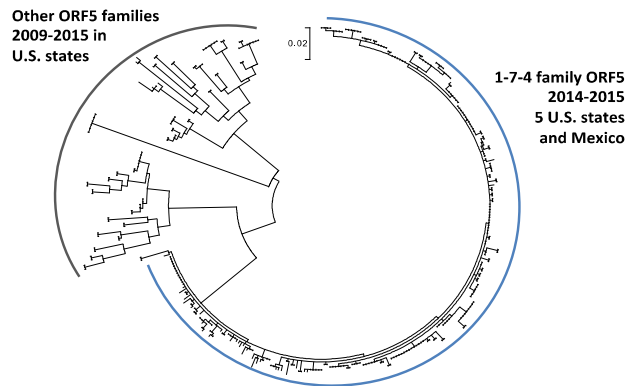
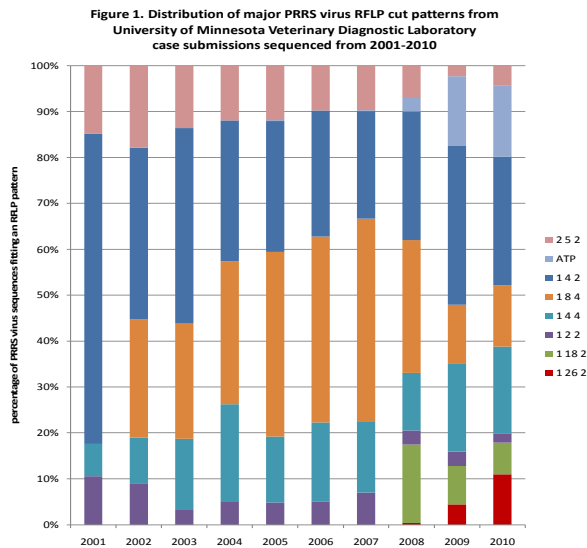


## PRRS RFLP 1-7-4 Summary

Some of our SHMP participants have been battling a particular strain of PRRS referred to as RFLP 1-7-4. This has been particularly problematic in North Carolina and several participants in the Midwest have also had cases. Observations common to all reporting veterinarians include:

- This strain first started wreaking havoc approximately 1 year ago.
- This strain appears to have evolved from the 1-8-4 family of PRRS viruses.
- This strain causes severe clinical signs in most infected herds including elevated sow mortality, reproductive disease and pre-weaning mortality.
- Decreased performance including up to 50% mortality has been observed in growing pigs.
- Infection has been detected in sow herds that are solidly vaccinated and / or have immunity from recent infection with other PRRS strains.
- Attempts to limit spread among sites have been stymied in high density regions.
- There is concern that time to achieve stability is longer than expected and there may be a higher recurrence rate in sow herds previously thought to be "stable".
- Response to interventions has been varied with no commonly recognized effective strategy.
- There is a unanimous call for investigations to gain a greater understanding of how to reduce spread, implications of infection and effective control strategies.

PRRS virus has a propensity to evolve and continually change its genetic make-up. We measure and compare this change by sequencing one virus gene, called ORF5. Each virus' sequence corresponds to a certain restriction fragment length polymorphism (RFLP) which presents a convenient naming system. Hence, we are familiar with virus RFLPs such as 2-5-2, 1-8-4 and 1-4-4. Jerry Torrison summarized the predominant RFLP patterns as detected at UMN VDL from 2000 to 2010. A new emerging RFLP pattern in 2014 is RFLP 1-7-4.



ORF5 sequencing shows that all 1-7-4 family strains, isolated from from multiple states and systems, cluster in one, nearly homogenous group (see circular tree). The tree strongly suggests that all outbreaks started from a single emergence event, whose origin is unknown. In about one year, the virus spread rapidly in NC, to sporadic Midwest pockets and Sonora, Mexico. Limited whole genome sequencing indicates strain variation in nonstructural protein (nsp) 2 due to insertion or deletion (indel) of sequence. The significance is not yet clear due to limited whole genome sequencing and lack of clinical and production data in outbreaks caused by the 1-7-4 variants.

All recent 1-7-4 family isolates are closely related, but mutations change the RFLP patterns occasionally. Dendrograms (trees) are more reliable than RFLP or pairwise similarity comparisons for determining relatedness.

The 1-7-4 family of viruses are easily distinguished from other PRRSV circulating in US swine and are unrelated to high path Chinese PRRS virus. The family is most similar to recent viruses in the general 1-8-4 family, including 1-22-2 and 1-18-2 type viruses.

Because of your participation in SHMP we have unprecedented capacity to understand PRRS virus evolution and spread. Therefore, we are starting a national, prospective PRRS virus sequence monitoring program. This is a long term, complex project that will require multiple levels of cooperation, data capture and collation. Your sharing of diagnostic information as well as locations of sites are two core elements. Equally important in the long run will be capturing real-time movement data. We should expect no value creation in the short term as we will be working mostly on the process as opposed to analysis. But if we have any hope of rapid detection and control of emerging pathogens, this is path to take. Thanks to Dr. Mike Murtaugh for providing this summary analysis of the 1-7-4 sequences.

Bob Morrison