

Phenotypic characterization of a New York *Phytophthora capsici* field population

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*Phytophthora capsici* is the oomycete pathogen responsible for Phytophthora blight. This vegetable disease causes significant losses to crops in the Solanaceae, Cucurbitaceae and Fabaceae families. Flooding events in the northeast, in recent years, have introduced *P. capsici* into growers' fields with no prior history of this pathogen. In addition, many growers are no longer able to use mefenoxam, a commonly used fungicide, to control *P. capsici*, due to an increase in the prevalence of pathogen insensitivity to this chemistry. Seventy isolates had been previously collected from a New York grower's field of mixed cucurbits that was infested with *P. capsici* for the first time. We assessed these isolates for several phenotypic traits: 1) sensitivity to mefenoxam; 2) growth rate; and 3) mating type. In addition, population structure was assessed using principle component analysis on genotypic data derived from genotyping-by-sequencing. Of the 70 isolates tested for sensitivity to mefenoxam, fifty-nine were sensitive, 3 intermediately sensitive, and 8 isolates were insensitive to the fungicide. Genotypic clustering was primarily consistent with mefenoxam sensitivity classification.