

Genetic diversity of grapevine Pinot gris virus (GPGV) in Australia

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Background

Grapevine Pinot gris virus (GPGV; Genus *Trichovirus*, family *Betaflexiviridae*):

- Causes leaf deformation and mottling disease (GLMD) in sensitive varieties¹
- Some GPGV strains may not be associated with disease
- Can cause reduced yield and low-quality fruit^{2,3}
- Spreads by
 - vegetative propagation
 - grafting of infected planting material
 - bud-blister mites
- Occurs globally, including Australia⁴
- Found in Australia in 2016⁵
- Association to GLMD disease is unknown

Project aim: A comprehensive study of the genetic diversity of GPGV in Australian vineyards to understand its potential risk to production in rootstock, table and wine grape varieties.

Methods:

- 27 GPGV isolates from infected rootstocks, wine and table grapes were collected from vineyards in New South Wales (NSW), South Australia (SA) and Victoria (VIC)
- Symptoms were recorded
- Each sample was tested by RT-PCR and high throughput sequencing
- Phylogenetic analyses compared a small (588nt) genomic region across the coat protein (CP) and movement protein (MP) genes previously used to differentiate between strains of GPGV associated with GLMD and asymptomatic vines^{6,7}
- Phylogenetic analyses compared whole genomes to investigate GPGV diversity amongst global isolates and to determine a possible origin of Australian strains

Results:

- GPGV was detected in 5 vines with GLMD-like symptoms, 10 vines with other symptoms (Figure 1) and 12 vines that were asymptomatic.
- There was no association between specific GPGV strains and disease based on the 588 nt CP/MP region (Figure 2)
- Full genomes of Australian GPGV isolates cluster closely with genomes of isolates from Europe, suggesting a European origin of Australian strains (Figure 3)
- There are four distinct clusters of Australian GPGV isolates but diversity exists within clusters, suggesting multiple introductions of the virus into Australia (Figure 4)
 - Pink clade: 97-100% nucleotide identity
 - Green clade: 97-99% nucleotide identity
 - Red clade: 96-99% nucleotide identity
 - Blue clade: 96-98% nucleotide identity
- Many Australian GPGV isolates share high nucleotide similarity and are therefore closely related (Figure 3 & 4), demonstrating spread after introduction of the virus.

Conclusions:

- GPGV has been introduced to Australia multiple times
- The association between disease and GPGV in Australia remains unclear
- Future inoculation studies will assist in determining if GPGV causes disease in Australia
- Use of virus tested high health planting material is recommended to prevent virus associated diseases

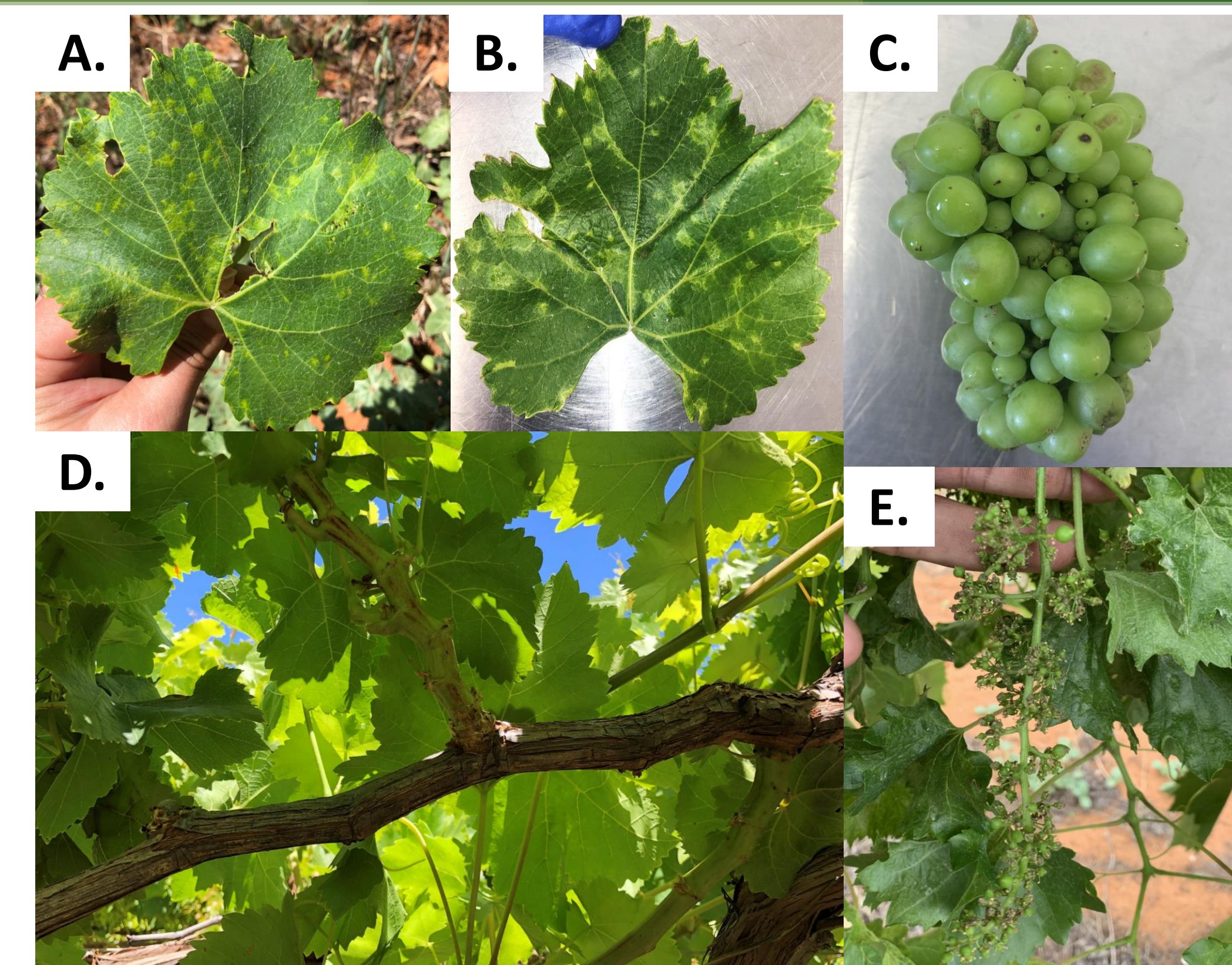


Figure 1. GLMD-like symptoms observed in Australian wine and table grape varieties.

- A. Leaf mottling in *Malbec*.
- B. Mottling and deformation in *Fiano*.
- C. Small bunches of fruit in *Nero d'Avola*.
- D. Zig-zag shoots in *Crimson seedless*.
- E. Poor growth of fruit in *Vermintino*.

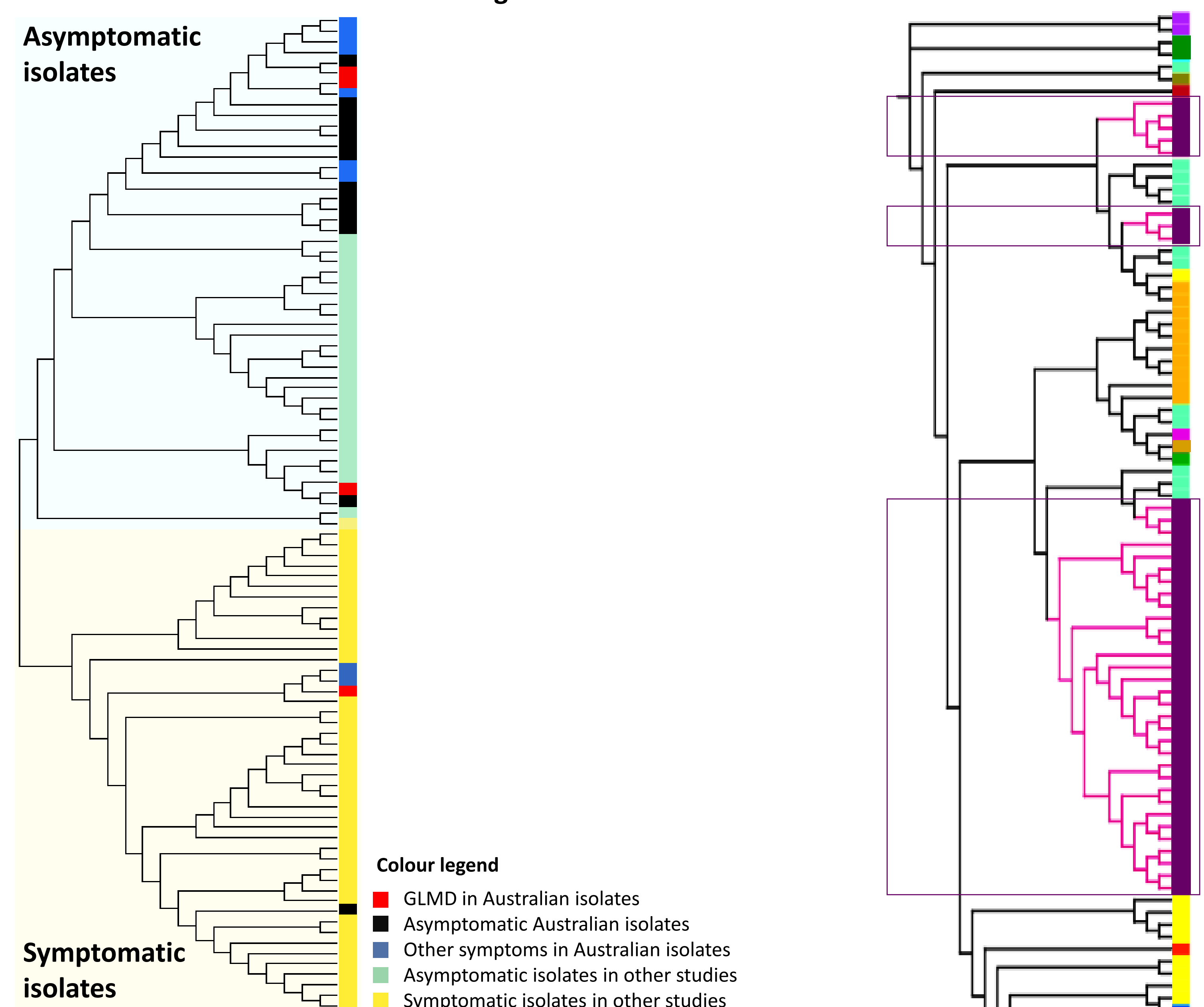


Figure 2. Maximum likelihood phylogenetic tree generated with 27 Australian GPGV isolates along with Italian isolates from Saldarelli et al, 2014 and Bertazzon et al, 2016, using the 588nt region across the movement protein and coat protein gene sequences.

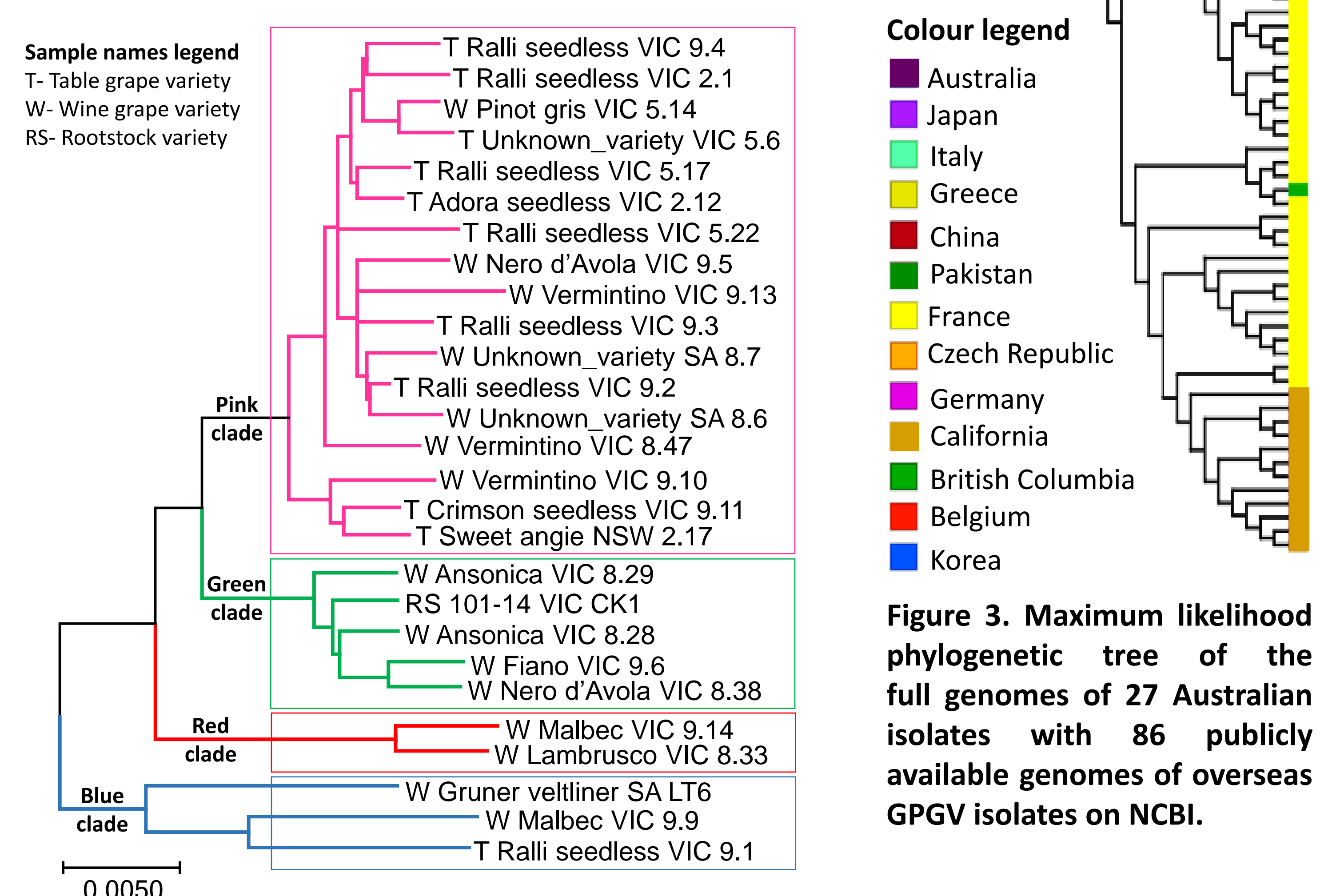


Figure 3. Maximum likelihood phylogenetic tree of the full genomes of 27 Australian isolates with 86 publicly available genomes of overseas GPGV isolates on NCBI.

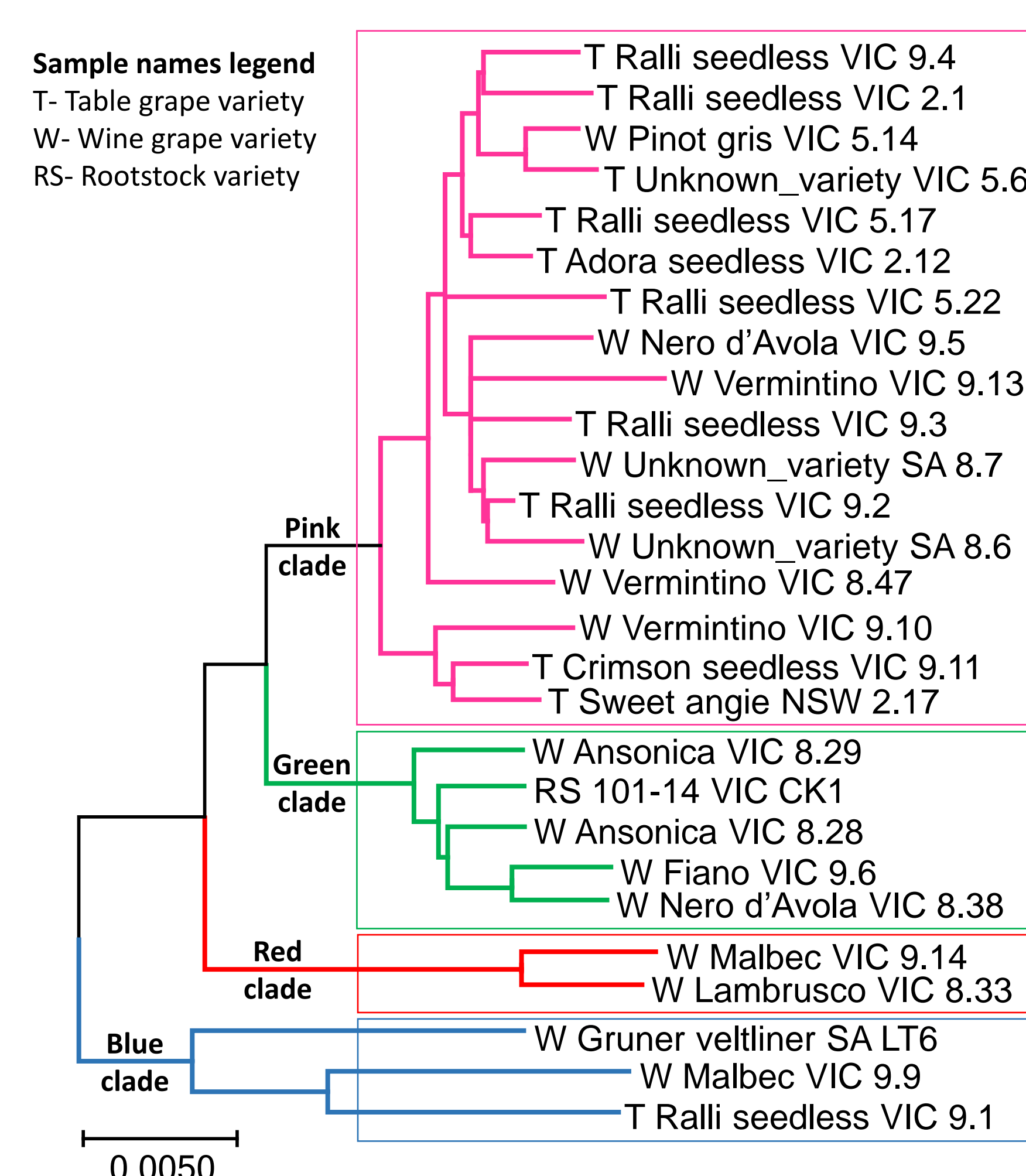


Figure 4. Maximum likelihood phylogenetic tree constructed with full genome sequences of 27 Australian GPGV isolates detected in HTS analysis.