**Supplementary materials**

**Fig. S5** Neighbor-joining tree constructed using the Jukes–Cantor model based on 16S rDNA sequences (1371 bp) of the present isolates and related bacterial species and pathovars. T, type strain of the species; PT, pathotype strain of the pathovars. Accession numbers for the sequences from the DDBJ, EMBL, and GenBank databases are in parentheses. Vertical lines and roman numerals on the right indicate *hrp* groups of the *Pseudomonas syringae* group bacteria. Numbers at nodes are bootstrap values (≥50%) expressed as percentages of 1000 replicates. Bar: 0.02 substitutions per nucleotide position



Fig. S5