PRRSv Exposure Dynamic in Growing Pigs in European Farms Part II

J. Angulo[1], O. Duran[1], E. Lewandowski[1], P.H. Rathkjen[1], I. Hernandez[1], S. Figueras[1], V. Torres[1], L. Eppink[1], A. Kirwan[1], N. Westenbroek[1], M. Steenaert[1], E. De Jonghe[1], A. Warzecha[1], N. Tommasini[1], R. Langhoff[1], E. Schacht[1], A. Negatsch[1], C. Keller[1]

[1] Boehringer Ingelheim AH European PRRS Solution Team

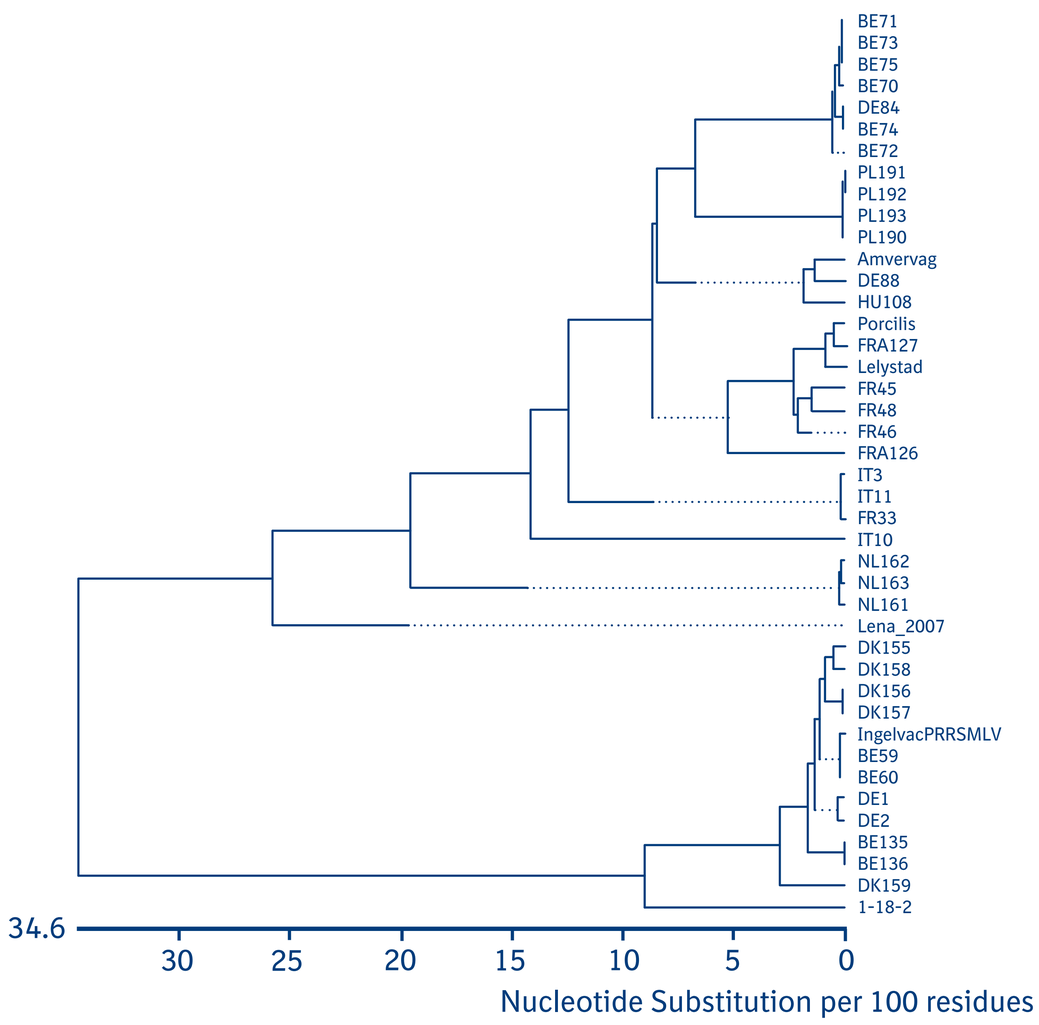
INTRODUCTION

The objectives of this study were to determine PRRSv exposure pattern and virus genetic diversity in growing pigs in European farms; to capture key information about common farm practices on biosecurity, diagnostic monitoring, and control tools and to capture mortality impact at the moment of sampling.

MATERIALS AND METHODS

34 farms were identified across Europe in 13 countries. A cross sectional sampling was implemented. We analyzed 396 PRRS PCR and 50 ORF5 sequences from selected + results. On farm questionnaire provided info on farm characteristics, biosecurity practices, diagnostic and control protocols. Part II includes PRRS sequences from 21 farms in 11 countries (AU, BE, DE, DK, FR, HU, IT, NL, PL, RO, UK) aligned with 5 references (Lelystad; Lena; Porcilis; Amvervac, Ingelvac MLV) getting a genetic distance table and tree (Fig 1). The analysis was based on ORF5 genetic distance considering >3 % as a cut off for classifying as different virus giving a nomenclature name specifically structured for this project starting as EPI with a consecutive number for different Wild-Type (WT) PRRS viruses identified in the genetic distance table. A regression analysis for mortality in nursery and finisher and WT PRRS prevalence was run (Fig 2). We analyzed data for descriptive stats on monitoring and control strategies from questionnaire.

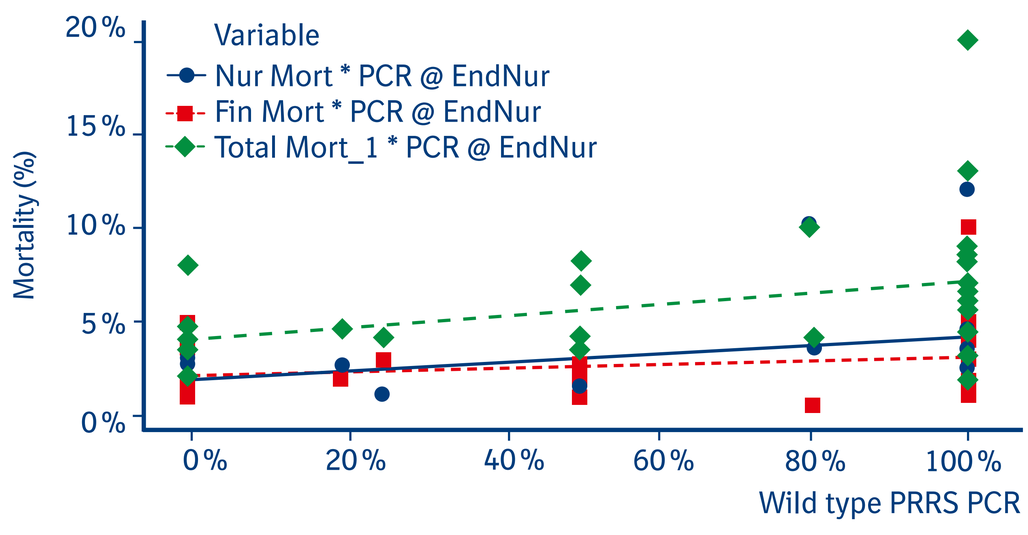
FIGURE 1: DENDOGRAM OF 36 SUCCESFULLY SEQUENCED SAMPLES REPRESENTING 19% OF ALL PCR POSITIVE SERUM SAMPLES.



RESULTS

Sequences distribution obtained: 26 % at weaning, 58 % end of nursery, 16 % mid finisher respectively. The majority of farms had a single variant of WT PRRS circulating in growing pigs. Same clade virus (EPI-2) was identified in farms in Belgium and Germany; also a farm in France and two farms in Italy shared same clade (EPI-3). A WT PRRS genotype II was observed in Denmark. Vaccine strains were identified in pig-flows with history of vaccination either in sows only or sows & pigs. Mortality mean in nursery was 3.08 % + 0.026 and 2.89 % + 0.019 in finisher at moment of sampling in + pig-flows finding a significant association ($p < 0.10$) between nursery mortality and WT PRRS prevalence at end of nursery but not between finisher mortality and prevalence at mid-finisher ($P > 0.10$). 70 % of farms used MLV as primary tool for PRRS control, out of these, 58 % applied mass vaccination, 42 % post farrowing/during gestation. Only 29 % of these farms vaccinated piglets. From all farms, 32 % had previous sequencing information; 68 % biosecurity program and 56 % monitoring in place. Regarding the semen source question; 62 %, 26 % and 12 % receive semen from external, internal and did not know. For farms receiving semen from external sources, PRRS status was positive in 19 % while 17 % did not know the boar stud status.

FIGURE 2: ASSOCIATION BETWEEN PRRS PCR AND MORTALITY RATE.



DISCUSSION AND CONCLUSION

1. Sequencing results confirmed end of nursery as the most important period for wild type PRRS circulation;
2. A single PRRS variant circulating per pig flow was a common observation.
3. Some farms shared the same virus variant, possibly related to transportation and/or area spread.
4. Mortality impact was associated to the nursery phase, suggesting this phase is critical for interventions to reduce the average and batch variability.
5. Understanding of risk related to the PRRS status of semen source is low.

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