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Full genome sequences of myxoma viruses

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Myxoma virus (MYXV) is a member of the *Leporipoxvirus* genus and causes myxomatosis in the European rabbit. For the examination of evolutionary relationships between leporipox viruses, we sequenced the genomes of six MYXV strains (four field isolates, MAV vaccine strain and ZA challenge strain) and compared them to the wild type strain Lausanne and the vaccine strain SG33. The genomes of the investigated strains differed from 147.6 kb (MAV) to 161.8 kb (Lausanne) and contained 153-171 open reading frames (ORFs). A/T contents varied from 55.6% to 56.4%. Phylogenetic analyses showed a close relationship between MYXVs, but all strains were affected by more or less extensive mutations covering 42-94 ORFs, respectively, resulting in amino acid residue (aa) substitutions, insertions, or deletions. Major differences were observed in the 31 immunomodulatory proteins (IMP). These ORFs are located within and in close proximity to the terminal inverted repeats (TIR). The MAV strain revealed mutations in 21 of these ORFs. Deletions of 14.3 kb in the left and right TIR accounted for the loss of nine IMP containing ankyrin repeats or belonging to the family of serine protease inhibitors. The field strain Munich-1 exhibited mutations in four IMP-ORFs and deletions of five IMP-ORFs. Further apparent mutations were identified in four ORFs encoding the putatively immunodominant envelope proteins M022L, M071L, M083L, and M115L in the MAV vaccine strain causing aa exchanges or protein truncation.

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