F324

RAPD analysis and chitinase isozyme patterns of 13 species in the genus *Fusarium*

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To clarify the taxonomical status among 13 *Fusarium* species, we investigated the use of the Random Amplification Polymorphic DNA(RAPD) method. To select primer that generated informative arrays of PCR products, we tested 30 primers, single arbitrary 10-mer primer. Each primer has its own RAPD patterns, and the size of the products were within the range 0.5 to 3.0kb. Genetic distances between each of these 13 species were calculated by UPGMA, and cluster analysis was used to generate a dendrogram showing relationships between them.

In addition, we studied the chitinase isozymes of these 13 *Fusarium* spp. using florescent substrate, 4-MU-GlcNAc to identify chitinolytic enzymes. And chitinase activities were measured by colorimetric assay using *p*NP-GlcNAc. As the results, the chitinase isozyme patterns were observed 1 to 3 bands within the range 50-100kDa, but there are no obvious differences among these 13 species. High chitinase and β-N-acetylglucosaminidase activities were found in the enzyme from *F. nivale, F. subglutinans, F. avenaceum.*

F325

The electrophoretic karyotypes and localization of 18s rDNA in Genus *Fusarium*

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The electrophoretic karyotype of *Fusarium* species and formae speciales has been established by using contour-clamped homogeneous electric field(CHEF) gel elctrophoresis. Intact chromosomal DNA was prepared from fungal protoplasts. Up to 11 distinct chromosomal bands were resolved after 228hrs of migration at 1.3v/cm, different pulsed time and 0.7% agarose concerntration. Polymorphic karyotypes were observed in different species of *Fusarium* and various formae speciales of *F. oxysporum.* Using the *Schizosaccharomyces pombe* and *Sccharomyces cerevisiae* chromosome as size standards, the genome size of *Fusarium* spp. was estimated to range from approximately 24 to 31.8Mb and that of *F. oxysporum* formae speciales genome was from 24.03 to 35.25. In addition, when 18s ribosomal DNA from *F. tricinctum* NRRL 3299, IGS region of *F. moniliforme* 7219 were used as probe and hybridized with genomic DNA, the 18s rDNA and IGS region were localized to the largest chomosome.