

## E和St基因组特异RAPD片在部分小麦族植物中的分布

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**摘要** 两个E基因组(包括Ee和Eb)特异RAPD片段和两个St基因组特异RAPD片段的序列分析表明, 4个片段均为新的DNA克隆片段。染色体原位杂交显示OPD-12 444为区域化连续高度重复序列, 而OPF-03 1296 (Eb特异)、OPB-08 525 (St特异)、OPN-01 817 (St特异)为弥散性高度重复序列。研究还显示: 大部分DNA高度重复序列在亲缘关系较近的小麦族植物基因组间是共享的, 差异可能主要是在重复次数及片段长度上, 而能否用RAPD技术扩增主要决定于某一基因组的这些重复序列中是否有与特定引物相匹配的区域。文中就这些重复序列在小麦远缘杂交后代外源遗传物质检测、多倍体物种染色体组组成研究中的潜在价值进行了讨论。

**关键词** [基因组](#) [RAPD标记](#) [克隆](#) [原位杂交](#) [Southern杂交](#)

分类号

## Distribution of E-and St-Specific RAPD Fragments in Few Genomes of Triticeae

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### Abstract

Two E genome-(including E<sup>e</sup> and E<sup>b</sup>) and two St-genome-specific RAPD markers were successfully cloned. Sequencing data indicated that the four DNA fragments were reported for the first time. Chromosome fluorescent in situ hybridization (FISH) showed that OPD-12<sub>444</sub> (E-specific) was a highly tandem repeat. OPF-03<sub>1296</sub> (E<sup>b</sup>-specific), OPB-08<sub>525</sub> (St-specific), and OPN-01<sub>817</sub> (St-specific) were highly dispersed repetitive sequences. The FISH and Southern hybridization of genomic DNA also revealed that all of the four highly repetitive sequences were shared among relatively closer genomes of triticeae. The difference was mainly in the fragment length and the copy number. Whether a genome can amplify a specific sequence via RAPD is mainly dependent on if there are priming sites at both ends of this sequence in the genome. We also discussed the potentiality of these highly repetitive DNA fragments in detection of alien chromatin in wheat and determination of genome constitution of polyploid triticeae species.

**Key words** [Genome RAPD marker](#) [Clone](#) [FISH](#) [Southern hybridization](#)

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