

蚕豆豆类胰岛素基因的cDNA克隆及序列分析 cDNA Cloning and Sequence Analysis of Leginsulin Gene in Broad Bean (*Vicia faba*)

谈建中¹, 楼程富², 张国英¹, 孙丙耀¹, 平野久³ TAN Jian-Zhong¹, LOU Cheng-Fu², ZHANG Guo-Ying¹, SUN Bing-Yao¹, HIRANO Hisashi³

1.苏州大学生命科学学院,苏州 215006; 2.浙江大学动物科学学院,杭州 310029; 3.横滨市立大学木原生物学研究所,横滨 244—0813,日本 1.College of Biological Science,Suzhou University,Suzhou 215006,China; 2.Animal Science College,Zhejiang University,Hangzhou 310029,China; 3.Kihara Institute for Biological Research,Yokohama City University,Yokohama,244-0813,Japan

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摘要 为探明豆科植物中豆类胰岛素基因的结构特征与进化关系,在已获得大豆豆类胰岛素基因的基础上,以蚕豆种子胚根mRNA为材料,采用RT-PCR技术,克隆了蚕豆豆类胰岛素基因的cDNA序列,编码的前体多肽包括信号肽、成熟型豆类胰岛素及另一多肽的45个氨基酸残基。DNA序列分析表明,克隆片段与大豆和豌豆的同源性分别为62.5%和58.7%。在氨基酸水平上分别具有44.2%和43.6%的同源性,其中存在着高度保守的半胱氨酸位点,它们在维持豆类胰岛素的空间结构与生理功能方面,可能具有重要的作用。

Abstract:In order to elucidate the relationship between the structural features of leginsulin gene in legume plants and their phylogenetic significance,we have cloned the cDNA sequence of leginsulin gene from radicles of broad bean (*Vicia faba*) via RT-PCR techniques according to the leginsulin gene sequence we previously obtained from soybean (*Glycine max*).The cloned cDNA encoded for a precursor protein consisting of the signal peptide,mature leginsulin and an additional 45 amino acids of another polypeptide.A sequence search for homology comparison revealed the cloned leginsulin cDNA fragment shares 62.5% and 58.7% similarity to soybean and pea,respectively.The results also shown that leginsulin cDNA from broad bean presents 44.2% and 43.6% amino acid sequence homology with soybean and pea (*Pisum sativum*),respectively,and that there exists highly conserved cysteine sites among the leginsulin cDNAs,which may play a crucial role in maintaining the three-dimensional structure and the physiological functions of leginsulin.

关键词 [蚕豆](#) [豆类胰岛素基因](#) [cDNA序列](#) [RT-PCR](#) **Key words** [broad bean \(*Vicia faba* L.\)](#) [leginsulin gene](#) [cDNA sequence](#) [RT-PCR](#)

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