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PRRSV-2 Lineage-Variant Nomenclature: March 6, 2025 Update

Purpose of report*:* To provide a brief overview of nomenclature updates of heightened interest.

Contents:

Questions: Kim VanderWaal (kvw@umn.edu).

[1] VanderWaal, K., N. Pamornchainavakul, M. Kikuti, J. Zhang, M. Zeller, G. Trevisan, S. Rossow, M. Schwartz, D. C. L. Linhares, D. Holtkamp, J.P. Herrera da Silva, C.A. Corzo, J.P. Baker, T.K. Anderson, D.N. Makau, and I.A. D. Paploski. 2025. "Prrsv-2 Variant Classification: A Dynamic Nomenclature for Enhanced Monitoring and Surveillance." *mSphere* 0 10: e00709-24.https://doi.org/10.1128/msphere.00709-24

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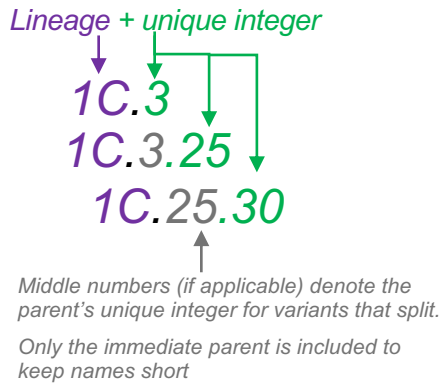
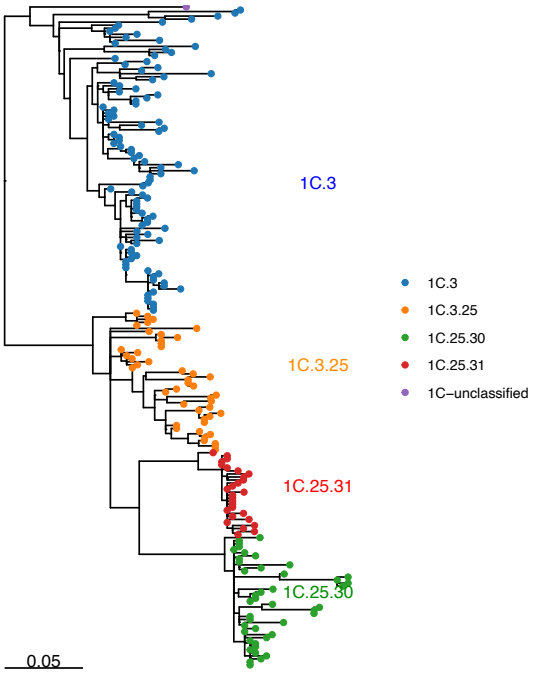
Naming conventions for variants that split

Viruses belonging to the same variant become more genetically diverse through time due to evolution. If genetic diversity of a variant exceeds ~5%, sub-groups that are genetically distinct from the original variant may receive a distinct variant ID. If a variant is split, then sequences most similar to the original variant retain the original ID, and genetically distinct sub-groups will receive new IDs. Standard criteria for splitting variants include: The new variant must be a minimum of >3% and a median of >5% different (ORF5) from the parent variant[1].

New variant IDs created from splits will incorporate the parent variant ID to communicate the relationship between the old and new variants involved in the split. Thus, variant IDs include the sub-lineage, followed by the immediate parent variant (if applicable), then an integer unique to the new variant within that sub-lineage. Only the immediate parent is included in the ID to ensure IDs do not become too lengthy.

Example: For variant 1C.3, a sub-group was flagged as substantially different (>5%) from other sequences belonging to variant 1C.3, meeting the criteria for being defined as a distinct variant. This new group was named 1C.3.25 (with 25 being the next unique integer within sub-lineage 1C). This new group subsequently split into two additional variants, named 1C.25.30 and 1C.25.31





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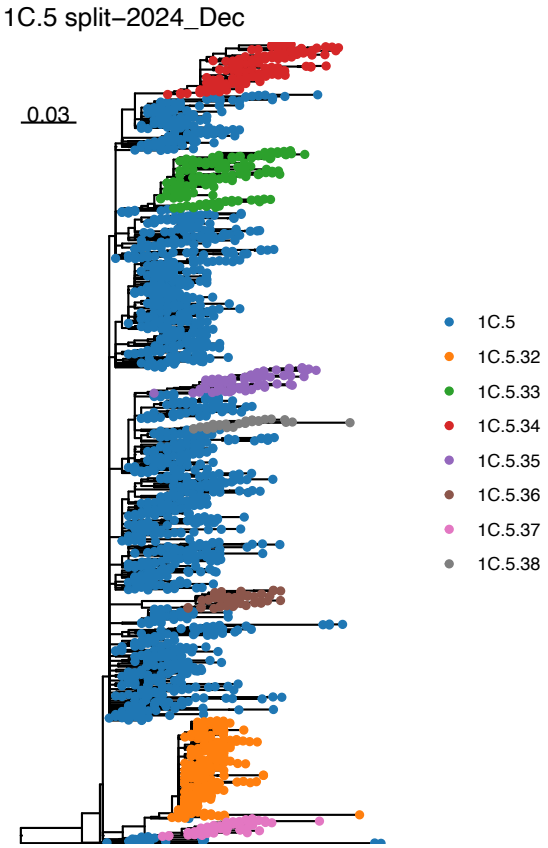
Variant 1C.5 split: Seven genetically distinct sub-groups receive new variant IDs

Context: Variant 1C.5 has been the most prevalent genetic variant in the U.S. for the past several years. Monitoring of 1C.5 occurrence through time has revealed seven sub-groups within the 1C.5 variant that have significantly diverged from the other 1C.5 sequences, such as the "clonal expansion" reported by ISU (link). It is unknown at this time if any of these groups of viruses have different clinical impacts than 1C.5.

Key update: Because of their genetic distinctiveness of these sub-groups and continued epidemiological significance of 1C.5, **seven new variant IDs** were created to identify these sub-groups to facilitate communication, monitoring, and investigations of these variants.



Standard criteria for splitting variants include: The new variant must be a minimum of >3% and a median of >5% different (ORF5) from the parent variant[1].

The new variants will be named **1C.5.32 – 1C.5.38**, following naming conventions laid out by the PRRSV nomenclature advisory group. This follows the general rule where variants IDs incorporate the sub-lineage, followed by the immediate parent variant (if applicable), then an integer unique to the new variant. Only the immediate parent is included in the ID to ensure IDs do not become too lengthy.

This change will be implemented **starting March 7** in the variant assignments available on PRRS-Loom and related platforms.

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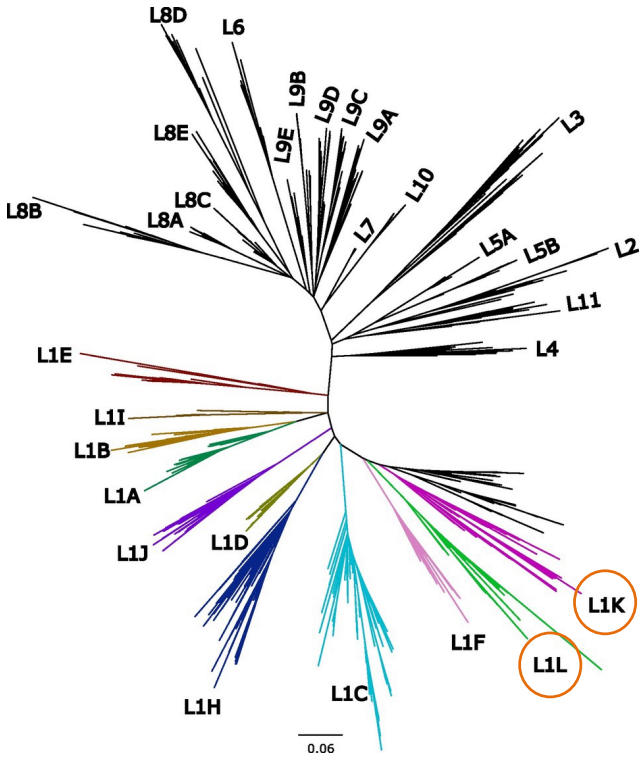
Two novel sub-lineages (1K & 1L) established based on analysis of new sequence data from Canada

Context: Recent updates of lineage-based classification for PRRSV-2 globally (Yim-im *et al.* 2023, *Microbiology Spectrum*) were based on only 165 ORF5 sequences from Canada. Recently, Herrera *et al.* analyzed >2,500 additional sequences from Canada. Two viral clades were identified that were 11.5 to 17% different from established lineages and sub-lineages, meeting the criteria to establish sub-lineages. These two clades were also ~11% different from one another.

Key update: Two new sub-lineages within Lineage 1 have been created to provide classifications for these Canadian groups of viruses: sub-lineages L1K and L1L.

One genetic variant present in the U.S. (previously known as variant 1C.23) belongs to sub-lineage 1K, which was previously unrecognized due to lack of data from Canada (i.e., 1C was the closest known sub-lineage at the time). These sequences are now classified as variant 1K.1 and 1K.2.

The L1K and L1L classifications will be implemented **starting March 7** in the variant assignments available on PRRS-Loom and related platforms.



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