Pseudomonas syringae pv. tomato race 1 strains have evolved to overcome genetic resistance in tomato. Here, we present the draft genome sequences of two race 1 P. syringae pv. tomato strains, A9 and 407, isolated from diseased tomato plants in California.

**Genomic DNA** was sequenced using the Illumina HiSeq 2500 (2 × 150-bp paired-end reads) at the Genome Center at the UC Davis DNA Technologies Core Facility. After the raw sequences were trimmed and their quality filtered (>Q30), the remaining reads were assembled de novo using the SPAdes assembler and draft genomes were generated for each isolate (9). Each genome was annotated with PROKKA (10) and the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok).

The final draft assembly of the P. syringae pv. tomato A9 genome consists of 188 contigs (>200 bp) with 70-fold genome coverage. P. syringae pv. tomato A9 harbors a single circular genome of 6,264,873 bp with a G + C content of 55.8%. Among the 57 type III effectors present in the P. syringae pan-genome (11), 27 are present in both P. syringae pv. tomato A9 and P. syringae pv. tomato 407. Detailed comparisons of related Pseudomonas strains exhibiting variable virulence will facilitate insight into molecular mechanisms regulating virulence and adaptation.

**Nucleotide sequence accession numbers.** The sequences have been deposited as whole-genome shotgun projects in GenBank under the accession numbers LNKY00000000 for P. syringae pv. tomato A9 and LNKZ00000000 for P. syringae pv. tomato 407.

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