

Alternative genes for exploring *Ranavirus* phylogenetics: Four core genes compared to the major capsid protein and the whole genome.

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The *Iridoviridae* is a family of virus that infects invertebrates and poikilothermic vertebrates such as amphibians, reptiles, and fish. *Ranavirus* is one of the five genera within the *Iridoviridae*. *Ranavirus* infections have been seen on every continent. The ranaviruses have 26 core genes, but our study focuses on the utility of: an immediate early protein ICP-46 [open reading frame (ORF) 91R in *Frog virus 3* (FV3)]; a transcription elongation factor TIIS (ORF 81R in FV3); Evrl/Air family protein (ORF 88R in FV3); and a hypothetical/putative protein of unknown function (ORF 94R in FV3) as alternative genes for phylogenetic reconstruction in this group. Gene sequences were obtained from GenBank, aligned using MAFFT, and trees were constructed in MEGA using the Neighbor-Joining method (with 1000 Bootstraps). The phylogenetic trees made from the 4 core genes will be compared to trees built in the same manner using the major capsid protein sequence (MCP, ORF 90R in FV3) and the whole genome. The MCP gene is commonly used to reconstruct phylogenetic relationships for ranaviruses because of its conserved nature. This is part of a larger project which seeks to understand which of the 26 core genes are the most phylogenetically informative.