

PRRSV diversity in the US based on RFLP patterns of samples submitted to the Minnesota VDL

Key Points:

- The same six RFLP patterns accounted for most of the PRRSV sequences obtained in the winters of 2011, 2012 and 2013
- Two different strains with RFLP patterns 1-7-4 and 1-3-4 were consistently sequenced during the winter of 2014
- The following was provided by Dr Albert Rovira. Bob Morrison

This report summarizes PRRSV ORF5 sequences from US isolates obtained at the University of Minnesota Veterinary Diagnostic Lab during the last 4 winters up to February 15, 2015. During the winters of 2011, 2012 and 2013, six RFLP patterns accounted for 70% of the sequences (Figure 1). Two of these patterns (2-5-2 and 1-4-2) represent mainly sequences associated with MLV vaccines. The other four patterns (1-8-4, 1-18-2, 1-26-2 and 1-4-4) represent PRRSV field strains that are common in US swine populations. The remaining 30% of sequences are made up of combinations of 82 different RFLP patterns. Many of these are closely related to the four main field virus patterns. For example, 1-18-4 strains are in most cases very similar to 1-18-2 strains but are counted under the "Others" category. During the last winter we have seen the emergence of two distinct PRRSV strains with RFLP patterns 1-3-4 and 1-7-4. It is important to note that the patterns themselves are not new. But the specific sequences of these recent strains are different from previous 1-3-4 and 1-7-4 strains.

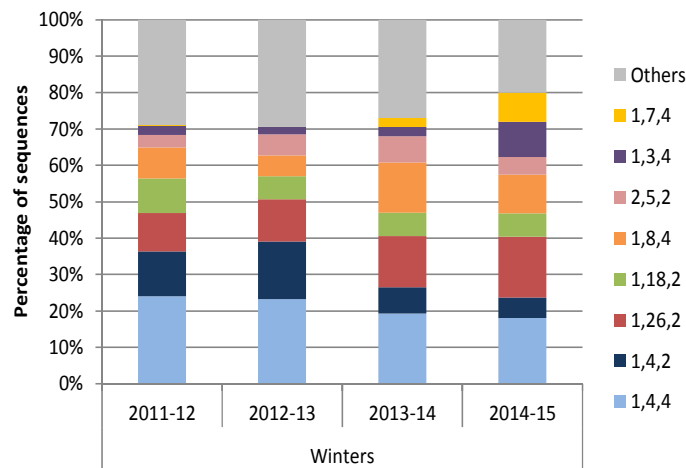


Figure 1: Predicted RFLP patterns based on ORF 5 sequences at the Minnesota VDL

When we look at these two new strain families in more detail, we find that the earliest case of recent 1-7-4 that was sequenced at the Minnesota VDL was from December 2013, while the first 1-3-4 sequence was from May 2014 (Figure 2). The 1-3-4 strain has been sequenced in cases from Minnesota and Wisconsin. The 1-7-4 strain has been found in cases from Minnesota, Iowa, Missouri, Ohio, North Carolina and South Carolina. The origin of these virus families have not yet been determined. We don't know at this point if these two strains will become established in swine populations or will die off. We will continue to monitor the frequency of these and other new PRRSV strains identified through sequencing at the Minnesota VDL.

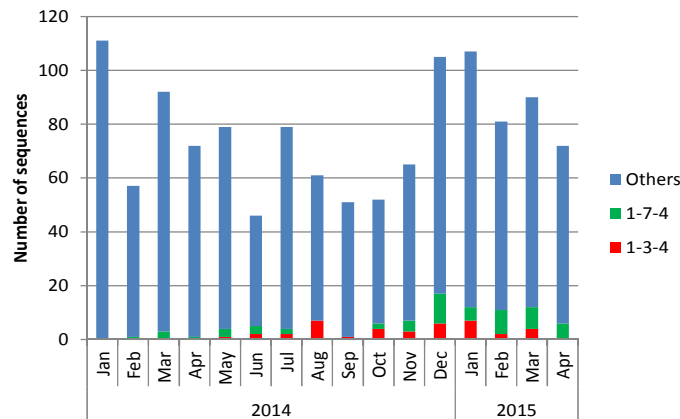


Figure 2