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## The role of allele specific expression (ASE) in genomic evolution

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Evolutionary adaptation to abiotic stresses is essential for the survival of living organisms. Previous studies have tested the evolutionary adaptation and phenotypic response of populations of the nematode worm *Caenorhabditis remanei* to heat stress. Genes responsible for growth, metabolism and development showed higher expression rates in populations under constant heat stress when compared with the control group. However, transcriptional expression in the evolved groups did not show significant differences in comparison with the ancestral population. These results suggest that processes other than transcriptional regulation may be responsible for rapid evolutionary adaptation. However, because neither the overall genes' expression rate nor the expression level of the heat stress response genes changed, changes in the allele frequencies, which resulted in structural and functional changes in stress response proteins, and/or alteration in the other stress response pathways may be responsible for the observed adaptation to environmental stress. This hypothesis is supported by a separate study of allelic expression in barley, which found that gene expression could be altered during adaptation to drought stress. The main goal of my current project is to analyze transcriptomic data of ancestral and stress-evolved populations of *C. remanei* and evaluate the role of ASE in the evolution of stress response, which will be presented during the poster session.

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