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Review & overall assessment of the Ph.D. thesis submitted by Tomáš Fér, “Study of plant dispersal in river corridors using molecular markers” at the Charles University Prag in 2008.

Overall assessment

The submitted Ph.D. thesis is a compendium comprises five chapters, a general introduction and summary (chapter 1), and four manuscripts (chapters 2-5) formatted to be published in scientific journals. The first chapter gives very good insight in the questions that were answered in the following chapters and the scientific background related. Special emphasis is given to the use of molecular markers in dispersal studies. The followed approach includes the analyses of four different taxa sampled along rivers in the Czech Republic, with molecular markers. Main emphasis is given to the discovery of clonal individuals (within the same or of different populations), the estimation of population structure and the estimation of the amount of gene flow among populations. Two different molecular marker systems are used in order to answer questions posed.

Overall Fér's Ph.D. is a timely and valuable contribution to the fields of population biology and ecology. One of the chapters of the thesis is already published in an international journal (Freshwater Biology, *Nuphar lutea* study in chapter 3), two others are submitted to international journals (chapter 2 to Molecular Ecology; chapter 4 to Aquatic Botany) which shows that the Ph.D. thesis is well embedded in the international botanical and ecological community and offers new insights in the reasons for diversity patterns along rivers. The approaches and methods used are up to date and the results are carefully and correctly interpreted and shown. All four studies were carried out carefully and relevant literature has been considered and discussed. The text is well written and understandable and has the potential of reaching a wide audience.

Specific questions to the defendant (onordered)

What are ways to define a “population”. How many different definitions do exist and which ones did you use in the study?

Population genetics aims to understand nature and processes in populations, but the term is frequently used to explain several kinds of populations, which is often confusing. This is a general, but interesting question to be discussed.

Why were populations sampled in this way? What are the advantages and disadvantages?

In most cases similar studies have a different sampling, i.e. including more individuals per population in order to be able to estimate allele frequencies in populations correctly which gives more power to analyses based on population genetic theory. Few included samples from many sites, but often less than three individuals per population.

Why were no “assignment tests” used?

There is one group of methods available that allow for assigning unknown individuals (e.g., AFLPop) to known populations. Could you briefly explain the idea of assignment tests and outline, whether such tests could be used in your studies?

Please explain spatial autocorrelation analysis and why this can be interpreted as undirected long-distance dispersal?

I regard this as a critical aspect of the studies. I think the interpretation that spatial autocorrelations within a certain geographical range does proof LDD is questionable. What would be alternative interpretations of such pattern? Could, e.g., high levels of pollen flow explain spatial autocorrelation?

How sure could you identify clones in the data sets with AFLPs or microsats?

Both molecular markers have error rates, i.e., results can be only obtained with a certainty under 100% . From which steps of the analysis procedure come these errors and how could molecular analysis improved to correctly find clones?

What would you do differently if you would start the study today regarding following aspects?

- Taxa chosen
- Molecular methods selected
- sampling scheme

What is the importance of rare floods for seed dispersal and establishment in the species chosen?

The answer to this question will be rather, speculative, but nevertheless. Simply based on your overall knowledge of the biology and morphology of the study taxa one would expect different “behaviour”.

Can you describe the approach of Bayesian model based clustering of populations and the interpretation of clusters obtained in *Phragmites* (chapter 4)? Why were clones not removed? What could be the reason for the very high number of clusters suggested by Bayesian analysis?

A straightforward interpretation would be lack of gene flow among populations, which is hard to believe in a wind dispersed, wind pollinated and dominant plant.

Can you offer alternative explanations for the higher diversity found in populations further downstream?

You explained that the higher diversity downstream is related to the “accumulation” of different genotypes originating from upstream areas. Nevertheless, could you find another reason for this pattern?

How do you, in a conclusive way, interpret the results from Mantel tests (i.e. correlation between genetic and geographic distance)?

In two species (summarized on page 20) there is a correlation in the other two there is not.