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## <u>The regulatory and transcriptional landscape associated with triterpenoid and lipid</u> <u>metabolisms by the bHLH-zip transcription factor SREBP in the medicinal fungus</u> <u>Ganoderma lingzhi</u>

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Ganoderic Acids (GAs) are well recognized as important <u>pharmacological</u> components of the medicinal species belonging to the basidiomycete genus Ganoderma. However, transcription factors directly regulating the expression of GA biosynthesis genes remain poorly understood. Here, the genome of *Ganoderma lingzhi* was de novo sequenced. Using DAP-seq, we identified putative targets of the transcription factor SREBP, including the genes of triterpenoid synthesis and lipid metabolism. Interactions between SREBP and the targets were verified by EMSA. RNA-seq showed that SREBP targets, mevalonate kinase and 3-hydroxy-3-methylglutaryl CoA synthetase in mevalonate pathway, sterol isomerase and lanosterol 14-demethylase in ergosterol biosynthesis, were significantly upregulated in the SREBP overexpression strain. In addition, 3 targets involved in glycerophospholipid/glycerolipid <u>metabolism</u> were up regulated. Then, the contents of mevalonic acid, lanosterol, ergosterol and 13 different GAs as well as a variety of lipids were significantly increased in this strain. Furthermore, the effects of SREBP overexpression on triterpenoid and lipid metabolisms were recovered when OE::SREBP strain were treated with exogenous fatostatin, a specific inhibitor of SREBP. Taken together, our genome-wide study clarified the role of SREBP in triterpenoid and lipid metabolisms of *G. lingzhi*.

Keywords: SREBP, DAP-seq, triterpenoid and lipid metabolisms, Ganoderma lingzhi.

## Biography

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