## BOLL WEEVIL (ANTHONOMUS GRANDIS) POPULATION GENOMICS AS A TOOL FOR MONITORING AND MANAGEMENT Tyler Jay Raszick Gregory A. Sword Texas A&M University College Station, TX Charles P.-C. Suh USDA-ARS College Station, TX Raul Ruiz-Arce

## Abstract

USDA-APHIS Edinburg, TX

Despite the success of eradication efforts across most of the cotton-producing regions of the U.S., the cotton boll weevil (Anthonomus grandis grandis Boheman) remains a major pest of cotton in much of the New World. The area along the Texas border with northern Mexico has been a particularly troublesome area for eradication efforts due to political and environmental constraints, and the fact that the region is the northern edge of the weevil's natural, sub-tropical range. In order to improve boll weevil eradication efforts, we have developed a robust population genomics approach to determine the genetic relationships and patterns of gene flow among weevil populations along the Texas-Mexico border. This approach enables identification of source populations for potential re-introductions in previously eradicated areas and helps guide control measures to reduce or prevent future reinfestations. Using double digest restriction site-associated DNA sequencing (ddRADseq), we generated 6901 SNP markers for 48 individual weevils from four major cotton-growing regions in northern and central Mexico, and from a domestic population in southern Texas. Despite limited sampling from Sonora (n = 5), Chihuahua (n = 4), and Durango (n = 5), we recovered estimates of both heterozygosity (H<sub>E</sub>, H<sub>O</sub>) and nucleotide diversity ( $\pi$ ) that were similar to those estimates from Tamaulipas (n = 16) and the domestic population in the Lower Rio Grande Valley (LRGV, n = 18). No populations appeared to differ with regards to the amount of within population diversity, and none appeared to deviate from the diversity estimates obtained from across all 48 sequenced individuals. Estimates of diversity were greater across all populations than they were within any one population, indicating that there is greater genetic diversity among populations than within any one population, which in turn, suggests some degree of population structuring. To test this hypothesis, we calculated two measures of pairwise population differentiation,  $F_{ST}$  and  $\rho_{ST}$ , for all five populations of interest. Both metrics of population differentiation showed that the Tamaulipas and LRGV populations are genetically indistinct, and likely represent two sampling areas from a single population that straddles the national border. We also found that the populations from Chihuahua and Durango are more similar to each other than either is to any of the other sampled populations. A principal components analysis (PCA) supported the results of our pairwise comparisons, and clearly illustrated the existence of three genetic clusters of populations that correspond to three geographic regions (western, central, and eastern) separated by two major mountain ranges. Our study provides evidence for the contiguousness of the weevil populations in southern Texas and northern Tamaulipas, but also reveals distinct geographical structuring of boll weevil populations in other areas of Mexico. Consequently, we believe that future eradication efforts in southern Texas and northern Tamaulipas need to consider an area-wide approach to successfully eradicate the boll weevil in both regions. We are in the process of expanding our geographic sampling across central and South America in order to completely resolve the population structure of this species across its entire range, as well as obtaining more specimens from the areas we had previously sampled. This will allow the application of a population level approach to management in all areas where the pest occurs, and allow for the identification of source populations when new or recurrent infestations occur