

Expressions of *Diorhabda*

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The evolutionary ecology of *Diorhabda carinulata* (Saltcedar leaf beetle) in its new range, the Southwestern United States, remains unstudied with regard to changes in genetic expression profiles. Native to regions of northern Africa, the Middle East and Asia, recent introductions of the beetle in novel environments are likely causing rapid evolution in distinct bio-molecular pathways. Populations of *D. carinulata* have been established in the western United States as a biocontrol of *Tamarix* spp. (Saltcedar). In the current study we shall attempt to characterize differences in gene expression between two distinct populations of *D. carinulata* (i.e., Fukang and Chilik) that were released at specific locations in Colorado, Nevada and Wyoming. Total RNA shall be extracted from brains of adult females awakened from diapause at the Colorado Department of Agriculture Insectary and compared to those harvested from the field. Suppressive Subtractive Hybridization (SSH) will be used to assess differences in expression between these populations. Observed differences in expression will be independently confirmed via PCR analysis. Genes differentially expressed between these populations will be fully characterized with regard to known molecular pathways. The results from the current study, when combined with the results of a planned future study utilizing direct RNA sequencing microarrays, will provide the scientific community with a baseline transcriptome for these populations, thus enabling investigators the opportunity to document how this species evolves in a novel environment. Once we have assembled the entire dataset, we shall also assess differences in expression with regard to photoperiod, voltinism and diapause and attempt to correlate the observed molecular differences with rates of tamarisk defoliation in the field.