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Evidence for Immuomodulatory function in the first full genome assembly of Equine herpesvirus 5

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Infection of the horse by equine gammaherpesviruses -2 and- 5 (EHV-2 and EHV-5) is common throughout the world, EHV-5 is commonly found in respiratory samples from clinically normal as well as sick horses, however recently it has been associated with equine multinodular pulmonary fibrosis (EMPF). Partial sequence information is available FOR EHV-5 (DNA pol) and full gene sequence of gB, gH and DNA terminase genes. This study describes the first full genome sequence of EHV-5 assembled using illumine short read platform. EHV-5 isolate 2-141 was propagated on primery equine foetal kidney cells, purified before the genomic DNA was extracted. Reads assembled Denovo to give EHV-5 consensus (Geneious 6.1.2 Java version 1.6.0_ 35-b10 (64 bit)). Ab initio gene prediction and annotation performed by Geneious, BLASTn, BLASTx and tBLASTx algorithm. Final assembly yielded a 173 bp sequences with an average G+C content of 55% throughout with some fluctuation in short repeat regions. Eighty four were annotated; including sixty four are EHV-2 homologue, twenty seven HVS homologue. Eighteen ORFs were unique to EHV-5, some with potential immunomodulatory functions. EHV-5 ORF eg 2 and ORF eg 10 assigned with a putative viroceptor and apoptosis regulator function. Homologue of at least six other ORFs were also detected and identified with immunomodulatory effects during herepsviral infection. ORF 74 found as exclusive homologue to HVS genome whereas ORF E7 is a homologue from EBV genome with putative viroceptor role. In conclusion, presences of host derived immunomodulatory putative genes may suggest a possible role for disease development by compromising host immunity or as co-factors for other organisms.

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