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甘草 β -香树酯醇合成酶编码区SNP与甘草酸含量的相关性研究投稿时间：2009-12-07 责任编辑：吕冬梅 [点此下载全文](#)引用本文：沈进云,刘春生,王学勇,呙未,李贝宁.甘草 β -香树酯醇合成酶编码区SNP与甘草酸含量的相关性研究[J].中国中药杂志,2010,35(7):813.

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中文摘要:目的:探讨甘草 β -香树酯醇合成酶(β -amyrin synthase,bAS)编码区SNP与甘草酸含量之间的相关性。方法:采用HPLC法测量80株人工栽培甘草的甘草酸含量,采用SAS 9.0软件将80株甘草按照甘草酸含量极差水平($P<0.00001$)进行分组,采用RT-PCR技术,扩增出甘草bAS编码区序列,运用DNAMAN分析软件找出该序列的SNP位点,进而分析该位点与甘草酸含量高低的相关性。结果:bAS基因编码区共有94,254 bp 2个突变位点,在94 bp位点发生G/A转换,为错义突变,导致该位点处甘氨酸→天冬氨酸转换,254 bp处发生G/T转换,为同义突变,根据序列变异将所测样品划分成G-T基因型、A-T基因型、G-C基因型和A/G-C基因型。结论:A-T基因型、G/A-C基因型和高含量甘草酸形成具有显著的相关性。

中文关键词:[甘草酸](#) [\$\beta\$ -香树酯醇合成酶](#) [单核苷酸多态性](#)

Correlation analysis between single nucleotide polymorphism of β -amyrin synthase and content of glycyrrhetic acid in *Glycyrrhiza uralensis*

Abstract: Objective :To analyze the correlation between content of glycyrrhetic acid and the single nucleotide polymorphism of β -amyrin synthase (bAS) in *Glycyrrhiza uralensis*. Method : glycyrrhetic acid content in 80 samples of the cultivated *G. uralensis* were determined by HPLC; According to the very significant level ($P<0.00001$), 80 samples in accordance with glycyrrhetic acid will be grouped by SAS 9.0; Using RT-PCR strategy to amplification the Open Reading Frame of β -amyrin synthase with the template of total RNA extracted from roots of *G. uralensis* and then using DNAMAN to analyze the relationship between glycyrrhetic acid content and the single nucleotide polymorphism of β -amyrin synthase (bAS). Result : There existed two mutation sites 94 bp and 254 bp, G/A conversion occurred at 94 bp site, which belonged to a missense mutation. G/A conversion led to the corresponding amino acid conversion (Gly→Asp); C/T conversion occurred at 254 bp site, which belonged to a synonymous mutation. According to sequence variation, the samples were divided into four genotypes: G-T genotype, A-T genotype, G/A-C genotype and G-T genotype. Conclusion : A-T genotype,G/A-C genotype and G-T genotype are correlated with the high content of glycyrrhetic acid .

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