

biocide action in killing microorganisms. Four main modes of biocide action are presented: oxidizing agents, cross-linking or coagulating agents, energy inhibitors, and structure-disrupting agents. In addition, the modes of action of various antibiotics (antibacterial, antifungals, antivirals, and antiparasitic drugs) are briefly analyzed.

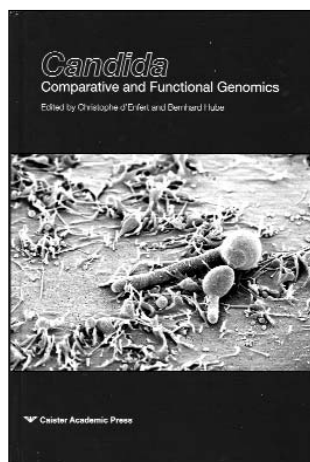
While a number of laboratory *in vitro* studies have demonstrated possible associations between the exposure of bacterial cultures to subinhibitory concentrations of biocidal molecules and changes in antibiotic susceptibility, currently there is little or no direct evidence that this is significant in the development of antibiotic resistance in clinical practice. Chapter 8, "Mechanisms of microbial resistance" considers the mechanisms by which bacteria may become less sensitive to biocide action and then examines potential links between antibiotic and biocide resistance. Resistance is the relative insusceptibility of a microorganism to a particular treatment under a particular set of conditions. The discussion of microbial responses to disinfectants and sterilants is confined to the

case of bacteria, because information regarding viruses and other microorganisms is still very limited. Resistance can be a natural property of an organism (intrinsic) or it can be acquired by mutation or horizontal transfer. Several intrinsic mechanisms of resistance have been studied extensively; of particular interest are those involving biofilms, extremophiles, and spores.

Uncontrolled and unwanted microbial growth continues to have dire medical, environmental, and economic consequences. *Antiseptics, disinfection, and sterilization* may contribute significantly to addressing some of the problems arising from contamination by improving our knowledge of modern disinfection and sterilization technologies and of their potential applications.

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## *Candida:* Comparative and Functional Genomics

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2007, Caister Academic Press,  
Norfolk, UK  
428 pp, 16 × 24 cm  
Price: US\$ 300  
ISBN: 978-1-904455-13-4

The last 25 years have seen a serious increase in the number of fungal infections due to a worldwide increase in the number of immunocompromised individuals. AIDS and cancer patients, those receiving immunosuppressive regimens or broad-spectrum antimicrobial therapies are at high-risk of developing disseminated fungal infections. Moreover, the use of indwelling catheters, artificial implants and surgical trauma further increases the risk of patients contracting nosocomial infections. *Candida* species are one of the main fungal pathogens responsible for causing opportunistic infections, and up until now, the high mortality rates associated with these have been partly associated to late diagnosis and the relative inefficiency of currently available antifungal treatments in the aforementioned situations. With the whole genome sequences for several medically relevant *Candida*

species now available, our understanding of the biology of these complex organisms has been revolutionized: post-genomic approaches have allowed for more detailed investigations and have changed the way *Candida* species are now studied and understood.

*Candida: comparative and functional genomics* is one of the most complete reviews on these organisms. This comprehensive book is a collection of 17 concise and straightforward chapters written by international experts, providing a broad coverage on the subject. The complete *Candida albicans* genome was the first in the genus to be sequenced and was made available in 2004. Therefore, the topics in most of the chapters refer to this organism. Nevertheless, there are other medically important *Candida* species such as *C. glabrata*, *C. parapsilosis*, *C. tropicalis* and *C. dublinensis*, all of which represent a therapeutic challenge.

Chapter 1 discusses the genome structure and dynamics in *C. albicans*. This species is both medically important and biologically interesting for a number of reasons. While normally a commensal of the skin and the gastrointestinal and genitourinary tracts, it can, on occasion, become pathogenic, generating opportunistic infections, and is responsible for the majority of the *Candida* bloodstream infections. This chapter concentrates on peculiarities of this organisms' highly-dynamic genome and its mitotic recombination. Chapter 2 discusses the mating systems of *Candida* species. It explains the similarities of *C. albicans* with *Saccharomyces cerevisiae* as well as its own peculiarities, and those of *C. dublinensis* and *C. glabrata* with attention to the possible relationship they may have to pathogenesis. The importance of this chapter lies in the role that *Candida*'s mating processes have on

its population dynamics as an important focus for future research. Chapter 3 further analyses this by zooming into the molecular epidemiology and population dynamics specific to *C. albicans*, whose population has been shown to be divided into five major clades through molecular typing. *C. albicans* is a heterozygous diploid species that possesses a clonal mode of reproduction predominantly, and it is likely that its heterozygosity has conferred it with a selective advantage.

All *Candida* species fall within the hemiascomycete group, of which *Saccharomyces cerevisiae* is the most well-known representative and has been one of the main models for the study of eukaryotic organisms. Chapter 4 deals with comparative genomics in hemiascomycetous yeasts. It reviews their major features (genome size and gene number or chromosomal structures such as centromeres, telomeres and replication origins) and discusses the evolutionary processes that led to differing genome compositions in these species. Chapter 5 goes more in depth to discuss the comparative genomics of *Candida* species. It describes the progress of the various genome sequencing projects and their possible status. The sequences of both pathogenic (*C. albicans*, *C. tropicalis*, *C. parapsilosis*, *C. lusitanae*, *C. glabrata*) and non-pathogenic (*C. guilliermondii*) species either have been, or are being determined. This will prove to be an extremely valuable resource by providing comparative data with regards to the processes that may have contributed to the success of different *Candida* species in becoming pathogenic. Chapter 6 discusses the use of *C. albicans*' global transcription profiles, which have revealed patterns of gene expression, in comparative analysis with other organisms, particularly with *S. cerevisiae*, given the large databases available. Chapter 7 talks about the molecular evolution of the *Candida* genetic code, which has been subjected to unique evolutionary forces. The leucine CUG codon, for example, is decoded as serine in *C. albicans* and other phylogenetically related *Candida* species. Due to evolutionary changes, the CUG codons in extant *Candida* species are not related to those present in the Open Reading Frames of other yeasts.

Huge amounts of data are being generated thanks to these post-genomic studies. It is the function of genome databases to collect, organize, display, and provide tools to analyze and explore this otherwise potentially overwhelming amount of information. Chapter 8 surveys the database resources and types of information available to the *C. albicans* research community, and considers the additional resources that will need to be developed in the future. Chapter 9 discusses how the recent availability of the complete *C. albicans* and *C. glabrata* genome sequences together with improvements in proteomics-based technologies are currently enabling the proteome characterization of these two human pathogens. Remarkably, *Candida* proteome analyses have also helped to unravel new concepts regarding cell envelope, virulence factors, host responses and drug resistance, intuiting the impor-

tance proteomics holds in the future of *Candida* research. In Chapter 10 we see how functional genomics, which was pioneered in *S. cerevisiae* is now within reach for *C. albicans*, *C. glabrata* and other *Candida* species whose genomes have been sequenced. The generation of knock-outs or conditional mutants show considerable promise for the identification of virulence factors as well as novel targets for the development of antifungals.

Chapters 11 to 17 represent some examples on how post-genomic analyses are bringing insight into key topics in our understanding of the biology of these species and their interaction with host cells. Virulence in *C. albicans* is dependent upon its ability to mount stress responses which protect it against host defenses. Chapter 11 explains how recent genomic studies have significantly contributed to our understanding of these stress responses and how they are regulated. Chapter 12 presents an overview of recent research into *C. albicans*' regulation processes underlying morphogenesis in response to external influences, such as those inducing filamentation. Chapters 13 and 14 discuss the cell wall biology and cell wall proteins of *Candida*, which are of vital importance in determining the nature of the host-pathogen interface. Chapter 15, called "Strategic analysis of *Candida albicans* gene function" explains how mutant analysis of transcription factors has been used to elucidate mechanistic information about biofilm formation and cell wall damage response. Chapter 16 summarizes how genomic tools can contribute to characterize the response of fungal pathogens to antifungal agents and the resistance mechanisms across several species. Finally, Chapter 17 summarizes the post-genomic view of *Candida*-host cell interactions, discussing the implications of *Candida* aforementioned responses (stress, morphogenesis, and interactions with host cells) with the organism's pathogenesis and its biology.

Overall, this book proves to be an essential reading for all *Candida* genome and molecular biology researchers and is a recommended text for scientists working on fungal genomics and molecular biology. In spite of its high price, it is recommended for a wide range of scientists interested in the biology of yeasts, fungal infections and also the basic mechanisms of the eukaryotic cell. As the book's editors, Christophe d'Enfert and Bernhard Hube conclude in their introduction, "the hope is that this system biology of the host-pathogen interaction will provide the foundation for a better management of *Candida* infections."

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