## 论文(设计)题目 大胡蜂核糖体蛋白 S5cDNA 克隆及序列分析

## 摘要

大胡蜂 Vespa (Magnifica) magnifica Smith 隶属于膜翅目(Hymenoptera) 胡蜂科 (Vespoidea)黄胡蜂属(Vespa),是一种分布比较广、飞行快速的昆虫。大胡蜂属名与种名的命名与地域的不同有关,而且不同属的大胡蜂其毒素组分存在较大差异,大胡蜂蜇伤人之后其毒素引起的过敏反应常能将人致死,并且近年来被胡蜂蜇伤的发病率也在提高。在其它国家,如今对胡蜂毒素的基因研究集中在过敏原性大分子量蛋白方面,但是,现在对于胡蜂蜇伤致病机制还不是很明确。

本次课题利用基因工程的相关技术,通过总 RNA 的提取、RNA 的检测、cDNA 文库的构建、PCR 扩增、琼脂糖凝胶电泳、序列比对等方法对大胡蜂核糖体 S5 蛋白进行分析。其目的是通过基因工程的相关技术利用所得片段序列与已知同属物种序列进行相似性对比,以此来为研究大胡蜂的毒素成分,并为大胡蜂的资源利用提供基础理论数据,在生物防治以及卫生药理等方面具有一定的意义,可以更清楚的了解并应用蜂毒。

关键词: 大胡蜂; 胡蜂毒素; cDNA 克隆; 核糖体蛋白; 序列分析

**Abstract** 

Vespa (Magnifica) magnifica Smith belongs to Hymenoptera, (Hymenoptera), (Vespoidea),

(Vespa), which is a widely distributed and fast flying insect. The nomenclature of the

genus wasp is often related to the region. There are great differences in the components of

wasp toxin among different genera. The rapid allergic reaction caused by wasp toxin often

leads to death, and the morbidity of the population is also increasing. In foreign countries,

the gene research of wasp toxin is focused on the allergy of large molecular weight protein,

but the pathogenesis of wasp stings is not clear. In this study, the ribosomal S5 protein of

wasp was analyzed by the methods of total RNA extraction, detection of RNA,

construction of cDNA library, PCR amplification, agarose gel electrophoresis, sequence

alignment and so on. The purpose of this study is to compare the sequence of fragments

obtained by genetic engineering with the sequences of known homologous species in order

to study the toxin components of wasp and to provide basic theoretical data for the

utilization of resources of wasp. It has certain significance in biological control and health

pharmacology, you can better understand and apply bee venom.

Keywords: Vespa (Magnifica) magnifica Smith; Wasp toxin; Ribosomal protein; cDNA

clone; sequence analysis

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