Preface

The avian influenza (AI) virus, which is the type A influenza virus adapted to an avian host, has been an important pathogen for the poultry industry worldwide for many years. Although the cause was unknown at the time, one of the first recognized outbreaks of highly pathogenic AI (HPAI) virus occurred in Europe in the 1870s. Since 1955, when the AI virus was first identified, there have been about 24 outbreaks of the HPAI virus in domestic poultry worldwide.

Of those, perhaps the most consequential HPAI virus strain to emerge has been the Asian H5N1 HPAI virus, which was first seen in Southeast Asia around 1997. Until sometime in 2003, this strain had been mainly involved in sporadic outbreaks and was relatively contained. Then in 2004, reports of infection in poultry increased throughout Asia at about the same time as fatal cases of human infections in several Southeast Asian countries were confirmed. By 2006, the virus had spread further throughout Asia, into Africa and Europe, and as far west as the United Kingdom.

In addition to the rapid and distant spread of the Asian H5N1 HPAI virus, and the low number of human infections with a high fatality rate (approximately 50–60%), this virus's lineage has developed unusual pathogenic properties in birds in that it can cause disease and even mortality in some species of ducks. These factors have contributed to an increasing focus on the AI virus as a basic research area, and surveillance for the virus in domestic poultry and wild bird species has also increased considerably in the past few years.

This volume focuses on both the essential virological methods that are foundational for AI virus research and diagnostics as well as some of the newest molecular procedures used for basic and applied research. Since the AI virus has had such a long history as a veterinary pathogen, many of the classical virological procedures for the basic manipulation and characterization of the virus have been in use for many years. Therefore, they are well established and well optimized. These tests will form the foundation for either research or diagnostics. The recently developed molecular methods focus on elucidating the virus pathogenesis (reverse genetics), and some methods focus on the avian host response to the AI virus. Although some of these methods are applicable to type A influenza in general, the focus is the AI virus and the avian host system.

The aim of this book is to create a resource that includes both basic methods that are currently used and well established as well as some of the most exciting new methods for studying the virus itself, and to include methods that focus on work with avian hosts, an area that has been greatly lacking. In that context, this volume will be of interest to both diagnosticians and researchers, but it does assume a basic knowledge of virology and molecular biology.

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