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# Draft Genome Sequence of antagonistic *Streptomyces* sp. Ru87 Isolated from Egyptian Soil

Authors
**Dina H. Amin[1], Chiara Borsetto[2], Assem Abolmaaty[3], Sahar Tolba[4], Nagwa A. Abdallah[5], Elizabeth M. H. Wellington[6]**
[1,4,5]Department of Microbiology, Faculty of Science, Ain shams University, Cairo, Egypt
[2,6]School of Life Sciences, University of Warwick, Coventry, CV4 7AL, United Kingdom
[3]Department of Food Science, Faculty of Agriculture, Ain Shams University, P.O. Box 68 Hadayek Shoubra, 11241 Cairo, Egypt
Corresponding Author
**Dina H. Amin**
Department of Microbiology, Faculty of Science, Ain shams University, Cairo, Egypt
Email: *d_hatemamin@yahoo.com*

**Abstract**
*Streptomyces sp. Ru87 was selectively isolated from Egyptian clay soil by sucrose gradient centrifugation method. It recorded antagonistic activity against some food and blood borne pathogens such as Staphylococcus aureus ATCC 6538, Pseudomonas aeruginosa ATCC 10145, Streptococcus mutans ATCC 25175 and Escherichia coli ATCC 51659. NRPS and PKS PCR assays revealed that our strain harbors Non ribosomal peptide synthases and polyketide synthases biosynthetic gene clusters. We reported here the draft genome sequence of strain Streptomyces sp. Ru87. The draft genome was 7, 662, 503 bp, with an average GC content of 73.12%was assembled in 629contigs using Illumina MiSeq and HiSeq 2500 platforms using 2X250bp paired-end technology. NCBI prokaryote pipeline annotation identified 6,527 coding sequences (CDS) with 6,051 coding genes, 3 recorded non-coding RNAs and 74 RNA genes with 62tRNAs. Previous data clarified, the significance of Streptomyces sp. Ru87in antibiotic production and drug discovery against resistant pathogens.*
**Keywords:** *Streptomyces-Antimicrobial-Next generation sequencing-Illumina platform-food borne pathogens.*

## Genome Annoucment

Genus *Streptomyces* is considered as the largest genus of Actinobacteria (Kämpfer,2006). Streptomycetes are Gram-positive with a high GC content. Soil and decaying vegetation are their dominant habitat (Williams et al., 1989). Streptomycetes are well known by their complex secondary metabolism. They generate above two-third of the essential recognized antibiotics used such as (cypemycin, grisemycin, bottromycins, neomycin and chloramphenicol) (de Lima Procópio et al., 2012).

In this study, we reported the draft genome sequence of *Streptomyces* sp. Ru87, isolated from a clay soil in North West of Egypt, 2008. It was isolated on selective humic acid vitamin agar

media and starch casein agar, by sucrose gradient centrifugation method (Yamamura et al., 2003; Hayakawa, 2008). This strain showed biological activity against some food and blood borne pathogens, such as *Staphylococcus aureus* ATCC 6538, *Pseudomonas aeruginosa* ATCC 10145, *Streptococcus mutans* ATCC 25175 and *Escherichia coli* ATCC 51659. NRPS and PKS PCR assays of the genome using specific primers showed positive results (Amos et al., 2015; Bredholt et al., 2007). This primary screening was reinforced by anti SMASH genome analysis that presented 19 biosynthetic gene clusters within *Streptomyces* sp. Ru87indicating a significant 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 (Williams and Davis, 1965). The genome was sequenced using Illumina MiSeq and HiSeq 2500 platforms using 2X250bp 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 (Bolger et al.,2014) and other software such as Samtools(Li et al., 2009) and bwa-mem (Li and Durbin, 2009)to quality filter the reads and assemble the genome. Gene annotation was performed via the NCBI Prokaryotic Genome Annotation Pipeline (Tatusova et al., 2016) and an additional annotation was done using Prokka version 1.1 (Seemann, 2014) to assist identifying gene clusters.

The assembly metrics provided by Microbes NG were calculated using QUAST. DNA sequencing resulted in 2,285Mb raw reads with130.274 coverage. The assembly consists of 629contigs. The draft genome was 7, 662, 503bp, with an average GC content of 73.12% (Table, 1). A total of 6,527 coding sequences (CDS) with 6,051 coding genes, 3 recorded non-coding RNAs and 74 RNA genes with 62tRNAs were identified by NCBI prokaryote pipeline. Preliminary information derived from the anti SMASH genomic data base indicated that the strain is able to produce Labyrinthopeptins. Labyrinthopeptins are a class of carbacyclicl antibiotics, which are ribosomally synthesized peptides produced by bacteria and actinomycetes and recorded antimicrobial activity against *S.aureus* (Meindl et al., 2010). The genome sequence of *Streptomyces* sp. Ru87 and their annotation would be a useful genetic resource for further exploration of antibiotic biosynthetic gene clusters and improve their genetic manipulation. Our study had a great impact on public health and combating the problem of multi drug resistant pathogens.

**Table (1):** Genome notification of *Streptomyces* sp. Ru87 provided by Microbes NG (http://www.microbesng.uk) using the assembly metrics calculated using QUAST software.

| Sample ID | *Streptomyces* sp. Ru87 |
|---|---|
| Median insert size | 448 |
| Mean coverage | 130.274 |
| Number of reads | 2285091 |
| contigs | 629 |
| Largest contig | 129784 |
| Total length | 7662503 |
| GC (%) | 73.12 |
| N50 | 20124 |
| N75 | 11601 |
| L50 | 103 |
| L75 | 227 |

**Nucleotide sequence accession number**

This Whole Genome Sequencing Bioproject has been deposited at EMBL/GenBank under no. PRJNA413750 (Bio Sample SAMN07765385, Accession PDIX00000000).

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**Conflicts of interest;** The authors declare no conflicts of interest

**References**


1. Amos, G. C., Borsetto, C., Laskaris, P., Krsek, M., Berry, A. E., Newsham, K. K., & Wellington, E. M. (2015). Designing and implementing an assay for the detection of rare and divergent NRPS and PKS clones in European, Antarctic and Cuban soils. *PloS one*, *10*(9), e0138327.
2. Bolger, A. M., Lohse, M., & Usadel, B. (2014). Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics*, *30*(15), 2114-2120.
3. Bredholdt, H., Galatenko, O. A., Engelhardt, K., Fjærvik, E., Terekhova, L. P., & Zotchev, S. B. (2007). Rare actinomycete bacteria from the shallow water sediments of the Trondheim fjord, Norway: isolation, diversity and biological activity. *Environmental microbiology*, *9*(11), 2756-2764.
4. de Lima Procópio, R. E., da Silva, I. R., Martins, M. K., de Azevedo, J. L., & de Araújo, J. M. (2012). Antibiotics produced by Streptomyces. *The Brazilian Journal of infectious diseases*, *16*(5), 466-471.
5. Hayakawa, M. (2008). Studies on the isolation and distribution of rare actinomycetes in soil. *Actinomycet-ologica*, *22*(1), 12-19.
6. Kämpfer, P. (2006). The family Streptomycetaceae, part I: taxonomy. In *The prokaryotes* (pp. 538-604). Springer New York.
7. Li, H., & Durbin, R. (2009). Fast and accurate short read alignment with Burrows–Wheeler transform. *Bioinformatics*, *25*(14), 1754-1760.
8. Li, H., Handsaker, B., Wysoker, A., Fennell, T., Ruan, J., Homer, N.,& Durbin, R. (2009). The sequence alignment/map format and SAM tools. *Bioinformatics*, *25*(16), 2078-2079.
9. Meindl, K., Schmiederer, T., Schneider, K., Reicke, A., Butz, D., Keller, S., & Brönstrup, M. (2010). Labyrinthopeptins: a new class of carbacyclic lantibiotics. *Angewandte Chemie International Edition*, *49*(6), 1151-1154.
10. Seemann, T. (2014). Prokka: rapid prokaryotic genome annotation. *Bioinformatics*, *30*(14), 2068-2069.
11. Tatusova, T., DiCuccio, M., Badretdin, A., Chetvernin, V., Nawrocki, E. P., Zaslavsky, L.,. & Oste ll, J. (2016). NCBI prokaryotic genome annotation pipeline. *Nucleic acids research*, *44*(14), 6614-6624.
12. Williams, S. T., & Davies, F. L. (1965). Use of antibiotics for selective isolation and enumeration of actinomycetes in soil. *Microbiology*, *38*(2), 251-261.
13. Williams, S. T. (1989). Genus Streptomyces Waksman and Henrici 1943. *Bergey's manual of systematic bacteriology.*, *4*, 2452-2492.
14. Yamamura, H., Hayakawa, M., & Iimura, Y. (2003). Application of sucrose-gradient centrifugation for selective isolation of Nocardia spp. from soil. *Journal of applied microbiology*, *95*(4), 677-685.