A new Densovirus isolated from the African cotton bollworm *Helicoverpa armigera Hbn.* (Lepidoptera: Noctuidae) in Egypt

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ABSTRACT

For studying the genomic diversity of the Egyptian Densovirus isolated from Mythimna loreyi (MlDNV), the epidemiological survey was done on the noctuid fauna of the lucerne alfalfa Medicago sativa on which the pests are the same that attack the cotton fields. During this work, we have isolated at El-Bahareya Oasis from dead larvae of the African Cotton Bollworm Helicoverpa armigera another 25 nm icosahedral non-enveloped DNA virus sharing the main biological and biophysical properties of densovirus that we named HaDNV. After characterization and partial cloning of the genome, the presence of antigenic cross-reactivity and some sequence homology indicates that HaDNV and MlDNV are not phylogenetically distant. The 6 kb genome of HaDNV was found to have high homology with members of the Densovirus genus as Galleria mellonella DNV, Junonia coenia DNVand MlDNV.

Key words: Densovirus, Helicoverpa armigera, Noctuidae, El-Bahareya Oasis, molecular characterization.

INTRODUCTION

The African Cotton Bollworm *Helicoverpa (Heliothis) armigera* Hübner as well as the Egyptian Cotton Leafworm *Spodoptera littoralis* Boisd. Both from Lepidoptera: Noctuidae are highly polyphagous agricultural pests. Host species for *H. armigera* come from a broad spectrum of families and include important agricultural crops such as cotton, maize, chickpea, pigeonpea, sorghum, sunflower, soyabean and groundnuts (Cunningham *et al.*, 1999). Females lay eggs on the flowering and fruiting structures of these crops, where voracious larval feeding leads to substantial economic loss. The ability of ovipositing females to locate and utilize a wide range of hosts from a number of families is one of the major factors contributing to the pest status of this moth. Modern pest management strategies for control of *H. armigera* rely upon an understanding of the oviposition behaviour of this insect. However, despite its importance, the host selection behaviour of this moth is still poorly understood (Cunningham *et al.*, 1999).

All the small non-enveloped icosahedral viruses which contain linear single-stranded DNA genome are classified into the family