

Detection and molecular characterization of selected swine enteric viruses in smallholder farms in Kenya and Uganda

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Summary

Virus induced enteritis is one of the serious problems accounting for maximum deaths in neonatal animals and human throughout the world. The absence of appropriate surveillance programs and laboratory facilities have resulted in scarcity of accessible data on virus associated diarrheas in pigs in the region. This study reports the incidence of selected enteric viral infections in nursing and weaned pigs on smallholder farms. A total of 251 swine fecal samples were screened for rotaviruses (RV), caliciviruses (CaV) and kobuviruses (KoV) using RT-PCR assay. Rotaviruses, CaV and KoV were detected in 42.6%, 12.7% and 13.1% of the samples, respectively. There were incidences of mixed infections involving RV, CaV and KoV. These viruses were detected in almost equal proportions in Kenya and Uganda, an indication of their endemicity on the tested farms. More nursing piglets shed RV (85.4%) and CaV (29.3%) than weaned piglets. However, KoV was more prevalent in post weaned pigs. More pigs that were either housed & free-range (82.4%) or tethered & free-range (45.1%) were RV positive than tethered (38.3%) or free-range (12.5%) or housed (33.3%) pigs. Pigs that were entirely housed shed more KoV (33.3%) while those that were housed & tethered shed more CaV(33.3%). Age and management system affected the prevalence of viral infections with nursing and confinement presenting higher risk for enteric viral infections. Partial sequencing of VP4 gene of selected positive samples revealed that different P genotypes (P[6], P[8] and P[13]) are circulating in the study region. The P[6] and P[8] RV genotypes detected were genetically closely related to human strains suggesting the possibility of interspecies transmission. Genetic analysis of the *kobuvirus* sequence revealed that they are more variable, sharing nucleotide identity ranging from 89.7-99.1% among them. Porcine astroviruses belonging to type 2 and type 3 *Mamastroviruses* were detected in 3 samples sequenced. This study reports the first detection and molecular analysis of porcine rotaviruses, caliciviruses, kobuviruses and astroviruses in Africa. The presence of these gastroenteritis-producing viruses in clinically healthy pigs represents a source of infection to pigs and possibly to humans. Further research is needed to determine their role in gastrointestinal infections of pigs in this region and to determine their genetic diversity in-order to develop accurate diagnostic tools and implement appropriate control strategies to improve pig health.

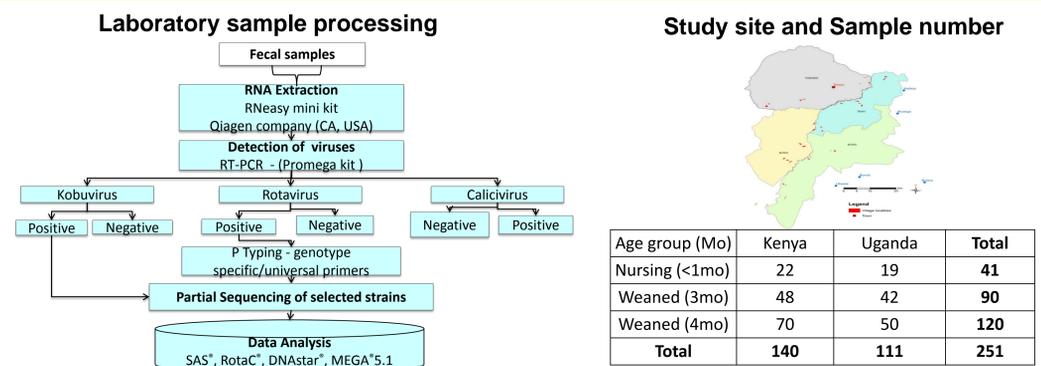
Introduction

- Small-scale pig production (free range or small backyard herds) constitutes >70% of the total pig farmers in Kenya and Uganda
- Viral diseases of swine represent the greatest challenges in the control and prevention of infectious diseases
- Viral diarrhea causes huge economic losses to pig farmers (esp. developing countries) due to loss of production; cost of treatment and control measures; and mortality
- Rotavirus-associated enteritis is a major problem in young calves (Saif & Jiang, 1994) and nursing and post-weaning piglets (Kapikian et al., 1996)
- Caliciviruses are recognized as the most common cause of non-bacterial acute gastroenteritis in persons of all age groups (Green, 1997)
- Porcine kobuvirus has been detected at high frequency in healthy pigs; however, a recent study in Korea reported an association between porcine kobuvirus detection and diarrhea in pigs (Park et al., 2010)
- Astroviruses are generally associated with either mild or severe enteric disease symptoms such as diarrhea and vomiting in a number of mammalian species (Jonassen et al., 2001)
- The prevalence of porcine RV, CaV and KoV in the East African is unknown but they are suspected to play an important role in diarrhea in suckling and weaned piglets

Objective

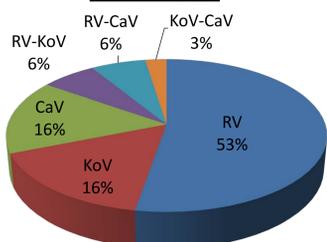
To investigate the prevalence and genetic diversity of rotaviruses, kobuviruses and caliciviruses in fecal samples from domestic pigs of various ages collected in Kenya and Uganda using RT-PCR assay and partial sequencing

Methods

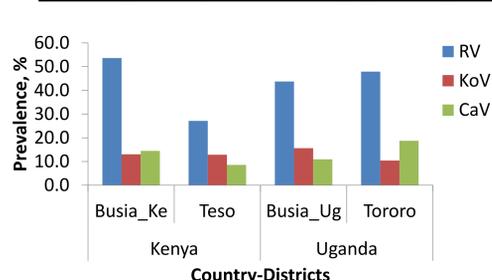


Results

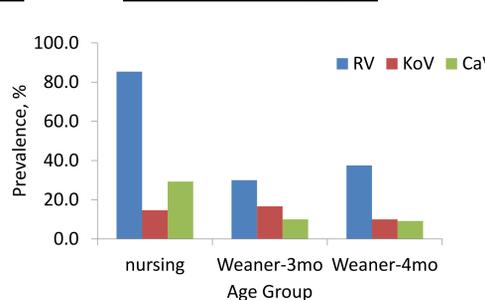
RVs were dominant in nursing and weaned pigs



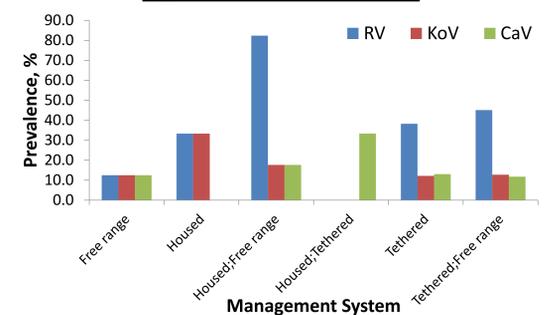
High incidence of enteric viruses in Busia and Tororo ✓ proximity to major town and pig density may play a role



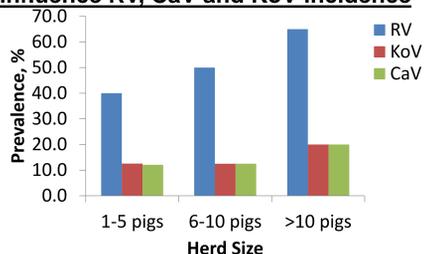
More nursing piglets shed RV and CaV than weaned piglets



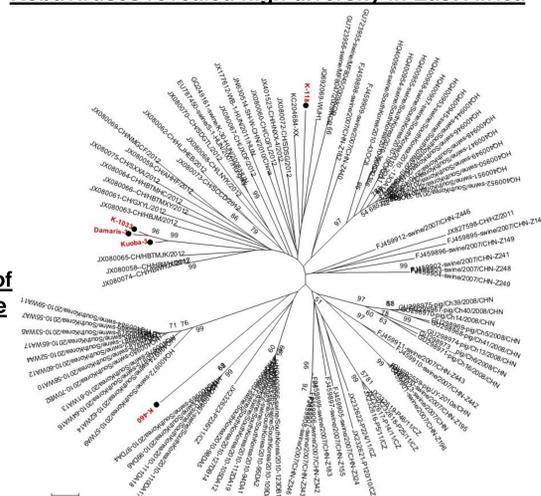
Housed;freerange management system showed higher risk for RV infection



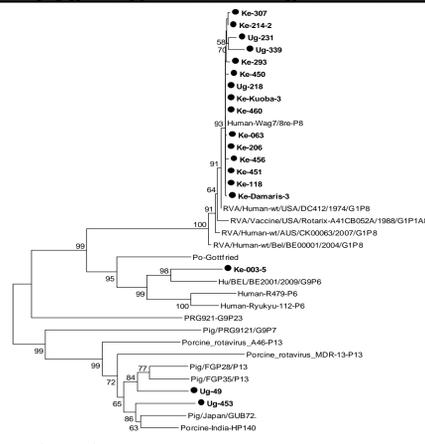
Number of pigs per household influence RV, CaV and KoV incidence



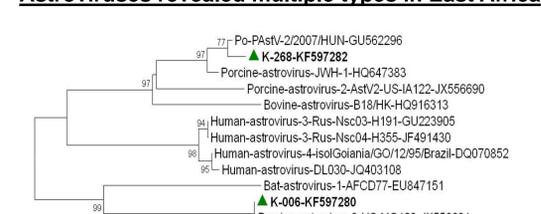
Phylogenetic analysis of the partial RdRp gene of Kobuviruses revealed high diversity in East Africa



Phylogenetic analysis of the partial VP4 gene of RVA revealed multiple P types – predominance of P[8] genotype resembling human strains



Phylogenetic analysis of the partial RdRp gene of Astroviruses revealed multiple types in East Africa



Conclusions

- This study confirms the presence of RVs, CaVs, KoVs and astroviruses in the swine population in E. Africa.
 - RV is the dominant virus** and both RV, CaV and KoV occur alone and in mixed infections.
 - Age and management system affected the prevalence of RV infections with **housed-freerange system showing the highest risk for RV infection.**
 - Different P genotypes (P[6], P[8] and P[13]) are circulating in the study region with **P[8] being more dominant and closely related to human strains.**
 - Epidemiological studies to investigate the prevalence and characterize the circulating RV, CaV and KoV strains in East Africa is an important step towards understanding the ecology, genetic diversity and their association with diarrhea in pigs.
 - The study is important for the development of accurate diagnostic tools; potential vaccines; and to aid in implementation of appropriate control strategies for enteric viral diseases in pigs leading to improved health.
- ✓ Improved pig health will lead to improved production and ultimately improved livelihood.

Acknowledgement

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