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Presence of Genotypes IX and X of African Swine Fever Virus in Apparently Healthy Domestic Pigs in South Kivu Province, Democratic Republic Congo

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Abstract

African swine fever (ASF) is an important viral disease of domestic pigs causing devastating outbreaks with huge impact on commercial and smallholder pig production in most of sub-Saharan African countries. Frequent suspected ASF outbreaks occur in South Kivu province with no data corroborating its presence and the circulating genotypes. The aim of this study was to determine the circulating ASFV genotypes and prevalence of ASF in domestic pigs in South Kivu province, DR Congo. Blood samples were collected from 267 clinically healthy pigs in different farms during the period of January-August 2016 to investigate presence of ASFV and ASFV strains using the C-terminal region of the B646L gene. A discrete and specific band of the expected size 257 base pairs was observed in 65 samples giving a prevalence of 24.3% (95% CI, 2.7- 9.5). ASFV infection was significantly higher ($p < 0.003$) in local (20.6%) than in improved pigs (2.2%). In addition, the statistical analysis results revealed that ASFV infection in domestic pigs varied significantly according to geographical location ($p < 0.001$) with the highest infection found in Uvira territory (40%) while the lowest was registered in Kabare (3.1%). Age and sex of pigs had no significant influence on ASFV infection ($p > 0.05$). Phylogenetic analyses based on part of the p72 and the complete p54 (E183L) genes revealed two circulating ASFV genotypes namely genotypes IX and X. Genotype IX clustered together with isolates from Kenya, Uganda and Congo Brazzaville, while genotype X clustered together with viruses responsible for recent ASF outbreaks in Burundi and Kenya. This is the first evidence of genotype X within the DR Congo. The genetic similarity of domestic pig-associated genotypes identified in healthy pigs from the border region between DR Congo, Uganda, Burundi and Congo Brazzaville, and the probability of trans-boundary transmission between these countries emphasizes the need for a regional approach for better control of ASF. More samples on suspected ASF-infected pigs will be required for developing an accurate sequence database and to understand the origin of the disease in the region.

Keywords: African swine fever virus, diagnosis, genotypes, healthy pigs, South Kivu province

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