

Genetic Diversity of *Verticillium dahliae* Isolates Infecting Sunflower in Argentina

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INTRODUCTION

Verticillium dahliae is a phytopathogenic soil fungus that infects about 250 species, including crops and weeds, in many cases without any recognizable disease symptoms. Sunflower *Verticillium* wilt (VW) is one of the most important and difficult diseases to control using chemical methods. This fungus can survive in soil for extended periods and colonize the xylem of its host plants.

In Argentina, four phytopathological races of *V. dahliae* infecting sunflower have been reported (Clemente et al., 2017). However, there is a lack of knowledge about the diversity and genetic structure of *V. dahliae* population in Argentina. Given that the characterization of isolates relies via pathogenesis assays, coupled with the unknown distribution of phytopathological races, we perform molecular characterization of Argentine isolates using ddRADseq methodology and evaluate their diversity in comparison to international isolates.

MATERIAL METHODS

Seventeen isolates of *V. dahliae* from symptomatic sunflower (*H. annuus*) plants isolated between 2001 and 2022 in Argentina (Fig. 1), 2 from France and 1 from the United States were analyzed. In addition, 34 genomes available in the NCBI database and 168 isolates from the work of Bautista-Jalón et al. 2021 were included in the analysis (Fig. 2).

MAT idiomorph markers were evaluated according to Usami et al. 2009.

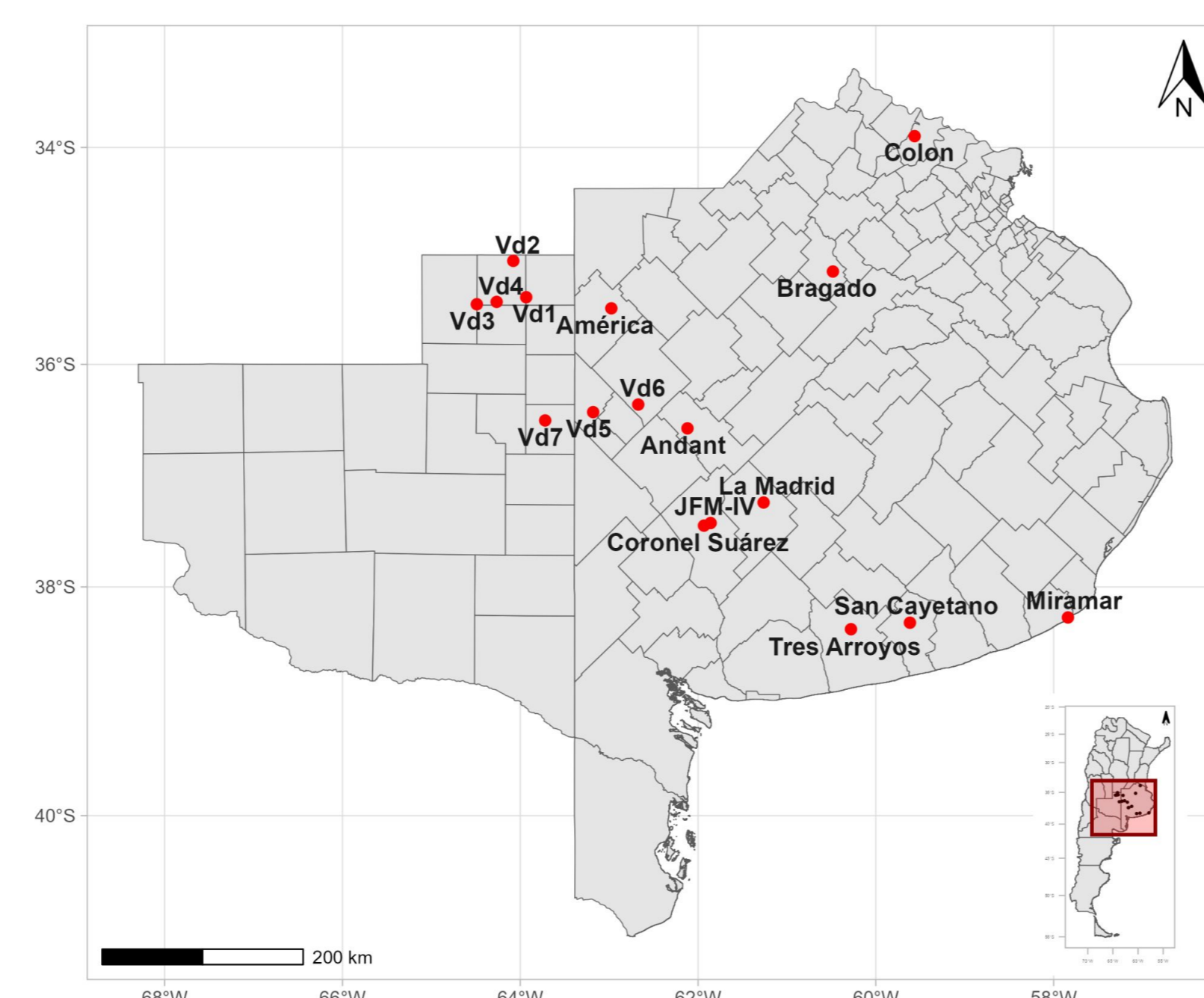


Fig.1: Locations in the provinces of La Pampa and Buenos Aires where the 17 isolates analyzed in this study were obtained.

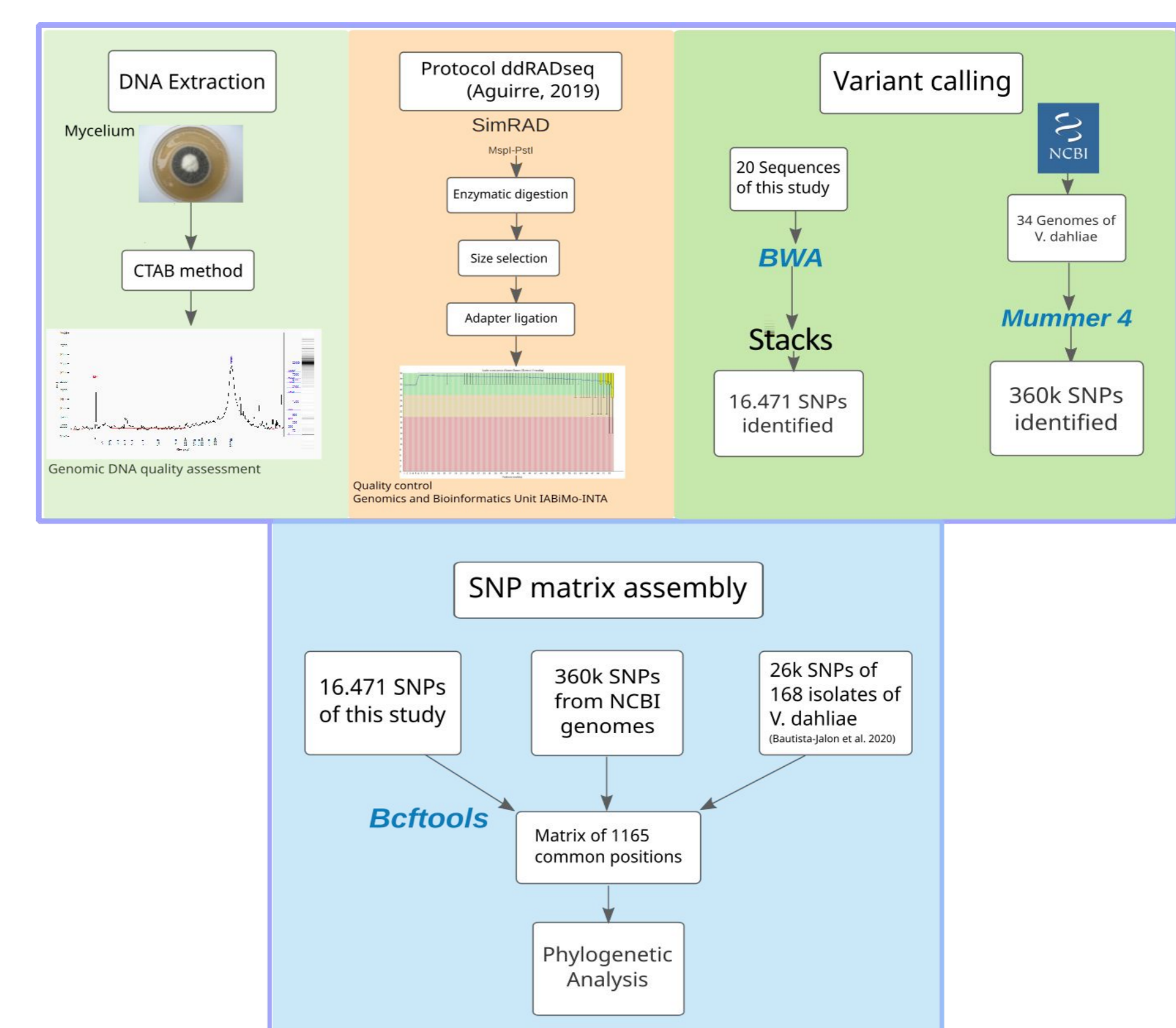


Fig.2 Protocol Diagram used for data collection and analysis.

RESULTS AND DISCUSSION

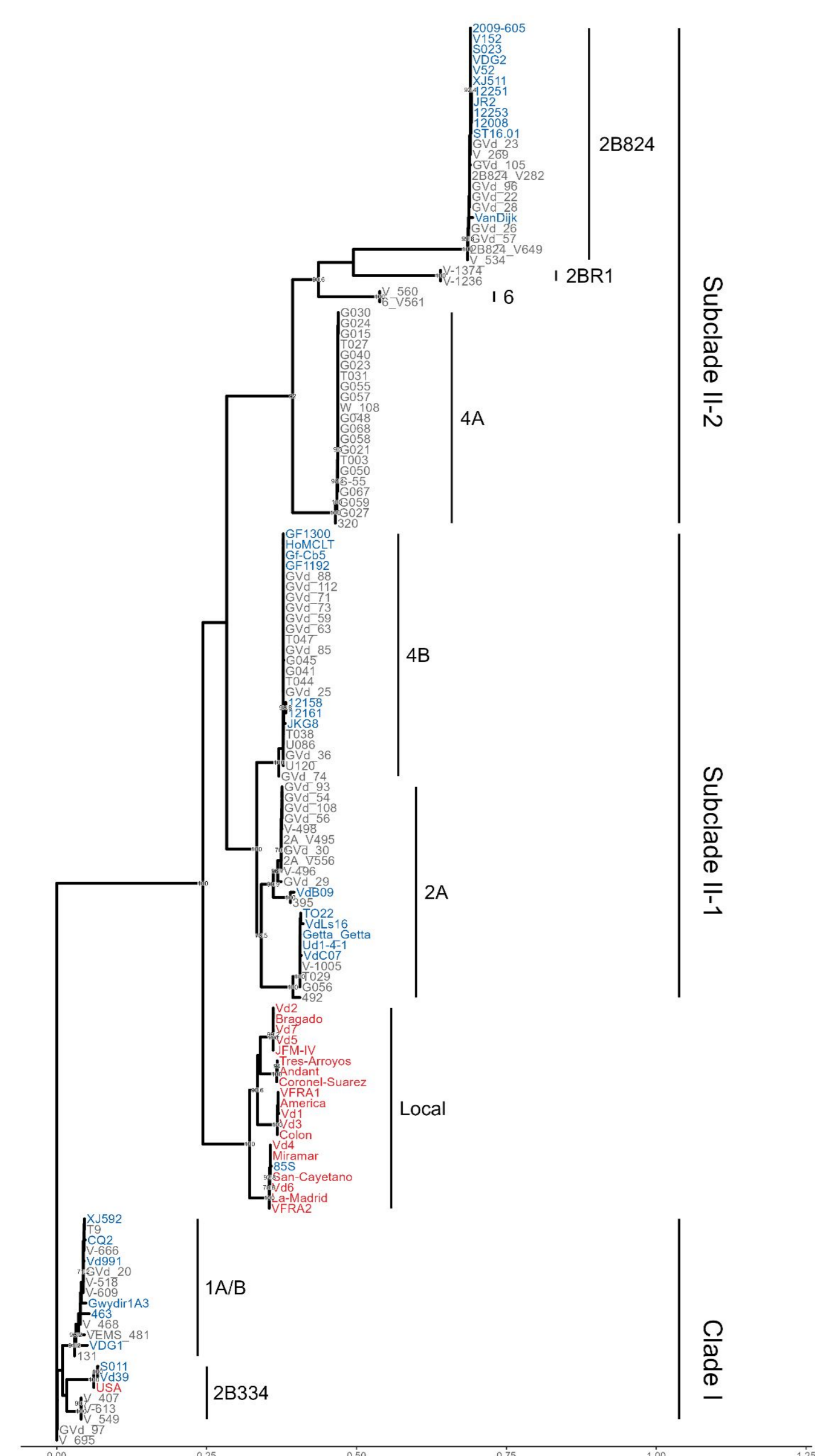


Fig. 3: Neighbor-joining tree inferred from 1165 SNPs of 222 *V. dahliae* isolates. Branches with less than 70% bootstrap support <70% were excluded. Colors indicate the origin of the dataset. Red: this study. Blue: NCBI Genome data. Gray: Bautista-Jalón et al. (2021) data (only 10 selected isolates belonging to lineage 4B were included to reduce the size of the figure).

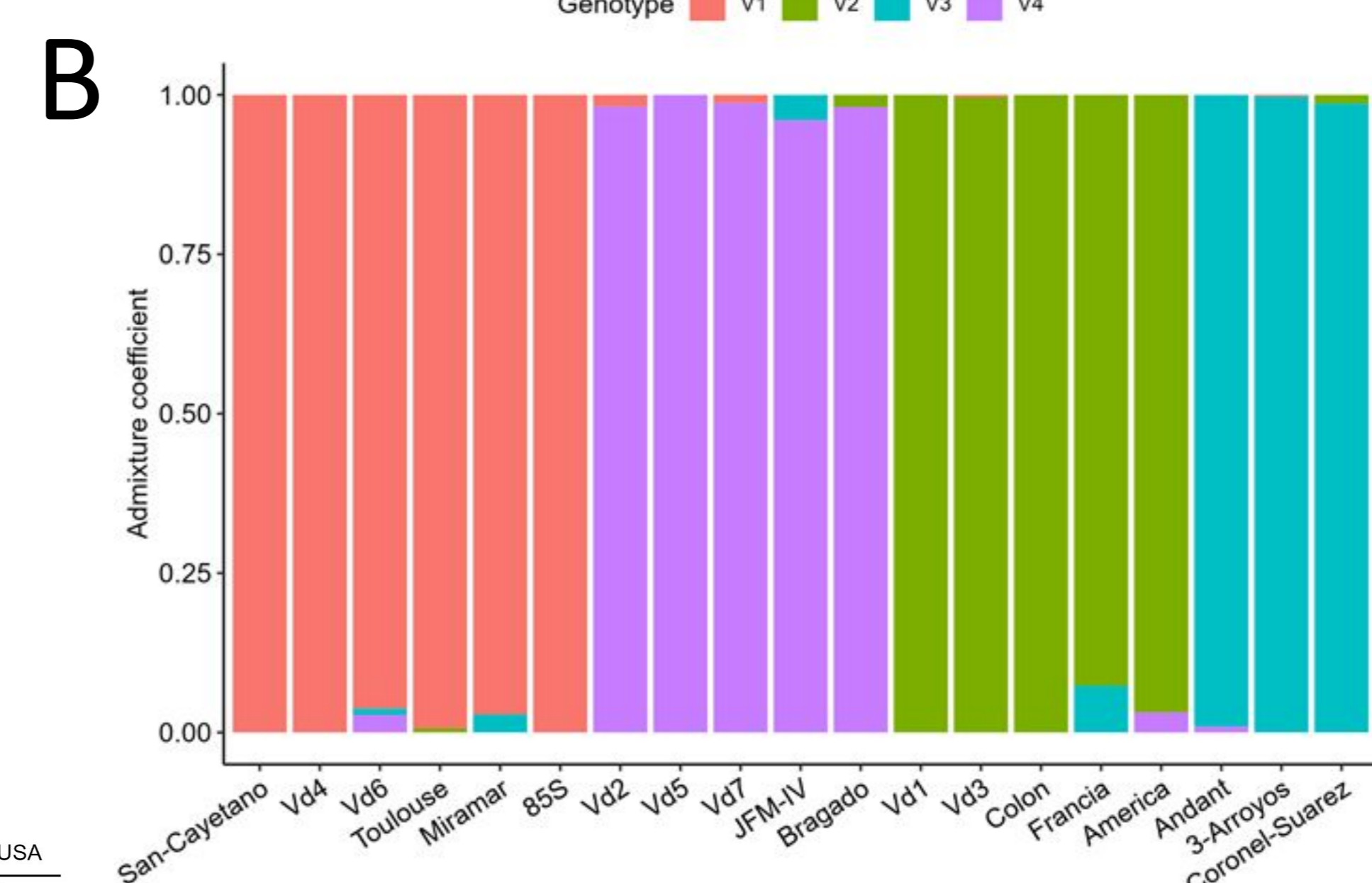
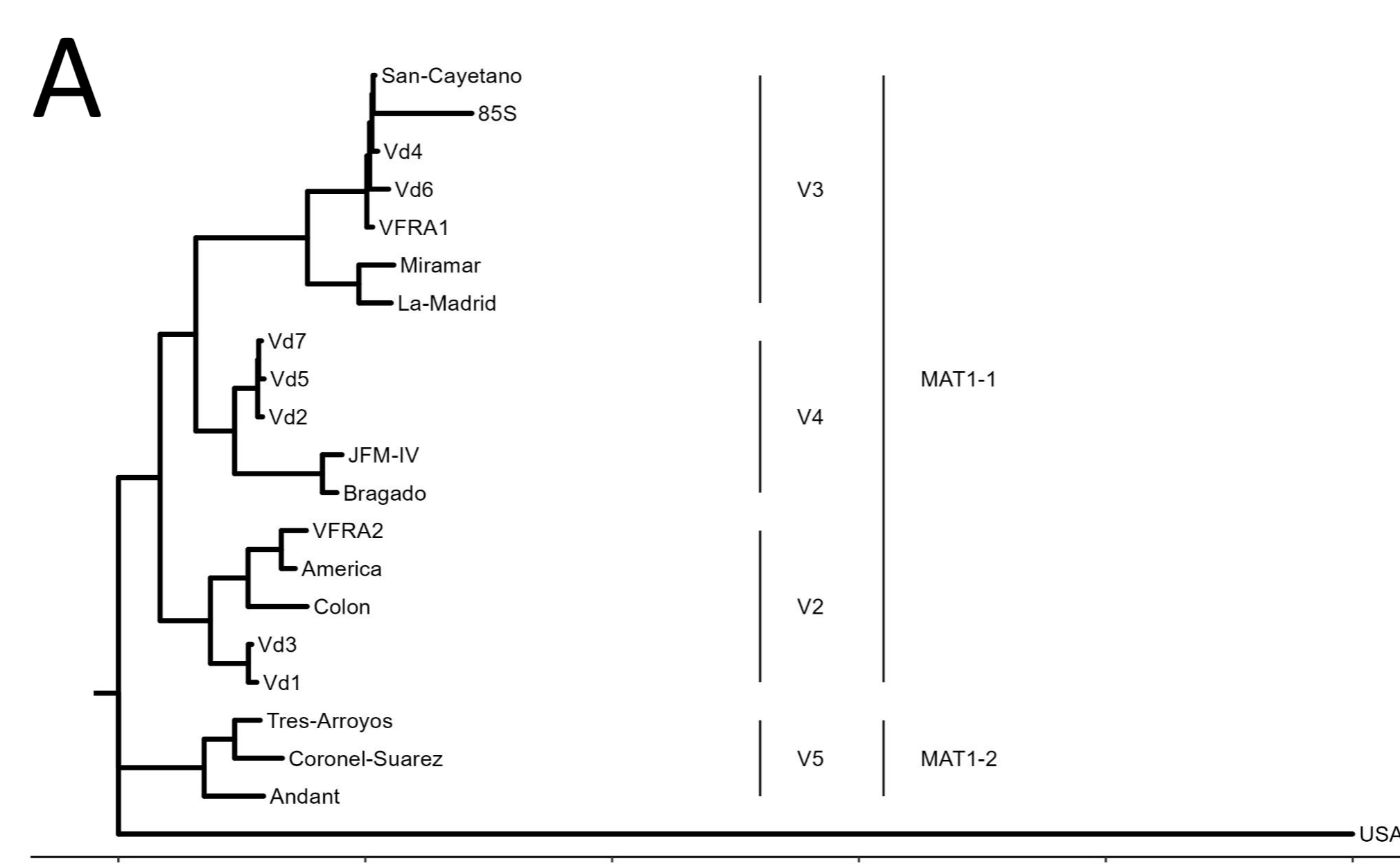
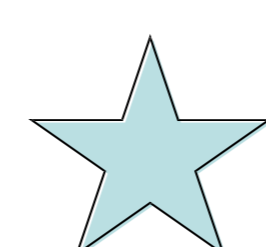


Fig.4: Analysis of population structure of *V. dahliae* using 16471 SNPs.

(A) Neighbor-Joining tree, the clustering generated by discriminant analysis (1, 2, 3, 4) and the characterization by MAT idiomorph (MAT1-1 and MAT1-2) are indicated. (B) snMF analysis, ancestry proportions of *V. dahliae* isolates for K=4. The colors indicate the different hypothetical ancestral populations.

- The Argentine isolates characterized in this study were grouped together with the French reference isolate 85S and another isolate of the same origin to form a putative new lineage (Fig. 3).
- This new lineage is divided into four possible clusters (Fig. 4 A and B) which could correspond to the phytopathological races previously described by Clemente et al. (2017).
- No differential clustering was observed based on the geographical origin of the local isolates. The MAT idiomorph marker showed that 3 isolates are MAT1-2, while the remaining 14 are MAT1-1 (Fig.4 A).
- This study allows the characterization of molecular variability and potential phytopathological races of *V. dahliae* which is essential for the control of VW.

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