

Stabilization of a sow herd in a Taiwanese farm endemically infected with PRRSV2 after mass vaccination with a PRRSV1 MLV

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Introduction

Currently, Porcine reproductive and respiratory syndrome type-1 (PRRSV1) and PRRS type-2 (PRRSV2) modified-live vaccine (MLV) are commercially available in Taiwan, where most of pig productions are infected with PRRSV2 belonged to lineages I and VI to X (1). Minimization of the impact of the disease is a primary objective and vaccination with MLV vaccines has been reported to achieve farm stabilization more quickly than other methods (2), a farm with stable PRRSV status is able to achieve an increase of 1.28 weaned piglets per sow per year if PRRSV stability is maintained for a one-year period (3).

This study aimed to evaluate the efficacy of using PRRSV1 MLV to improve the stability of a sow herd in a Taiwanese pig farm endemically infected with PRRSV2.

Materials and methods

From December 2021 to January 2022, a 3000 sow-farrow-to-finish farm with over 2 years PRRSV1 MLV (UNISTRAIN® PRRS, HIPRA) vaccination history (60-day pregnant in cycle vaccination), suffered a new PRRS outbreak, this resulted in 20% abortion and a decrease in the number of weaned piglets.

Sequences of ORF5 gene were done to check the homology between the PRRS virus circulating in the farm during the outbreak and the current commercial vaccine strain.

Mass vaccination with the current PRRSV1 MLV in the sow herd was done in January 2022. Vaccine efficacy in PRRS control was evaluated on the basis of these criteria: viremia-positive rate in weaned piglet and reproductive performance (average number of weaned piglets and farrowing rate).

Results

Sow herd PRRS stability improved at 68 days after PRRSV1 MLV mass vaccination, from positive unstable to positive stable status due to 100% of monthly samples from the herd tested negative (Figure 1).

The reproductive parameters were back to baseline performance in 3 months, the farrowing rate and the average number of weaned piglets improved from 73.8% to 81.2% and from 10.7 to 11.5 respectively (Table 1).

The results of complete ORF5 gene phylogeny (Figure 2) of PRRS virus isolates which were circulating during the epidemic in this production belonged to the PRRSV2, lineage III. The strains divergence between these isolates ranged from 0.0 to 2.7%, whereas comparing with commercial MLV strains VR2332 and UNISTRAIN® PRRS were 21.0 to 21.7% and 49.7 to 51.6% respectively.

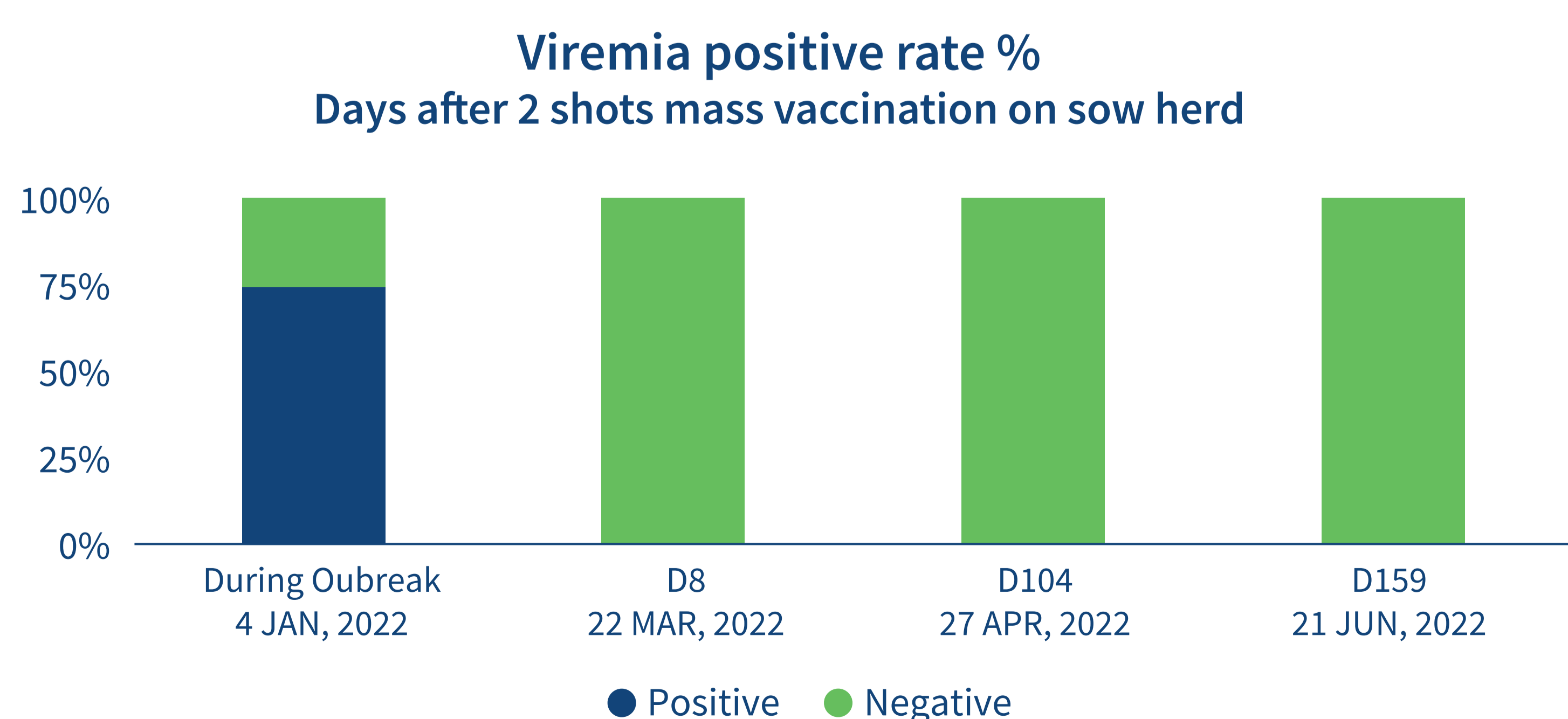


Figure 1. Positive rate of PRRS virus viremia in weaned piglets

Table 1. Reproductive performance

	Before Epidemic (JAN-NOV 2021)	During outbreak (DEC 2021-FEB 2022)	After outbreak (MAR-JUL 2022)
Farrowing rate	84.8%	73.8%	81.2%
Avg. number of weaned piglet	12.2	10.7	11.5

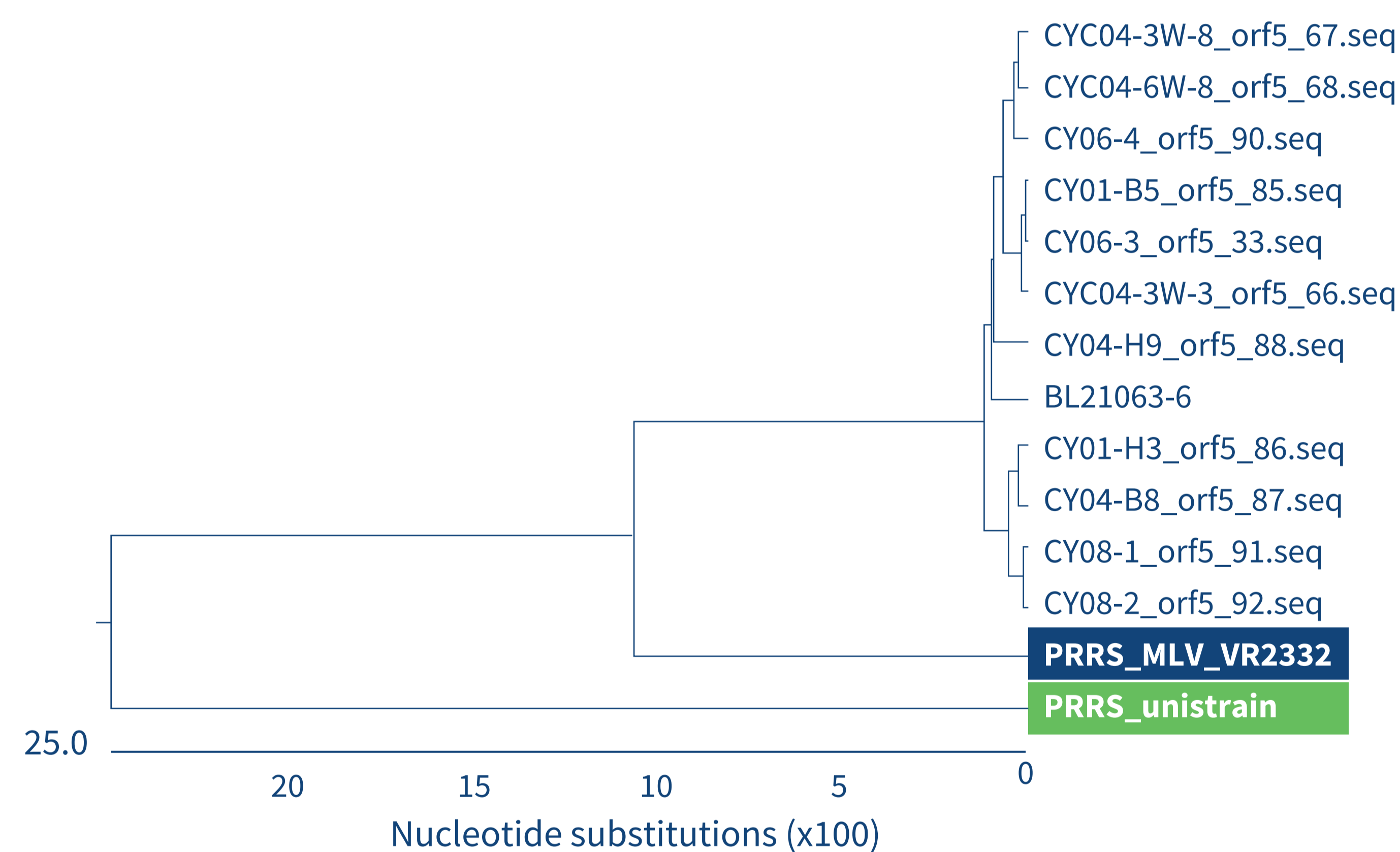


Figure 2. Sequencing and phylogenetic analysis

Discussion and conclusion

This study concluded that PRRSV1 MLV was effective against PRRSV2 field infection due to the achievement of sow herd stability and an improvement of the reproductive performance. For the sequencing and phylogenetic analysis, the PRRSV2 which was circulating in this farm belongs to lineage III, which is different from the results of the molecular epidemiology survey published in 2015 (1); however, PRRSV1 MLV conferred a solid heterologous protection with scientific evidence.

It was noteworthy that the time to stability (TTS) and the time to baseline production (TTBP) in this study was 68 days and less than 3 months, remarkably shorter than the known scientific publications either using PRRSV1 or PRRSV2 MLV in Taiwan, in which TTS was 3 and 9 months respectively (4,5).

References

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