

Pathogenicity and molecular diversity of *Fusarium solani* from different cucurbits in Taiwan

Benjapon Sritongkam¹⁾, Wen-Hsin Chung^{1,3)}, Pei-Hsin Chung²⁾

¹⁾Department of Plant Pathology, National Chung Hsing University, Taiwan.

²⁾Taichung District Agricultural Research & Extension Station, Council of Agriculture Executive Yuan, Taiwan

³⁾Innovation and Development Center of Sustainable Agriculture (IDCSA), Taiwan

Purpose: *Fusarium solani* (Teleomorph: *Nectria heamatococca*) is the most worldwide distribution fungus caused in several economic plants. It was considered to be plant pathogen and saprophyte. Among the pathogenic *F. solani*, the *F. solani* f. sp. *cucurbitae* (FSC) is important pathogen to cause crown rot and fruit rot of several cucurbit plants. Two races of FSC have been reported that race1 cause crown rot, root rot, stem rot and fruit rot on cucurbit plant and race2 only cause fruit rot. The purpose in this study is to carry out the pathogenicity and virulence of *F. solani* isolates from different cucurbits and analyze its characteristics.

Methods: A total of 34 isolates of *F. solani* from stem and fruit of pumpkin, cucumber, luffa, bitter gourd and muskmelon were identified following morphology and ITS rDNA. For pathogenicity test, these isolates (1×10^6 spore/ml) were inoculated on stem with 2 to 3 true leaves of plants and fruits based on wound inoculation. The total DNA extraction followed to use 5-7 days old mycelia and be extracted by DNA extraction Kit. The races identification was used the specificity primers of Fsc1-EF1/Fsc1-EF-2 and Fsc2-EF1/Fsc2-EF3. The ITS rDNA and TEF-1 α gene were analyzed for the relationship between theses isolates.

Results and conclusions: The pathogenic test showed that the *F. solani* isolates from different cucurbits might have cross pathogenicity on different cucurbits. Races analysis demonstrated that most of isolates could not be detected by specific primers. The phylogenetic analyses indicated that *F. solani* isolates could not be formed as one molecular phylogenetic group. These results revealed that the *F. solani* isolates from different cucurbits are not monogenic pathogen in Taiwan.