Relatedness of baculovirus and gypsy retrotransposon envelope proteins

ABSTRACT

These analyses provide a link between envelope proteins from a group of insect retrovirus-like elements and a baculovirus protein family that includes low-pH-dependent envelope fusion proteins. The ability of gypsy retroelements to transpose from insect into baculovirus genomes suggests a pathway for the exchange of this protein between these viral families.

INTRODUCTION

Background Baculoviruses are a diverse family of insect viruses that are pathogenic for insects particularly members of the Lepidoptera, Diptera and Hymenoptera. They have large double-stranded, circular, supercoiled, DNA genomes of 100-180 kb and are characterized by the occlusion of their virions in crystalline protein matrices. There are two genera of baculoviruses, the nucleopolyhedroviruses (NPVs) in which many virions are occluded in large polyhedron-shaped occlusion bodies, and the granuloviruses (GVs) which normally occlude a single nucleocapsid per small granular occlusion body. A novel feature of these viruses is the production of two types of virions. One, the occlusion derived virion (ODV) type, is present in occlusion bodies and spreads the infection between insects, whereas the other, the budded virion (BV) type, spreads the infection between cells within insects or in cell culture. A major difference between these two types of virions is their envelope proteins. The envelope of ODV is not well characterized; and although it may be composed of multiple proteins, the mechanism by which it facilitates the initiation of infection of insect midgut cells is unclear [reviewed in]. In contrast, BV envelopes contain an envelope fusion protein that causes the merging of the virion envelope and the membrane of cellular endocytic vesicles when exposed to low pH. Current evidence suggests that lepidopteran baculoviruses may be divided into two phylogenetic groups based on the envelope fusion proteins of budded virions. One group that includes Autographa californica multinucleocapsid nucleopolyhedrovirus (AcMNPV) and Orgyia pseudotsugata MNPV (OpMNPV), contain GP64 in their budded virion envelopes. Homologs of gp64 are also found in a genus of orthomyxoviruses, the thogotoviruses. Recently a number of complete baculovirus genome sequences have been described and were found to lack an open reading frame with homology to gp64. Analysis of the genome of the Lymantria dispar MNPV (LdMNPV), revealed a single orf (ld130) with predicted signal and transmembrane domains. Characterization of LD130, indicated that it localizes to the membrane of infected cells, is a component of budded virions, and is N-glycosylated. Uninfected cells transiently transfected with a plasmid encoding LD130, showed localization of the protein to the cell membrane and low-pH mediated cell fusion suggesting that LD130 is the envelope fusion protein of LdMNPV. Similar results have been reported for the LD130 homolog in SeMNPV. Homologs of ld130 are found in the genomes of all the sequenced gp64-minus viruses including LdMNPV, SeMNPV, Plutella xylostella GV (PxGV) and Xestia c-nigrum GV (XcGV). In addition, homologs of ld130 are also found in gp64-containing viruses, although they do not appear to be capable of mediating low-pH-dependent membrane fusion (Pearson et al, unpublished). In contrast to the close relatedness of baculovirus gp64 homologs, the LD130 homologs are highly variable suggesting that gp64 was recently incorporated into a baculovirus genome where it displaced the envelope fusion function of the ld130 homologs. Database searches with LD130 and its homologs routinely identify, not only

homologous baculovirus proteins, but some members also showed significant levels of homology with the predicted envelope proteins of a number of insect retrovirus-like elements from Drosophila and Lepidoptera, (also see genbank documentation for AcMNPV orf23 in the AcMNPV sequence). Evidence suggests that at least some of these retrovirus-like elements are infectious and have been classified as insect retroviruses or errantiviruses. In this report, we provide evidence for an evolutionary link between this newly characterized family of baculovirus envelope proteins and the envelope proteins predicted for a variety of insect retrovirus-like retrotransposons. These relationships suggest a possible common origin of the envelope fusion proteins for these two groups of viruses.

CONCLUSION

Conclusions The relatedness of a class of low pH-dependent baculovirus envelope fusion proteins to envelope proteins of gypsy retrovirus-like elements was demonstrated to be highly significant. Transposon mediated exchange provides a documented pathway for the movement of this gene between insect cells, and two different types of viruses.