
Plant Molecular Biology Reporter **22:** 85–86, March 2004

Publish by Abstract

An Improved Enrichment Procedure to Develop Multiple Repeat Classes of Cotton Microsatellite Markers

SIVA P. KUMPATLA*, MARILYN K. MANLEY, ERIN C. HORNE, MANJU GUPTA and STEVEN A. THOMPSON

Department of Trait Genetics and Technologies, Dow AgroSciences LLC, 9330 Zionsville Road, Indianapolis, IN 46268

Abstract. The availability of a large number of molecular markers is a prerequisite, especially in cotton, for identifying a sufficient number of informative markers for mapping and genetic analysis. Despite the global importance of the cotton crop, few informative microsatellite markers are available, primarily because of the cost associated with their development. This report describes an improved and cost-effective strategy for developing microsatellite markers. Genomic DNA was randomly sheared with nitrogen gas to obtain unbiased representation of the genome, and the fragments containing microsatellites were captured by using biotinylated oligos and streptavidin-based recovery. Six libraries enriched for 14 microsatellite motifs were constructed and screened. Nearly 4900 simple sequence repeat (SSR)–containing sequences were identified, leading to the development of more than 1200 markers in a small amount of time.

Full text†: This article, in detail, is available only in the electronic version of the *Plant Molecular Biology Reporter.*

Contents: This article contains Introduction, Materials and Methods, Results and Discussion, 16 references, and 3 illustrations.

Illustrations:

Table 1. Repeat motif composition, the number of clones generated for the simple sequence repeat (SSR)–enriched libraries, and the number of putative SSR-containing clones obtained from the screening of high-density replica filters of the libraries.

*Author for correspondence. Present address: Department of Trait Genetics and Technologies, Building 306/C2, Dow AgroSciences LLC, 9330 Zionsville Road, Indianapolis, IN 46268; e-mail: spkumpatla@dow.com; fax: 317-337-5989; ph: 317-337-3422.

†Editor's note: Although the scientific content of this article has been reviewed, the full-text Web publication has not been edited in detail.

Figure 1. Outline of the strategy used for the selective capture and cloning of cotton genomic DNA fragments containing SSRs.

Figure 2. Nebulization of genomic DNA to generate randomly sheared fragments in the desired size range.

Key words: biotinylated oligos, cotton, enriched libraries, microsatellites, nebulization, polymorphic