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Molecular Diagnosis of the Causal Agent of the Root and Corm Rot of Taro (*Colocasia esculenta*) in the Aunu'u Island of American Samoa

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ABSTRACT

Recently, taro (*Colocasia esculenta*) growers in Aunu'u have been complaining of a new disease characterized by the taro root and corm rot. *Pythium* spp. usually cause this type of disease. But, it was puzzling when the morphological features of the fungus isolated from diseased taros did not match those of *Pythium*. More sophisticated tools were needed. The objective of this study was to use molecular techniques for identification of this pathogen.

Potato dextrose broth (PDB) was inoculated with five agar plugs cut from one week-old pure cultures of the pathogen grown on potato dextrose agar (PDA). After 10 days incubation at 24 C, mycelia were collected by centrifugation, and genomic DNA was extracted, using the CTAB method. The DNA was used to PCR-amplify a fragment of the ITS-rRNA gene, using universal fungal ITS primers. The amplicons were sequenced with BigDye Terminator V3.1, and the reactions were shipped to Hawaii for resolution on a DNA analyzer. The Sequencher software was used to build a 795-nt consensus sequence, which was submitted for similarity searches, using the NCBI Blast program.

The Blast search returned *Phytophthora* taxon *cyperaceae* as the best match. This the first time this species of *Phytophthora* is implicated on taro disease.

Key Words: American Samoa, Aunu'u, *Colocasia esculenta*, Root and Corm Rot, Taro

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