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1-1-2009

Preface to *Lesser Known Large dsDNA Viruses. Current Topics in Microbiology and Immunology* 328

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Van Etten, James L., "Preface to *Lesser Known Large dsDNA Viruses. Current Topics in Microbiology and Immunology* 328" (2009). *Papers in Plant Pathology.* Paper 210.
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Published in James L. Van Etten (ed.) *Lesser Known Large dsDNA Viruses. Current Topics in Microbiology and Immunology* 328 (2009), pp. v–vii. Copyright © Springer-Verlag Berlin Heidelberg 2009. Used by permission.

Preface

Several large dsDNA-containing viruses such as poxviruses (smallpox) and herpes viruses are well known among the scientific community, as well as the general populace, because they cause human diseases. The large dsDNA insect-infecting baculoviruses are also well known in the scientific community because they are used both as biological control agents and as protein expression systems. However, there are other large dsDNA-containing viruses, including the giant 1.2-Mb mimivirus, which are less well known even though all of them play important roles in everyday life. Seven of these virus families are reviewed in this book.

Examples of their importance include the virus that causes white spot disease of shrimp (WSSV) (a single representative in the family *Whispoviridae*). WSSV is responsible for the loss of millions of dollars in the commercial shrimp farming industry every year. Likewise, some iridoviruses, such as members in the genus *Megalocytivirus*, cause serious diseases in commercial fish farms throughout Asia. Other Iridovirus members in the genus *Ranavirus* are the causative agent for approximately 50% of the documented cases of amphibian mortality reported in the United States between 1996 and 2001.

African swine fever virus (ASFV) (a single representative in the family *Asfarviridae*), which is vectored by argasid ticks and may actually be a tick virus, is usually lethal to domestic swine and outbreaks of the virus have led to large swine kills in Southern Europe, primarily in Spain.

Large dsDNA viruses that infect algae, family *Phycodnaviridae*, are also just beginning to be appreciated by the scientific community because of their influence on the global environment. That is, more than 50% of the CO_2 fixed on the planet is by marine microorganisms, called phytoplankton. The majority of these microorganisms are photosynthetic cyanobacteria. However, a significant number of these microorganisms are eukaryotic algae. Studies in the past 10 years indicate that approximately 20% or more of these photosynthetic microorganisms are infected with a virus at any one time; thus viruses are playing a large role in the turnover of these microorganisms and their role in global CO_2 fixation is only beginning to be appreciated by many marine scientists. Phycodnaviruses also contribute to the disappearance of some massive algal blooms, often referred to as red tides or brown tides.

The huge *Mimivirus*, which was originally reported to only infect protozoans belonging to the *Acanthamoeba* (amoebe) genus, may be involved in some human pneumonia-like diseases, although this role is still subject to verification. Currently, *Mimivirus* is the only member in the family *Mimiviridae*, but other relatives have been discovered recently and their genomes are being sequenced. Also, the massive genomic sequencing projects that are occurring, e.g., DNA from the Sargasso Sea, are revealing many genes that are related to *Mimivirus genes*, indicating that these large viruses are probably more common than expected.

Members of the virus family *Ascoviridae* infect insects. Ascoviruses primarily infect lepidopterous insects and they have a fascinating life style.

Some viruses reviewed in this book, specifically ASFV, *Mimivirus*, the iridoviruses, and the phycodnaviruses, along with the poxviruses, probably have a common evolutionary ancestry. Collectively, these viruses are referred to as nuclear, cytoplasmic, large dsDNA viruses, abbreviated as NCLDV. As mentioned in the chapter on the *Ascoviridae*, the ascoviruses have a strong evolutionary connection to the iridoviruses and so eventually they will probably be included as a member of the NCLDVs.

The NCLDVs are gaining the attention of some scientists interested in evolution for two reasons. First, accumulating evidence indicates that the NCLDVs may be ancient viruses; in fact, there is a suggestion that the predecessor of the NCLDVs may have existed at about the time eukaryotes and prokaryotes diverged and that these viruses might even represent the fourth domain of life. A separate cladistic study suggests that the *Phycodnaviridae* δ DNA polymerases may be near the origin of all eukaryotic δ DNA polymerases. Second, other investigators have suggested that an NCLDV predecessor may have been the origin of the nucleus in eukaryotic cells or that the nucleus is the origin of the NCLDVs.

The evolutionary origin of some of these other large dsDNA viruses is a complete mystery. For example, currently WSSV does not seem to be related to any other family of viruses. Of its predicted 181 open reading frames (ORFs), only approximately 25% match proteins in the public databases; however, another 40 of these proteins are structural proteins associated with the virus particles.

The large bacteriophage (~500 kb genome) Phage G, which infects *Bacillus megaterium*, was always considered to be an abnormality. Although, the phage was first described roughly 40 years ago, it was essentially ignored until recently. However, scientists have recently isolated more of these giant, plaque-forming bacteriophage from nature. Ironically, many of these large dsDNA bacteriophage were missed because the agar concentrations used to plaque the phage were so high that the viruses did not have time to diffuse in the soft agar on the plates.

It should also be noted that many of these large viruses, such as *Mimivirus*, are trapped in filters commonly used to remove bacteria from nat-

ural samples. Consequently, they can be easily missed unless special precautions are taken. Without doubt many more large dsDNA-containing viruses remain to be discovered.

Finally, as editor of this volume, I want to thank each of the authors for their contributions. However, only one, Greg Chinchar and his co-authors, actually met the original deadline for their chapter and so he receives a gold medal. A special thank you goes to Chu-Fang Lo and her co-authors for agreeing at the last minute to write the chapter on the Whispovirus, after the original author backed out of the assignment. Finally, I want to thank Anne Clauss and her assistants at Springer for making this book happen.

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