Diversity and zoonotic potential of rotaviruses in swine and cattle across Europe.

Group A rotaviruses can infect both humans and animals. Individual rotavirus strains can occasionally cross species barriers and might hereby contribute to the emergence of new genotypes in heterologous hosts. The incidence and impact of zoonotic rotavirus are not well defined, and one reason for this is a lack of data about strains circulating in suspected reservoir animal hosts. In this study we report the incidence, genetic diversity, and molecular epidemiology of rotaviruses detected in domestic cattle and swine in 6 European countries. From 2003 to 2007, 1101 and more than 2000 faecal specimens were collected from swine and cattle, both healthy and diarrhoeic, and tested for rotaviruses. Viruses from positive stools were genotyped and a subset of strains was characterized by nucleotide sequencing and phylogenetic analysis of the VP7 (G) and VP4 (P) genes. Rotaviruses were detected in 43% of bovine samples and in 14% of porcine samples. In cattle, 10 different combinations of G and P types were identified and the most common strains were G6P[11] and G6P[5]. In swine, the number of identified G–P combinations was higher (n = 21), however, no single combination was predominant across Europe. Newly described genotype specificities, P[27] and P[32], were identified in swine. When compared at the nucleotide sequence level, the identified porcine rotavirus strains and contemporary human strains grouped together phylogenetically, whereas bovine rotavirus strains formed separate clades. These data demonstrate large genetic diversity of porcine and bovine rotavirus strains across Europe, and suggest that livestock herds may serve as potential reservoirs for human infections.