

## **Morphology and Molecular Systematics of *Alternaria* and Allied Genera**

Seung Hun Yu, Hye Sun Cho<sup>1</sup>, and Myung Soo Park<sup>2</sup>

*Department of Applied Biology, Chungnam National University; <sup>1</sup>National Institute of Agricultural Biotechnology; <sup>2</sup>Korea Research Institute of Bioscience and Biotechnology.*

To establish a taxonomic system of *Alternaria* and allied genera in Korea, the *Alternaria* spp., *Stemphylium* spp. and *Ulocladium* spp. isolated from Korea were classified based on conidial morphology and catenulation, and molecular phylogenetic relationships of the species were evaluated using a variety of molecular techniques. Based on conidial catenulation, *Alternaria* spp. were segregated into three sections; Longicatenate, Brevicatenate and Noncatenate. Phylogenetic analysis of 28S rDNA, ITS rDNA and EF-1  $\alpha$  gene sequences revealed that the *Stemphylium* spp. were phylogenetically distinct from the *Alternaria* and *Ulocladium* spp. but the *Ulocladium* spp. were included in a large *Alternaria* clade. *A. longissima*, *A. helianthi* and *A. padwickii* were distantly related to the other *Alternaria* spp., as well as the *Ulocladium* and *Stemphylium* spp. Phylogenetic analysis of ITS rDNA and EF-1  $\alpha$  gene sequences showed that it was possible to distinguish species of the *Alternaria* belonging to the section Brevicatenate, however, it was not possible to distinguish species belonging to the sections of the Longicatenate and Noncatenate. Analysis of histone H3 gene sequence and URP-PCR were found to be useful for establishing systemic relationships among *Alternaria* spp. belonging to the section Noncatenate. Based on phylogenetic analysis of *gpd*, EF-1  $\alpha$  and calmodulin gene sequences and URP-PCR polymorphism analysis of *Stemphylium* spp., the molecular groups were well correlated with morphological species.