Fig. S1. Flow chart summarizing the bioinformatic tools used in this study.

Only the second tier bioinformatic tools are included.

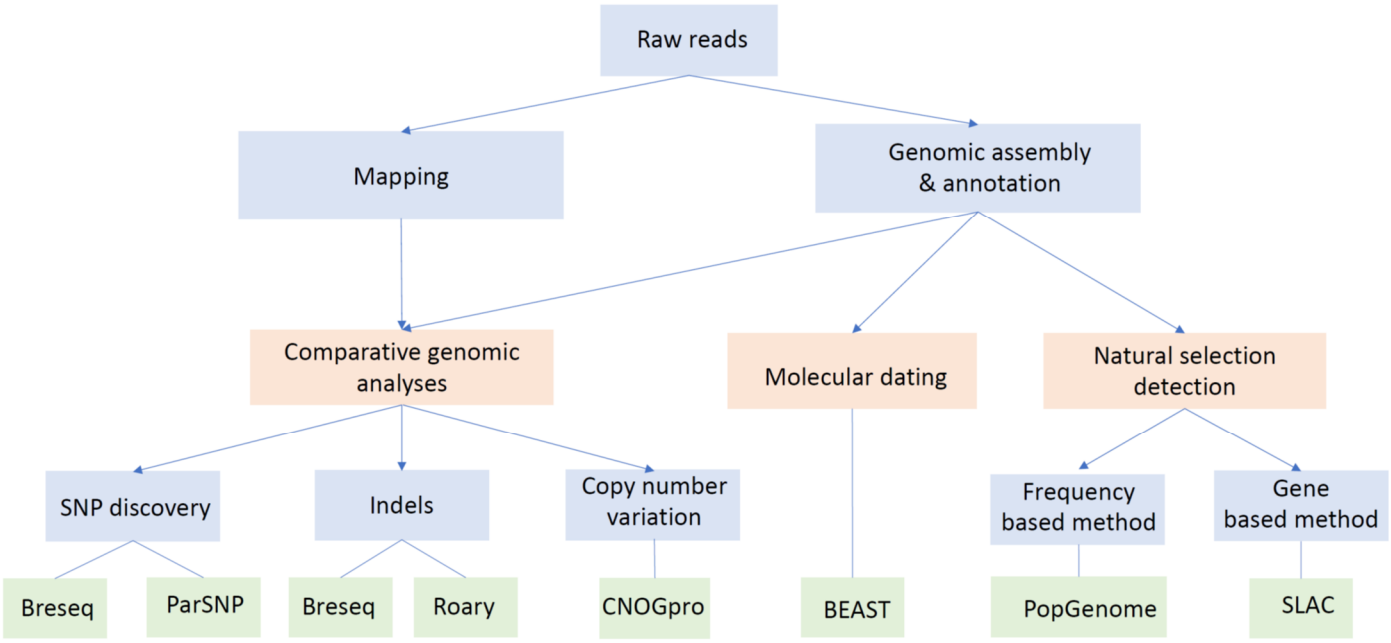


Fig. S2. Dating the introduction of *X. fastidiosa* in Apulia, Italy.

The 95% HPD have been added on the main nodes.

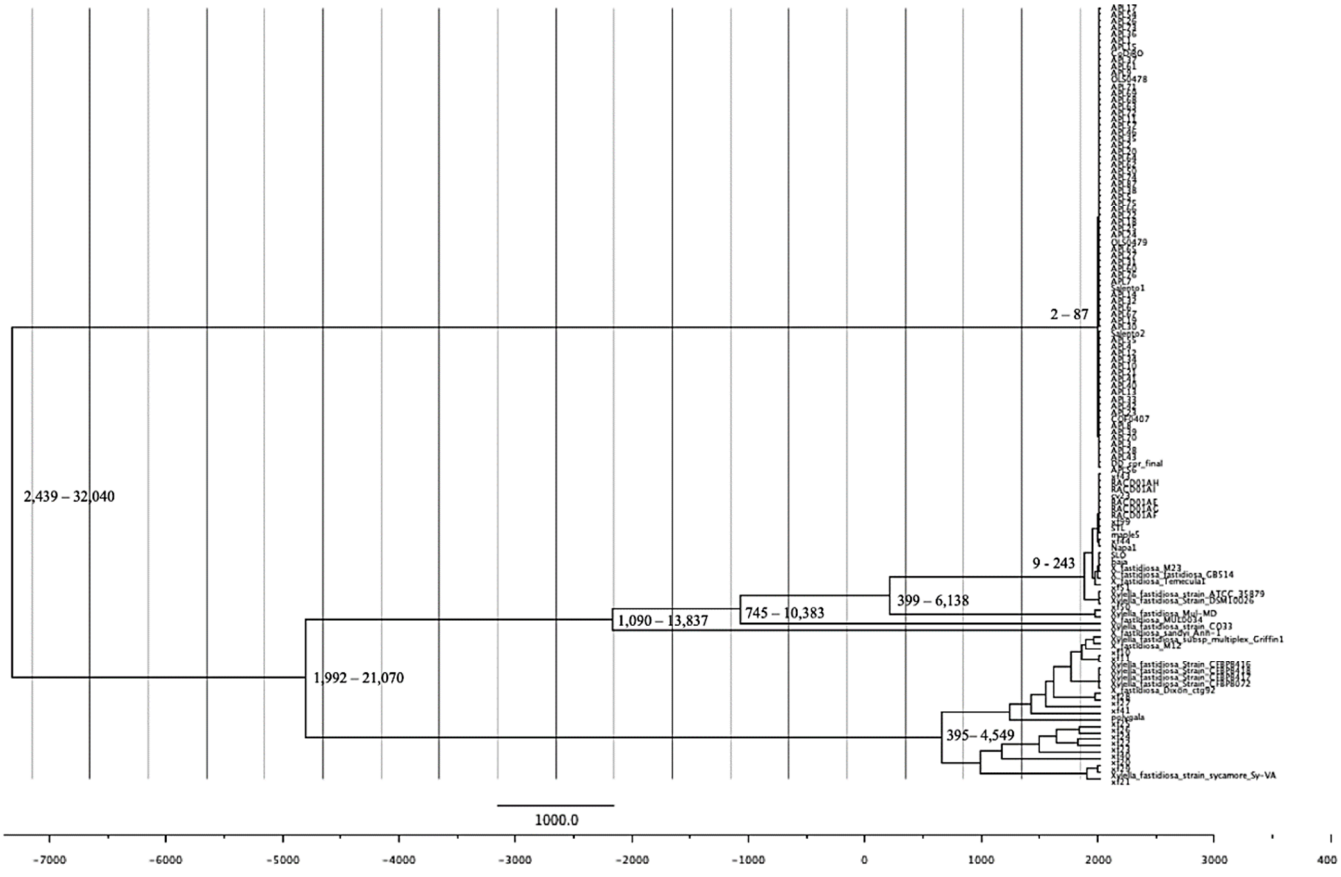


Fig. S3. Ancestral and recent recombination events within the ST53 clade.

No ancestral event was detected within ST53 (A) while four recent recombination events were observed (B): two introgression events of the APL-COF lineage (blue) into OLS0478 (0.410-0.429 Mb and 1.013-1.037 Mb) and two introgression events of an unknown lineage (black) into COF0407 (0.961-0.962 Mb) and APL38 (0.993-0.101 Mb). The OLS lineage containing the two Costa Rican strains isolated from oleander is depicted in red.

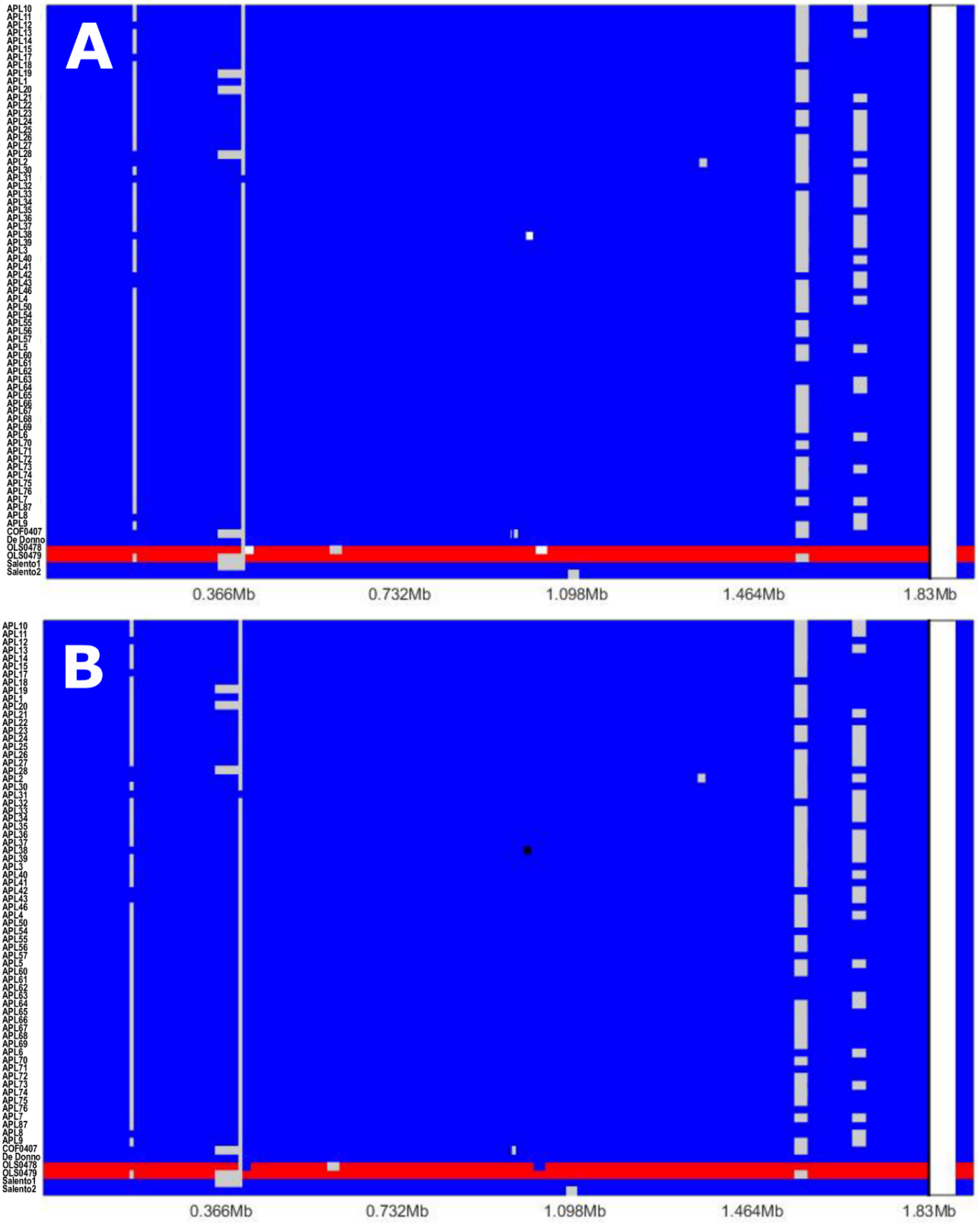


Fig. S4. Pangenome of the ST53 clade.

ST53 pangenome pie (A) and Venn diagram (B). COG categories of the ST53 core genome are shown in (C). S: no functional prediction, J: translation, including ribosome structure and biogenesis, M: cell wall structure and biogenesis and outer membrane, E: amino acid metabolism and transport, L: replication, recombination and repair, C: energy production and conversion, K: transcription, O: molecular chaperones and related functions, H: coenzyme metabolism, P: inorganic ion transport and metabolism, F: nucleotide metabolism and transport, G: carbohydrate metabolism and transport, I: lipid metabolism, T: signal transduction, U: Intracellular trafficking and secretion, V: Defense mechanisms , D: cell division and chromosome partitioning, Q: Secondary metabolites biosynthesis, transport and catabolism.

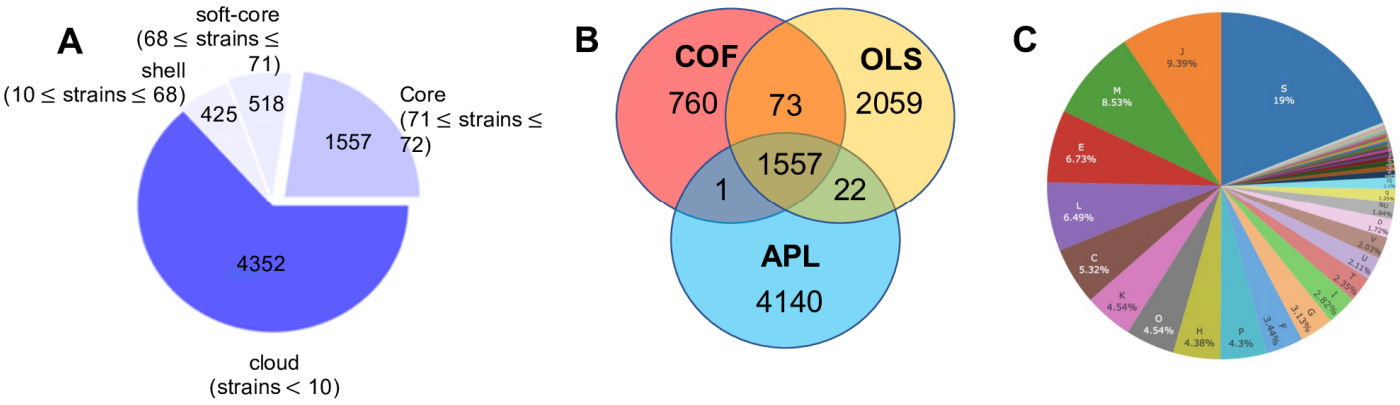
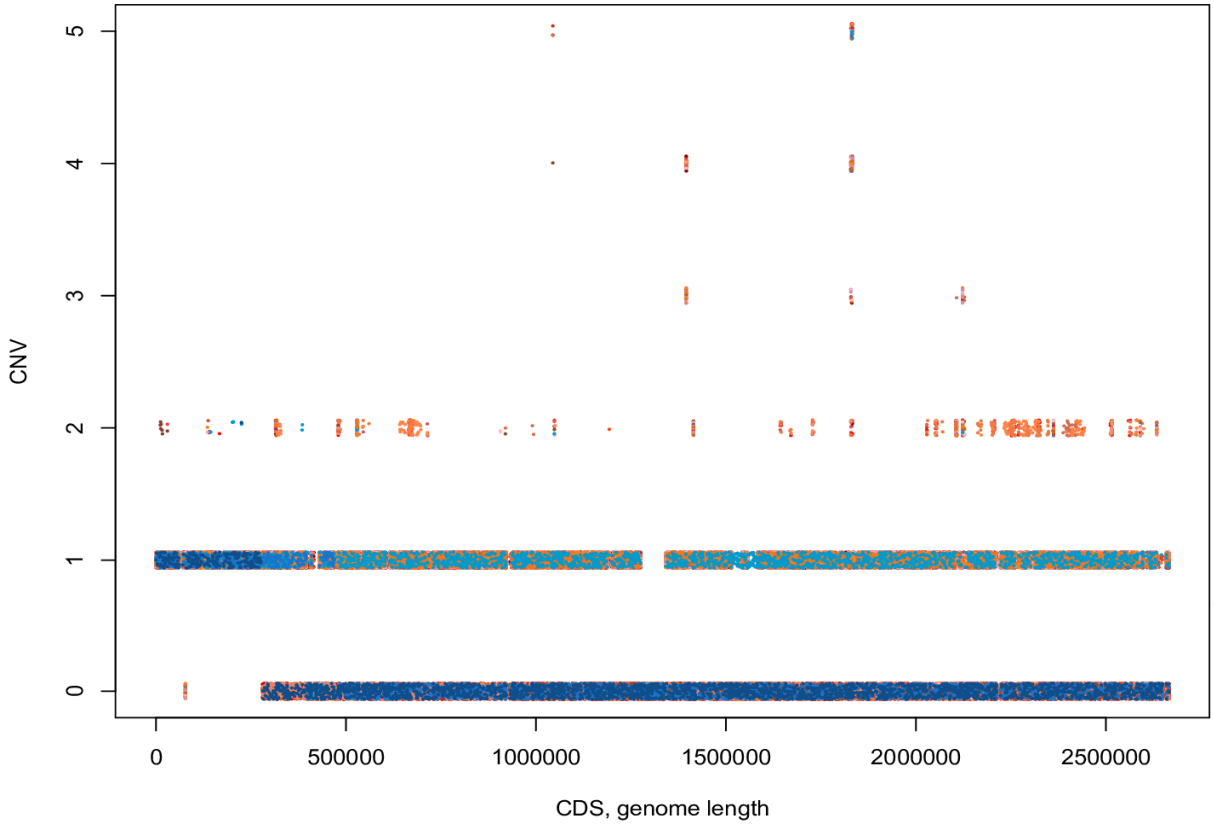
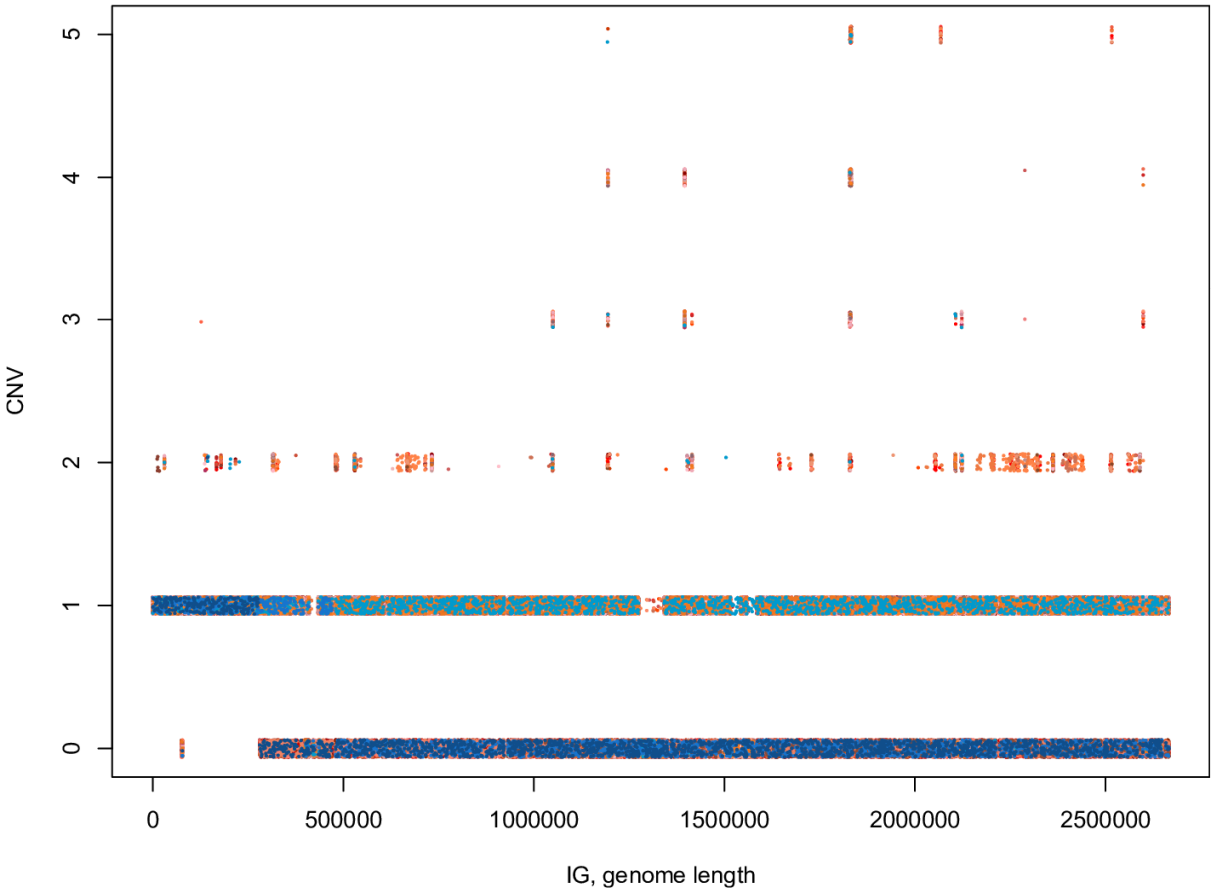


Fig. S5. Copy number variations (CNV) in each ST53 isolate using subsp. *pauca* strain *Pr8x* as a reference.

CNV in both coding sequences (CDS) and intergenic regions (IG) are shown. No duplication events were shared by all the Apulian isolates (orange or red dots). The Costa Rican strains COF0407 and OLS0478/OLS0479 appear in dark and light blue respectively.


CNV
0
1
2
3
4
5
0
500000
1000000
1500000
2000000
2500000
CDS, genome length


CNV
0
1
2
3
4
5
0
500000
1000000
1500000
2000000
2500000
IG, genome length