Draft Genome Sequence of *Serratia* sp. Strain M24T3, Isolated from Pinewood Disease Nematode *Bursaphelenchus xylophilus*

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Here we report the draft genome sequence of *Serratia* sp. strain M24T3, which is associated with pinewood nematode *Bursaphelenchus xylophilus*, the causative agent of pine wilt disease. *Serratia* sp. strain M24T3 has been identified as a bionematocide for *B. xylophilus in vitro*, and multiple genes potentially involved in virulence and nematotoxity were identified.

The pinewood nematode (PWN), *Bursaphelenchus xylophilus* is considered the causative agent of pine wilt disease (PWD). Native to North-America, it was introduced to Japan and has spread into China, South Korea, and Europe (5). Lately, bacteria have been suggested to play a role in the disease (8), but their specific functions and contributions to disease are still unclear. Isolation of *Serratia* sp. strain M24T3 was achieved from trails made on R2A by *B. xylophylus* from PWD *Pinus pinaster* (6). Sequencing of the 16S rRNA gene was performed, and the strain was tested for the ability to kill nematodes (6). Culture supernatants of Gram-negative *Serratia* sp. strain M24T3 (classified as *Serratia* sp. strain M24T3 in reference 6) killed *B. xylophilus* nematodes *in vitro* within 24 h of incubation (D. N. Proença, unpublished results).

Reads were generated by 454 GS FLX sequencing (4), and raw data were assembled using GS De Novo Assembler ("Newbler") version 2.5.3. The assembled contigs were submitted to the RAST annotation server for subsystem classification and functional annotation (1). Coding sequences (CDSs) were assigned using BLASTp with KEGG Orthology (KO). The G+C content was calculated using an in-house Perl script. The NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) was employed for gene annotation in preparation for submission to GenBank (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html).

The draft genome sequence of *Serratia* sp. strain M24Tt3 comprises 5,257,417 bases, representing 53-fold coverage of the genome. The assembled genome consists of 97 large contigs with more than 500 bp (N_{50} contig size of approximately 110,827 bp). The G+C content was 49.03%. The genome contains 4,858 putative coding sequences (CDSs). The draft genome sequence contains eight ribosomal RNAs and 63 tRNA loci. For the CDSs, 84% corresponding to 4,030 proteins could be assigned to the Cluster of Orthologous Groups (COG) families (7). Comparison with genome sequences available at RAST showed that 30 of the closest strains belong to eight genera (*Citrobacter*, *Erwinia*, *Escherichia*, *Klebsiella*, *Salmonella*, *Serratia*, *Shigella*, and *Yersinia*).

The *Serratia* sp. strain M24T3 genome carries multiple genes potentially involved in nematotoxic activity, such as genes coding for colicin V and bacteriocin biosynthesis, the *yafQ* gene coding for an endoribonuclease (YafQ toxin), and a gene that contains a bacterial RTX (repeats in the structural toxins) toxin-activating protein C signature.

The phylogenetically closest relative, *Serratia plymuthica*, can be used to protect against plant-pathogenic *Agrobacterium* (2) and induces systemic resistance against various rice pathogens (3).

Serratia sp. strain M24T3 has a set of genes typical for plant niche adaptation, like nitrogen regulatory protein P-II (ammonia assimilation), putative polysaccharide deacetylase (putatively involved in nodulation), and acetoin (diacetyl) reductase (plant protection against fungal and bacterial infections). Additionally, it is tempting to speculate that the *Serratia* sp. strain M24T3 may also be used as bionematocide against certain nematodes.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited in DDBJ/EMBL/GenBank under accession no. AJHJ00000000. The version described in this paper is the first version, AJHJ01000000.

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