PROQUEST

KOMODITAS: KAPAS

PLANT PROPOGATION (2 jdl)

Somatic embryogenesis and plant regeneration in two wild cotton species belong to G genome/ Shu-Feng Yan, Qiao Zhang, Jing-Er Wang, Yu-Qiang Sun, M K Daud, Shui-Jin Zhu.
In Vitro Cellular & Developmental Biology.: Plant Columbia:Jun 2010. Vol. 46, Iss. 3, p. 298-305
Abstract:

The present work describes the plant regeneration via somatic embryogenesis in two wild cotton species belonging to G genome: Gossypium nelsonii Fryx and Gossypium australe F Muell. The role of plant hormones and carbohydrates was also evaluated for somatic embryogenesis and somatic embryo development. Normal plants were obtained from G. nelsonii Fryx; abnormal plants and somatic embryos were obtained from G. australe F Muell. The best medium for callus induction for these G genome wild cotton species was MSB^sub 5^ supplemented with 0.1 mg L^sup -1^ KT and 0.1 mg L^sup -1^ 2,4-D. For embryogenic callus proliferation, the best medium used was MSB^sup 5^ supplemented with 0.2 mg L^sup -1^ KT and 0.5 mg L^sup -1^ IBA. The medium MSB^sup 5^ supplemented with 0.15 mg L^sup -1^ KT and 0.5 mg L^sup -1^ NAA was used successfully for root initiation and plant growth. In addition, adding CuSO^sub 4^ and AgNO^sub 3^ in the callus-inducing and proliferation medium resulted in a number of somatic embryos. Glucose and maltose, the carbon sources in somatic culture, were used for callus induction, but maltose worked even better than glucose for proliferation of embryogenic callus and development of somatic embryos. [PUBLICATION ABSTRACT]

Imazamox Tolerance in Mutation-Derived Lines of Upland Cotton/ Efrem Bechere, Dick L Auld, Peter A Dotray, Lyndell V Gilbert, Hirut Kebede.
Crop Science. Madison:Sep/Oct 2009. Vol. 49, Iss. 5, p. 1586-1592
Abstract:

Induction of genes conferring herbicide resistance by mutagenesis could facilitate use of imidazolinone herbicides in upland cotton (Gossypium hirsutum L.). In 1997 and 1998, seeds of eight High Plains cotton cultivars were treated with 2.45% v/v ethyl methanesulfonate. The resulting M^sub 3^ and M^sub 4^ generations were sprayed with imazethapyr, and the M^sub 5^ and M^sub 6^ generations were sprayed with imazamox. Four stable M^sub 6^ to M^sub 7^ lines with tolerance to imazamox were identified in 2004. During 2005 and 2006, tolerant mutants and their nonmutated parents were treated at the four-leaf stage with topical applications of imazamox applied at five rates (0, 88, 175, 350, and 700 g a.i. ha^sup -1^). Elevated levels of tolerance to imazamox were observed in all mutants. Imazamox did not impact fiber length. Preliminary investigation indicated that tolerance to imazamox was controlled by a partially dominant single gene. An allelism test revealed that the tolerance genes in the four mutants are either alleles in the same locus or are very tightly linked. [PUBLICATION ABSTRACT]

PLANT GENETICS AND BREEDING (28 jdl)

Evaluation of a Heterogeneous Population of Cotton (Gossypium hirsutum L.) Developed with Recurrent Mass Selection in an Ultradense Population/ S Hague, C W Smith.
Crop Science. Madison:Mar/Apr 2011. Vol. 51, Iss. 2, p. 579-584 (6 pp.)
Abstract:

The pedigreed system is commonly used to develop improved genotypes of upland cotton (Gossypium hirsutum L.); however, this system can be resource intensive compared to mass selection methods. A project was initiated in 1995 to develop improved germplasm using recurrent mass selection in an ultradense plant population configuration. A composite population (CP) resulting from six cycles of selection was compared to two high-performing cultivars at three plant population densities (203,858 plants ha^sup -1^, 101,929 plants ha^sup -1^, and 33, 975 plants ha^sup -1^). Traits of interest included lint yield, plant morphology, and fiber quality. Genotype had a significant effect on lint yield and fiber qualities. Population densities affected plant morphology. Lint yield potential of the CP was not competitive against cultivars at any of the three population densities. Fiber traits generally were unaffected by plant density. The CP was earlier maturing and plant height remained more constant across population densities in comparison to the two check cultivars. This type of recurrent mass selection system may be more effective if initial breeding lines with a high percentage of fixed alleles make up the initial population. The existing CP population may still have value as a source of individual plants with enhanced stress tolerance. [PUBLICATION ABSTRACT]

Germplasm Potential for Continuing Improvement of Fiber Quality in Upland Cotton: Combining Ability for Lint Yield and Fiber Quality/ Linghe Zeng, William R Meredith Jr, Deborah L Boykin.
Crop Science. Madison:Jan/Feb 2011. Vol. 51, Iss. 1, p. 60-68 (9 pp.)
Abstract:

Exotic germplasm, that is, germplasm without commercial applicability, can broaden the genetic base in upland cotton (Gossypium hirsutum L.). The objectives of this study were to determine combining ability and identify parents from exotic germplasm for breeding. Twelve regionally adapted exotic germplasm lines were crossed with one cultivar and three elite germplasm lines in a North Carolina Design II scheme. The 48 F^sub 2^ hybrids were evaluated at two locations with 4 and 3 replicates each in 2008 and 2009, respectively. General combining ability (GCA) effects were significant (p ≤ 0.001) for lint yield and all fiber properties. General combining ability effects were more important than specific combining ability (SCA) effects for most traits. Significant (p ≤ 0.05) favorable GCA effects were detected in all exotic germplasm parents for different fiber properties. Positive GCA effects for lint yield and favorable GCA effects for at least one fiber property were detected in some exotic parents: SP156 and SP224 for lint yield and strength; SP192, SP205, and JC65 for lint yield, micronaire, and elongation; and SP192 and SP224 for lint yield and short fiber content and fineness, respectively. Significant high parent heterosis (HPH) for lint yield was detected in F^sub 2^ hybrids of FM832 × SP205 (14%) and MD15 × SP205 (26%). These results provide evidence for the potential of these germplasm lines in breeding for continuing improvement of lint yield and fiber quality. [PUBLICATION ABSTRACT]

Genetic detection of node of first fruiting branch in crosses of a cultivar with two exotic accessions of upland cotton/ Yufang Guo, Jack C McCarty, Johnie N Jenkins, Chuanfu An, Sukumar Saha.

Euphytica. Dordrecht:Apr 2009. Vol. 166, Iss. 3, p. 317-329

Abstract:

Flowering time has biological and agricultural significance for crops. In Upland cotton (Gossypium hirsutum L.), photoperiodic sensitivity is a major obstacle in the utilization of primitive accessions in breeding programs. Quantitative trait loci (QTLs) analysis was conducted in two F2 populations from the crosses between a day-neutral cultivar Deltapine 61 (DPL61) and two photoperiod sensitive G. hirsutum accessions (T1107 and T1354). Node of first fruiting branch (NFB) was used to measure relative time of flowering. Different flowering time genetic patterns were observed in the two populations. Two QTLs were found across five scoring dates, accounting 28.5 (qNFB-c21-1) and 15.9% (qNFB-c25-1) of the phenotypic variation at the last scoring date in Pop. 1107 (DPL61 by T1107); whereas, one major QTL (qNFB-c25-1) can be detected across five scoring dates, explained 63.5% of the phenotypic variation at the last scoring date in Pop. 1354 (DPL61 by T1354). QTLs with minor effects appeared at various scoring date(s), indicating their roles in regulating flowering at a lower or higher node number. Genetic segregation analysis and QTL mapping results provide further information on the mechanisms of cotton photoperiodic sensitivity. [PUBLICATION ABSTRACT]

Heterotic Effects in Topcrosses of Modern and Obsolete Cotton Cultivars/ B T Campbell, D T Bowman, D B Weaver.

Crop Science. Madison:Mar/Apr 2008. Vol. 48, Iss. 2, p. 593-600 (8 pp.)

Abstract:

Historically, reselection, pedigree, and massselection breeding methods have been used, to develop open-pollinated cultivars of upland cotton (Gossypium hirsutum L.). As a result, modern cotton cultivars should have accumulated additive genetic effects with time, while also possessing fewer nonadditive gene effects than obsolete cultivars. A topcross test was conducted to compare the heterotic effects of obsolete and modern cultivars for yield, yield components, and fiber quality. Significant differences were detected between heterosis values for the modern and obsolete cultivar groups for seed cotton yield, lint yield, lint percentage, and boll weight. No significant heterotic effects were detected for fiber quality. The obsolete group of cultivars showed average lint yield heterosis values of 34% compared with 23% for the modern cultivars. Both cultivar groups displayed significant, but similar heterosis values for the number of bolls per square meter (17 and 15%, respectively). The major yield component associated with lint yield heterosis for both groups was bolls per square meter, although boll weight heteror sis also contributed to lint yield heterosis for the obsolete cultivars. Although modern cultivars produced considerable heterotic effects for yield, this study demonstrates that obsolete cultivars may provide an additional source of nonadditive genetic effects that can be exploited in a hybrid production system. [PUBLICATION ABSTRACT]

Identification of Molecular Markers Associated with Root-Knot Nematode Resistance in Upland Cotton/ Chen Niu, Doug J Hinchliffe, Roy G Cantrell, Congli Wang, et al. ***Crop Science***. Madison:May/Jun 2007. Vol. 47, Iss. 3, p. 951-960

Abstract:

Cotton breeding for resistance to root-knot nematode (RKN) [Meloidogyne incognita (Kofoid and White) Chitwood] is hindered by the lack of convenient and reliable screening methods for resistant plants. The identification of molecular markers closely linked to RKN resistance will facilitate the development of RKN resistant cultivars through marker-assisted selection (MAS). Our objective was to identify and develop new DNA markers that are associated with RKN resistance in cotton. Using three pairs of near-isogenic (NIL) resistant (R) and susceptible (S) lines, two AFLP markers, two RAPD markers, and three RGA markers were identified to bepolymorphic between the NIL-R and NIL-S lines. One RAPD marker was converted into a sequence-tagged site (STS) marker. In an F^sub 2^ population of 'ST 474' × 'Auburn 634 RNR', the two RAPD markers and the STS marker were mapped to the same linkage group containing several markers that were previously reported to be linked with the RKN resistance gene rkn1 on chromosome 11 in 'Acala NemX'. All these markers were found to be associated with a major RKN resistance gene, presumably Mi^sub 2^ in the resistant line Auburn 634 RNR, suggesting that rkn1 and Mi^sub 2^ are either allelic or closely linked. In addition, no susceptible recombinants were found in a resistance screen of 200 F^sub 2^ plants from the cross Acala NemX × Auburn 634 RNR. The utility of the two RAPD markers and the converted STS marker were evaluated using 23 R and 8 S germplasm lines. The RAPD and STS markers, along with other previously reported markers associated with RKN resistance will be useful in germplasm screening, MAS for RKN resistance, and map-based cloning for RKN resistance genes. [PUBLICATION ABSTRACT]

Reniform Nematode Resistance in Upland Cotton Germplasm/ David B Weaver, Kathy S Lawrence, Edzard van Santen.

Crop Science. Madison:Jan/Feb 2007. Vol. 47, Iss. 1, p. 19-24

Abstract:

Cotton (Gossypium spp.) is attacked by parasitic nematodes including the reniform nematode (Rotylenchulus reniformis Linford and Oliveira). Options for management of reniform nematode are limited. No cultivars of upland cotton (G. hirsutum L.) have genetic resistance. Our objectives were to evaluate the USDA G. hirsutum collection for reaction to parasitism by R. reniformis, and determine the value of measurement of eggs (reproduction) or vermiform stages (nematode survival) as an indicator of nematode resistance. In groups of 50, accessions were evaluated in the greenhouse, using single plants in four replicates. Accessions were planted in sterile soil and inoclated with a mixture of R. reniformis isolates. After 60 d, soil populations of vermiform nematodes were determined, and eggs were extracted from the root system and counted. Paymaster 'PM 1218' was included as a check in every experiment. Out of 1973 accessions with at least one replication, none showed high levels of resistance. Seven accessions had lower population development than PM 1218 after repeated evaluations. Results indicated egg counts and vermiform counts were correlated, but not closely. Egg counts were higher and more variable than vermiform counts. While some accessions showed levels of resistance that might be useful in cotton improvement, evaluation remains difficult and introgression of genes for reniform nematode resistance remains a long-term breeding objective. [PUBLICATION ABSTRACT]

Heritability and Correlations of Agronomic and Fiber Traits in an Okra-Leaf Upland Cotton Population/ Mauricio Ulloa.

Crop Science. Madison:Jul/Aug 2006. Vol. 46, Iss. 4, p. 1508-1514

Abstract:

In cotton (Gossypium hirsutum L.), the cost and time to develop and evaluate appropriate genetic populations have limited the number of intensive and complete heritability studies. Herein, three agronomic and 17 fiber quality traits were assessed for heritability and correlation analyses on progeny rows in an okra-leaf cotton population of 208 families. Progenies were advanced in succeeding generations by a single-seed descent. Comparison between F^sub 2:3^ and F^sub 2:6^ generations for individual traits and individual progeny by trait revealed significant differences between the two generations. Heritability estimates (h^sup 2^ > 0.60), and correlations within and between (r > 0.55) F^sub 2:3^ and F^sub 2:6^, generations have practical applications for the simultaneous improvement of multiple fiber traits. Fiber strength was positively correlated to 2.5 and 50% fiber span length and negatively correlated to short fiber content. Number of neps was positively correlated to number of seed coats, and short and immature fiber content, and negatively correlated to mean fiber fineness and maturity ratio. The genetic potential for improving agronomic and fiber traits may exist in populations with this alternative leaf morphology, okra-leaf type. Mass selection may be effective for improving most of the above traits (h^sup 2^ > 0.60). However, pedigree, sibs, and progeny tests need to be used to achieve higher genetic progress. Selection

may be applied as early as the F^sub 3^ when selection units can be replicated. Thereafter, antagonistic trait correlations may become neutral or favorable in later generations, facilitating improvement of fiber quality. [PUBLICATION ABSTRACT]

T1 locus in cotton is the candidate gene affecting lint percentage, fiber quality and spiny bollworm (Earias spp.) resistance/ Qun Wan, Zhengsheng Zhang, Meichun Hu, Li Chen, Dajun Liu, Xiao Chen, Wei Wang, Jing Zheng.
Euphytica. Dordrecht:Nov 2007. Vol. 158, Iss. 1-2, p. 241-247
Abstract:

A genetic linkage map of chromosome 6 was constructed by using 270 recombinant inbred lines originated from an upland cotton cross (Yumian 1 × T586) F^sub 2^population. The genetic map included one morphological (T^sub 1^) and 18 SSR loci, covering 96.2 cM with an average distance of 5.34 cM between two markers. Based on composite interval mapping (CIM), QTL(s) affecting lint percentage, fiber length, fiber length uniformity, fiber strength and spiny bollworm resistance (Earias spp.) were identified in the t^sub 1^ locus region on chromosome 6. The allele(s) originating from T586 of QTLs controlling lint percentage increased the trait phenotypic value while the alleles originating from Yumian 1 of QTLs affecting fiber length, fiber length uniformity, fiber strength and spiny bollworm resistance increased the trait phenotypic value.[PUBLICATION ABSTRACT]

Genetic mapping of quantitative trait loci for fiber quality and yield trait by RIL approach in Upland cotton/ Xinlian Shen, Wangzhen Guo, Qiongxian Lu, Xiefei Zhu, Youlu Yuan, Tianzhen Zhang.
Euphytica. Dordrecht:Jun 2007. Vol. 155, Iss. 3, p. 371-380
Abstract:

The improvement of cotton fiber quality has become more important because of changes in spinning technology. Stable quantitative trait loci (QTLs) for fiber quality will enable molecular marker-assisted selection to improve fiber quality of future cotton cultivars. A simple sequence repeat (SSR) genetic linkage map consisting of 156 loci covering 1,024.4 cM was constructed using a series of recombinant inbred lines (RIL) developed from an F^sub 2^ population of an Upland cotton (Gossypium hirsutum L.) cross 7235 × TM-1. Phenotypic data were collected at Nanjing and Guanyun County in 2002 and 2003 for 5 fiber quality and 6 yield traits. We found 25 major QTLs (LOD ≥ 3.0) and 28 putative QTLs (2.0 < LOD < 3.0) for fiber quality and yield components in two or four environments independently. Among the 25 QTLs with LOD ≥ 3, we found 4 QTLs with large effects on fiber quality and 7 QTLs with large effects on yield components. The most important chromosome D8 in the present study was densely populated with markers and QTLs, in which 36 SSR loci within a chromosomal region of 72.7 cM and 9 QTLs for 8 traits were detected.[PUBLICATION ABSTRACT]

Germplasm Potential for Trait Improvement in Upland Cotton: Diallel Analysis of Within-Boll Seed Yield Components/ Paul Irwin Ragsdale, C Wayne Smith.
Crop Science. Madison:May/Jun 2007. Vol. 47, Iss. 3, p. 1013-1017 (5 pp.)
Abstract:

Within-boll seed yield components (seed per boll, motes per boll, ovules per boll, and seed-setting efficiency [SSE]) were evaluated in a diallel analysis of eight upland cotton (Gossypium hirsutum L.) genotypes. Genotypes included four converted race stock (CRS) accessions representing putative extremes for SSE and four commercial types representing Texas, mid-South, and eastern cotton production regions. Parents and their F^sub 1^ progeny without reciprocals were evaluated in 2000 and 2001 near College Station, TX. General combining ability (GCA) effects and specific combining ability effects (P = 0.05) were found for each trait, indicating potential for improvement of seed yield components in this population. The CRS accession M-9044-0162 had the best mean performance and GCA effects for each trait, suggesting that it would be a good parent for improving within-boll seed yield components in upland cotton. [PUBLICATION ABSTRACT]

Genetic Variation for Yield and Fiber Quality Response to Supplemental Irrigation within the Pee Dee Upland Cotton Germplasm Collection/ B T Campbell, P J Bauer.
Crop Science. Madison:Mar/Apr 2007. Vol. 47, Iss. 2, p. 591-599 (9 pp.)
Abstract:

Water availability is a major factor influencing cotton cultivar performance and sustainable cotton (Gossypium hirsutum L.) production in the southeastern USA. An increased understanding of the response of diverse cotton germplasm lines to supplemental irrigation could aid in future efforts to develop cultivars targeted to irrigated or dryland environments. In this study, 13 germplasm lines were selected from the Pee Dee (PD) germplasm collection and evaluated to measure the effect of supplemental irrigation on a number of agronomic and fiber quality traits important to cotton production systems. Most PD germplasm lines receiving supplemental irrigation had increased plant height and lint percent, while boll weight, seed index, fiber length, fiber strength, uniformity index, and micronaire decreased. Cultivars PD-2 and FM-966 did not show a significant response to supplemental irrigation for any of the traits measured. In contrast, PD5377 and PD93009 showed differential responses to supplemental irrigation for 5 out of the 12 traits measured. This study shows the importance of comparing individual genotype response to supplemental irrigation for agronomic and fiber quality traits to efficiently target genotypes for irrigated or dryland environments. [PUBLICATION ABSTRACT]

Genetic Effects of Thirteen Gossypium barbadense L. Chromosome Substitution Lines in Topcrosses with Upland Cotton Cultivars: II. Fiber Quality Traits/ Johnie N Jenkins, Jack C McCarty, Jixiang Wu, Sukumar Saha, et al.
Crop Science. Madison:Mar/Apr 2007. Vol. 47, Iss. 2, p. 561-572

Abstract:

Thirteen chromosome substitution lines (CS-B) lines with individual 3-79 Gossypium barbadense L. chromosome or arms substituted into TM-1, G. hirsutum L., were crossed with five Upland cultivars and additive and dominance effects for fiber micronaire, elongation, length, and strength were measured over four environments. Additive genetic effects were considerably larger than dominance or environmental interaction effects. Fiber strength of 3-79 and FM966 were 282 and 240 kN m kg^sup -1^, respectively. FM966 had greater additive effects for fiber length (1.13 mm) and strength (12.90 kN m kg^sup -1^) than arty CS-B line; however, CS-B25 had the greatest additive effects (8.97 kN m kg^sup -1^) for strength among CS-B lines. The greatest negative additive effect for fiber length was -1.29 mm (CS-B22sh). Although several CS-B lines had negative additive effects on strength, none was more negative than TM-1 (-5.31 kN m kg^sup -1^). CS-B02 and CS-B25 had additive effects on strength of 2.36 and 8.97 kN m kg^sup -1^. SG747 had the greatest negative additive effect (-12.13 kN m kg^sup -1^) for strength among cultivars and CS-B lines. CS-B07 and CS-B18 had negative additive effects for fiber strength but had significant and positive dominance effects with FM966. When individual CS-B lines were crossed with elite cultivars beneficial alleles for fiber properties were uncovered on specific chromosomes or chromosome arms that should aid introgression of alleles from 3-79 into Upland. [PUBLICATION ABSTRACT]

QTL mapping of fiber quality in an elite hybrid derived-RIL population of upland cotton / Baohua Wang, Wangzhen Guo, Xiefei Zhu, Yaoting Wu, Naitai Huang, Tianzhen Zhang.

Euphytica. Dordrecht:Dec 2006. Vol. 152, Iss. 3, p. 367-378

Abstract:

Xiangzamian 2 (XZM2) was the most widely cultivated cotton hybrid planted as F^sub 1^ hybrids and as selfed F^sub 2^ seeds in China before the release of transgenic Bt hybrids. By crossing two parents of XZM2, Gossypium hirsutum cv. Zhongmiansuo12 (ZMS12) and G. hirsutum acc. 8891, and through subsequent selfings, we obtained F^sub 8^ and F^sub 9^ populations of 180 recombinant inbred lines (RILs). A RIL population was cultivated in two cotton-growing regions in China for 2 years. The purpose of the present research was to detect quantitative trait loci (QTL) fiber quality and provide information applicable to cotton breeding. A genetic map was constructed mainly using SSR markers. QTL controlling fiber quality traits were determined at the single-locus and two-locus levels, and genotype-by-environment interactions were analyzed. Among the main-effect QTL, a fiber length QTL qFL-D2-1 and a reflectance QTL qFR-D2-1 were simultaneously detected at two growing regions in 2 years, which suggested a high degree of stability in different environments, and might be of particular value for a marker-assisted selection (MAS) program. The results suggested that epistatic effects, as well as additive effects, of QTL play important roles in fiber quality in these RILs. In our research, the phenomenon of QTL clusters was detected in the cotton genome.[PUBLICATION ABSTRACT]

QTLs for node of first fruiting branch in a cross of an upland cotton, Gossypium hirsutum L., cultivar with primitive accession Texas 701/ Yufang Guo, Jack C McCarty, Johnie N Jenkins, Sukumar Saha.

Euphytica. Dordrecht:Sep 2008. Vol. 163, Iss. 1, p. 113-122

Abstract:

Primitive cottons (Gossypium spp.) represent resources for genetic improvement. Most primitive accessions are photoperiod sensitive; they do not flower under the long days of the U.S. cotton belt. Molecular markers were used to locate quantitative trait loci (QTLs) for node of first fruiting branch (NFB), a trait closely related to flowering time in cotton. An F2 population consisted of 251 plants from the cross of a day neutral cultivar Deltapine 61, and a photoperiod sensitive accession Texas 701, were used in this study. Segregation in the population revealed the complex characteristics of NFB. Interval mapping and multiple QTL mapping were used to determine QTLs contributing to NFB. Three significant QTLs were mapped to chromosome 16, 21, and 25; two suggestive QTLs were mapped to chromosome 15 and 16. Four markers associated with these QTLs accounted for 33% of the variation in NFB by single and multiple-marker regression analyses. Two pairs of epistasis interaction between markers were detected. Our results suggested that at least three chromosomes contain factors associated with flowering time for this population with epistasis interactions between chromosomes. This research represent the first flowering time QTL mapping in cotton. Makers associated with flowering time may have the potential to facilitate day neutral conversion of accessions. (PUBLICATION ABSTRACT)

Combining ability for yield and fibre characteristics in Tanzanian cotton germplasm / Everina P Lukonge, Maryke Tine Labuschagne, Liezel Herselman.

Euphytica. Dordrecht:Jun 2008. Vol. 161, Iss. 3, p. 383-389

Abstract:

In Tanzania, cotton is of great economical importance, representing a large percentage of agricultural exports, but yield and lint quality is still relatively poor. The aim of this study was to identify parents to improve boll and lint yield and quality. Parents and F1 progeny of a 7 × 7 diallel were evaluated in four different environments. Results indicated significant variation for especially yield components, yield, ginning outturn and fibre quality. Parents with high and positive GCA like NTA 93-21, Delcot 344, Auburn 56 and MZ561 and combinations with high and positive SCA for the characteristics were identified. Additive genetic effects were seen for most of the characteristics, except for fibre strength at one locality. Parents with high GCA effects for certain characteristics produced combinations with high SCA effects for the same characteristics. This study indicated that there is enough genetic variability for boll and lint yield and quality for effective selection, and good parents that can be included in the breeding programme. (PUBLICATION ABSTRACT)

Comparative yield component analysis in Gossypium hirsutum parents using fibre quality grouping/ Shankar Lal Ahuja, L S Dhayal, Ram Prakash.

Euphytica. Dordrecht:Jun 2008. Vol. 161, Iss. 3, p. 391-399

Abstract:

The usual practice of estimating association and direct and indirect effects among various traits in Gossypium hirsutum is with ungrouped genetic material based on staple length and strength. During 2003-2004 and 2004-2005 genotypic and phenotypic association among ten characters were estimated in G. hirsutum genotypes: (i) set-1: 10 genotypes of low fibre strength (≤196.2 mN/tex) and medium staple length (≤25.0 mm), (ii) set-2: 10 genotypes of high fibre strength (≥235.44 mN/tex) and long staple length (≥28 mm) and (iii) set-3: 20 genotypes of set-1 and 2. The differences in the estimates of associations, direct and indirect effects for different characters in fibre quality groups were examined. The complete analysis of variance for the characters under study viz; days to 50% flowering, plant height (cm), number of monopodial and sympodial branches per plant, seed cotton yield per plant (g), boll weight (g), total number of bolls per plant, lint %, 2.5% span length (mm) and fibre strength (mN/tex) indicated highly significant genotypic differences for genotypes, years and genotype × years interaction. Variation within medium staple length and low strength (set-1), high staple length and high strength genotypes (set-2) and their interaction with year were also significant. Medium staple length and low strength (set-1) versus high staple length and high strength component (set-2) was significant for all the traits indicating significant variability between the sets. A true relationship and direct selection were observed for days to 50% flowering, number of monopodial and sympodial branches per plant with seed cotton yield in the three sets suggesting that separation of genetic material based on staple length and fibre strength for improvement of seed cotton yield through these traits is not required. Magnitude and direction of direct effect and association with yield of the other traits; plant height, number of total bolls per plant, boll weight, lint %, staple length and fibre strength differed between the sets. This study concluded that more successful planning of a breeding programme can be made through path coefficient analysis if the genetic material is grouped based on staple length and fibre strength. (PUBLICATION ABSTRACT)

Interrelationship among and repeatability of seven stability indices estimated from commercial cotton (Gossypium hirsutum L.) variety evaluation trials in three Mediterranean countries/ Dimitrios Baxevanos, Christos Goulas, Stergios Tzortzios, Athanasios Mavromatis.

Euphytica. Dordrecht:Jun 2008. Vol. 161, Iss. 3, p. 371-382

Abstract:

Multi-environment trial data are required, to obtain variety stability performance parameters as selection tools for effective cultivar evaluation. The interrelationship among seven stability parameters and their association with mean yield, along with the repeatability of these parameters across consecutive years was the objective of this study. Cottonseed yield data of 31 cotton cultivars, proprietary of Delta and Pine Land Co and other companies, evaluated in 20 locations over the 1999-2005 year period in Greece, Spain and Turkey were used for combined analysis of variance in four datasets. Across locations in a single evaluation year (dataset A), across locations in each of two single consecutive evaluation year (dataset B), across locations and two consecutive years (dataset C) and across locations and three consecutive years (dataset D). For each dataset, cultivar phenotypic variance (Ã^sub p^^sup 2^ was appropriately partitioned in its components and the h^sup 2^ and Ã^sub ge^^sup 2^ component estimated. Furthermore, following the appropriate stability analysis b^sub i^, sd^sub i^^sup 2^, Ã^sub i^^sup 2^, YS^sub i^ and AMMI1 along with the GGE Biplot distance (GGED) and instability (GGEIN) parameters were obtained. The interrelationship among the parameters and their association with mean yield based on Spearman rank correlation was studied in each of the seven single evaluation years (dataset A). Rank correlation coefficients were also used as estimates of the repeatability of these stability parameters across consecutive year combinations (dataset B, C and D). The parameters GGED and YS^sub i^ were consistently highly correlated with each other and mean yield in five out of seven single evaluation years. The data provided evidence that single year evaluation across locations might be sufficient to reliably rank cotton cultivars, based on mean yield along with GGED and YS^sub i^. Combined analysis across two consecutive years (dataset C) was more effective as compared to single year evaluation. GGED was relatively more repeatable than YS^sub i^ and mean yield in single (dataset B) and 2-year comparisons (dataset C). Although GGED is an index depended and proportional to yield, provides a superior way to integrate mean performance and stability into a single measure, which can be assessed visually on biplots. Regarding the other stability parameters, the results were contradicting and of low repeatability across single years and two consecutive years. Cultivar evaluation combined across locations in 3 years did not improve the repeatability of cultivar variance effects but resulted in very high repeatability of GGED, YS^sub i^ and mean yield. (PUBLICATION ABSTRACT)

Agricultural Sciences; New agricultural sciences study findings recently were reported by X.Q. Zhang and co-researchers/ Anonymous.
Journal of Farming. Atlanta:Mar 31, 2008. p. 52
Abstract:

The range of heterosis was ranged from -32.18 ('HaiA' x 'LuR') to 20.59% ('HaiB' x 'JiR') for seed cotton yield, -42.22 ('HaiA' x 'LuR') to 8.60% ('JiA' x 'LuR') for lint yield, -23.80 ('HaiB' x 'JiR') to 0.75% ('JiA:x 'LuR') for lint per cent, -31.50 ('LuA'x 'HiR') to 3.87% ('JiA'x 'LuR') for boll weight and -15.71 ('JiA' x 'JiR') to 106.43% ('HaiB' x 'JiR') for bolls/plant, -3.90 ('JiA' x 'JiR') to 27.29% ('HaiR' x 'LuR') for fibre length, -6.37 ('JiA' x 'JiR') to 35.93% ('LuA' x 'HR2') for fibre strenght, -2.19 ('JiA' x 'JiR') to 4.38% ('JiA' x 'HR1') for fibre elongation and -0.42 ('HaiA' x 'LuR') to 3.53% ('JiR' x 'HaiR') for fibre uniformity.

Genetic association of lint yield with its components in cotton chromosome substitution lines/ Jixiang Wu, Johnie N Jenkins, Jack C McCarty, Sukumar Saha, Richard Percy.
Euphytica. Dordrecht:Nov 2008. Vol. 164, Iss. 1, p. 199-207
ABSTRACT:

Dissection of the genetic relationship between lint yield and its yieldcomponents at the chromosome level may provide an additional avenue for yield enhancement in cotton (Gossypium hirsutum L.). Based on the conditional additive-dominance (AD) genetic model, we investigated the genetic structures of lint yield with its three component traits, lint percentage, boll weight, and boll number, using a two-location data set containing cotton chromosome substitution lines (chromosome or chromosome arm substituted from G. barbadense L. into G. hirsutum L., TM-1) which are defined as CS-B lines and their F2 hybrids with CS-B recurrent parent TM-1. We calculated the conditional variance components, contribution ratios, and contribution effects subject to the additive and dominant components. Our results showed that boll number or boll number with boll weight greatly reduced the conditional variance components and phenotypic variance for lint yield and thus indicated that boll number plays a more important role in lint yield than the other two component traits. We demonstrated that the G. barbadense chromosomes in CS-B16, CS-B18, and CS-B4sh were directly associated with reduced lint yield. Substituted chromosome arms14sh, 22sh, and 22Lo were associated with reduced additive effects for lint yield through the component of boll weight, thus suggesting that some substituted chromosomes or chromosome arms may be indirectly associated with lint yield through yield component traits. This study provides a better understanding of cotton yield and its component traits at the chromosome level and this information should be useful in cotton breeding. [PUBLICATION ABSTRACT]

Variability within cotton cultivars for yield, fibre quality and physiological traits/ I S Tokatlidis, C Tsikrikoni, J T Tsialtas, A S Lithourgidis, P J Bebeli.
The Journal of Agricultural Science. Cambridge:Aug 2008. Vol. 146, Iss. 4, p. 483-490 (8 pp.)
Abstract:

Selection within elite cotton cultivars is ineffective; it is believed that they are genetically homogeneous. Research in other crops, however, has verified significant intra-cultivar variation based either on phenotypic differentiation or molecular analysis techniques. The present study primarily investigated possible intra-cultivar variation for seedcotton yield. Honeycomb selection within three elite cotton cultivars, on the basis of single-plant seedcotton yield and under the ultra-low density of 1·2 plants/m2, was performed. From each cultivar, six selfed (hand-pollinated) plants were selected and seed of each selected plant constituted a separate line. The 18 first generation lines were evaluated in three locations at a density of 1·2 plants/m2. Within each line, the 10 selfed plants which yielded the highest were selected. Mixed seed from these selected plants constituted the respective second generation line. Offspring performance of the 18 second generation lines was also tested in three locations at a density of 1·2 plants/m2. The results were indicative of intra-cultivar variation, since significant differentiation between lines of each cultivar was found for seedcotton yield per plant, averaged across two years and three locations. Additionally, significant intra-cultivar variation was found for fibre quality properties (length and micronaire, but not strength and uniformity) averaged across two years in a single location, as well as for physiological traits (leaf carbon isotope discrimination, ash content and K concentration) averaged across two years and three locations. In comparison with the original cultivars the second generation lines had higher seedcotton yields supporting the existence of exploitable genetic variation. The conclusion was that honeycomb selection in the absence of competition could be an effective technique in breeders' seed treatment in order to avoid gradual degeneration and beneficially exploit any latent or newly developed genetic variation. [PUBLICATION ABSTRACT]

Genetic association of cotton yield with its component traits in derived primitive accessions crossed by elite upland cultivars using the conditional ADAA genetic model / Jack C McCarty, Jixiang Wu, Johnie N Jenkins.
Euphytica. Dordrecht:Jun 2008. Vol. 161, Iss. 3, p. 337-352
Abstract:

Boll number, lint percentage, and boll weight are three component traits for lint yield of upland cotton, Gossypium hirsutum L. Selecting high yielding lines or hybrids depends on the ability to dissect the genetic relationship of lint yield with these component traits. In this study, 14 day-neutral lines with desirable fiber quality derived from primitive accessions were top crossed with five commercial cultivars. The F2 populations and parents were grown in one location in 1998 and two locations in 1999 at Mississippi State, MS. The F3 populations and parents were grown in two locations in 2000. Lint yield and three component traits were measured and analyzed by the ADAA genetic model with the mixed model based conditional approach. Results showed that boll number or boll number with lint percentage or boll weight contributed to the majority of the phenotypic variance and variance components for lint yield. Boll number was more important than the other two component traits in terms of various genetic effects. The results also showed that the combination of boll number and boll weight greatly increased the contribution to lint yield even though boll weight itself had no significant contribution to lint yield compared to boll number alone. The genetic contribution effects were also predicted due to single component traits or their combinations for parents and crosses. The results revealed that the balanced selection of boll weight and boll number should be considered to obtain high yielding hybrids or pure lines. (PUBLICATION ABSTRACT)

Genetic transformation of green-colored cotton/ Sheng-Wei Zhu, Peng Gao, Jing-San Sun, Hai-Hua Wang, et al.
In Vitro Cellular & Developmental Biology.: Plant Columbia:Sep/Oct 2006. Vol. 42, Iss. 5, p. 439-444 (6 pp.)
Abstract:

This study reports an Agrobacterium-mediated transformation of green-colored cotton (Gossypium hirsutum L.). A tissue culture procedure was optimized to induce callus formation from hypocotyl expiants and subsequent differentiation into the embryogenic type. Callus formation could be induced by growing explants on Murashige and Skoog medium containing 2,4-dichlorophenoxyacetic acid and kinetin. Among the four genotypes studied, embryogenic calli and plant regeneration were observed only in var. G9803. Agrobocterium-medialed transformation of G9803 with the fiber-specific expansin gene GhExp1 was achieved based on the establishment of these tissue culture methods. A total of 32 individual regenerants resistant to kanamycin were generated within 7 mo., with a transformation frequency of 17.8%. Transformation was confirmed by Southern blot analysis and RT-PCR. These results represent the first step towards genetic manipulation of the colors and fiber quality of green-colored cottons by biotechnology. [PUBLICATION ABSTRACT]

Genetic Effects of Thirteen Gossypium barbadense L. Chromosome Substitution Lines in Topcrosses with Upland Cotton Cultivars: I. Yield and Yield Components/ Johnie N Jenkins, Jixiang Wu, Jack C McCarty, Sukumar Saha, et al.
Crop Science. Madison:May/Jun 2006. Vol. 46, Iss. 3, p. 1169-1178
Abstract:

Gossypium barbadense L. line 3-79 is lower in yield, has smaller bolls and longer, finer, and stronger fibers than upland cotton G. hirsutum L. Thirteen chromosome substitution (CS-B) lines with individual 3-79 chromosomes or arms substituted into TM-1, G. hirsutum, were top crossed with five elite cultivars and additive and dominance effects for the yield components, lint percentage, boll weight, seed cotton yield, and lint yield, were measured over four environments. Additive effects were greater than dominance effects for all traits. CS-B lines had smaller additive and homozygous dominance effects than the cultivars for most traits. Many CS-B lines had negative additive effects; however, chromosome substituted arms 22sh and 22Lo showed additive effects for lint yield that were significantly greater than homologous chromosome arms in TM-1. Hybrids of DP90 × CS-B15sh, ST 474 × CS-B17, and FM 966 × CS-B02 had positive dominance effects for lint yield significantly greater than the homologous chromosomes in TM-1. Several chromosomes or arms were associated with significant negative additive or dominance effects. These data provide a valuable baseline on yield components for the utility of these CS-B lines in commercial breeding programs. When individual chromosomes or chromosome arms, via CS-B lines, are used in crosses with cultivars, alleles for yield components on specific G. barbadense chromosomes were uncovered that showed positive interactions with alleles in elite germplasm. [PUBLICATION ABSTRACT]

A Microsatellite-Based, Gene-Rich Linkage Map Reveals Genome Structure, Function and Evolution in Gossypium/ Wangzhen Guo, Caiping Cai, Changbiao Wang, Zhiguo Han, et al.
Genetics. Bethesda:May 2007. Vol. 176, Iss. 1, p. 527-41 (14 pp.)
Abstract:

The mapping of functional genes plays an important role in studies of genome structure, function, and evolution, as well as allowing gene cloning and marker-assisted selection to improve agriculturally important traits. Simple sequence repeats (SSRs) developed from expressed sequence tags (ESTs), EST-SSR (eSSR), can be employed as putative functional marker loci to easily tag corresponding functional genes. In this paper, 2218 eSSRs, 1554 from G. raimondii-derived and 754 from G. hirsutum-derived ESTs, were developed and used to screen polymorphisms to enhance our backbone genetic map in allotetraploid cotton. Of the 1554 G. raimondii-derived eSSRs, 744 eSSRs were able to successfully amplify polymorphisms between our two mapping parents, TM-1 and Hai7124, presenting a polymorphic rate of 47.9%. However, only a 23.9% (159/754) polymorphic rate was produced from G. hirsutum-derived eSSRs. No relationship was observed between the level of polymorphism, motif type, and tissue origin, but the polymorphism appeared to be correlated with repeat type. After integrating these new eSSRs, our enhanced genetic map consists of 1790 loci in 26 linkage groups and covers 3425.8 cM with an average intermarker distance of 1.91 cM. This microsatellite-based, gene-rich linkage map contains 71.96% functional marker loci, of which 87.11% are eSSR loci. There were 132 duplicated loci bridging 13 homeologous At/Dt chromosome pairs. Two reciprocal translocations after polyploidization between A2 and A3, and between A4 and A5, chromosomes were further confirmed. A functional analysis of 975 ESTs producing 1122 eSSR loci tagged in the map revealed that 60% had clear BLASTX hits (<1e^sup -10^) to the Uniprotdatabase and that 475 were associated mainly with genes belonging to the three major gene ontology categories of biological process, cellular component, and molecular function; many of the ESTs were associated with two or more category functions. The results presented here will provide new insights for future investigations of functional and evolutionary genomics, especially those associated with cotton fiber improvement. [PUBLICATION ABSTRACT]

QTL mapping for economic traits based on a dense genetic map of cotton with PCR-based markers using the interspecific cross of Gossypium hirsutum × Gossypium barbadense/ Dao-Hua He, Zhong-Xu Lin, Xian-Long Zhang, Yi-Chun Nie, Xiao-Ping Guo, Yan-Xin Zhang, Wu Li.
Euphytica. Dordrecht:Jan 2007. Vol. 153, Iss. 1-2, p. 181-197
Abstract:

A high-density molecular marker linkage map of cotton based entirely on polymerase chain reaction-based markers is useful for a marker-assisted breeding program. Four kinds of markers--simple sequence repeats (SSRs), sequence-related amplified polymorphism (SRAP), random amplified polymorphic DNA (RAPD), and retrotransposon-microsatellite amplified polymorphism (REMAP)--were used to assay an F^sub 2^ population from a cross between "Handan208" (Gossypium hirsutum) and "Pima90" (Gossypium barbadense). Sixty-nine F^sub 2^ plants were used for map construction using 834 SSRs, 437 SRAPs, 107 RAPDs, and 16 REMAPs. Linkage analysis revealed that 1,029 loci could be mapped to 26 linkage groups that extended for 5,472.3 cM, with an average distance between 2 loci of 5.32 cM. The corresponding 69 F^sub 2:3^ families were grown, arranged in two replicates, and scored for eight phenotypes. Quantitative trait loci (QTL) analysis was performed by means of composite interval mapping using WinQtlCart ver 2.0. A total of 52 distinct QTLs were detected: 4 QTLs for lint index, 8 for seed index, 11 for lint yield, 4 for seed cotton yield, 9 for number of seed per boll, 3 for fiber strength, 5 for fiber length, and 8 for micronaire value. The present map and QTL analysis may provide a useful tool for breeders to transfer desirable traits from G. barbadense to the mainly cultivated species, G. hirsutum.[PUBLICATION ABSTRACT]

A Wealth of Genetics Technology Under One Roof/ Jim Core.
Agricultural Research. Washington:Jul 2006. Vol. 54, Iss. 7, p. 20-21 (2 pp.)
Abstract:

The BAC physical map will be a useful tool for identifying genes that affect production traits and could act as the backbone for future efforts to sequence the catfish genome. The lab also assisted Earl Taliercio, a molecular biologist in the Stoneville crop genetics lab, in determining 70,000 expressed sequence tags (ESTs) from upland cotton ovules, young fiber stems, and roots.

Molecular Marker Diversity and Field Performance in Commercial Cotton Cultivars Evaluated in the Southwestern USA /Jinfa Zhang, Y Lu, R G Cantrell, E Hughs.
Crop Science. Madison:Jul/Aug 2005. Vol. 45, Iss. 4, p. 1483-1490 (8 pp.)
Abstract:

Genetic diversity in modern upland cotton cultivars (Gossypium hirsutum L.) is thought to be narrow, thus limiting genetic advance. Robust information on the genetic relatedness among currently grown cotton cultivars is lacking. The objectives of the present study were to field test a sample of elite commercial cotton cultivars, including many transgenic cultivars representing the major cottonseed companies, and to evaluate their genetic divergence using simple sequence repeat (SSR) markers. Eighty-eight SSR primer pairs were chosen for genotyping that provided 177 SSRs. Jaccard's genetic similarity coefficients among 24 genotypes ranged from 0.694 to 0.936, with an average of 0.772, indicating that sufficient genetic diversity does exist within our sample of commercial upland cotton. Genetic similarities among cultivars from the same seed companies were generally higher than the mean of all cultivars and grouped into six major groups: two Deltapine (DP), one Stoneville (ST), one FiberMax (FM), and two New Mexico (NM) Acalas. One California Acala cultivar of New Mexico origin, developed by Phytogen (PHY), did not group with New Mexico Acala germplasm. Texas High Plains stripper type cultivars were distant from picker types and formed independent groups. Under New Mexico growing conditions, DP and ST cultivars yielded higher but produced lower fiber quality, while NM Acala cotton had lower yield but higher fiber quality. The PHY and FM cultivars were intermediate in cotton yield and fiber quality. Six SSR markers were identified to be significantly correlated with fiber yield or quality among the cultivars tested, providing impetus to validate the marker-trait associations. [PUBLICATION ABSTRACT]

Selection for Water Use Efficiency Traits in a Cotton Breeding Program: Cultivar Differences/ Warwick N Stiller, John J Read, Gregory A Constable, Peter E Reid.
Crop Science. Madison:May/Jun 2005. Vol. 45, Iss. 3, p. 1107-1113
Abstract:

Water stress adversely affects both yield and fiber quality of cotton (Gossypium hirsutum L.) and any improvement in components of water use efficiency (WUE) would be expected to partially reduce these adverse affects. Six field experiments in Australia and one in Texas using four Australian and three Texas cultivars determined genetic differences in physiological WUE parameters. Four of the experiments were grown

under dryland conditions and three under irrigated conditions. Cultivar differences for net photosynthesis (A) were found in only 30% of comparisons, ratio of intercellular CO2 concentration to ambient CO2 concentration (C^sub i^/C^sub a^) in 20%, and carbon isotope ^sup 13^C discrimination (”) in 69%. Cultivars Cascot 014 and Sicot 189 had significantly (P ≤ 0.05) higher A than Siokra 1-4 and Siokra L23 and these differences were consistent across experiments. A significant (P ≤ 0.05) cultivar × experiment interaction suggests C^sub i^/C^sub a^ would be an environment specific measure enabling confident distinction of cultivar differences. Tamcot Sphinx and Cascot 014 had significantly higher ” (P ≤ 0.001) than Siokra L23, with the ranking differing in only one irrigated experiment. Broad sense heritability estimates were 0.65, 0.68, and 0.56 for A, ”, and lint yield, respectively. Cultivar variation for these physiological traits measured in single leaves of cotton, and related indirectly to plant WUE, indicate potential for genetic advancement through selection. Further studies to determine heritability of these physiological traits in segregating populations are needed to confirm their usefulness in a cotton-breeding program. [PUBLICATION ABSTRACT]

Trends over Time among Cotton Cultivars Released by the Oklahoma Agricultural Experiment Station/ Melanie B Bayles, Laval M Verhalen, William M Johnson, Bradley R Barnes.

Crop Science. Madison:May/Jun 2005. Vol. 45, Iss. 3, p. 966-980 (15 pp.)

Abstract:

Twelve cotton (Gossypium hirsutum L.) cultivars, released by the Oklahoma Agricultural Experiment Station (OAES) between 1918 and 1982 inclusive, were evaluated in multiple environments to estimate selection progress over time for lint yield, six fiber properties, eight agronomic characters, and three diseases. Lint yield increased 1.2 to 3.0 kg ha^sup -1^ yr^sup -1^ on dryland and 3.7 to 5.6 kg under irrigation. Five of six experiments indicated that a selection plateau had not yet been reached for lint yield. Increases in fiber length of 0.04 to 0.06 mm yr^sup -1^ and of 0.02 mm yr ' were observed for 2.5 and 50% span lengths, respectively. Uniformity index and micronaire displayed significant differences among cultivars, but no significant trends over time. T^sub 0^ fiber strength increased by 0.5 kN m kg^sup -1^ yr^sup -1^. Initially, T^sub 1^ fiber strength declined; but since the mid-1940s, its trend was upward by 0.6 kN m kg^sup -1^ yr^sup -1^ in a generally linear fashion. Picked and pulled lint percentages increased rapidly at first but reached a plateau in the mid-1940s. Boll size increased over time, and bur size increased slightly. Weight of lint per boll increased through 1955, but has since remained essentially constant. Relatively large improvements were made in lint index through 1964; but since then, the trait has remained stable. Seed index increased by 0.02 g (100 seed)^sup -1^ yr^sup -1^ on dryland and by 0.03 g under irrigation. Lock tenacity increased by 1.7 g force yr^sup -1^. Positive trends over time were also noted for resistance to bacterial blight [caused by Xanthomonas campestris pv. malvacearum (Smith) Dye] and to the Fusarium wilt [caused by Fusarium oxysporum Schlect. f. sp. vasinfectum (Atk.) Snyd. & Hans.]-root-knot nematode [Meloidogyne incognita (Kofoid & White) Chitwood] complex but not for tolerance to Verticillium wilt (caused by Verticillium dahliae Kleb.). The above findings were compared with those in numerous other breeding programs. This information

provides a historical perspective on genetic gain for a number of traits among the cotton cultivars released by the OAES. [PUBLICATION ABSTRACT]
Abbreviations: CE, cultivar × environment; CL, cultivar × location; CY, cultivar × year; CYL, cultivar × year × location; OAES, Oklahoma Agricultural Experiment Station

PLANT PHYSIOLOGY-REPRODUCTION (1 jdl)

A Target Region Amplified Polymorphism Marker for Fertility Restorer Gene Rf^sub 1^ and Chromosomal Localization of Rf^sub 1^ and Rf^sub 2^ in Cotton/ Fei Wang, Bing Yue, Jinguo Hu, J McD Stewart, Jinfa Zhang.
Crop Science. Madison:Sep/Oct 2009. Vol. 49, Iss. 5, p. 1602-1608 (7 pp.)
Abstract:

Cytoplasmic male sterility (CMS), a maternally inherited trait characterized as an inability to produce functional pollen, is an important biological system for economically producing hybrid seed to enhance crop yield and studying cytoplasmic and nuclear gene interactions. In cultivated tetraploid cotton (Gossypium hirsutum L.), male fertility in two systems CMS-D2 and CMS-D8 is restored by two restorer genes Rf^sub 1^ and Rf^sub 2^, respectively. The objectives of the present study were to identify additional molecular markers for the two restorer genes and to determine their chromosomal location in the cotton genome. Two backcross (BC^sub 1^F^sub 1^) populations were developed with D2 and D8 restorers containing their respective cytoplasms as female in crosses with the same Upland cotton maintainer as male and recurrent parent. One pentatricopeptide repeat (PPR)-based target region amplified polymorphism (TRAP) marker was developed to be tightly linked to the Rf^sub 1^ gene with a genetic distance of 0.8 cM, while three more simple sequence repeat (SSR) markers (NAU2232-550/650, NAU2232-750/850, and NAU 2801-250) were identified to be closely linked to Rf^sub 2^. Using two common SSR markers, a consensus linkage group was constructed to include both Rf^sub 1^ and Rf^sub 2^ loci that were anchored in a 14.0-cM region by the two PPR gene-based markers. Based on four chromosome-anchored SSR markers, Rf^sub 1^ and Rf^sub 2^ were localized on chromosome D5 within a genetic distance of 1.4 cM, providing an incentive for further investigations of this Rf^sub 1^/Rf^sub 2^-containing region. [PUBLICATION ABSTRACT]

PEST OF PLANTS (3 jdl)

Introgression of Root-Knot Nematode Resistance into Tetraploid Cottons/ P A Roberts, M Ulloa.
Crop Science. Madison:May/Jun 2010. Vol. 50, Iss. 3, p. 940-951 (12 pp.)
Abstract:

Root-knot nematode (RKN) resistance introgression into tetraploid cotton (Gossypium spp.) and its ancestral genome origin were examined. Resistance sources ('Acala NemX', 'Clevewilt 6', Auburn 623 RNR) were compared with diverse germplasm using simple sequence repeat (SSR) markers from chromosomes 7, 11, and 14 and DNA sequence information. Differences ($P < 0.05$) were observed for mean root galling index (GI; scale 0-10) between the 56 resistant and susceptible entries. In resistance sources, GI ranged from 0.3 to 2.9, but no consistent differences were observed at allele-marker or DNA sequence level. Except for CIR316 allele (206-207 bp) on chromosome 11, no alleles from other SSRs were observed on resistant entries (GI < 3). Allotetraploid G. hirsutum L. (AD^sub 1^) and G. barbadense L. (AD^sub 2^) showing the same SSR marker alleles as G. arboreum L. (A^sub 2^) might suggest resistance introduction from the diploid cotton A^sub 2^ genome (genetic distance 0.19 to 0.27). However, percent sequence identity from MUCS088 and CIR316 revealed G. barbadense and resistant G. hirsutum (206-207 bp) also were close to diploids G. herbaceum L. (A^sub 1^), G. thurberi Tod. (D^sub 1^), and G. trilobum (DC.) Skovst. (D^sub 8^). Other G. hirsutum DNA sequences were closer to G. raimondii Ulbr. (D^sub 5^). These analyses indicated resistance introgression into G. hirsutum allotetraploid cottons occurred by artificial hybridization with ancestral genome origin from G. arboreum as well as G. thurberi and not during cotton genome evolution. [PUBLICATION ABSTRACT]

Identification of Molecular Markers Associated with Root-Knot Nematode Resistance in Upland Cotton/ Chen Niu, Doug J Hinchliffe, Roy G Cantrell, Congli Wang, et al.
Crop Science. Madison:May/Jun 2007. Vol. 47, Iss. 3, p. 951-960 (10 pp.)
Abstract:

Cotton breeding for resistance to root-knot nematode (RKN) [Meloidogyne incognita (Kofoid and White) Chitwood] is hindered by the lack of convenient and reliable screening methods for resistant plants. The identification of molecular markers closely linked to RKN resistance will facilitate the development of RKN resistant cultivars through marker-assisted selection (MAS). Our objective was to identify and develop new DNA markers that are associated with RKN resistance in cotton. Using three pairs of near-isogenic (NIL) resistant (R) and susceptible (S) lines, two AFLP markers, two RAPD markers, and three RGA markers were identified to be polymorphic between the NIL-R and NIL-S lines. One RAPD marker was converted into a sequence-tagged site (STS) marker. In an F^sub 2^ population of 'ST 474' × 'Auburn 634 RNR', the two RAPD markers and the STS marker were mapped to the same linkage group containing several markers that were previously reported to be linked with the RKN resistance gene rkn1 on chromosome 11 in 'Acala NemX'. All these markers were found to be associated with a major RKN resistance gene, presumably Mi^sub 2^ in the resistant line Auburn 634 RNR, suggesting that rkn1 and Mi^sub 2^ are either allelic or closely linked. In addition, no susceptible recombinants were found in a resistance screen of 200 F^sub 2^ plants from the cross Acala NemX × Auburn 634 RNR. The utility of the two RAPD markers and the converted STS marker were evaluated using 23 R and 8 S germplasm lines. The RAPD and STS markers, along with other previously reported markers associated with RKN resistance will be useful in germplasm screening, MAS for RKN resistance, and map-based cloning for RKN resistance genes. [PUBLICATION ABSTRACT]

Association of Root-Knot Nematode Resistance Genes with Simple Sequence Repeat Markers on Two Chromosomes in Cotton/ Pavathi Ynturi, Johnie N Jenkins, Jack C McCarty Jr, Osman A Gutierrez, Sukumar Saha.

Crop Science. Madison:Nov/Dec 2006. Vol. 46, Iss. 6, p. 2670-2674 (5 pp.)

Abstract:

The pots and greenhouse beds were filled with screened, methyl bromide-fumigated Wickham sandy loam soil (fine-loamy, mixed, semiactive, thermic Typic Hapludults). DNA from 150 mg stored leaf samples of five individual plants of each of the parental lines and 86 individual F2 plants of the RNIL X SNIL cross was extracted using a DNeasy Plant Mini Kit (Qiagen, Santa Clarita, CA) following the manufacturer's protocol. The genomic DNA sample was amplified using SSR primers in 10 μM reactions containing Ix Gene Amp PCR Gold Buffer, 0.15 μM SSR primers, 2.5 mM MgCl2, 0.5 units Ampli Taq Gold DNA polymerase, 0.2 mM dNTPs, and 20 ng of the template DNA sample.

Linkage Mapping of Resistance to Reniform Nematode in Cotton following Introgression from Gossypium longicalyx (Hutch. & Lee) / Nilesh D Dighe, A Forest Robinson, Alois A Bell, Monica A Menz, Roy G Cantrell, David M Stelly.

Crop Science. Madison:Jul/Aug 2009. Vol. 49, Iss. 4, p. 1151-1164 (14 pp.)

Abstract:

Reniform nematodes (Rotylenchulus reniformis Linford & Oliveira) decrease U.S. production of Upland cotton (Gossypium hirsutum L., 2n = 52, 2[AD]^sub 1^) by more than US$100 million yr^sup -1^. We report here on the mapping of a gene for extreme resistance that was introgressed from the African species G. longicalyx (Hutch. & Lee, 2n = 2x = 26; 2F^sub 1^). The responsible allele, designated Ren^sup lon^, was localized to chromosome 11 by first screening A-subgenome simple sequence repeat (SSR) marker loci for parental polymorphism and then for association with resistance. The three most strongly coupled SSRs and a G. longicalyx gene conferring green seed fuzz, designated Fzg^sup lon^, were screened against 984 resistant and susceptible individuals of multiple backcross generations. We used marker data and pedigrees to identify nonrecombinant heterozygous parents and thereby avoid bias from repeated sampling of a recombination event. We constructed linkage maps after progeny testing a small population (147) and after implementing three alternative approaches better suited to larger populations-marker-assisted genotyping analysis,
applying a cut-off value as population-wide genotyping criterion, and genotype-selective sampling. The maps concordantly indicated the order to be Fzg^sup lon^-Ren^sup lon^-BNL3279_114-BNL1066_156-BNL836_215, with most Ren-proximal bilaterally flanking markers within 6 cM of each other. The results will clearly facilitate use of Ren^sup lon^ in breeding, additional mapping, genomics, and prospective cloning. [PUBLICATION ABSTRACT]

PLANT STRUCTURE (1 JDL)

Quantitative inheritance of leaf morphological traits in upland cotton/ J J Hao, S X Yu, Z D Dong, S L Fan, Q X Ma, M Z Song, J W Yu.
The Journal of Agricultural Science. Cambridge:Oct 2008. Vol. 146, Iss. 5, p. 561-569 (9 pp.)
Abstract:

Genetic manipulation of leaf architecture may be a useful breeding objective in cotton (Gossypium spp.). The present study reports quantitative genetic analysis of leaf traits from two intraspecific crosses of inbred lines in upland cotton (Gossypium hirsutum L.) viz. Kang3xChaoji463 and Han109xJi98. Six leaf morphological traits (leaf area (LA), leaf perimeter (LP), main lobe length (LL) and width (LW), petiole length (PL), and main LL/LW ratio) were recorded from multiple generations (P1, F1, P2, BC1, BC2, and F2) in the two crosses. Generation mean analyses were conducted to explain the inheritance of each leaf morphological trait. The six-parameter model showed a better fit to an additive-dominance model for LA, main LW, PL, and main LL/LW ratio in the two crosses, suggesting the relative importance of epistatic effects controlling leaf morphology. A simple additive-dominance model accounted for the genetic variation of the main LL in the Kang3xChaoji463 cross. Different models were selected as appropriate to explain LP in the two crosses. The differences between broad- and narrow-sense heritability values for the same trait were not constant in the two crosses. The estimated minimum number of genes controlling each leaf morphological trait ranged from 0 to 2 for both the crosses. Moreover, the sums of the minimum number of genes controlling leaf morphology were 6 and 2 in the Kang3xChaoji463 and Han109xJi98 populations, respectively. Most data suggested that there existed a substantial opportunity to breed cottons that transgress the present range of leaf phenotypes found. [PUBLICATION ABSTRACT]

HUMAN NUTRITION (1 jdl)

Engineering cottonseed for use in human nutrition by tissue-specific reduction of toxic gossypol / Ganesan Sunilkumar, LeAnne M Campbell, Lorraine Puckhaber, Robert D Stipanovic, Keerti S Rathore.
Proceedings of the National Academy of Sciences of the United States of America. Washington:Nov 28, 2006. Vol. 103, Iss. 48, p. 18054
Abstract:

Global cottonseed production can potentially provide the protein requirements for half a billion people per year; however, it is woefully underutilized because of the presence of toxic gossypol within seed glands. Therefore, elimination of gossypol from cottonseed has been a long-standing goal of geneticists. Attempts were made to meet this objective by developing so-called "glandless cotton" in the 1950s by conventional breeding techniques; however, the glandless varieties wercommercially unviablebecause of the increased susceptibility of the plant to insect pests due to the systemic absence of glands that contain gossypol and other protective terpenoids. Thus, the promise of cottonseed in contributing to the food requirements of the burgeoning world population remained unfulfilled. We have successfully used RNAi to disrupt gossypol biosynthesis in cottonseed tissue by interfering with the expression of the ´-cadinene synthase gene during seed development. We demonstrate that it is possible to significantly reduce cottonseed-gossypol levels in a stable and heritable manner. Results from enzyme activity and molecular analyses on developing transgenic embryos were consistent with the observed phenotype in the mature seeds. Most relevant, the levels of gossypol and related terpenoids in the foliage and floral parts were not diminished, and thus their potential function in plant defense against insects and diseases remained untouched. These results illustrate that a targeted genetic modification, applied to an underutilized agricultural byproduct, provides a mechanism to open up a new source of nutrition for hundreds of millions of people. [PUBLICATION ABSTRACT]