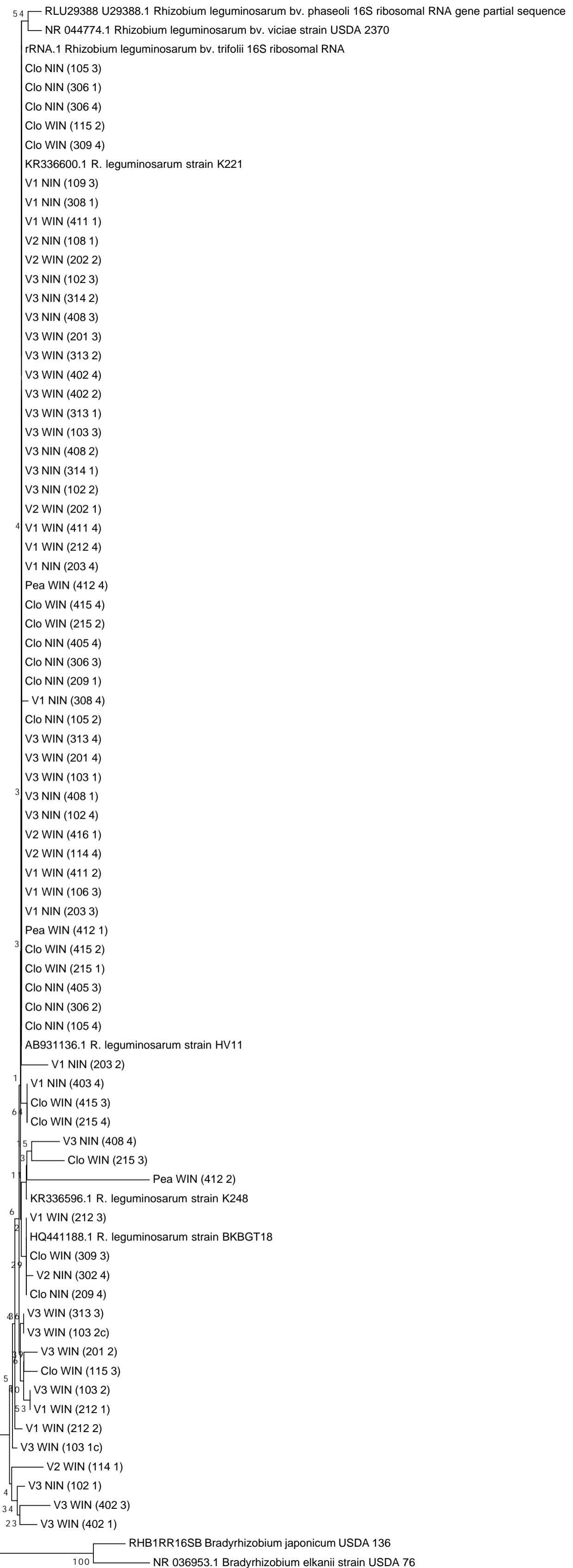


**Figure 2.** Phylogenetic tree showing the relationship of *Rhizobium* strains isolated from legume cover crops (V1, V2, V3, Clo and Pea) in Lambertton with *R. leguminosarum* species based on partial 16S rRNA gene sequences (550 bp). Phylogenetic analysis was conducted in MEGA, version 7. The evolutionary history was inferred using the Neighbor-Joining method. The optimal tree with the sum of branch length = 0.26513004 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. The analysis involved 82 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated.



0.010