ABSTRACT

Viral enteritis is a serious problem accounting for deaths in neonatal animals and humans worldwide. The absence of surveillance programs and diagnostic laboratory facilities have resulted in a lack of data on rotavirus associated diarrheas in pigs in East Africa. Here we describe the incidence of group A rotavirus (RVA) infections in asymptomatic young pigs in East Africa. Of the 446 samples examined, 26.2% (117/446) were positive for RVA. More nursing piglets (78.7%) shed RVA than weaned (32.9%) and grower (5.8%) pigs. RVA incidence was higher in pigs that were either housed_free-range (77.8%) or tethered_free-range (29.0%) than those that were free-range or housed or housed-tethered pigs. The farms with larger herd size (>10 pigs) had higher RVA prevalence (56.5%) than farms with smaller herd size (24.1-29.7%). This study revealed that age, management system and pig density significantly ($p<0.01$) influenced the incidence of RVA infections, with housed_free-range management system and larger herd size showing higher risks for RVA infection. Partial (811-1604nt region) sequence of the VP4 gene of selected positive samples revealed that different genotypes (P[6], P[8] and P[13]) are circulating in the study area with P[8] being predominant. The P[6] strain shared nucleotide (nt) and amino acid (aa) sequence identity of 84.4-91.3% and 95.1-96.9%, respectively, with known porcine and human P[6] strains. The P[8] strains shared high nt and aa sequence identity with known human P[8] strains ranging from 95.6-100% to 92-100%, respectively. The P[13] strains shared nt and aa sequence identity of 83.6-91.7% and 89.3-96.4%, respectively, only with known porcine P[13] strains. No P[8] strains yielded RNA of sufficient quality/quantity for full genome sequencing. However analysis of the full genome constellation of the P[6], two P[13] and one untypeable strains revealed that the P[6] strain (Ke-003-5) genome constellation was G26-P[6]-I5-R1-C1-M1-A8-N1-T1-E1-H1, P[13] strains (Ug-049 and Ug-453) had G5-P[13]-I5-R1-C1-M1-A8-N1-T7-E1-H1 while the untypeable strain (Ug-218) had G5-P[?]-I5-R1-C1-M1-A8-N1-T1-E1-H? In conclusion, P[6] and P[8] genotypes detected were genetically closely related to human strains suggesting the possibility of interspecies transmission. Further studies are required to determine the role of RVA in swine enteric disease burden and to determine the genetic/antigenic heterogeneity of the circulating strains for development of accurate diagnostic tools and to implement appropriate prophylaxis programs.