

Supplementary Materials

Table S1. Biochemical and antibiotic resistance profile of *Xanthomonas arboricola* pv. *juglandis* strain J303 employed in this study.

Reaction/Enzyme	Xaj J303 WT
Reduction of nitrates to nitrites	-
Reduction to nitrates to nitrogen	+
Indole production	-
Glucose fermentation	-
Arginine Dihydrolase	+
Urease	+
Esculin hydrolysis	+
Gelatin hydrolysis	+
B-galactosidase	+
Carbohydrate assimilation	
Glucose	+
Arabinose	-
Mannose	+
Mannitol	-
N-Acetyl-Glucosamine	+
Maltose	-
Potassium Gluconate	-
Capric Acid	-
Adipic Acid	-
Malate	+
Trisodium Citrate	+
Phenylacetic Acid	-
Antibiotic resistance profile (mm)	
Gentamicin	22 ± 0,2
Streptomycin	32 ± 0,7
Oxytetracycline	37 ± 0,5

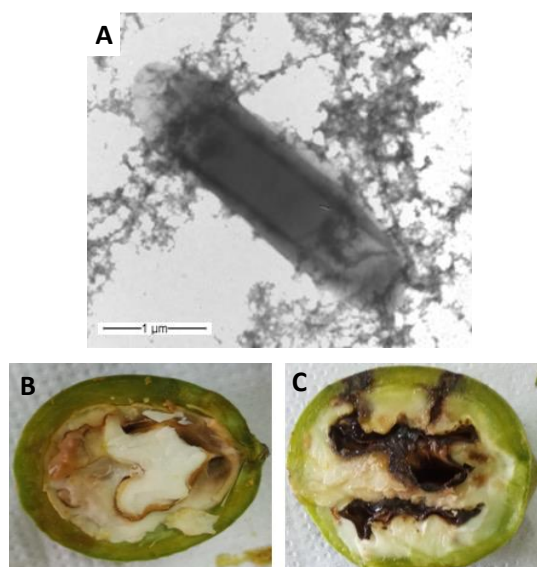


Figure S1. Characterization of *Xanthomonas arboricola* pv. *juglandis* J303 employed for isolation and propagation of bacteriophages. (A) Transmission electron microscopy of *X. juglandis* strain J303 (bar 1 μ m). Necrotic damage in immature walnut fruit: Control PBS (B) and *X. juglandis* J303 (C).

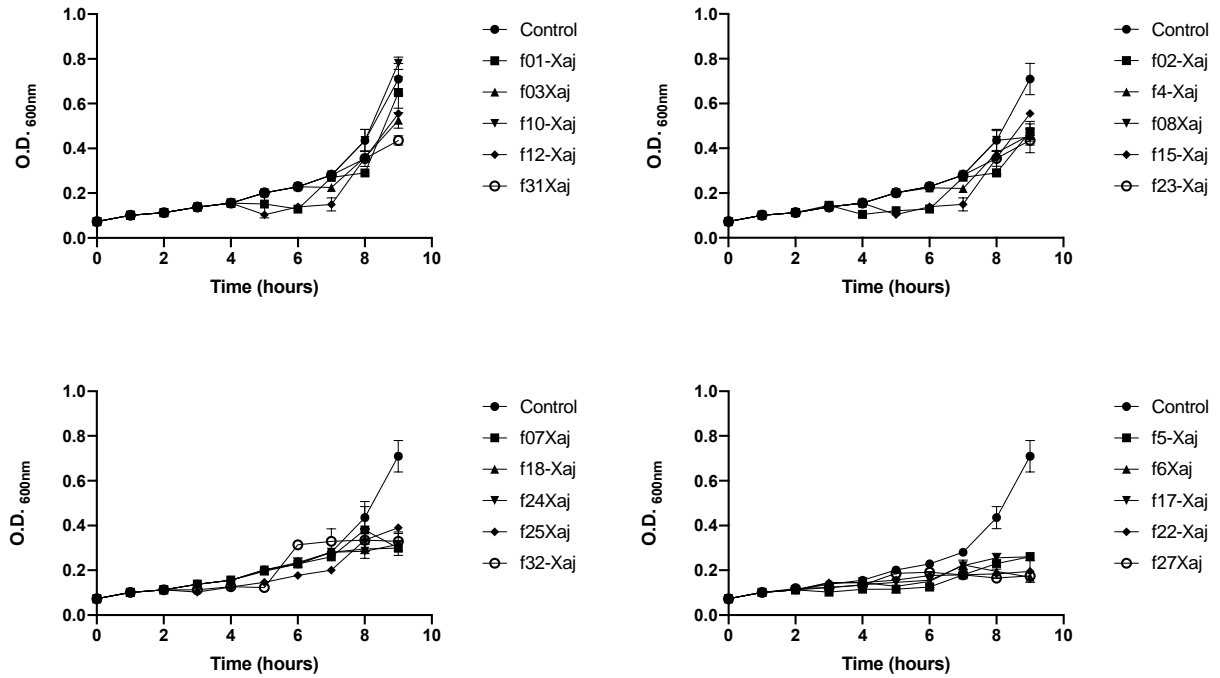


Figure S2. In vitro activity assay of bacteriophages against *Xanthomonas arboricola* pv. *juglandis* J303. The phages were grouped in each graph according to the OD600nm ranges they reached at the end of the assay. All experiments were employed in three independent replicates.



Figure S3. Alignment analysis of tail tubular protein of f20-Xaj and f30-Xaj bacteriophages. (A) Schematic depicting nucleotide changes between sequences performed with Geneious Prime® 2022.0.2 software. (B) Alignment of putative bacteriophage tail tubular proteins A and B performed with online Clustal-Omega server. Only the amino acid sequence of tubular protein A is indicated with the upper red line.