

Booth: 227

Conservation Genetics of *Penstemon Albomarginatus*

Presenter(s): Timothy NeCamp, Susan Fassnacht

Advisor(s): Andrea Wolfe

Biological Sciences

Laura Kubatko

Mathematical and Physical Sciences

*Penstemon albomarginatus* is a rare flowering plant endemic to the Mojave Desert of Nevada, California and Arizona. This unique plant has evolved adaptations to its shifting sand habitat. Due to the plant's already limited distribution and threats caused by human development, *P. albomarginatus* is an important focus for conservation efforts. By understanding the genetic structure of *P. albomarginatus*, the degree of population isolation and genetic diversity can be analyzed. Eight microsatellite loci were used to determine the genotypes of 230 individuals collected from 12 different populations distributed across their range. By applying a variety of statistical approaches and microsatellite analysis programs, information was obtained on various population parameters and the overall population structure. We report on the genetic differentiation both within and between these 12 populations, as well as discuss inferences about past demographic events. In this project, we consider the implications of our study to future conservation efforts for *P. albomarginatus*.

Booth: 269

Crystallization of a Bacterial Single Stranded Annealing DNA Repair Protein

Presenter(s): Alburuj Rahman

Advisor(s): Charles Bell

Biological Sciences

Single-stranded annealing (SSA) protein is a protein that binds to single-stranded DNA (ssDNA) and participates in pairing homologous DNA and double-stranded breaks. I studied RecT and  $\beta$  proteins from bacteria *Escherichia coli*. The human equivalent Rad52 protein promotes the same reactions as RecT and  $\beta$ , and is involved in multiple DNA repair pathways. Cells and DNA have mechanisms to repair mutations but failure to do so may lead to cancer. Chemotherapy requires the study of repair mechanisms. Therefore, it is important to understand the DNA repair processes of RecT and  $\beta$  protein. Electron Microscopy studies propose that the proteins form oligomeric rings and helical filaments, but no information on the fold of the proteins and on the accurate DNA binding sites is available. However, this can be obtained from high resolution images of a protein's structure. To determine the mechanism by which SSA proteins bind to ssDNA and promote the annealing of complementary DNA and study how proteins recognize and repair damaged sites of DNA in cells, crystals were produced from RecT and  $\beta$  protein and the structure was studied through x-ray diffraction. A sample of RecT is purified and screened to grow initial crystals whose conditions are optimized to grow larger crystals. Once large crystals form, x-ray diffraction is used to solve the three-dimensional atomic structure of the protein in complex with DNA substrates. I have formed the first large crystals of RecT that can diffract 7 Angstroms, which is a significant step toward understanding the protein repair mechanism needed in applications such as cancer treatment.

Booth: 200

Determining the cDNA Sequence of the Gene Clock in *Culex Pipiens*

Presenter(s): Allison Barnes

Advisor(s): Megan Meuti

Biological Sciences

The Northern House mosquito, *Culex pipiens*, is the major vector of West Nile Virus. Diapause is an arrested state of development, which insects enter to survive unfavorable conditions. *C. pipiens* enters an adult diapause in response to short daylength in the late larval and early pupal stages. How insects interpret daylength to program diapause is unknown. Researchers have speculated that clock genes, which regulate daily behavior, might also be involved in measuring daylength. If clock genes are involved in programming diapause, the sequence of circadian genes, such as *Clock*, may differ between mosquitoes that enter diapause (*C. pipiens*) and those that do not (*C. quinquefasciatus*). To test this hypothesis, we extracted RNA from 50 female mosquito heads,