

Processes structuring desmid communities - phylogenetic approach



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Questions asked:

Do desmid communities show phylogenetically based composition?

What are the key processes structuring desmid communities?

Are there any differences in role and intensity of structuring processes along environmental gradients?

Background:

Our study was focused on processes forming ecological communities. As a model we used desmid communities in peat bogs. We took advantage of a method which includes evolutionary history of species into ecological research – phylogenetic structure of communities. It is useful tool for revealing processes structuring those communities. Phylogenetic information can be used as a proxy of species functional similarity - this is very helpful when studying protist organisms where traits are difficult to identify and measure.

Two significant phylogenetic structures could be identified: i) underdispersion - community containing more closely related species, and ii) overdispersion – community with more distantly related species. The main idea of this method is that communities facing environmental stress contain closely related species because they share traits favoring them in harsh conditions – environmental filtering. Overdispersion arises when biotic interaction (such as competition) are dominant forces in structuring communities (Webb et al. 2002).

Desmids:

Desmids are streptophyte green algae (Desmidiales, Zygnematophyceae) closely related to vascular plants. Order Desmidiales is monophyletic with distinctive morphological feature – cell divided into two semicells. In peat bogs they are one of the most dominant micro-phytobenthic groups (Figure 1). It is well studied group and it has been showed that community composition correlates with pH and conductivity (Neustupa et al. 2012).



Figure 1: Example of desmid community; light microscope, scale bar 100 μm

Abbreviations:

PSV - Phylogenetic Species Variability
PSE - Phylogenetic Species Evenness

References:

Coesel, P.F.M. (1982). Structural Characteristics and Adaptations of Desmid Communities. *The Journal of Ecology*, 70. / Černá, K. & Neustupa, J. (2009). The pH-related morphological variations of two acidophilic species of Desmidiales (Viridiplantae) isolated from a lowland peat bog, Czech Republic. *Aquatic Ecology*, 44. / Helmus, M.R., Bland, T.J., Williams, C.K., Anthony, R. & Ives, A.R. (2012). Phylogenetic Measures of Biodiversity, *The American Naturalist*, 169 (3). / Neustupa, J., Černá, K. & Št'astný, J. (2012). Spatio-temporal community structure of peat bog benthic desmids on a microscale. *Aquatic Ecology*, 46. / Webb, C.O., Ackerly, D.D., McPeck, M. & Donoghue, M.J. (2002). Phylogenies and Community Ecology. *Annual Review of Ecology and Systematics*, 33.

Results:

Most of examined communities were phylogenetically structured. However, no predominant pattern of phylogenetic structure was discovered (Table 1).

Table 1: Observed and permuted mean PSV and PSE values

	PSV	PSE
mean observed	0.4694	0.3322
null model richness	0.3890 overdispersed	0.3890 overdispersed
null model frequency	0.4760 underdispersed	0.4007 underdispersed
null model trial swap	0.4701 random	-

Whereas the phylogenetic structure of communities with $pH \leq 5$ was underdispersed (PSVobs = 0.4159, PSVnull2 = 0.4340), communities with $pH > 5$ were found to be overdispersed (PSVobs = 0.5459, PSVnull2 = 0.5219). (Figure 2)

The only environmental factor explaining variability in PSV is pH (pH sum of square [SS] = 0.44987, residuals SS = 1.73000, adjusted R2 = 0.1984) (Figure 3). Variability in PSE can be also explained mainly by pH, and to smaller extent by geographical position of communities. There was no effect of conductivity on phylogenetic structure of communities.

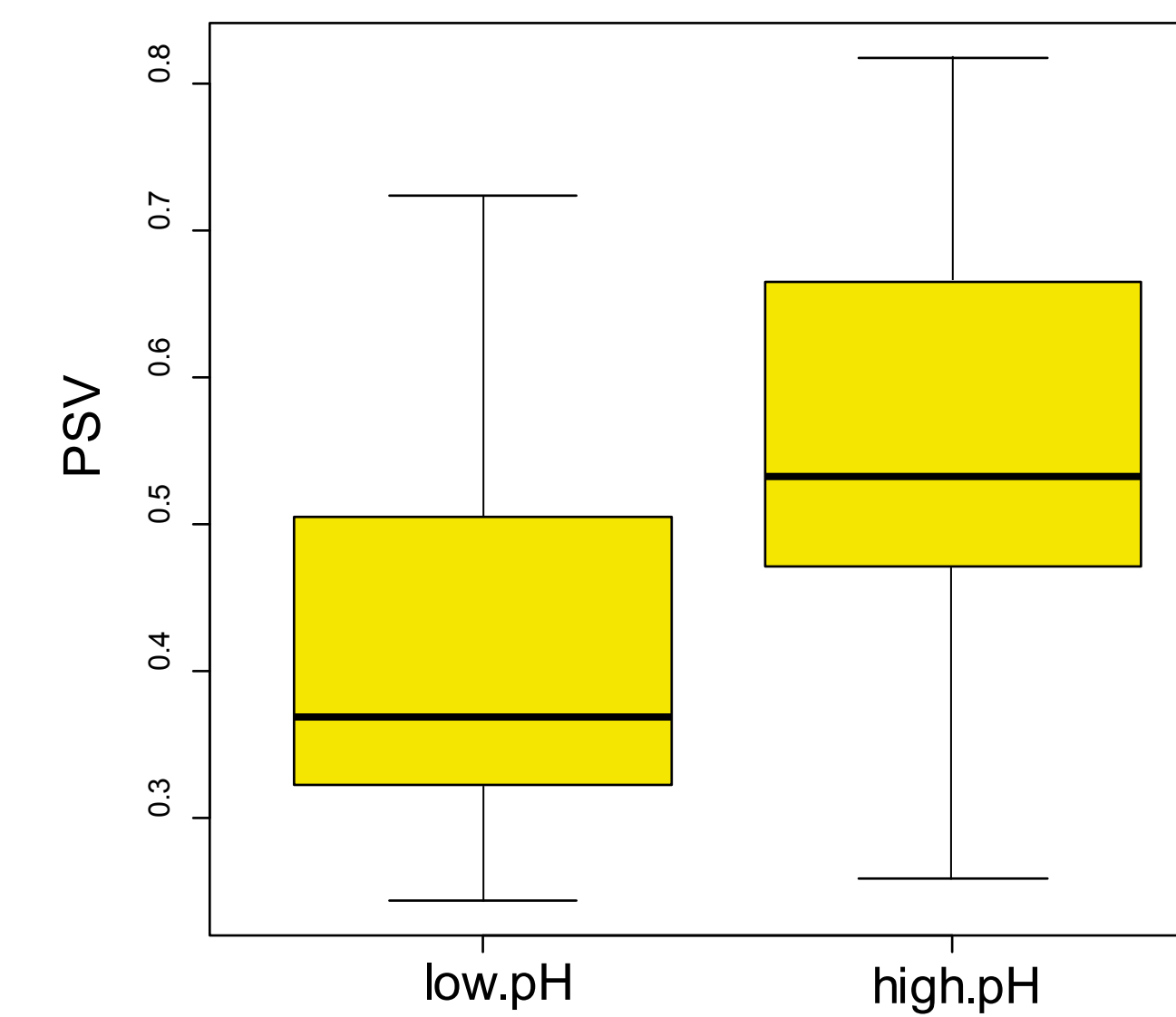


Figure 2: Box plot diagrams; phylogenetic species variability in low and high pH communities; there is significant difference in variability between those two subsets (Kruskal-Wallis test: $p < 0.001$)

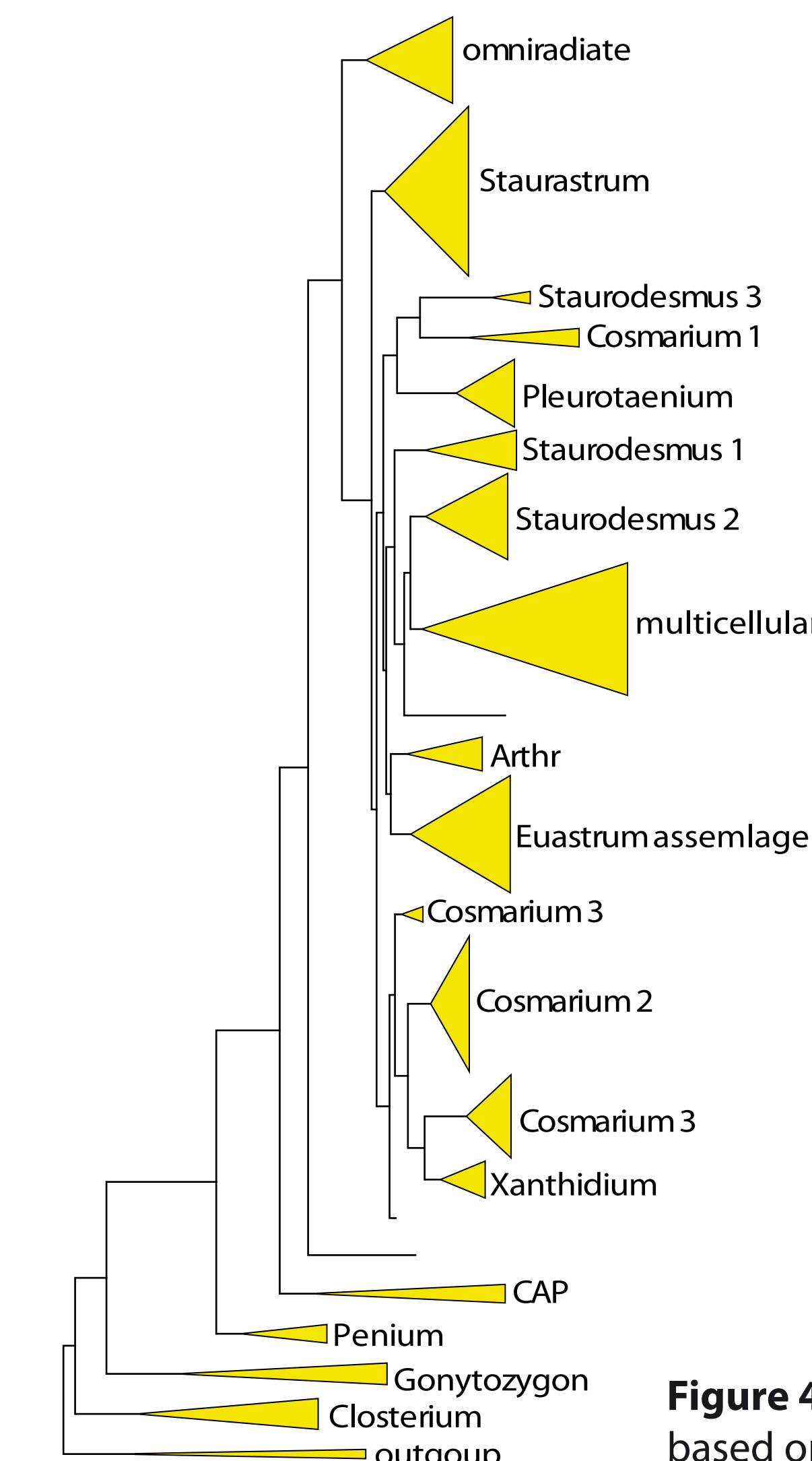


Figure 4: Phylogeny of Desmidiales; Bayesian analysis based on rbcL sequences, important clades are stressed

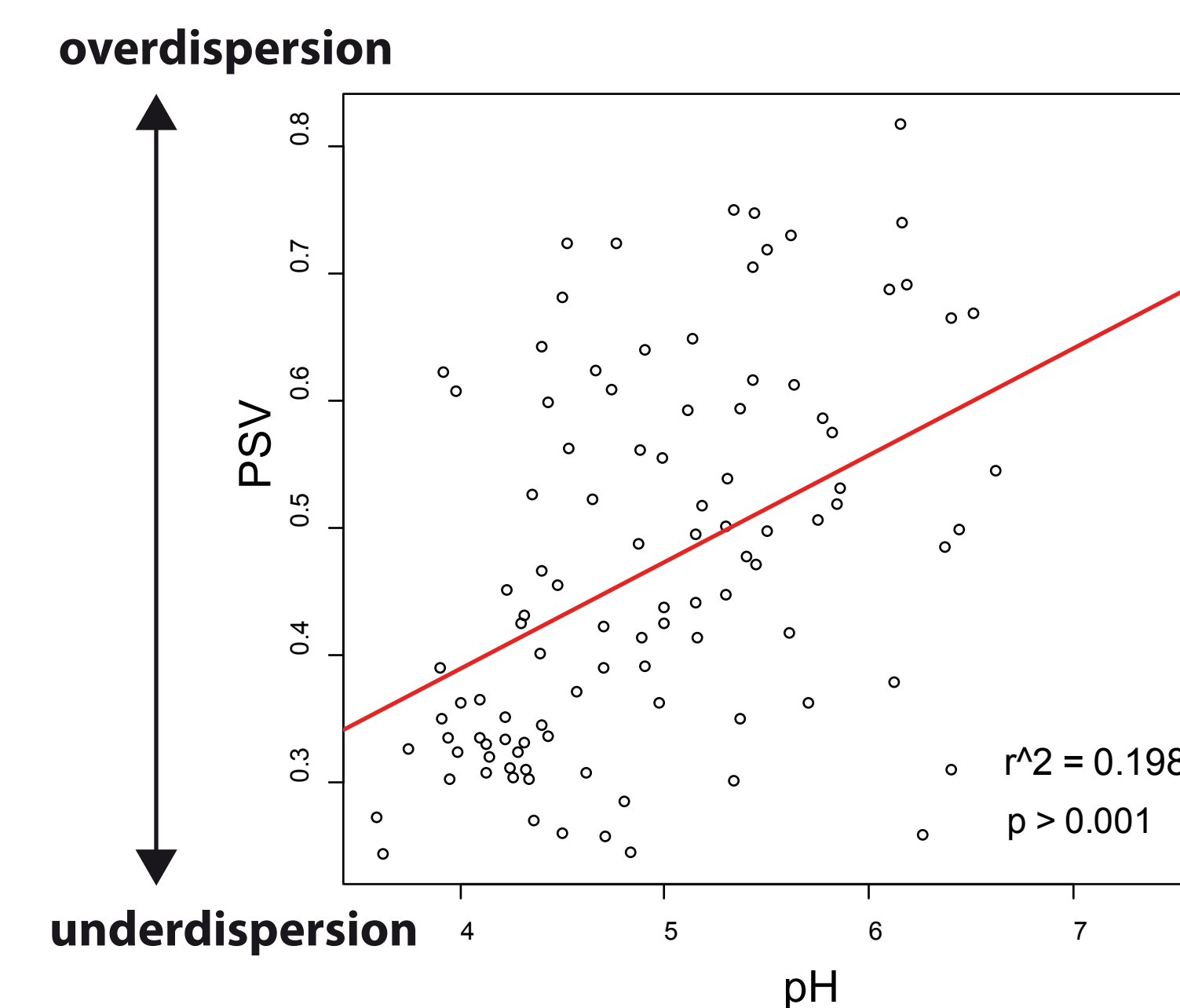


Figure 3: Least square regression of phylogenetic species variability (PSV) and pH

Conclusions:

Examined desmid communities show phylogeny based composition, however there is no predominant pattern. The inconsistency between results from different null models can be explained by differences in species prevalence; the most prevalent species are more distantly related than expected. After accounting for those, different communities are composed of closely related species.

Large portion of variation in phylogenetic structure can be explained by pH. Communities contain more closely related species as pH decrease. Whereas the communities in low pH are significantly phylogenetically underdispersed, those in higher pH are overdispersed. Since the other measured environmental factors had no significant influence we can assume pH to be the most dominant environmental driver of phylogenetic composition.

It is clear that low pH acts as a stress factor and strong environmental filter. This is in correspondence with previous studies showing that in low pH the shape of desmid cells is changing towards simpler morphology with higher surface-to-volume ratio (Coesel 1982; Černá & Neustupa 2009). On the other hand, environmental stress is loosen in higher pH, so that biotic processes like competition are dominant in structuring, causing overdispersion in desmid communities.



Methods:

Through years 2010-2013 we sampled 102 desmid communities from peat bog in Europe (Czech Republic, Sweden, Norway, and Ireland). We measured pH, conductivity and geographic position at each site. We identify desmid taxa in light microscope and estimates abundances by counting first 200 cells per sample. As a measure for evolutionary relatedness of species we used phylogenetic relationships inferred from nearly four hundred unique rbcL sequences (Figure 4). We calculated several measures of phylogenetic structure (phylogenetic species variability (PSV), phylogenetic species evenness (PSE) (Helmus et al. 2012)) and compared obtained results with permuted communities created by three null models richness, frequency and trial swap. By linear least square regression we estimated role of abiotic factors on phylogenetic structure. We also divided samples to two subsets - one with $pH \leq 5$ and the second $pH > 5$ and compare if the subsets significantly differ in PSV values.

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