

**Mitochondrial genetic diversity in three isolated populations of Mexican Fruit Flies (*Anastrepha ludens*)
in the Rio Grande Valley**

Kari Skalitsky¹, Raul Ruiz-Arce², Hugh E. Conway², Sarah Kowalski¹, Christopher Vitek¹

1Department of Biology, University of Texas-Pan American, Edinburg, TX

2United States Department of Agriculture, Animal and Plant Health Inspection Services, Plant Protection and Quarantine, Mission Laboratory, Edinburg, TX

The Mexican Fruit Fly (*Anastrepha ludens*) is a major pest of citrus and mango. It has a wide distribution in Mexico and Central America. Occasional infestations occur in California, Florida, and in the lower Rio Grande Valley region in South Texas. In an effort to reduce the infestations by Mexican fruit fly (Mexfly), the USDA APHIS PPQ along with Texas Department of Agriculture established a Preventive Release Program that relies on the Sterile Insect Technique (SIT). The Willacy strain flies originating from Willacy County, TX are currently being mass reared at the Mexican Fruit Fly Mass Rearing Facility at Moore Airbase in Edinburg, Texas. However, various strains of Mexfly are often tested prior to being mass reared in order to determine the most appropriate set of individuals to release. Distinguishing among the various strains is important because traits associated to the competitive nature of the fly that are beneficial to management programs may be strain-specific. For the present study, we examine the utility of the COI barcode for distinguishing among three geographic strains of Mexfly. A 592bp fragment from the COI mtDNA region was sequenced in 45 Mexflies. Flies were sampled from Willacy County, Donna and Mercedes for the current study. The collections revealed one haplotype, no variation. Our findings show that the COI region does not provide sufficient resolution to distinguish among the strains tested. Future work will utilize recently developed microsatellite molecular markers for distinguishing among Mexfly strains.