

Figure S1. Distance matrix of pairwise MAFFT-based comparison of the complete coding sequence (9,279-9,288 nt; 3,092-3,095 aa) of eleven isolates of Wisteria vein mosaic virus (WVMV) and one isolate of kudzu chlorotic ring blotch virus (KudCRBV). The percentage of nt and aa sequence identities are shown below and above the diagonal, respectively. The analysis was performed using Sequence Demarcation Tool (SDT) software, version 1.2. All sequences are identified by their accession number, virus and isolate names, country of origin. Three-letter codes are used for country names, as defined in the ISO 3166-1 standard [94]. The WVMV isolate Bari, the object of this study, is highlighted and its identity values are reported in bold. Detailed information on individual isolates can be found in [Table S1](#).

[illegible]