

Supplementary Information

Table S1. Basic information of *Xal* JG43 and *Xsa* DD13.

Table S2. Repeat contents from genome sequence of *Xal* JG43 and *Xsa* DD13.

Table S3. Genes in plasmid from the genome of *Xal* JG43. (.xls)

Table S4. Carbohydrate-active enzymes (CAZys) in *Xal* JG43 and *Xsa* DD13.

Table S5. Comparative pathogenomics of *X. albilineans* JG43 and its related *X. sacchari* DD13. (.xls)

Table S6. Genomic island and prophages of *Xal* JG43 and *Xsa* DD13. (.xls)

Table S7. Resequencing of 23 *X. albilineans* strains.

Table S8. Genomic variations (SNPs and SVs) obtained from 23 sequenced *X. albilineans* strains against JG43.

Table S9. SNP mutations in 23 strains of *X. albilineans*.

Table S10. Mutations at the DNA level in 23 strains of *X. albilineans*.

Table S11. List of primers used in this study.

Fig. S1. Diseased sugarcane plant with leaf scald disease and chlorotic streak disease symptoms.

Left side: *X. albilineans* cause leaf scald disease. (a), (c) and (d) show leaf scald symptoms after *X. albilineans* invade sugarcane; (b) Colony of *X. albilineans* isolated from diseased sugarcane plant;

Right side: *X. sacchari* cause chlorotic streak disease. (a), (c) and (d) show chlorotic streak symptoms after *X. sacchari* infect sugarcane; (b) Colony of *X. sacchari* isolated from the diseased sugarcane plant.

Fig. S2. Type III secretion system (T3SS) (a), and SPI-1 family (b) of six *Xanthomonas* species.

Fig. S3. Type IV secretion system (T4SS) (a), T5SS and T6SS (b) of six *Xanthomonas* species.

Fig. S4. Potential pathogenic factors of six *Xanthomonas* species, including CRISPR system, Lipopolysaccharide transport system protein, Glycogen, Type III secretion

regulators, Two-component system regulators, Three-component system, and TALEs.

Fig. S5. Verification of *rpfC* and *rpfH* mutations. (a) PCR amplification from the upstream and downstream 500 bp of *rpfC*. M: 2000 bp; Lane 1: *rpfC* Gene left arm; Lane 2: *rpfC* gene right arm. **(b) Validation of enzymic fragment ligated with *PK18mobsacB*, a 500bp upstream and downstream fragment of *rpfC* gene.** M: 5000 bp; Lane 1,2,3: Validation of *rpfC* recombinant plasmid fragment by enzyme digestion; Lane 4 not included in this experiment. **(c) PCR amplified from mutants and its wild type JG43.** M:1000 bp; Lane 1, 2, 3; PCR fragment amplified with mutants; Lane 4: PCR fragment amplified with JG43 as template; Lane 5: Water control; Lane 6, 7, 8: Internal primer verification of the target fragment missing in 123, none, which proves the successful deletion of *rpfC* gene; Lang 9: Internal primer fragment of PCR amplified with JG43 as template. **(d) PCR validation of *rpfH* gene.** M:1000 bp; Lane 1: *Xcc* 8004; Lane 2: DD13; Lane 3: JG43; Lane 4: Water control; Lane 5: not included in this experiment.

Fig. S6. *rpf* gene cluster of six *Xanthomonas* species.

Fig. S7. PCR validation of single-base SNPs mutations. (a) PCR validation of single-base SNP mutations of candidate genes in FS 12. M:2000 bp; Lane 1: 1312440-G-C-L; Lane 2: 1312440-G-C-R; Lane 3: 1316566-A-G-L; Lane 4: 1316566-A-G-R; Lane 5: 1316572-A-G-L; Lane 6: 1316572-A-G-R; Lane 7: 1316840-G-A-L; Lane 8: 1316840-G-A-R; Lane 9: 1316855-T-C-L; Lane10: 1316855-T-C-R; Lane 11: 1316974-A-G-L; lane12: 1316974-A-G-R; lane13: 1317164-T-C-L; Lane 14: 1317164-T-C-R; Lane 15: 3055754-G-A-L; Lane 16: 3055754-G-A-R. **(b) PCR validation of single-base SNP mutations of candidate genes in FS12 (Lanes 1 and 2), FS25 (Lanes 3 and 4), FS63 (Lanes 5 and 6) and NM10 (Lanes 7 and 8).** M:2000 bp; Lane 1: 3055807-G-C-L; Lane 2: 3055807-G-C-R; Lane 3: 2749153-C-T-L; Lane 4: 2749153-C-T-R; Lane 5: 1508978-C-A-L; Lane 6: 1508978-C-A-R; Lane 7:1510223-A-C-L; Lane 8: 1510223-A-C-R. **(c) SNP point mutation fusion fragment in FS12.** M:2000 bp; Lane 1: 1312440-G-C; Lane 2: 1316566-A-G; Lane 3: 1316572-A-G; Lane 4:1316840-G-A; Lane 5: 1316855-T-C; Lane 6:1316974-A-G; Lane 7: 1317164-T-C. **(d) SNP point mutation fusion fragment in FS12.** M: 2000 bp; Lane 1:3055754-G-A; Lane 2:3055807-G-C; Lane 3: 3055836-T-G. **(e) SNP point mutation fusion fragment in FS25 (Lane 1:2749153-C-T), FS63 (Lane 2: 1508978-C-A), and NM10 (Lane 3: 1510223-A-C).** M:5000 bp.