

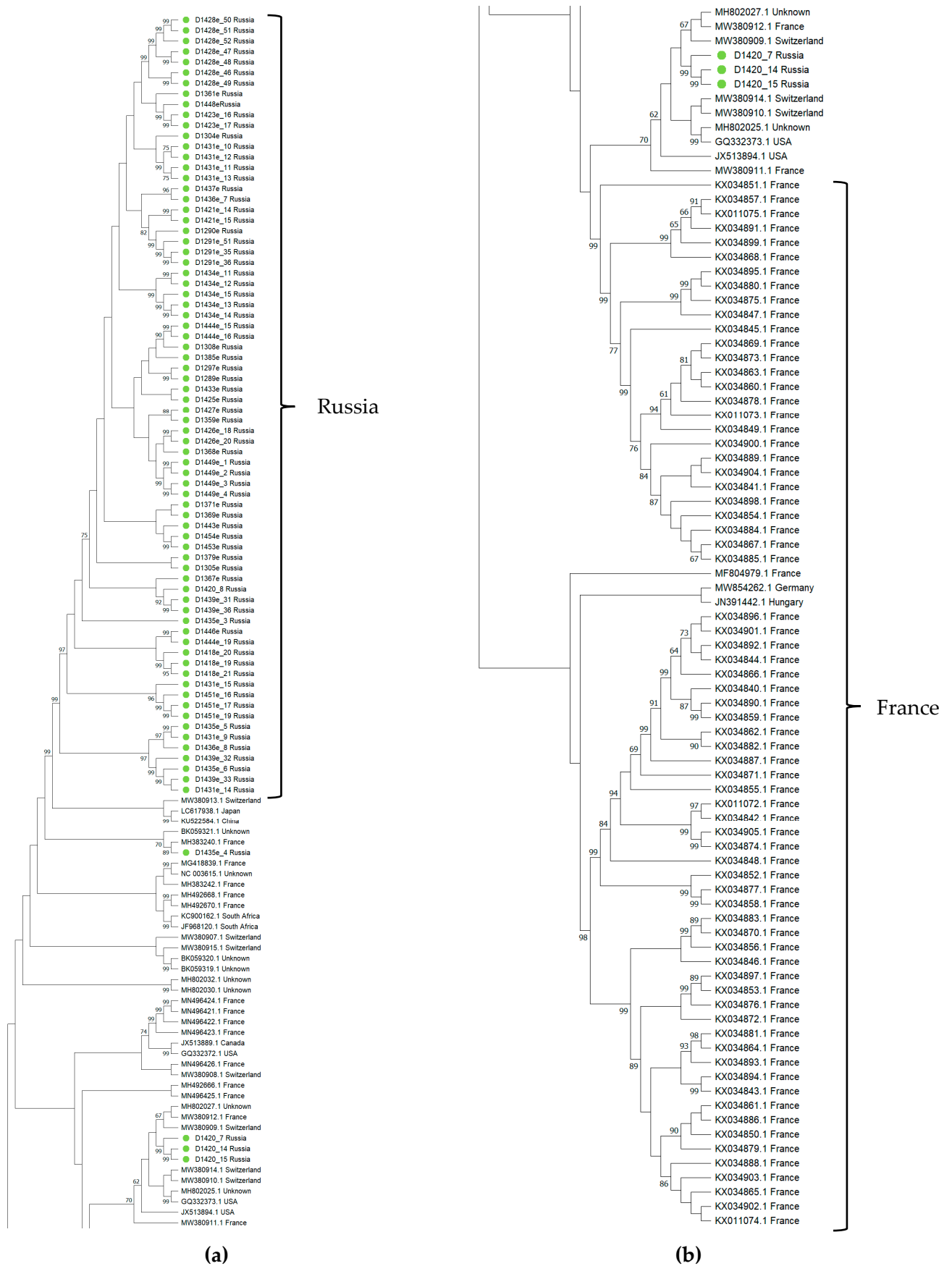
Metagenomic Analysis of Ampelographic Collections of Dagestan Revealed the Presence of Two Novel Grapevine Viruses

Darya Shvets, Kirill Sandomirsky, Elena Porotikova and Svetlana Vinogradova *

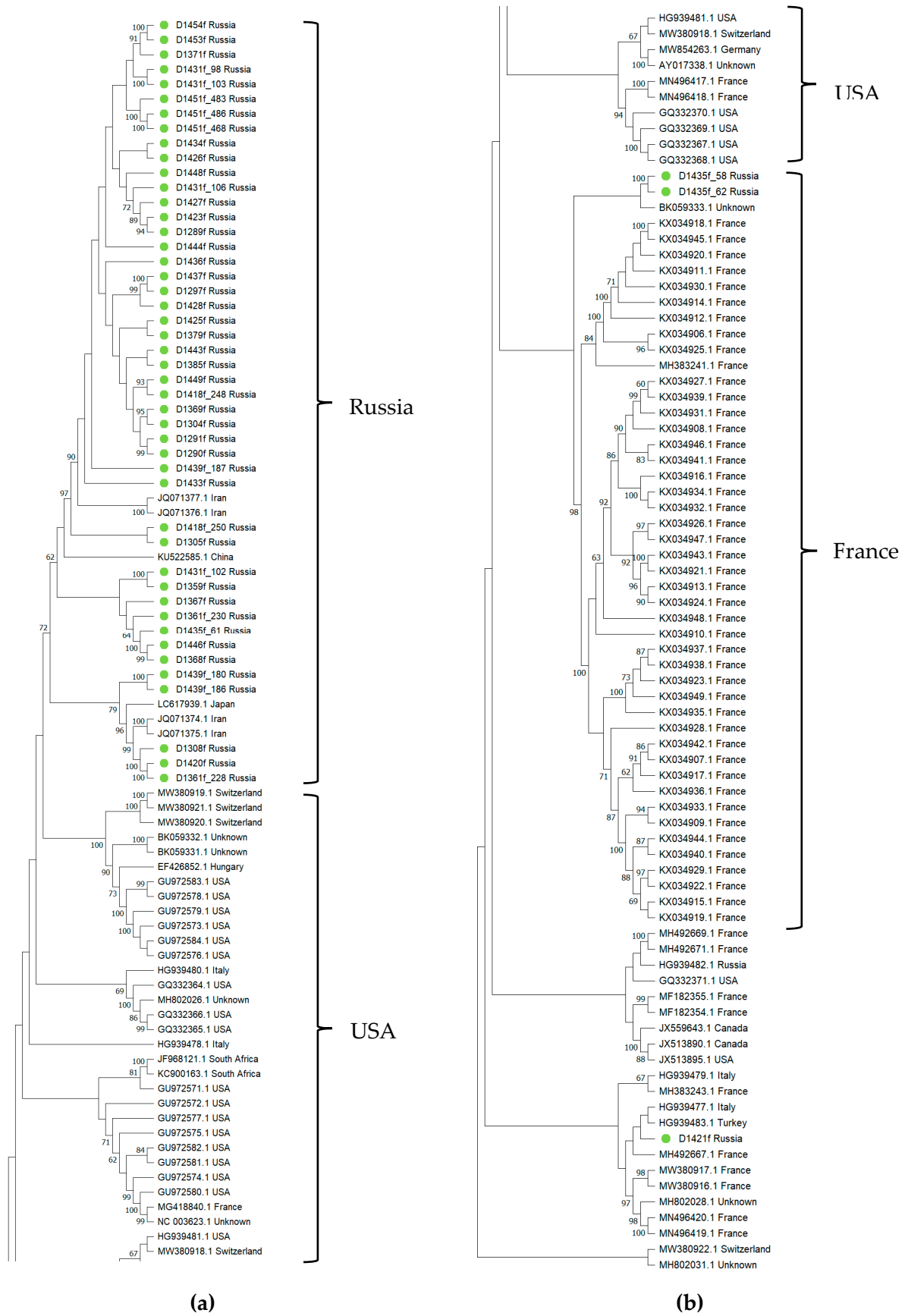
Skryabin Institute of Bioengineering, Research Center of Biotechnology of the Russian Academy of Sciences, Leninsky Prospect, 33, Build. 2, 119071 Moscow, Russia

* Correspondence: coatprotein@bk.ru

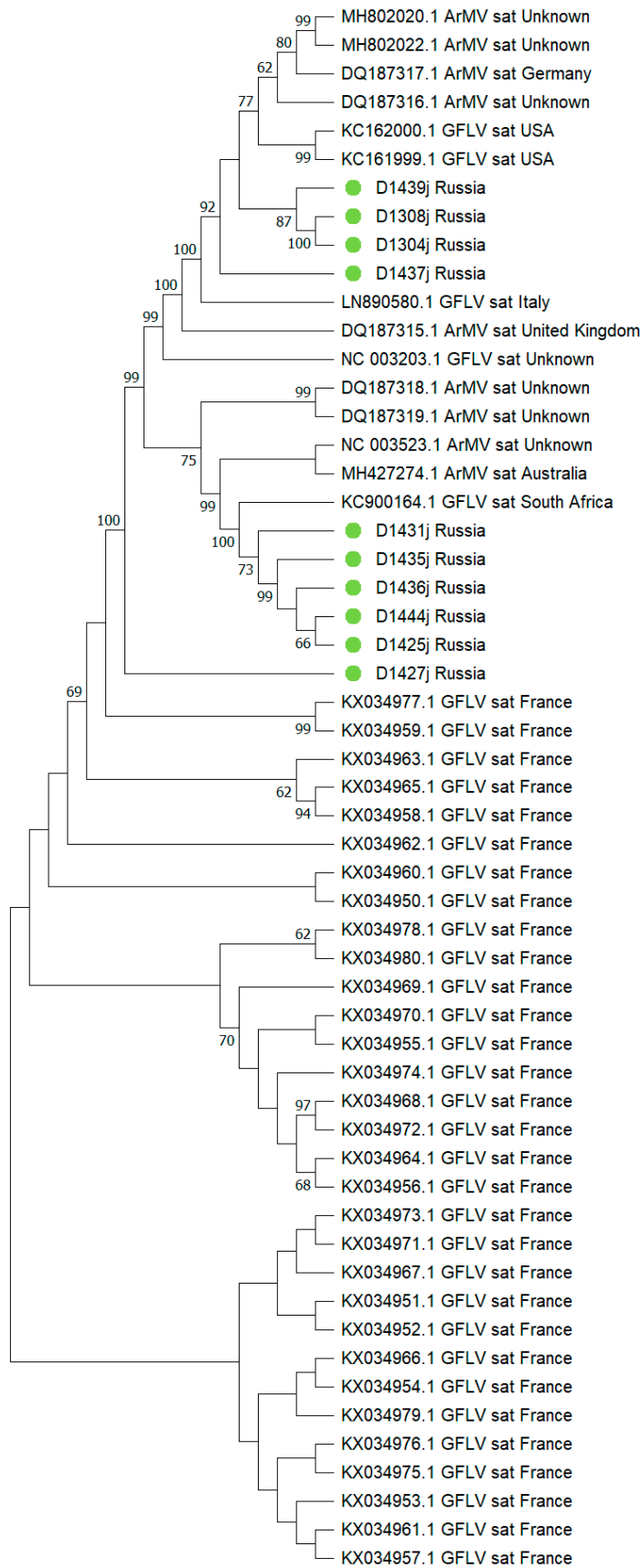
Supplementary Materials



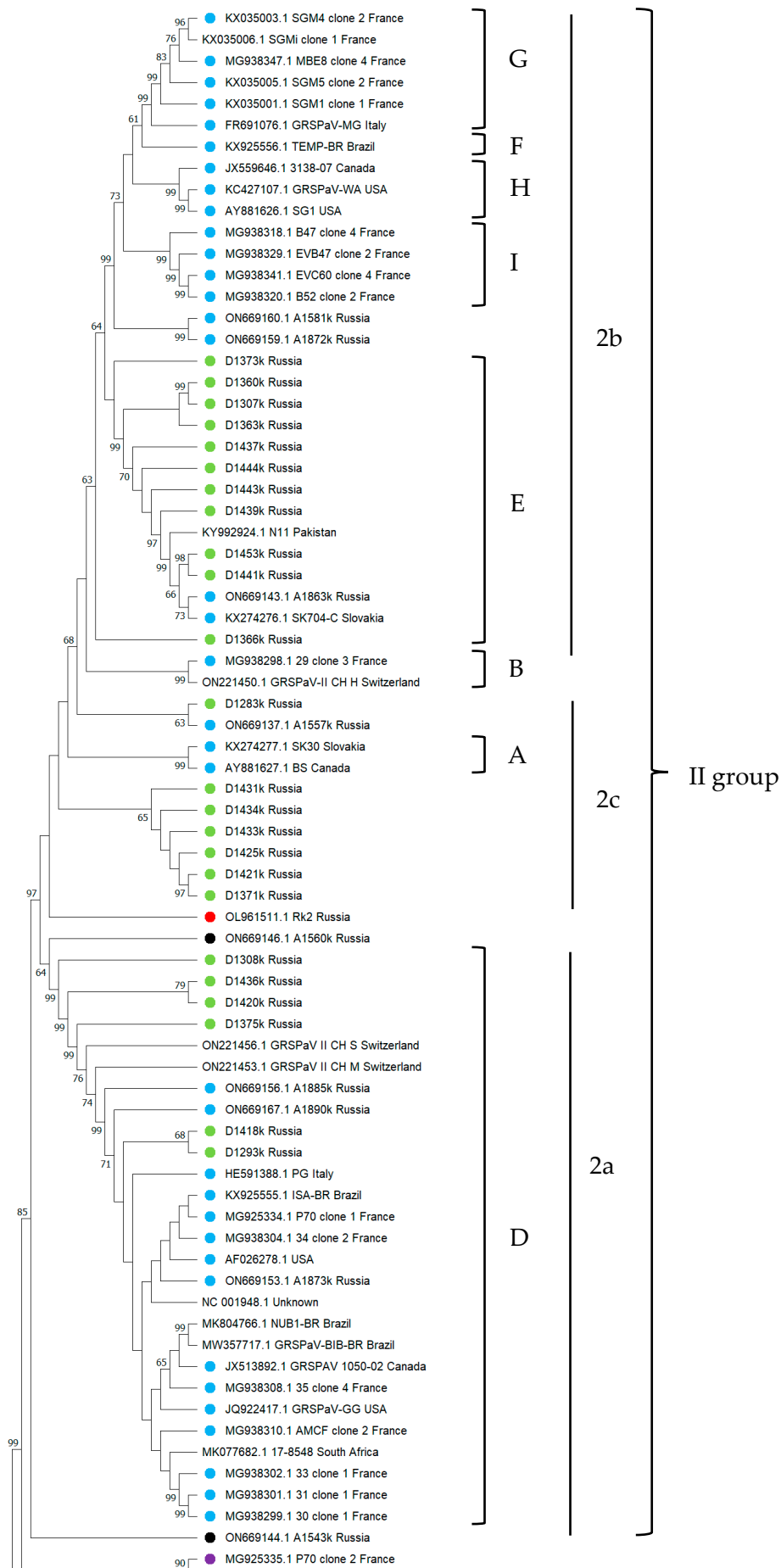
Supplementary Figure S1 (a, b). Neighbor-joining tree showing the distribution of complete nucleotide sequences RNA1 of Russian grapevine fanleaf virus (GFLV) isolates (●) and world isolates. Bootstrap values >60% (1000 bootstrap replicates) are shown.



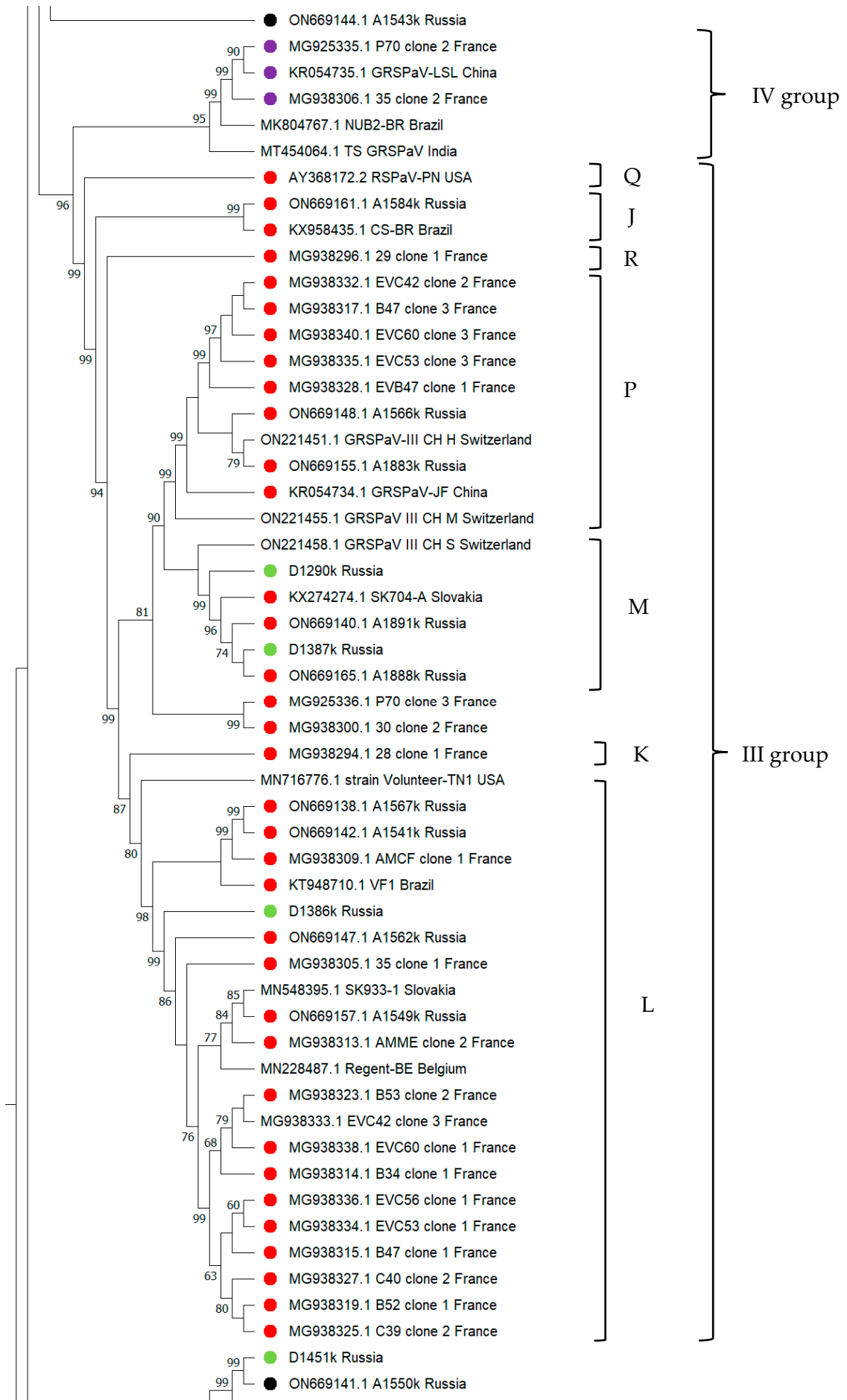
Supplementary Figure S2 (a, b). Neighbor-joining tree showing the distribution of complete nucleotide sequences RNA2 of Russian grapevine fanleaf virus (GFLV) isolates (●) and world isolates. Bootstrap values >60% (1000 bootstrap replicates) are shown.



Supplementary Figure S3. Neighbor-joining tree showing the distribution of complete genome nucleotide sequences of Russian grapevine fanleaf virus satellite RNA (GFLV sat) isolate (●) and world GFLV sat and Arabis mosaic virus satellite RNA (ArMV sat) isolates. Bootstrap values >60% (1000 bootstrap replicates) are shown.



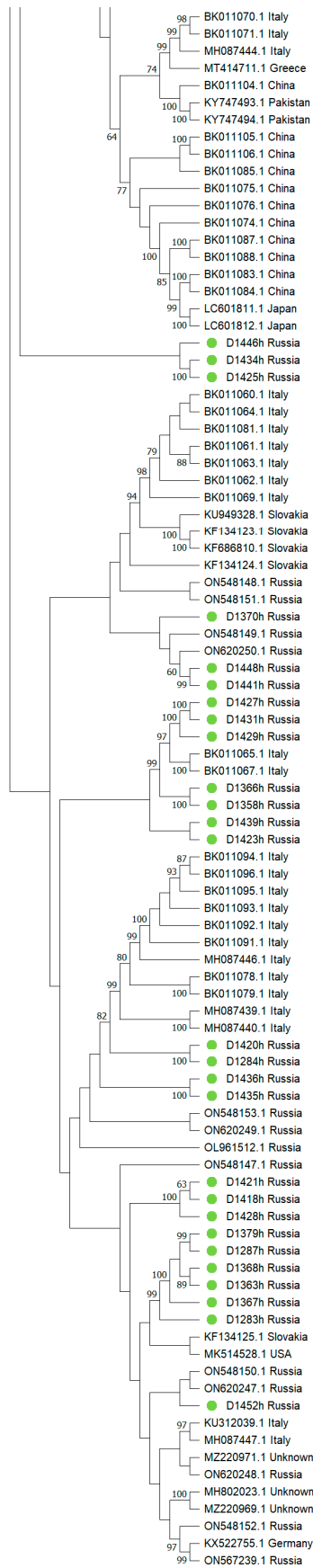
(a)



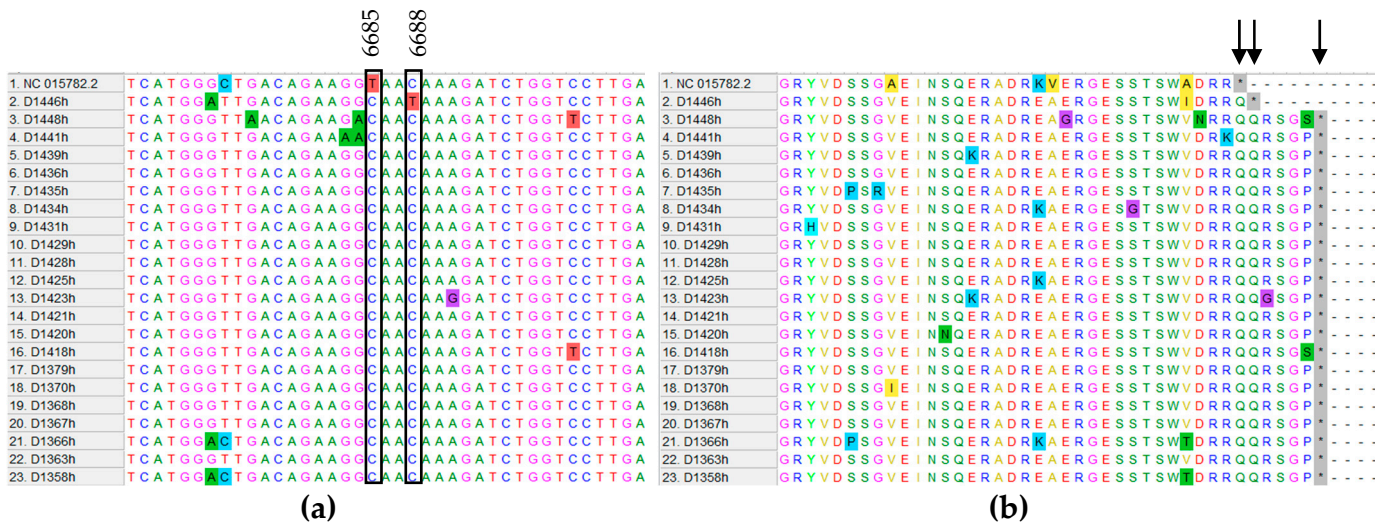
(b)



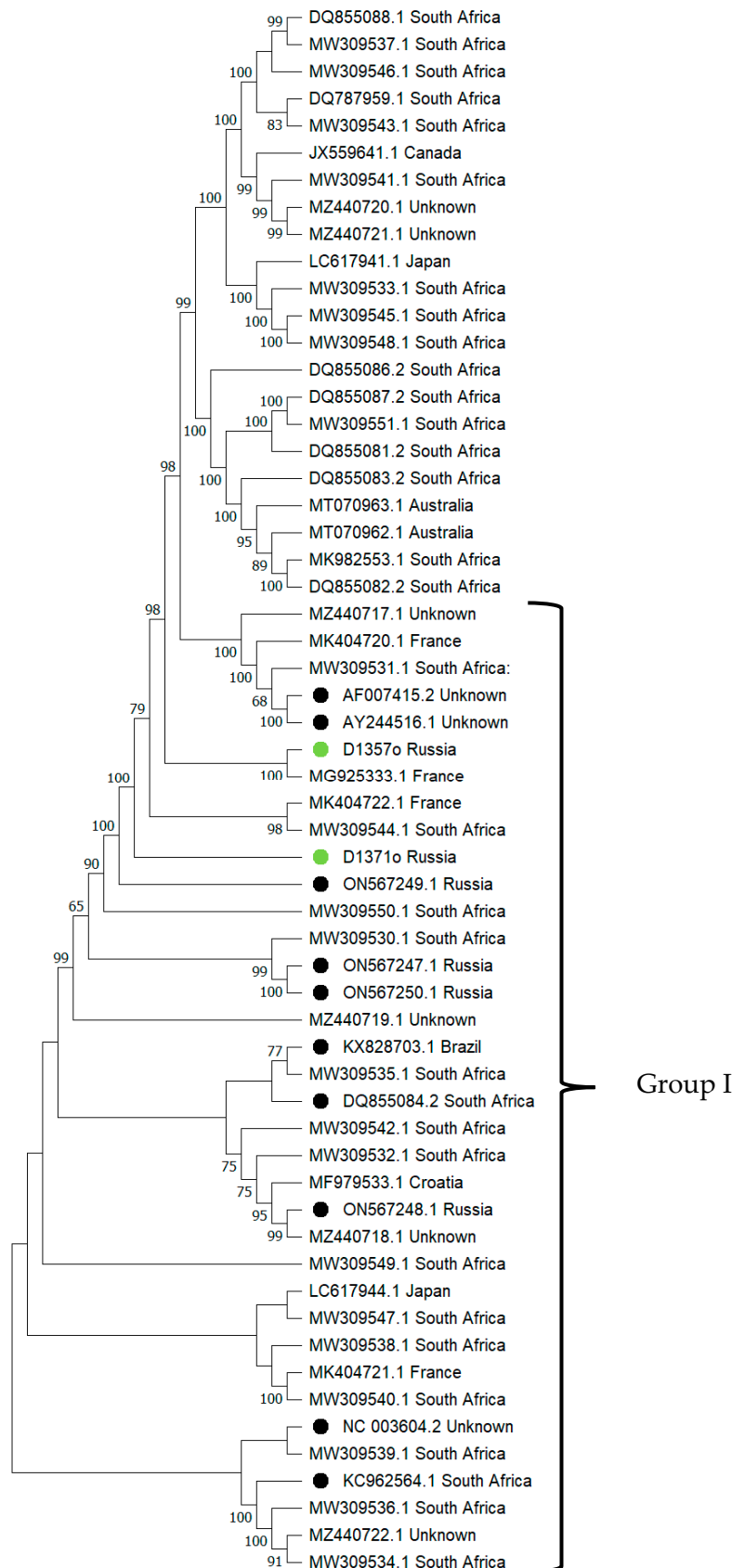
Supplementary Figure S4 (a-c). Neighbor-joining tree showing the distribution of complete genome nucleotide sequences of Russian grapevine rupestris stem pitting-associated virus (GRSPaV) isolates (●) and world isolates. I, II, III and IV molecular groups are indicated as (●), (●), (●) and (●), respectively. Bootstrap values >60% (1000 bootstrap replicates) are shown.



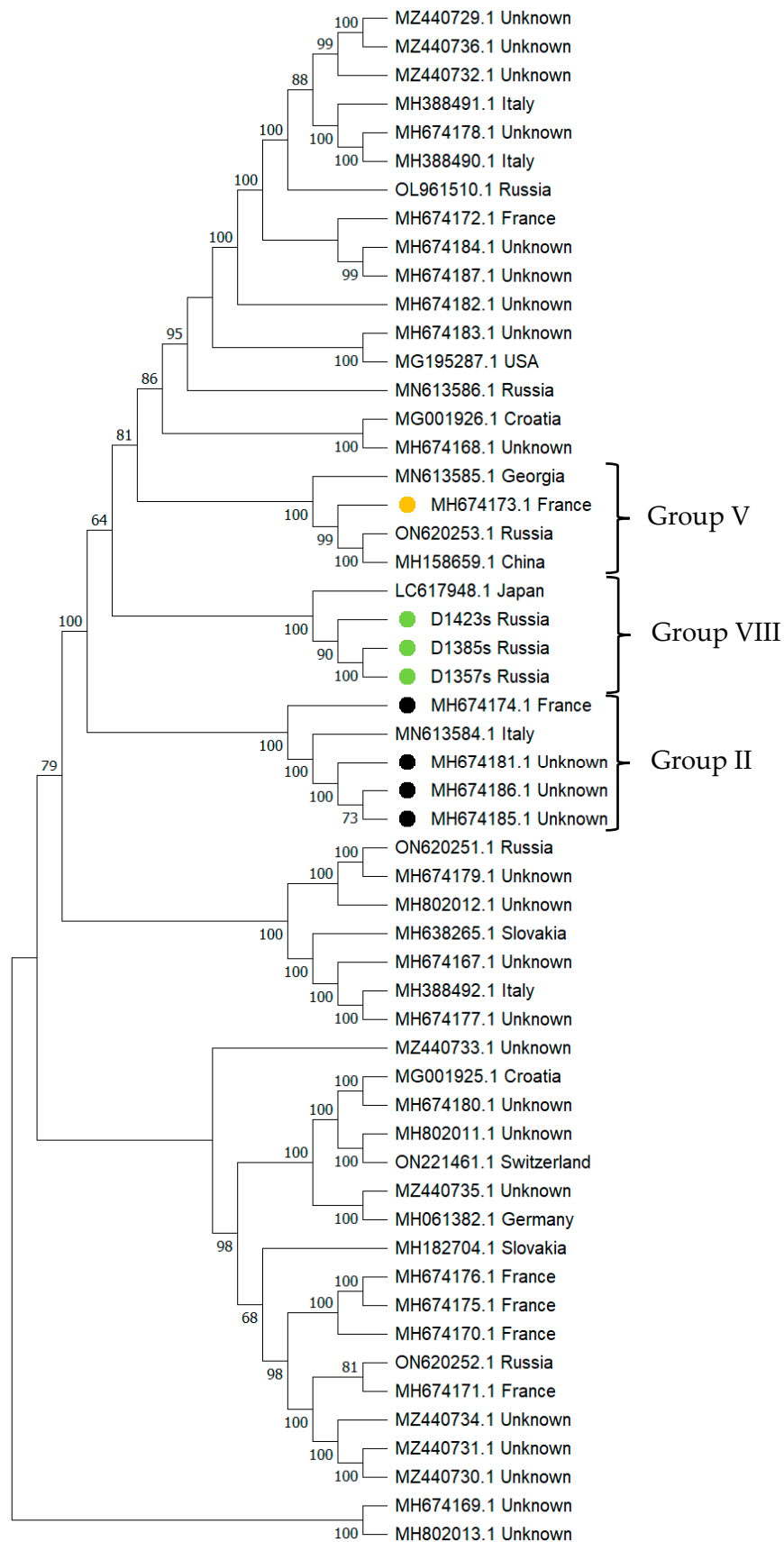
Supplementary Figure S5. Neighbor-joining tree showing the distribution of complete genome nucleotide sequences of Russian grapevine Pinot gris virus (GPGV) isolate (●) and world isolates. Bootstrap values >60% (1000 bootstrap replicates) are shown.



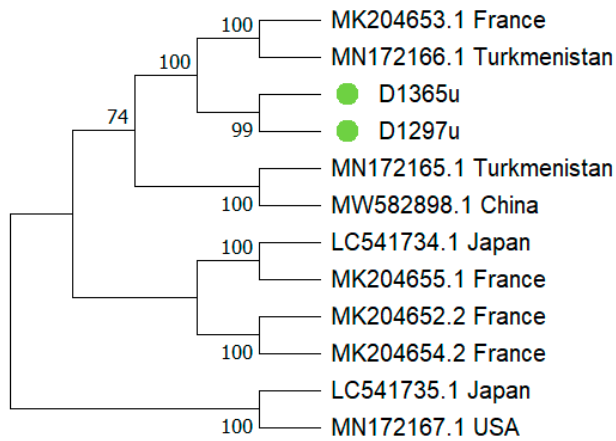
Supplementary Figure S6 (a, b). Alignment of (a) MP/CP nucleotide sequences; (b) movement proteins (MP) of Russian grapevine Pinot gris virus (GPGV) isolates and reference isolates (NC_015782.2). 6685 and 6688 T/C polymorphisms are marked in boxes. The stop codons are indicated by gray stars.



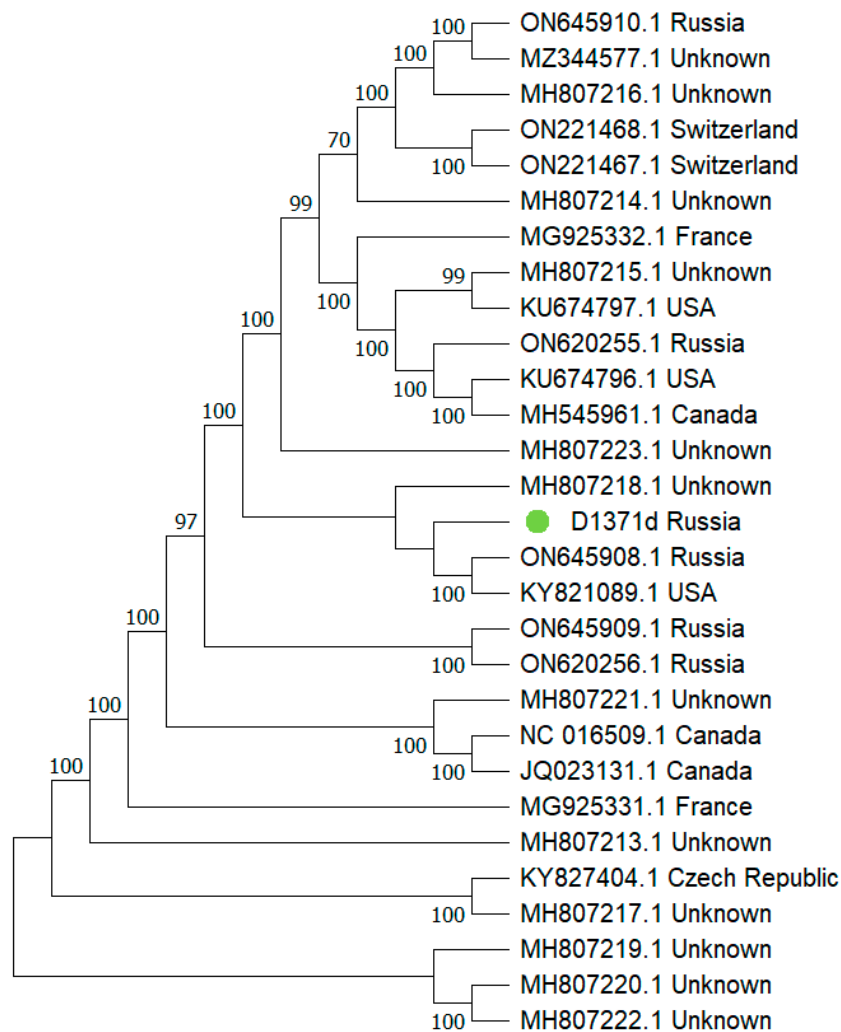
Supplementary Figure S7. Neighbor-joining tree showing the distribution of complete genome nucleotide sequences of Russian grapevine virus A (GVA) isolates (●) and world isolates. Representative isolates from I molecular group are indicated as (●). Bootstrap values >60% (1000 bootstrap replicates) are shown.



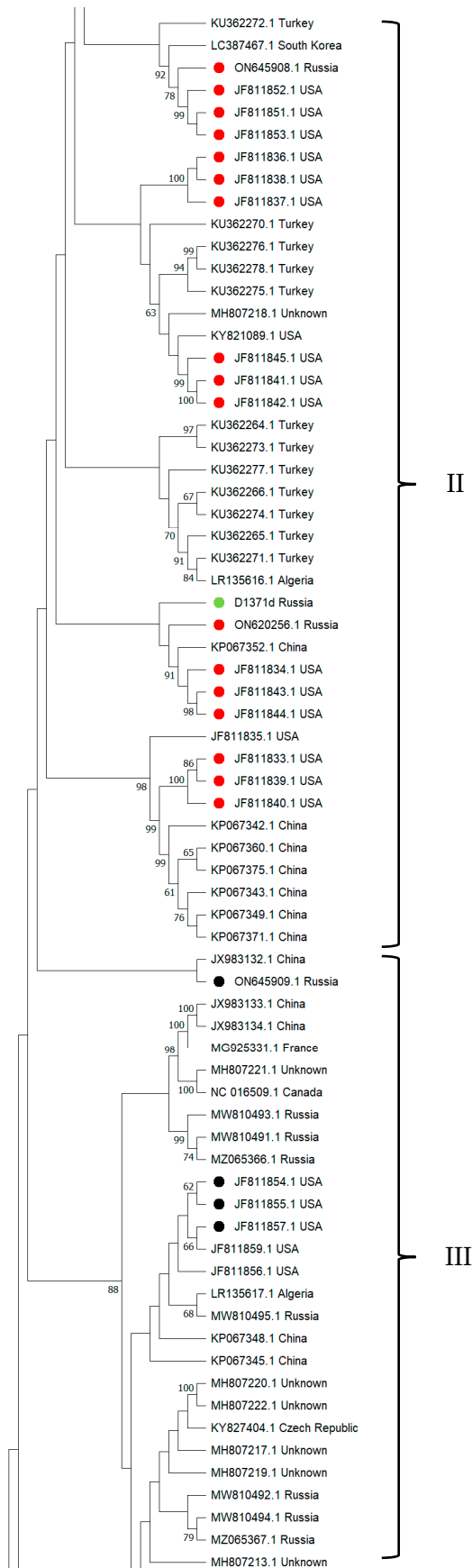
Supplementary Figure S8. Neighbor-joining tree showing the distribution of complete genome nucleotide sequences of Russian grapevine virus T (GVT) isolates (●) and world isolates. II and V molecular groups are indicated as (●) and (●), respectively. Bootstrap values >60% (1000 bootstrap replicates) are shown.



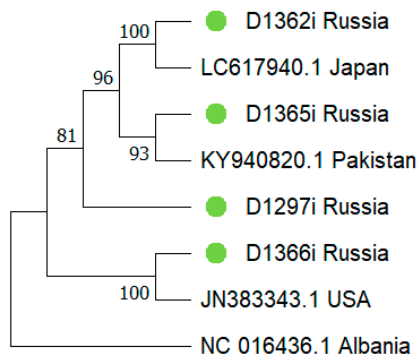
Supplementary Figure S9. Neighbor-joining tree showing the distribution of complete genome nucleotide sequences of Russian grapevine Kizil Sapak virus (GKSV) isolates (●) and world isolates. Bootstrap values >60% (1000 bootstrap replicates) are shown.



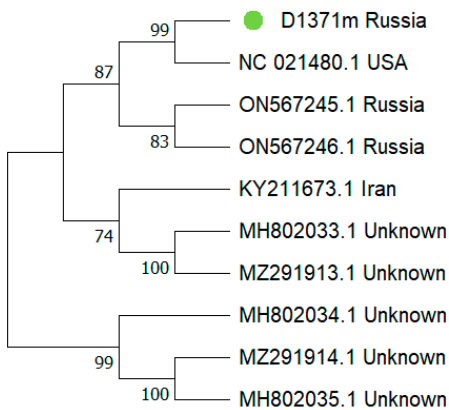
Supplementary Figure S10. Neighbor-joining tree showing the distribution of complete genome nucleotide sequences of Russian grapevine leafroll-associated virus 1 (GLRaV-1) isolate (●) and world isolates. Bootstrap values >60% (1000 bootstrap replicates) are shown.



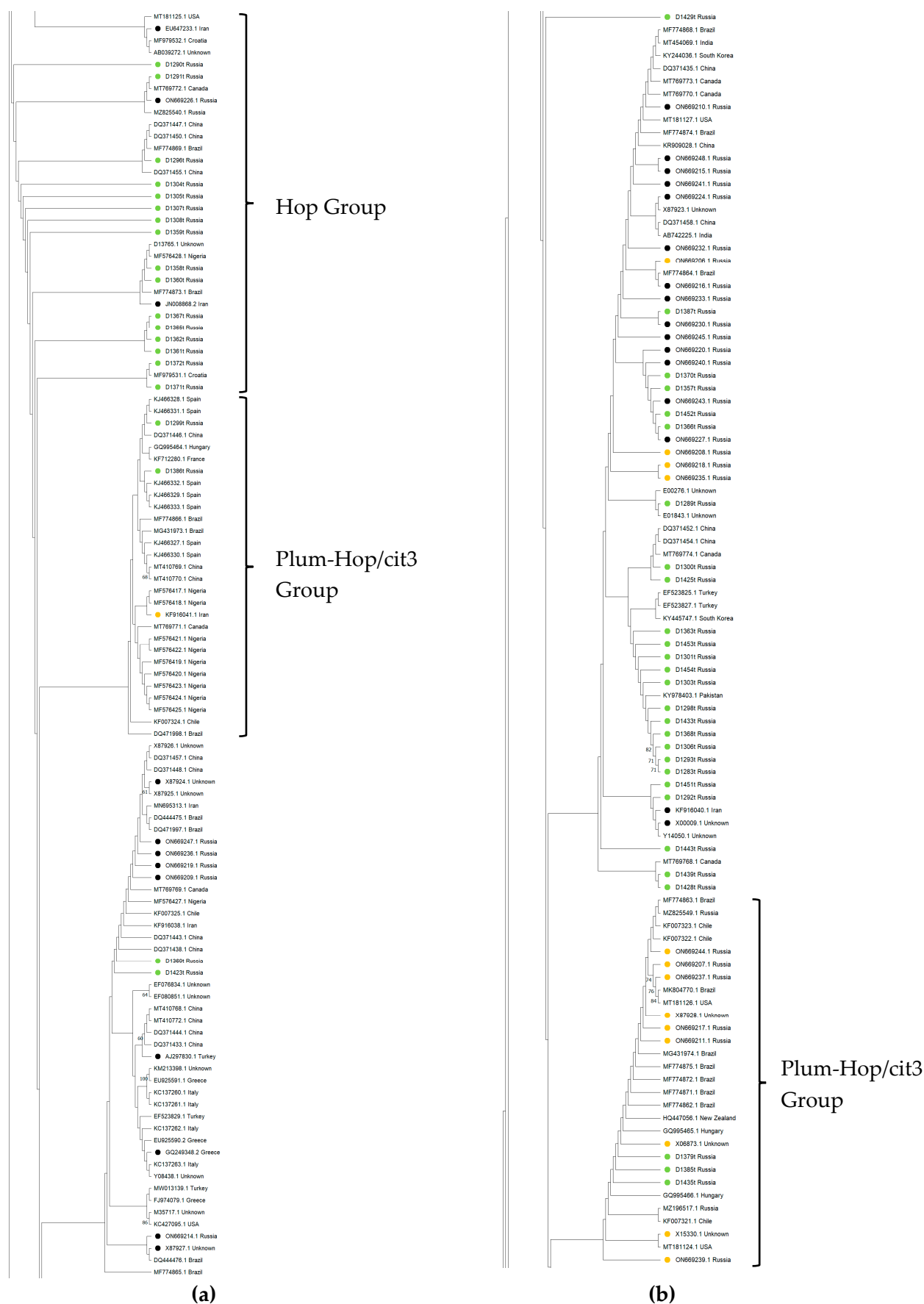
Supplementary Figure S11. Neighbor-joining tree showing the distribution of coat protein nucleotide sequences of Russian grapevine leafroll-associated virus 1 (GLRaV-1) isolate (●) and world isolates. II and III molecular groups are indicated as (●) and (●), respectively. Bootstrap values >60% (1000 bootstrap replicates) are shown.



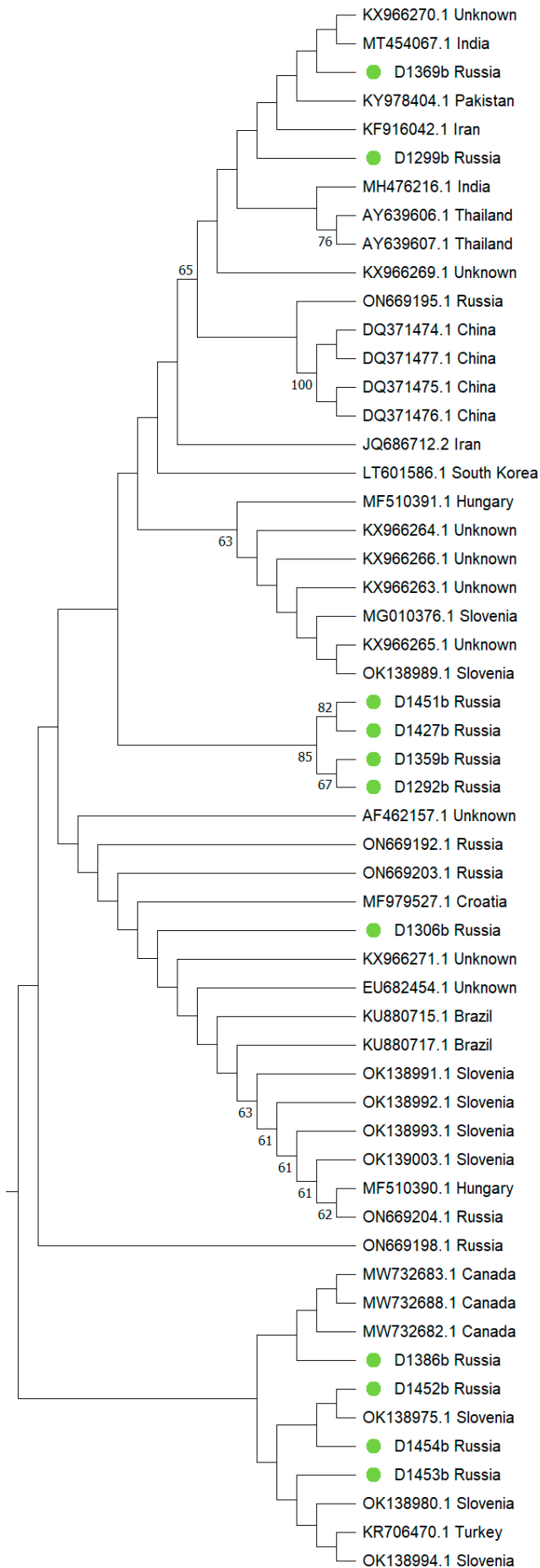
Supplementary Figure S12. Neighbor-joining tree showing the distribution of complete genome nucleotide sequences of Russian grapevine leafroll-associated virus 7 (GLRaV-7) isolates (●) and world isolates. Bootstrap values >60% (1000 bootstrap replicates) are shown.



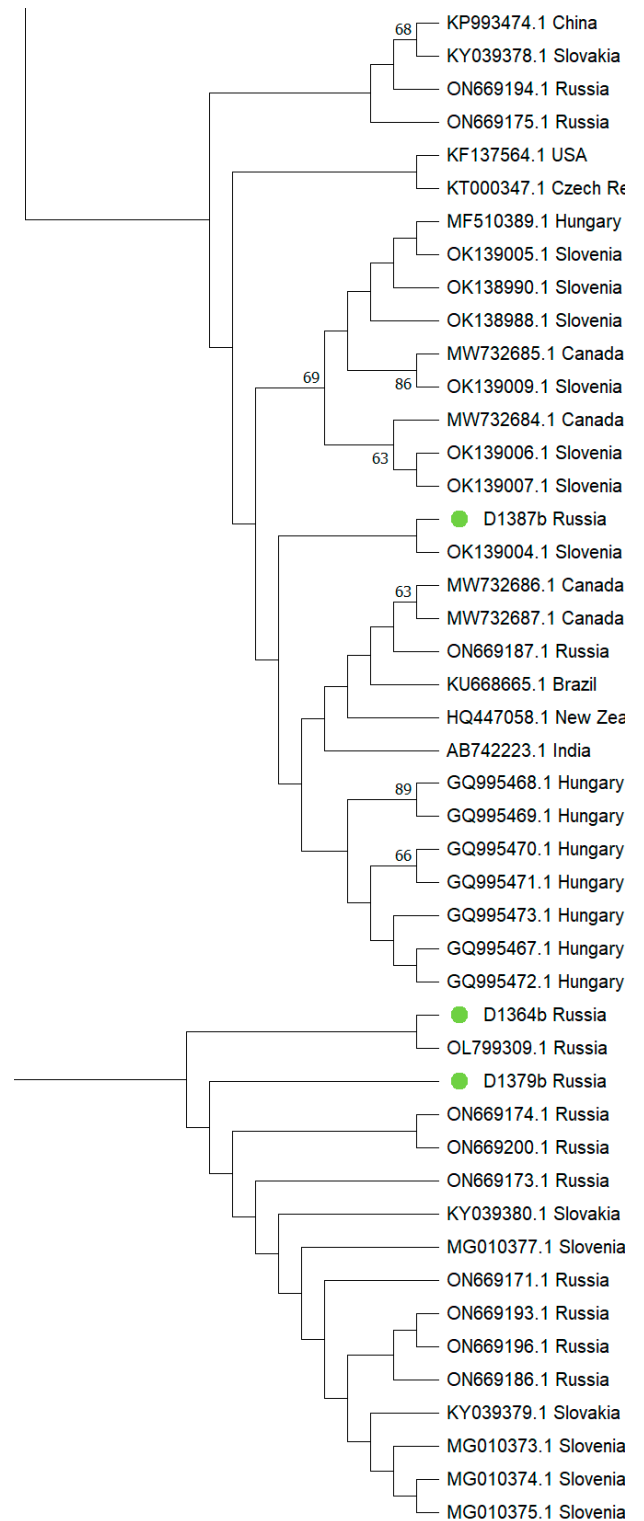
Supplementary Figure S13. Neighbor-joining tree showing the distribution of complete genome nucleotide sequences of Russian grapevine satellite virus (GV-Sat) isolate (●) and world isolates. Bootstrap values >60% (1000 bootstrap replicates) are shown.



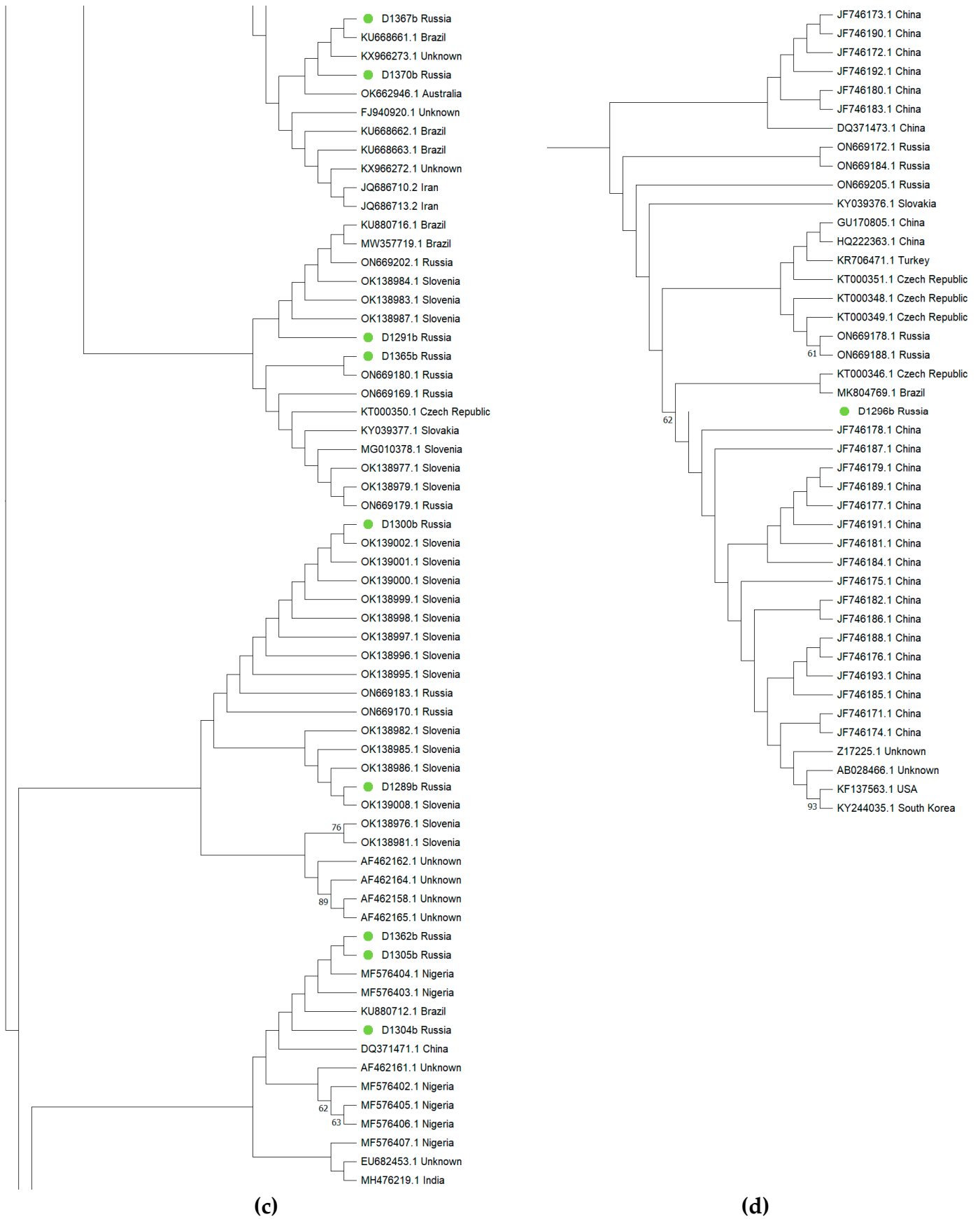
Supplementary Figure S14 (a, b). Neighbor-joining tree showing the distribution of complete genome nucleotide sequences of Russian hop stunt viroid (HSVd) isolates (●) and world isolates. Hop and Plum-Hop/cit3 molecular groups are indicated as (●) and (●), respectively. Bootstrap values >60% (1000 bootstrap replicates) are shown.



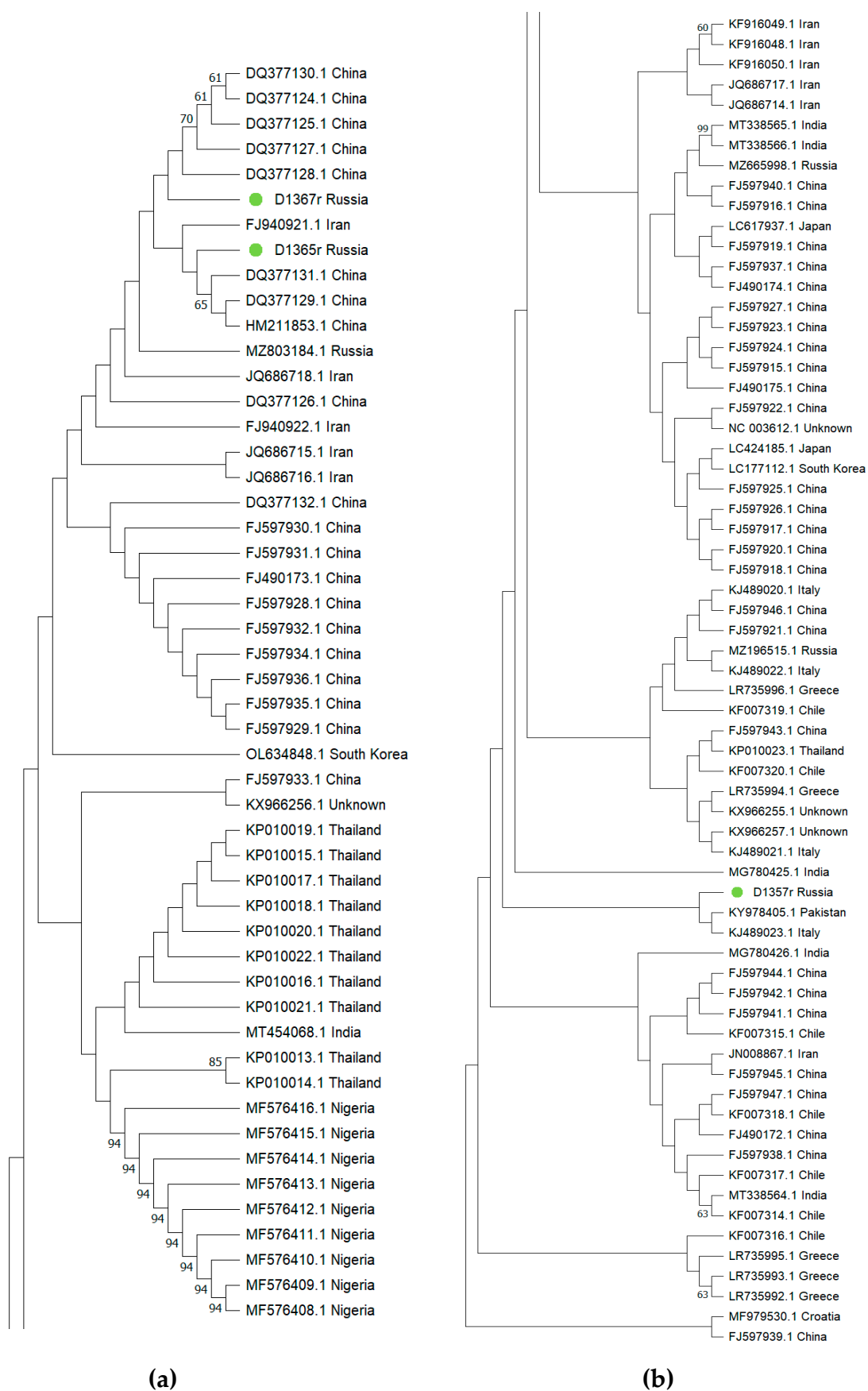
(a)



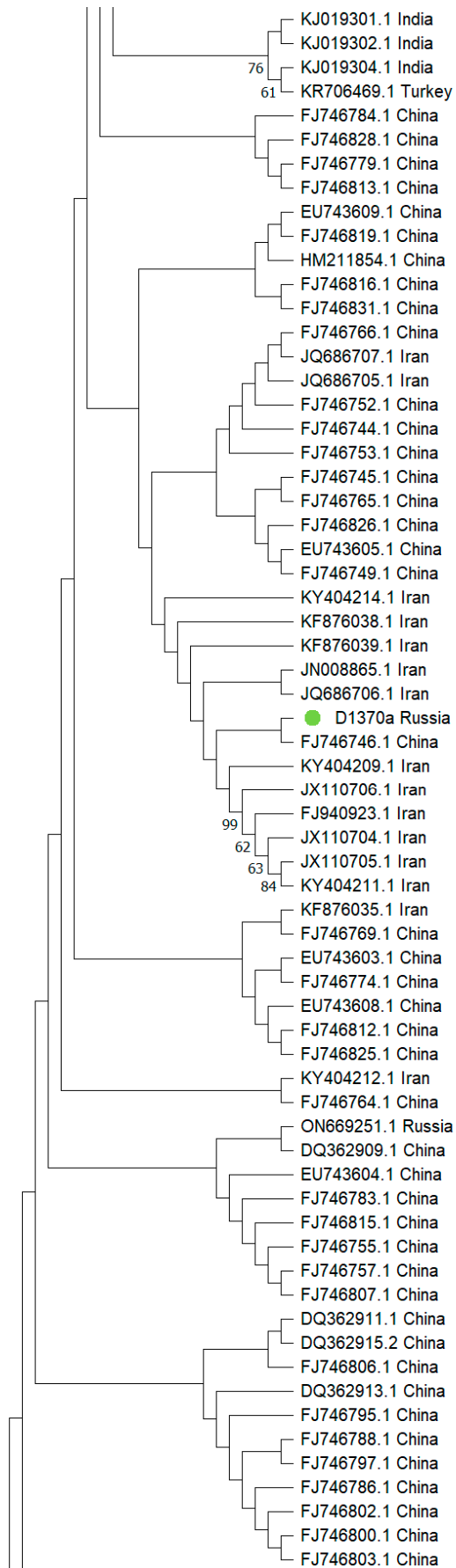
(b)



Supplementary Figure S15 (a-d). Neighbor-joining tree showing the distribution of complete genome nucleotide sequences of Russian grapevine yellow speckle viroid 1 (GYSVd-1) isolates (●) and world isolates. Bootstrap values >60% (1000 bootstrap replicates) are shown.



Supplementary Figure S16 (a, b). Neighbor-joining tree showing the distribution of complete genome nucleotide sequences of Russian grapevine yellow speckle viroid 2 (GYSVd-2) isolates (●) and world isolates. Bootstrap values >60% (1000 bootstrap replicates) are shown.



Supplementary Figure S17. Neighbor-joining tree showing the distribution of complete genome nucleotide sequences of Russian Australian grapevine viroid (AGVd) isolate (●) and world isolates. Bootstrap values >60% (1000 bootstrap replicates) are shown.