During a severe outbreak of diarrhoea and vomiting in a pig herd in Central Eastern Europe, faecal samples were tested positive for porcine epidemic diarrhoea virus (PEDV) and negative for transmissible gastroenteritis virus (TGEV) using a commercial RT-qPCR assay that can detect both of these coronaviruses. However, further analyses, using other TGEV- and PEDV-specific RT-qPCR assays, provided results inconsistent with infection by either of these viruses. Sequencing of an amplicon (ca. 1.6 kb), generated by an RT-PCR specific for the PEDV S-gene, indicated a very close similarity (ca. 99% identity) to recently described chimeric viruses termed swine enteric coronaviruses (SeCoVs). These viruses (with an RNA genome of ca. 28 kb) were first identified in Italy in samples from 2009 but have not been detected there since 2012. A closely related virus was detected in archived samples in Germany from 2012, but has not been detected subsequently. Building on the initial sequence data, further amplicons were generated and over 9 kb of sequence corresponding to the 3′-terminus of the new SeCoV genome was determined. Sequence comparisons showed that the three known SeCoVs are ≥98% identical across this region and contain the S-gene and 3a sequences from PEDV within a backbone of TGEV, but the viruses are clearly distinct from each other. It is demonstrated, for the first time, that pigs from within the SeCoV-infected herd seroconverted against PEDV but tested negative in a TGEV-specific ELISA that detects antibodies against the S protein. These results indicate that SeCoV is continuing to circulate in Europe and suggest it can cause a disease that is very similar to PED. Specific detection of the chimeric SeCoVs either requires development of a new diagnostic RT-qPCR assay or the combined use of assays targeting the PEDV S-gene and another part of the TGEV genome.