Epidemiology of Rotavirus C in Czech pig farms

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INTRODUCTION

Rotavirus C (RVC) was first described in 1980 as a causative agent of diarrhoea in piglets and also detected in humans, cows, ferrets, dogs and minks. Several studies have shown an association between porcine RVCs and gastroenteritis in pigs of different age categories. It is assumed that RVC continuously circulates in the pig holdings resulting in a much broader genetic diversity of RVCs in pigs than in other hosts.

This makes the pig the main reservoir for RVC and poses a major risk of incidental zoonotic porcine-to-human (and vice versa) transmissions which have been described previously.

The aim of the ongoing project is, among other things, to determine the current epidemiological situation in pig farms in terms of rotavirus infection and to evaluate the occurrence of RVC genotypes.

RESULTS

|	Suckling piglets/%	Weaned/%	Total/%
RVA+	29 / 26.1	7 / 6.8	36 / 16.8
RVB+	4 / 3.6	4 / 3.9	8 / 3.7
RVC+	5 / 4.5	10 / 9.7	15 / 7.0
RVA+ RVB+	15 / 13.5	15 / 14.6	30 / 14.0
RVA+ RVC+	13 / 11.7	3 / 2.9	16 / 7.5
RVB+ RVC+	3 / 2.7	1 / 0.97	4 / 1.9
RVA+ RVB+ RVC+	6 / 5.4	56 / 54.4	62 / 29.0
RVA+ RVB+ RVC+ RVH+	0	1 / 0.97	1 / 0.5
Negative	36 / 32.4	6 / 5.8	42 / 19.6
Total	111	103	214

METHODS

❖ RNA extracted with the use of TRI Reagent (Sigma) from 10% suspension of faeces in PBS

❖ detection of rotaviruses A, B and C with the use of RT-qPCR; primers targeting the conserved NSP3 gene of RVAs (own design) and VP6 of RVB and RVC[1]

❖ detection of RVH is being carried out by end-point RT-PCR with primers targeting VP6[2]

❖ genotyping of RVC-positive samples was carried out through the sequencing and analysis of nucleotide sequence of VP7 (whole cds), VP4 (partial cds – 800 bp) and VP6 (whole cds – 1353 bp) genes coding structural proteins[3]

LITERATURE

[1] Marthaler, D., Homwong, N., Rossow, K. et al. Rapid detection and high occurrence of porcine rotavirus A, B, and C by RT-qPCR in diagnostic samples. J Virol Methods 2014;209:30–34.

[2] Puente H., Cortey M., de Nova P.J.G. et al. First identification and characterization of rotavirus H in swine in Spain. Transbound Emerg Dis 2021;68:3055-3069.

[3] Lee S.-G., Youn S.-H., Oh M.-H et al. Molecular characterization of two strains of porcine group C rotavirus. J Microbiol 2011; 49:1058-1062.

[4] Euling B., Harzer M., Vahlenkamp T.W. Extended analyses of rotavirus C (RVC) G-types and P-types reveal new cut-off value for the G-types and reclassification of strains. J Virol 2025;00049-25

ACKNOWLEDGEMENT
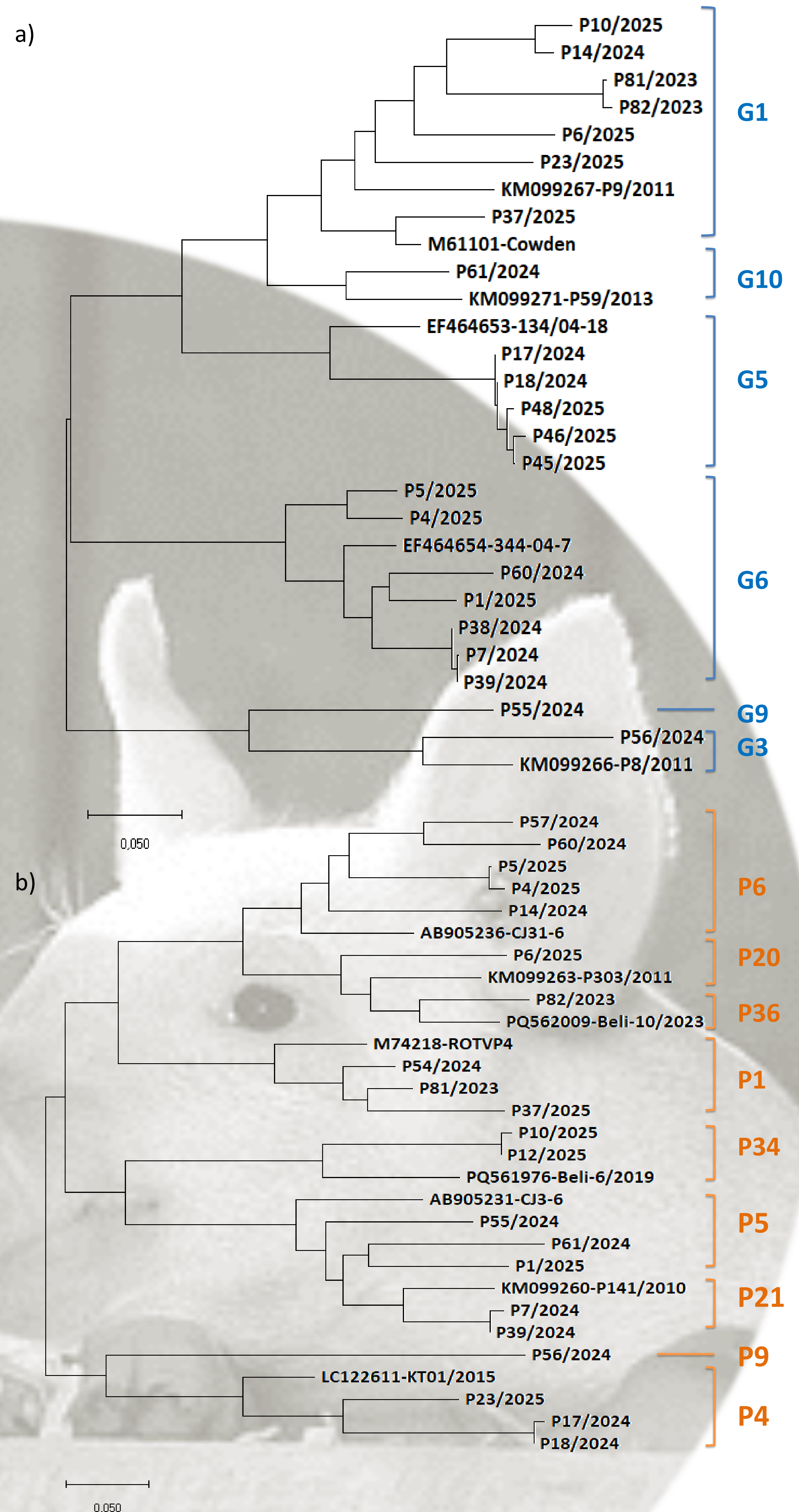
Phylogenetic trees based on nucleotide sequence of the whole coding sequence of VP7 (a) and partial cds of VP4 (b) genes. The Czech newly described RVC strains are those without GenBank accession number. The respective genotypes are indicated on the side.[4]

CONCLUSIONS

❖ in the set of 214 faecal samples 172 (80%) were positive for at least one rotavirus

❖ the most common RVA was detected in 145 (68%) of all samples

❖ RVH was found in Czech pigs for the first time

❖ VP6 genotypes were successfully detected in 19 RVC+ samples; I13 was the most abundant (13x), I11 was found 5x and I12 once

❖ phylogenetic analyses of RVC showed great variability of VP7 and VP4 genes with 6 different VP7-genotypes and 9 VP4-genotypes

❖ 14 combinations of G- and P-genotypes in RVC+ samples were found; G6P6 in 3 samples, G1P1 and G6P21 both in 2 samples, other combinations were singular