Frequency of PRRS live vaccine virus (European and North American genotype) in vaccinated and non-vaccinated pigs submitted for respiratory tract diagnostics in North-Western Germany

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Introduction
A basic requirement of live vaccine virus strains is that natural transmission of vaccine virus is minimal or non-existent (3). The objectives of this study were (a) to determine the frequency of the EU and the NA genotype PRRS vaccine viruses in a large sample of pigs from North-Western Germany, (b) to assess the association between vaccine isolate detection and vaccination history and (c) to characterise the identified vaccine isolates considering their origin.

Material and Methods
During January and December 2007, 1,970 pigs were submitted to the Field Station for Epidemiology for post-mortem examination. Nine hundred and two of these pigs aged between 1 and 25 weeks of life had a history of respiratory disease and/or emaciation and were included in the study. The 902 pigs originated from 439 herds and were submitted by 141 different veterinary practices. Lung tissue from these pigs was tested for PRRSV by a nonaplex RT-PCR. Those samples positive for PRRSV were selected for further examination and genetic typing. The vaccination history was obtained from the veterinary surgeons who had submitted the pigs. Telephone interviews were conducted that followed a standardised questionnaire consisting of six closed (predefined range of answers or yes/no) questions on PRRS vaccination management/history of the herds of origin. It was hypothesised that these variables were related to the detection of the vaccine and/or wild-type viruses.

Results
Overall, 18.5% of the samples were positive for the EU wild-type virus. EU genotype vaccine virus was detected in 1.3% and the NA genotype vaccine virus in 8.9% of all samples. The production stage-specific detection rates for EU wild-type virus and NA genotype vaccine virus showed the highest values in weaning and growing pigs (Fig. 1).

Material from 168 of the 259 samples found positive in the diagnostic laboratory was available for genetic typing by amplifying and sequencing the ORF5. Of these, 104 were of the EU genotype, and 64 of the NA genotype. The ORF5 nucleotide sequence of 11 of the EU genotype isolates had 99.1–100%, identity with the corresponding ORF of the Porcilis PRRS DV strain. Nucleotide identities of the remaining EU genotype isolates with the Porcilis PRRS-DV strain were between 85.3 and 91.7%, allowing their classification as EU wild-type virus. Nucleotide identities of the ORF5 of the NA genotype isolates with the Ingelvac PRRS MLV vaccine strain were between 96 and 100%. The detection of the EU vaccine was significantly higher in pigs vaccinated with the corresponding vaccine (OR = 9.4). Pigs vaccinated with NA genotype had significantly higher detection chances for the corresponding vaccine virus when compared to non-vaccinated animals (OR = 3.34) animals, however, NA vaccine was also frequently detected in non-vaccinated pigs.

Discussion
The spread of vaccine virus within herds has been demonstrated in several studies (1, 2). However, data on age-dependent detection rates of live PRRS vaccine virus have not been published. The evident similarities in the dynamics of the NA genotype vaccine virus and the EU wild-type virus strongly support the contention that spontaneous transmission of the Ingelvac PRRS MLV is a common occurrence in those countries using this vaccine. Known that an eradication of PRRSV from infected herds would require a fundamental knowledge of the dynamics of PRRS virus infection and epidemiology, the results of this study show that this is not only needed for the PRRS wild-type virus but also for live vaccine viruses. Obvious differences in the potential of spontaneous spread of different PRRS vaccine viruses should be considered when choosing vaccines to be used in an eradication program.

References
(1) Botner A. et al. (1997) Vet Rec 141
(2) Botner A. et al. (1999) Vet Microbiol 68
(3) Mateu E. et al. (2008) Vet J 177