عنوان مقاله:

Highlights on the Genetic Relationships Between Some Honey Bee Viruses Using Various Techniques

نویسنده:

Hossam Abou-Shaara - *Department of Plant Protection, Faculty of Agriculture, Damanhour University, Damanhour, Egypt*

خلاصه مقاله:

Introduction: Honey bees are used intensively to boost the agricultural and economic sectors worldwide. Many viruses attack honey bees and cause severe problems to the bee colonies, and constitute a real challenge for beekeeping development. Hence, understanding the genetic characteristics of bee viruses is necessary to highlight the phylogenetic relationships between them, and to find out similarity aspects based on sequences. Materials and Methods: Some public resources and free genetic analysis programs were utilized to perform this study. The complete sequences for some viruses were downloaded and analyzed using various programs and methods. Results: Some viruses shared the same base composition pattern in regards to percentage of A, T, C, and G. The phylogenetic relationships among the investigated viruses were presented and discussed. The phylogenetic trees constructed using three bioinformatics programs based on different methods emphasized the relationship between Kashmir bee virus (KBV) and Israeli acute paralysis virus (IAPV), and between deformed wing virus (DWV) and Kakugo virus (KV). These genetic relationships were also confirmed using enzymatic digestion to the sequences, gene cluster families, and open reading frames (ORFs). Conclusions: This study has presented new trends to analyze genetic similarities between organisms utilizing sequences. Different results for the phylogenetic relationships could be obtained when performing the analysis using various methods without impacting the relationships between closely related organisms.

.This study encourages the performance of additional studies to figure out functional components of these viruses

کلمات کلیدی:

Phylogeny, Honey Bees, Viruses, Bioinformatics

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