

Identification of QTL and QEI for Fiber-related Traits in *Gossypium Hirsutum* L.

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Abstract

Background

Cotton is one of the most important cash crops in the world, depending on fiber quality, yield, seed oil and protein content. Identifying QTL for fiber related and other agronomic traits will facilitate the genetic improvement in cotton.

Results

In this study, forty-seven QTL for fiber related traits were identified across four different environments and six of these QTL were detected in more than one environment, including two for lint percentage (qLP-D03-1 and qLP-D09-1), two for fiber length (qFL-A07-2 and qFL-D11-1), and two for fiber micronaire (qFM-A08-1 and qFM-D11-1), respectively. Four QTL clusters contained 12 QTL were distributed on four chromosomes including two in At subgenome and two in the Dt subgenome. Moreover, thirteen QTL by environment interactions (QEI) were recognized, including one for lint percentage, five for fiber length, three for fiber strength, two for fiber micronaire, one for fiber uniformity and one for fiber elongation, respectively.

Conclusion

Six QTL were detected in more than one environment and two environmentally stable QTL (qLP-D03-1 and qFM-A08-1) interacted significantly environment. The QTL detected in more than one environment could be useful for further fine-mapping and marker assisted selection in cotton.

Background

Genus *Gossypium* comprises of approximate 50 species and four of them are cultivated species [1]. Of the cultivated species, *Gossypium hirsutum* L. offers the most important source for natural fiber, and occupies more than 90% of cotton production worldwide because of its high yield and broad adaptability [2]. High fiber yield and excellent fiber quality traits are very important goal for plant breeders to improve cotton through the breeding programs and any other biotechnology tools. The yield, fiber quality and other agronomic traits of cotton are quantitative traits which are highly effected by the environmental conditions, and also the negative genetic correlation between fiber quality and fiber yield added a lot of difficulties and challenges to improve cotton through classic breeding, which depends on phenotype selection alone [3-5]. However, molecular markers supply a powerful tool to map the quantitative traits loci (QTL), and improve the complex traits through markers-assisted selection (MAS) [6]. In cotton, more than thousands of QTL controlling fiber quality traits have been identified according to CottonQTLdb [7, 8], but most of the QTL explained small effects or were unstable in different environments [9, 10]. Furthermore, the low polymorphism of simple sequence repeat (SSR) markers in cotton resulted in insufficient linkage between markers and traits, which hindered the favorable QTL pyramiding through MAS. Single nucleotide polymorphism (SNP) markers with genome wide abundance characterized by

high-throughput genotyping can meet the requirement for high density genetic map construction and QTL dissection. In recent years, a lot of QTL for yield, fiber quality and other agronomic traits have been identified with SNP marker genetic maps in cotton, including restriction-site associated DNA sequencing (RAD-seq) [11, 12], genotyping-by-sequencing (GBS) [13, 14], amplified fragment sequencing (SLAF-seq) [15-18], and SNP-array [19]. In addition to fiber, cotton is also regarded as the most important source of vegetable protein and oil [20, 21]. Previous study has demonstrated that the negative relationship exists between cottonseed oil content and fiber yield [22], and cottonseed oil content is also negatively related to seed protein content [23-25]. Our previous studies have shown that major QTL for lint percentage, crude protein content, crude oil content and fiber quality traits are identified at morphological loci N_1 , Lc_1 , and Lg [26, 27]. Our recent study has constructed a high density SLAF-seq SNP genetic map and identified QTL for seed size, oil and protein content with a RIL population developed from a cross between high fiber quality cultivar Yumian 1 and high oil content line M11 [18]. This study identified QTL for fiber-related traits and QTL by environment interactions (QEI) under four different environments. The result could facilitate the future studies about the molecular breeding in cotton.

Results

Phenotypic data analysis

The statistical analysis for fiber related traits, including lint percentage (LP), fiber elongation (FE), fiber uniformity (FU), fiber strength (FS), fiber micronaire reading (FM), and fiber length (FL), and the phenotypic data of these six traits from two parents and the RIL population under four different environments were summarized in (Table1). Almost under all environments, the fiber length and fiber strength of Yumian 1 were higher than M11's. In general, all these six traits were observed to show continuous variation and transgressive segregation. The Skewness and the kurtosis tests granted that all these traits were approximately normally distributed.

One-way ANOVA analysis for all the six traits were carried out and summarized in (Table 2). The result showed that all of them, except fiber uniformity, had significant genetic and environmental effects ($p < 0.05$).

Correlations among the tested traits, based on phenotypic data from four environments for the RIL population, were shown in (Table 3). Among them, fiber length presented significant correlation with the other four fiber quality traits. Fiber strength was significantly negative correlated with fiber micronaire and was significantly positive correlated with fiber elongation. Lint percentage had significant negative and positive correlations with fiber strength and fiber micronaire respectively.

QTL identification for fiber related traits

A total of forty-seven QTL for fiber related traits were identified across four environments and distributed on twenty-one chromosomes (Table 4; Fig. 1). The phenotypic variation explained (PVE) value of these QTL ranged from 10.1 to 21.1 %, and their LOD value ranged from 2.0 to 4.4. At subgenome carried thirty-

one QTL, while Dt subgenome contained sixteen QTL, and almost all chromosomes carried one or more QTL with the exception of chromosomes A06, D02, D06, D07 and D13. Six stable QTL, including two for lint percentage, two for fiber length and two for fiber micronaire, were identified under more than one environment. These six stable QTL were thought to be environment-stable QTL.

Lint percentage (LP)

Seven QTL for lint percentage were detected on seven chromosomes, with PVE value ranged from 10.1% to 20.6 % and LOD values ranged from 2.0 to 4.3. Notably, favorable alleles of most QTL, except qLP-D05-1, were contributed by Yumian 1. Besides, two QTL were identified in three environments, including qLP-D03-1 and qLP-ChrD09-1.

Fiber Length (FL)

Thirteen QTL for fiber length were identified on 10 chromosomes, with LOD values range from 2.0 to 4.4 and PVE value from 10.1 to 21.1 %. The favorable alleles of qFL-A05-2, qFL-A09-2, qFL-A11-1, qFL-A13-1, and qFL-D11-1 were provided by Yumian 1, and the others were provided by M11. In addition, two QTL (qFL-A07-2 and qFL-D11-1) were identified in two different environments.

Fiber Strength (FS)

Six QTL for fiber strength were detected on five chromosomes, including five QTL on the At subgenome and one QTL on the Dt subgenome. The PVE value of these QTL ranged from 10.6% to 14.9%, and the LOD value of them ranged from 2.1 to 3.0. M11 provide favorable alleles to qFS-A10-1. The favorable alleles of the other five QTL were contributed by Yumian 1.

Fiber Micronaire (FM)

Eleven QTL for fiber micronaire were identified, with LOD values from 2.0 to 3.6. The PVE values of these QTL ranged from 10.1% to 17.6%. The favorable allele of qFM-A07-1, qFM-A08-1 and qFM-D09-1 were contributed by Yumian 1, and the other eight QTL were provided by M11. Besides, qFM-A08-1 and qFM-D11-1 was detected in two environments.

Fiber Uniformity (FU)

Six QTL for fiber uniformity ratio were identified on five chromosomes. The LOD value of these QTL ranged from 2.1 to 3.0, and the PVE value ranged from 10.5% to 16.2 %. Only the favorable allele of qFU-A05-1 was provided by Yumian 1, while the favorable alleles of the others were contributed by M11.

Fiber Elongation (FE)

Four QTL for fiber elongation were detected on four chromosomes, with PVE values ranged from 10.3 to 16.3 % and LOD values from 2.0 to 3.0. Among them, the favorable alleles of qFE-A02-1 and qFE-D08-1 were contributed by Yumian 1, the other two QTL were derived from M11.

QTL clusters

Four QTL clusters that located on chromosomes A05, A10, D09, and D11 were detected and summarized in (Table 5). The favorable alleles of QTL from cluster-A05 were all contributed by Yumian 1, whereas the favorable alleles of QTL from cluster-A10 were all provided by M11. Remarkably, cluster-D09 contained the stable lint percentage QTL qLP-D09-1 and cluster-D11 contained the stable fiber micronaire QTL qFM-D11-1.

QTL by environment interaction

Through QEI analysis, a total of thirteen QEI were identified, including one QEI for lint percentage, five QEI for fiber length, three QEI for fiber strength, two QEI for fiber micronaire, one QEI for fiber uniformity and one QEI for fiber elongation. The details of each QEI were listed in (Table 6). Except for QEI-FS-A03-2, whose environment effect made higher phenotypic contribution than the additive effect, the other 12 QEI showed stability across environments. By comparing the QEI results with QTL identified through individual environment, QEI-LP-D03-1, QEI-FL-D01-1, QEI-FL-D09-1, QEI-FS-A03-1, QEI-FS-A05-1 and QEI-FM-A08-1 were found to be located in the same region with qLP-D03-1, qFL-D01-1, qFL-D09-1, qFS-A03-1, qFS-A05-1, and qFM-A08-1, respectively. This result indicated that qLP-D03-1 and qFM-A08-1 were environmentally stable QTL with QTL by environment interaction.

Discussion

Environmentally stable QTL and QTL by environment interaction

The identification of QTL for important agronomic traits is a main part of MAS. However, few QTL were successfully applied in MAS breeding in spite of numerous QTL were identified in cotton, as well as other crops. The main reason is the poor consistency of QTL effects across environments [28, 29]. Therefore, environmentally stable QTL need to be identified and multi-environmental analysis need to be applied [29, 30]. In the present study, both QTL identification across individual environment and multi-environmental analysis was applied, and six environmentally stable QTL and thirteen QEI were detected. Of the thirteen QEI, six were also detected by individual environmental analysis, indicating that they have certain interaction effect with environments, but the additive effect made higher phenotypic contribution than the environmental effects. Moreover, two environmentally stable QTL, qLP-D03-1 and qFM-A08-1 identified in more than one environment by individual environmental analysis were also detected by multi-environmental analysis with environmental effects lower than additive effects. This result indicated that some environmentally stable QTL interacts significantly with the environment. The QTL detected in more than one environment could be useful for further fine-mapping and MAS in cotton.

Common QTL across different genetic backgrounds

Out of forty-seven QTL, forty QTL for fiber quality traits were identified in this study. Comparing with the QTL identified in our previous studies, which used high quality cultivar Yumian 1 as the common parent

of RIL populations [26, 31] (Zhang et al. 2009, Tang et al, 2015), also Ali et al 2018) [17], we found that six QTL were identified in two or three different populations. For instance, qFS-A10-1 was identified in all three populations, four QTL (qFS-A03-1, qFS-A05-1, qFE-A09-1 and qFM-D04-1) were detected in population (Yumian 1 × M11) and population (Yumian 1 × CA3084), and one QTL (qFE-A10-1) was identified in population (Yumian 1 × M11) and population (Yumian 1 × 7235). Except for qFE-A09-1 and qFS-A10-1, the favorable alleles of other four were all derived from Yumian 1. The QTL detected in more than one genetic background could be also useful for MAS.

QTL for multiple traits

Two of the environmentally stable QTL (qLP-D03-1 and qLP-D09-1) detected in the present study also are found to be stable QTL for oil content in our previous study [18]. The favorable alleles of qLP-D03-1 and qLP-D09-1 derived from Yumian 1, whereas favorable alleles for oil content derived from M11. Our previous studies have shown that major QTL for lint percentage, crude protein content and crude oil content were identified at morphological loci N_1 [26, 27]. These linkage or pleiotropy QTL could explain partially the negative relationship between fiber yield and cottonseed oil content.

Conclusions

Six QTL fiber quality were detected in more than one environment, and two environmentally stable QTL (qLP-D03-1 and qFM-A08-1) interacted significantly with environment. The QTL detected in more than one environment could be useful for further fine-mapping and marker assisted selection in cotton.

Methods

Population and traits examination

RIL population is the same population used in our previous study [18]. High oil content line M11 and high fiber quality cultivar Yumian 1, as well as the RIL population, were planted in single-row plot, 0.7 m wide and 5 m long, in four environments (summer of 2017 at Anyang of Henan, summer of 2018 at Anyang of Henan and Kuerle of Xinjiang, and winter of 2018 at Sanya of Hainan), including representative ecological cotton-producing regions of China: Anyang in the Yellow River cotton-growing area, and Kuerle in the northwestern cotton-growing area. For each plot, fifty mature bolls were manually harvested and ginned fiber. Lint percentage of a given line was measured by the weight ratio of lint to cottonseed, and fiber samples were measured for fiber quality traits with the HVI900 instruments at the Supervision Inspection and Testing Cotton Quality Center of the Ministry of Agriculture, Anyang, China. The fiber quality traits included upper half mean length (FL, mm), fiber strength (FS, cN/tex), fibre elongation (FE), fibre micronaire reading (FM), fiber uniformity ratio (FU, %). The statistical analysis performed by parameters of SAS version 9.4 and Statistics 8.1.

QTL analysis

The QTL for fiber quality traits were detected using the MQM mapping of MapQTL 6.0 [32], and a threshold of log of odds ratio (LOD) ≥ 2.0 was used to declare suggestive QTL as suggested by Lander and Kruglyak [33]. The positive additive effects indicated the favorable alleles derived from M11, whereas the negative additive effects indicated the favorable alleles derived from Yumian 1. The QTL detected in two or more environments were exact to be possible the stable QTL [34]. QEI mapping of QTL was carried out by the multi-environment trials (METs) function and the inclusive composite interval mapping (ICIM) method of ICIMapping 4.0 [35], as described by Liu et al [10]. The QTL nomenclature was designated as, starting with 'q', followed by a trait abbreviation and the chromosome number, then by the number of QTL affecting the trait on the same chromosome.

Abbreviations

Chr: Chromosome; LOD: Log of Odds; PVE: Phenotypic variance explained; QTL: Quantitative trait locus/loci; RAD: Restriction-site associated DNA; RIL: Recombinant inbred line ; SNP: Single nucleotide polymorphism; FE: Fiber elongation; FL: Fiber length; FM: Fiber micronaire; FS: Fiber strength; FU: Fiber uniformity and LP :Lint percentage ; TS transgressive segregation ; Mb: million base and cM: centiMorgans; QEI: QTL by environment interactions.

Declarations

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Authors' contributions

ZZ conceived the study, participated in its design and modified the manuscript design; AS contributed to manuscript writing and data analysis; PY, JM and NA contributed to DNA extraction; WW and XL contributed to data analysis; ZT contributed to field work.

Consent for publication

All authors have read the final manuscript and agreed to publication.

Competing interests

The authors declare that they have no competing interests.

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Tables

Due to technical limitations, table 1-6 is only available as a download in the Supplemental Files section.

Figures

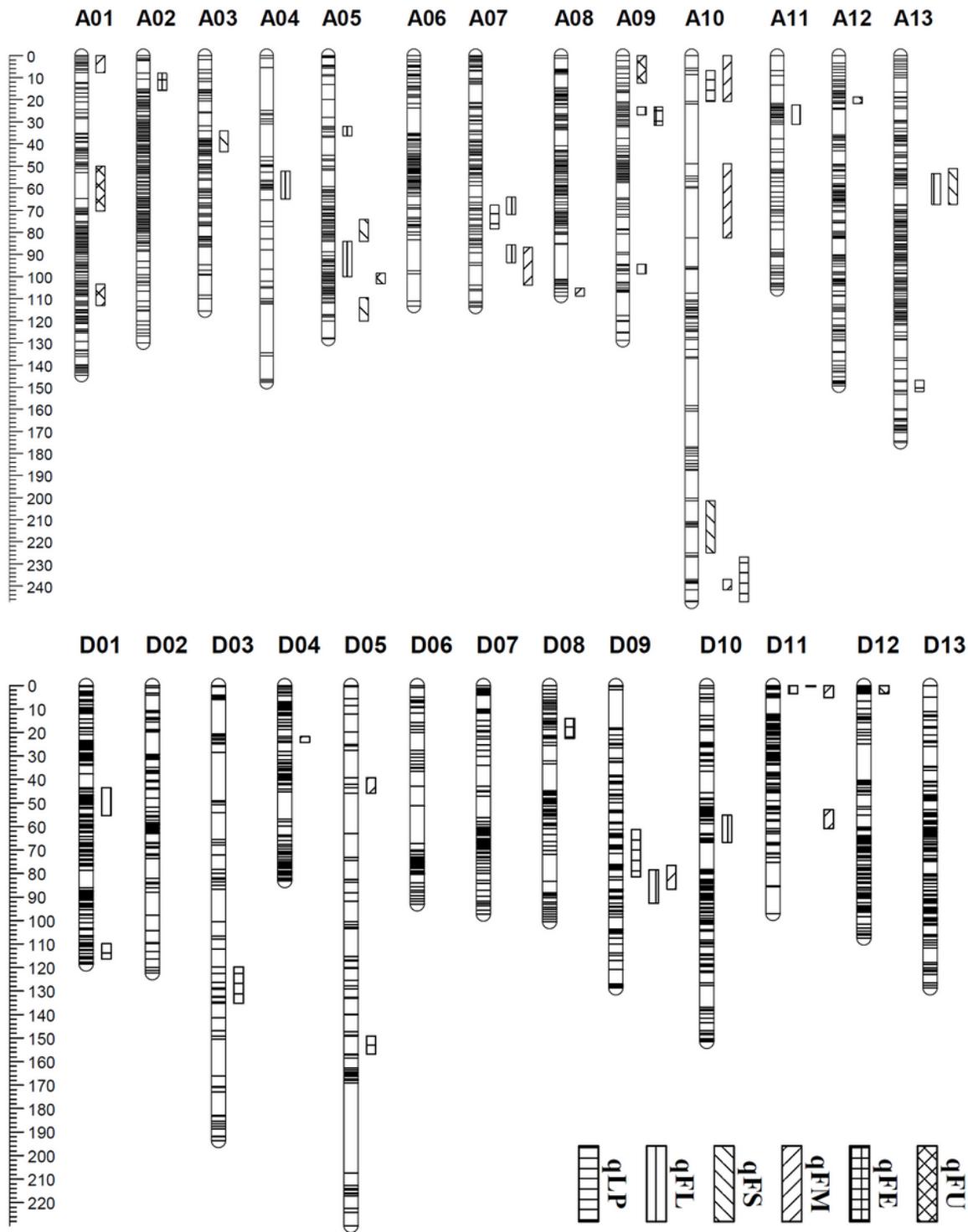


Fig 1. QTL for fiber-related traits in M11 x Human1 RIL population

Figure 1

Figure 1

Supplementary Files

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