

Assessment of the thesis entitled ‘Genome size studies in plants – from intraspecific variation to ecological consequences’ by Magdalena Lucanova

The thesis presents the results of a series of distinctive and interesting case studies (six in total) which aim to (i) explore the role of genome size across different environmental scales and its impact and relevance to a range of ecological processes (case studies I to V), and (ii) develop new approaches to preserving plant material suitable for flow cytometry to extend the application of this method to environments where the collection of fresh plant material is challenging. All the case studies are underpinned by very extensive and high-quality genome size datasets that have been generated by the candidate, together with a range of different analytical and statistical approaches to explore the biological significance of the data. It is to be commended that most of the work presented has already been published, with papers dating from 2010 – 2015. Only the first case study remains to be submitted.

Given the long period over which the data have been generated, analysed and published, it is apparent that, for example, the statistical approaches, and the discussions of some of the Case studies do not reflect the current status of knowledge in these particular areas of research, especially the earlier papers (e.g. Cases studies IV and V, published in 2010). To some extent this is addressed in the Introductory chapter which provides an overview of the field of genome size research, with particular focus on the areas addressed in the six case studies presented. Nevertheless, while this introduction is indeed broad, it is noted that, perhaps some of the more recent and significant publications in the field are missing which is a shame. For example, in the discussion on intraspecific variation in genome size, it is surprising that there is no mention of recent papers such as that of Bilinski *et al.* (*PLoS Genetics* **14**: e1007162; 2018). In addition, it would have been nice to see some discussion of the more recent literature and the new insights they bring to the Case studies in the final chapter ‘Key results and conclusions’. For example, in the discussion of Case study V (page 157) on the role of genome size in naturalization and invasiveness of species in the Czech flora (published in 2010), it would have been nice to see some mention of the relevance of more recent studies on the topic such as Schmidt *et al.* (*Ecology and Evolution* **7**: 10289-10300; 2017). Finally, it would have been good to see some discussion as to how the development of new molecular, statistical, and phylogenetic approaches may enhance the understanding and interpretation of the biological significance of the data generated. (Perhaps these suggestions reflect differences in the style of a Czech PhD with that of from the UK, in which case, I apologise for mentioning this.)

Overall, the thesis represents a nice collection of studies that have clearly contributed towards advancing our understanding in several areas of plant genome size research. Certainly, it is clear that the importance of the published papers is already being recognised by the research community, with the number of citations for the five papers ranging from 10 to 92 (Google Scholar, 15th September 2018). This, together with the candidate’s h-index of 15, which is strong for a scientist at this stage of a scientific career, especially since it that includes a period of maternity leave, suggests that Magdalena Lucanova is a good candidate who is worthy of a PhD.

General questions:

1. What did you enjoy most about your thesis – and what do you consider to be the most important findings that have made the biggest contribution to the field of genome size research?
2. Given your clear expertise in generating such high-quality genome size data (i) what do you consider are the most important factors that need to be taken into consideration in order to

generate reliable genome size data, and (ii) where do you see the next big advances to be made in this area which will advance the field of plant genome size research.

3. To what extent do you think the findings from your research presented are applicable across other angiosperms and, indeed to other land plant groups such as gymnosperms, monilophytes and bryophytes?
4. Do you think intraspecific variation (excluding polyploidy) in genome size is indeed rare as stated in the Introduction or are there just insufficient number of thorough studies conducted to the highest standards (as demonstrated by your own exquisite skills) to show that it is actually widespread?
5. The thesis has examined genome size evolution across different scales – from the intraspecific level (Case studies I, II and III) to between genera (Case study IV) and across whole floras (Case study V). What do you think are the main evolutionary drivers underpinning the diversity of genome sizes encountered at these different scales– and to what extent do you think you're your results contribute to the explaining why most angiosperms have small genomes.