

P55

Phylogenetic analysis of *Fusarium oxysporum* complex in Korea

Jae-Min Park, Jae-Dong Lee and Man Kyu Huh¹

Department of Micrology, Pusan National University, Busan

¹Department of Molecular Biology, Dong-eui University, Busan

The goal of this study was to determine that the phylogenetic analysis of *Fusarium oxysporum* and formae speciales. Identification of *Fusarium oxysporum* and formae speciales has been difficult due to confusing phenotypic classification systems. The genetic relationship of forty-one formae speciales of *Fusarium oxysporum* causing plant disease was determined by sequencing of Internal transcribed spacer region. ITS1, ITS2, 5.8S rDNA regions were amplified by PCR using ITS universal primers ITS1 and ITS4. The PCR products which has 550 bp long were sequenced respectively. Clustal G analysis of ITS sequencing data did not show any specific classification to explain phylogenetic relation of *Fusarium oxysporum* and formae speciales. For the accurate phylogenetic analysis the fusaric acid which is important secondary metabolite in *Fusarium oxysporum* and formae speciales was also examined. Summarize ITS sequencing data and fusaric acid analysis, the phylogenetic relationship of *Fusarium oxysporum* and formae speciales was still impossible to determine.