**Supplementary materials**

**Fig. S6** Neighbor-joining tree constructed using the Jukes–Cantor model based on **a** *gap1* (860 bp), **b** *gltA* (573 bp), **c** *gyrB* (910 bp) and **d** *rpoD* (804 bp) sequences from the present isolates and related bacterial species and pathovars. T, type strain of the species; PT, pathotype strain of the pathovars. Accession numbers of the sequences from the DDBJ, EMBL, and GenBank databases are in parentheses. Numbers at nodes are bootstrap values (≥50%) expressed as percentages of 1000 replicates. Bar: 0.01 substitutions per nucleotide position



a

b



d



c

Fig. S6