

技术与方法

基于比较基因组学的玉米ESTs定位方法

张祖新^{1,2}, 张绍鹏^{1,2}, 郑用琰²

1. 河北农业大学农学院,保定 071001; 2. 华中农业大学作物遗传改良国家重点实验室,武汉 430070

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摘要

描述了以水稻基因组数据和玉米与水稻的比较遗传图谱为桥梁, 基于水稻和玉米间存在的标记和序列水平上的广泛的共线性, 对大量的玉米ESTs初步定位于玉米连锁群上新方法, 为对ESTs开展进一步的基因组学研究和基因克隆提供参考信息。对139条玉米ESTs的定位发现, 96条玉米ESTs (69%) 可在水稻基因组中找到同源序列, 77条ESTs (55%) 可使用该策略进行定位, 证实了该方法的可行性和有效性。

关键词 [表达序列标签 \(ESTs\)](#); [比较作图](#); [基因组](#); [分子标记](#)

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A Strategy Based on Comparative Genomics to Align ESTs of Maize

ZHANG Zu-Xin^{1,2}, ZHANG Shao-Peng^{1,2}, ZHENG Yong-Lian²

1. *College of Agronomy, Hebei Agricultural University, Hebei Baoding 071001, China;*
2. *National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Hubei Wuhan 430070, China*

Abstract

In this study, a new strategy to locate ESTs on maize linkage groups was described. In the strategy, the rice (*Oryza sativa* L.) genomic sequence database of was employed to locate maize EST on rice linkage groups, and then to locate on maize linkage group by comparative genetics mapping between rice and maize genome. The aligned ESTs information should available for further study on genomics and gene cloning. As an example, 139 ESTs of maize were assayed, and 96 maize ESTs (69%) were homologous with rice genomic sequence, 55% (77/139) ESTs were located on maize linkage groups based on the strategy, indicating that the locating approach of ESTs is feasible and available.

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Key words [expression sequence tags \(ESTs\)](#) [comparative mapping](#) [genome](#) [molecular marker](#)

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· 张祖新	
· 张绍鹏	
· 郑用琰	