Complete genome sequencing of Streptomyces sp. MOE7 that produces biologically active extracellular polysaccharide

Members of the genus *Streptomyces* are filamentous bacteria, considered the largest genus of *Actinobacteria*. Bacteria of this genus are considered among the most important soil bacteria as they are well known sources of many important biologically active compounds, including antimicrobial, antifungal, antiviral and anticancer agents. Thus, more tools have been developed for genetic manipulation of *Streptomyces* species to improve the production of these biologically active compounds and modify the routes of synthesis. Extracellular polysaccharides (EPS) are considered one of the important biologically active macromolecules due to the unique structures and pharmacological activities. The production of EPS from *Streptomyces* species has not been extensively studied compared to other bacterial and fungal sources.

The complete genome sequence is now an essential and powerful research tool for discovering the secondary metabolites produced by this microbe as well as potentially improving the productivity of these metabolites.

In this work, a new *Streptomyces* named *Streptomyces sp.* MOE7 was isolated from agricultural soil of Columbia, Missouri, USA. This newly isolated strain produced EPS that inhibited the spread as well as reduced the motility of the human breast cancer cells. Thus, we were interested in sequencing its whole genome in order to identify genes responsible for EPS production.

The DNA of strain MOE7 was isolated and sequenced by PacBio RSII at the University of Maryland Institute for Genome Sciences. Unlike other bacteria but relatively common in *Streptomycetes*, the genome was found to be a linear chromosome consisting of 8,399,509 bp with high G+C content of 72.0 % and a centrally located origin of replication.

Automated annotation of the genome sequence also identified 6,782 protein coding sequences in addition to 67 tRNA, 21 (seven 5S, seven16S, seven 23S) rRNA and 3 ncRNA genes. Moreover, the terminal regions of the linear chromosome showed the presence of an inverted repeat consisting of 19,413 bp. In addition the whole genome revealed the presence of genes responsible for the production of EPS as well as other secondary metabolites.

In conclusion, this whole genome sequencing is considered a powerful tool to improve the production of the extracellular polysaccharide as well as to discover other biologically active compounds produced by *Streptomyces* sp. MOE7.

The whole-genome sequence has been deposited in DDBJ/ENA/GenBank under the accession no. CP019779. The version described in this paper is the first version, CP019779.1.

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