

The *Agrotis* baculovirus complex: multiple viruses for multiple pests

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Larvae of the genus *Agrotis* (Lepidoptera: Noctuidae) are known to be severe soil pests on a wide range of field crops and vegetables in Europe, Asia and Africa. *Agrotis spec.* are highly susceptible for a broad number of baculoviruses and in the past, two Alphabaculoviruses (AgseNPV-A and AgseNPV-B) and one Betabaculovirus (AgseGV) were isolated from the common cutworm *A. segetum*. From larvae of the black cutworm *A. ipsilon* another Alphabaculovirus, *Agrotis ipsilon nucleopolyhedrovirus* (AgipNPV), was isolated. Bioassay analysis demonstrated the cross-infectivity of all four baculoviruses for both hosts, which made them potential biocontrol agents for the control of cutworms. Especially in terms of resistance management the usage of a combination of different baculoviruses is regarded to be useful. In order to develop methods for identification of the different viruses we developed

a multiplex polymerase chain reaction (PCR) and quantitative PCR (qPCR) based method. The genome of AgseNPV-B was completely sequenced and a comparative genome analysis of AgseNPV-B, AgseNPV-A and AgipNPV was conducted. Phylogenetic analysis confirmed the close relationship of AgseNPV-B and AgipNPV by a high sequence similarity, although the genome length and number of open reading frames (ORF) of AgseNPV-B and AgseNPV-A were more alike.

For biological characterization bioassays and the determination of the median lethal dose (LC50) of AgipNPV and AgseNPV for their common host *A. segetum*, were performed. This work is the basis to analyze the molecular and cellular interaction of these viruses in mixed infections and to optimize the application of these viruses for *Agrotis* control.