

**Essential Fungal Genetics.** David Moore and Lily Ann Novak Frazer. Springer-Verlag, New York. 2002. 357 pp. Price US \$ 69.95.

Standard textbooks of genetics describe the general principles of genetics as applied to diverse organisms, using one system to explain the corollaries in other systems. Such an approach, while showing the commonality of principles in different organisms, falls short of a comprehensive understanding of one system, such as fungi. It is this lacuna that this book purports to fill.

The opening chapter traces the fungi as being distinct from plants and sharing a common ancestor with the animal kingdom, after an earlier divergence of plants from a common eukaryotic ancestor 1 billion years ago. The authors discount a common misconception that fungi belong to the plant kingdom. Some evolutionary studies suggest that they may be the common ancestors of plants and animals, and may have aided the colonization of land by plants. Because of their long evolutionary history, fungi can serve as model systems for studying the genetic and molecular processes in higher eukaryotes.

The munificence of fungi owes greatly to their sexual mode of reproduction, underpinned by a variety of mating-type systems. The budding and fission yeasts have two alternative mating types, which predominantly undergo switching to the opposite mating type. The switching directionality in the budding yeast is regulated by a higher-order folding of chromatin, dictated by a distinct DNA sequence and the cognate binding factor/s. On the other hand, the switching competence of the recipient *mat1* locus in the fission yeast is dictated by a cryptic, strand-specific imprint, whose conversion into a double-strand break results in asymmetric switching during DNA replication. Thus, these two distantly related species execute switching asymmetry by different mechanisms. The different cell types generated by the mating-type factors communicate with each other through pheromones, which initiates the sexual cycle. Evolution of the sexual cycle has imparted a distinct edge to fungal species as it increases the chance of genetic variation, provides an escape route from DNA parasites and is a means of repair of DNA damage.

Existence of distinct sexual types has facilitated the use of meiotic recombination to map genetic distances between linked genes. The statistical approaches used to determine the genetic distances between linked genes in diverse fungi are

well-described, a strong point of this book.

A particularly instructive treatment is in the area of genomics. The progress in mapping techniques has been well-described. The complete DNA sequence of the budding yeast reveals several unique features. With nearly 5600 genes, the yeast genome has a high density of coding genes (~2 kb/gene), leaving very short regions to perform regulatory functions, like transcription, replication and chromatin maintenance. Most interestingly, 40% of the genes are duplicated in regions referred to as cluster homology regions – large segments on two or more chromosomes that share duplicated genes in the same order. The duplicated genes are generally involved in membrane processes, protein conformation and DNA/RNA processing. Such duplications may allow redundancy of functions and may have arisen as a part of evolutionary strategy to protect cells from accidental loss of function.

A unique epiphany of yeast genome relates to evolutionary origins. The genes involved in nuclear functions, like transcription, replication and cell cycle, are closely related to the archeal genes, while those involved in metabolism, stress response, detoxification and protein conformation are closer to the bacterial genes. These observations suggest that eukaryotes arose from endosymbiosis of an archaeal cell into a bacterial cell: over time, the former lost its metabolic functions, while the latter lost its gene-expression functions. Furthermore, a large number of genes involved in basic biological processes are conserved from yeast to *Drosophila* to humans. Thus, a study of gene function in yeast can yield quicker insights into the function of the orthologues in humans, particularly the genes related to diseases, including cancer. Such insights, along with the potential commercial spin-offs, have justified the enormous investments into the sequencing efforts and provided further impetus to sequencing of other fungal genomes. Fungi have been exploited to produce better baking and brewing characteristics and for production of cholesterol-lowering and immunomodulatory drugs. Lately, using a large variety of promoters, yeasts have been exploited for producing high-value therapeutics and recombinant vaccines.

Genetic analysis of fungi can also be instructive in studying phylogenetic relationships and determining the evolutionary distances between species. Sequence information can help in study of gene polymorphism in populations and in

understanding the host-pathogen gene-to-gene interactions. The large number of progeny resulting from fungal reproduction has facilitated the study of evolution in captivity using organisms like *Fusarium*. Interestingly, results of such studies appear to support the theory of punctuated equilibrium.

Fungi have also provided one of the best-understood models of gene regulation – the galactose gene cluster, wherein the interplay of the regulatory molecules, GAL4, GAL80 and GAL3 facilitates either expression or repression of the *Gal1*, *GAL10* and *GAL7* genes. Functions of the regulatory molecules can be modulated either by mutations or by altering the growth conditions. In addition, budding yeast has also provided important paradigms for chromatin remodelling and the epigenetic mechanisms of gene silencing that target the nucleosome structure. Other epigenetic means of gene regulation include DNA methylation, quelling, RIP, MIP, protein turnover by ubiquitination and prions. Fungi have provided excellent models for these phenomena as well.

The advent of proteomics provides a means for understanding the complex protein-protein interaction networks that maintain not only homeostasis but also allow organisms to function as multi-molecular entities, continuously evolving in adaptation to the environment. Such questions can be best addressed in fungi.

The scope of the book, as defined in its preface as comprehensive and succinct, has been well-achieved as it attempts to cover a large and representative canvas. Each chapter starts with 'revision concepts', summarizing its main points. The theme of each chapter is developed in a coherent and lucid manner, which makes the reading easy. However, an important area of cell cycle and check-point control mechanisms, which were recently recognized in the form of a Nobel Prize, has been omitted. Further, the book could be improved by more in-depth coverage of areas like stress response, protein trafficking and various epigenetic phenomena as well as some pertinent illustrations. Nevertheless, the comprehensive subject matter makes it a good reference book for students of fungal genetics.

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