

Molecular and genomic characterization of a novel equine molluscum contagiosum-like virus

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Abstract

Cases of pox-like lesions in horses and donkeys have been associated with poxviruses belonging to different genera of the family *Poxviridae*. These include the orthopoxviruses vaccinia virus (VACV), horsepoxvirus (HPXV) and cowpoxvirus (CPXV), as well as a potentially novel parapoxvirus and molluscum contagiosum virus (MOCV). However, with the exception of VACV, HPXV and CPXV, the genomic characterization of the causative agents remains largely elusive with only single short genome fragments available. Here we present the first full-length genome sequence of an equine molluscum contagiosum-like virus (EMCLV) directly determined from skin biopsies of a horse with generalized papular dermatitis. Histopathological analysis of the lesions revealed severe epidermal hyperplasia with numerous eosinophilic inclusion bodies within keratinocytes. Virions were detected in the lesions in embedded tissue by transmission electron microscopy. The genome sequence determined by next- and third-generation sequencing comprises 166 843 nt with inverted terminal repeats (ITRs) of 3473 nt. Overall, 20 of the predicted 159 ORFs have no equivalents in other poxviruses. Intriguingly, two of these ORFs were identified to encode homologues of mammalian proteins involved in immune signalling pathways, namely *secreted and transmembrane protein 1* (SECTM1) and *insulin growth factor-like family receptor 1* (IGFLR1), that were not described in any virus family so far. Phylogenetic analysis with all relevant representatives of the *Poxviridae* suggests that EMCLV should be nominated as a new species within the genus *Molluscipoxvirus*.

Keywords: IGFLR1; SECTM1; equine molluscum; novel poxvirus, Molluscipoxvirus.