The **Reference** in **Prevention** for **Animal Health**

CONTROLLING PRRSV AND PREVENTING RECOMBINANTS: A CASE REPORT

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BACKGROUND & OBJECTIVES

Mutation and recombination are common processes inherent to PRRSv to the point that most existing strains are considered as mosaics. The literature reports recombination cases involving (modified live vaccine) MLV and wild virus or PRRSv1 and PRRSv2. Some people in the pig industry are afraid of creating new strains with enhanced virulence – but there is no evidence that recombinant strains are more pathogenic than their parental strains. We set out to establish if a recombinant strain that was causing clinical problems could be controlled by a change in vaccine protocol

MATERIALS AND METHODS

250 PRRSv positive sows (three-week batch) on a farrow-to-finish farm in Northern Ireland where vaccination protocols included MLV for sows (4 blankets/year) and 3 weeks-old piglets (two different products from the same company but same strain). Clinical respiratory problems were occurring on 12 -16 weeks-old pigs causing mortality (>5% each batch) and production. Diagnostic investigations supported by laboratory results had identified PRRSv as the cause of the problems and ORF2 to ORF7 sequencing of isolates from severe lesions had identified as a recombinant PRRSv strain (MLV + wild virus). Part of the genome was similar to a wild-virus strain for which we have not previous isolate, and rest of the sequence was very similar to the strain 94881 found in Reprocyc® PRRS (BI Animal Health).

These ongoing problems with the piglets-growers forced the decision to immediately replace the current MLV vaccines with UNISTRAIN® PRRS ID with no cooldown period. Following this, PRRSv status was monitored over the next 12 months by serology, PCR and occasional sequencing.

RESULTS

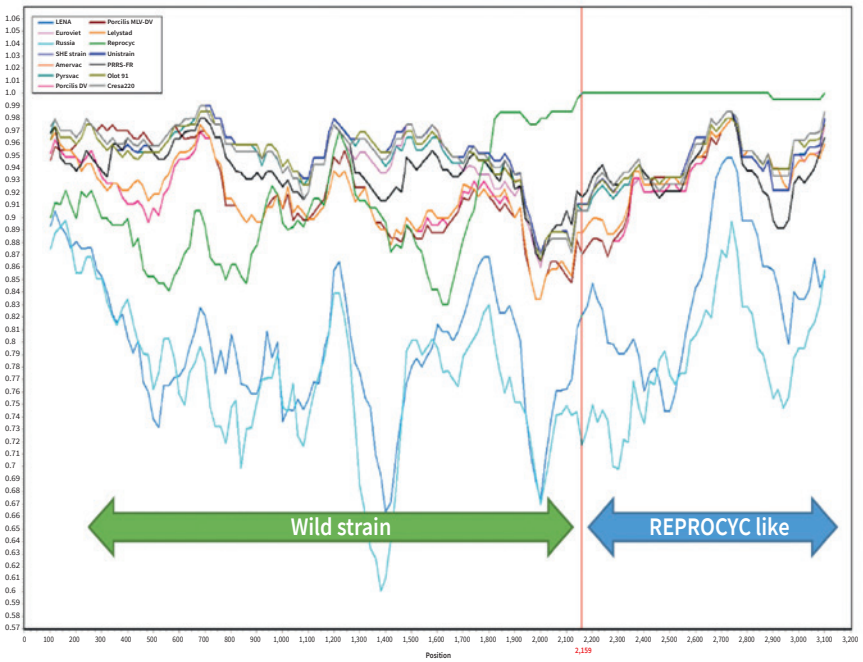
Viremia was found in 4 and 16 week-old pigs on multiple occasions during the monitoring period. Veterinary inspections identified various events and accidents that may have undermined vaccination efficacy including wrong fridge temperature, frozen vaccines, vaccines kept out of the fridge and biosecurity breaches. PCR work and sequencing detected a new (not identified before in this farm) field virus circulating but the new vaccination protocol prevented PRRSv disease and fine-tuning the vaccination timing prevented to viremia in growers. The incidence of respiratory disease was significantly reduced and PRRSv was not found linked to respiratory problems. The recombined MLV-wild virus was never found again, and stabilization was finally achieved (weaners were PRRSv negative and no viremia occurred in growers).

Table 1: PRRSV detection by PCR during the monitoring period in different age groups.

	DATE	4 WEEKS-OLD	10 WEEKS-OLD	16 WEEKS-OLD	REMARKS
Sows: Reprocyc® PRRS (3 mass vaccinations per year).	Sep19			+	Detection of a wild virus (1)
Pigs: Ingelvac® PRRS periweaning	Nov 19	+ / + / - / -	+ / + / + / +	+ / + / + / -	Recombinant strain found in lesions.
Sows: UNISTRAIN® PRRS Intradermal (3 mass vaccinations per year).	Jan 20	- / - / -	+ / + / +	+ / + / -	
Pigs: UNISTRAIN® PRRS Intradermal periweaning	Jul 20	+ / + / -	+ / + / -	- / - / -	Detection of a new different wild virus (2)
Sows: UNISTRAIN® PRRS Intradermal (3 mass vaccinations per year).	Sept 20	+ / -	+ / +	+ / -	
Pigs: UNISTRAIN® PRRS Intradermal 1 week after weaning	Nov20	- / - / -	+ / + / +	- / - / -	Detection of a new different wild virus (3)

Each symbol "+" or "–" separated by an "/" represent the "+" positive or "-" negative detection in PCR for PRRSv on each of the 2 to 4 pools tested per age group. In Brackets info from the sequencing.

Figure 1: Capture of the ORF2-7 sequencing form the recombinant strain. Sequencing results and graphics courtesy of Biosellal (Dardilly, France).



DISCUSSION & CONCLUSIONS

In this case, the recombinant strain implicated in the disease, but both disease and virus stopped being detected once the farm was stabilized. The virulence of the parental wild strain is unknown, but the recombinant (wild virus + the BI strain 94881) virus recombinant virus was no more virulent (evaluations made on clinical lesions and productive impact) than other PRRSv strains found in clinical cases in Ireland. Increasing use of PRRSv genome sequencing may allow the identification of more recombinant strains causing viremia or clinical disease. Good vaccination practices are paramount to control PRRSv but other aspect related to external and internal biosecurity must not be disregarded.