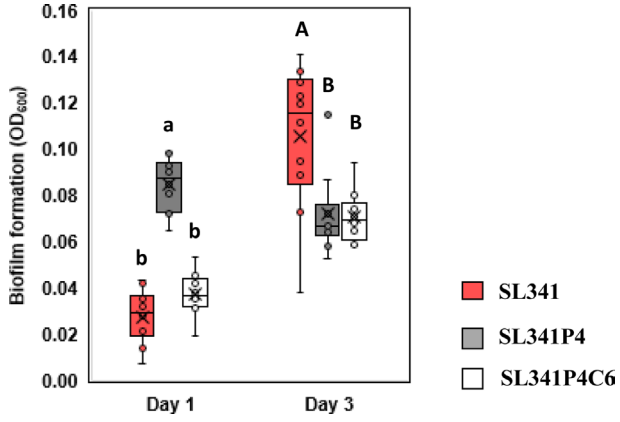
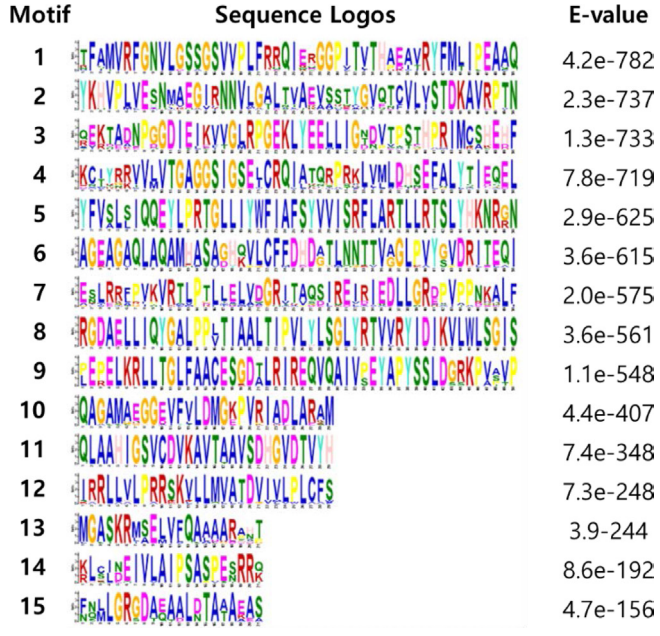
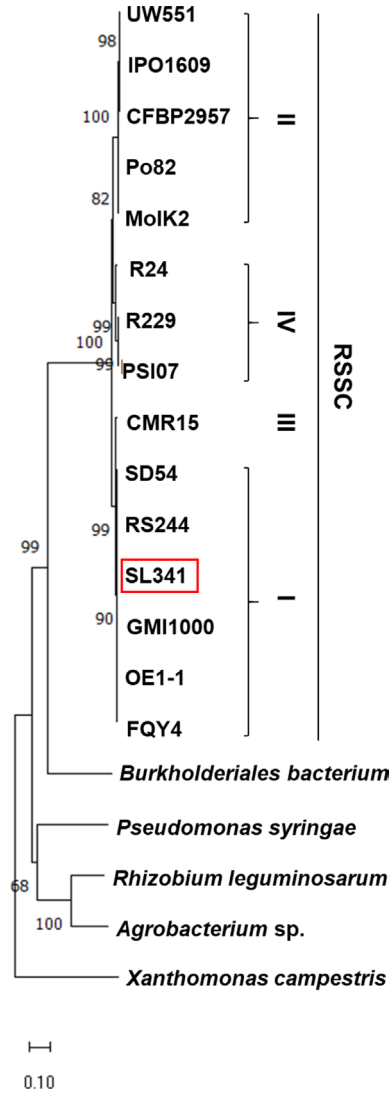


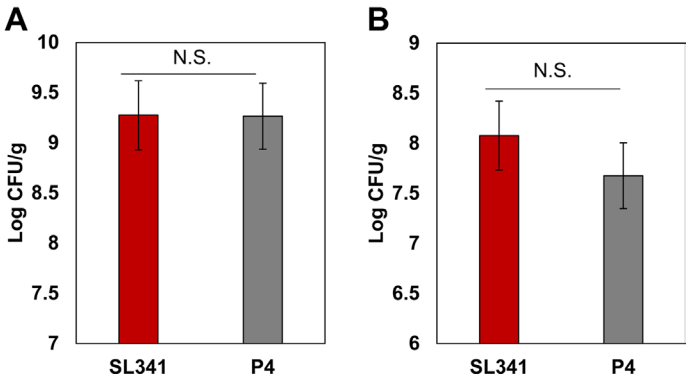
Supplementary Fig. 1. The measurement of biofilm formation in *Ralstonia pseudosolanacearum* SL341, SL341P4, and SL341P4C6 by crystal violet staining method. Different letters above the bar represent the significant difference in Tukey's means comparison ($P = 0.05$).



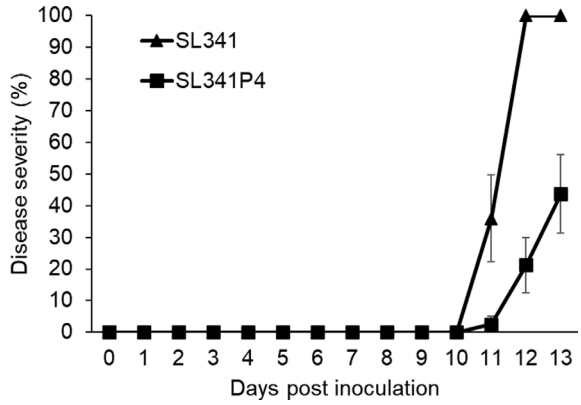
Supplementary Fig. 3. Fifteen conserved motifs in NDP-sugar epimerase proteins of 20 different bacterial phytopathogens. Sequence logos represent 15 significant conserved motifs in NDP-sugar epimerase proteins in Fig. 2. The height of letter designating the amino acid residue at each position represents the degree of conservation. The numbers on the x-axis represent the residue positions in the motifs. The y-axis represents the information content measured in bits. E-value of motifs indicate the statistical significance of each motif estimated by MEME suite tool.



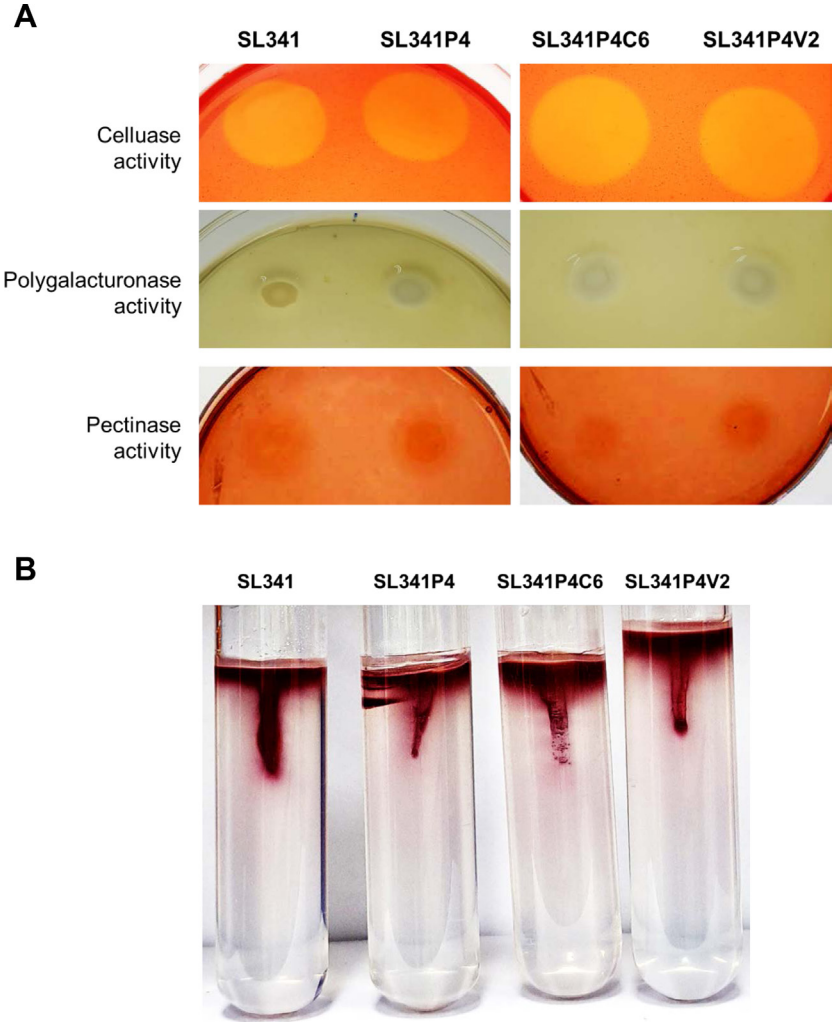
Supplementary Fig. 2. Phylogenetic tree of NDP-sugar epimerase proteins in 20 different bacterial phytopathogens. The evolutionary history was inferred using the Neighbor-Joining method. The optimal tree is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1,000 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method and are in the units of the number of amino acid substitutions per site. This analysis involved 20 amino acid sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 748 positions in the final dataset. Evolutionary analyses were conducted in MEGA11. RSSC, *Ralstonia solanacearum* species complex.



Supplementary Fig. 4. Bacterial multiplication in tomato plants (cv. Zuiken) inoculated with *Ralstonia pseudosolanacearum* wild-type strain SL341 and the NDP-sugar epimerase mutant strain SL341P4 by soil-soaking method. For each strain, three plants were used, and the number of bacteria were measured by dilution plating from mid-stem (A) and rhizosphere soils (B) at 14 dpi. Different letters above the box-plot represent the significant difference among treatment by ANOVA and least significant difference *post hoc* test ($P = 0.05$).



Supplementary Fig. 5. Disease responses on tomato plants Hawaii 7996 inoculated with *Ralstonia pseudosolanacearum* strain SL341 and SL341P4 by petiole injection. Disease severity of bacterial wilt was investigated for 13 days post inoculation of *R. pseudosolanacearum* strains.



Supplementary Fig. 6. Diverse virulence assay of SL341 and mutant strains *in vitro*. (A) Cell wall degrading enzyme activity. (B) Swimming motility.