

Preface

Henipaviruses form a new genus of emerging paramyxoviruses that are the deadliest human pathogens within the *Paramyxoviridae* family. Nipah and Hendra virus, prototype members of this *Henipavirus* genus, are zoonotic pathogens present in alarmingly high frequencies in its natural reservoir, the asian fruit bat. Henipavirus infections can cause respiratory and encephalitic illness in humans with mortality rates that exceed 70 %. Discovered around the turn of the century, the spillover of henipaviruses into animal and human populations dramatically illustrate the threat posed by emerging zoonoses when human and environmental factors force the unintended overlap of otherwise naïve ecological niches. Horses and pigs serve as amplifying reservoirs for Hendra and Nipah virus, respectively, but direct bat-to-human and human-to-human transmission, at least for Nipah virus, has been increasingly documented. Although Nipah and Hendra virus spillover events are currently limited to Southeast Asia and Australia, respectively, serological and molecular evidence for henipavirus-related pathogens in bat species has been documented in places as distant as West Africa, and most recently, in Central and South America. Indeed, as this book goes to press, an international consortium of virologists and viral ecologists led by Christian Drosten reports the identification of 19 novel viral species within the Henipavirus genus, which can now be classified into at least 23 distinct viral clades.¹ The phylogenetic diversity of henipaviruses is thus vastly greater than what was thought previously. Henipaviruses also exhibit a much broader species tropism than other paramyxoviruses, largely due to the highly conserved protein receptors that these viruses use. In the various taxonomic schemes proposed for the transitional dynamics of zoonotic pathogens,² all these features justifiably place henipavirus at or close to the penultimate stage for sustained transmission in human outbreaks.

¹ Drexler JF et al (2012) Bats host major mammalian paramyxoviruses. *Nat Commun* 3:796.

² Wolfe ND et al (2007) Origins of major human infectious diseases. *Nature* 447:279–283; Lloyd-Smith JO et al (2009) Epidemic dynamics at the human–animal interface. *Science* 326:1362–1367.

This timely volume deals with the many facets of henipavirus biology, and covers our current understanding regarding the ecology, molecular virology, and pathogenesis of henipavirus infections. It is an international effort written by a multidisciplinary panel of experts at the front lines of research into this lethal emerging group of paramyxoviruses. The first section introduces the epidemiology and ecology of Nipah and Hendra viruses in their respective endemic areas, including a first-hand account of the discovery of Nipah virus during its initial outbreak in Malaysia; the next section documents the molecular virology of henipaviruses, and the substantial advances made towards understanding the unique features of henipavirus entry and tropism; and this is followed by accounts of the clinical and pathologic features of henipavirus infections in their human and naturally infected animal hosts. The next sections on pathogenesis provide a comprehensive reference on how henipaviruses counteract the innate immune system, and the relevant pathogenic features in animal challenge models developed to test potential therapeutic strategies. The final sections describe our current and future capabilities for diagnosis and control, including an account of potentially effective immunization strategies that are currently being tested. This book will not only serve as a useful reference for the henipavirus field; it will be useful to basic and animal virologists, ecologists, epidemiologists, physicians, and others interested in emerging infectious viral diseases, as it showcases the multidisciplinary efforts required to understand the genesis, spread and hopefully, control, of a lethal emerging zoonotic pathogen.

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Henipavirus

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