

Pathotype dynamics and genetic variability of *Colletotrichum scovillei* causing pepper anthracnose in Taiwan

Zong-Ming Sheu, Ming-Hsieh Chiu, Reuy-Jean Chang, Jaw-Fen Wang, Lawrence Kenyon
World Vegetable Center, Taiwan, R.O.C

Purpose: Fruit anthracnose caused by *Colletotrichum acutatum* sensu lato has been known the main pathogen constraints pepper production in Asia including Taiwan. This study aims to clarify the species following the recent taxonomy updates and analyze the temporal and spatial distributions on the pathotype and genetic diversity of Taiwan populations.

Methods: A total of 168 isolates collected from main production areas of Taiwan were analyzed. The virulence of all isolates was tested by inoculating fruits of two differential host genotypes. Forty-four strains, arbitrarily selected from diverse geographic origin and collection time, were used for sequencing of the nuclear ribosomal internal transcribed spacer (ITS) and AFLP assay. Twelve representing strains were further chosen for fungal identification through multi-locus phylogenetic analyses using combined sequences of the ITS, the β -tubulin (TUB2), actin (ACT), calmodulin (CAL) and GAPDH genes.

Result and Conclusions: *C. scovillei* was identified and 3 pathotypes within the species were determined. Among these strains, 77 and 98 strains were CA1 and CA2 pathotypes, respectively. Only 11 strains were CA3 and all of them showed weak virulence on both genotypes. CA2 were more virulent than CA1 and caused susceptible reactions on a pepper genotype derived from PBC932, which was resistant to CA1. CA2 was first found in 1997 but soon replaced CA1 in many locations of Taiwan. Since 2000, CA2 predominated in southern (78%) and eastern (96%) Taiwan; however, the CA1 was dominant in central Taiwan (59%). AFLP analysis showed that CA1 were genetically diverse, whereas CA2 were homogenous, mostly clonal.