

Mutation Accumulation Experiments in *Arabidopsis thaliana* Natural Populations

Mao-Lun Weng¹

@MaoLunW

mweng@westfield.ma.edu

Jon Ågren² Eric Imbert³ Detlef Weigel⁴ Claude Becker⁵ Henning Nottbrock⁶ Matthew Rutter⁷ Charles Fenster⁸

¹ Department of Biology, Westfield State University, Westfield MA

² Department of Ecology and Genetics, Uppsala University, Sweden

³ Institute of Evolution Sciences of Montpellier, France

⁴ Department of Molecular Biology, Max Planck Institute for Developmental Biology, Tübingen, Germany

⁵ Gregor Mendel Institute of Molecular Plant Biology, Austrian Academy of Sciences, Vienna BioCenter (VBC), Austria

⁶ Department of Plant Ecology, The University of Bayreuth, Germany

⁷ Department of Biology, College of Charleston, Charleston SC

⁸ Department of Biology and Microbiology, South Dakota State University, Brookings SD

Although the mutation spectrum has been documented in a variety of species, the assessment of spontaneous mutation from natural populations is still limited. To assess the mutation spectrum from natural populations, we generated 374 mutation accumulation (MA) lines of *Arabidopsis thaliana* that were derived from eight natural founder individuals collected in Sweden and France. With whole genome sequencing and reciprocal transplanting, we aim to investigate:

1. Whether the mutation spectrums were genotype background dependent?
2. How do mutational effects on fitness change between environments?

Single nucleotide mutation (SNM) rate varied among genomic regions (Fig. 1) with the highest rate at the TE position consistent with Columbia accession MA line (Weng et al. 2019). SNM rate did not differ significantly among natural founder populations, but the indel mutation rate was higher in natural population than Columbia MA lines (Fig. 2).

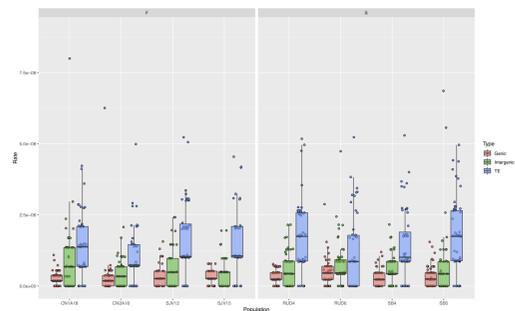


Figure 1: Single nucleotide mutation rate at different genomic regions

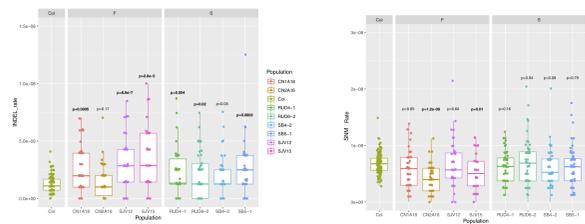


Figure 2: SNM and INDEL mutation rate from different populations

Single nucleotide mutation rate does not differ between populations but indel mutation rate does

Mutation becomes more deleterious at stressful environments due to the shift of fitness landscape

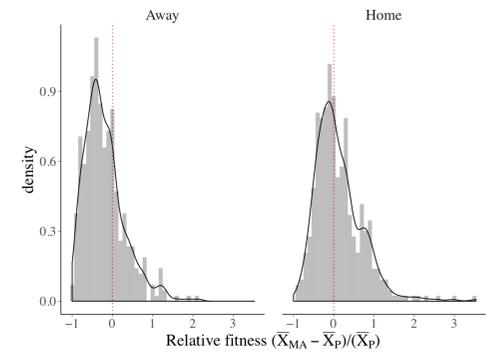


Figure 3: Relative fitness at home and away field sites

Mutational fitness effects biased toward deleterious at away site (Fig. 3) can be explained by the reduced and shifted fitness landscape (Fig. 4). At away site the number of MA lines that have lower fitness than the founder increased (Fig. 3). When the measurement of stress was accounted for, we showed that mutational variance and selection strength was increased under stress condition (Fig. 5) consistent with (Agrawal and Whitlock 2010). In addition, using non-fitness traits as approximate, we showed that fitness optimum at away site is reduced and shifted compared to the home site.

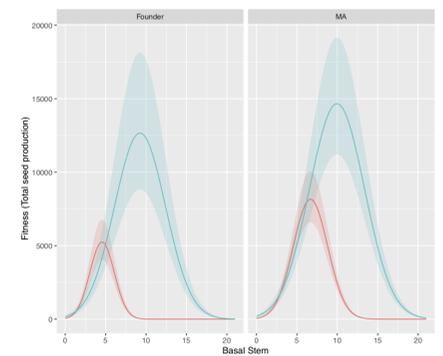


Figure 4: Fitness landscape at home and away field sites

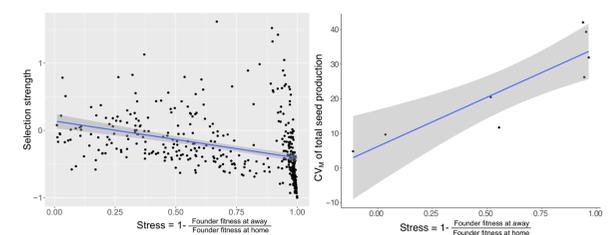


Figure 5: Correlation between stress and selection strength and mutational variance

The poster design was inspired by Mike Morrison and produced by posterdown package



Agrawal, Aneil F., and Michael C. Whitlock. 2010. "Environmental Duress and Epistasis: How Does Stress Affect the Strength of Selection on New Mutations?" *Trends in Ecology & Evolution* 25 (8): 450–58. <https://doi.org/10.1016/j.tree.2010.05.003>.

Weng, Mao-Lun, Claude Becker, Julia Hildebrandt, Manuela Neumann, Matthew T. Rutter, Ruth G. Shaw, Detlef Weigel, and Charles B. Fenster. 2019. "Fine-Grained Analysis of Spontaneous Mutation Spectrum and Frequency in *Arabidopsis thaliana*." *Genetics* 211 (2): 703–14. <https://doi.org/10.1534/genetics.118.301721>.

