

Figure S3. Distance matrices of pairwise MAFFT-based comparison of the (a) complete (948-957 nt; 316-319 aa) or (b) N-terminal (1-300/309 nt; 1-100/103 aa) sequences coding for the P1 proteinase (P1-Pro) 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 diagonals, 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][illegible]