

Draft genome sequencing of *Streptomyces exfoliatus* FT05W, a biological control strain against plant soil-borne pathogens

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“*Streptomyces exfoliatus*” FT05W is a biocontrol strain showed antagonisms to a variety of soil-borne pathogens. In this study, we used Miseq PE300 next-generation sequencing platform to perform its genome sequencing, and obtained 6914188 reads. The SPAdes software was used to splice a total of 1836 contigs with a total genome length of 7699129 bp and a GC ratio of 71%, in which the length of the coding gene sequence is 6037181 bp, and 7434 protein-coding genes are predicted, which are predicted to encode 7233 proteins. Subsequently, through the comparison and analysis of databases such as GO, COG, KEGG, NR and TCDB, the genome prediction and basic function annotations were completed. The gene annotation information thus obtained lays an important foundation for further research on its biological control mechanism in plant. The basis of the study will help promote the excavation and utilization of “*Streptomyces*” sp. functional genes and provide a theoretical basis for further development and application of “*Streptomyces exfoliatus*” FT05W as biopesticides.