

Resistance to Oxidative Stress in *Drosophila*: Providing Insight Into Complex Disease

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Aerobic organisms are susceptible to damage by reactive oxygen species. Oxidative stress resistance is a quantitative trait with population variation attributable to the interplay between genetic and environmental factors. *Drosophila melanogaster* provides an ideal system to study the genetics of variation for resistance to oxidative stress. We used 167 wild-derived inbred lines of the *Drosophila* Genetic Reference Panel for a genome-wide association study of acute oxidative stress resistance to two oxidizing agents, paraquat and menadione sodium bisulfite. For a subset of 40 of the DGRP lines we have also collected basal whole transcriptome data in order to identify natural variation in transcript abundance associated with resistance to oxidative stress. Lastly, we have assayed the transcriptional response on both treatments during the first 10 hours. Using these tools we have identified enriched cellular networks comprising DNA metabolism and neuronal development, consistent with targets of oxidative stress-inducing agents. These results form the basis for future translational studies to identify oxidative stress susceptibility/resistance genes that are evolutionary conserved and might play a role in human disease.