Usage of highly specific indel mutations for distinguishing Cydia pomonella granulovirus isolates

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Various isolates of the Cydia pomonella granulovirus (CpGV) has been used as an insect pest control agents against codling moth (CM, Cydia pomonella L), a main pest in apple orchards, worldwide since the 1980s. Commercial formulations are based on *in vivo* produced CpGV occlusion bodies (OBs) that are sprayed in aqueous suspensions on leafs and fruits, where they are ingested by CM first larval instar initiating a quick and fatal viral infection. A production of qualitative stable and consistent OB suspensions is important to guarantee the right CpGV isolate composition since isolates, such as CpGV-M, CpGV-S and CpGV-E2, exhibit different virulence to known CpGV resistant field and laboratory CM populations. Furthermore, population of CM were known to host potentially latent CpGV infection, challenging the propagation process. Recently, isolates CpGV-M, -S and -E2 were NGS deep sequenced and characterized for their intra-genetic composition based on single nucleotide polymorphisms. In the present study, the NGS data was used to identify highly isolate specific insertion/deletion (indel) locations that allow the rapid detection and identification of these three CpGV isolates by PCR techniques. Two different open reading frames, namely pe38 and orf47, as well as, an intergenic region with specific indel mutations were chosen for this approach. Indels were not smaller or larger than 19 to 25 bp, respectively. The PCR approach was used for the identification of populations of susceptible and resistant CM populations to detect CpGV latency offering a rapid tool in quality control for CpGV OB production.