

Acanthamoeba Biology and Pathogenesis

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viii + 290 pp., February 2009

ISBN 978-1-904455-43-1 \$319/£159

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This book provides the first comprehensive review of *Acanthamoeba* research to be published. Everything that is known about *Acanthamoeba* is critically reviewed and divided into easy-to-follow sections. This book presents the current state of research on every aspect of this organism, detailing major advances in areas such as genomics, molecular and cellular biology, life cycles, geographical distribution, role in ecosystem, morphology, motility, phylogenetics, genotyping, metabolism, regulation of morphogenesis, host-parasite interactions, the molecular and immunological basis of pathogenesis, methods of transmission, epidemiology, clinical manifestation, diagnosis, treatment, new target development and drug resistance, as well as its role as a Trojan horse of the microbial world, including viral, bacterial, protozoal and fungal pathogens, and much more. There is a significant emphasis on our knowledge of *Acanthamoeba* infections that has grown in the molecular era. In addition, this book provides a historical perspective on *Acanthamoeba* research that will be of considerable interest.

This compilation will serve as an essential reference for microbiologists, immunologists, and physicians in the field of basic and medical microbiology, as well as an invaluable reference for new and experienced researchers who wish to understand this organism better. This book is the definitive guide to current research on this increasingly important organism.

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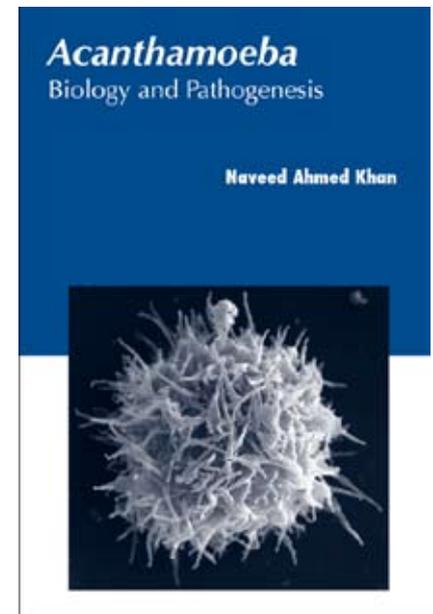
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Microbiology and Molecular Biology Reviews. Microbiology Resource Announcements. Microbiology Spectrum. Molecular and Cellular Biology. mSphere. mSystems. With respect to pathogenesis, most relevant substrates of T1SS are hemolysins (reviewed in reference 33). An example of a T1SS encoded by a PAI is the paradigmatic hly operon of UPEC, which is responsible for synthesis, activation, and transport of α -hemolysin (see also Uropathogenic E. coli below).

An organism's genome provides vital information about its biology and evolution. The genome of *Entamoeba histolytica* was sequenced and assembled in 2005 and provided many insights into the biology of the pathogen. A number of additional *E. histolytica* genomes and those of pathogenic and nonpathogenic relatives have followed, a process aided in no small part by the advent of second-generation sequencing technology. In this review, we mention in general each of the different factors of pathogenesis in amebiasis. Although many alphaviruses have been well studied, little was known about the biology and pathogenesis of CHIKV at the time of the 2005 outbreak. Over the past 5 years there has been a multidisciplinary effort aimed at deciphering the clinical, physiopathological, immunological and virological features of CHIKV infection. This Review highlights some of the most recent advances in our understanding of the biology of CHIKV and its interactions with the host. PMID: 20551973.