

ANALYZING PHYLOGENETIC RELATIONSHIPS AMONG RANAVIRUSES: MYRISTILATED MEMBRANE PROTEIN AND OTHER POTENTIAL ALTERNATIVES TO MAJOR CAPSID PROTEIN

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Ranaviruses are globally distributed emerging infections of ectothermic and poikilothermic vertebrates. They are responsible for countless morbidity and mortality events around the globe, and they are known to affect several endangered species. Therefore, understanding the evolutionary relationships among different strains of *Ranavirus* becomes important if we are to predict the consequences of their emergence. Past best practice for classifying different *Ranavirus* isolates has mainly been based on the major capsid protein (MCP), which is a highly conserved gene. However, this approach does not appear to capture the full sequence diversity of isolates. Twenty-six core genes have been identified for ranaviruses, some of which may better demonstrate the true phylogenetic relationships among different isolates. Here, we use the myristilated membrane protein (open reading frame 2L in *Frog virus 3*; MMP) as an alternative to the MCP gene for constructing *Ranavirus* evolutionary trees. We compare trees obtained using full length genomes, only the MCP gene sequences, and only the MMP gene sequences. Trees are built using the Neighbor-Joining method (1000 Bootstraps) and an appropriate nucleotide substitution model using MEGA6. Trees are then compared visually for similarities and differences. The same methods will be used to compare myristilated membrane protein A (ORF 53R in FV3), unknown protein A (ORF 41R in FV3), and unknown protein B (ORF 12L in FV3), all of which are members of the twenty-six core genes, as suitable alternatives or supplements to MCP.

Keywords: *Ranavirus*, emerging infection, myristilated membrane protein, major capsid protein, phylogenetic reconstruction