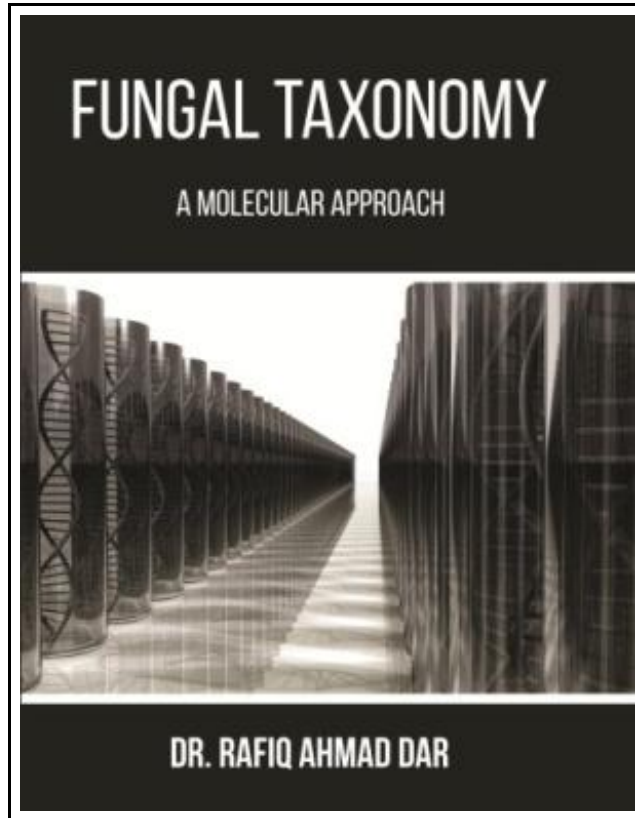


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Ebooks2go Inc, 2017. Paperback. Condition: New. Language: English . Brand New Book ***** Print on Demand *****.The distribution of fungi among the various ecological niches of the biosphere seems to be infinite. Estimates suggest a total of 1.5 million fungal species; only less than a half has been merely described yet. This implies a backlog demand, which comes along with a rising importance of novel techniques for a rapid and unambiguous detection and identification of fungi to explore the fungal diversity as a coherent whole. Molecular techniques, particularly the technology of the polymerase chain reaction, have revolutionized the molecular biology and the molecular diagnosis of fungi. The incorporation of molecular techniques into what has been traditionally considered as morphology-based taxonomy of fungi helps us in the differentiation of fungal species and varieties. Databases of genomes and genetic markers used as sources for molecular barcodes are being created and the fungal world is in progress to be unveiled with the help of bioinformatics tools. Genome projects provide evidence for ancient insertion elements, provirus or prophage remnants, and many other patches of unusual composition. Consequently, it becomes increasingly important to pinpoint genes, which characterize fungal organisms at different taxonomic levels without the necessity of previous cultivation. Unfortunately, the initiative of an excessive use of molecular barcoding has been hampered by a lack of sufficient and novel synapomorphic nucleotide characters and signature sequences. Moreover, high intraspecific variability of conventional molecular characters makes it difficult to identify species borders. However, DNA sequences and other genetic markers provide large amounts of data which are cultivation-independent and do not depend on physiological inconsistencies. Genetic markers constantly reflect the identification treasure hidden in the genetic information and allow to control the degree of resolution by choosing the appropriate genes. In this book, we highlight the advances of...



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