USING HIGH TRHOUGHPUT SEQUENCING TO LINK COTTON FLEAHOPPER GUT CONTENT TO HOST PLANTS

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Abstract

The cotton fleahopper (CFH), *Pseudatomoscelis seriatus* (Reuter), is an early season cotton pest whose feeding can result in square abortion, irregular plant growth, and delayed plant maturity. This Texas native generalist has been documented feeding on over 160 host plants across 35 families. For the most part, identification of host plants was accomplished through field observation and/or controlled feeding studies under lab conditions. As an opportunistic or obligatory feeder, these results may not accurately represent the plant hosts used by the cotton fleahopper. Previous studies have demonstrated that it is possible to identify host plant families consumed by insects based on analysis of plant DNA found in the insect gut. In these studies, plant DNA was extracted from the gut of large chewing insects or whole small-bodied, sponging-feeding insects. We present a proof-of-concept study to determine if this technique can work in the cotton fleahopper, a small piercing-sucking insect. Initial tests were conducted on newly emerged nymphs reared solely on green beans or horsemint. Then sweep samples for nymphs were collected from horsemint, cotton, and croton. Finally, we collected nymphs weekly throughout spring from fields with known mixed plant compositions at various locations in the Brazos River Bottom. Nymph samples were stored in alcohol at -80°C until DNA was ready to be extracted. DNA was extracted with the Qiagen QiaAmp kit, quantified, and stored at -20°C. We found that plant DNA from the CFH gut was successfully amplified with chloroplast-specific primers using Polymerase Chain Reaction (PCR). This was documented by running the PCR product on a 2% agarose gel using electrophoresis. Future directions are to prepare amplicon libraries, sequence the chloroplast DNA obtained from field-collected CFH on the Illumina MiSeq, and BLAST results to a sequence database to identify host plants to the family or species level. Results will be cross-referenced with plant composition from the location nymphs were sampled to validate the families that were detected. Applying this method to the CFH may give insight as to what adults fed on before infesting cotton or what nymphs developed on in fields of mixed composition. More importantly, this process may also prove useful for identifying host plants used by other piercing-sucking pests such as lygus and stink bugs.