XYLELLA FASTIDIOSA GENES AND PHENOTYPES RELATED TO HOST SPECIFICITY

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ABSTRACT
Xylella fastidiosa (*Xf*) strains differ in host specificity, although the molecular basis of the specific plant-bacteria interactions has not been identified. There is also evidence of variability in host range among isolates collected from within the same host species. Due to the lack of knowledge about the relationship between host specificity and genetic variability among *Xf* strains, this project was implemented to identify traits involved in *Xf* host preference. A collection of *Xf* isolates was screened for genetic and phenotypic characteristics that may be related to the interaction with the host. The preliminary collection consists of 24 *Xf* isolates collected from diverse plant hosts and multiple geographic locations in the US. For the genetic characterization, Multi Locus Sequence Analysis (MLSA) was performed using 10 candidate environmentally-mediated genes. Selected genes are hypothesized to be influenced by environmental factors and include genes related to surface attachment, motility, virulence, chemotaxis, and membrane transport functions. Primers for PCR amplification of these genes were designed and validated, and phylogenetic analyses were conducted on sequence information obtained from the amplified genes. For phenotypic characterization, traits related to interaction with the plant hosts and insect vectors, such as twitching motility and attachment, were analyzed *in vitro*. Preliminary genotypic and phenotypic results indicate that differences in environmentally-mediated gene sequences and differences in the motility and attachment of *Xf* isolates are related to the host plant from which the isolate was collected. Future expansion of this work will include adding more strains to the culture collection and including new genes and phenotypic traits in the analysis.

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