

Updated epidemiological curve of cases associated with the new Lineage 1C RFLP1-4-4 variant

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As we continue to monitor the detection of the newly described PRRSv Lineage 1C RFLP 1-4-4 variant, we would like to update the epidemiological curve of cases associated with this variant. The updated epidemiological curve of the number of cases per week is shown in Figure 1. As of our last update, a total of 355 sequences from 15 MSHMP participating production systems have been detected in 294 sites (194 growing pig farms, 57 breeding herds, and 43 with no information on site type). Coordinates or State information was available for 94% of cases. This strain continues to be detected in MN, IA, IL, SD and WI, with 97% of cases occurring in MN and IA. It is important to highlight that this analysis is based on sequence data obtained by the UMN, ISU, and SDSU Veterinary Diagnostic Laboratories of MSHMP participating systems; therefore, non-MSHMP production systems are not represented in this graph and may also be experiencing cases.

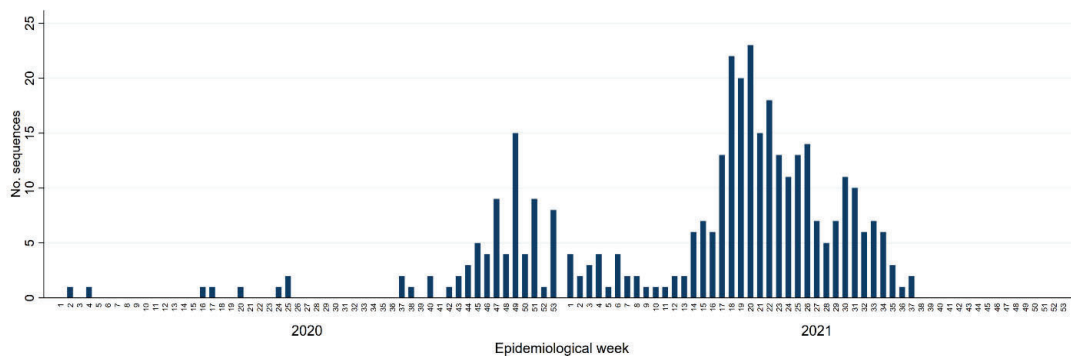


Figure 1. Epidemiological curve of the PRRSv Lineage 1C RFLP 1-4-4 newly emerged variant.

We would like to point out different ways in which the transmission of the newly emerged L1C variant has been captured by our weekly charts in this report. The two main differences between the epidemiological curve presented here and the weekly report charts are that 1) The weekly report charts represent only breeding herds, and 2) They represent all 38 MSHMP participating systems (all regions monitored by MSHMP). Therefore, the transmission and dissemination of the newly emerged L1C variant has been accounted for in the cumulative incidence graph. This is observed by the end (e.g. May) of the 2020-2021 season, when there is a steep increase in incidence due mostly to the occurrence of the new variant. Secondly, on the EWMA graph, the regular seasonality the virus has had for over a decade has been broken as for the first time and during the months of May-June 2021 an important epidemic was observed, again due mostly to the transmission of the new variant.

Once again, we would like to thank the MSHMP participants for their willingness to share information. If you have any comments/suggestions on this topic or would like to raise a different topic to be investigated with the MSHMP data, do not hesitate to contact Cesar Corzo at corzo@umn.edu and Mariana Kikuti at mkikuti@umn.edu.