技术与方法

几种全长cDNA文库构建方法比较

毛新国，景蕊莲，孔秀英，赵光耀，贾继增

中国农业科学院作物科学研究所，农作物基因资源与基因改良国家重大科学工程，农业部作物种质资源与生物技术重点开放实验室,北京100081

摘要　　全长cDNA文库是高效、大规模获得基因全序列信息的一条有效途径，尤其是对基因组庞大，近期内尚不能进行全基因组测序的生物来说，是一条开展功能基因组研究的重要途径。本文对几种全长cDNA文库的构建方法进行了概述，针对各种方法的原理及优缺点做了分析、比较，并结合本实验室的结果，重点介绍了Cap-trapper法在小麦全长cDNA文库中的应用及文库中全长基因比例判定方法。

关键词　　Oligo-cap法,Cap-jumping法,SMART法,全长cDNA文库,Cap-trapper法,Capture法

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Compare of Full-length cDNA Library Construction Methods

MAO Xin-Guo, JING Rui-Lian, KONG Xiu-Ying, ZHAO Guang-Yao, JIA Ji-Zeng

National Key Facility for Crop Gene Resources and Genetic Improvement, Key Laboratory of Crop Germplasm & Biotechnology/the Ministry of Agriculture, Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing 100081, China

Abstract

Full-length cDNA library is the cornerstone to find new genes in high-throughput manner, especially in huge genome organisms that cannot carry out whole genome sequencing. In this review, the authors compared the theories and characters of several cDNA construction methods, and introduced Cap-trapper method and standard to judge full-length cDNA in detail according to the utilization of this method in wheat full-length cDNA construction.

Key words　Capture method　Oligo-capping method　Cap-jumping method　SMART method　Capture method　Full-length cDNA library

通讯作者

贾继增

jzjia@mail.caas.net.cn

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