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Sequence Analysis of the Fibroblast Growth Factors Found in the Baculoviridae and Iridoviridae

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Genomic sequences reveal that homologues to vertebrate fibroblast growth factors (FGFs) are found in all species of the genera Alphabaculovirus and Betabaculovirus in the family Baculoviridae, as well as in several species in the genus Ranavirus of the family Iridoviridae. Single copies of these viral FGFs (vFGFs) are found in the genomes of the alphabaculoviruses, one or two copies are found in the ranaviruses, while the betabaculoviruses all possess three different types of vFGF, which are termed vFGF-1, vFGF-2, and vFGF-3. Previous research from other laboratories on the alphabaculovirus FGFs has established them as important virulence factors that appear to be involved in promoting systemic infection within the host. The primary structures of all these vFGFs vary considerably, but multiple sequence analysis and phylogenetic trees show that the vFGFs cluster into clades based on their source species and type (e.g. vFGF-1, 2, and 3). Pfam annotation shows that the vFGF-2 from *Spodoptera litura* granulovirus contains two FGF cores within a single polypeptide chain, a highly unusual feature that is shared by only two other proteins among the 845 sequences contained in the FGF family in this database. We report that this second FGF core is shared by other betabaculovirus vFGF-2 sequences. Homology modeling of several vFGFs suggests that their FGF cores will conserve much of the secondary structure seen in other FGFs, but with greater variability seen in the solvent exposed loops and the amino and carboxy terminal regions. Analysis of the predicted signal sequences, transmembrane regions, secondary structures, and receptor binding residues for all known vFGF sequences will also be reported.