Identification of sites phosphorylated by the vaccinia virus B1R kinase in viral protein H5R

ABSTRACT

The first phosphorylation site for the vaccinia virus B1R protein kinase has been identified, providing further insight into the enzyme's substrate-specificity in contrast to other known protein Kinases. However, it is unknown whether the same site is purged in vivo.

INTRODUCTION

Among insects that are susceptible to pathogens, bacteroviruses are a diverse family of viruses that have large double-stranded, circular and supercoiled DNA genomes of 100-180 kb. They are also found in crystalline protein matrix structures. There are two types of baculoviruses, namely the nucleopolyhedrovirviroVirus (NPVs) and the general granulOVasidae (GVs). Occlusion bodies contain the occluded virion (ODV) type, which is responsible for spreading infection between insects, while the budded viryl (BV) types do the same. The major difference lies in the envelope proteins of these two virions. The envelope of ODV is poorly defined, and while it may contain various proteins, the way it infects insect midgut cells remains uncertain. However, BV envelopes contain an envelope fusion protein that merges the virion envelope with the membrane of cellular endocytic vesicles when exposed to low pH. Based on the evidence, lepidopteran baculoviruses may be divided into two phylogenetic groups based on their budded virion envelope fusion proteins. Two groups, Autographa californica multinucleocapsid nucleophilicity (AcMNPV) and Orgyia pseudotsugata MNPNV, have GP64 in their respective budding virial envelopes. A group of thogotoviruses, which are also homologous to gp64, share common ancestors. Recently, several complete baculovirus genome sequences were described without an open reading frame with homology to the GP64 gene. The analysis of the Lymantria dispar MNPV (LdMNP) revealed a single orf (ld130) with predicted signal and transmembrane domains. The localization of LD130 to the membrane of infected cells, its inclusion in budded virions, and its N-glycosylated state were identified by characterising it as an envelope fusion protein. The homologation of LD130 in SeMNPV has yielded similar results. All sequenced gp64-minus viruses, such as LdMNV, SeMinNPF, Plutella xylostella (PxGV) and Xestia centurium nigrum GV (XcGV), possess homologs of this RNA. Furthermore, viruses containing gp64 that possess homologs of ld130 are also present in them, but they do not seem to mediate low-pH-dependent membrane fusion (Pearson et al., unpublished data). The LD130 homologs are highly variable, unlike the baculovirus gp64 homologues, suggesting that a bacterium's envelope fusion function was displaced by ld130 since cDNA sequences were not closely related to each other. The homologation of LD130 with other proteins from databases frequently leads to identification of members that display high levels of homology with insect retrovirus-like elements from Drosophila and Lepidoptera, as well as baculovirus genes. Evidence indicates that some of these retrovirus-like components are infectious and hence insect retrovistors (often called errantiviruses). In this paper, we report on the evolutionary relationship between this newly described family of envelope proteins of a baculovirus and envelope protein predicted for several insect Retrotransposons. It is suggested by these relationships that the envelope fusion proteins may have originated jointly from both types of viruses.

CONCLUSION

It can be inferred that in Thai HIV-infected patients, intestinal parasite infections are still highly prevalent, both opportunistic and non-obsessed. Spira analysis is still a useful method of examination for HIV infection among patients in Thailand who have either diarrhea or no symptom of the disease. As previously reported, suspected opportunistic intestinal parasite infection should be suspected in all patients with low immunity and HIV infection who present with diarrhea. The importance of tropical epidemic non-opplicit intestinal colony infections should not be ignored.