



Draft Genome Sequence of *Micromonospora* sp. Rc5 Isolated from desert Egyptian Soil

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Abstract

Micromonospora sp. Rc5, a rare actinomycetes isolated from Egyptian desert. It showed antimicrobial activity against some food and blood borne pathogens. NRPS and PKS biosynthetic gene clusters were recorded in our strain. Previous findings ensure that, *Micromonospora* sp. Rc5 is a promising source for novel antibiotic production against multi drug resistant pathogens.

Keywords: *Micromonospora*-Antimicrobial-Next generation sequencing-Illumina platform-food borne pathogens.

Genome Annoucement

Micromonospora is the type genus of the family *Micromonosporaceae*, which are Gram positive, filamentous, aerobic bacteria which have diverse habitats such as soil, water, marine sediment and mangrove⁽¹⁻³⁾. This family produces many of the well-known antibiotics such as the aminoglycosides gentamicin and amikacin⁽⁴⁾.

In this study, we reported the draft genome sequence of *Micromonospora* sp. Rc5, isolated from a sandy soil in Sinai Desert, North East of

Egypt, 2009. It was isolated on selective humic acid vitamin agar media and starch casein agar, by rehydration and centrifugation method⁽⁵⁾. This strain showed biological activity against some food and blood borne pathogens, such as *Staphylococcus aureus* ATCC 6538, *Pseudomonas aeruginosa* ATCC 10145, *Klebsiella pneumonia* ATCC 10031, *Streptococcus mutans* ATCC 25175, *Escherichia coli* ATCC 51659 and *Salmonella enterica* ATCC 25566. Hemolytic effect on blood agar plates was also tested and

resulted positive with a small zone of clearance. In addition, probing of the genome using specific primers for polyketide synthase and nonribosomal peptide synthetase gene clusters revealed several hits^(6,7). This preliminary screening was supported by genome analysis which yielded in excess of 20 clusters indicating a considerable bioactive potential.

DNA was extracted from mycelium using the Promega Wizard Genomic DNA Purification kit, the mycelium was recovered from a liquid culture of seven days grown in starch casein broth⁽⁸⁾. The genome was sequenced using Illumina paired-end technology by Microbes NG (<http://www.microbesng.uk>), which is supported by the BBSRC (grant number BB/L024209/1). The bioinformatic analysis were provided by the sequencing company, which used Trimmomatic to trim raw reads⁽⁹⁾ and other software such as Samtools⁽¹⁰⁾ and bwa-mem⁽¹¹⁾ to quality filter the reads and assemble the genome. Gene annotation was performed via the NCBI Prokaryotic Genome Annotation Pipeline⁽¹²⁾ and an additional annotation was done using Prokka version 1.1⁽¹³⁾ to assist identifying gene clusters. The assembly metrics provided by Microbes NG were calculated using QUAST.

DNA sequencing resulted in 2,252Mb raw reads with 128.284 coverage. The assembly consists of 513 contigs. The draft genome was 7,702,789 bp, with an average GC content of 73.64%. A total of 6,792 coding sequences (CDS) with 6,504 coding genes, 3 recorded non-coding RNAs and 63 RNA genes with 50 tRNAs were identified by NCBI prokaryote pipeline (Table, 1).

Preliminary information derived from the genomic data indicated that the strain harbored a gramicidin-like gene cluster. The cluster also resembled a surfactin synthase subunit, which have been previously reported in *Micromonospora* sp.⁽¹⁴⁾.

Table (1): Genome notification of *Micromonospora sp. Rc5* provided by Microbes NG (<http://www.microbesng.uk>) using the assembly metrics calculated using QUAST software.

Sample ID	<i>Micromonospora sp. Rc5</i>
Median insert size	476
Mean coverage	128.284
Number of reads	2252025
contigs	513
Largest contig	123083
Total length	7702789
GC (%)	73.64
N50	28785
N75	15228
L50	87
L75	181

Nucleotide sequence accession number

This Whole Genome Sequencing Bioproject has been deposited at EMBL/Gen Bank under no. PRJNA354176 (BioSample SAMN06041774, Accession MQMK00000000).

Conflicts of interest

The authors declare no conflicts of interest.

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