

2002.V030-033.02. *Poxviridae*

It is proposed to:

2002.V030.02. Remove *Melanoplus sanguinipes entomopoxvirus* from Genus *Entomopoxvirus B*.

2002.V031.02. Create a fourth *Entomopoxvirus* genus in the Family *Poxviridae*.

2002.V032.02. Name the genus created by Proposal 2, *Entomopoxvirus D*.

2002.V033.02. Nominate *Melanoplus sanguinipes* as the type species of Genus *Entomopoxvirus D*.

Rationale:

The *Entomopoxviridae* are divided into three genera based on virion morphology and insect host. Virus genera are designated as A (coleopteran), B (lepidopteran and orthopteran), C (dipteran). The genus *Entomopoxvirus B* contains fourteen species. Nine species infect lepidopteran hosts, whereas the remaining five infect members of the orthopteran order. Like that of baculoviruses, entomopoxviruses (EPV) are named after the latin binomial of the insect from which it was first isolated.

Limited DNA sequence analysis of a number of members of Genus *Entomopoxvirus B*, and the complete genomic sequences of grasshopper (orthopteran) *Melanoplus sanguinipes entomopoxvirus* (MsEPV), and of the red hairy caterpillar (lepidoptera) *Amsacta moorei entomopoxvirus* (AmEPV) have suggested that entomopoxviruses infecting different insect orders are phylogenetically distinct. The spheroidin protein of MsEPV shows approximately 20% amino acid identity with spheroidin protein of *Melolontha melolontha* EPV (Genus *Entomopoxvirus A*) and other lepidopteran EPV of Genus *Entomopoxvirus B* (*Heliothis armigera*, HaEPV; AmEPV and *Choristoneura biennis*, CbEPV). In contrast the spheroidin proteins of AmEPV, HaEPV and *Choristoneura fumiferana* EPV all lepidopteran viruses of Genus *Entomopoxvirus B* have amino acid identities of greater than 79%.

The MsEPV genome is not collinear with genomes from other lepidopteran viruses from Genus *Entomopoxvirus B*. The spheroidin and NPH-I homologues are separated by approximately 20 kbp in MsEPV, whereas in the examined genomes of lepidopteran viruses of Genus *Entomopoxvirus B*, they are in juxtaposition. The availability of the complete genomic sequence of AmEPV, the type species of Genus *Entomopoxvirus B*, provided the basis for the most complete determination of the genetic relatedness of MsEPV with a lepidopteran virus of Genus *Entomopoxvirus B*. A comparison of the spatial distribution of eighteen homologous genes between AmEPV and MsEPV revealed no significant gene order conservation. In addition, 136 ORFs (35.1% of the genome) were unique to AmEPV and were not represented in MsEPV, other insect viruses, or the vertebrate poxviruses. In contrast, limited comparative alignment of two lepidopteran Genus *Entomopoxvirus B* viruses, AmEPV and HaEPV, does reveal some degree of co linearity.

The preponderance of data supports the creation of a fourth genus with *Melanoplus sanguinipes* as the type species. We anticipate that as more DNA genomic sequence information becomes available for other orthopteran viruses of Genus *Entomopoxvirus B*, they will also be placed into Genus *Entomopoxvirus D*.

References:

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