Agricultural Sciences in China
2008, 7(11): 1290-1297

Available online at www.sciencedirect.com
ScienceDirect

November 2008

Genetic Effect on Yield and Fiber Quality Traits of 16 Chromosome Substitution Lines in Upland Cotton

LUAN Ming-bao, GUO Xiang-mo, ZHANG Yong-shan and YAO Jin-bo

Key Laboratory of Cotton Germplasm Improvement, Ministey of Agriculture/Cotton Research Institute, Chinese Academy of Agricultural Sciences (CAAS), Anyang 455000, P.R.China

Abstract

Evaluation of the genetic effect on yield and fiber quality can provide useful information on cotton breeding. Sixteen CSB lines and TM-1 introduced from USDA/ARS were used as male and top-crossed with three elite cultivars and the 51 F_1 hybrids, 16 CSB lines, TM-1, and 3 elite cultivars were planted at the Cotton Research Institute of CAAS, Anyang, Henan Province and Xiajin, Shandong Province, China. The yield traits and fiber quality data were obtained and additive and dominance effect on each trait were measured by AD model. Boll weight takes the largest additive proration, whereas boll number takes the least additive proration. The largest and the least dominant proration for lint yield and boll weight were measured, respectively. Fiber length has the additive and dominance effect, and dominance effect was slightly more than additive effect. Larger additive and no dominance effect on uniformity, micronaire, and fiber strength were measured. Significantly, positive additive effect on boll weight of CSB06 and CSB12Sh was observed. CSB14Sh and CSB01 have significantly positive additive effect on 4 and 3 traits of fiber quality, respectively. CSB01 has the greatest dominant effect on lint yield among CSB lines. The dominant effect on fiber length of CSB lines showed positive. It is beneficial to use CSB06 and CSB12Sh as parents to improve boll size, to use CSB14Sh and CSB01 as parents to improve fiber quality. As for hybrid cotton breeding, it is reasonable using CSB01 to improve lint yield traits, and using CSB01, CSB11Sh, and CSB06 to improve fiber length.

Key words: chromosome substitution lines in upland cotton, additive genetic effect, dominance genetic effect, AD model

INTRODUCTION

Germplasm is the basis of plant breeding, and the creation of superior variety relied on the abundant germplasm. Evaluation of the introduced elite germplasm can provide important information for germplasm utilization. There have been many reports concerning the genetic research on the yield and fiber quality of upland cotton. The significant additive effect can be measured in traits related to yield (Fan *et al*. 2003; Guo and Zou 1994; Ji *et al*. 1996; Wu *et al*. 1985), but some results reviewed that dominative effect or combining effect of additive and dominative control yield trait (Han and Liu 2002; Liu and Zhu 2007; Sun *et al*. 2004; Xing *et al*. 2007). According to the published literature, fiber length, strength, fineness, and uniformity usually belong to quantity traits and controlled by tiny polygene and mainly controlled by additive effect (Cao and Kang 2006; Han *et al*. 2002; Yuan *et al*. 2002a, b; Yuan *et al*. 2005). Whereas there are important effects belonging to predominant effect and epistasis in fiber length, strength, and fineness according to some experiments (Li *et al*. 2000; Lin and Zhao 1988). It is an important path to improve upland

This paper is translated from its Chinese version in *Scientia Agricultura Sinica.*

LUAN Ming-bao, E-mail: luanmingbao2002@126.com; Correspondence GUO Xiang-mo, E-mail:gxm214@126.com

cotton through special chromosomes of Sea Island cotton, substitution lines, in which a pair of chromosomes of upland cotton is substituted by the corresponding chromosome of Sea Island cotton. The path can conquer the malpractice of long separation generations and polarizing toward parents. Some reports reviewed that some traits were in association with special chromosomes (Kohel *et al.*1977; Ma and Kohel 1983; Ren and Zhang 2001; Saha and Wu 2004). Kohel *et al.* (1977), Ma and Kohel (1983), and Ren and Zhang (2001) evaluated 2, 6, and 7 chromosome substitution lines, respectively. With the increase of number of chromosome substitution line, Saha and Wu (2004) evaluated 13 CSB lines to determine main trait associated with substituted chromosome. But there are few reports related to genetic analysis about CSB lines. Saha *et al.* (2006), Jenkins *et al.* (2006, 2007), and Jia *et al.* (2006) analyzed genetic effects for yield and fiber quality traits of 14, 13, and 7 CSB lines using traditional AD model, respectively. They only used a few CSB lines in their research. Seventeen CSB lines were developed (Stelly and Saha 2005). Sixteen CSB lines introduced from USDA/ARS were used in this research. Compared with the 14 CSB lines that were used before, CSB01, CSB11Sh, CSB12Sh are new, and CSB25 is absent. In the research of Saha *et al.* (2006) and Jenkins *et al.* (2006), some important indexes related to yield and fiber quality, such as boll number per plant and fiber uniformity, were not analyzed. Sixteen CSB lines and TM-1 introduced from USDA/ARS were used as male and top-crossed with three elite cultivars in this research, and 51 F_1 hybrids, 16 CSB lines, TM-1, as well as three elite cultivars, were planted at the Cotton Research Institute of CAAS, Anyang, Henan Province, and Xiajin, Shandong Province, China. The yield traits and fiber quality data were obtained and genetic effects on each trait were measured by AD model. This research evaluated the value of each CSB lines to provide useful information in breeding program.

MATERIALS AND METHODS

Materials

Sixteen CSB lines and their common parent TM-1, introduced from USDA/ARS, were used as male parents and top-crossed with 3 elite cultivars, Zhong 41, Zhong 43, and SG506. The crosses were conducted at the Cotton Research Institute of CAAS, Anyang, Henan Province, China, in 2005. Sixteen CSB lines were CSB01, CSB02, CSB04, CSB05Sh, CSB06, CSB07, CSB11Sh, CSB12Sh, CSB14Sh, CSB15Sh, CSB16, CSB17, CSB18, CSB22Sh, CSB22Lo, and CSB26Lo. Each of them had a corresponding pair of chromosomes (or chromosome arms) of *G. barbadanse* L., 3-79 in *G. hirsutum* L. inbred TM-1 background. For example, CSB01 means chromosome 1 of TM-1 was replaced by the chromosome 1 of 3-79, CSB05Sh means the short arm of chromosome 5 was replaced by the same arm of 3-79, and CSB22Lo means the long arm of chromosome 22 was replaced by the same arm of 3-79. Thus, 51 F_1 and 20 parents were used in the test. Development of each alien species chromosome substitution lines are as follows: (1) to cross monosome lines with TM-1 and backcross for 5 generations to get TM-1 monosome, (2) to cross TM-1 with 3-79, and backcrossed 6-7 generations to get purified materials, and (3) to self-cross monosome in order to get CSB lines.

Methods

Fifty-one F_1 hybrids, 16 CSB lines, TM-1, and 3 upland cotton cultivars were planted at the Cotton Research Institute of CAAS, Anyang, Henan Province, China, and Xiajin, Shandong Province, China, in 2006. The experiment design was randomized block design with 3 replications. Each plot had 3 rows with 6 m length and 0.8 m apart. Eighteen plants were cultivated in each row and the standard cultural practices were followed in each environment.

Boll number per plant, seed cotton yield, and lint cotton yield per plant were investigated. The 20-boll sample was hand harvested in each plot. The samples were ginned on a 10-saw laboratory gining machine. Fiber length, strength, uniformity, micronaire value, and elongation were measured in the Cotton Quality Inspection, Supervision, and Test Center of Agriculture Ministry of China.

Statistical methods

AD model provided by Zhu (1992) was used for the