for freshwater lake diatom
393 communities in several previous studies (e.g., Hall & Smol, 1992; King et al., 2000; Lim et
394 al., 2001; Soininen, 2007). In addition, pH was found as one of the most influential variables
395 for subarctic ponds' contribution to β -diversity of diatom communities (Teittinen et al., 2017).
396 In turn, some publications targeting β -diversity assessments reported that LCBD was not well
397 determined by local environmental characteristics, for instance, in case of stream insects
398 (Heino & Grönroos, 2017) and invertebrates (Tonkin et al., 2016).

399

400 *Species contribution to β -diversity*

401 With respect to species contribution to β -diversity, results published for different biota and
402 ecosystems are congruent, however, abundance- and incidence-based calculations displayed
403 fundamentally distinct patterns similarly to our findings. Gaston et al. (2006) emphasized the
404 tight link between abundance, its spatial variation and the number of occupied sites by a given
405 species, which may be related to our observations that diatom species occupying a high
406 number of lakes and represented by high abundance contributed the most to overall β -
407 diversity. That is, contrary to our hypothesis, common diatom species such as *Achnanthydium*
408 *minutissimum*, *Amphora pediculus* and *Cocconeis placentula* with extensive ecological

409 amplitude (Hofmann et al., 2011) and variable abundance at different sites exerted the greatest
410 impact on β -diversity. This pattern prevailed only in case of abundance-based SCBD similarly
411 to observations by Heino & Grönroos (2017) for stream insects and by Vilmi et al. (2017) for
412 stream and lake diatom communities. Our incidence-based calculations revealed that species
413 with intermediate occupancy had the largest contribution to β -diversity, which was also
414 observed by Heino & Grönroos (2017). This may be due to the fact that occupancy of these
415 species can vary largely across the sites (Gaston et al., 2006). Species with the highest
416 incidence-based SCBD were *Eolimna minima*, *Halamphora veneta*, *Nitzschia palea* var.
417 *tenuirostris*, *N. palea* var. *debilis* and *N. supralitorea*, which are relatively common and
418 possess intermediate-sized niches (Hofmann et al., 2011). Also, their total abundance was
419 intermediate in our data set but in this case, the relationship between SCBD and species'
420 abundance was statistically not significant. However, it is important to note that both
421 dependent (SCBD index) and explanatory variables (occupancy and species' total abundance)
422 of the models are not independent mathematically, since each of them is conducted from the
423 same raw community data (even abundance or presence-absence), which might have affected
424 the strong relationship between them (Legendre & De Cáceres, 2013; Heino & Grönroos,
425 2017).

426

427 **Conclusions**

428 At intermediate spatial scale (2-400 km) of a mid-latitude region, where physical and
429 chemical parameters across small freshwater lakes are relatively, but not extremely
430 heterogeneous, benthic diatoms were assembled conforming most to the mass-effect
431 metacommunity concept. However, because patterns are largely dependent on several factors
432 (such as scale of heterogeneity, environmental variables considered during the study, dispersal
433 rates, size of species pool and stochastic processes), conclusions should be drawn with

434 caution. The high α -diversity (average of local species richness) found in the region, is in line
435 with the mass-effect paradigm, which is, in turn, inconsistent with the high β -diversity
436 enhanced mainly by species turnover. Freshwater lakes in the Carpathian Basin with the
437 highest contribution to overall β -diversity (and with the highest ecological uniqueness in
438 terms of turnover, too) hosted a lower number of diatom species than the average, however,
439 biodiversity conservation, in general, focuses on preserving species-rich sites. Furthermore, β -
440 diversity was related mainly to the regionally common species that have medium-sized or
441 broad niches, instead of the ecologically restricted ones. Therefore, we advocate the previous
442 suggestions made by Heino & Grönroos (2017) and Vilmi et al. (2017) that if a study aims
443 comprehensive conservation planning, a simultaneous application of LCBD and SCBD
444 indices combining with the focus on species-rich ecosystems and rare species would be
445 sufficient. Moreover, although abundance-based and incidence-based analyses led us to the
446 same conclusions regarding metacommunity concept and sites' ecological uniqueness, they
447 displayed different patterns of SCBD. Consequently, for assessing species' ecological
448 uniqueness during an extensive research of metacommunities, we recommend conducting the
449 analyses both on species abundance and binary data, especially in case of conservation
450 objectives.

451

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458

459 **Conflict of Interest**

460 The authors declare that they have no conflict of interest.

461

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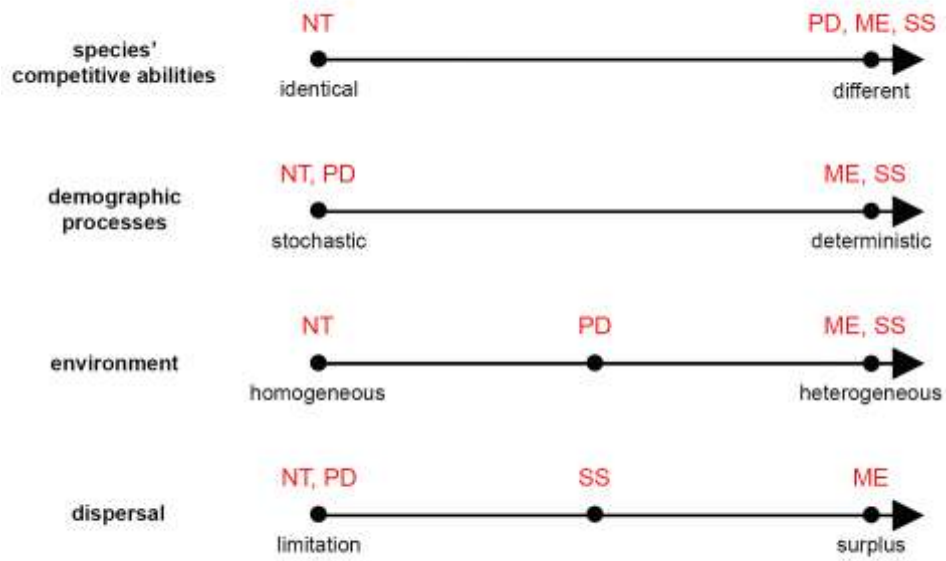
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685

686 **Table 1** Results of GAMs (beta regression family with logit link function) testing relationship
687 of local contribution to β -diversity (LCBD_{D%diff}, LCBD_{DS}) with local species richness
688 (richness), and the relationship of species contribution to β -diversity (SCBD_{ab}, SCBD_{pa}) with
689 the number of sites occupied by a given species (occup) and the species' total abundance
690 (abund). edf = The estimated degrees of freedom accounting for smoothing function, Ref. df.
691 = Reference degrees of freedom, χ^2 = Chi-square test statistic, adj. R² = The proportion of
692 variance explained by the model, Dev. expl. = The proportion of the null deviance explained
693 by the model, P = p-value
694

	smooth term	edf	Ref. df	χ^2	adj. R ²	Dev. expl. (%)	P
LCBD _{D%diff}	s(richness)	1.000	1.000	2.09	0.032	5.6	0.148
LCBD _{DS}	s(richness)	4.034	4.915	68.06	0.644	64.6	<0.001
		8.155	8.795	281.40			<0.001
SCBD _{ab}	s(occup)+s(abund)	8.918	8.996	4171.20	0.996	99.1	<0.001
		8.437	8.891	4687.79			<0.001
SCBD _{pa}	s(occup)+s(abund)	1.002	1.003	0.11	0.963	96.2	0.741

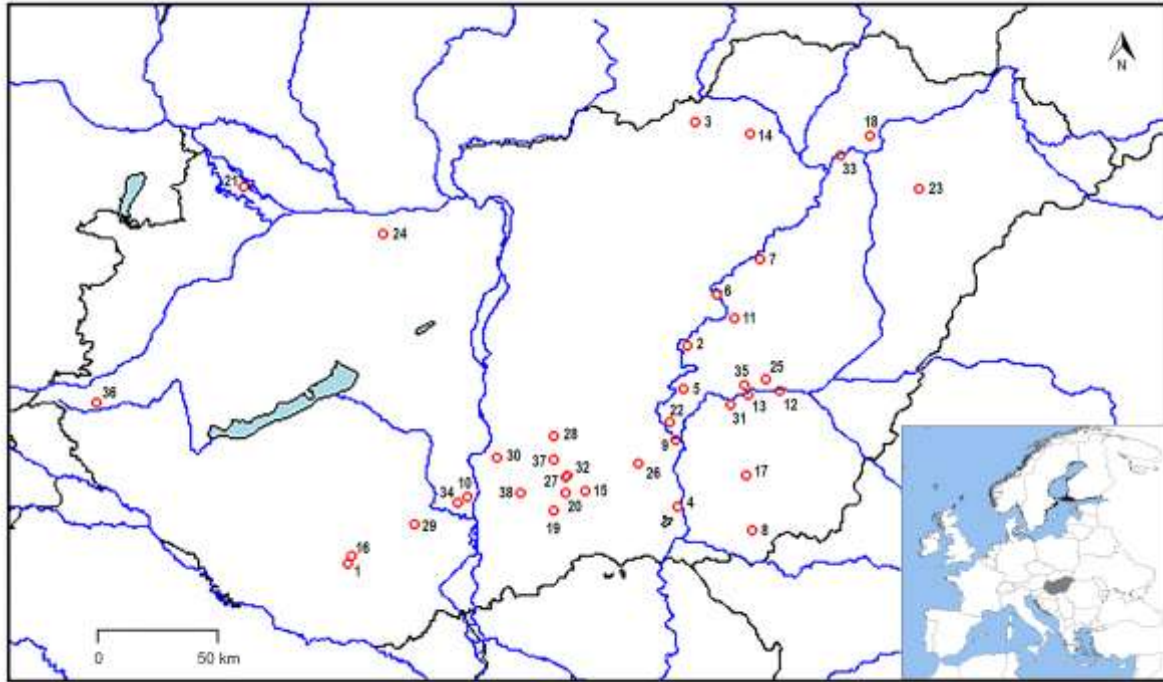
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697 **Fig. 1** Summary of assumptions about the main processes in the four metacommunity
 698 concepts (NT = neutral theory, PD = patch dynamics, ME = mass-effect, SS = species sorting)

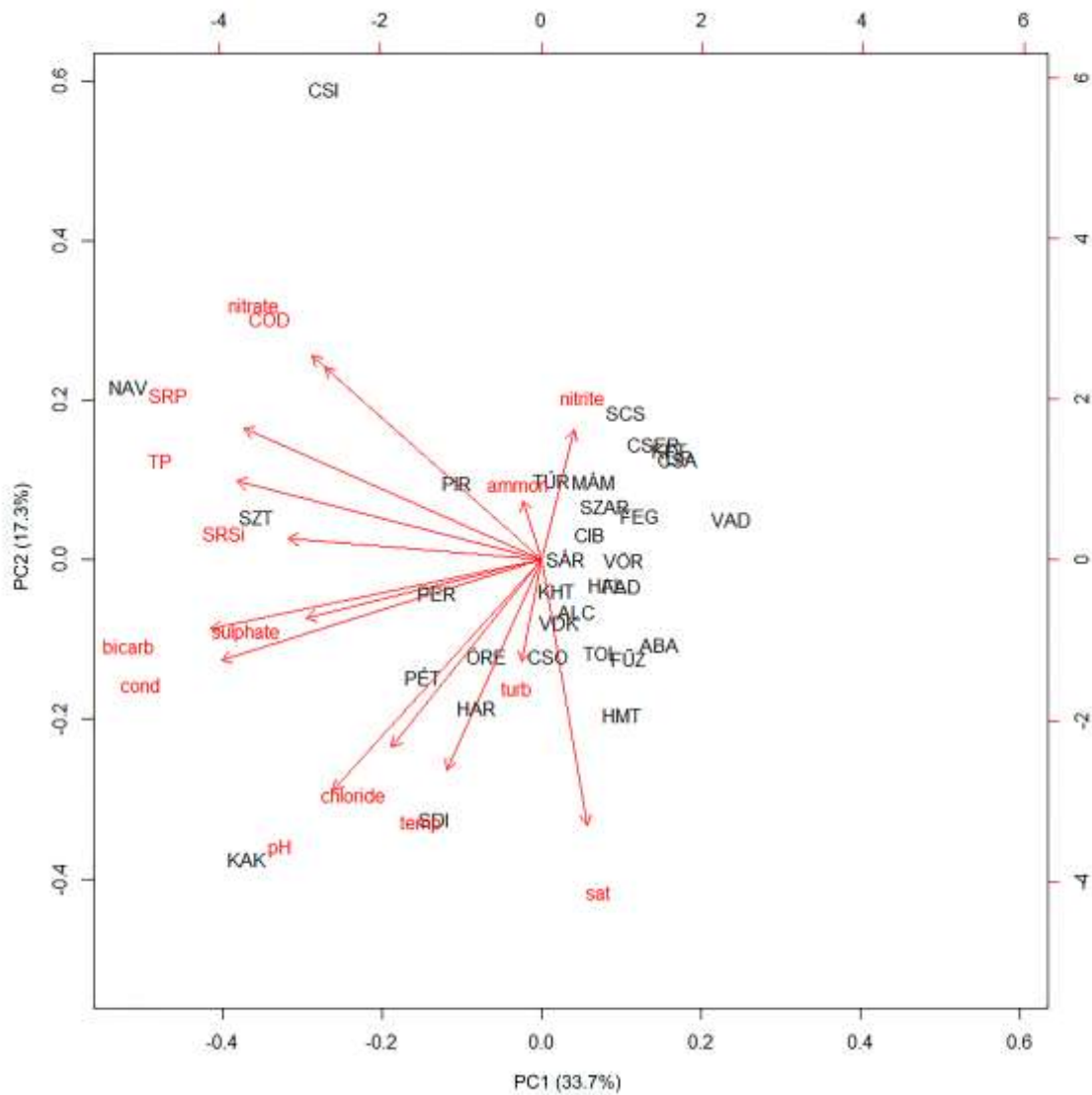
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701 **Fig. 2** Location and schematic map of Hungary and the sampling sites. Lake codes for the
702 numbers are listed in Table S2

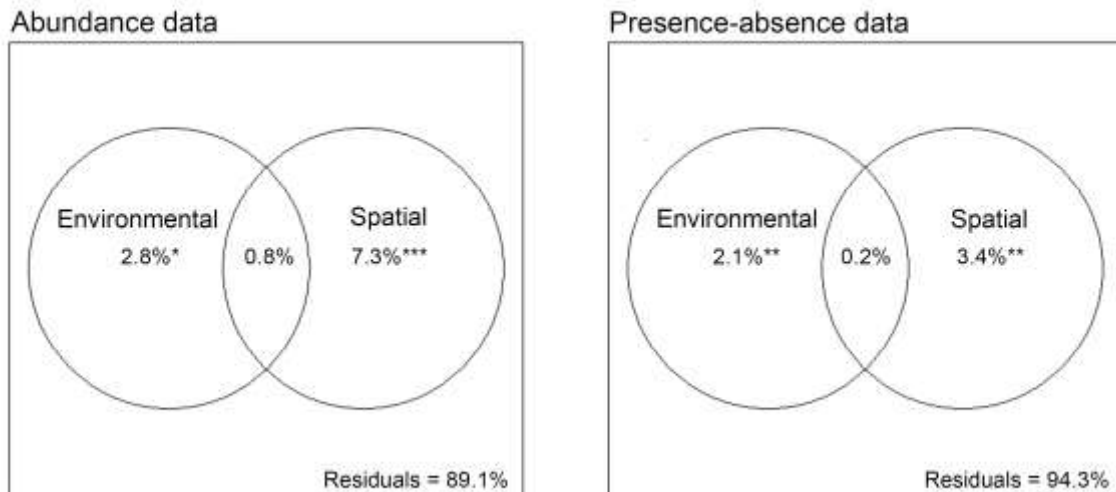
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705 **Fig. 3** PCA biplot representing sample codes and environmental variable vectors (cond =
 706 conductivity, sat = O₂ saturation, temp = water temperature, turb = turbidity, bicarb = HCO₃⁻,
 707 chloride = Cl⁻, sulphate = SO₄²⁻, COD = chemical oxygen demand, nitrite = NO₂⁻, nitrate =
 708 NO₃⁻, ammon = NH₄⁺, SRP = soluble reactive phosphorus, TP = total phosphorus, SRSi =
 709 soluble reactive silica). Proportion of variance explained by PC1 and PC2 axes are indicated

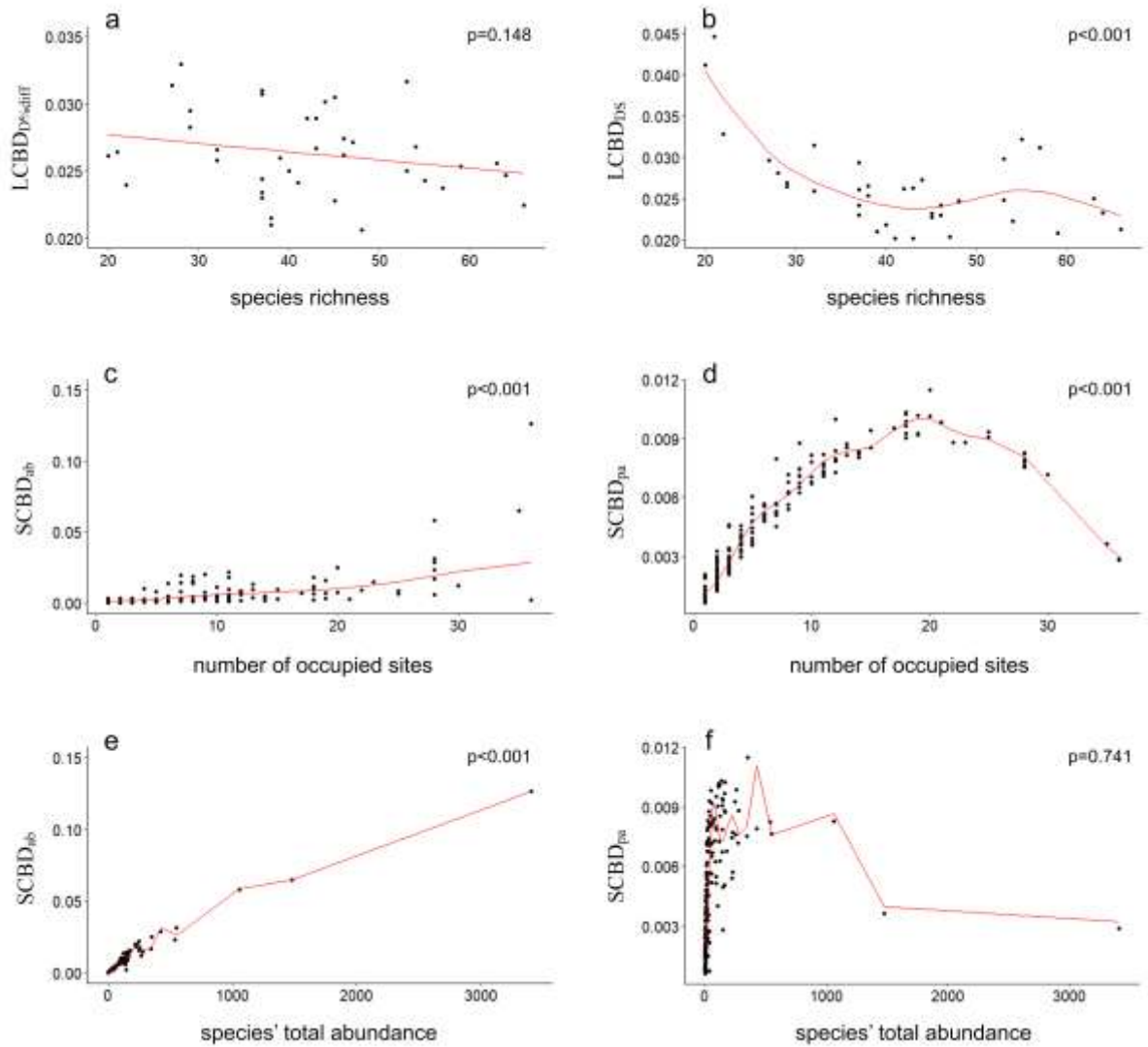
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712 **Fig. 4** Results of variation partitioning conducted on Hellinger transformed abundance and
 713 presence-absence data. Adjusted R^2 values are shown to indicate the relative importance of
 714 environmental heterogeneity (Environmental) and spatial distance (Spatial) in the total
 715 community variation. Unexplained variances are represented by the residuals. Significance of
 716 testable fractions is shown as follows: *** = 0.001, ** = 0.01, * = 0.05. P values were
 717 computed using ANOVA of RDA models

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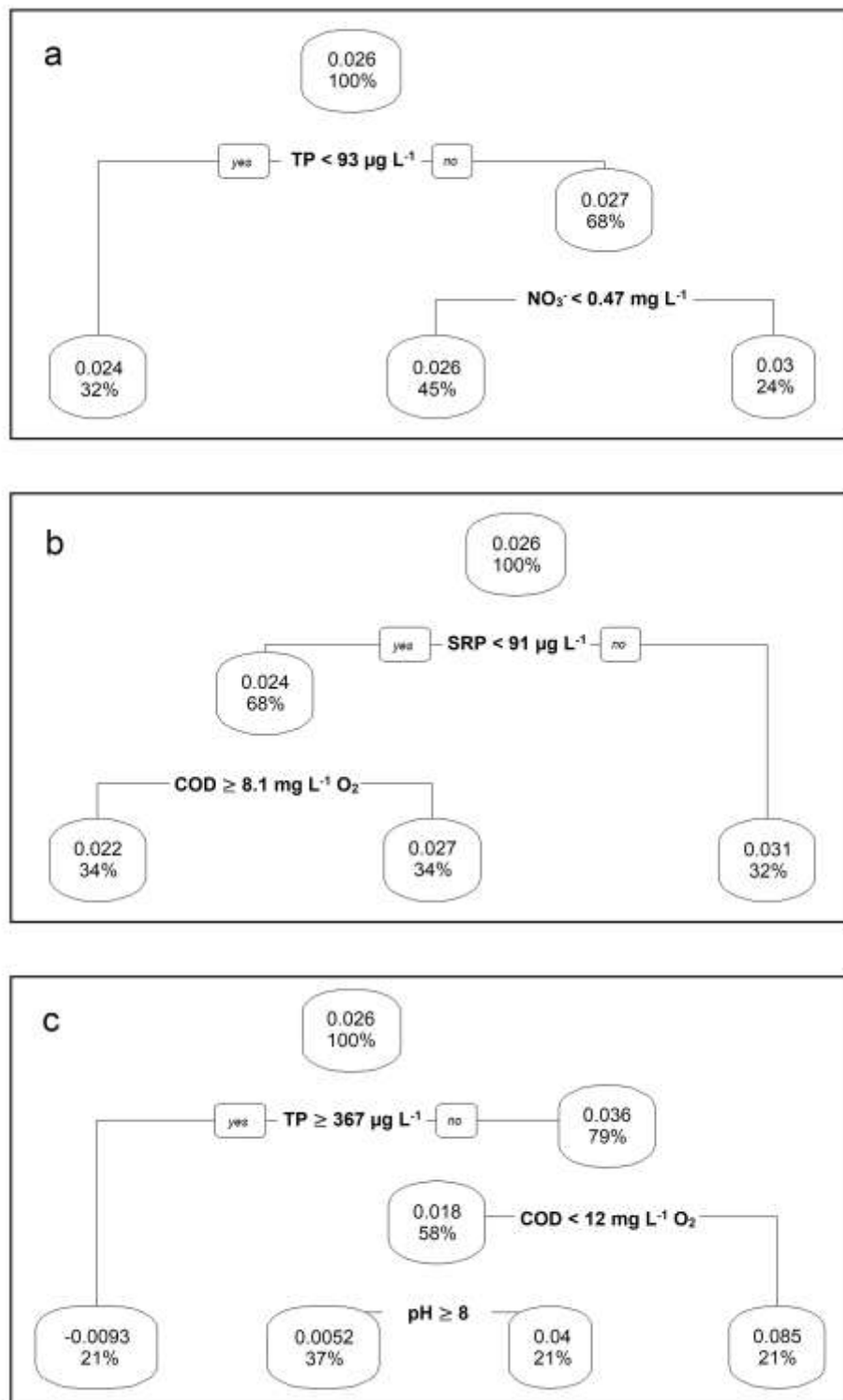
720 **Fig. 5** The relationship of local contribution to β -diversity ($LCBD_{D\%diff}$, $LCBD_{DS}$) with local

721 species richness and the relationship of species contribution to β -diversity ($SCBD_{ab}$, $SCBD_{pa}$)

722 with the number of occupied sampling sites and with the total abundance of a given species.

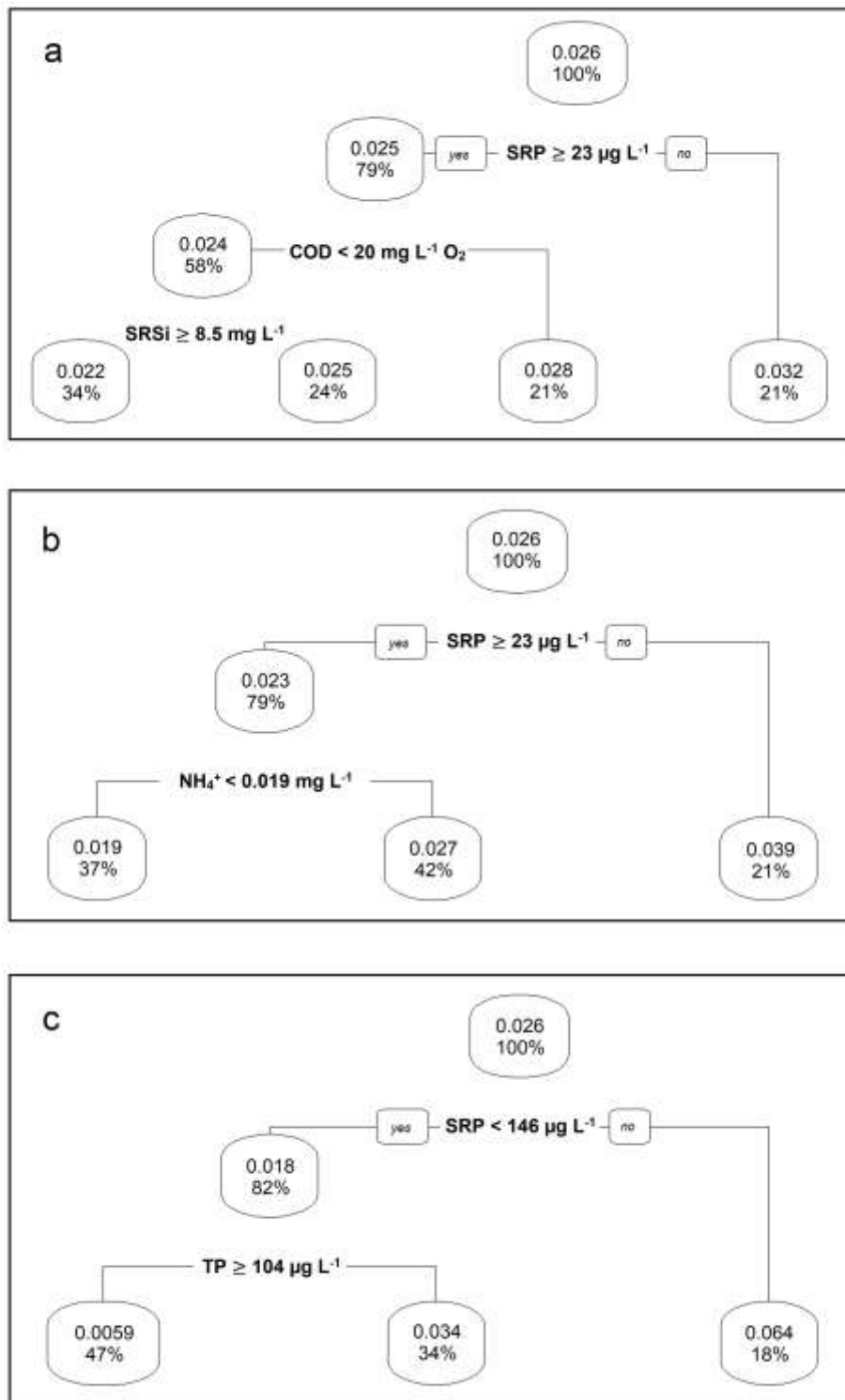
723 Solid lines show the fitted GAM using beta regression family with logit link function

724



725

726 **Fig. 6** Regression trees for predicting a) $\text{LCBD}_{\text{D}\% \text{diff}}$, b) $\text{LCBD}_{\text{RepIB}\% \text{diff}}$ and c) $\text{LCBD}_{\text{NesB}\% \text{diff}}$
 727 from the set of environmental parameters. Each node shows the predicted LCBD value (i.e.
 728 the mean LCBD value) and the percentage of observations in the node



730

731 **Fig. 7** Regression trees for predicting a) $LCBD_{DS}$, b) $LCBD_{RepIBS}$ and c) $LCBD_{NesBS}$ from the
 732 set of environmental parameters. Each node shows the predicted LCBD value (i.e. the mean
 733 LCBD value) and the percentage of observations in the node