Thesis Plan / Rose McKeon / Sep 2019

According to Ramsey and Ramsey (2014), polyploidisation is thought to be fundamental in the diversification of plant species due to polyploidy being a ubiquitous feature in the lineages of most plant taxa. While polyploids have been studied for over a century, the factors that drive the success of their establishment in the face of reproductive disadvantages and high extinction rates are still unclear. Polyploidisation has been found to coincide with around 25% of plant speciation events (Wood et al. 2009), however, a study by Arrigo and Barker (2012) on the extinction rates of polyploids has suggested that many of these new lines are evolutionary dead ends. They conclude that polyploids tend to become extinct at the establishment phase due to reproductive disadvantages such as lack of mates, diploid pollen swamping, and triploid sterility. Therefore, understanding demographics at the establishment phase is critical to predicting polyploidisation of plant species. Benefits associated with polyploidy may offset these costs: Polyploids are frequently linked with distinct traits such as “gigas effects”, which include increases in plant organs, reversal of selfing inhibition, enhanced capabilities for buffering of deleterious mutation (due to increased heterozygosity), and hybrid vigour (heterosis) (Woodhouse et al. 2009; Ramsey and Ramsey 2014). These traits are thought to overcome the reproductive disadvantages of polyploidy and instead make this mutation key to the invasive and adaptive potential of plants, ultimately shaping broader patterns of plant diversification.

In natural populations, polyploids maintain distinct spatial distributions relative to progenitors and other diploids, suggesting the importance of polyploidy as a mechanism of ecological divergence (Ramsey and Ramsey 2014). Recent niche modelling, however, has not supported this theory and proposes that glacial retreat and environmental disturbance (conditions which correlate with increased polyploid frequency) may be more influential (Godsoe et al. 2013). This research will aim to advance theoretical understanding of the evolution of polyploids in plant systems by examining the interplay between whole-genome duplication events, environmental factors and traits which embue individuals with costs/benefits. **The exact question for my project is not compeletely nailed down. I'm attempting to find the key gap in our undestanding of the theory in order to choose an appropriate question to test.**

0.1 Methodology:

This study aims to advance theoretical understanding of the evolution of polyploids by means of an individual based model (IBM), a method which has not yet been fully applied to this problem. By simplifying a complex biological system into a model one, then manipulating its variables and underlying biological processes, biological patterns (such as species distribution) can be revealed. Analysis of these patterns can make sense of relationships which are hard to pinpoint in natural environments.

The model will be developed based on the DisturPloidy R package which I created over the summer. Additions/improvements will be made according to the specifics of the research question. Simulated plants will be initialised on a spatially explicit landscape. Their genomes will be modelled so that polyploidy can occur mechanistically. Fitness costs and benefits of polyploidy will also be represented genomically so these traits can arise naturally, vary between individuals and be subject to selection. Repeated simulations will be run with atleast 30 replicates per simulation. Method of analysis will depend on the exact requirements of the question, but bootstrapped confidence intervals of the replicates will no doubt be created.

0.1.1 Ethics:

There are no ethics concerns for this project.

0.1.2 Timetable of Planned work:

I have set up a private GitHub repository for the writing of my thesis. Project management will be carried out here; milestones, project cards, and issues already in progress have been added accordingly. I have invited you as a collaborator so you can access all aspects here.

0.1.3 Summary of Resources Required:

I will need computing power to run replicate simulations.

References

Arrigo N., Barker M.S. (2012) Rarely successful polyploids and their legacy in plant genomes. *Current Opinion in Plant Biology*, 15 (2), pp. 140–146.

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Ramsey J., Ramsey T.S. (2014) Ecological studies of polyploidy in the 100 years following its discovery. *Phil Trans R Soc B*, 369.

Wood T.E., Takebayashi N., Barker M.S., Mayrose I., Greenspoon P.B., Rieseberg L.H. (2009) The frequency of polyploid speciation in vascular plants. *Proceedings of the National Academy of Sciences of the United States of America*, 106 (33), pp. 13875–9.

Woodhouse M., Burkart-Waco D., Comai L. (2009) Polyploidy. *Nature Education*, 2 (1), p. 1.