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GENOME ANNOUNCEMENT

Whole-Genome Sequence of *Enterobacter* sp. Strain SST3, an Endophyte Isolated from Jamaican Sugarcane (*Saccharum* sp.) Stalk Tissue

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***Enterobacter* sp. strain SST3 is an endophytic bacterium isolated from *Saccharum* spp. Here we present its annotated draft genome that may shed light on its role as a bacterial endophyte of sugarcane. To our knowledge, this is the first genome announcement of a sugarcane-associated bacterium from the genus *Enterobacter*.**

Sugarcane is an important crop plant that contributes to the economy of many countries, including Jamaica. Due to its economic importance, research addressing the growth and protection of sugarcane is a priority. There are examples in the literature of sugarcane research from countries such as Brazil and India that pertain to bacteria (8, 9). However, the same is not true for Jamaica even though the sugarcane industry is integral to Jamaica's economy.

Besides sugar production, sugarcane is valuable for other commodities, such as molasses, press mud (a solid residue before sugar crystallization), and biogases (fibrous matter that remains after juice extraction). In addition, this crop has recently garnered significant attention as perhaps the most economically competitive source for ethanol production (1).

The sequenced bacterium (SST3, for sugarcane stalk tissue) was isolated from an endophytic screen of stem tissues of sugarcane obtained from a farm in Savanna La Mar in the Westmoreland parish of Jamaica. SST3 was initially identified as an *Enterobacter* sp. strain by sequence analysis of the variable 3 region of the 16S rRNA gene (3). Strain SST3 was shown to produce bacterial cell-to-cell communication signals of the acyl-homoserine-lactone (AHL) family (3).

Nitrogen fertilization for sugarcane growth is very costly. As such, we are interested in the identification of sugarcane-associated nitrogen-fixing bacteria. A recent study showed that two *Enterobacter* strains from sugarcane roots and rhizosphere soil from China increase the biomass and nitrogen content of sugarcane seedlings to facilitate growth and development (6). The identification, sequencing, and annotation of the genome of this Jamaican sugarcane-associated bacterium have the potential to broaden our understanding of the role(s) that endophytic bacteria have in sugarcane growth and development.

The genome sequencing of *Enterobacter* sp. SST3 was performed using the Illumina MiSeq (150-bp paired-end reads). The reads were trimmed and assembled *de novo* using CLC Genomics Workbench 5.0 (CLC Bio, Denmark). Prodigal 2.60, tRNAscan-SE 1.3, and RNAmmer 1.2 were used to predict open reading frames (ORFs), tRNAs, and rRNAs, respectively (4, 5, 7). Subsequent genome annotation was performed using Blast2GO 2.5.1 (2). The *de novo* assembly results in 54-fold coverage of a 4,626,853-bp draft genome contained in 63 contigs with an average GC content of 56.05%. The contig N_{50} was approximately 150 kb, and the longest contig assembled was approximately 330 kb. A total of 4,267 ORFs, 73 tRNAs, and 3 rRNAs were predicted from the draft genome.

Consistent with the AHL-positive phenotype of strain SST3, an AHL synthase gene was identified at contig 40. The protein sequence of this AHL synthase displays 88% similarity to CroI from *Citrobacter rodentium* strain CC168. Strain SST3 contains the complete enzyme set required for the conversion of sucrose into an energy source. Interestingly, an *iaaH* ortholog which may be involved in the production of auxin-like compounds that contribute to the promotion of sugarcane growth and development was also identified in the genome of strain SST3.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ALNS00000000. The version described in this paper is the first version, ALNS01000000.

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