

Relatedness of baculovirus and gypsy retrotransposon envelope proteins

ABSTRACT

A connection between envelope proteins from a group of insect retrovirus-like elements and bacterial protein family (envelope fusion proteins) is established by these analyses. The transposition of gypsy retroelements from insect to baculovirus genomes indicates that this protein may be exchanged between these families.

INTRODUCTION

Baculovirus is a coronavirus that causes gastroenteritis and is endemic in the UK. It is spread through contact with contaminated food or water. It is also spread through contact with contaminated surfaces, such as surfaces of hands, feet, mouth or eyes.

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The virus is transmitted through contact with contaminated Bacteria belong to a diverse group of viruses, including those found in insects such as Lepidoptera, Diptera and Hymenoptera. They have virions that are occlusionary, with the former being present in 100-180 kb DNA genomes. There are two types of baculoviruses: the nucleopolyhedrovirus (NPV) and the budded virion (BV) which spread infection between insects and cells. The MVN proteins facilitate infection process. There is currently no clear indication of two phylogenetic differences between lepidopteran baculoviruses, with the AcMNPV and OpMSPV being among the groups that contain GP64 in their budded virion envelopes. All sequenced gp64-minus viruses, including LdMNPV, SeMNV, Plutella xylostella (PxGV) and Xestia C-nigrum (XcG), have homologs of LD130, which are also present in GHp 64-containing viruses. However, the high variability of the LD130 homologues implies that they were recently inserted into a single baculovirus genome that could have mediated low-pH-dependent membrane vp120, suggesting that GD132 as referred to as In routine database searches, the homologs of LD130 and its homologues identified not only homology with some baculovirus proteins but also predicted envelope proteins of several insect retrovirus-like elements from Drosophila and Lepidoptera (see genbank documentation for AcMNPV orf23 in the AcPNV sequence). Evidence suggests that at least some of these retrovirally-eleven elements are infectious and have been classified as insect Retroviruses or errantivirus. In this report, we show that an evolutionary link between this newly characterized family of

CONCLUSION

Remarkable conclusions The significance of a class of envelope fusion proteins related to gypsy retrovirus-like elements was established by

showing significant correlation between low pH-dependent baculoviruses and envelope proteins. Transposon mediated exchange provides coding for the movement of this gene between insect cells and two different types of viruses.