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Project title: Whole genome sequence analysis of the *Streptomyces rimosus* (ASM2276019v1)

Introduction

Actinomycetes are Gram positive bacteria which are found in soil rich with organic content as well as in complex environments. These have high G+C content and highly developed with substrate and aerial mycelium. They are also capable of forming spores and can be found in different complex habitats (1). *Streptomyces* spp. is the most important among them and are well known for synthesis of bioactive products (2). They can produce secondary metabolites like biopesticide amines, antibiotics, hormones, antitumor compounds, antiviral agents, pigments, and many more enzymes which have great economic importance for industrial applications. The possibility of getting more important and potent isolates from environment is highly desirable since only 10% of actinomycetes are known to be isolated from nature to date (1).

Among these, *Streptomyces rimosus*, is the most important species, producing the first broad-spectrum antibiotic, oxytetracycline. *Streptomyces* species have complex genomes with high GC content often exceeding 70%. These microorganisms can also contain one or more linear plasmids, sometimes reaching over 1 Mb in size and designated giant linear plasmids (GLPs). The GC content was slightly higher in the chromosome (at 72.0%) than in the plasmid (at 69.6%) (3).

Research question:

1. Does the genome have a potential gene that can produce the special metabolites useful for industrial applications?
2. Will the quality of the assembled genome sequence resulted from combining both the long read (Nanopore fast base-calling) and short reads (Illumina), be the same as the assembled genome sequence generated by long reads only (Nanopore high accuracy base-calling) using DORADO software installed at the supercomputer.

Method:

The whole genome sequence is analyses by using high accuracy rate software like DORADO. As the organism genome has the data from both NGS and oxford nanopore technology, use of best software though supercomputer on both long and short read gene can generate better result.

References

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