9.17 Molecular Characterization of a New Entomopathogenic Fungus *Isaria poprawskii*: A Potential Biocontrol Agent for *Diaphorina citri*. Development of *Isaria*-Specific Molecular Markers

de León, J.H.1, Cabanillas, H.E.1, Humber, R.A.2, Murray, K.D.1, Moran, P.1, Jones, W.A.3

1USDA, ARS, Weslaco, TX, USA
2USDA, ARS, Ithaca, NY, USA
3USDA, ARS, Stoneville, MS, USA

We genetically characterized *Isaria poprawskii* sp. nov., a new entomopathogenic fungal species similar to *Isaria javanica* (= *Paecilomyces javanicus*). Biological, ecological, and morphological data will be presented elsewhere. The fungus was discovered during natural epizootics on the sweet potato whitefly (*Bemisia argentifolii*) in the Lower Rio Grande Valley of Texas (LRGV), USA. Phylogenetic analyses of *I. poprawskii* inferred from β-tubulin (TUB2) sequence data was performed along with standard *Isaria* TUB2 sequences obtained from GenBank. Fifteen previously un-sequenced fungal isolates, eight of which were field collected from the LRGV, were also included in the analyses. *I. poprawskii* was shown to be closely related to *I. javanica* ex-type; however, it formed its own unique clade, thus confirming its status as a new fungal species. In addition, our analyses confirmed that *I. poprawskii* could be recovered from the fields of the LRGV. The results showed that both *I. javanica* and *I. poprawskii* are present in the LRGV in sympatry. Polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) diagnostic assays reliably distinguished isolates belonging to the *I. javanica* and *I. poprawskii* clades. Inter-simple sequence repeat-polymerase chain reaction (ISSR-PCR) DNA fingerprinting also distinguished the ex-type isolates of *I. javanica* and *I. poprawskii*. PCR-RFLP assays were also developed toward *I. fumosorosea* and *I. tenuipes*, and the four assays were tested for their utility on important isolates presently being used in biocontrol programs against *Diaphorina citri*. These assays, along with the phylogenetic data, uncovered 11 misidentified fungal isolates. Correct identifications are critical to biological control programs.