

1 Stream diatom assemblages as environmental indicators

2 – a cross-regional assessment

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23 **Running title:** Diatoms as environmental indicators

24 **Key words:** bioindicators, biomonitoring, predictive modelling, stream diatoms

25 **Abstract**

26 Ongoing climatic change and anthropogenic pressure highlight the importance of reliable
27 assessment of the ecological status of freshwaters. Bioindicators are used widely in
28 ecological assessments as biotic assemblages reflect the environmental conditions in current
29 ecosystems. However, the robustness of bioindicators relies on the transferability of indices
30 and models outside the regions they were derived from. We tested the reliability of stream
31 diatom assemblages as indicators of water chemistry and climatic factors in a cross-regional
32 assessment by developing a predictive model with diatom assemblage data from Sweden and
33 using it to model stream conditions in Finland. The inference models and predictions were
34 performed using the Boosted Regression Trees (BRT) method, separately in species and
35 genus levels. The predictive performance of the calibration models in Sweden were good or
36 moderate for both water chemistry and climatic variables, both at species and genus levels.
37 The most important climatic (growing degree days, $r^2 = 0.57$) and water chemistry variables
38 (pH, $r^2 = 0.65$; and total phosphorus (TP), $r^2 = 0.52$) could be inferred from diatom
39 assemblages relatively well. However, predictive performances of the cross-regional models
40 were low ($r^2 \leq 0.13$). Nevertheless, water chemistry variables, conductivity ($r^2 = 0.13$) and TP
41 ($r^2 = 0.12$), were predicted the best. The most important diatom indicators for climatic and
42 environmental variables varied between Sweden and Finland. The study showed that diatom
43 assemblages can be robust indicators of water chemistry and climatic variables within the
44 region where the inference models are calibrated. However, their indicator ability may be
45 weak between regions. The reason for the low transferability of the diatom inference models
46 may stem from between-region differences in species realized niches, species pools and/or
47 ecosystems, local adaptation or species identification. Hence, models should only be used
48 with caution in geographical contexts other than the one where they were developed. The
49 calibration data should cover as large geographical area as possible to give reliable

50 predictions when applied in smaller regions.

51

52 **1. Introduction**

53 Water is an essential element for life. However, ongoing climate change and increasing
54 anthropogenic pressures affect the quality of all kinds of aquatic ecosystems (Foley et al.
55 2005, Wrona et al. 2006). Freshwater ecosystems are especially threatened (Heino et al.
56 2009). In order to monitor and predict the changes caused by the changing climate and land
57 use, robust methods are necessary. Although assessments of water quality using bioindicators
58 are conducted around the world, many regions do not have a robust system for water quality
59 assessments (Taylor et al. 2007, Chen et al. 2016, Tan et al. 2017). Furthermore, the potential
60 effect of climatic factors on bioindicators is typically not integrated in existing biotic indices,
61 which are calibrated mainly with water chemistry. This may hinder the reliability of these
62 indices under rapidly changing climatic conditions and in cross-regional assessments.

63 Bioindicators are widely used to infer the ecological status of ecosystems. The robustness of
64 bioindicators relies on the known environmental preferences of indicator species (Smol &
65 Stoermer 2010). Depending on the life-cycles of the studied taxa, biological assemblages
66 reflect the conditions for a variable period of time rather than reflecting conditions only
67 during a snapshot like water chemistry sampling does (Sandin & Verdonschot 2006).
68 Additionally, communities reflect the overall conditions, i. e. the mixture of chemical
69 compounds, physical environment and biological interactions providing a cost-efficient
70 method for environmental surveys. In freshwaters and especially in fluvial ecosystems, the
71 most commonly used bioindicators are macroinvertebrates and microscopic algae, especially
72 diatoms (Resh 2008). Diatoms (Bacillariophyceae) are microscopic unicellular algae, living
73 in almost any kind of waters, and can be identified typically to species and variety level by

74 their unique siliceous cell wall (Round et al. 1990). Environmental preferences of many
75 diatom species are known relatively well (Smol & Stoermer 2010) and many species have a
76 specific range of tolerance for pH or nutrient enrichment, for instance (e.g. van Dam et al.
77 1994). Currently used diatom indices, such as IPS (Cemagref 1982) or ACID (Andr en &
78 Jarlman 2008), are based on these known tolerances.

79 Traditionally, indices are built using simple methods such as weighted averaging (Cemagref
80 1982, Kelly & Whitton 1995, Coste et al. 2009). A disadvantage of weighted averaging is that
81 it assumes a unimodal response of species to environment, which often is not the case in
82 nature. A more novel method would be a machine learning approach such as Boosted
83 Regression Trees (BRT), which takes into account more complex responses, interactions
84 between predictors and thresholds above or below which species may occur (Elith et al.
85 2008).

86 There are other problems with the accuracy of diatom indices (e.g. Besse-Lototskaya et al.
87 2011). As a growing number of countries are developing their own indices for water quality
88 assessment, many still use indices developed in some other geographical region (Taylor et al.
89 2007, Chen et al. 2016, Tan et al. 2017). Recently, it has been shown that the observed optima
90 and tolerances of diatom species might vary between geographical regions (Rimet et al. 2007,
91 Soininen et al. 2019; but see Bennett et al. 2010). This observed variation among species'
92 responses indicates that the indices developed in one region may not be transferable across
93 regions. This is disappointing since the usage of diatoms as indicators (e.g. of water
94 chemistry) relies on the concept that diatom distributions are ubiquitous and restricted only
95 by local environmental variables to similar degree across regions (Smol & Stoermer 2010).
96 Although, this might be the case for many cosmopolitan species, a number of studies suggest
97 that endemism, local adaptation and dispersal limitation occur among diatom species

98 (Vanormelingen et al. 2008, Jüttner et al. 2010). In fact, ultimate factors, such as climate,
99 geology and land use, can in some circumstances explain more variation in diatom
100 communities and species distributions than local environmental factors (Pajunen et al.
101 2016a).

102 We studied the usefulness of stream diatom assemblages as indicators of water chemistry and
103 climatic factors across two boreal regions. We developed a predictive model using Swedish
104 diatom data and used it to model stream conditions in a neighboring country, Finland. A
105 recent study has shown that diatom assemblages can be good indicators for both local
106 environmental and climatic factors (Pajunen et al. 2016b); however, the applicability of such
107 predictive model have not yet been tested outside the regions they were calibrated.

108

109 **2. Materials and methods**

110 *2.1. Diatom and physico-chemical data*

111 Two extensive data sets of stream diatom assemblages were obtained from the neighboring
112 countries Sweden (55° – 70° N, 10° – 25° E) and Finland (60° – 70° N, 20° – 32° E) in order
113 to conduct a cross-regional assessment of the reliability of bioindicators (Fig. 1). The
114 Swedish data set consisted of 571 stream sites (Table 1). The Swedish samples were collected
115 for the national and several regional routine sampling programs across Sweden during
116 autumn. Diatoms were sampled by brushing stones with a toothbrush, according to the
117 recommendations of EU standards ((European Committee for Standardization 2014a; 2014b).
118 At least five replicate, pebble-to-cobble sized stones (5-15 cm) were selected randomly from
119 five to 10 cross-stream transects. They were brushed and the diatom suspension was placed in
120 a small plastic bottle and preserved in ethanol (70%). In the laboratory, organic materials

121 were cleaned from diatom samples by wet combustion with hydrogen peroxide and mounted
122 in Naphrax or Dirax. At least 400 valves per sample were counted using phase contrast light
123 microscopy (magnification 1000x) and identified to the lowest taxonomic level possible
124 using the literature in the Swedish standard (Jarlman et al. 2016). Identifications were done
125 by experts who had previously harmonized their identification routines within the Nordic-
126 Baltic Network for Benthic Algae in Freshwater (NorBAF; Kahlert & Albert 2005), meaning
127 that their counts were as similar as counted replicates, and diatom names were harmonized
128 according to conventions adopted by NorBAF (Kahlert et al. 2009). Sampling for water
129 chemistry and other local parameters are part of those routine sampling programs, and water
130 chemistry values consist of either spot values taken simultaneously with diatom samples or
131 monthly mean values. Both diatom and other data are stored in the national database
132 (Department of Aquatic Sciences and Assessment SLU 2010).

133 The Finnish data set comprised 227 stream sites collected between 1986 and 2004. The sites
134 were located in the five ecoregions in Finland and covered broad gradients in water chemistry
135 (Soininen et al. 2004) (Table 1). All sampling was conducted during low flow conditions in
136 July and August. At the majority of the sites, water samples were taken simultaneously with
137 the diatom samples and analyzed for total phosphorus (TP), pH, conductivity and water color.
138 For less than 20% of the sites, water chemistry data were taken from the national water
139 quality database (Finnish Environment Institute 2019), using results from the nearest
140 sampling occasion in space and time. Current velocity and stream width were measured and
141 shading by riparian vegetation was assessed at each site along 10 transects perpendicular to
142 the flow covering the whole sampling area. Diatom samples were collected and prepared
143 following standard protocols as in Sweden, with the exception that combustion was done with
144 acid ($\text{HNO}_3\text{:H}_2\text{SO}_4$; 2:1) (European Committee for Standardization 2014a; 2014b). For each
145 sample, 250–500 valves were counted using phase contrast light microscopy. Species were

146 identified to the lowest level possible according to Krammer & Lange-Bertalot (1986-1991)
147 and Lange-Bertalot & Metzeltin (1996) by two analysts who had harmonized their species
148 identification routines by working together.

149 The Swedish and Finnish data sets were carefully harmonized by diatom experts following
150 the NorBAF conventions, involving the merging of subspecies and matching of both data
151 sets. After harmonization the datasets comprised 878 species in Sweden and 213 in Finland
152 (see Appendix A, Table A.1). All taxa not found in both data sets (n=699) were removed
153 keeping the relative abundances of each species as in original full data. Thus, the summed
154 relative abundances in the Swedish data set ranged from 27.5 to 100 % (md 82.2 %), and in
155 the Finnish data set from 61.3 to 100 % (md 91.3 %). Additionally, diatom genera data were
156 generated by merging this new reduced species data into diatom genera. In the end, both
157 Swedish and Finnish data sets contained the same 196 species and 65 genera.

158 2.2. Climatic data

159 Climate data (averages for the years 1979–2013) were obtained from the CHELSA climate
160 data base (Karger et al. 2017a, 2017b). The data set includes high resolution (30 arc sec \approx 1
161 km) climatic data for the earth land surface areas, including monthly mean temperature and
162 precipitation patterns. Frost degree days (FDD, defined as temperature < 0 °C), growing
163 degree days (GDD, defined as temperature > 5 °C), mean annual precipitation (MAP) and
164 water balance (WAB) were defined for each Finnish and Swedish stream site from the
165 climatic data rasters. FDD indicates the length and severity of the frozen winter period,
166 whereas GDD can be seen as a proxy for temperature and overall productivity of the stream
167 and its catchment. MAP and WAB indicate the amount of atmospheric water supply to the
168 whole catchment area, potential run-off and flow regime.

169 2.3. Data analyses

170 Covariance between the local and climatic variables was assessed using Spearman's rank
171 correlation separately for both countries. Climatic and environmental data exhibited strong
172 collinearities ($\geq |0.70|$) between some variables in both data sets (Table A.2). Coordinates (i.
173 e. latitude and longitude), FDD and MAP were later excluded from the predictions due to the
174 strong correlations with other variables, such as GDD and WAB. GDD and WAB were
175 selected as they reflect the overall climatic conditions in the growing season. Overlying
176 histograms (Fig. A.1) show that the ranges of climatic and environmental variables were
177 much larger in the Swedish data set than in the Finnish data set. To avoid extrapolation,
178 Swedish data were chosen to be used as the calibration data to predict Finnish environmental
179 conditions. Principal component analysis (PCA) was used to further explore the
180 environmental data of both data sets (Fig. A.2, Table A.3). Environmental variation was
181 much larger in the Swedish data set than in Finnish data set. This supports the decision to use
182 Swedish data as the calibration data for the predictions.

183

184 The most important variables for diatom assemblages in the data sets were investigated by
185 using RDA, both at species and genus level. The strongly correlated variables (coordinates,
186 FDD and MAP) were removed prior the analyses. To further visualize the relationships
187 between diatom assemblages and the climatic and environmental variables, we performed
188 non-metric multidimensional scaling (NMDS) for all data sets (Figs. A.3 and A.4). PCA,
189 RDA and NMDS analyses were performed in R (version 3.2.2; R Development Core Team,
190 2016) applying VEGAN package (Oksanen et al. 2015).

191

192 *2.4. Calibration and inference models*

193 The prediction models were conducted by using Swedish data as calibration data and Boosted
194 Regression Trees (BRT) as a modelling approach. BRT is a machine learning method where

195 predictions with minimized loss function (such as deviance) are created by a boosting
196 technique in which a sequence of simple regression trees is progressively grown fitting one
197 tree at a time to the sequence (Friedman et al. 2000, De'ath, 2007, Elith et al., 2008). All
198 models were fitted using R software (version 3.2.2; R Development Core Team 2016).
199 Models were conducted separately for the species and genera data. In model calibration,
200 GDD, WAB, pH, TP, conductivity and water color were set as response variables and the
201 diatom abundance of 196 taxa or 65 genera from 571 sites as predictors. The BRT model was
202 fitted using functions from the gbm package version 2.1.3 (Ridgeway 2017) based on
203 Friedman's (2001) gradient boosting machine. The interaction depth in the model was set to
204 6. The learning rate, determining the contribution of each tree to the growing model, was set
205 to 0.005 and the maximum number of trees was set to 1000. A Gaussian distribution of errors
206 was used to model the six variables. Leave-one-out cross-validation (LOO) was used to
207 assess the performance of the models. Model performance was estimated by the coefficient of
208 determination (r^2) and the root-mean-square error of prediction (RMSEP). The relative
209 importance of the predictor variables was first estimated according to Friedman (2001) and
210 then scaled to sum up to 100. The higher value a predictor variable gets, the stronger its
211 influence on the response variable. Additional calibration models were performed using
212 Finnish data in order to estimate the relative importance of species and genera in Finland.
213 Finally, the Swedish calibration models were used to predict climatic and environmental data
214 for Finnish data.

215

216 Alternative models were conducted to guard against potential differences among calibration
217 models, datasets and used modelling techniques. Firstly, the performance of calibration
218 models using Finnish dataset and their predictive ability in Swedish data were tested.
219 Secondly, a subset of Swedish dataset ($n = 396$ sites, subsampled to match the ranges in

220 Finnish data, see Appendix C, Table C.1) was used as calibration data to infer climatic and
221 environmental variables for Finnish data. Thirdly, a weighted averaging method was used to
222 repeat the original calibration and inference models (Swedish data as calibration dataset (n =
223 571 sites) for sites in Finland). The WA models were fitted using functions from the RIOJA
224 package version 0.9-21 (Juggins 2019) in R. The performance of the calibration models was
225 assessed using leave-one-out cross-validation and model performance was estimated by the
226 coefficient of determination (r^2) and the root-mean-square error of prediction (RMSEP).

227

228 **3. Results**

229 PCA analyses showed much larger variation in environmental and climatic variables in
230 Swedish than in Finnish data set (Fig. A.2, Table A.3). The first two components collectively
231 explained 67% of the variation in Swedish data and 66% in Finnish data. In Swedish data,
232 latitude, longitude and FDD had high positive and GDD a negative loading on the first
233 component, while MAP and WAB had high positive and pH a negative loading on the second
234 component. In Finnish data, latitude and FDD had high negative and GDD a positive loading
235 on the first component, whereas pH had a high negative loading on the second component.
236 Based on the RDAs, pH, GDD and TP were the most important factors explaining variation
237 in diatom species composition of the set of variables tested in Sweden, whereas GDD,
238 conductivity and TP were the most important factors in Finland (Fig. 2, see also Appendix B,
239 Table B.1). The most important factors for diatom genera did not differ from those for
240 species, except that in Finnish data, where TP was slightly more important than conductivity
241 (Fig. B.1, Table B.2).

242

243 Within Sweden, the predictive performance of the calibration models was moderate ($r^2 \geq$
244 0.27) for all variables (Table 2, Figs. 3 and B.2). The highest coefficients of determination
245 between observed and diatom inferred values were for pH ($r^2 = 0.65$ with species data and r^2
246 $= 0.71$ with genus data), GDD ($r^2 = 0.57$ and $r^2 = 0.53$) and TP ($r^2 = 0.52$ with both species
247 and genus).

248

249 When predicting from Sweden to Finland, the predictive performance of all the models was
250 low ($r^2 = 0.002$ to 0.13) (Table 2, Figs. 4 and B.3), although evaluation of the prediction
251 models showed moderate performances for the most important variables, GDD, pH, TP and
252 conductivity ($r^2 = 0.31$ and 0.33). Nevertheless, water chemistry variables conductivity ($r^2 =$
253 0.13 (species) and 0.11 (genera)) and TP ($r^2 = 0.12$ and 0.10) were best predicted. On
254 average, environmental variables could be predicted slightly better using species than genus
255 models. None of the alternative models showed significant improvement in the model
256 performances (Tables C.1, C.3 and C.4). The predictive performances of the alternative
257 models showed moderate to good performance for Swedish data and poor to moderate
258 performance for Finnish data. The level of model performance did not considerably change
259 whether a country was used as calibration dataset or being inferred for, i.e. calibration models
260 using Finnish dataset had poor performance in Finland yet they could infer for Swedish data
261 reasonably well.

262

263 The most important species and genera as predictors for each variable varied between
264 Sweden and Finland (Figs. 5 and B.4). In the top ten of the most important species, only two
265 (for color, conductivity and TP) or three (for GDD, WAB and pH) species were the same in
266 both countries (Fig. 5). The ten most important genera included four (for conductivity, TP

267 and GDD), five (for pH and WAB) or six (for color) genera that were among the ten most
268 important in both countries (Fig. B.4).

269

270 **4. Discussion**

271 The performances of the calibration models within Sweden demonstrated that the most
272 important climatic and water chemistry variables can be inferred from diatom assemblages
273 relatively well, both with species and genus level taxonomy. The predictive ability for pH and
274 TP showed similar or better accuracy than diatom inference models conducted previously in
275 streams in other regions (e.g. USA (pH and TP; Pan et al. 1996), Finland (pH; Soininen &
276 Niemelä 2002), Finland (TP; Pajunen et al. 2016b)). GDD was also well-predicted within the
277 calibration set when compared with inference models created earlier in Finland with the same
278 method (Pajunen et al. 2016b). These results indicate that diatom assemblages are robust
279 indicators of both local environmental and climatic variables, when the inference models are
280 being used in the same geographical region where they have been calibrated.

281 However, we found only low transferability of our predictive models from Sweden to Finland
282 for both local environmental and climatic variables. Although some differences among
283 species responses were expected between the two boreal neighboring countries, such a poor
284 predictive performance for Finland was surprising even if the performances of the calibration
285 models were good or moderate. This result is especially unexpected concerning pH and TP,
286 which are variables typically well-predicted by diatom assemblages (Pan et al. 1996,
287 Soininen & Niemelä 2002, Pajunen et al. 2016b). The failure of the cross-regional predictions
288 could be caused by several reasons: 1) between-region differences in species realized niche
289 brought about by competition or stressors, 2) different species pools and ecosystems in the
290 study regions, or 3) identification differences and the effect of data selection. Below, we

291 discuss these aspects in more detail.

292 4.1. *Fundamental vs realized niche*

293 The poor predictive performance could result from different realized niches for species in
294 Sweden and Finland. A species has a fundamental ecological niche, which is often described
295 as an optima and range of tolerance for environmental conditions (Hutchinson 1957).

296 However, in the presence of competition or environmental stressors, a species is forced to use
297 only a part of its range of tolerance (Hutchinson 1959, Soberón & Peterson 2005, Peterson
298 2011). As the size and composition of regional species pool, environment and the dominance
299 of competitive species may differ among geographical regions, the realized niches of species
300 may vary among different regions (Soberón & Peterson 2005, Pearman et al 2008). This
301 creates a problem in species based inference models as species' fundamental niches can
302 seldom, or never, be fully covered in natural environments (Jackson & Overpeck 2000,
303 Jiménez et al. 2019). In contrast, the observed niches of diatom species in nature are typically
304 the realized niches in a certain geographical area. Thus, the inference models are most likely
305 to perform better in the region they have been calibrated than outside the calibration region.

306 The differences in the realized niches between the regions influence the optima and
307 tolerances of species used in diatom indices. In fact, many studies have found a discrepancy
308 in the indicator values of some diatoms species. For example, Potapova & Charles (2007)
309 pointed out that some studies have reported low nutrient optimum for *Ulnaria ulna* (Kelly &
310 Whitton 1995, Soininen & Niemelä 2002), yet some have found it to indicate high-nutrient
311 conditions (Rott et al. 1997). Such differences in species' responses to environmental
312 variables between regions may be caused by the variable degree of biotic interactions, local
313 adaptation, or different environmental conditions, but then, these differences may also stem
314 from identification problems (see section 4.3). Also, the ranges of environmental variables in

315 the datasets influence the derived values of species' optima and tolerances. Models calibrated
316 from larger geographical areas may perform better as they include wider ranges of
317 environmental variables and may thus be able to detect the species' realized niche more
318 reliably. Additionally, mean values of temporal environmental measurements can reflect more
319 robustly the environmental conditions affecting species than snapshot water chemistry
320 measurements. On the other hand, environmental interactions, interspecific interactions or
321 even microevolution may increase the noise in such datasets, which again could reduce the
322 performance of models based on these datasets.

323 *4.2 Different species pools and ecosystems*

324 Differences in the species pools and environmental conditions between the regions where the
325 calibration and inferred data sets originated may decrease the predictive ability of diatom
326 inference models. Here, Swedish and Finnish data sets consisted of the same 196 species,
327 which generally represented the majority of individuals in sites in both countries (median
328 coverage in Finland was 91.3% and in Sweden 82.2% of the individuals). However, in some
329 sites the species assemblages were dominated by species not occurring in the original data set
330 of the neighboring country. This indicates a difference in species pools between these two
331 neighboring countries, yet also, the variation in species assemblages may stem from
332 environmental differences (Table 1, Fig. A.4) between Sweden and Finland. Based on the
333 RDA results, the most influential water chemistry variable for Finnish diatom communities
334 was conductivity, whereas in Sweden, pH was the most important environmental factor. This
335 shows that the main drivers of diatom community composition differ between the two
336 countries indicating different environmental settings and limiting resources. The poor
337 performance of Finnish calibration models (Table C.1) compared to earlier studies using the
338 same data set with full species data (Pajunen et al. 2016b) indicate that the subset of Finnish

339 diatom assemblages used in this study lack the ability to indicate environmental conditions in
340 Finland.

341 The differences between species pools in Sweden and Finland could also reflect some
342 dispersal limitation due to dispersal barriers (e.g. the Baltic Sea). Additionally, both countries
343 may contain some peculiar ecosystems, such as heavily polluted, acidic or brownified
344 streams, not found in the other country (or at least not covered in the data set), and these
345 ecosystems may cover such environmental conditions and gradients that harbor specialist
346 taxa. For instance, the relative abundances of the indicator species used in the models covered
347 only 27.5% out of the total abundance (500 cells) in the site with the highest water color (535
348 mg Pt L⁻¹) in Sweden. This indicates that the dominant species in this site is especially
349 tolerant of high water color, and its absence in Finnish data set may be due to the smaller
350 range of water color in the Finnish data set.

351 Generally, one reason for the models' poor ability to infer environmental variables may be the
352 lack of specialized species in the data sets. Therefore, the indication ability of the
353 assemblages is weak due to the lack of joint indicator species between the data sets. Many
354 good indicator species are rare as they have a clear optima for a certain environmental
355 variable and a narrow range of tolerance. However, integrating these rare species into
356 inference models is problematic as their low occurrence can cause noise and instability to the
357 models. In this study, rare species were not systematically left out, since the species data from
358 Sweden and Finland were matched to consist of all the species present in both data sets. Thus,
359 keeping all the species in the models would probably enhance the predictive ability of the
360 calibration set, but not the inference model.

361 *4.3 Problems in identification or data selection*

362 In addition to cryptic species, diatom models can also suffer from other problems in species

363 identification (Kahlert et al. 2012, Werner et al. 2016). The identification process is very
364 detailed and the accurate interpretation of complex structures is in the end subjective.
365 Therefore, the probability of differences in identification is greater when more analysts have
366 participated in the species identification. However, such differences can be minimized by
367 identifying diatoms to genus level only. In this study, the differences between the predictive
368 ability of species and genera based models were only minor, indicating that our
369 harmonization efforts had been successful and species identification did not seem to cause
370 major problems in this study. The similar performance of the two models may also indicate
371 that the whole diatom genera responded to environment quite similarly and/or that the use of
372 genus level in identification overall decreased the between-analyst differences in species
373 identification, and models performed well even if the sensitivity of genus level to indicate
374 environmental conditions may be somewhat lower than the species level.

375 Finally, we note that the inconsistencies in observed species optima and the range of
376 tolerance between different geographical areas can be caused by differences in ranges of
377 environmental variables in each data set. It has been shown that the relative importance of an
378 environmental variable for diatom community depends on its range of variation in the data set
379 (Potapova & Charles 2002). Moreover, in streams, environmental conditions can fluctuate
380 rapidly, and thus, a snapshot measurement of a water chemistry variable may not reflect the
381 actual conditions faced by the biota accurately enough. This may have partly caused the poor
382 predictive ability of environmental variables in Finland as the water chemistry values in
383 Finnish dataset were based on snapshot measurements whereas the Swedish environmental
384 data consisted of mean values from different sampling occasions. Furthermore, the
385 unidirectional flow may increase the potential mass effects, i.e., a constant dispersal of
386 species from high-quality patches to sink habitats (Pulliam 1988, Terui et al. 2014, Jamoneau
387 et al. 2018). Therefore, species may occur at a site that does not match their preferences

388 because of such metapopulation dynamics.

389

390 **5. Conclusions**

391 The present study shows that diatom assemblages are reliable indicators of water chemistry
392 and climatic variables within the region where the inference models are calibrated, yet their
393 indicator ability shows low transferability across regions. The underlying reasons for the
394 weak performance of the diatom inference models may be related to between-region
395 differences in species realized niche, species pools and/or ecosystems, local adaptation or
396 species identification. These findings highlight the importance of being careful when using
397 models based on regional datasets in a different geographical context.

398

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405

406 **Appendices**

407 Supplementary data associated with this article can be found, in the online version:

408 *Appendix A*: The results of data analyses, including species data, covariance matrixes,
409 overlying histograms, NMDS and PCA.

410 *Appendix B*: The results of RDAs, and the calibration and inference models for genus data.

411 *Appendix C*: The results of alternative calibration and inference models.

412

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1 **TABLE 1.** Summary (minimum, maximum, range, median and standard deviation (Sd)) of the measured variables from 571 stream sites in
 2 Sweden and 227 stream sites in Finland.

3

Variable	Unit	Sweden					Finland				
		Min	Max	Range	Median	Sd	Min	Max	Range	Median	Sd
Growing degree days (GDD)		450.9	1680.1	1229.2	1352.0	253.2	450.1	1349.1	899.0	1143.1	252.8
Frost degree days (FDD)		0	1818.1	1818.1	243.6	429.3	337.1	1811.0	1473.9	893.3	396.3
Precipitation (MAP)	mm	415.5	997.2	581.7	611.8	93.3	371.7	732.9	361.2	612.3	71.7
Water balance (WAB)	mm	102.4	784.0	681.6	255.9	98.5	126.5	441.4	314.9	274.9	48.3
Total phosphorus (TP)	$\mu\text{g L}^{-1}$	1.0	332.0	331.0	23.0	38.1	2.0	190.0	188.0	21.0	32.1
Conductivity	$\mu\text{S cm}^{-1}$	0.7	143.0	142.3	7.6	15.9	0.9	36.6	35.7	4.0	7.9
pH		3.6	9.2	5.6	7.0	0.8	4.5	8.2	3.7	6.9	0.6
Water color	mg Pt L ⁻¹	3.5	535.0	531.5	100.0	84.2	5.0	400.0	395.0	80	71.2

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1 **Table 2.** Summary of model performances shown as the model predictive ability (i.e. how
 2 well the model was transformed from Sweden to Finland) (r^2). The results of the model
 3 evaluations (r^2), i.e. the performances of the calibration models (in Sweden), are shown in
 4 parenthesis.

	Species	Genera
GDD	0.05 (0.57)	0.02 (0.53)
WAB	0.00 (0.33)	0.02 (0.30)
pH	0.01 (0.65)	0.01 (0.71)
TP	0.12 (0.52)	0.10 (0.52)
Conductivity	0.13 (0.31)	0.11 (0.33)
Water color	0.04 (0.29)	0.01 (0.27)

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1 **Figure legends**

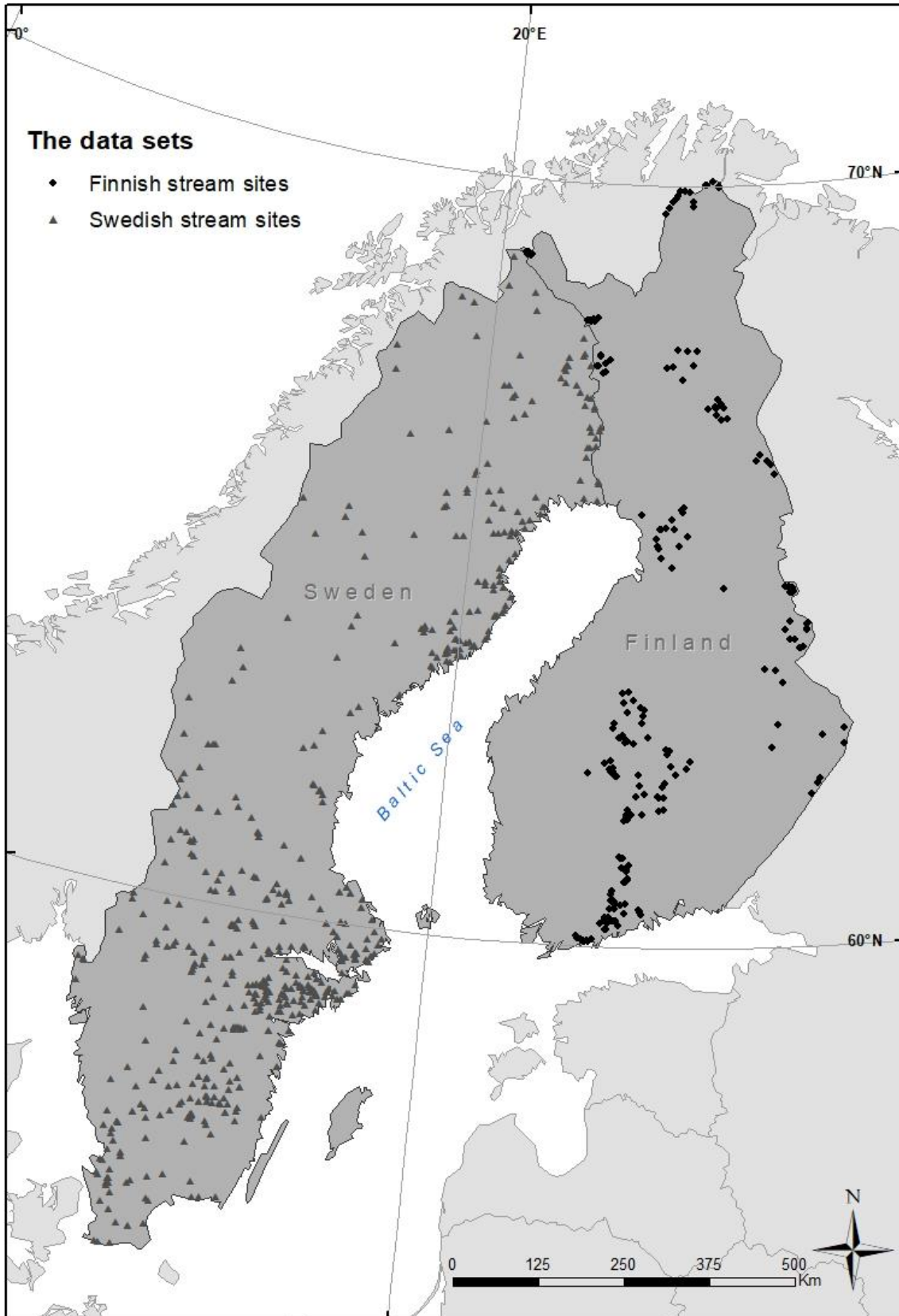
2 *Figure 1.* Locations of the stream sites in Sweden (n=571, 55° – 70° N, 10° – 25° E) and
3 Finland (n=227, 60° – 70° N, 20° – 32° E) Finnish (n=227), in northern Europe.

4
5 *Figure 2.* The ordination plots of Redundancy Analysis (RDA) on the species data using the
6 climatic and environmental variables for 571 stream sites in Sweden and 227 stream sites in
7 Finland. Total phosphorus (TP), conductivity and water color were log-transformed. The
8 other abbreviations stand for growing degree days (GDD) and water balance (WAB). The
9 circles represent stream sites.

10
11 *Figure 3.* Relationships between observed and diatom species inferred values for climatic and
12 local environmental variables in the calibration models (i.e. within Sweden). Models were
13 conducted using Boosted Regression Trees (BRT) method. Each plot shows the coefficient of
14 determination (r^2) and root-mean-square error of prediction (RMSEP).

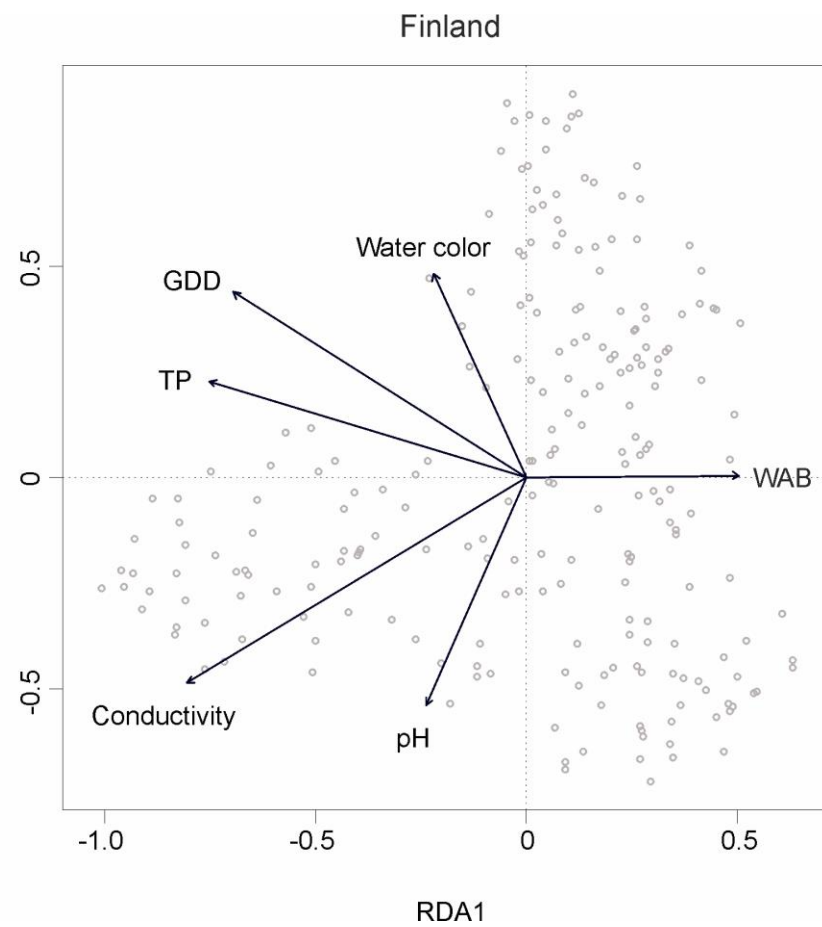
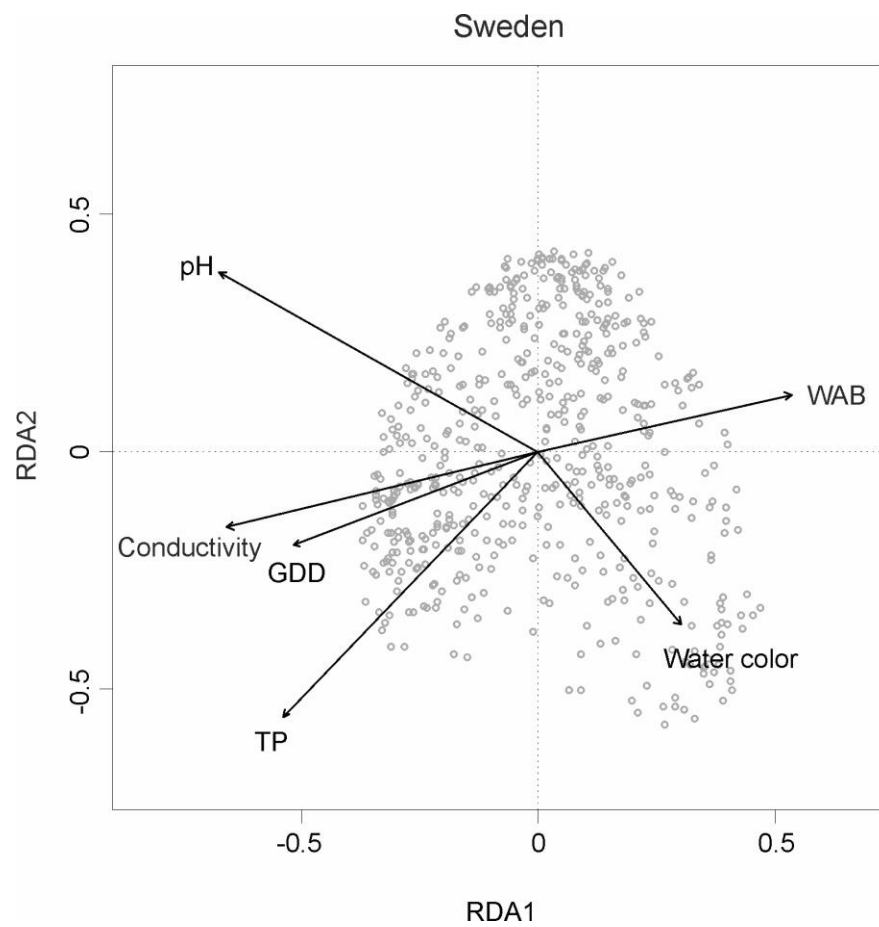
15
16 *Figure 4.* Relationships between observed and diatom species inferred values for climatic and
17 local environmental variables in Finland using the Swedish calibration models for prediction.
18 Models were conducted using Boosted Regression Trees (BRT) method. Each plot shows the
19 coefficient of determination (r^2) and root-mean-square error of prediction (RMSEP).

20
21 *Figure 5.* The ten most important species for each climatic and environmental variable in
22 Sweden and Finland. The importance of each species is shown as relative importance (%),
23 which are estimated by using Boosted Regression Trees (BRT) method.



1

2 FIG. 1



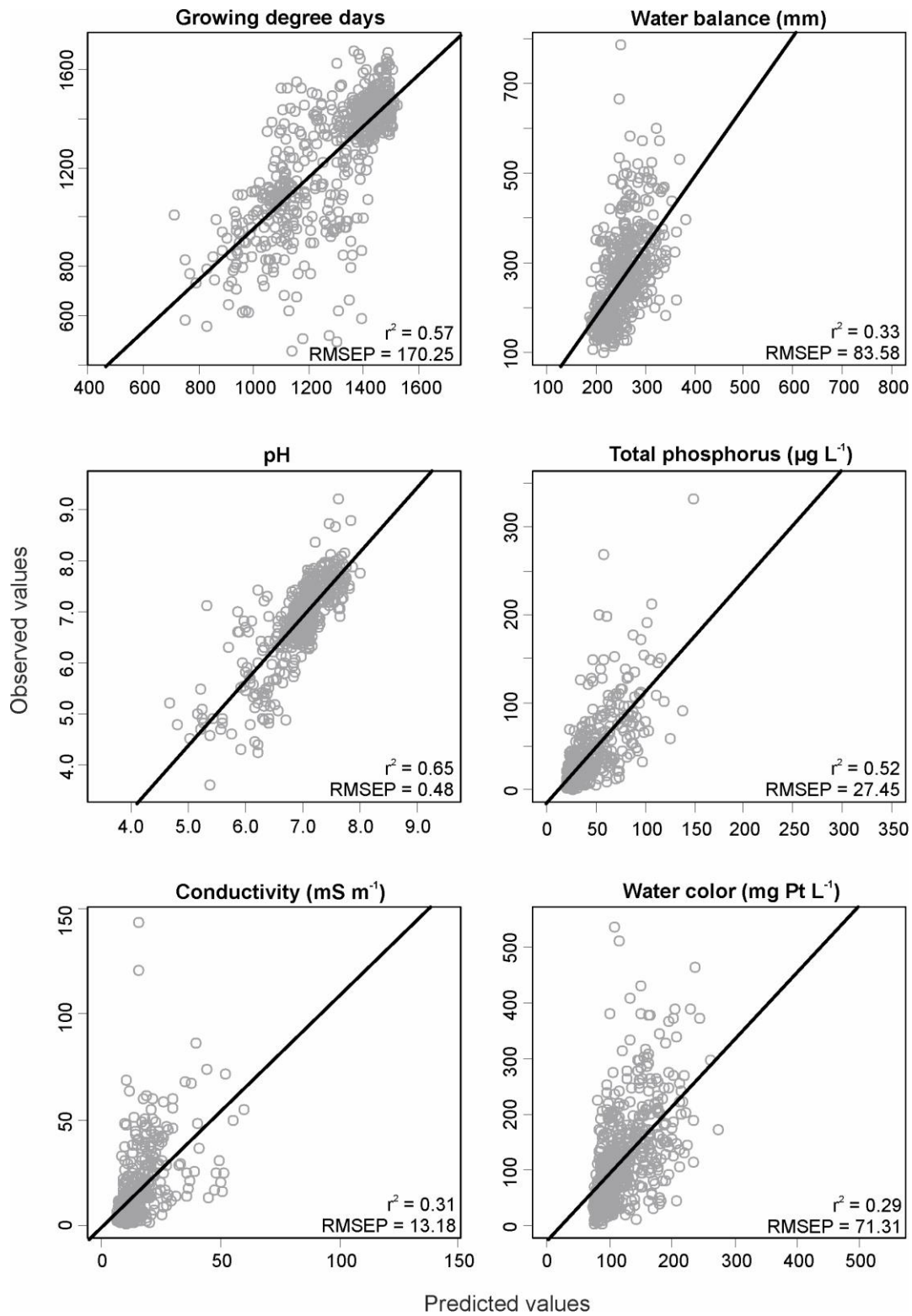
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2 FIG. 2

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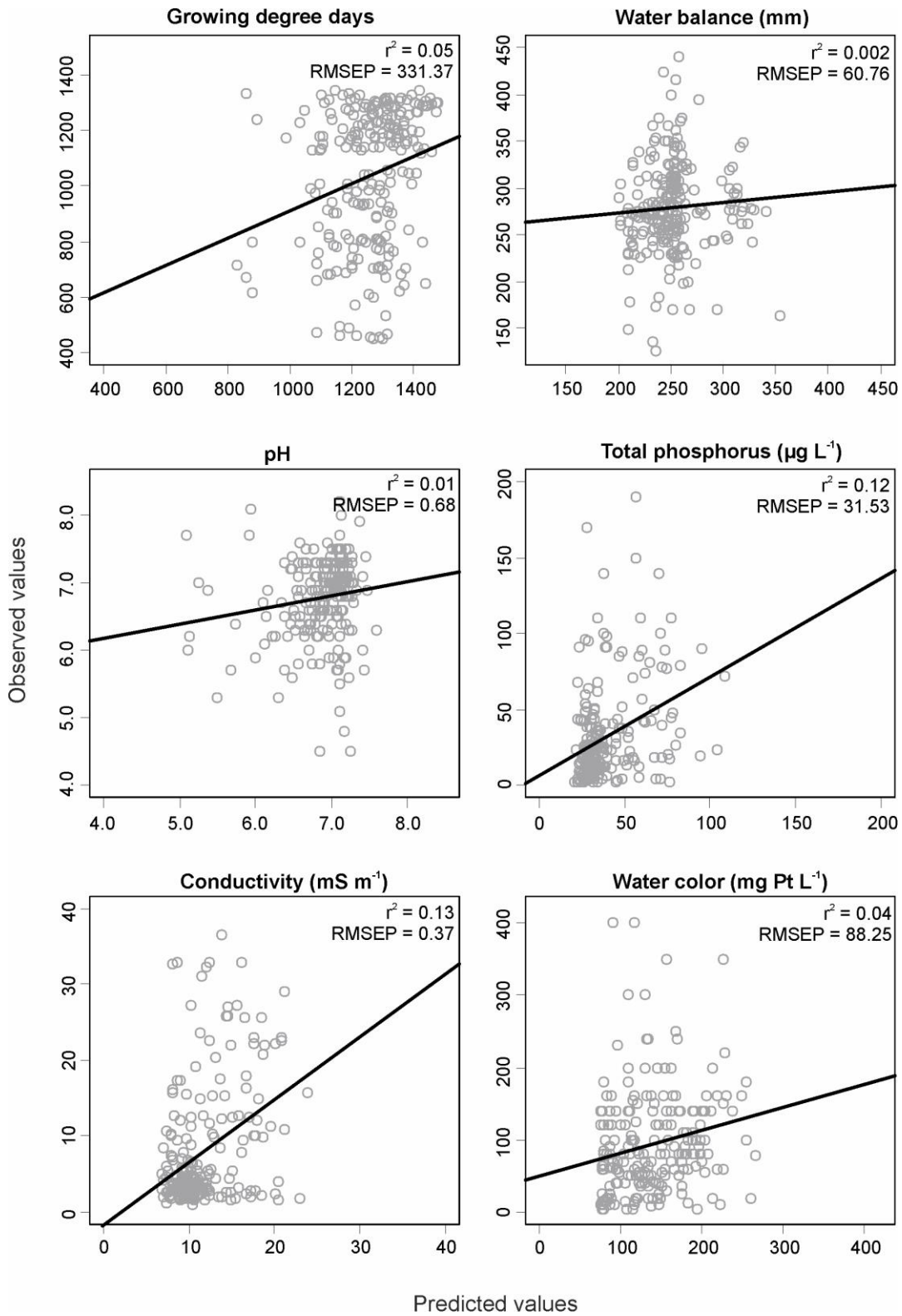
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2 FIG. 3

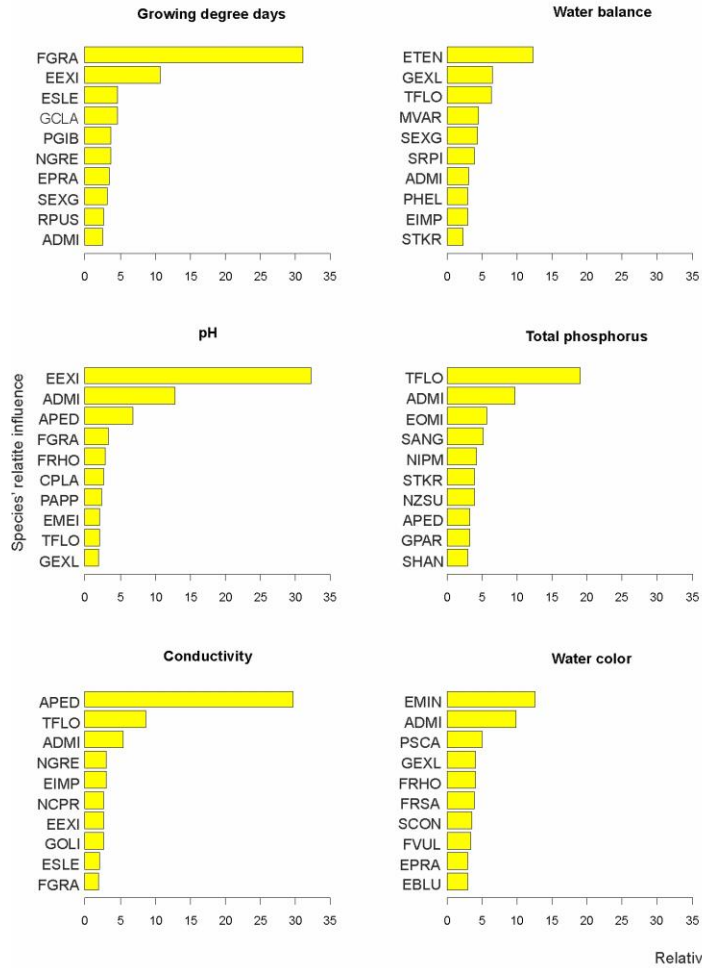


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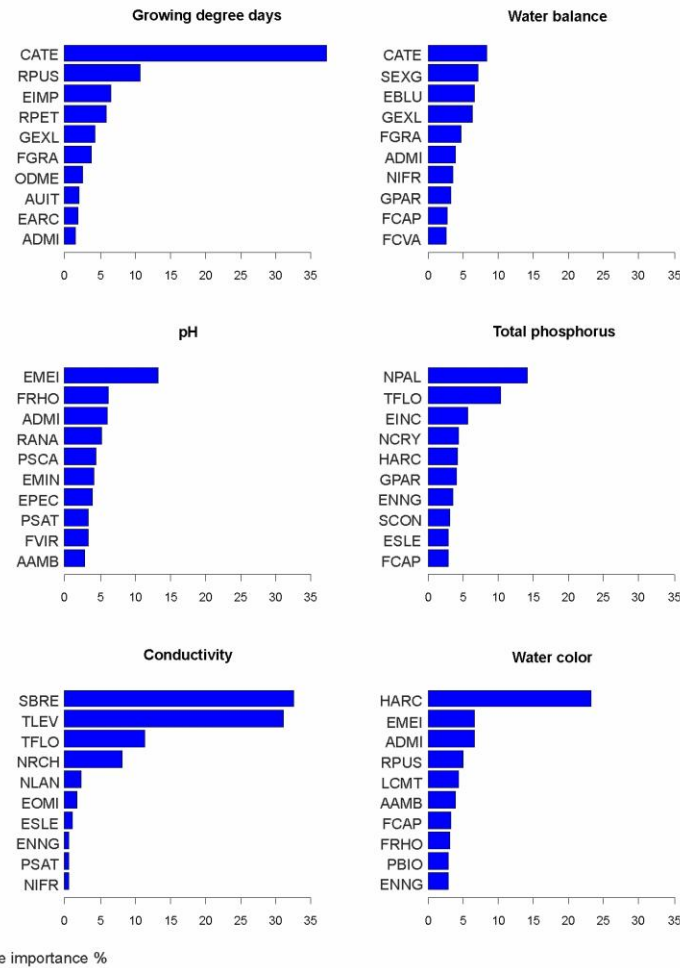
Predicted values

2 FIG. 4

Sweden



Finland



Abbreviations

AAMB *Aulacoseira ambigua*
 ADMI *Achnanthydium minutissimum*
 APED *Amphora pediculus*
 AUIT *Aulacoseira italica*
 CATE *Caloneis tenuis*
 CPLA *Cocconeis placentula*
 EARC *Eunotia arcus*
 EBLU *Eunotia bilunaris*
 EEXI *Eunotia exigua*
 EIMP *Eunotia implicata*
 EINC *Eunotia incisa*
 EMEI *Eunotia meisteri*
 EMIN *Eunotia minor*
 ENNG *Encyonema gracile*
 EOMI *Eolimna minima*
 EPEC *Eunotia pectinalis*
 EPRA *Eunotia praeurupta*
 ESLE *Encyonema silesiacum*
 ETEN *Eunotia tenella*
 FCAP *Fragilaria capucina*
 FCVA *Fragilaria vaucheriae*
 FGRA *Fragilaria gracilis*
 FRHO *Frustulia rhomboides*
 FRSA *Frustulia saxonica*
 FVIR *Fragilariforma virescens*
 FVUL *Frustulia vulgaris*
 GCLA *Gomphonema clavatum*
 GEXL *Gomphonema exilisimum*
 GOLI *Gomphonema olivaceum*
 GPAR *Gomphonema parvulum*
 HARC *Hannaea arcus*
 GPAR *Gomphonema parvulum*
 ENNG *Encyonema gracile*
 LCMT *Lindavia comta*
 MVAR *Melosira varians*
 NCPR *Navicula capitatoradiata*
 NCRY *Navicula cryptocephala*
 NGRE *Navicula gregaria*
 NIFR *Nitzschia frustulum*
 NIPM *Nitzschia perminuta*
 NLAN *Navicula lanceolata*
 NPAL *Nitzschia palea*
 NRCH *Navicula reichardtiana*
 NZSU *Nitzschia subalittorea*
 ODME *Odontidium mesodon*
 PAPP *Pinnularia appendiculata*
 PBIO *Psammothidium bioretii*
 PGIB *Pinnularia gibba*
 PHEL *Psammothidium helveticum*
 PSAT *Psammothidium subatomoides*
 PSCA *Pinnularia subcapitata*
 RANA *Rossethidium anastasiae*
 RPET *Rossethidium petersenii*
 RPUS *Rossethidium pusillum*
 SANG *Suriella angusta*
 SBRE *Suriella brebissonii*
 SCON *Staurosira construens*
 SEXG *Stauriforma exiguiiformis*
 SHAN *Stephanodiscus hantzschii*
 SRPI *Staurosirella pinnata*
 STKR *Stauroneis kriegeri*
 TFLO *Tabellaria flocculosa*
 TLEV *Tryblionella levidensis*

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2 FIG. 5