
Genetic variation of transcriptomic expression in *Lymnaea stagnalis* exposed to a redox-cycling pesticide

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Abstract

Population response to stress may have a genetic component which, if additive, forms the basis for adaptive evolution to local conditions. Although adaptive processes have been traditionally investigated through integrated responses involving polygenic characters, a growing number of studies now focuses on gene expression. Indeed, like quantitative traits, gene expression may entail a heritable genetic component, and thus have some evolutionary adaptive potential. Genetic variation in gene expression has been found in various taxa, and gene expression is thus expected to be at least partly influenced by evolutionary forces. Although stabilizing selection seems to be the primary force acting at this level, this hypothesis may sometimes be difficult to disentangle from neutrality, and may be challenged by new findings in population genomics. We investigated the evolutionary potential of transcriptomic expression induced by a pro-oxidant herbicide, diquat, using lines from natural populations of the pond snail *Lymnaea stagnalis*. Populations exhibited significant neutral differentiation (microsatellites) as well as genetic adaptive divergence in several life history traits (*QST-FST*). In the laboratory, F1 families were exposed during five hours to 222 µg/L diquat *vs* control conditions to assess transcriptomic reaction norms. RNAseq was used to estimate diquat-induced differential expression. DESeq2 analysis showed that molecular responses depend highly on the source population, whereas common effects were restricted to a very small subset of transcripts. Most DE transcripts were down-regulated, and involved in various molecular pathways, while those found up-regulated in all tested populations matched

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with genes involved in glutathione metabolism, oxidative phosphorylation, signal transduction, oxygen transport, ATP binding, transcription factors, and uncharacterized proteins. A remarkable consistency was found between neutral F_{ST} and correlation of expression, suggesting a predominant role of random genetic drift on global gene expression. Results will be discussed in terms of relevance to ecological risk assessment.