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# Making practice decisions with PRRS sequence information

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## Introduction

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PRRS virus has been a very frustrating pathogen to deal with in herds. Virus sequencing has been used to try to understand more about the epidemiology of the virus. At the farm level SVC uses sequence information to:

- Determine if PRRS outbreak is a re-break of the farm strain of virus or an introduction of a new strain.
- Identify the number of strains of virus present in the herd.
- Monitor replacement stock in acclimation procedures.
- Help establish biosecurity pyramids and protocols within a system.

Sequencing is a crude, if highly scientific, tool we have used. Remember that the only information we learn from virus sequencing today is whether one virus strain is similar to other virus strains. In sequencing virus strains, if the strains are less than 0.5% different, they are considered the same virus. This may be a high as 1.5–2.0% different. However, differences in U.S. isolates can be as much as 17% different, and European isolates over 30% different. Among the important things we still don't know from sequencing are the locations of the critical areas in the virus that determine the pathogenicity of the virus or what area or sequence is required to stimulate protection by the immune system.

## Identifying the strain in a clinical outbreak

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After an outbreak, one of the first questions asked in a PRRS positive herd is: "Is this a new strain of the virus, or a re-break of an existing strain of the virus in the herd?" This is where sequencing can be very helpful in determining if the virus isolated from affected animals is different from previously isolated and sequenced viruses. If the virus that is identified is a strain that is already present in the herd, we have to evaluate the control program in the herd:

- Was there some type of stress event that allowed the virus an opportunity to flare up again—for example,

allowing the gestation barn temperature to fall below 68 degrees in any area?

- other disease breaks?
  - swine influenza?
  - erysipelas?
- Did herd immunity wane allow for the outbreak from the older sows in the herd?
- Did gilt acclimatization program work properly?
- Were gilts not exposed to field virus?
- Were gilts exposed to field virus too late to allow for the development of adequate immunity before entering the herd?

If the virus is a new strain to the herd:

- Is it similar to other viruses in the production system?
- How closely does it match up with the vaccine strain?
- Is it similar to other known strains of virus?
  - e.g., similar to other virus strains in the neighborhood

## Identifying the number of strains in the herd

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Identifying the number of strains in a herd is useful as we look at long-term decisions about control programs for the herd. Certain strains—such as the Oklahoma, south-east Iowa and 1, 8, 4 strains—are more pathogenic than others. Gilt acclimation programs need to include the strains present in the herd. When using natural exposure to the virus strains, it's important to make sure that the strains are active in the acclimation area and that there has been adequate cool down time before gilts are introduced back into the herd. If a gilt development site supplies multiple farms, one must monitor and make sure that new strains have not entered the system (such as the highly virulent 1, 8, 4 strain that has been identified).

- If there are several virus strains present in the herd, can one strain be identified as a more predominate strain?

## Establishing biosecurity protocols within a system

In systems that have more than one positive herd, it is important to understand the number of strains in the system—this will avoid making biosecurity mistakes that could allow for more problems in the system. An example would be a farm that has more severe clinical signs and a different virus strain (such as the 1, 8, 4). The production system wants to avoid spreading this strain through the rest of the system.

- By knowing the virus types present in the system, the pig flow transportation and people flow can be manipulated in the system to avoid potential cross-contamination of farms.
- Dedicated to flow of production from farms with similar strains of virus
  - Nurseries
  - Finishers
  - Wean-to-finish barns
- Locate the flow of pigs to sites that are distant from multipliers, boar studs or other sow farms that don't have these strains of virus.
- Important areas to consider include:
  - transport systems (isoweans, culls, replacement gilts, etc.)
    - dedicated trailer to problem farms
    - dedicated wash site for these trailers
  - semen route deliveries to farms
    - order based on the strains of virus present on the farm
  - feed deliveries
    - follow biosecurity guidelines based on strains of virus present
      - trucks washed and allowed to sit empty overnight before returning to other farms
  - management
    - farm staff: if employees need to transfer between units:
      - must follow downtime rules based on strains present
- 2 nights to return to farms that don't have this strain of virus
  - supervisor and veterinary staff:
    - schedule visits so other farms don't have to be visited after these problem farms and biosecurity protocol can be followed.

nology just tells us if the viruses are similar or not. There is more work to be done by the virologists and epidemiologists to help understand these differences. Today however, we can use this information practically in our day-to-day operation of the farm.



## Summary

The use of sequencing has been a valuable tool for understanding the differences in strains of PRRS virus on farms. There is still much more that needs to be learned to make better use of this information. We have to remember not to over-interpret the use of sequences because this tech-