



## 正、副高职称

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### 个人简历

#### 科研领域描述

本实验室主要兴趣在于:

1. 植物系统进化学及植物分子生物学的研究
2. 拟南芥野生居群的遗传多样性及分子适应性的研究
3. 植物基因家族的功能和进化研究

研究对编码CHS、水稻胰蛋白酶抑制剂等基因家族的分子进化,发现多数植物的CHS基因可被分为两类,一类进化速率较慢,另一类进化速率较快且受到正选择的作用。CHS基因在裸子植物中的拷贝数较少,而在被子植物中拷贝数变化很大。水稻中Bowman-Birk型胰蛋白酶抑制剂(RBBI)10个成员的系统树及编码基因的5'和3'非编码区的序列分析发现有两个结构域受到了正向选择。对长城两侧的六种植物的居群遗传分化进行了分析,发现两侧的植物亚居群发生了显著的遗传分化,证明了长城在一定程度上阻断了两侧植物的基因流,或因其两侧的环境的微小差异造成了植物居群的变异。收集了全国约10个省份的30多个野生拟南芥居群,对其遗传多样性及分子系统树的研究表明,有一些居群可能很早就分布于中国,并在中国迅速扩张;对不同居群在逆境下的表达谱分析则发现明显的差异,进一步深入的研究正在进行中。

#### Research Description:

- 1 Systematic and evolutionary botany and plant molecular biolog
- 2 Studies on genetic diversity and origin of the natural Arabidopsis thaliana populations in China
- 3 Studies on function and evolution of certain plant gene families

Studies on the evolution of gene families such as those coding for CHS, trypsin inhibitor, etc. The studies have found that CHS genes in most plant families could be classified into two groups based on their base substitution rates. One group has fast rates and the other group has relatively low rates. It has also been found that the gymnosperm plants have few copies of CHS gene in a particular nuclear genome, but copy number varies greatly in the angiosperm plants. About 10 genes are found in the rice genome encoding Bowman Birk trypsin inhibitor. The phylogenetic analysis and sequence comparison of the 5' and 3' UTR showed that the genes with three-repeat structure evolved from the genes with two-repeat structure. Further analysis showed that the second repeat in the genes has been under the positive selection. The function of the 10 genes is under investigation now. Many factors can cause plant population to diverge. A recent study by this research team on the plant populations separated by the Great Wall of China has showed that the subpopulations along two sides of the Wall were significantly differentiated genetically. The research group has also collected about 30 natural populations of Arabidopsis thaliana from about 10 provinces of China, and the studies on the genetic diversity and phylogenetic trees revealed that most of the Chinese populations formed a monophyletic

group and their distribution in China may be resulted from one founder effect. The analysis on the transcription profiles of different populations under stress treatments showed significant differences among populations and it may be correlated with environmental factors to which they have been adapted. Further studies on the possible molecular mechanisms will be the main focus.

#### 代表性论文

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