

Genetic diversity of new Chinese *Cydia pomonella granulovirus* isolates

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Cydia pomonella granulovirus (CpGV) is an efficient biological agent to control codling moth in pome fruit orchards. Different geographic CpGV isolates originating from Mexico, Canada and elsewhere have been commercialized since 1980s to control CpGV-susceptible and resistant codling moth populations. Five genome groups (termed as group A, B, C, D and E) representing different phylogenetic lineages, were proposed according to analyses of full genome sequences of different CpGV isolates. Isolates from these groups have differing biological activity against different types of CpGV resistance. In the light of resistance management, it is important to determine the genetic diversity of naturally occurring CpGV isolates.

Seven Chinese CpGV isolates (ZY, JQ, ALE, KS1, KS2, ZY2, WW) were completely sequenced by Illumina next generation sequencing (NGS), using a self-assembled workflow in the galaxy server of the Julius Kühn-Institut to assemble sequencing reads and determine single nucleotide polymorphisms (SNPs). Based

on specific SNPs of genome A to E, SNP markers of each new isolate were classified into different groups which provide information to determine composition of each isolate. We found isolate ZY, KS1 and KS2 are composed of genome group A and E with 76.8% and 22.7%, 69.2% and 30.3%, 85.8% and 13.8% respectively. Isolate ALE and WW are nearly composed of genome group D (92.5%) and E (99%), respectively. Both JQ and ZY2 are comprised of genome group C with 82.6% and 18%, meanwhile JQ and ZY2 containing 17% genome group E and 18% genome group C, respectively. In addition, we found 54, 167, 93, 42, 45, 133 and 38 of non-genome group SNPs in the Chinese isolates. Combining the ratio of different genome group in isolate with its efficacy against different types of resistant codling moth, it points out the way how to optimize the components ratio of CpGV genome group.

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