

Viral Metagenomics Demonstrates That Domestic Pigs Are A Potential Reservoir For Ndumu Virus

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Abstract:

Background The rising demand for pork has resulted in a massive expansion of pig production in Uganda. This has resulted in increased contact between humans and pigs. Pigs can act as reservoirs for emerging infectious diseases. Therefore identification of potential zoonotic pathogens is important for public health surveillance. In this study, during a routine general surveillance for African swine fever, domestic pigs from Uganda were screened for the presence of RNA and DNA viruses using a high-throughput pyrosequencing method. **Findings** Serum samples from 16 domestic pigs were collected from five regions in Uganda and pooled accordingly. Genomic DNA and RNA were extracted and sequenced on the 454 GS-FLX platform. Among the sequences assigned to a taxon, 53% mapped to the domestic pig (*Sus scrofa*). African swine fever virus, Torque teno viruses (TTVs), and porcine endogenous retroviruses were identified. Interestingly, two pools (B and C) of RNA origin had sequences that showed 98% sequence identity to Ndumu virus (NDUV). None of the reads had identity to the class Insecta indicating that these sequences were unlikely to result from contamination with mosquito nucleic acids. **Conclusions** This is the first report of the domestic pig as a vertebrate host for Ndumu virus. NDUV had been previously isolated only from culicine mosquitoes. NDUV therefore represents a potential zoonotic pathogen, particularly given the increasing risk of human-livestock-mosquito contact.