

A few years ago, a new endotheliotropic herpes virus was described in African elephants (*Loxodonta africana*), which, when crossing species barriers, may cause lethal haemorrhages in Asian elephants (*Elephas maximus*).

A phylogenetic analysis of viruses from diseased animals showed that at least 2 major groups of EEHV exist, one apparently infecting only African elephants (EEHV2), whereas the other (EEHV1) infects both elephant species. The latter is even further divided into two subgroups (EEHV1 & 1b). Interestingly, EEHV1b has so far only been found in Asian Elephants.

Because glycoprotein B (gB) is a herpes viral envelope protein known to induce a neutralizing antibody response, we sequenced the entire EEHVgB gene from isolated of several diseased elephants. Four different gB variants were found. Computer-aided methods were used to predict functionally important regions within EEHVgB.

An extra-cytoplasmic region of 153 amino acids was predicted to be under positive selection and may potentially contain antigenic determinants useful for future serologic assays developments.

more publications (before 2003)

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