

Re-winding the tape: experimental evolution of resistance to herbicides

Supervisory team:

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Project description:

The evolution of resistance to herbicides in plant (weed) populations is a classic example of rapid, human-induced evolution. Herbicide resistance is a global phenomenon, causing significant economic impacts through the loss of weed control in agroecosystems. Two mechanisms of resistance have been described; target-site resistance (TSR) which is conferred by single nucleotide polymorphisms (SNPs) in herbicide target genes, and non-target site resistance (NTSR) which involves the upregulation of metabolic enzymes that underpin detoxification and cellular sequestration of herbicides. A major remaining challenge is to understand the fitness landscape and evolutionary trajectory of herbicide resistance in plant populations under contrasting selection regimes to inform best management practices to slow or mitigate the evolution of resistance.

These studies of 'evolution in action' are hampered in higher plant populations by long generation times, small experimental population sizes and often, by a lack of molecular genetic resources. In previous research, we have established *Chlamydomonas reinhardtii* as a suitable model organism to study the experimental evolution of herbicide resistance. This work focused on phenotypic characterisation of evolved *Chlamy* populations following a series of selection experiments that explored the impacts of herbicide cycling (Lagator et al., *Evolutionary Applications*, 2012), mixtures (Lagator et al., *New Phytologist*, 2013) and sequences (Lagator et al., *Proceedings of the Royal Society B*, 2014) on evolution of resistance. We also explored the impacts of sex and migration on resistance evolution (Lagator et al., *Evolution*, 2014).

A full genome sequence is available for *C. reinhardtii* and we are now in a position to extend these studies to identify the genomic basis of adaptation to herbicides. These studies will enable us to identify the mutations that underlie de novo evolution of resistance, establish genotype-phenotype relationships and quantify co-variation with other life history traits, including fitness costs and cross-resistance between diverse herbicide modes of action. Having established the mutations responsible for adaptation to herbicides and their phenotypic consequences, we will be able to perform a series of hypothesis-driven selection experiments to understand interactions between the fitness landscape for herbicide resistance and the efficacy of different management strategies to slow or prevent the evolution of resistance.

This exciting inter-disciplinary project will bring the combined power of experimental evolution and genomics to bear on a pressing issue in global food security, addressing fundamental questions relating to the evolutionary dynamics of adaptation to novel stresses and applied questions concerning pesticide resistance management.