

生物技术·植物遗传育种

cDNA文库构建策略及其分析研究进展

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摘要 cDNA文库构建和筛选是基因克隆的重要方法之一, 它是目前发现新基因和研究基因功能的基本工具。从cDNA文库中可以筛选到目的基因, 并直接用于该基因的表达。经典 cDNA文库存在克隆的片段短等缺点, 而全长cDNA文库则能提供完整的mRNA信息, 从而克隆cDNA全长; 对文库进行均一化处理即均一化cDNA文库, 可以增加克隆低丰度mRNA的机会; 差减cDNA文库在研究生物体某一时期基因差异表达上具有重要的意义; 改进的固相cDNA很大程度上提高了建库的效率和质量。本文以阐述基本原理为主, 介绍几种近年来常用的cDNA构建的方法及其优缺点。

关键词 [cDNA文库](#) [cDNA全长](#) [基因克隆](#) [均一化cDNA文库](#) [差减cDNA文库](#) [固相cDNA文库](#) [快速扩增cDNA末端 \(RACE\)](#)

分类号

Advances of the Studies on Construction Strategy and Analysis of cDNA Library

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Abstract

cDNA library construction and screen is one of the important methods of gene cloning. Up to date, it is basic tool of finding new genes and researching gene function. Target genes can be selected from cDNA library, and used to analyze the expression of the genes. Cloned fragments from classical cDNA library is short. However, full-length cDNA library can provide the full information of mRNAs and their relevant gene structure. The normalized cDNA library can increase the opportunity of selecting the mRNA with low expression. Subtractive library has the important significance in researching gene differential expression of tissues at different periods. To some extent, the solid phase DNA library enhances the efficiency and the quality of constructed cDNA library. The paper mainly explains basic principles, several methods of cDNA library construction, and their advantages and disadvantages.

Key words

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