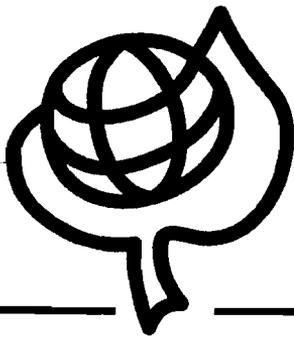


Analysis of several Colombian *Phthorimaea operculella granulovirus* isolated from *Tecia solanivora*: Detection of a new variable region in the PhopGV genome

Xavier Léry¹, Laura Villamizar², Carlos Espinel², Jean -Louis Zeddami³,
Alba Marina Cotes², Miguel López-Ferber⁴

¹IRD, Centre de Recherche, 30380 St Christol-les-Alès, France; ²CORPOICA, Km 14 vía Mosquera, Bogotá, Colombia; ³IRD, PUCE, Quito, Ecuador; ⁴LGEI, Ecole des Mines, Alès, France

Abstract: Five isolates of *Phthorimaea operculella granulovirus* (PhopGV), obtained from *Tecia solanivora* larvae sampled from three different regions of Colombia were studied. One isolate was obtained from an infected larva collected in the north-east near the frontier with Venezuela, one from the south-west near the frontier of Ecuador and the three others from the center of Colombia. They were amplified on larvae of *T. solanivora* reared in laboratory conditions. Isolates were characterized using 12 specific restriction endonucleases and the amplification by PCR of the four variable regions already mentioned for PhopGV, using specific set of primers. The results indicated differences between the strains. The three isolates from the center part of Colombia present the same profiles, and the two others present submolar bands either with REN or with PCR analysis. The Colombian isolates were compared with several PhopGVs originated from Peru, Ecuador and Tunisia and isolated from *P. operculella*, *T. solanivora* and *S. tangolias*. Using the 4 set of primers, the three isolates from the center part of Colombia present a profile specific to *T. solanivora* isolates. In the two other isolates, the submolar bands are the same than the ones found in *P. operculella* profiles, indicating the presence in the genome of at least 2 different profiles. A new variable region was detected in the 90-91 gene region using another set of primers. With this set of primers, a 630 bp band appears, different from the 789 bp band usually found with the other PhopGV strains. The sequence of this part of the genome indicates a deletion in the repetitive part of the 90-91 genes. This deletion appears to be a specific modification only found in viral strains obtained from *T. solanivora* in Colombia.



**IOBC
OILB**

WPRS / SROP

Insect Pathogens and Insect Parasitic Nematodes



editors:

Ralf-Udo Ehlers, Jürg Enkerli, Itamar Glazer,
Miguel Lopez-Ferber & Cezary Tkaczuk

**IOBC wprs Bulletin
Bulletin OILB srop**

Vol. 31, 2008