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Sommario/riassunto

Aquareoviruses cause infection in bony fish and shellfish and thus, constitute a significant threat to aquaculture industries worldwide. Aquareoviruses, belonging to the family Reoviridae, have genomes consisting of 11 segments of double-stranded RNA contained within a core ($T = 1$) surrounded by a double-layered icosahedral capsid with a $T = 13$ symmetry in general. These viruses not only physically resemble mammalian orthoreoviruses, but also show the highest amino acid identity. More than hundred aquareoviruses have been isolated from both saline water and freshwater origins; however, literary sources elucidating aquareovirus biology are very limited. Given the increasing pace of discovery, it is imperative to make a clear, systematic filing of key aspects of aquareoviruses. Therefore, the aim of writing this book is to provide insights into the molecular mechanisms of evolution, pathogenesis, and host response in aquareovirus infection. This book offers a state-of-the-art report on recent discoveries concerning the aquareovirus genome evolution, gene encoded protein functions, and pathogenesis by comparison with its sister genus Orthoreovirus, including avian and mammalian reoviruses. It mainly focuses on advances made over the past 30 years in research on the general and molecular biology, protein structure and function, infection and replication, epidemiology and diagnosis, immunological prevention and medical treatment, and host antiviral immunity against aquareovirus infection. This book will help curious graduate students or interested researchers acquire an overall picture of aquareovirus infection and pathogenesis, as well as yield benefits in fisheries to better prevent and control diseases caused by aquareovirus infection.
