

Complete nucleotide sequence of an endogenous retrovirus from the amphibian, *Xenopus laevis*

Abstract

We report the first full-length sequence of an endogenous amphibian retrovirus derived from the African clawed toad *Xenopus laevis*. The virus, termed Xen1, has one of the largest endogenous retroviral genomes described to date of over 10 kb in length and it also has a relatively complex genomic organisation consisting of LTR-orf1, orf2, gag, pol, env-LTR. Orfs 1 and 2 are novel, duplicated genes of unknown function. Phylogenetic analysis indicates that Xen1 is most closely related to the ϵ -retroviruses WDSV and WEHV types 1 and 2, which are large, complex exogenous retroviruses present within Walleye fish.