Baculovirus isolated from *Lymantria dispar* larvae as an example of possible virus adaptation to a new host

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Among the different forest insects, the gypsy moth is a species that is highly susceptible to viral infections. In presented work, baculovirus isolated from gypsy moth dead larvae in Biebrza National Park in Poland (LdMNPV-BNP) shows similar bioactivity to other LdMNPVs used as pest control agents (Gypcheck). However its fully sequenced genome seems to be distant from known LdMNPVs. Genome organization and GC content indicate that LdMNPV-BNP may be recognized as a new species isolated from *Lymantria dispar.* Next-generation sequencing of LdMNPV-BNP revealed gene content (e.g., photolyase) that is not present in any LdMNPV isolate sequenced to date. Because the nucleotide sequences for the *polh*, *lef-8* and *lef-9* genes are very similar to those found in LymoNPV in the GeneBank database, one can draw the conclusion that these two viruses have a common ancestor. Both *Lymantria monacha* and *Lymnatria dispar* moths are present in Biebrza National Park. Caterpillars of these species normally feed on different types of trees (coniferous and deciduous trees, respectively), but during their gradation, when not enough food is present, both can start to consume any available source of food. The isolate characterized in the presented work may be an example of virus transmission and adaptation to a new host on secluded area.

Genomics of alphabaculovirus isolates infecting *Mamestra* species from North America and Eurasia.

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Alphabaculoviruses infecting *Mamestra configurata* (Bertha armyworm) in North America and *Mamestra brassicae* (cabbage moth) in Eurasia are closely related and complete genomes of several isolates from both host species have been published. The alphabaculovirus isolates from *M. configurata* separate into two species, MacoNPV-A and MacoNPV-B. In contrast those from *M. brassicae*, MbMNPV, are most closely related to MacoNPV-B. The M. configurata and M. brassicae alphabaculovirus isolates appear to have wide host ranges. We sequenced complete genomes of additional isolates that were derived from widely dispersed *M. brassicae* populations from across Eurasia. We show that some of these isolates from *M. brassicae* are MacoNPV-A type viruses. In addition, MacoNPV-B type isolates were also identified but were found to contain some ORFs more closely related to MacoNPV-A homologues. None of the MacoNPV-B type viruses contained a homologue of *lef-7* which is found in all MacoNPV-A type viruses. The most variability in ORF content among the MacoNPV-A genomes is concentrated between *hr1> bro-b* and *bro-b> calyx*. Similarly in MacoNPV-B type genomes, most variation in ORF content is concentrated between *hr1> bro-a* and *bro-b> he65*. Oral infectivity bioassays showed that there were minimal differences in infectivity for MacoNPV-A and MacoNPV-B type isolates in *M. configurata* 2nd instar larvae; while the MacoNPV-B type isolates were typically more infectious for *Trichoplusia ni* 2nd instar larvae than were the MacoNPV-A isolates. The high degree of sequence homology, gene synteny and biological differences between MacoNPV-A and MacoNPV-B type isolates, respectively, suggest a relatively recent evolutionary diversion of these virus species.

Improved insecticidal activity of Chilo iridescent virus expressing an insect specific neurotoxin

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Previously we have generated a recombinant Chilo iridescent virus (CIV), by placing the green fluorescent protein gene (gfp) to the CIV 157L open reading frame (ORF) locus and have shown that the obtained recombinant was fully infectious both in cell culture and in larvae. This study opened us new venues toward valuable strategies for increasing the viral pathogenicity of CIV by inserting virulence genes into its genome. In this study, to improve the viral pathogenicity, we constructed a recombinant CIV (rCIV-D157L/gfp-AaIT), by replacing the 157L ORF with the AaIT neurotoxin gene from the scorpion *Androctonus australis* and the gfp gene under individual viral major capsid protein (mcp) promoters. Recombinant virus was purified by successive rounds of plaque purification in cell culture. The infectivity of rCIV-D157L/gfp-AaIT was compared to the wild-type and rCIV-Δ157L-gfp, CIV, in *Spodoptera frugiperda* (Sf-9) cells. One-step growth curves for recombinant and wild-type CIVs were similar. Toxin expression in infected third instar *Galleria mellonella* larvae was confirmed by western blot analysis using an antibody against the AaIT protein. Recombinant virus caused a rigid paralysis in the infected *G. mellonella* larvae two days after injection. Bioassays on these larvae demonstrated that the speed of action (LT50) and pathogenicity (LC50) of the recombinant virus were strikingly enhanced compared to wild-type CIV. These results suggest that this recombinant form of CIV provides further opportunities to develop a commercial product to control susceptible pest insects.This study was supported by The Scientific and Technological Research Council of Turkey (TUBITAK, Project No. 113Z748).

Characterization of the Baculovirus-Densovirus interaction when co-infecting the same host

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Accumulating evidences suggest that mixed viral infections are abundant in the nature, yet studies trying to understand virus interactions when co-infecting the same host are rare. Such studies might be indispensable to have clear view about the possible interactions between pests and viral enemies when designing new biopesticides. Among insect viruses, Baculoviruses (BVs) are widely