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CHARACTERIZATION AND PHYLOGENETIC ANALYSIS OF A NEW BACULOVÍRUS: MYTHIMNA SEQUAX NUCLOPOLYHEDROVIRUS

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Resumo

The wheat caterpillar of the species *Mythimna sequax* is the main pest of some crops including wheat, oats, barley and rice in southern Brazil. The baculovirus insect viruses when applied in plantations may be an alternative method of control and that does not harm the ecosystem. However, there are no reports of baculoviruses isolated from *M. sequax*. The Embrapa-Soja virus database contains an extract from wheat laages with symptoms of baculovirus infection. Previous analyzes showed the presence of polyhedra in the extract. Thus, we aim to characterize at the molecular level the putative baculovirus found in the wheat caterpillar extract. We extracted the DNA by previously described methods and sequenced using the 454 platform (Macrogen, South Korea). After sequencing, the data obtained was submitted to *de novo* assembly and annotated the ORFs with the Geneious R9 program. Moreover, BlastX to identify homologous genes. We found the complete genome of a baculovirus, named *Mythimna sequax nucleopolyhedrovirus* (MyseNPV). The genome has a size of 148.403bp and a G+C percentage of 40.3%, with 169 CDS, and 13 ORFs are unique. The virus presents all core genes and after phylogenetic analysis, we found that the virus belonged to the genus *Alphabaculovirus* of Group II, which exclusively infect lepidoptera. The virus is close to the ancestor of the group containing baculoviruses that infect other pests of agricultural importance of MacoNPV-A, MacoNPV-B, MbMNPV and HaMNPV. We found a high degree of identity and syntenia between these genomes. A gain and loss reconstruction was performed within the group, and the main differences were: (1) absence of *helicase-2* in MyseNPV and an independent loss in MacoNPV-A; (2) *lef-7* is only present in MyseNPV and MacoNPV-A, whose absence in others suggests a loss in the ancestor of this group; And (3) *Viral enhancing factor* is absent in MyseNPV. In addition, we found that the *BRO-A* gene has similarity to an ascovirus, that suggests a horizontal acquisition during a co-infection between them in a host cell. Importantly, the position of *chitinase* and *cathepsin* are in contrast to other baculoviruses because they are more distant in the genome, but phylogenetic analyzes and tree reconstructions do not suggest an independent gain and more studies are needed. The analysis of this genome is of extreme importance to study the importance of these genes in viral infection and to develop a bioinsecticide. **Financial support:** Cnpq, FAP/DF

Palavras-chave: baculovírus, wheat pest, MyseNPV, alphabaculovirus, bioinseticide