



Evolutionary analysis of the ubiquitin gene of baculovirus and insect hosts

S.S. Ma, Z. Zhang, H.C. Xia, L. Chen, Y.H. Yang, Q. Yao and K.P. Chen

Institute of Life Sciences, Jiangsu University, Zhenjiang, Jiangsu, China

Corresponding author: K.P. Chen

E-mail: kpchen@ujs.edu.cn

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ABSTRACT. Baculovirus is the only virus that has been found to encode the ubiquitin protein. In this study, ubiquitin sequences from 16 insects and 49 viruses were collected and compared. The resulting sequences were aligned with virus genomes. Then MAGE 5.0, k-estimated software, as well as other software programs were used for systemic evolutionary, selection pressure, and evolutionary distance analysis. The results of the pairwise ratio of non-synonymous to synonymous substitution values and evolutionary distances showed that ubiquitin from baculovirus and insect hosts have been under purifying selection during evolution and are thus evolutionarily conserved. Moreover, genes from insect hosts were more conserved than those in baculovirus. Analysis of the non-synonymous to synonymous substitution rates at each site and entropy calculations revealed the evolutionary status of every site in the ubiquitin genes of baculovirus and their hosts. Genome locations and phylogenetic trees indicated that granuloviruses and non-photosynthetic vegetation evolved, and granulovirus evolution was more similar to that of insect hosts. Our results suggest that the ubiquitin gene in baculovirus may have been acquired through horizontal transfer from the host.

Key words: Baculovirus; Conservation; Evolution; Insect hosts; Ubiquitin