

Reviewer's Dissertation Thesis Report



Institute of Biophysics ASCR
Roman Hobza, Ph.D.
Department of Plant Developmental Genetics
Královopolská 135, 61200, Brno
e-mail: hobza@ibp.cz

Dissertation Thesis Title: How predictable is genome evolution? Insights from convergent adaptations across Brassicaceae

Student: Magdalena Bohutínská

The Thesis is subdivided into two major sections, Part A and Part B. The first part comprises of Introduction, Aims, Methods, Results, Discussion and References. I appreciate short version which, in fact, clearly explains all aspects of complex thesis. The logic and beautiful illustrations summarizing hypotheses and principal findings (Fig. 1 and Fig. 2) suggest great ability of the author to summarize complex data.

The second part consists of 5 papers published in PNAS (first author), The Plant Journal, Nature Communications, 2x Molecular Biology and Evolution (first author) and manuscript deposited in BioRxiv. To be honest, it is almost inappropriate to evaluate such collection of great achievements. Number of evaluators has already corrected and discussed presented results. Anyway, it raises my first question. **What was the most discussed or problematic point (if any) during reviewing process (no need to discuss all papers)?** As I mentioned at the beginning, PhD candidate is “summarizing” expert. **Did you consider writing a review on topic of thesis?**

Author selected great model system to study parallel evolution. **What do you think about studying parallel evolution in process of domestication (independently domesticated lineages within the same crop)? Can you pick other model systems (not only crops or Arabidopsis species) worth to study in plants?**

Everything seems to be smooths in the logic and outputs of dissertation. Anyway, if you start again would you change something in experimental design (sequencing method, number of samples....)?

I miss little bit broader discussion about mechanistic explanation of parallel evolution phenomenon. I wonder if e.g. 3D nucleus structure, targeting of retroelements into specific motifs of promoters, generally retroelement “vigor” during process of adaptation (at least in polyploids) ... can be drivers of what is in the end seen as a result (pool of genes showing

parallel signature of positive selection). **Can you briefly discuss impact of non-genic regions in the process of parallel evolution and adaptation in general?**

What about role of microRNAs in parallel evolution? Did you try to analyse microRNA profiles in parallel with gene expression?

What about epigenetics? Did you consider to analyse epigenetic patterns in process of parallel evolution?

On the experimental side, various designs have been employed, mostly using microbes (parallel replay experiments). Can you pick advantages of plant systems in such experiments?

As far as I understand, author suggests that allele reuse in case of some meiotic genes enable autotetraploids to survive the unstable post-WGD phase and to escape an extinction („The reused genes mostly encoded a set of physically and functionally interacting proteins governing meiosis crossover number and distribution.“). **How about that polyploidy increases accessibility of meiosis to the regions with very low meiotic rate in diploids and as a consequence increases variability (ability to adapt)?**

The thesis convincingly demonstrates Magdalena Bohutínská ability to work scientifically to the highest standards, yielding many new insights that she has also turned into very strong publications. PhD thesis clearly fulfils all criteria needed and I fully and without any hesitation recommend it strongly for the successful defense procedure.

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Roman Hobza, Ph.D.