Assessment of the Ph.D. thesis of Magdalena Bohutínská

The Ph.D. candidate, Magdalena Bohutínská, has presented a written Ph.D. thesis titled "How predictable is genome evolution?" compiling six manuscripts, five of which are published and three of which are the first-author contributions. This impressive research work can be roughly subdivided into two parts: parallelism in local alpine adaptation and parallel adaptation to intrinsic challenges of whole-genome duplications. She investigated adaptive evolution across several plant lineages within the Brassicaceae family, where she has been involved at every step of the process, starting from field sampling, data generation, data analysis, and writing manuscripts.

The central hypothesis of the presented research is that divergence between the investigated lineages is one of the main limiting factors to parallel evolution. Indeed, this work shows that at shallow divergence levels probability of adaptation to the same selection pressure by the same adaptive allele in different populations is high due to the presence of such shared alleles in incompletely sorted lineages. Although in lineages with ongoing gene flow it would be hard to infer if such adaptation was truly independent and therefore parallel unless the adaptation occurs by a different mutation on the same gene. At deeper divergence levels, it seems that even gene reuse is a rare event, and parallelism can be mostly observed on the functional level of genes underlying the adaptation. In the outlook of her research, Magdalena Bohutinska suggests focusing future work on investigating the limitations to parallel adaptation, specifically, pleiotropic constraints in the context of regulatory networks, which I find very interesting.

As most of the work in this Ph.D. thesis has been already published and therefore went through a peer-review process, my questions do not concern any technical procedures or drawn conclusions, but rather more wide interpretations and understanding of parallel evolution.

Question 1: Would similar limitations to genetics underlying convergence apply to (1) parallel adaptation to the same selection pressure and (2) parallel evolution of a trait?

Question 2: What would be the effect of polyploidization on the genetic constraints to parallel evolution such as pleiotropy? What would be your ideal or most optimal experiment to test such an effect if any?

Question 3: In Case study 5 titled "Novelty and convergence in adaptation to whole-genome duplication" where you studied genomics of adaptation to polyploidy in *Cardamine amara* - polyploids seem to occupy different geographical regions compared to diploids. What would be the follow-up experiments one could do to clearly distinguish between signals of local adaptation and adaptation to polyploidy in this case?

Question 4: What could be the main selection pressure, in your opinion, at the transition to the higher ploidies than four? The question is related to Case study 6, where the possibility to investigate this question presented itself, however was not fully developed in the manuscript.

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