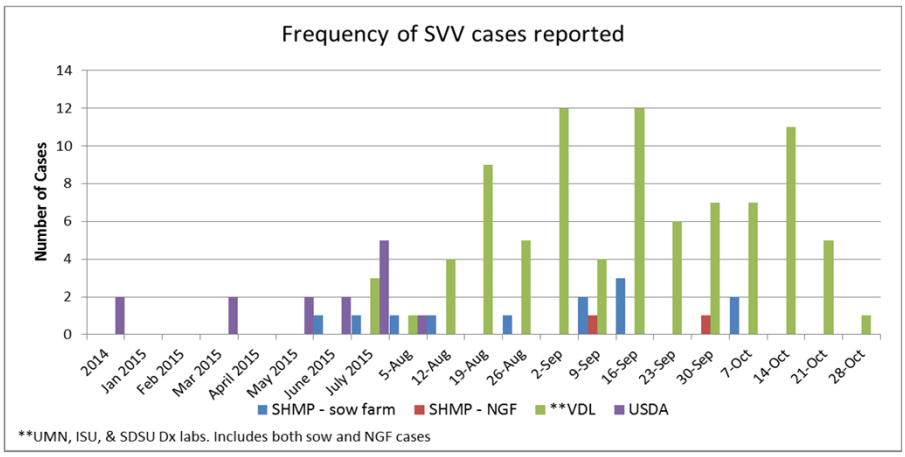
Seneca Valley Virus Update



Virulent PRRSV Families Come and Go. Will the 1-7-4 family behave the same?

Xiong Wang, Michael Murtaugh

Key Points:

- The 1-7-4 family of viruses is particularly serious because the virus can spread rapidly and widely in systems with immunity and biosecurity programs that effectively controlled and eliminated other strains.
- Rapid spread of newly introduced viruses indicates lack of immunity, which raises questions about cross-protection if herds were using vaccination, virulent virus exposure, or other methods.
- Outbreaks are due more likely to introduction of new viruses.
- Conserved subgroups appear in many branches of Type 2 PRRSV. The ability to spread rapidly without substantial genetic change is independent of genotype.
- Conserved subgroups die out. They do not mutate into resistant forms that take over and establish endemic populations that continue to evolve.
- Resolution of outbreak events is consistent with increased levels of immunity. Improvements in biosecurity will also contribute to elimination.

Recently, five production systems shared their PRRSV sequence databases with SHMP to analyze the pattern of virulent 1-7-4 family outbreaks. A total of 6,744 PRRSV ORF5 were put into a dendrogram, resulting in a never-seen-before perspective of genetic diversity showing distinct clusters of viruses, many with a sub-cluster of highly conserved isolates found in a limited time frame. The dendrogram in Figure 1 shows a series of viral families which are clearly different, just like a herd of zebras that show individual variation when looked at very closely. Within every family is a highly conserved group, shown as a heavy black line. In many cases, the group was observed in a limited span of time, defined by the start of an outbreak, and ending with its eradication. Some of these outbreak events are familiar, including the 1-4-4 outbreak family in 2010-2012, the 1-18-2, 1-22-2, and 1-22-6 families that were prominent in 2007-2008, and the recent 1-7-4 family, with 241 independent isolations. Except for the 2-5-2 family of Ingelvac MLV field re-isolates throughout the sampling period of 1998 to the present, these outbreak events had a clear onset and a clear termination.

These findings, using entirely diagnostic sequence samples, have important implications that will stimulate further investigation.