

食品—研究报告

地黄实时定量PCR内参基因的筛选

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摘要:

本文通过RT-qPCR分析了地黄中7个传统内参基因18S、EF-1 α 、ACT11、UBQ10、UBQ5、TUB5、GAPDH和4个新报道的内参基因PP2A、RP II、HSP90、TIP41的mRNA表达差异情况,分别利用Ct值比较,GeNorm、NormFinder和BestKeeper软件分析它们在两个发育时期、八种不同组织器官中表达稳定性。结果表明:在地黄花器官中(花瓣、花托、雄蕊、雌蕊、子房),TIP41和UBQ10表达稳定;在地黄生殖生长期和营养生长期不同器官中(根、茎、叶),TIP41和UBQ5表达稳定。因此,以上两组基因分别适宜作为不同营养器官的内参基因。

关键词: 地黄

Selection of the Reference Genes for Gene Expression Studies in *Rehmannia glutinosa* by Real-time Quantitative PCR

Abstract:

A total of eleven reference genes were systematically compared in different tissues of *Rehmannia glutinosa* using RT-qPCR, including seven traditional reference genes (ACT11, 18S, TUB5, GAPDH, EF-1 α , UBQ10 and UBQ5) and four novel candidates reference gene (HSP90, PP2A, RP II and TIP41) in this study. The mRNA levels of these genes were analyzed among the organs of flowers, roots, stems and leaves representing the vegetative growth phase and the generative growth phase. The stabilities of the eleven candidate reference genes were ranked by the Ct value comparison and three softwares (GeNorm, NormFinder and BestKeeper). The results showed that the expression of TIP41 and UBQ10 was stable in different tissues of sepals, petals, stamens, pistils, and ovary from flower. For the case of the roots, stems and leaves sampled in vegetative growth phase and generative growth phase, UBQ5 and TIP41 were expressed stably. As a result, the two groups of candidate genes were selected as reference genes for *Rehmannia glutinosa*.

Keywords: *Rehmannia glutinosa*

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