Detection of Bemisia Tabaci Meam1 and Med Cryptic Species in Oklahoma

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Introduction

- *Bemisia tabaci* (Gennadius) (Hemiptera: *Aleyrodidae*) are small pests (1-2m in length) that rapidly develop insecticide-resistance.
- Thus, causing difficulties controlling populations from infesting targeted plants i.e., pepper, sweet potatoes, cucumber, tomatoes, beans, hibiscus, etc.
- Two cryptic species of *B. tabaci* cause agricultural damage in the U.S, B. *tabaci* MEAM1 (Middle East Asia Minor 1, also called biotype B) and *B. tabaci* MED (Mediterranean, biotype Q).
- *B. tabaci* feeding causes black sooty mold to build up on leaves, preventing photosynthesis, decreasing efficiency of affected crop.

[Photo: Tomasz Klejdysz/ Shutterstock.com]

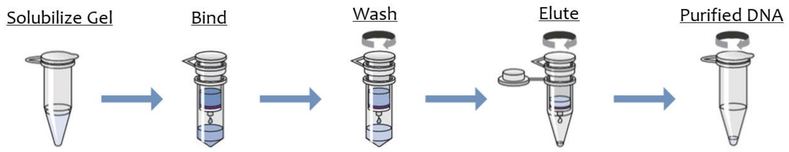
Figure 1. Close-up picture of a *Bemisia tabaci* (Whitefly)

Materials and Methods

Sample Collection and RNA Extraction:

Figure 2. Flow chart of methods used for the detection and identification of MEAM 1 and MED

Gel Purification of Amplified PCR Products:



- All DNA samples were first subjected to PCR analysis to differentiate MEAM1 from MED using the primer pair Bem23Fand Bem23R, which amplifies a microsatellite locus of about 200 bp or 400 bp for MEAM1 versus MED, respectively (De Barro et al. 2003, Kontsedalov et al. 2012).
- The generic insect primers C1-J-2195 and TL2-N-3014 (Table 2) were also used to amplify a fragment of the mtCOI gene (Frohlich et al. 1999). The PCR products were visualized by electrophoresis in 1% agarose gel stained with SYBER Safe DNA Gel Stain (Invitrogen).

Figure 2. Sampled B. tabaci with glass pipette connected to tubing secured with gauze filter to prevent escape.

Results

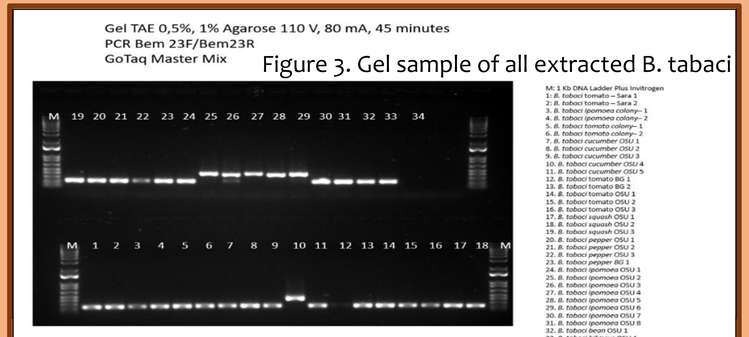


Figure 3. Gel sample of all extracted B. tabaci

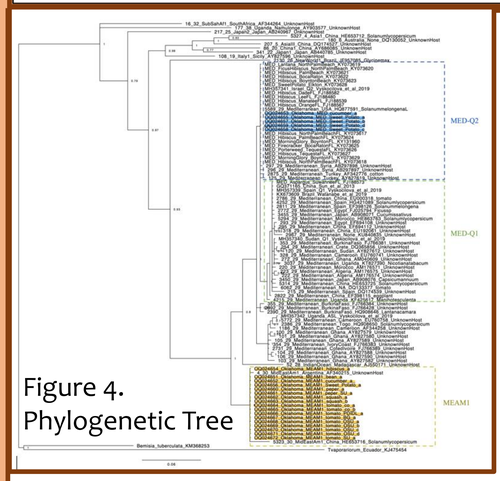


Figure 4. Phylogenetic Tree

Fig 3. Gel sample sequences match up with either MEAM 1 or MED. Any raised sequence translates as MEAM otherwise, all samples were MED.

Fig 4. The mtCOI fragment sequences ranged from 602 to 625bp in length. Multiple sequence alignment was prepared using MAFFT (Katoh and Toh 2008) within the Geneious 9.1.8 software. Subsequently, Bayesian analyses were conducted using Mr Bayes v. 3.2.2 (Ronquist and Huelsenbeck 2003) and Trees were visualized, edited, and rooted using FigTree v1.4.4.

Objective

- Identify population of *B. tabaci* cryptic species in Oklahoma and ecological niches of the different cryptic species

Conclusion

1. Prior to our findings, *B. tabaci* MED hadn't been reported in the state of Oklahoma
2. The correct identification of *B. tabaci* cryptic species contributes to structure management strategies, identifying the ecological niches, and pest movement.

References

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