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GENOMICS OF A NOVEL BACULOVIRUS ISOLATED FROM A LEGUMINOUS PEST, *URBANUS PROTEUS* (LINNAEUS, 1758) (LEPIDOPTERA: HESPERIIDAE)

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Resumo

Baculovirus are insect viruses that naturally controls population of insects including agricultural pests. They are divided into four genera, one them *Alphabaculovirus* are infectious to the larval stage of moths and butterflies. The Embrapa-Soja has a robust collection of viruses with almost 100 extracts of caterpillars that showed symptoms of baculovirus infection. We received part of an extract identified as *Urbanus proteus* NPV (UrprNPV) to analyze. *Urbanus proteus* belongs to the family HesperIIDae, one of the butterfly families that causes severe loss in beans, peas, and fava beans crops during the larval stage. In this work, we sequenced the genome of the putative virus using 454-pyrosequencing. The genome were *de novo* assembled and annotated using Geneious-R9 and BLAST-X. We also reconstructed the virus phylogeny using a set of 38 conserved genes. The genome of UrprNPV is 105 kbp long with a G+C content of 34.7%. We found 119 ORFs of at least 50 amino acid residues; 109 showed similarity to other baculovirus. We found the *f protein*, typical of group II alphabaculoviruses, *iap-2* and *iap-3*, both related to the inhibition of cellular apoptosis. Nine ORFs were shown to be unique and only one presented no hit with any other organism in GenBank. The genome lacks *chitinase*, *cathepsin*, and typical homologous regions. Phylogenetic analysis based on the concatenated dataset of the 38 baculovirus core genes confirmed that UrprNPV is a group II *Alphabaculovirus* and belongs to a lineage that includes *Adoxophyes honmai nucleopolyhedrovirus* (AdhoNPV) and *Adoxophyes orana nucleopolyhedrovirus* (AdorNPV). UrprNPV presents the smallest genome among all alphabaculovirus sequenced to date. In order to understand such small genome, we investigated the loss and acquisition of genes and intergenic spaces in comparison to other closely related viruses. Regarding AdorNPV and AdhoNPV, UrprNPV did not present 17 genes, including 15 hypothetical proteins, one *bro* and the *p43*. The intergenic space was reduced as well. Two hypotheses could explain that genome shortening: UrprNPV belongs to a lineage that reduced independently its genome or this lineage resembled an ancestor that had not acquired genes and intergenic spaces. Importantly, most of the individual phylogenies of each core gene did not reconstruct the phylogeny based on the concatenated dataset, indicating high diversity in this virus lineage depicting resemblance to the ancestor or restricted dataset. **Financial Support:** CNPq

Palavras-chave: *Alphabaculovirus*, agricultural pests, biological control, *Urbanus proteus* NPV, genomics