A sequence comparison of the VP72 gene of African Swine Fever Virus.

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African Swine Fever Virus (ASFV) is the sole member of a virus class, being related to both the iridoviridae by morphology[1-3] and the poxviridae by genome and cytoplasmic replicative cycle[4-7]. It has a genome size of between 170 and 195 kb, depending on the isolate and it has an icosahedral capsid and a membrane, but no coat glycoprotein.

VP72 is a gene coding for a 72 kilodalton coat protein which is expressed late in infection. We are studying the sequence and organisation of its promoter with the aim of identifying transcription factors involved in VP72 gene expression.

We have isolated a clone (LMw9) of the VW2 gene in λEMBL3 vector from a Malawi isolate of ASFV (LIL21). We have subcloned a 2.4 kb Hind III/Sal I fragment from LMw9 containing the transcription start site and approximately 1.4 kb of upstream sequence into the Bluescript M13 vector. From this subclone we have produced two truncated subclones which should enable us to make suitable reporter gene constructs for a transcription analysis of the VP72 gene.

We have carried out preliminary sequence analysis of these subclones, comparing both upstream and coding regions of the VP72 gene to similar regions of a Spanish ASFV isolate with a view to possibly identifying conserved upstream sequences which are likely to be involved in the expression of the gene. Any such conserved sequences might be probable sites of transcription factor binding which could be further investigated. These sequence comparisons are shown in Figures 1 and 2.

![TTATGGTGATAAAGCGC'CGCCGAAGCGAATGT](image1)

**Figure 1 VP72 coding region sequence comparison.**

The nucleotide differences in the Spanish isolate are shown below the sequence of the Malawii isolate. The region shown is around amino acid residue 330.

![G-TTTTTTTTCTGCCAGCAACCAGGCTGTC](image2)

**Figure 2 VP72 upstream sequence comparison.**

The upper line is the sequence of the Malawii isolate from about -20 from the ATG. The lower sequence is the Spanish isolate. Dashes indicate deletions within the gene is much greater than that upstream of the coding region, although there are some regions of higher conservation. These may be the motifs likely to be involved in gene regulation, possibly as transcription factor binding sites. We are currently working on studies of the proteins which bind at these sites in infected cells.

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