Primary structure of the SSAV tether–RNase H endonuclease (pol) region deleted in SSV

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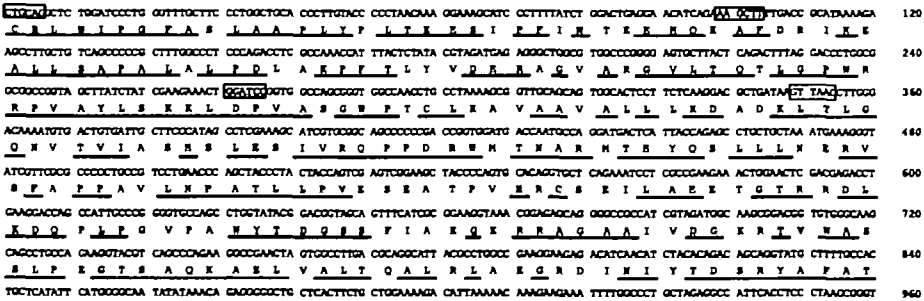
The v-sis bearing simian sarcoma virus (SSV) contains a deleted pol gene relating to only the 3' endonuclease section and therefore requires an associated helper virus (SSAV) for replication. Sequence analysis of an SSAV pol region not contained in SSV was carried out with subcloned SSAV pol fragments (map positions 7.8 - 9 and 0 - 0.8 of B11 (1)) derived from the molecular SSAV clone pB11 (provided by E.P. Geiduschek). The complete nucleotide sequence given below was assigned to tether, RNase H and part of the endonuclease according to (2). Alignment of the translated tether and RNase H amino acid sequence with the corresponding pol sequences of baboon endogenous virus (BaEV) and murine leukemia virus AKV yielded a slightly higher score for BaEV (identical amino acids underlined in figure). The 5' endonuclease showed only weak similarity (not marked in figure).
The SSAV sequence is related to human endogenous retroviral element S71 as shown by phylogenetic analysis (4). Comparisons of the tether sequences of SSAV, BaEV, AKV and S71 with each other indicates that this region is as well conserved as the RNase H domain. The SSAV sequence between position 1337 and 1431 is identical to the SSV pol sequence between position 2903 and 2997 with a single A/C mismatch at 1348/2914. Together with the SSV endonuclease sequence (3) this overlap enables construction of a 2.2 kb SSAV/SSV sequence encompassing all pol domains downstream of the reverse transcriptase.

Restrictions sites present in the map of (1): PstI (1-6), HindIII (99-104), BamHI (271-276), HpaI (349-353), SalI (1054-1059), EcoRII (1154-1159), HpaI (1177-1182), PstI (1251-1256). Additional restriction site: Sac I (1130-1135). Border: tether/RNase H: 617; RNase H/endonuclease 1084 (2)



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