Molecular cloning and promoter analysis of squalene synthase and squalene epoxidase genes from *Betula platyphylla*

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**Introduction**

*Betula platyphylla* contains important secondary metabolites, and one such group of pharmaceutical secondary metabolites are the Birch triterpenoids (TBP), which include betulin, betulinic acid and oleanolic acid. These TBP have great potential in the development of anti-cancer and anti-human immunodeficiency virus (HIV) therapeutics. In the Birch triterpenoids synthetic pathway, squalene synthase (SS) and squalene epoxidase (SE) are two important rate-limiting enzymes. The content and activity of SS and SE determine the yield of the subsequent product.

**Results & Discussion**

Here, we cloned the squalene synthase (SS) full length cDNA sequences from *Betula platyphylla*. Neighbor-joining phylogenetic trees were constructed with the MEGA 6.0 software program from different organisms that were retrieved from the NCBI GenBank database. The *BpSS* was included in a separate clade consisting of members of the *Theobroma cacao* family to which *BpSS* belongs. Subcellular localization of the *BpSS*:GFP fusion protein in onion epidermal cells. The fusion construct pCAMBIA1303-*BpSS* (p35S-*BpSS*::GFP) and control pCAMBIA1303 (p35S-GFP) were mobilized in Agrobacterium tumefaciens strain GV3101. These results indicated that *BpSS* is localized in the cytoplasm.

**Conclusions**

In this study, we cloned and detected the expression patterns of the gene encoding the enzyme *BpSS* that involved in birch triterpene biosynthesis. And we isolated *BpSS* promoters and analysis cis-acting elements. The yeast expression vector pYES2-*BpSS* and pYES2-*BpSE* were constructed and transformed into the yeast INVSc1 strain. The squalene content of galactose-induced *BpSS* expression yeast cells and the squalene epoxidase activity of induced *BpSE* expression yeast cells was significant increase.

**Acknowledgments:** Natural Science Foundation of China (31200428, 31570589).