

Supporting S1 to

Grapevine Pinot gris virus is present in different non-*Vitis* hosts

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Figure S1. Field view of sampled maintained vineyards at Szekszard, Eger, and Tokaj.



Figure S2: Field view of sampled neglected vineyard at Mogyorod.

Chenopodium album

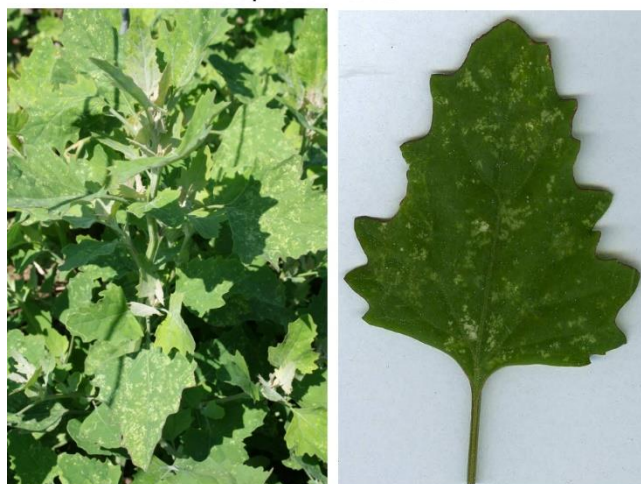


Figure S3: Symptoms of *Chenopodium album* collected at Szekszard that proved to be GPGV infected.

Asclepias syriaca



Ailanthus sp



Rosa canina



Crataegus sp



Sambucus nigra



Figure S4: Symptoms of sampled plants collected at Mogyorod that proved to be GPGV infected.



Figure S5: Symptoms of *Rosa canina* collected at Eger that proved to be GPGV infected.

Rubus sp



Figure S6: Symptoms of sampled *Rubus sp.* that proved to be GPGV infected.

Fraxinus sp



Figure S7: Symptoms of *Fraxinus sp.* collected at Jaszszentlászlo that proved to be GPGV infected.

MP/CP coding region

- Szekszard
- Mogyorod
- Eger
- Tokaj
- Jaszszentlaszlo

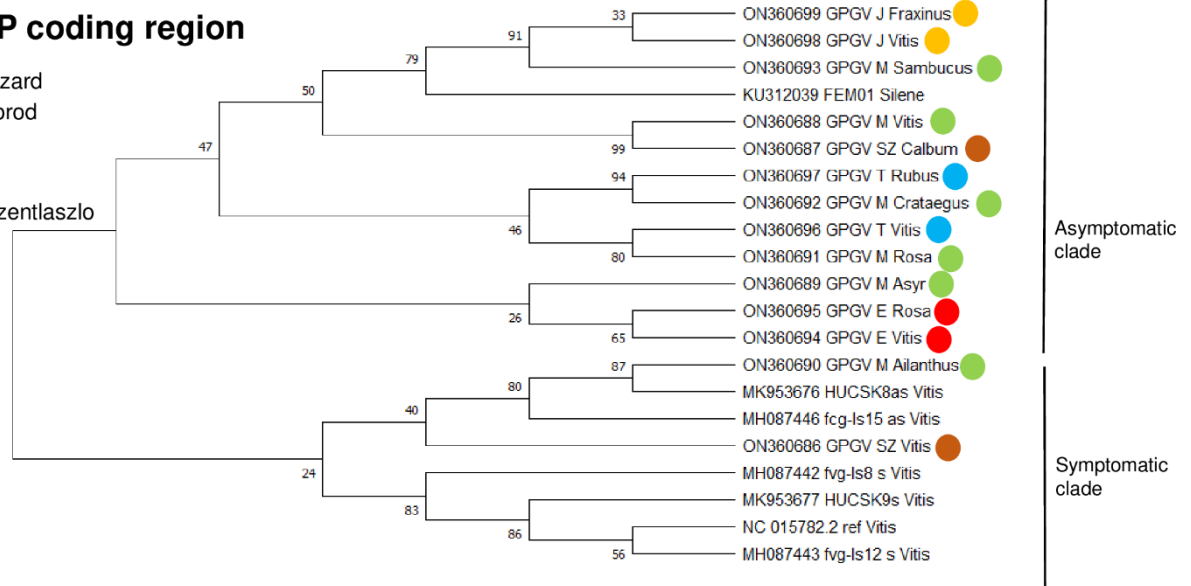


Figure S8. Evolutionary analysis of 411 bp part of MP/CP coding region of GPGV by maximum likelihood method.

The evolutionary history was inferred by using the maximum likelihood method and Tamura-Nei model [1]. The bootstrap consensus tree inferred from 1000 replicates [2] is taken to represent the evolutionary history of the taxa analysed. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test 1000 replicates) are shown next to the branches [2]. Evolutionary analyses were conducted in MEGA11 [3]. Colour circles indicates the geographical origin of the strains. HUCSK8as and HUCSK9s are asymptomatic and symptomatic GPGV strains described in Hungary [4]. Ref is the GPGV reference genome from grapevine, while FEM01 strain was described from *Silene* [5]. Symptomatic (s) and asymptomatic (as) GPGV isolates Fvg-is-8_s, 12_s, 15_as were described by Tarquini et al [6].



Figure S9: Polymorphism in movement coding region of asymptomatic and symptomatic GPGV variants.

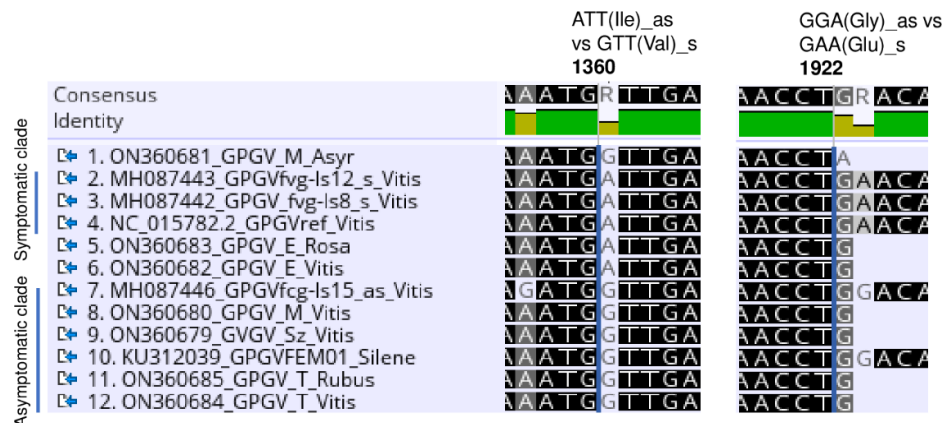


Figure S10: Polymorphism in replicase coding region of asymptomatic and symptomatic GPGV variants.

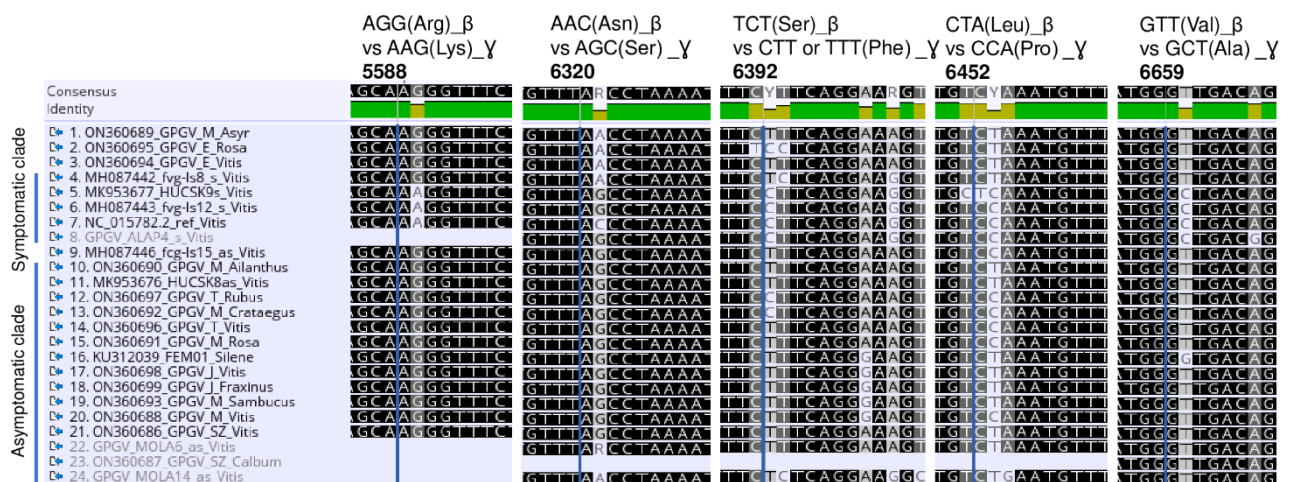


Figure S11: Polymorphism in movement protein coding region of asymptomatic and symptomatic GPGV variants in position differentiating between clade β and γ.

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