研究论文

自身基因组原位杂交揭示植物基因组重复 DNA沿染色体的分布自身基因组原位杂交揭 示植物基因组重复DNA沿染色体的分布

佘朝文 $^{1,~2}$,刘静宇 $^{2,~3}$,刁 英 $^{2,~4}$,胡中立 2 ,宋运淳 2

- 1. 怀化学院生物系, 怀化 418008;
- 2. 武汉大学生命科学学院植物发育生物学教育部重点实验室, 武汉 430072;
- 3. 华中科技大学生命科学与技术学院人类基因组研究中心,武汉 430074;
- 4. 重庆文理学院生命科学系, 重庆 400068
- 收稿日期 2006-6-5 修回日期 2006-7-9 网络版发布日期 2007-4-17 接受日期

摘要

重复DNA沿染色体的分布是认识植物基因组的组织和进化的要素之一。本 研究采用一种改良的基因组原位杂交程序,对基因组大小和重复DNA数量 不同的6种植物进行了自身基因组原位杂交(self-genomic in situ hybridization, self-GISH)。在所有供试物种的染色体都观察到荧光 标记探针DNA的不均匀分布。杂交信号图型在物种间有明显的差异,并与 基因组的大小相关。小基因组拟南芥的染色体几乎只有近着丝粒区和核 仁组织区被标记。基因组相对较小的水稻、高粱、甘蓝的杂交信号分散 分布在染色体的全长,但在近着丝粒区或近端区以及某些异染色质臂的 分布明显占优势。大基因组的玉米和大麦的所有染色体都被密集地标 记,并在染色体全长显示出强标记区与弱标记或不标记区的交替排列。 此外,甘蓝染色体的所有近着丝粒区和核仁组织区、大麦染色体的所有 近着丝粒区和某些臂中间区还显示了增强的信号带。大麦增强的信号带 带型与其N-带带型一致。水稻自身基因组原位杂交图型与水稻Cot-1 DNA 在水稻染色体上的荧光原位杂交图型基本一致。研究结果表明,自身基 因组原位杂交信号实际上反映了基因组重复DNA序列对染色体的杂交,因 而自身基因组原位杂交技术是显示植物基因组中重复DNA聚集区在染色体 上的分布以及与重复DNA相关联的染色质分化的有效方法。

关键词 <u>自身基因组原位杂交;植物基因组;重复DNA;染色质分化;基因组组织</u>

分类号

The Distribution of Repetitive DNAs Along Chromosomes in Plants Revealed by Selfgenomic in situ Hybridization

Chaowen She^{1, 2,①}, Jingyu Liu^{2, 3}, Ying Diao^{2,4}, Zhongli Hu², Yunchun Song^{2,①}

- 1. Department of Biology, Huaihua University, Huaihua 418008, China:
- 2. Key Laboratory of MOE for Plant Developmental Biology, Wuhan University, Wuhan 430072, China;
- 3. Human Genome Research Center and College of Life Science and Technology, Huazhong University of Science and Technology, Wuhan 430074, China;
- 4. Department of Life sciences, Chongqing University of Arts and Sciences, Chongqing 400068, China

扩展功能

本文信息

- ▶ Supporting info
- ▶ <u>PDF</u>(340KB)
- ▶[HTML全文](317KB)
- ▶参考文献

服务与反馈

- ▶把本文推荐给朋友
- ▶加入我的书架
- ▶加入引用管理器
- ▶复制索引
- Email Alert
- ▶文章反馈
- ▶浏览反馈信息

相关信息

- ▶ 本刊中 包含
- "自身基因组原位杂交;植物基因组;重复DNA;染色质分化;基因组组织"的相关文章
- ▶本文作者相关文章
- · 佘朝文
- 刘静宇
- <u>刁 英</u>
 - 胡中立
 - 宋运淳

Abstract

<P> The distribution of repetitive DNAs along chromosomes is one of the crucial elements for understanding the organization and the evolution of plant genomes. Using a modified genomic in situ hybridization (GISH) procedure, fluorescence in situ hybridization (FISH) with genomic DNA to their own chromosomes (called self-genomic in situ hybridization, self-GISH) was carried out in six selected plant species with different genome size and amount of repetitive DNA. Nonuniform distribution of the fluorescent labeled probe DNA was observed on the chromosomes of all the species that were tested. The signal patterns varied among species and were related to the genome size. The chromosomes of the small Arabidopsis genome were labeled almost only in the pericentromeric regions and the nucleolus organizer regions (NORs). The signals in the relatively small genomes, rice, sorghum, and Brassica oleracea var. capitata L., were dispersed along the chromosome lengths, with a predominant distribution in the pericentromeric or proximal regions and some heterochromatic arms. All chromosomes of the large genomes, maize and barley, were densely labeled with strongly labeled regions and weakly labeled or unlabeled regions being arranged alternatively throughout the lengths. In addition, enhanced signal bands were shown in all pericentromeres and the NORs in B. oleracea var. capitata, and in all pericentromeric regions and certain intercalary sites in barley. The enhanced signal band pattern in barley was found consistent with the N-banding pattern of this species. The GISH with self-genomic DNA was compared with FISH with Cot-1 DNA in rice, and their signal patterns are found to be basically consistent. Our results showed that the self-GISH signals actually reflected the hybridization of genomic repetitive DNAs to the chromosomes, thus the self-GISH technique would be useful for revealing the distribution of the regions where repetitive DNAs concentrate along chromosomes and some chromatin differentiation associated with repetitive DNAs in plants. </P>

Key words <u>self-genomic in situ hybridization (self-GISH)</u> <u>plant genome repetitive DNA chromatin differentiation genome organization</u>

DOI: