

Newly emerging PRRSV Lineage 1C variant nomenclature

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As mentioned in previous science pages, recent outbreaks caused by a highly similar PRRSV variant have been reported. As we move forward with investigations of these farm-level outbreaks, we continue to confirm that these form a tight genetic cluster not similar (using a 98% nucleotide identity as a cutoff) to any other sequences from our dataset. Because this is such a specific variant and because the common nomenclature used in the field has been restriction fragment length polymorphism (RFLP) typing, a review of the limitations of different PRRSV classification systems is warranted. Particularly, we want to clarify that although these outbreaks were initially reported as RFLP patterns 1-4-4, RFLP classification alone is not specific enough when referring to this variant. A main limitation of RFLP classification is that it does not always correlate with genetic distance, nor does it communicate meaningful info about relatedness amongst variants. An alternative classification would be phylogenetic lineage/sub-lineage classification based on the ancestral relationships and genetic distance of the isolates (1,2). This variant has been classified as Lineage 1C.

Using our MSHMP sequence database spanning 1998-2021, as an example, about 13% (over 4,000 sequences) of all sequences (n>30,000) were classified as RFLP 1-4-4. If we were to classify those into lineages, which the average nucleotide distance is around 11% between lineages and around 5% between sub-lineages, we can see that RFLP pattern 1-4-4 sequences can be very different genetically (Figure 1). Taking 2020 as an example, only 31% of all RFLP type 1-4-4 sequences belongs to the same sub-lineage (Lineage 1C) as the newly described variant. Thus, it is important to keep in mind that most RFLP type 1-4-4 PRRS currently circulating are not closely related to the variant found in the previously described outbreaks that caught the industry's attention in late 2020.

Of all RFLP 1-4-4 Lineage 1C PRRS that were present in our database, 72% comprised that specific variant associated with the late 2020 outbreaks. The combination of both classifications would have a 98% sensitivity and 89% specificity in correctly identifying the cases associated with those outbreaks. Sensitivity is not 100% because some cases within that outbreak comprised RFLP 1-4-3 Lineage 1C sequences, thus would be missed if using RFLP pattern in the case definition. For that reason, while we do not yet have a standardized PRRSV variant designator established, we recommend the temporary adoption of the "newly emerging PRRSV Lineage 1C variant" nomenclature when referring to sequences belonging to this epidemic event, as it more accurately describes the cases involved. The term variant is an important addition, as the lineage 1C is historically the second most prevalent lineage/sub-lineage within our MSHMP database, thus using this terminology alone would also relate to several sequences unrelated to this epidemics.

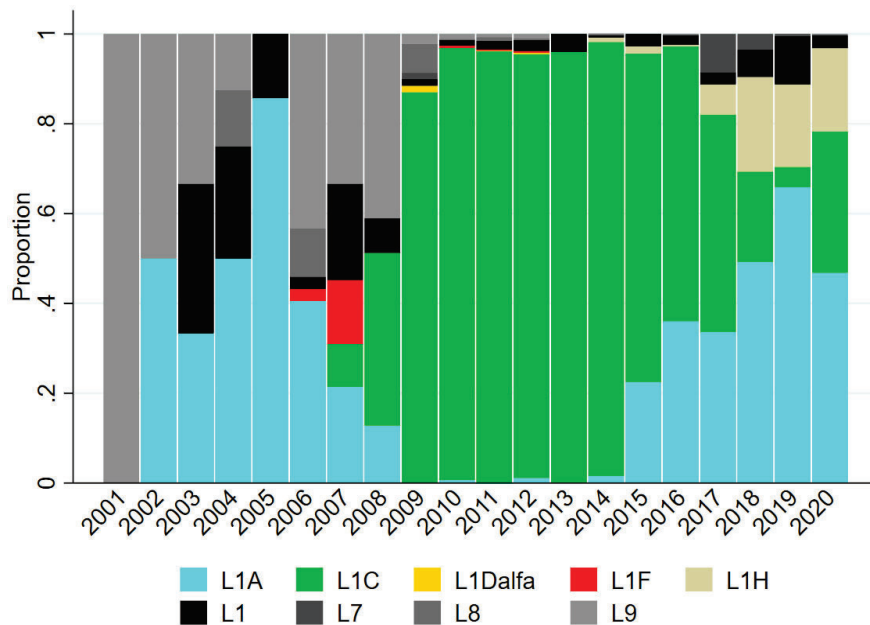


Figure 1. Lineage classification of all PRRSV RFLP type 1-4-4 within the MSHMP sequence database.

References

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