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STUDY ON INHERITANCE OF EARLINESS AND IT'S RELATIVE TRAITS OF SHORT-SEASON COTTON AND QTLS MAPPING

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Abstract

Genetic effect and its environment interaction were studied for short season cotton of Upland cotton (*Gossypium hirsutum* L.) by Mixed linear model approaches using a 9×9 incomplete dialelle crosses in three ecological environments. The results reviewed that the hereditability in narrow sense(h^2_N) for earliness traits were low, only 16.1%,and it's environment interaction was significant, about 17.5%, especially first fruiting branch node and squaring with the lowest hereditability and the highest environment interaction, but growth date, plant height and flowering with higher hereditability and lower environment interaction when same experiment materials planted in different test places were affected. The h^2_N for yield traits were 20.1%, and it's environment interaction was low, about 7.4%, Lint percent, boll weight and seed index are three most important traits in short season cotton yield breeding because of their relative higher h^2_N and lower environment interaction. Interaction between genetic effect and environment for five fiber qualities were significant or mighty significant. The h^2_N of fiber qualities were 28.6%, and its environment interaction was about 6.9%. The average h^2_N for earliness of short season cotton in Anyang, Yuncheng and Shihezi were 46.0%, 10.9%, 12.3% respectively. Average h^2_N of cotton plant properties including earliness, yield and fiber quality: Anyang>Yuncheng > Shihezi. The results explained and developed the different views of the former about the hereditability of the first fruiting branch node and squaring.

Primary contradiction among earliness, yield and fiber quality were found by the canonical correlation analysis for three main short season cotton breeding environments, respectively. In order to solve the main problem of breeding and realize the objective to earliness, high yield and fine fiber quality, corresponding breeding strategies were brought forward. For Anyang, the key was that the period from sowing to squaring should be prolonged properly and concentrative boll opening should be selected so that pre-frost lint yield would be increased. At the same time, fiber strength and micronaire would be improved with paying attention to the selection of high lint index. For Yuncheng, the key was to make the period from sowing to flowering long properly for improving the fiber length of short season cotton. But bolls growth must be rapidly during the period of flowering to boll opening. In addition, breeding materials with high lint percent should be selected in order to keep fine fiber strength and micronaire. For Shihezi, the key was to shorten the period from sowing to flowering properly to increase fiber micronaire and maturity. At the same time, the selection of lines with short stage from flowering to boll opening should be intensified for high pre-frost lint yield. But the increase of fiber micronaire went against fiber length and strength. This problem could be solved by high seed index selection. The results mentioned above were expected to offering scientific evidence to adjust the current selection strategies of short season cotton in three main areas.

The genetic analysis of short season cotton earliness and its relative traits by mixed major gene and poly gene model showed that earliness and its relative traits were not only controlled by major gene generally, but also modified by minor effect polygene. There was one major gene at least expressing at different growth and development stages. Major genes controlling cotton plant traits were different in number, effect, direction and hereditability. Except of the days from sowing to squaring and plant height, genetic effect and hereditability of major gene, 30.23%~66.79%, was higher than that of polygene, 2.83%~35.07%. Plant traits were categorized to three classes: the first class traits were dominated by major gene with little genetic effect of polygene, including days from sowing to flowering, days from sowing to boll opening, lint percent, days from squaring to flowering, days from flowering to boll opening and plant bolls. The hereditability of major gene and polygene were about 36.85%~66.79% and 2.83%~12.64%, respectively. The second class traits which major gene effect was important but polygene genetic effect couldn't be neglected, including first fruiting branch node, boll weight, fiber length, fiber strength, micronaire and cotyledon size. The hereditability of major gene and polygene was about 30.23%~63.33% and 21.78%~28.17%, respectively. The third class traits were dominated by polygene, major gene genetic effect was too little to be examined, including days of from sowing to squaring and plant height. Three fit selection ways and means for different classes of traits were put forward in accordance with their hereditability of major gene and polygene.

CCRI36, a short season cotton variety, and TM-1 were used to create 207 F2 segregating population in Anyang. The two parents were used to screen 73 polymorphism markers from 518 pair SSR primers, 1200 RAPD primers and 153 pair SRAP primers. The 207 F2 populations were tagged and mapped with 73 polymorphism markers, including 25 SSR, 35 RAPD and 13 SRAP markers. 43 of the informative loci were used in linkage map construction and were assigned into 5 linkage groups. The linkage map was composed of 9 SSR loci, 28 RAPD loci and 6 SRAP loci. The total length is about 1174.0cM, covering 23.48% of the whole cotton genome. The linkage distance ranged from 11.8cM to 48.9cM. The marker number associated with particular group was from 2 to 23 while 30 loci were not linked to the map. 7.16%~39.73% phenotype variance could be explained in F2 generation, 12 QTL's were examined, among which 8 QTL's were clustered on the first linkage group from this paper. More than 30% phenotype variance in F2 segregation population was explained by 3 QTL’s relative to the days from sowing to boll opening, the days from sowing to flowering and percent of pre-frost lint respectively. The linkage map construction for study on short season cotton, QTL’s of earliness mapping and clustering haven’t been reported before. The results are valuable to further research for earliness MAS of short season cotton