

FIG. S1. Alignment of the nucleotide (nt) sequences of the variable region (left intergenic region [LIR], C4 gene and the 5' end of the C1 [Rep] gene; see Fig. 2C) of isolates of three genotypes of Tomato leaf deformation virus (ToLDeV). Vertical brackets show isolates of the ToLDeV PA98-1 and PA98-2 variants and the PA10 strain. The nt sequences were aligned using MUSCLE and were presented using Jalview v.2 (73). Intensity of the shading reflects the relative sequence identity among genotypes. Dark shading shows identical nts in all genotypes, light shading shows identical nts in two genotypes and no shading shows nts different in the genotypes. The TAATATTAC sequence of the conserved stem-loop structure is indicated in a box, and the inverted repeats that constitute the stem (RAS, right arm stem and LAS, left arm stem) are indicated with arrows. The thick red and black arrows on the top of sequences indicate the location of the C4 gene and the 5' end of the C1 (Rep) gene, respectively. Horizontal brackets indicate potential recombination junctions.

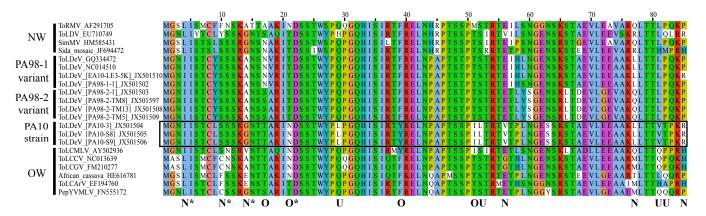


FIG. S2. Alignment of the AC4/C4 amino acid (aa) sequences of New World (NW) bipartite begomoviruses and Old World (OW) monopartite begomoviruses that are most closely related to the C4 sequences of the three genotypes of Tomato leaf deformation virus (ToLDeV): the PA98-1 and PA98-2 variants and the PA10 strain. The aa sequences were aligned using MUSCLE and were presented using Jalview v.2 (73). Color shading reflects the relative identity/similarity of aas based on their biochemical properties according to the ClustalX code. Residues of the C4 sequences of isolates of the PA10 strain (shown in the black box) that are unique (U), shared only (N) or predominantly (N*) with AC4 sequences of NW begomoviruses or C4 sequences of the other ToLDeV genotypes or shared only (O) or predominantly (O*) with C4 sequences of OW begomoviruses are shown below the alignment. AC4/C4 sequences were obtained from GeneBank and the accession numbers of the viruses are listed in Fig. 3, except for Pepper yellow vein Mali virus-(PepYVMLV) [BF:Ban:09] which was added to this alignment.