

## **Enhanced discrimination of African swine fever virus isolates through nucleotide sequencing of the p54, p72, and pB602L (CVR) genes**

### **Abstract:**

Complete sequencing of p54-gene from 67 European, American, and West and East African Swine Fever virus (ASFV) isolates revealed that West African and European ASFV isolates classified within the predominant Genotype I according to partial sequencing of p72 were discriminated into four major sub-types on the basis of their p54 sequences. This highlighted the value of p54 gene sequencing as an additional, intermediate-resolution, molecular epidemiological tool for typing of ASFV viruses. We further evaluated p54-based genotyping, in combination with partial sequences of two other genes, for determining the genetic relationships and origin of viruses responsible for disease outbreaks in Kenya. Animals from Western and central Kenya were confirmed as being infected with ASFV using a p72 gene-based PCR assay, following outbreaks of severe hemorrhagic disease in domestic pigs in 2006 and 2007. Eleven hemadsorbing viruses were isolated in macrophage culture and genotyped using a combination of full-length p54-gene sequencing, partial p72-gene sequencing, and analysis of tetrameric amino acid repeat regions within the variable region of the B602L gene (CVR). The data revealed that these isolates were identical in their p72 and p54 sequence to viruses responsible for ASF outbreaks in Uganda in 2003. There was a minor difference in the number of tetrameric repeats within the B602L sequence of the Kenyan isolates that caused the second Kenyan outbreak in 2007. A practical implication of the genetic similarity of the Kenyan and Ugandan viral isolates is that ASF control requires a regional approach.