

ABSTRACT

In this study, swine fecal specimens (n = 251) collected from nursing and weaned piglets raised under smallholder production systems were screened for the presence of kobuviruses by RT-PCR. Porcine kobuviruses were detected in 13.1 % (33/251) of the samples. We demonstrated that porcine kobuvirus infections exist in indigenous pigs in Kenya and Uganda and that the prevalence was higher in young piglets than older pigs: nursing piglets (15 %), post-weaning (3-month-old) pigs (17 %), 4-month-old pigs (10 %). Genetic analysis of the partial RNA-dependent RNA polymerase (RdRp) region (690 nt) revealed that kobuviruses circulating in East Africa are diverse, sharing nucleotide sequence identities ranging from 89.7 to 99.1 % and 88 to 92.3 % among them and with known porcine kobuviruses, respectively. The nucleotide sequence identities between our kobuvirus strains and those of human, bovine and canine kobuviruses were 69.4-70.7 %, 73.1-74.4 % and 67-70.7 %, respectively. Additionally, upon sequencing selected samples that showed consistent 720-bp RT-PCR bands while using the same primer set, we detected porcine astroviruses in our samples belonging to type 2 and type 3 mamastroviruses. To our knowledge, this study reports the first detection and molecular analysis of both porcine kobuviruses and astroviruses in an African region. Further studies are required to determine the role of these viruses in gastrointestinal infections of pigs in this region and to determine the genetic diversity of the circulating strains to develop accurate diagnostic tools and implement appropriate control strategies.