Evidence of new recombinations among equid herpesvirus

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Equid herpesviruses (EHV) belong to the Herpesviridae family and are divided into three subfamilies known as Alpha, Beta and gammaherpesviruses. Within alphaherpesvirus, there are 6 viruses with different hosts such as Horses, donkeys, zebras known.

Previous studies have reported interspecific recombinations between EHV1 and 4. Others have suggested recombinations between EHV1 and 8.

Here, we realized a bioinformatic study from EHV1, 4, 8, and 9 genomes present in GenBank. All these sequences were analyzed with RDP4, SplitsTree and Simplot for recombination evidence. In total, 13 events were found, some of them present in more than a genome.

These recombinations are present in EHV1 being the minors parents EHV4 and EHV9. Two events are in EHV8 being EHV1 and 4, the minor and major parents respectively.

Most episodes are targeting the same gene previously described: ICP4.

ICP4 is a gene with two copies located in the repetitive regions. It’s associated with transcriptional regulations. The presence of recombination events with different breakpoints makes us believe ICP4 is a hot spot. ICP4 events were evidenced in EHV1 with both EHV4 and EHV9 as minor parents. Future studies of in vitro replication should be displayed to prove the importance of ICP4 as a facilitator of interspecific recombination.

Episodes of recombinations between EHV1 and EHV9 are also associated with another repetitive gene, ICP22, which gives us the idea that repetitive regions tend or allow recombination. Another EHV1 with EHV9 recombination event involved genes from the unique long zone (UL). EHV8 recombinations also entailed UL genes.

Emerging interspecific recombinant viruses could generate unknown pathogenesis and be able to infect new hosts. We report previously not described recombinations, some involving EHV9 as the minor parent and affecting EHV1 zebra borne type strains. These recombinations might be conferring EHV1 the capacity to infect hosts others than horses.

1. What is your pathogen? Multiple options possible (e.g. if working on coinfections)

Other viruses : Equid herpesvirus

2. On a scale of 1-5 is your work mostly eco/epidemiological or evolutionary? 5 (100% evolutionary)

3. On a scale of 1-5 is your work mostly theoretical or experimental/empirical?
5 (100% empirical)

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