

Use of Whole Genome Sequencing during a PRRSv outbreak investigation

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Key Points:

- Viral recombination is documented in PRRSv
- Whole Genome Sequencing can provide the detailed information to better understand recombination and PRRSv dynamics

Porcine reproductive and respiratory syndrome continues to challenge the swine industry. As an RNA virus, it is well documented that this virus changes through time which dramatically increases viral diversity generating more challenges. This virus changes through mutation or recombination with another strain that is concurrently infecting the same pigs. Currently, producers and practitioners work intensely to protect herds from new introduction of viruses as the cost of an outbreak is significant. Within the prevention measures adopted, biosecurity programs play an important role as they are a first line of defense in avoiding transmission. However, in certain regions of the country, in addition to biosecurity, the establishment of herd immunity also plays a role. Immunity can be established after an outbreak of PRRSv, or through exposure to the virus by the use of live and killed vaccines. Vaccines are currently seen as a tool to mitigate the impact of this virus. Today vaccines are used in sows, gilts, and growing pigs. In certain occasions, both the wild-type virus and the vaccine virus can be present in one pig increasing the chances of new strain generation. The case described here summarizes the recombination of two PRRSv vaccine strains.

This case occurred in a PRRSv stable sow farm. The herd had been meeting production targets until an increase in abortions was observed. Serum from 10 sows that had aborted was sent to the University of Minnesota Veterinary Diagnostic Laboratory for PRRSV diagnostics. While all samples yielded a PCR-positive result, 7 out of the 10 had a cycle threshold value below 30. An ORF5 sequence was obtained from these 7 samples and virus isolation was performed in 3 samples. All of the ORF5 sequences were 98% similar to one of the modified-live PRRSv commercial vaccines. However, the farm had not used this modified-live vaccine (vaccine A) in this herd for 2 years. It was unclear whether this PRRSV strain was a close relative to vaccine A. If so, why was it associated with clinical signs? To try to solve these questions the whole genome of this strain was sequenced using next generation sequencing.

The results from this investigation clearly demonstrated a recombination event. As with ORF5, other genes such as ORF4, ORF5a, ORF6 and ORF7 were found to be similar to Vaccine A. However, ORF1b, ORF2, ORF2b and ORF3 genes were similar to another vaccine (vaccine B), the one that the farm was currently using. A recombination analysis comparing this PRRSV genome with that of vaccine A and vaccine B showed that there was not just one but multiple recombination events that had accumulated in this PRRSV strain. Additionally, a deletion in ORF1b gene was detected. Hence, whole genome sequence analysis clearly showed that this was not vaccine A, but a new PRRSV strain derived from the mutation (deletion) and recombination of two commercially available vaccines. This new strain may be more virulent than the original vaccine strains, as it was isolated from sows that had abortions.

Recombination of RNA virus, especially PRRSv is not a new event as it has been previously reported on different occasions. The possibility of viral recombination should be kept in mind with the use of a live vaccine. In this case, Whole Genome Sequencing had a deeper discriminatory power and provided more information when compared to classical ORF5 Sanger sequencing. The use of this technology and the higher level of discernment it provides can aid in the understanding of PRRSV dynamics in pig populations.