GENETIC ANALYSIS OF YIELD, FIBER QUALITY AND ABOITIC STRESS TOLERANCE IN PIMA COTTON

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Abstract

As Pima cotton is grown in the arid southwest and west United States, abiotic stress is one of the major production problems facing sustainable agriculture. The most practical solution to the problem is to develop drought and salt tolerance cultivars for these areas. However, information on yield, fiber quality and abiotic stress tolerance and associated molecular markers in Pima cotton is currently lacking. In this study, 165 recombinant inbred lines (RILs) from an intraspecific cross between Pima S-6 and a Sea-Island cotton germplasm were developed and have been tested in both the field and greenhouse conditions in 2014 and 2015. The main objectives of this study were to identify the most promising lines for salt and drought tolerance with high yield potential and good fiber quality, and to identify markers associated with yield, fiber quality, and abiotic stress tolerance. The field trials were conducted in two locations (Las Cruces, NM and Lubbock, TX) and two years for yield and fiber quality using a randomized complete block design with two replications. Before mechanical harvests for yield, boll samples were collected from each field plot to determine yield component traits such as boll weight, lint percentage, lint index, seed index, and fiber quality traits including fiber length, strength and micronaire. The same RIL population was tested in the greenhouse for osmotic and salt stress tolerance in three replicated tests in a hydroponic system in 2015. The osmotic stress and control treatments were conducted using 10% of polyethylene glycol (PEG) and water, respectively, while the salt and control treatments were conducted using 200 mM of NaCl and water, respectively. The treatments started when at the second true-leaf seedling stage and lasted for three weeks. The growth traits measured were chlorophyll readings, plant height, fresh shoot and root weights. Three main statistical analyses were performed to analyze the data including analysis of variance (ANOVA) using SAS, linkage mapping using the JoinMap software and QTL mapping using QTL ICLMapping. The ANOVA showed that all the source of variances were significant for all the traits including fiber quality, agronomic traits, osmotic and salt stress tolerance except for genotype by treatment interactions under salt stress for chlorophyll readings, plant height and fresh root weight. The result indicates that genotypes perform in a similar trend between the control and salt treatment conditions. Thus, control plants are not needed when evaluating different genotypes for salt tolerance for this RIL population. Heritability estimates were moderate for agronomic traits, fiber quality and abiotic stress tolerance. A total of 114 polymorphic simple sequence repeat (SSR) markers were placed onto 17 chromosomes. A total of 31 QTL were detected including 16 QTL for agronomic traits, 8 for fiber quality traits and 7 for abiotic stress tolerance. Importantly, 15 common QTL were detected, indicating that the field and greenhouse tests are consistent even though genotypes by environment interactions were detected. For example, two common QTL were detected for fresh shoot weight on chromosome 12 under PEG and NaCl treatments. These common and consistent QTL will be useful for marker-assisted selection and the understanding of the genetic basis for drought and salt tolerance.