Detection of Vaccinia Virus in Dairy Cattle Serum Samples from 2009, Uruguay

Technical Appendix

Technical Appendix Figure 1. A) Antibody titers for virus neutralization in 125 cattle serum samples from Durazno, Uruguay. The samples were considered positive if they reduced at least 70% of the virus plaques. B) A56R (HA) gene nucleotide identity matrix. The analysis involved 18 nt sequences. Evolutionary analyses were conducted in MEGA 6.
Technical Appendix Figure 2. A) Nucleotide sequence of the vaccinia virus (VACV) Uruguay A56R hemagglutinin (HA) gene (indicated by dot) compared with homologous sequences from several other *Orthopoxviruses*. VACV Uruguay showed one polymorphism (A→T) in comparison with other VACVs. B) Phylogenetic tree based on nucleotide sequences of orthopoxvirus HA gene (indicated by dot). The tree was constructed with HA sequences by using the neighbor joining method with 1,000 bootstrap replicates and the Tamura 3-parameter model in MEGA6 (http://megasoftware.net/). Bootstrap values are represented on branches; only values >60% are shown. Nucleotide sequences were obtained from GenBank. Scale bar represents 0.05 substitutions per nucleotide position.