

Supplementary Dataset

The Supplementary dataset files includes the results of the phylogenetic and geotemporal analysis conducted using WNV Nextstrain [1] workflow (<https://github.com/nextstrain/wnv>), available through the INSaFLU-TELEVIR platform v.2.2.2 (<https://insaflu.insa.pt>; <https://github.com/INSAFLU/WNV>, as of 2026-02-12) [2,3].

The analysis included a total of 3,126 international WNV lineage 1A genome sequences (>10,000 bp) publicly available, obtained from the Nextstrain build (as of 2026-02-05), and confirmed to correspond to the same non-redundant sequences available at Pathoplexus (<https://pathoplexus.org/>, accessed on 2026-02-05). To further refine the phylogenetic and geotemporal analysis, the Nextstrain subtree in which the 2025 Portuguese sequences clustered was zoomed in, including a subset of 34 sequences (eight from Portugal, 24 from Spain, and two from Senegal). For this focused analysis, higher-resolution geographic metadata were used when available, namely NUTS III regions for Portuguese sequences from the present study and Province information for Spanish sequences, as reported in the literature [4,5] or in <https://nextstrain.clinbioinfospa.es/wnv> (accessed as of 2026-02-13).

The full phylogenetic trees can be explored interactively at <https://auspice.us/> using the JSON files provided as Supplementary Dataset (first drag&drop both JSON files, and then the metadata TSV file to enhance exploration of the subtree). The phylogenetic sub-branch depicted in Figure 1 can be delineated by the C4302G mutation (relative to the reference NC_009942.1 used for mutation annotation), which is exclusive to this branch in the global tree.

References

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