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**"In an Earlier Study (BONO et al., 2011 PNAS) My Lab has Examined the Gene Expression Changes Occuring in the Lower Reproductive Tract of the Female *Drosophila Mojavensis* (Cactophilic Fruit Flies) Immediately Following Copulation"**

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### **Faculty Mentor:**

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### **Project Summary:**

In an earlier study (Bono et al., 2011. PNAS) my lab has examined the gene expression changes occurring in the lower reproductive tract of female *Drosophila mojavensis* (cactophilic fruit flies) immediately following copulation. Furthermore, we observed that in addition to the previously known transfer of proteins and sperm through the ejaculate, males apparently also transfer RNA transcripts (mRNA). To examine the role of these transcripts and to determine if they are being translated into proteins we have set out to isolate actively translating ribosomes from the lower reproductive tract tissue of *D. mojavensis*. As ribosomes are processing mRNA transcripts approximately 24 base pairs of sequence is protected within the ribosome structure. We have isolated ribosomes, removed any mRNA overhang and extracted the protected 24 base pair fragments. These fragments represent and actively translated mRNA. We have begun to sequence these fragments using next generation sequencing technology. By the time all the sequencing is completed millions of 24 bp sequence fragments will be produced which will assist in identify genes. These genes will be cross-referenced with our prior study to determine if the transcripts being transferred are being translated.

### **Student Duties:**

The most appropriate student for this project would be a Biology Major/Computer Science minor or vice-versa, but I am willing to look at other interested students. Participant must be interested in utilizing computational tools to answer important biological questions. Under my supervision the student will learn the latest bioinformatic tools to identify the genes actively being translated in the reproductive tract of *D. mojavensis*. Additionally, the next generation sequencing results will allow the student to determine the level of translation, by essentially examining how often a sequence fragment is found. The student will utilize both the computational resources in the lab as well as the Alabama Supercomputer Center. The student will be an active participant in the bioinformatic analysis as well as participate in the collection of further lower reproductive tract samples.

### **Mentor Supervision and Interaction:**

I plan to guide the student throughout the project, although I will allow her/him the opportunity to determine paths of analysis and troubleshoot, which are valuable lessons in research. I will personally meet with the student once a week to allow her/him to update me in the progress of the analysis. This of course is in addition to sitting down with and going over the analyses methods. The ultimate goal will be to eventually produce a peer-reviewed publication in which the student would be an author. Lastly,

the student will give a presentation to the entire research group on the results of the summer work during one of the first weekly lab meetings of the Fall semester.