USING POPULATION GENOMICS TO REVEAL TEMPORAL PATTERNS OF HOST USE IN THE COTTON FLEAHOPPER (*PSEUDATOMOSCELIS SERIATUS*)

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<u>Abstract</u>

The cotton fleahopper (CFH), Pseudatomoscelis seriatus (Reuter, 1876) (Hemiptera: Miridae), is a pest of commercial cotton (Gossypium hirsutum L.) with over 100 known host plants across its range. Both adults and nymphs attack small, developing squares, leading to abscission of the square. A new transgenic cotton cultivar has been developed that has shown some resilience to CFH damage. However, due to potential host plant association which has been documented in this species, a genetically differentiated host-race may exist which is associated with cultivated cotton. If the CFH genotypes associated with cotton do not share gene flow with genotypes associated with other host plants, then this species could quickly develop resistance to the transgenic cotton. Because cotton is only available as a host plant during parts of the year, populations found on cotton must shift to alternative host plants outside of the cotton-growing season. However, whether this host shift results in gene flow between cottonassociated populations and those associated with other host plants is unknown. Woolly croton (Croton capitatus Michx.) is an important overwintering host plant that is hypothesized to be a year-end site of admixture between populations coming from a variety of different host plants, including commercial cotton. Using high-throughput sequencing, we have elucidated a temporal pattern of gene flow between a focal population of CFH in cotton interacting with populations of CFH that are associated with C. capitatus in the Brazos Valley, TX. We collected fleahopper nymphs from the focal cotton field three times, once each in the months of June, July and August, 2015. We also reared out nymphs from eggs collected at four surrounding croton sites in February, 2015. From these samples, we used double digest restriction site-associated DNA sequencing (ddRADseq) to generate 3107 informative SNP markers that were used for population genomic analysis. By comparing pairwise F_{ST} calculated from these markers across all eight collections, we revealed a mid-season host shift from cotton onto croton. In June, cotton and croton populations were significantly distinct from one another, and croton populations were not significantly different from each other. In July and August; however, there was no significant difference between croton-associated and cotton-associated populations. Furthermore, cotton populations collected in June, July, and August, were never significantly different from each other. This indicates that there is gene flow from cotton into croton during the middle of the cotton-growing season. Though fleahopper movement from cotton onto croton during the cotton-growing season is well documented, our study is the first that shows that this movement contributes to gene flow between the populations associated with the different host plants. Further directions for this work include expanding our sampling into other alternative host plants and into other geographic areas where croton may not be available.