

Preface to this Edition

In the previous volume of this series on Lower Groups, algal genomics was represented in Rhodophyceae in detail. Genomics of fungi was presented in the phytopathogen *Leptosphaeria*, powdery mildew and oyster mushroom. In addition, comparative genomics of several phytopathogens and genomic redundancy in yeast were critically reviewed. The genomics of lichens, liverwort sex chromosomes, the functional genomics of mosses and organellar transcription of Bryophytes formed the core matter of the other chapters.

The coverage of the present volume which fills up the lacuna of and is supplementary to the earlier one is very wide, starting with the most emerging study in Genomics—the RNA world—ancient to modern—a metabolic story in detail. The structural features of all the different ribozymes and their functioning as well as all the non coding RNAs—their role, chemical basis of action and catalytic mechanisms have been critically reviewed in the backdrop of genome structure and evolution.

The subsequent chapters on genomics of algae deal with groups which are of great phylogenetic significance and biodiversity. These include origin of plastids, diversity, origin and evolution of dinoflagellates and diatoms from the molecular perspective.

The fungal genomics in relation to phylogeny has been covered in hemi, archi and euscomycete with special reference to comparative

genomics and evolution, The biodiversity in basidiomycetous yeast such as Ustilaginales, Uredinales and Hymenomycetes has been critically reviewed in terms of DNA sequence analysis. In the yeast group, a special feature is the analysis of cactophilic yeast growing on decaying cactus tissue, from an evolutionary and ecological standpoint. The molecular data of these habitat and insect specific yeast show clear interstrain and interspecific variations and throw light on the intercommunity relationship.

The molecular phylogeny of the genus *Aspergillus* with the two subgenera—the source of drugs and enzymes has been presented in detail along with the evolution of mycotoxin production, which is presumed to have evolved several times in course of evolution.

The genomic study of *Fusarium* – a highly destructive fungus has been focussed towards its phylogenetic analysis and its detection using molecular tools.

The host pathogen co-evolution with the aid of nuclear DNA and microsatellite markers in two co-colonizing fungi *Philaphora* and *Plectosporium* and a negative correlation between the two pathogens could be established.

The articles on Bryophytes deal with a comprehensive analysis on role of nuclear and organellar DNA in evolution and biodiversity. The importance of ITS spacers of nuclear ribosomal DNA and the role of intergenic spacers of chloroplast DNA in the analysis of phylogeny and plant systematics and evolution of this group have been discussed. In *Plagiochila*—the Jungermanniales, the data on phylogeny and interactions between species of intercontinental ranges have been presented. The molecular evidences indicate interconnecting link between the taxa of neotropics and Africa with the Atlantic, Europe and the Americas and the Asian *Plagiochila* with the Holarctic.

This volume thus provides an in depth and comprehensive analysis on genomics in evolution from the ancient RNA world to the modern day land plants passing through all hierarchy of algae, fungi and bryophytes. It will be of immense use to all engaged in the molecular studies of different groups with their impact on genetics, evolution and agriculture.

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