

GLRaV-1 Coat protein gene

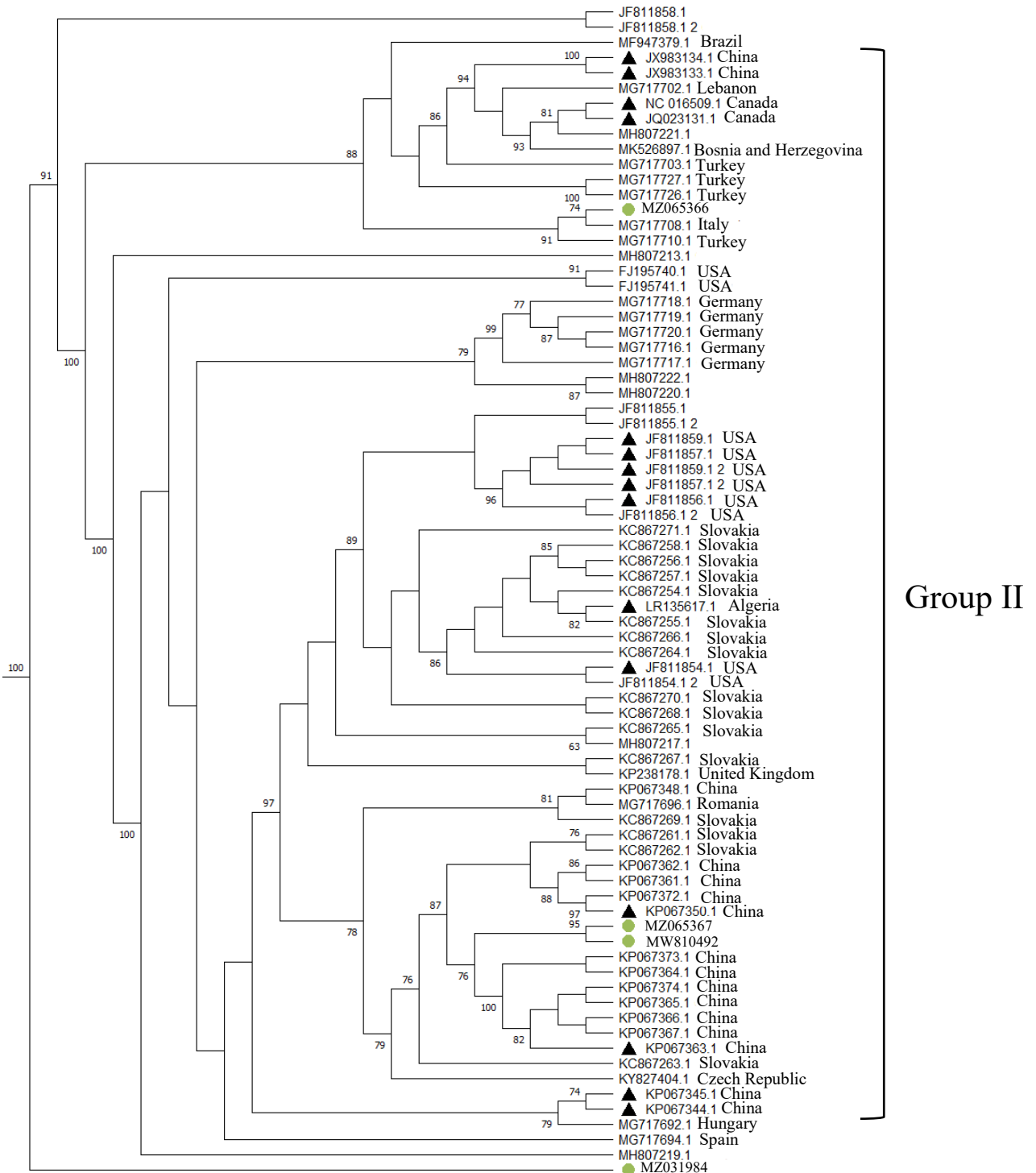


Figure S1. Phylogenetic analysis of global isolates of GLRaV-1 based on nucleotide sequences of the coat protein (cp) gene. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by 'green mark'; ▲ - representative sequence for the group. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

GLRaV-2 Coat protein gene

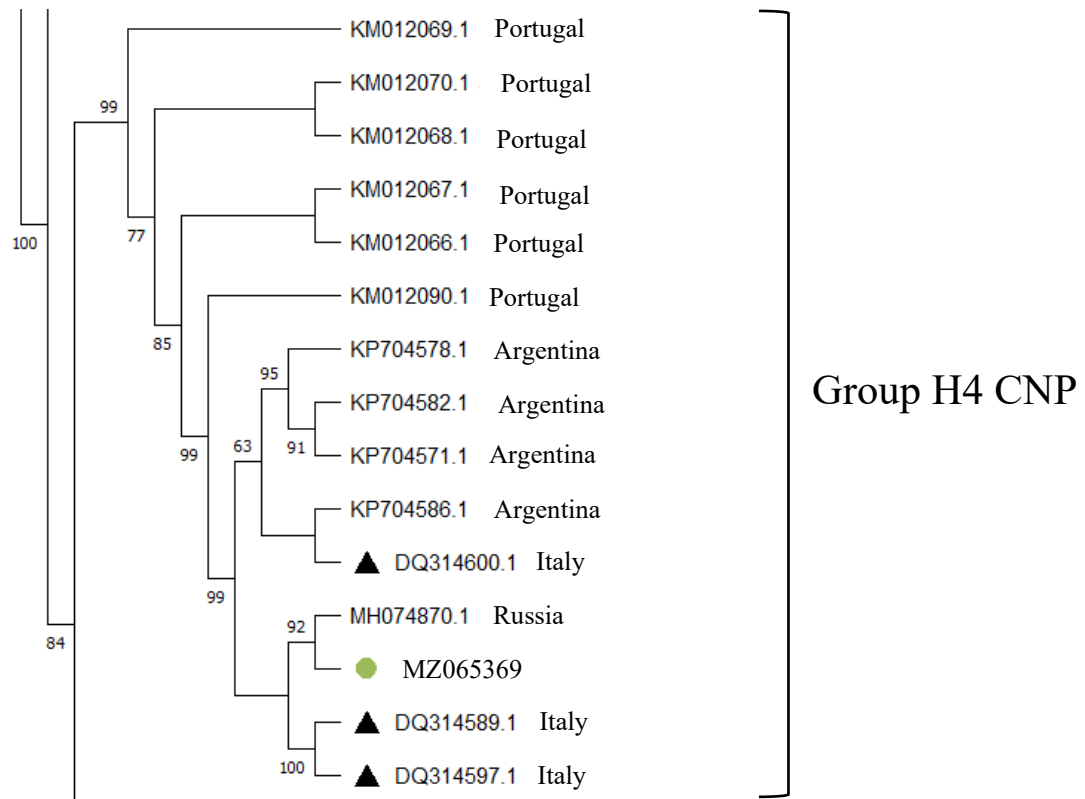


Figure S2. Phylogenetic analysis of global isolates of GLRaV-2 based on nucleotide sequences of the coat protein (cp) gene. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by 'green mark'; ▲ - representative sequence for the group. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

GLRaV-3 Coat protein gene

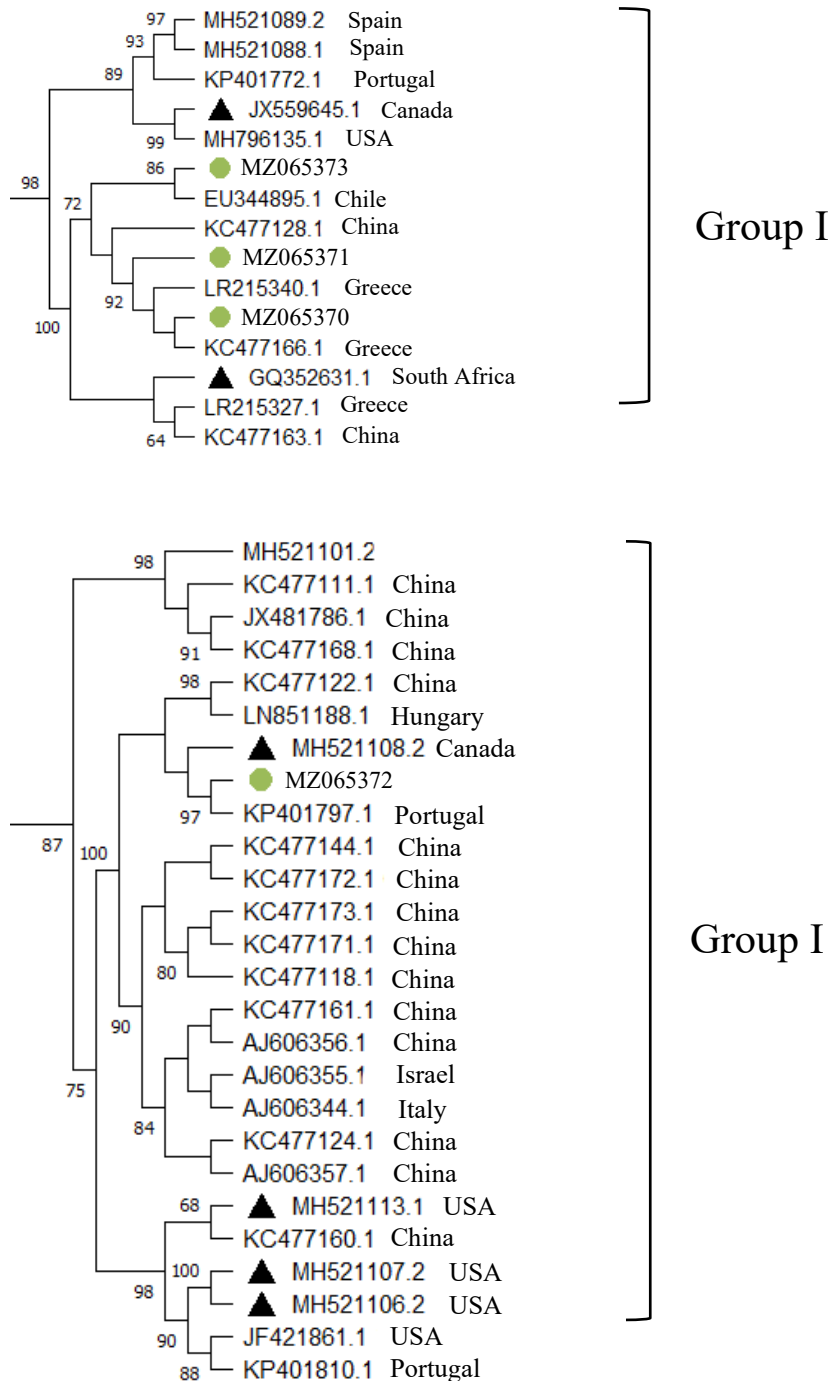


Figure S3. Phylogenetic analysis of global isolates of GLRaV-3 based on nucleotide sequences of the coat protein (cp) gene. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by 'green mark'; ▲ - representative sequence for the group. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

GLRaV-4 HSP70 like protein

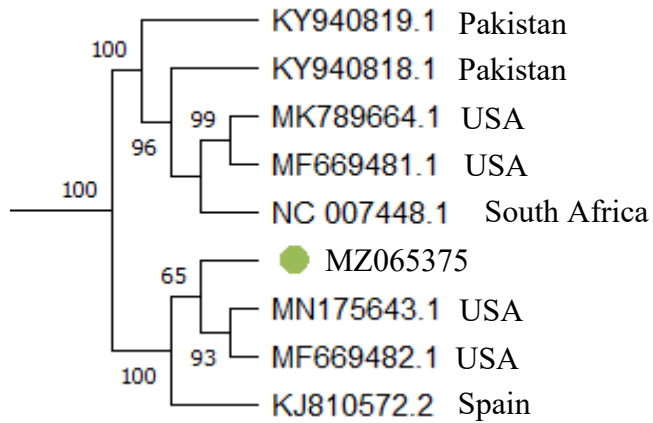


Figure S4. Phylogenetic analysis of global isolates of GLRaV-4 based on total nucleotide sequences from NCBI. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by 'green mark'. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

GFLV Polyprotein gene

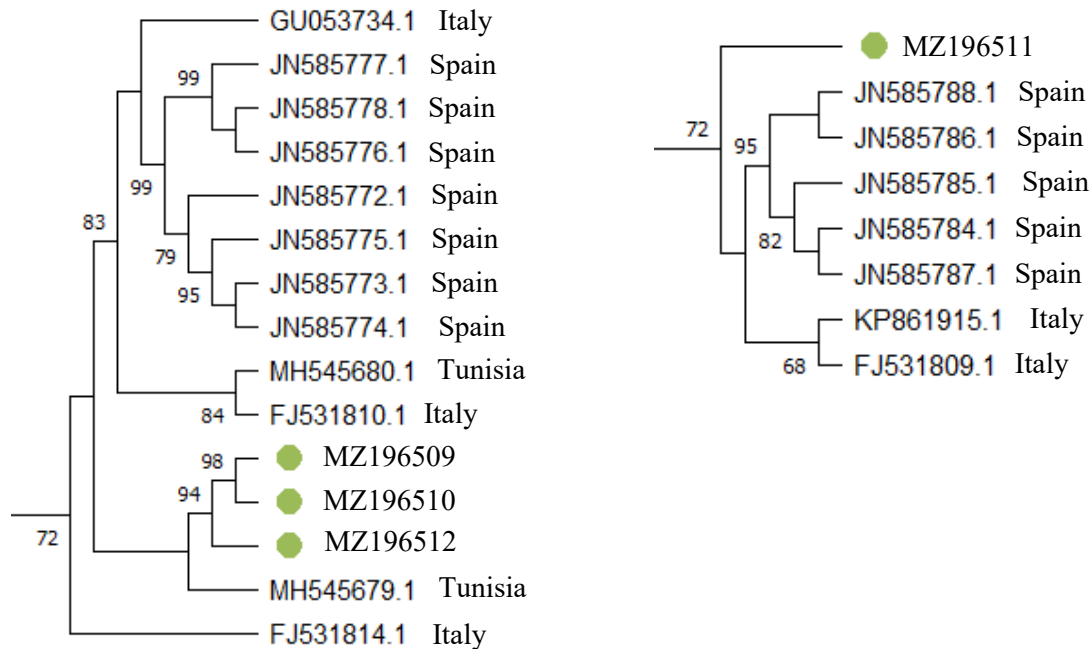


Figure S5. Phylogenetic analysis of global isolates of GFLV based on nucleotide sequences of the polyprotein gene. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by 'green mark'. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

GVA Coat protein gene

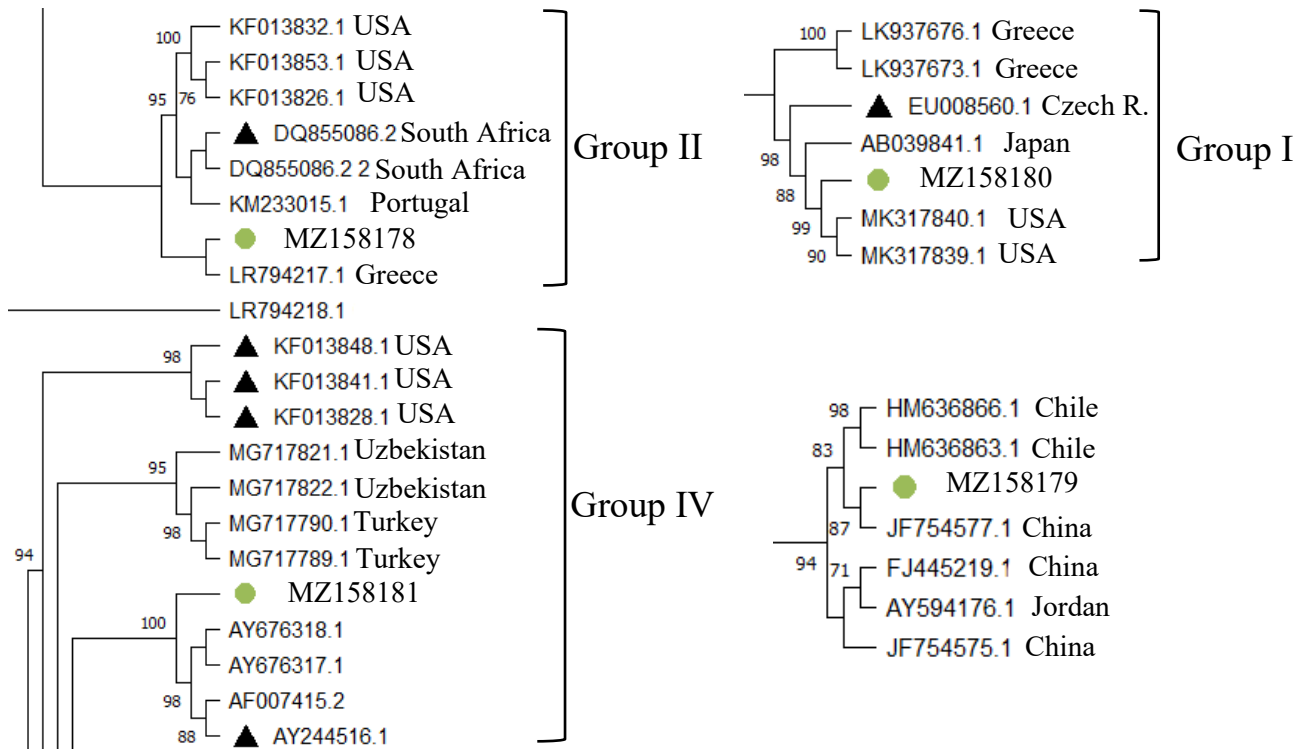


Figure S6. Phylogenetic analysis of global isolates of GVA based on nucleotide sequences of the coat protein (cp) gene. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by 'green mark'; ▲ - representative sequence for the group. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

GRSPaV Coat protein gene

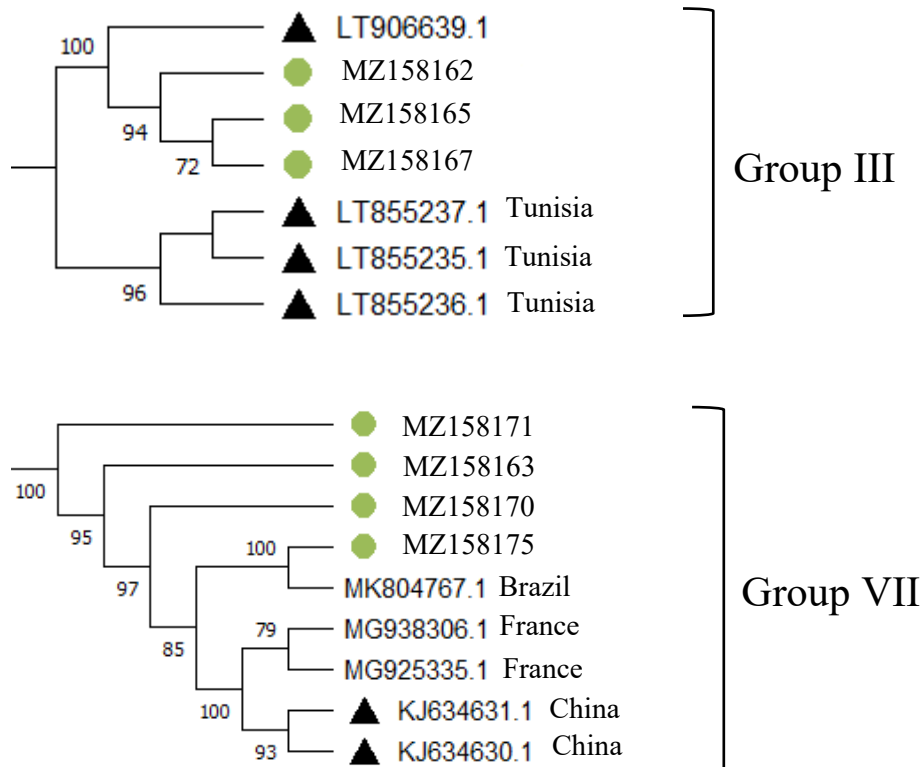


Figure S7. Phylogenetic analysis of global isolates of GRSPaV based on nucleotide sequences of the coat protein (cp) gene. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by 'green mark'; ▲ - representative sequence for the group. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

GVT Coat protein gene

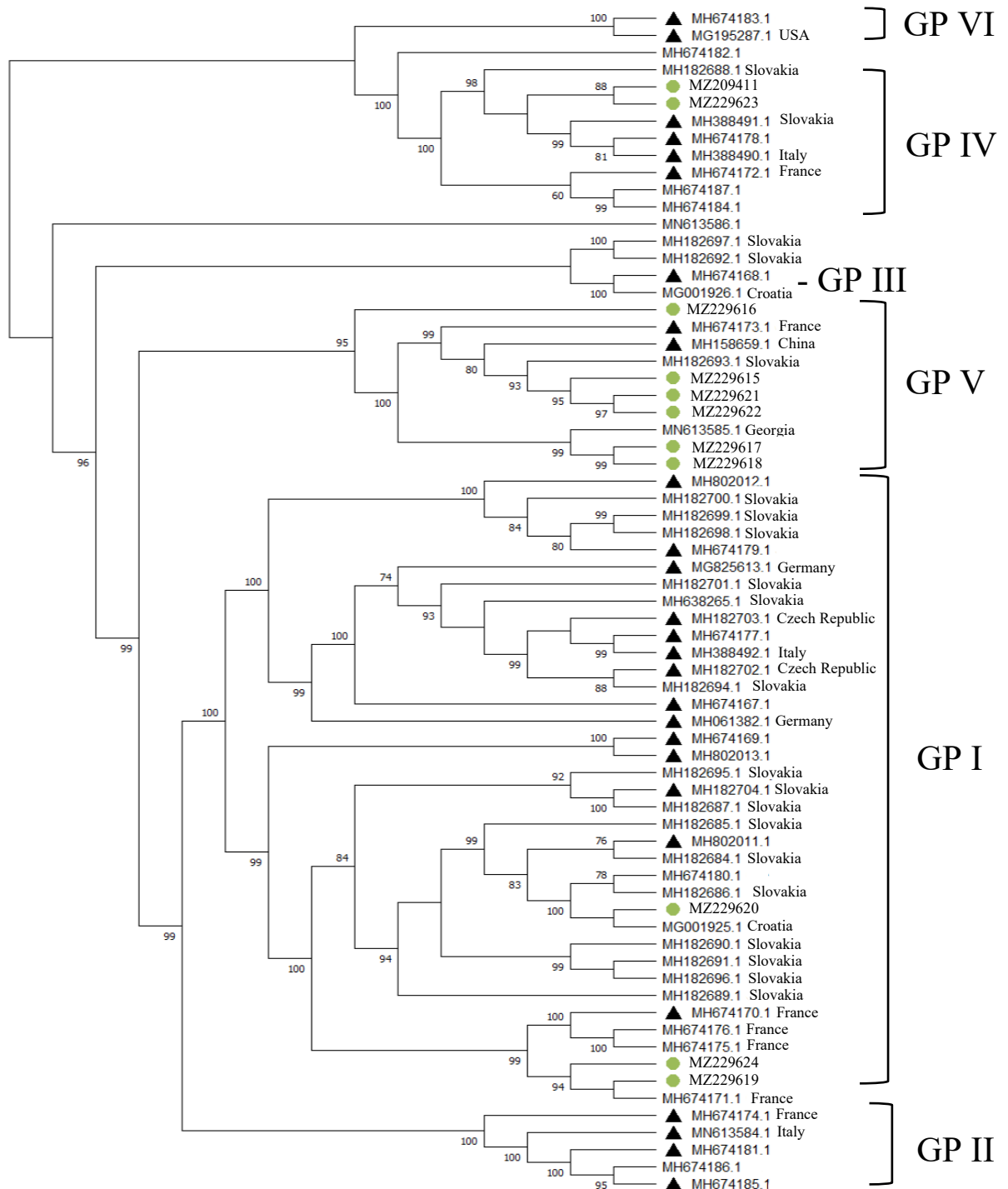


Figure S8. Phylogenetic analysis of global isolates of GVT based on total nucleotide from NCBI. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by 'green mark'; ▲ - representative sequence for the group. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

GPGV Coat protein gene

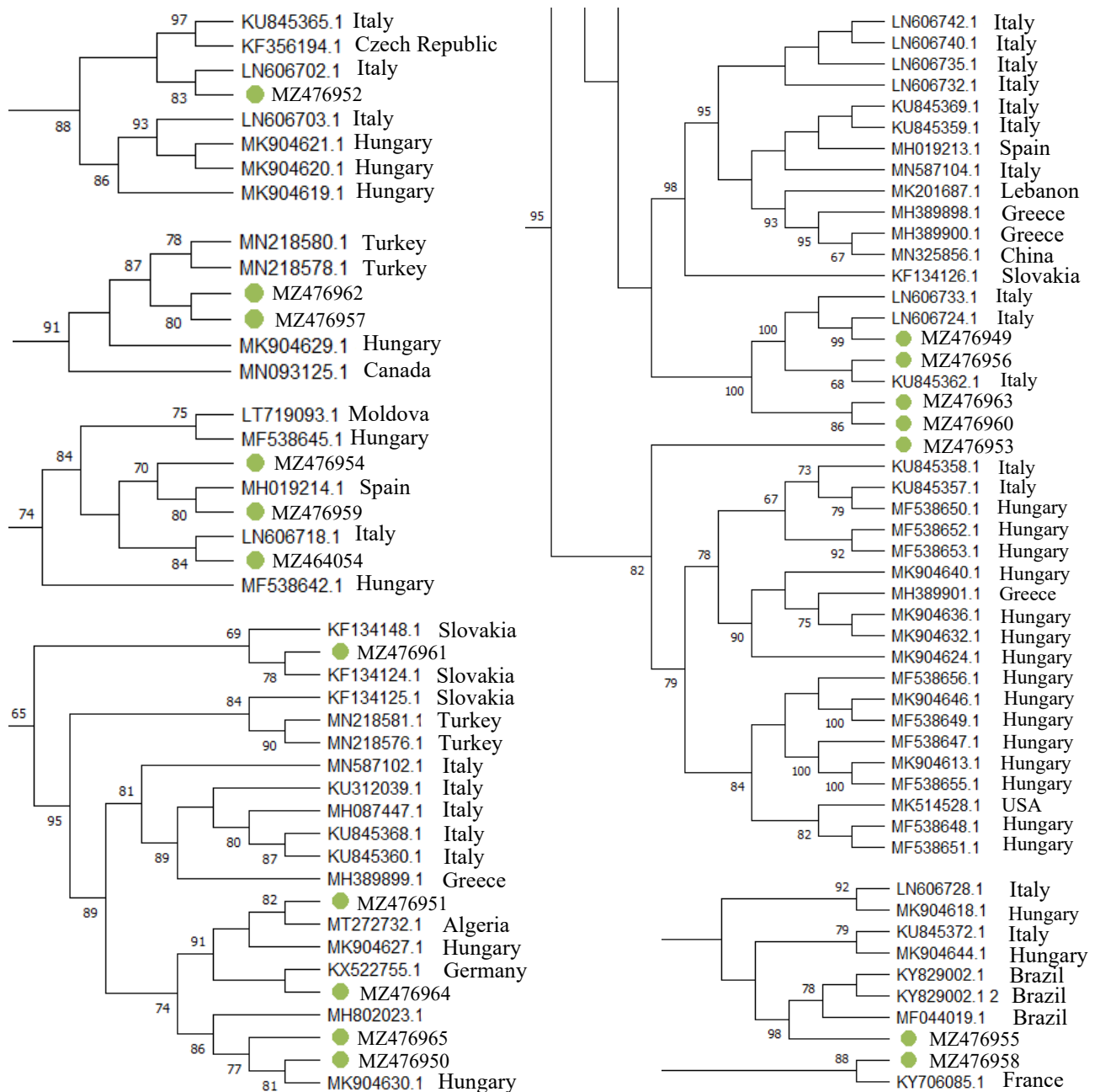


Figure S9. Phylogenetic analysis of global isolates of GPGV based on nucleotide sequences of the coat protein (cp) gene. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by 'green mark'. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

GFkV Coat protein gene

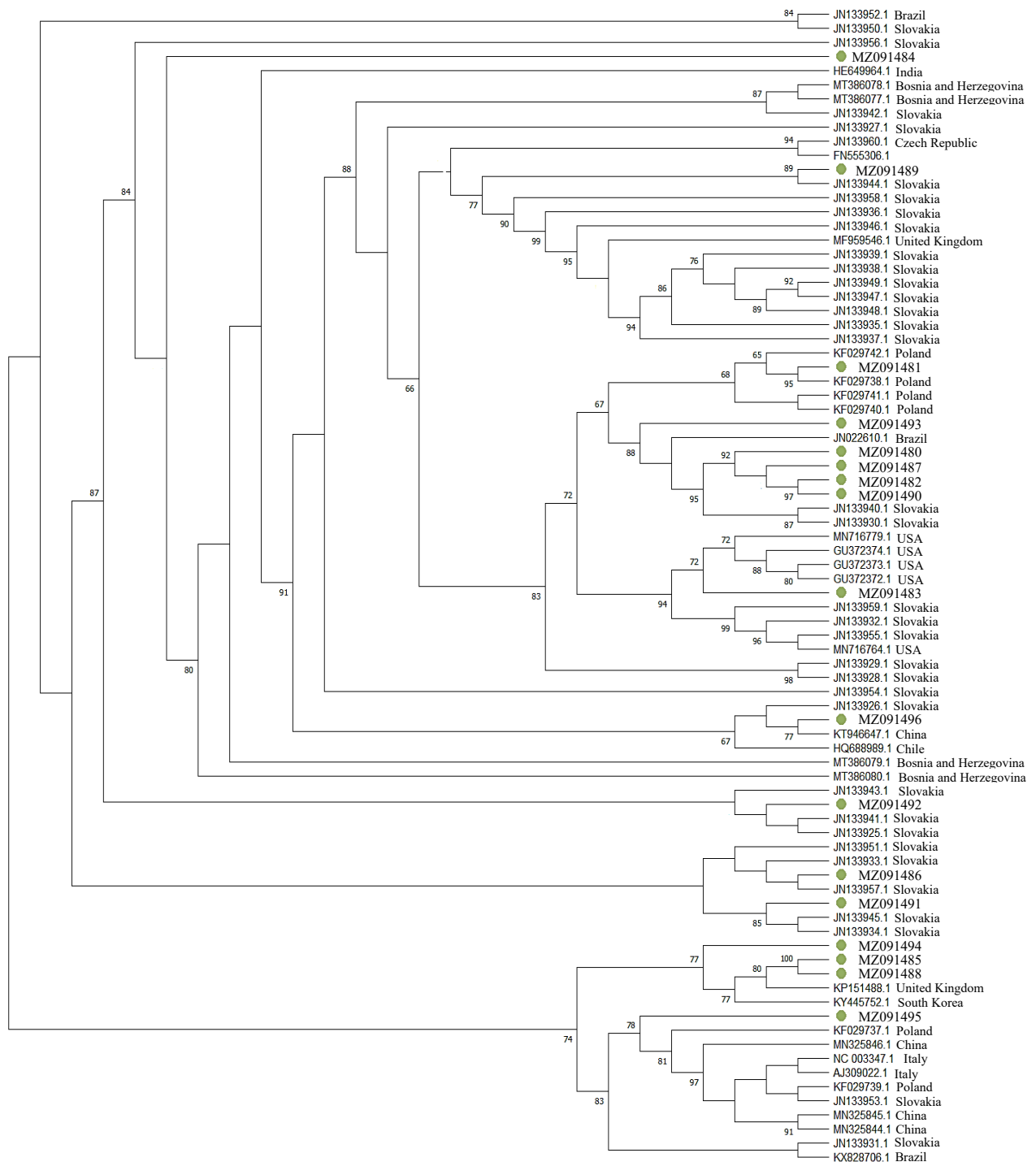


Figure S10. Phylogenetic analysis of global isolates of GFkV based on nucleotide sequences of the coat protein (cp) gene. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by ‘green mark’. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

GRVFFV Polyprotein gene

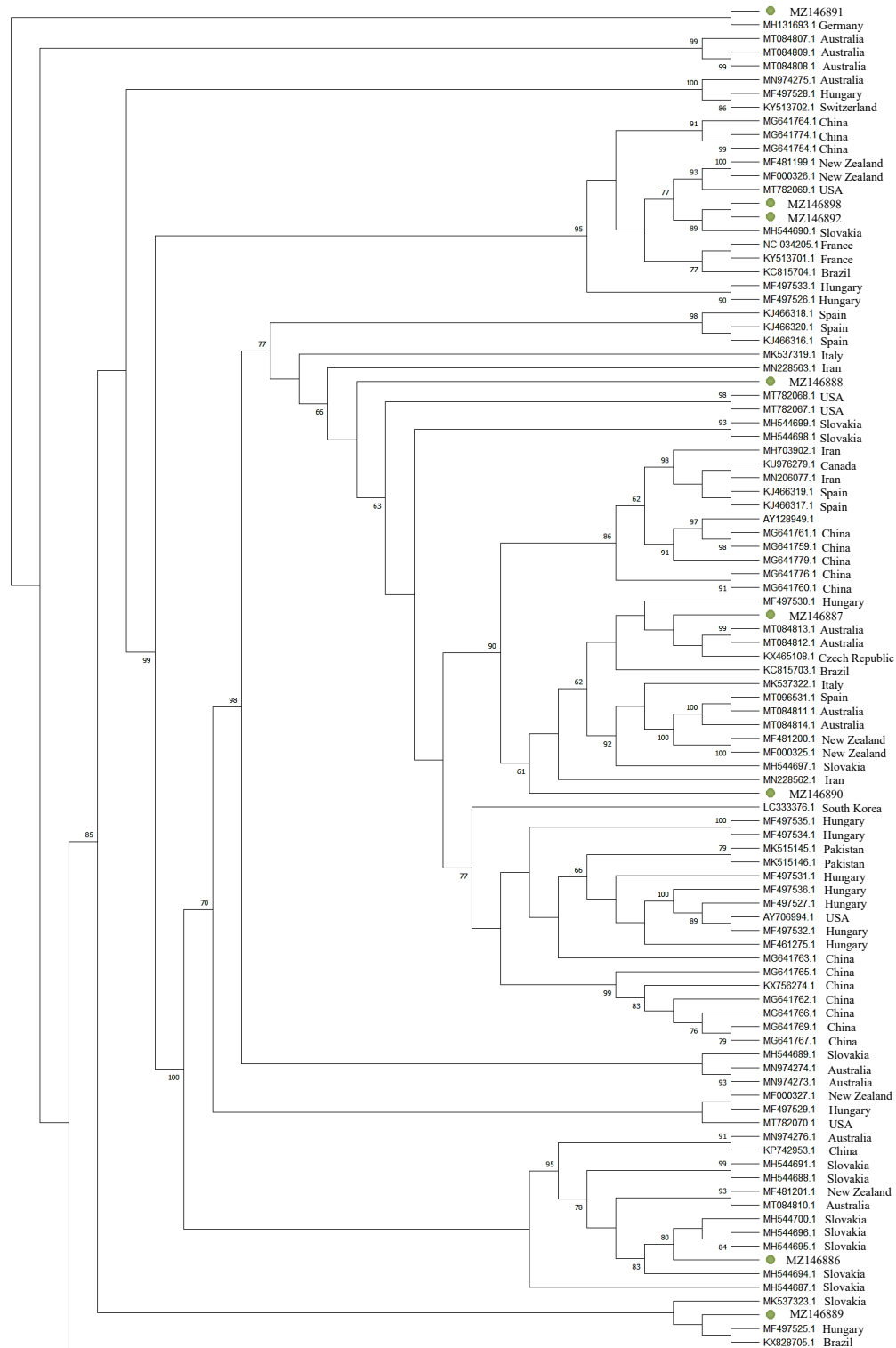


Figure S11. Phylogenetic analysis of global isolates of GRVFFV based on total nucleotide sequences from NCBI. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by ‘green mark’. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

GSyV-1 Coat protein gene

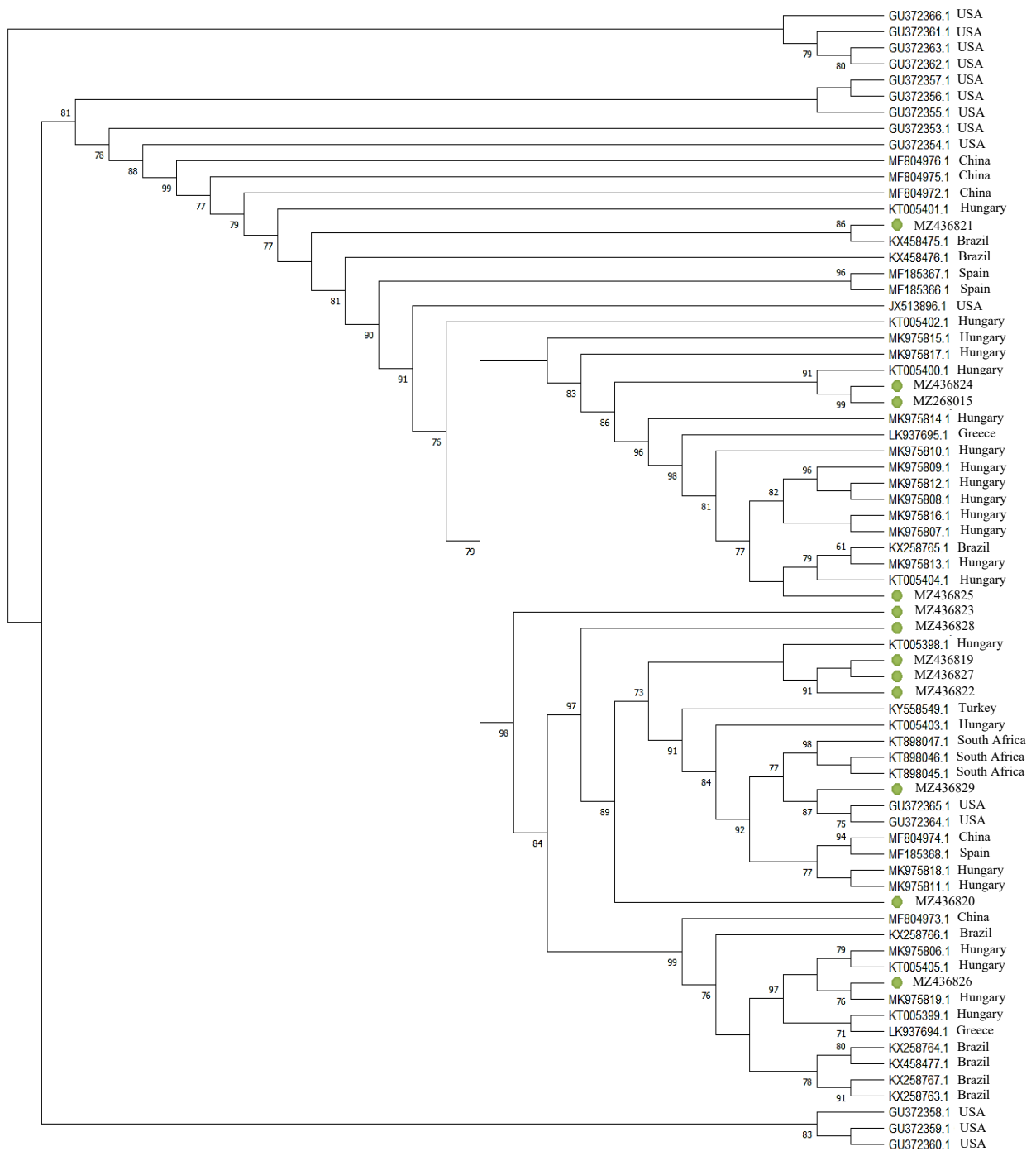
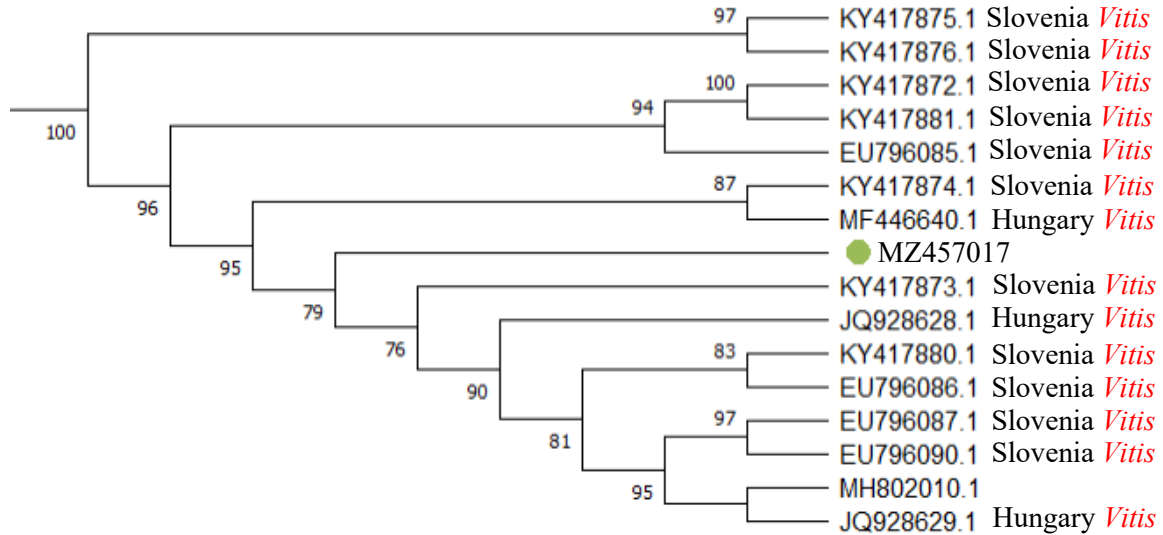


Figure S12. Phylogenetic analysis of global isolates of GSyV-1 based on nucleotide sequences of the coat protein (cp) gene. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by 'green mark'. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

RBDV – RNA2



RBDV – RNA1

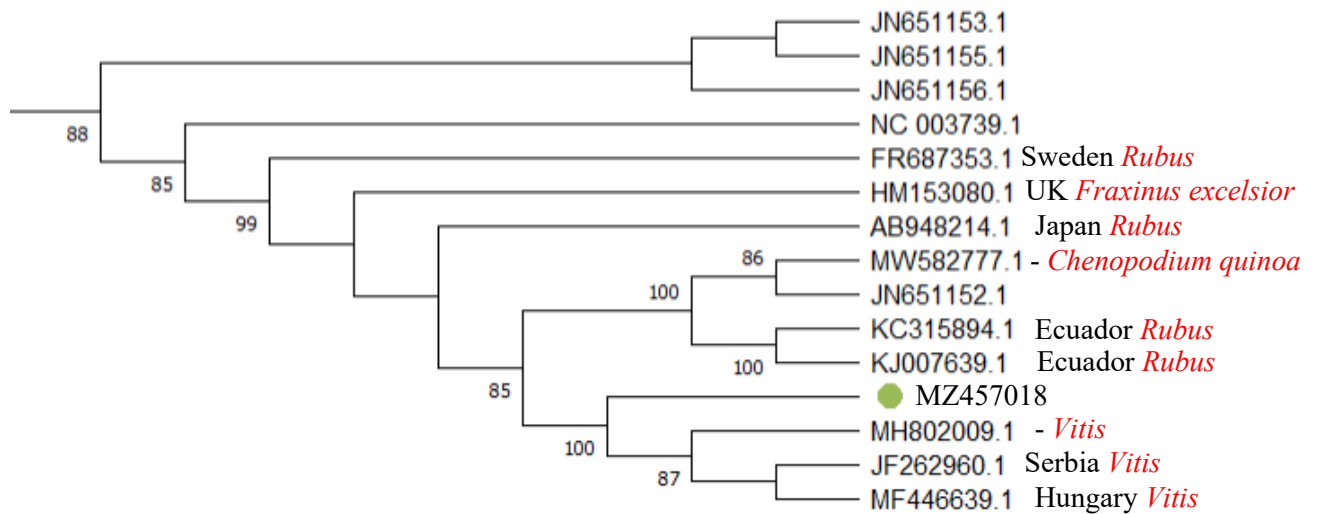


Figure S13. Phylogenetic analysis of global isolates of RBDV based on based on total nucleotide from NCBI. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by ‘green mark’. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

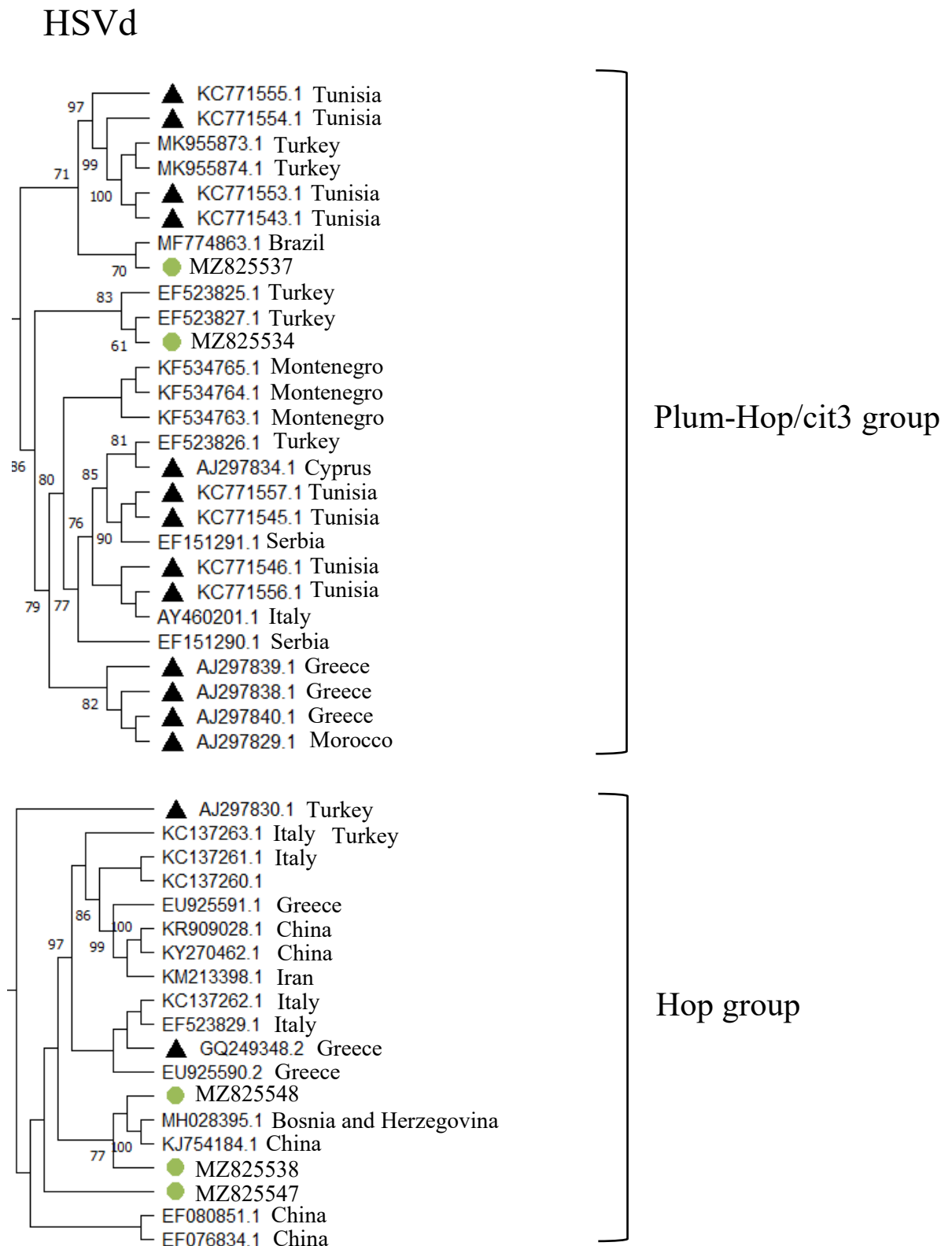


Figure S14. Phylogenetic analysis of global isolates of HSVd based on based on total nucleotide from NCBI. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by ‘green mark’, ▲ - representative sequence for the group. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

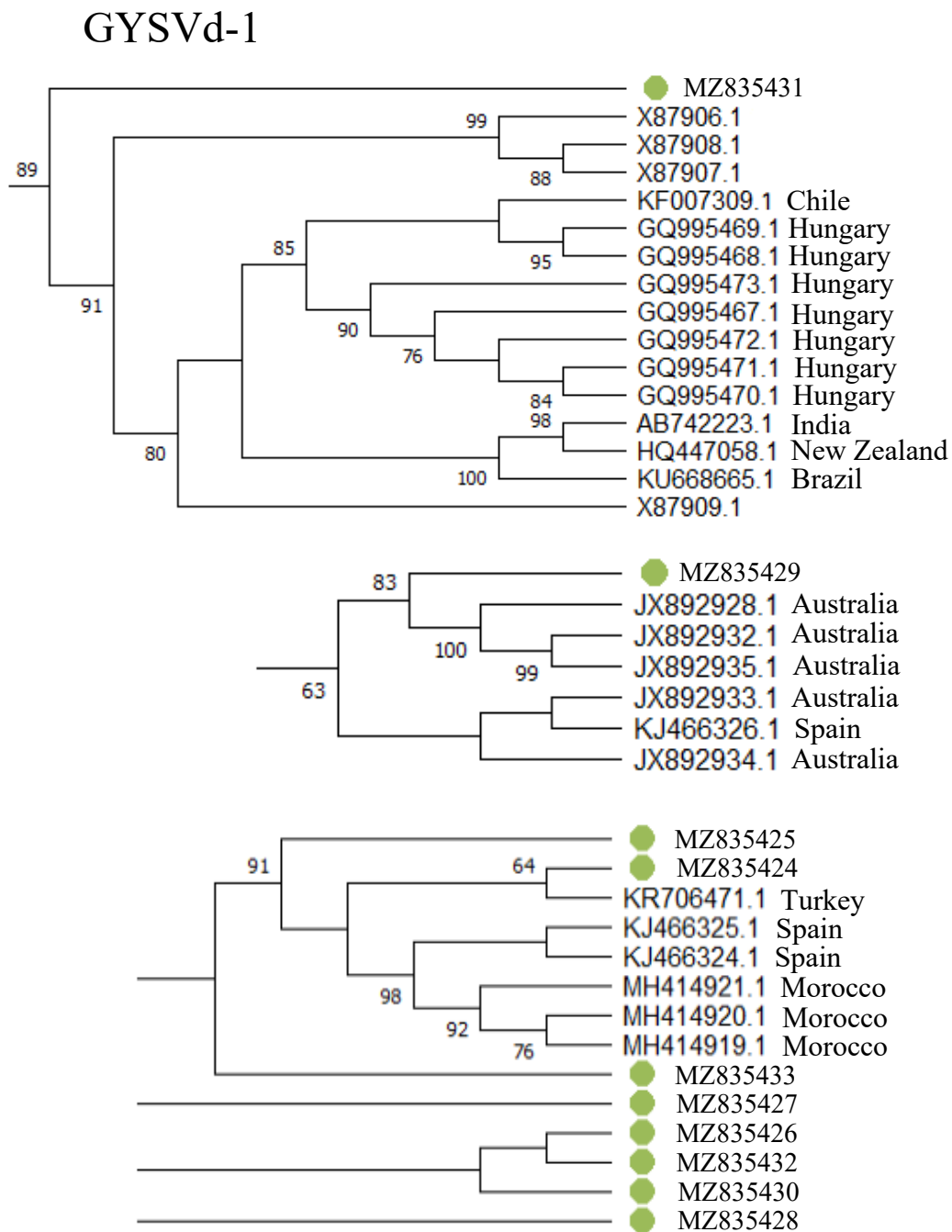


Figure S15. Phylogenetic analysis of global isolates of GYSVd-1 based on total nucleotide from NCBI. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by 'green mark'. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

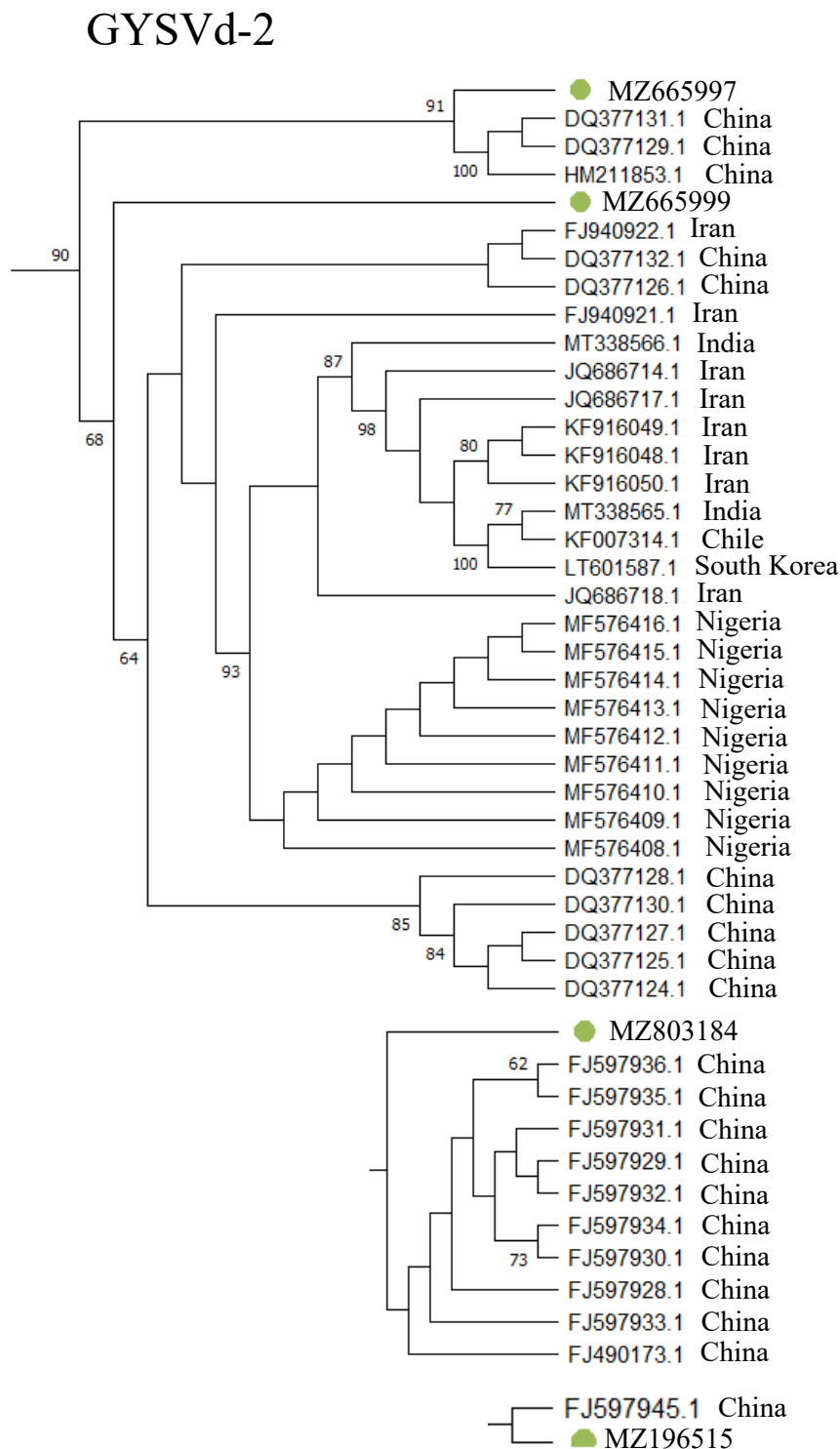


Figure S16. Phylogenetic analysis of global isolates of GYSVd-2 based on total nucleotide from NCBI. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by ‘green mark’. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.

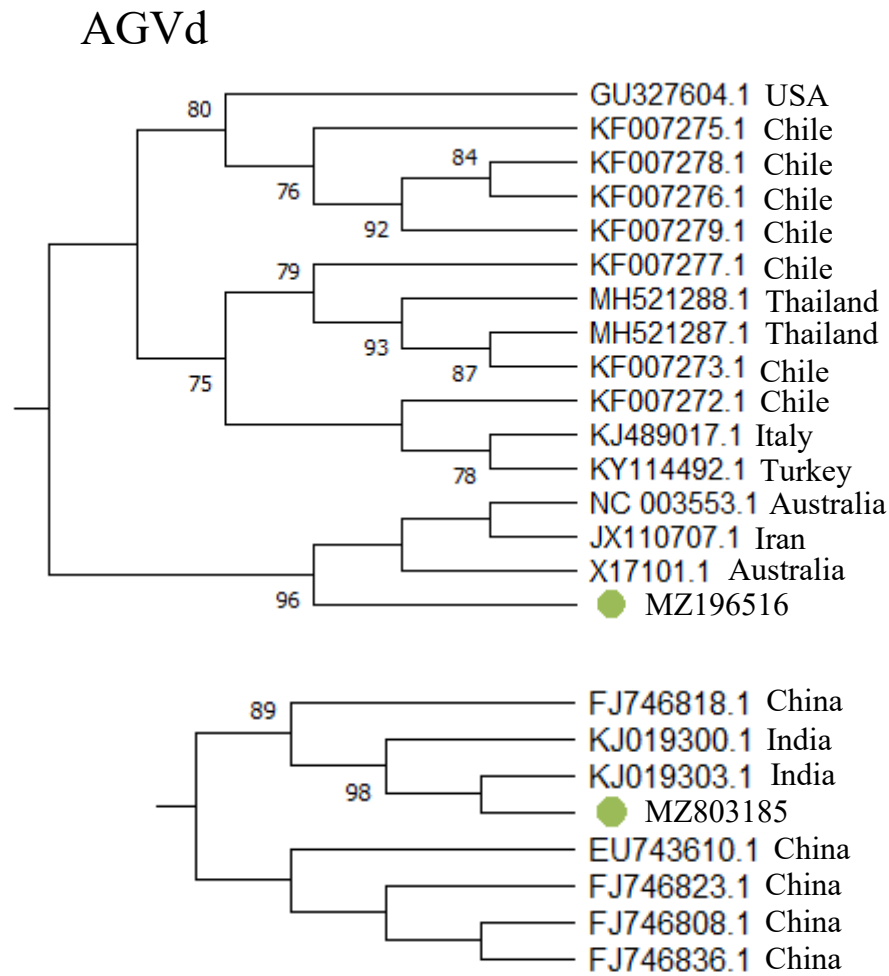


Figure S17. Phylogenetic analysis of global isolates of AGVd based on based on total nucleotide from NCBI. Sequences previously reported by us and the corresponding sequences available from GenBank are identified by their isolate names, followed by their GenBank accession number and source. The isolates obtained in this study are indicated by 'green mark'. The tree was constructed using the Maximum Likelihood method. The numbers at the nodes indicate bootstrap support (1,000 replicates). Values below 60% are not shown.