淫羊藿花蕾 cDNA 文库的构建与鉴定

姜天亮1,黎云祥1*,杨子松2,韩素菊1,陈光登1

(1. 西华师范大学,四川省环境科学与生物多样性保护重点实验室,四川南充 637002; 2. 阿坝高等师范专科学校,四川汶川 623000)

摘 要:基于 smart 技术构建了淫羊藿花蕾 cDNA 文库并检测了其质量。结果表明,该文库重组率为 95%,平均插入片段大小为 1095~bp,文库滴度为 $2\times10^6~pfu/mL$,是一个高质量的淫羊藿花蕾 cDNA 文库。此文库的建立将有助于克隆与次生代谢相关的基因,特别是淫羊藿黄酮特异合成代谢的基因,其次是克隆与花发育相关的基因。

关键词: cDNA 文库; 花蕾; 淫羊藿

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Construction and Identification of a cDNA Library for the Flower buds of *Epimedium brevicornu* Maxim

JIANG Tian-Liang¹, LI Yun-Xiang¹*, YANG Zi-Song², HAN Su-Ju¹, CHEN Guang-Deng¹

 Sichuan Provincial Key Laboratory of Environmental Science and Biological Diversity Conservation, China West Normal University, Nanchong, Sichuan 637002, China; 2. Aba Teachers College, Wenchuan, Sichuan 623000, China)

Abstract: A cDNA library for flower buds of *Epimedium brevicornu* Maxim was constructed which based on SMART technology. Our results showed that the titer of unamplified library from flower buds was 2 × 10⁶ pfu/mL. The percentage of recombinants was 95% and the average length of the insert cDNA fragments was 1095 bp. It suggested that one high quality cDNA library for flower buds of *E. brevicornu* were successfully constructed. Construction of cDNA library will help to clone the relevant genes associated with secondary metabolism, first, the special genes in the course of flavonoid biosynthesis; second, the genes related with development of flower buds in *E. brevicornu* Maxim.

Key words: cDNA library; Flower buds; Epimedium brevicornu Maxim

As a traditional Chinese medicine and important genus, *Epimedium* has been used for a long time, and is the hotspot of modern pharmaceutical studies for its wide and good curative effects. The recent studies focus on the chemical constituents and their corresponding chemical structures, taxonomic system, ecophysiology, cultivation, pharmacognosy and so on^[1-4]. Flavonoids are main component as a medicine, such as icariin, anhydroicaritin, epimedoside A, etc^[5-10].

In flowers, seeds, nuts, vegetables and fruits, flavonoids occur naturally. They belong to a class of secondary metabolites in plants that are involved in many important functions. For examples, protection against overexposure to ultraviolet light, floral pigmentation for attracting pollinators and antimicrobial activi-

ty as phytoalexins^[11,12]. Being an integral part of the human diet, flavonoids possess health-promoting properties acting as antioxidants and being involved in vaso-dilator processes. The amount and content of flavonoid compounds in plants can be modified by altering expression levels of the enzymes involved in thepathway^[12]. The way of flavonoid biosynthesis is very clear in many species such as in bilberry^[13] and many enzymes, such as chalcone synthase (CHS), chalcone isomerase (CHI), flavanone-3-hydroxylase (F3H), dihydroflavonol-4-reductase (DFR), flavonol synthase (FLS), rhamnosyl transferase (RT) are key enzymes in this course of biosynthesis^[14,15].

Constructing cDNA library will lay solid foundation for finding relevant genes and investigating their

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作者简介:姜天亮(1979-),男,吉林四平人,硕士研究生,从事植物分子生态学研究。

^{*} 通讯作者(E-mail: yx_li@263.net)。