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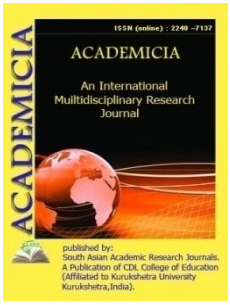

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MOLECULAR-GENETIC IDENTIFICATION AND TAXONOMIC RELATIONSHIPS OF FUNGI BELONGING TO FUNGI IMPERFECTI

R.M. Artikova*; M.R.Zakirova; N.F.Yusupova*****

[1,3]Tashkent Pharmaceutical Institute
Email id: Yusupova69@mail.ru

ABSTRACT

To identify phytopathogenic and entomopathogenic fungi, mostly belonging to the classes Ascomycetes and Deuteromycetes we used standard and changed primers to amplify mitochondrial small subunits of rRNA (NMS3, NMS4), nuclear small subunit18S rRNA (NS7, NS8) and the two of internal transcribed spacer regions (ITS1, ITS2), between the genes 18S and 28S rRNA. Using the standard primers NMS1 and NMS2, ITS1 and ITS2 did not lead to the amplification of DNA of the fungi in PCR. It was interesting to note that only when the region of the small subunit 18 S RNA (NS7 and NS8) was used could positive results be obtained amplifying the DNA of both entomopathogenic and phytopathogenic fungi. Using the modified primers provided means for the differentiation of 13 strains of entomopathogenic fungi and 6 strains of Ascomycetes from different geographic zones.

KEYWORDS: *Rrna, Ribosomal DNA, Kanamycin, Phytopathogenic, Tag-Polymerases.*

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