

Taxonomy and phylogeny of *Alternaria* and *Stemphylium* in Korea

Seung Hun Yu

Department of Applied Biology, Chungnam National University

Alternaria and *Stemphylium* are dictyosporic genera of the family Dematiaceae, Hypomycetes, Fungi imperfecti. Species of *Alternaria* and *Stemphylium* are frequent parasites on numerous agricultural crops, economic garden plant and weeds. They are also common components of the flora of seeds or saprophytes living on various substrates and constitute groups of fungi whose importance has been well known for a long time, in mycology as well as in plant pathology. Classic taxonomy of the genera *Alternaria* and *Stemphylium* is based on morphology. However, it is complicated by variability in their morphological characters, which are affected not only by environmental conditions but also by intrinsic factors. Molecular methods may overcome the problems of species delimitation and are increasingly being used for identification and phylogenetic studies.

Alternaria

Two hundred and seventy isolates of *Alternaria* collected in Korea were classified by morphological analyses. They were separated into three groups (sections) according to the catenulation pattern and conidial morphology. Sections Longicatenatae, Brevicatenatae and Noncatenatae contained 11, 10 and 21 species of *Alternaria*, respectively. However, morphological characters often vary among isolates of the same species, and show significant overlap among species. Some species in the Brevicatenatae included isolates that produce solitary spores and some Noncatenatae species appeared in short chains of two to three. Catenulation was also influenced by conditions of growth. *A. brassicae* and *A. panax* hardly formed chains on host plants but easily formed short chains in culture. To elucidate relationships among *Alternaria* species, nuclear large subunit (28S), internal transcribed spacer (ITS) and mitochondrial small subunit (SSU) rDNA, translation elongation factor 1 alpha (EF-1 α) gene and histone H3 gene sequences from 41 *Alternaria*, five *Stemphylium* and one *Ulocladium* species were determined and compared. Phylogenetic analysis of the 28S and ITS rDNA and EF-1 α gene sequences revealed that *A. helianthi*, *A. longissima* and *A. padwickii* were phylogenetically distinct from the other *Alternaria* spp., as well as the *Stemphylium* spp. The three species of *Alternaria* should belong to the different genera because they had genetically and morphologically unique characteristics. The ITS and mt SSU variability within the

small-spored *Alternaria* spp. was relatively limited. A number of small-spored Longicatenatae taxa such as *A. alternata*, *A. arborescens*, *A. citri*, *A. gaisen*, *A. longipes*, *A. mali* and *A. tenuissima* could not reliably be distinguished from each other using this method. However, cluster analysis of universal rice primer(URP)-PCR fragment patterns was useful for establishing relationships among the species of small-spored *Alternaria*. Sequence analysis of ITS rDNA and EF-1 α gene was able to distinguish the Brevicatenatae species of *Alternaria*, however, it was not possible to distinguish the Longicatenatae and Noncaterenatae species of *Alternaria*. Based on phylogenetic analysis of histone H3 gene sequence, the large-spored Noncaterenatae *Alternaria* spp. were clustered into several distinct species-clades, most of which correlated with species-groups previously established based upon morphological characteristics. URP-PCR analysis was also useful for establishing systematic relationships among the large-spored *Alternaria* spp. Of the 41 species of *Alternaria* found in Korea, eight species were confirmed as new species.

Stemphylium

Seventy nine isolates of *Stemphylium* were collected from 35 species of host plants in Korea. Eight species were identified based on morphological characteristics such as size and shape of conidia and conidiophores. However, species delimitation and identification is notoriously difficult. To elucidate relationships among *Stemphylium* spp., ITS rDNA, glyceraldehyde-3-phosphate dehydrogenase(gpd) gene, EF-1 α gene and calmodulin gene sequences from 8 species were determined and compared. The analysis of gpd, EF-1 α and calmodulin genes were found to be more useful for establishing systemic relationships among the species and isolates of *Stemphylium* than that of ITS. URP-PCR fingerprinting analysis of the isolates of *Stemphylium* using 9 URP primers revealed that differentiation of the species was recognised, and *S. lycopersici* had genetic diversity among isolates. Based on phylogenetic analyses and URP-PCR polymorphism analyses of *Stemphylium*, the molecular groups were well correlated with morphological species, and the *Stemphylium* sp. isolated from *Symphytum officinale* was considered as a new species.

Referances

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