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The terpenoid biosynthesis pathway of *Hypsizigus marmoreus* genome

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Hypsizigus marmoreus that is also known as brown beech is an edible mushroom. It is native to East Asia, one species of the genus *Hypsizigus* with the white beech mushroom, white clamshell mushroom, buna-shimeji etc. It is also industrialized due to its rich nutrition and medicinal value. Anti-tumor, antioxidant, anti-inflammatory, anti-bacterial and anti-viral activities are reported. *Hypsiziprenol A9* was reported to be responsible to the anticancer activity. RDA and Korea University consortium launched the genome sequencing project in 2014. The strain Haemi was collected in Korea. The two haploid strains 51987-8 and Haemi-18 were generated from the diploid. 71X Illumina sequencing data lead the genome feature with 30.3 Mb and 15561 protein coding genes. About 70% of the annotated genes have no hits, 22% of genes involved biological process were predicted to play roles in metabolic process. There have been found 23 terpenoid synthesis genes. One of them is considered to function for the biosynthesis of hypsiziprenols. It harbors genes for polyprene synthesis and oxygenation but lacks cyclase.

Biography

Jeong-Gu Kim has completed his PhD from Seoul National University, South Korea. He is working for Genomics Division, Institute of Agricultural Sciences, Rural Development Administration (RDA), South Korea. As an Agricultural Researcher, he is carrying out research projects on microbial genome and one project on development of plant disease suppressing substances from *Streptomyces*. He has published more than 10 papers in international journals and patented for biological activities of microbial metabolites, detection methods for microbes.

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