Five phylogenetic groups identified in the coat protein gene of grapevine leafroll-associated virus 3 obtained from Portuguese grapevine varieties

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Abstract The genetic variability and population structure of grapevine leafroll-associated virus 3 (GLRaV-3) variants were updated by examining the diversity within the viral coat protein (CP) gene among 174 isolates belonging to a collection of Vitis vinifera representing most of the Portuguese varieties. Phylogenetic analysis revealed the existence of five well-defined clusters. Three of these correspond to previously defined groups, another corresponds to variants from Chile for which only one sequence has been previously identified, and an additional new group includes only Portuguese variants. A typing tool based on asymmetric PCR-ELISA (APET) was developed within the frame of this population structure. This tool was used to assess the prevalence of each phylogenetic group among the infected grapevine varieties. Although most of the isolates harbour variants from groups 1 and 2, variants from the remaining three groups exist in a number of varieties, reinforcing the notion that they are genuine genomic variants and are not isolated, atypical cases.

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