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Heritability and Genetic Correlation in Experimental and
Natural Populations of *Arabidopsis Thaliana*

Plant genetics studies using the model species *Arabidopsis thaliana*, thale cress, tend to focus on the exotic or rare genes in which mutations cause serious changes in a plant's appearance, growth and life cycle, overlooking the many genes that regulate far more subtle aspects of the phenotype. My research employs a large random sample of knock-out mutant plants from a comprehensive mutant library to investigate these less notorious genes on a population level. In any population of phenotypically variable plants, expression of traits depends on both underlying genetic variation and environmental variation. Phenotypic plasticity is an organism's capacity to change its phenotype in response to environmental changes. The phenotypic plasticity of a trait does not diminish the importance of the trait's heritability, a quantification of the proportion of genetic variation that contributes to phenotypic variation. Also critically important is genetic correlation, the potential for pairs of traits to be strongly related to each other and therefore co-inherited and paired evolutionarily. My analyses estimate heritabilities and genetic correlations using data from an experiment that grew 27 single knock-out mutants and 26 non-mutants natural ecotypes in the constant growing conditions of a growth chamber and a much more variable greenhouse environment. Many of the traits showed high heritability. The genetic correlation between rosette diameter and number of good fruits showed constancy across environments, remaining positive across both environments. The correlation between days to bolting and mean fruit length changed from being negative in the greenhouse to being positive in the growth chamber. We scored several fitness components such as fruit productivity, timing of reproduction, and the sizes of leaves and fruits. A focus on heritability and genetic correlation is relevant not only for evolutionary biology but also for plant breeders selecting for, say, the largest tomatoes but inadvertently selecting for a much longer flowering period, requiring adjustment in an entire crop rotation schedule. Working with this annual model organism allows me to study the same traits in a tiny plant with a very short life cycle, yet agriculturally relevant especially to plants in the *Brassicaceae* family such as broccoli or canola oil. Finally, a better understanding of the joint impacts of genetics and environment on a plants' phenotypes could lead to smarter and more efficient farming and vegetation management practices, especially in this time of climate change.