Comparative genomic variation in porcine species could lead to species-specific responses to ASF


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Target Audience: Researchers, Animal health workers

Abstract

African Swine Fever (ASF) is a highly contagious viral disease of pigs and is of utmost concern due to its presence in list A diseases by the United Nations Office International des Epizooties (OIE). It causes significant economic losses in affected countries due to resulting high mortality rates associated. In contrast, the porcine species endogenous to Africa tolerate infection. The ability of the virus to persist in one host, while killing another genetically related host implies that the disease may influence by the hosts genetic variation. This study identify genetic polymorphism among three suidae family species in susceptibility to ASFV based on five genes such as RELA, NFATCI, PPIA, PPP3CB, NKBIA. It alsopredicts the protein structure of each gene and draw phylogenetic trees of each gene using human as an out-group. The nucleotide and amino acid sequence (AAS) of the 5 genes of pig, warthog and Babyrus were downloaded from the National Center for Biotechnology information (NCBI) data base, United State of America and Universal protein resources (Uniprot) database, United Kingdom. Data and phylogenetic trees were constructed using MEGA7. The variation observed at position 531 in RELA gene between warthog and domestic pig may be a significant factor behind the susceptibility or tolerance to ASFV. This study could give genomic bases to the discovery of a potent vaccine for prevention, control and prophylaxis.

Key words: African Swine Fever, Pigs, Warthogs, Babirusa