

MIGHT GREAT VARIABILITY OF PORCINE ROTAVIRUS A HAMPER THE VACCINE EFFICACY IN PIGS?

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Introduction

Rotaviruses (RV) are known for their complex epidemiology, pathogenicity and great genetic diversity. Currently, nine species of rotaviruses (marked by the letters A-D, F-J) are known. So far, rotaviruses A, B, C, and H have been detected in pigs; all of these rotavirus species can cause diarrhoea. From a veterinary point of view, RVA represents one of the most important causes of acute diarrhoea of young animals. Apart from the first days of life, piglets are at great risk of RV infection during the weaning period. Detailed characterization of rotaviruses provides valuable information on the presence of new genetic variants that may escape vaccine-induced herd immunity, as observed in the case of the human RVA vaccines. In Czech pig farms, an inactivated vaccine against rotavirus and E. coli infections is used for active immunization of pregnant sows and gilts. This vaccine contains one inactivated strain of porcine RVA (OSU); the genes for its major surface antigens are assigned to the G5P[7] genotype.



	Suckling	Weaned	Total
RVA+	16	0	16
RVB+	3	2	5





RVC+	0	2	2
RVA+B+C+	3	17	20
RVA+B+	10	14	24
RVA+C+	8	0	8
RVB+C+	0	1	1
Negative	18	0	18
Total	58	36	94

Methods

The examined feces samples collected in 2021-2023 were processed according to the previously described methodology.¹ From the prepared complementary DNA (cDNA), the genomes of RVA (own modification)², RVB and RVC were detected using real-time PCR with a hydrolysis probe (qPCR).³ In the selected positive samples, the entire section of the gene encoding the surface antigen VP7 and the variable part of the gene encoding VP4 were amplified according to previously published procedures.^{4,5} These PCR products were sequenced (Eurofins Genomics, Germany) and the sequences were analyzed in the Blast program. Based on the nucleotide similarity of the sequences, the genotype of VP7 (G-type) and VP4 (P-type) was determined.

Conclusions

Fig. Detected genotypes of porcine RVA in samples of faeces collected in Czech pig farms during 2021-2023.

Results

- RVA was detected in 72.3% of screened samples (58/94)
- In weaned piglets 100% of samples was positive for at least one rotavirus species.
- In 88.9% of samples from weaned piglets (32/36) a coinfection with two or three rotavirus species was detected.
- RVB and RVC were mostly present in samples co-infected with another rotavirus species.
- The most abundant G-types were G9 (46.7%), G4 (17.8%), G5 (13.1%), and G11 (11.2%).
- The epidemiology of porcine rotaviruses is very complex and highly dynamic.
- The genotypes present in a porcine RVA vaccine (G5 and P[7] in combination with other G- and P-types) were detected only in 13.1% and 10.2% of all positive samples.
- The newly emerging novel genetic variants can evade herd immunity against the vaccine strains, as observed with human RVA vaccines, RotaTeq and Rotarix.
- P-types most frequently detected were P[13] (48%) and P[6] (26%).
- The most prevalent RVA genotype combinations were G5P[13] (n = 23) and G4P[13] (n = 11).
- The most common genotypes in samples detected earlier (2016-2018) were G5P[6] and G4P[6] (26.8%).

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