

SEQUENCING AS A COMPLEMENTARY TOOL INTEGRATED IN A PRRS MONITORING PROJECT IN EUROPEAN SOW FARMS

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INTRODUCTION

Porcine Reproductive and Respiratory Syndrome (PRRS) is an endemic swine disease causing significant productive and economic losses in pig farms. In many countries there is a lack of systematic and periodic monitoring of PRRS virus (PRRSV) which limits the knowledge on PRRSV infections incidence or prevalence over time on the real PRRS status of the farms. The aim of this study was to establish an epidemiological investigation through PRRSV sequencing.

MATERIALS AND METHODS

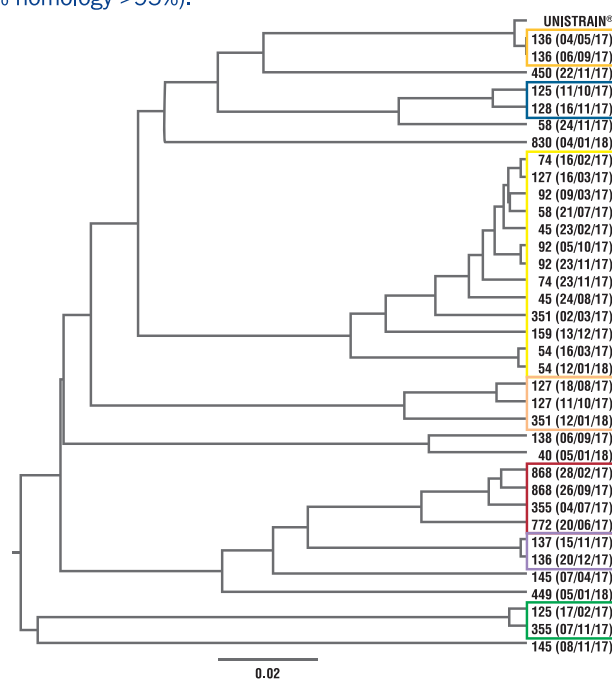
From February 2017 to January 2018, 40 breeding herds belonging to one large integrated group located in South East Europe, enrolled in a one-year program for PRRSV systematic monitoring. This program was designed following the AASV guidelines for the PRRS farm's classification¹.

According to these guidelines, serum samples from 30 piglets at weaning age were taken monthly to classify positive PRRS farms as stable or unstable. Pooled samples (5 pools of 6) were tested by PCR. Farms were established as stable after 4 consecutive all-negative sampling and as unstable when at least one of the pools was tested positive. Additionally, selected positive samples with epidemiologic relevance were tested to obtain PRRSV ORF-5 sequence by Sanger method. Percentage of homology between sequences was calculated to make the phylogenetic analysis and to investigate epidemiologic relationship between PRRSV strains.

RESULTS

A total of 46 positive samples (Ct values between 18 and 34) were tested for sequencing. 35 of these samples (Ct values between 18 and 31) from 21 different farms were successfully sequenced. According to ORF-5 homology between sequences, we identified 15 different PRRSV-strain origins (Fig 1). In 9 farms we obtained just one PRRSV sequence while in 12 farms we obtained 2 or more PRRSV sequences at different moments. In those farms where 2 or more sequences were obtained, we identified recirculation of the same PRRSV 7 times and introduction of a new PRRSV also 7 times. In 2 farms, we both identified recirculation and introduction of a new PRRSV. Moreover, 6 of the identified sequences were found in more than one farm.

Figure 1. Phylogenetic analysis of the PRRSV strains sequenced. Samples reference: farm code (sampling date). Groups of strains into the same color box indicates strong phylogenetic relationship (% homology >95%).



CONCLUSIONS

The results of this study suggest that both PRRSV recirculation and lateral infections can play a critical role for the control of PRRS in sow's farms. So, internal and external biosecurity are both key points in the PRRSV control strategies. At the same time, these findings indicate that PRRSV strain-sharing among farms of the same production group or system can be found very often indicating a significant epidemiologic relationship between them.

Altogether, it reinforces the necessity to include PRRSV sequencing as systematic tool for better understanding of the epidemiology of PRRSV and for better investigation of the epidemiologic relationships between farms of the same production systems or closely located.

REFERENCES

¹ Holkamp *et al.* Terminology for classifying swine herds by porcine reproductive and respiratory syndrome virus status. *J Swine Health and Prod.* 2011;19(1):44-56.