Complete Genome Sequences of Five *Chrysodeixis chalcites* Nucleopolyhedrovirus Genotypes from a Canary Islands Isolate

Alexandra Bernal, Trevor Williams, Delia Muñoz, Primitivo Caballero, Oihane Simón

INSTITUTO DE AGROBIOTECNOLOGÍA, CSIC-Gobierno de Navarra, Mutilúa Baja, Navarra, Spain; Instituto de Ecología AC, Xalapa, Veracruz, Mexico; Departamento Producción Agraria, Universidad Pública de Navarra, Campus Arrosadia, Pamplona, Navarra, Spain

The *Chrysodeixis chalcites* single nucleopolyhedrovirus (*ChchSNPV*) infects and kills *C. chalcites* larvae, an important pest of banana crops in the Canary Islands. Five genotypes present in the most prevalent and widespread isolate in the Canary Islands were sequenced, providing genetic data relevant to the genotypic and phenotypic diversity of this virus.

Received 24 September 2013 Accepted 27 September 2013 Published 24 October 2013


Copyright © 2013 Bernal et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

Address correspondence to Oihane Simón, oihane.simon@unavarra.es.

The *Chrysodeixis chalcites* single nucleopolyhedrovirus (*ChchSNPV*) (*Baculoviridae: Alphabaculovirus*) has great potential to be a complement or alternative to chemical control of its natural host, *C. chalcites* (*Lepidoptera: Noctuidae*), as occurs with many other baculovirus-host systems (1), particularly for banana protection in the Canary Islands, Spain. A Canadian isolate, ChchSNPV-TF1wt (*ChchTF1*), obtained from a *C. chalcites*-infected larva collected during a natural epizootic in banana crops, is the most prevalent and widespread isolate in the Canary Islands and displays the highest pathogenicity and virulence values compared to previously described strains from the Netherlands (2) and Spain (3, 4). This strain is composed of multiple genotypes, which have been cloned in vitro (5). The complete genome sequences of the three most abundant genotypes, namely, *ChchTF1-A*, *ChchTF1-B*, and *ChchTF1-C*, and the two scarcest ones, *ChchTF1-G* and *ChchTF1-H*, were determined by 454 sequencing, assembled with Newbler version 2.3 software, and checked in detail manually.

The genomes of *C. chalcites* *ChchTF1-A*, *ChchTF1-B*, *ChchTF1-C*, *ChchTF1-G*, and *ChchTF1-H* are 149,684, 149,080, 150,079, 149,039, and 149,624 bp long, respectively, very similar to the genome of the *ChchSNPV* type isolate, *C. chalcites* ChchSNPV-NL (149,622 bp) (*GenBank accession no. AY864330*), from the Netherlands. All five isolates have a 39% G+C content, also similar to that of ChchSNPV-NL (2). The unique ChchSNPV gene, open reading frame (ORF) 53, was not identified in the *ChchTF1-A*, *ChchTF1-B*, *ChchTF1-C*, or *ChchTF1-H* genome due to a single nucleotide mutation in the start codon (TGC). Hence, a total of 150 ORFs were predicted in *ChchTF1-A*, *ChchTF1-B*, *ChchTF1-C*, and *ChchTF1-H*, and 151 ORFs were predicted in the *ChchTF1-G* genome. Fifty-eight ORFs are 100% homologous in the six *ChchSNPV* genomes sequenced to date. The 62 genes conserved in other lepidopteran baculoviruses were also similar to that of ChchSNPV-NL (2). The unique ChchSNPV genome sequences of the three most abundant genotypes, *ChchTF1-A*, *ChchTF1-B*, and *ChchTF1-C*, and the two scarcest ones, *ChchTF1-G* and *ChchTF1-H*, show 98 to 99% homology at the nucleotide level. This analysis also demonstrated that variable genomic regions are located principally in the *hoar* and *bro-d* genes, which represent a major source of intraspecific variability among genotypes in many baculoviruses (7–9). Finally, phylogenetic analysis grouped the five Spanish genotypes and the Dutch genotype in three pairs of clusters: ChchSNPV-NL with ChchTF1-G, ChchTF1-A with ChchTF1-B, and ChchTF1-C with ChchTF1-H.

In all, our work will be helpful for further exploring the genetic diversity of this virus and the genes involved in insecticidal traits.

**Nucleotide sequence accession numbers.** The complete genome sequences of ChchSNPV-TF1-A, ChchSNPV-TF1-C, ChchSNPV-TF1-B, ChchSNPV-TF1-G, and ChchSNPV-TF1-H were submitted to GenBank under the accession no. JX535500, JX560539, JX560540, JX560541, and JX560542, respectively.

**ACKNOWLEDGMENTS**

This work was sponsored by the Instituto Nacional de Investigaciones Agrícolas (RTA2010-00016-C2-02), the Government of Navarra (IIQ14065.RI1), and the Comisión Interministerial de Ciencia y Tecnología (AGL2011-30352-C02-01).

**REFERENCES**


