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7. Title

Improving Cotton through Genetic Research

12. Investigator Name(s) (Last Name and Initials)

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40. Period Covered (mo/da/year): 01/01/2011 TO 12/31/2011

Outputs:

A quick and efficient and nondestructive method for identifying reniform nematode egg masses on cotton roots was developed. The importance of additive genetic variance on improving cotton fiber traits was confirmed and demonstrated to cotton breeders. A mixed model analytical framework was developed to provide robust marker-trait association analyses. Data on regional performance of elite cotton genotypes was generated and shared among the cotton industry. One refereed journal article and five conference presentations were used to disseminate research results.

Outcomes/Impacts:

A quick and simple greenhouse screening method was developed and optimized for visual indexing of reniform (Rotylenchulus reniformis Linford & Oliveria) nematode egg masses on cotton roots using Trypan blue. The method works as a rapid screening tool and is being adopted by other researchers. Influential cotton lines are those that contributed a larger proportion of genes to modern cotton cultivars than other lines. Ten influential cultivars from 16 cotton breeding programs were identified based on pedigree analysis of 260 cultivars released from 1970-90. Diallel analysis across two environments calculated highly significant GCA mean squares for bolls/plant, boll weight, lint percentage, seed index, and lint index, indicating importance of additive gene effects. While SCA effects were highly significant for a few traits, the ratios of mean squares determined that additive effects were more important in trait inheritance than non-additive effects. Association mapping principles were applied to upland cotton genotypes to examine population structure and marker trait associations. A set of 232 genotypes were genotyped using AFLP markers generating 568 polymorphic markers. Population structure analysis indicated the existence of six subpopulations, in agreement with geographical origin. The mixed and mixed-multiple regression (MMR) models identified significant markers for lint yield and fiber traits. Out of an initial 568 AFLP markers, 255 were detected using the traditional Mixed Linear Model approach. Inclusion of MMR improved the model, reducing the significant markers to 111. MMR-based epistatic interactions revealed 49 QTLs responsible for eight fiber traits. Mixed MMR models reduced Type I error. This sequential validation of marker is an improved method for reducing false positives and identifying truly significant associations. Fifty seven cross populations was developed to meet program goals. In early segregating populations (F2-F3) developed in prior years, modified bulks were based upon superior agronomic phenotype and are being evaluated for their fiber properties. Individual plant selections were made in the F4 generation. Seed increases of 139 lines previously selected were done as a prelude to entry into the yield testing program. The yield testing program evaluated 136 different experimental lines across six different tests at four locations. Extremely dry and hot weather after planting limited data collection, particularly at two locations. Yields were uniformly disappointing on an absolute basis. On a relative basis in comparison to the standards, across all yield trials at both locations, an average of 13.6% of experimental entries were superior to the best standard in their respective test.

Publications:

Lu, H. and G.O. Myers. 2011. Combining abilities and inheritance of yield components in influential Upland cotton varieties. Aust. J. Crop Sci. 5(4):384-390.

Myers, G.O., J.E. Jones, J.I. Dickson, and C. Overstreet. 2011. Egg mass indexing as a tool for selecting reniform nematode resistance in cotton. In: Proc. Beltwide Cotton Conf., Atlanta, GA. 4-7 Jan. 2011. Natl. Cotton Counc. Am., Memphis, TN.

Badigannavar, A. and G.O. Myers. 2011. Population structure and association mapping of fiber traits in upland cotton (Gossypium hirsutum L.). World Cotton Research Conference V. Nov. 7-11, 2011. Mumbai, India.

Participants:

Gerald Myers (PI), Bikash Bhandari, David Caldwell, Patrick Colyer, Ivan Dickson, LSU AgCenter; Ted Wallace, Mississippi State; C. Wayne Smith, David Stelly, Steve Hague, Peggy Thaxton, Texas A&M; Vasu Karuparthy, Peng Chee, UGA; Michael Gore, Jack McCarty, Todd Campbell, Mauricio Ulloa, Richard Percy, USDA-ARS; Don Jones, ASU; David Weaver, Auburn; Freddie Bourland, University of Arkansas; Jinfa Zhang, NMSU; Jane Deaver; Cotton Incorporated (Partner organization).

Target Audiences:

Graduate students in plant breeding and genetics (classroom, laboratory, and practicum), cotton industry.

Project Modifications:

Nothing significant to report during this reporting period.

Approved (Signature)	Title	Date