

## Article

# A Genetic Linkage Map of BC<sub>2</sub> Population Reveals QTL Associated with Plant Architecture Traits in *Lagerstroemia*

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**Abstract:** Plant architecture improvement is of great significance in influencing crop yield, harvesting efficiency and ornamental value, by changing the spatial structure of the canopy. However, the mechanism on plant architecture in woody plants is still unclear. In order to study the genetic control of plant architecture traits and promote marker-assisted selection (MAS), a genetic linkage map was constructed, and QTL mapping was performed. In this study, using 188 BC<sub>2</sub> progenies as materials, a genetic map of *Lagerstroemia* was constructed using amplification fragment length polymorphisms (AFLP) and simple sequence repeats (SSR) markers, and the QTLs of four key plant architecture traits (plant height, crown width, primary lateral branch height and internode length) were analyzed. The genetic map contains 22 linkage groups, including 198 AFLP markers and 36 SSR markers. The total length of the genome covered by the map is 1272 cM, and the average distance between markers is 6.8 cM. Three QTLs related to plant height were located in LG1, LG4 and LG17 linkage groups, and the phenotypic variation rates were 32.36, 16.18 and 12.73%, respectively. A QTL related to crown width was located in LG1 linkage group, and the phenotypic variation rate was 18.07%. Two QTLs related to primary lateral branch height were located in the LG1 and LG7 linkage groups, and the phenotypic variation rates were 20.59 and 15.34%, respectively. Two QTLs related to internode length were located in the LG1 and LG20 linkage groups, and the phenotypic variation rates were 14.86 and 9.87%. The results provide a scientific basis for finely mapping genes of plant architecture traits and marker-assisted breeding in *Lagerstroemia*.

**Keywords:** *Lagerstroemia*; genetic map; QTL; plant height; branching; internode length



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## 1. Introduction

Plant architecture refers to the morphological characteristics of various tissues and organs of the above-ground part of the plant and their arrangement, including plant height, crown width, primary lateral branch height, internode length, etc. The formation of plant architecture is mainly determined by the layout and activities of the shoot apical meristem, axillary meristems, intercalary meristems, lateral or secondary meristem and the subsequent development of stems, leaves, branches and inflorescences [1]. Plant architecture plays an important role in crops, horticultural crops, and ornamental plants. Plant architecture is not only important for improving yield, environmental adaptability, and competitiveness, but also for enriching ornamental horticulture [2,3].

Humans have never stopped in their research and improvement of plant architecture, and the Green Revolution gene is one of the milestone discoveries. The successful appli-

cation of the rice semi-dwarf gene *sd1* has effectively solved the contradiction of “high yield and lodging” [4]. In addition to the *sd1* gene regulating plant height by participating in gibberellin synthesis, *D2* and *DLT* are also another important pathway for regulating plant height by participating in brassinolide synthesis [5]. Tiller is a unique research trait in rice, and its number and angle affect rice plant architecture. *MOC1* is an important gene controlling rice tillers. Mutations in this gene cause rice to produce no tillers and only one main stem [6]. The up-regulated expression of *TAC1* leads to an increase in tiller angle [7]. *LAZY1* regulates the tiller angle of rice by regulating the polar transport of auxin [8]. The wheat green revolution gene *rht* leads to suppression of wheat cell elongation and shortening of the stems, inducing lodging resistance and increased yield, but it also leads to the production of a large number of ineffective tillers and light blocking and competition among the leaves [9]. Thus, people have turned to genetic improvement of ideal plant architecture varieties. The *TB1* gene in maize has extremely reduced the number of branches, resulting in a species with only one main stem at present, which has become an important cultivated crop for humans [10]. With in-depth study of the ideal plant architecture of maize, it was found that too high a plant height will reduce the cultivation density and cause lodging. Only a reasonable plant height and ear height ratio can effectively increase the yield [11].

In woody plants, researchers have focused more on dwarfing, branching, and weeping. Dwarfing can improve harvesting efficiency, and the main genes controlling apple dwarfing are *Co*, *Dw* and *Md* [12–14]. Through an *Agrobacterium*-mediated method, researchers have successfully introduced *ipt*, *rolA*, *rolB* and *rolC* genes into apples and leading to exhibition of dwarfing traits [15–17]. The dwarf gene *Dw* from peach was accurately located within a distance of 277 kb. The results of this study will help the cloning of dwarf genes and molecular-assisted breeding of peach dwarf traits [18]. In terms of branching, *MdCCD7* and *MdCCD8* genes in apple can restore the multi-branched phenotype of *Arabidopsis max3* and *max4* to wild type [19]. The *TAC1* gene, which controls the branching angle of peach, was located within 2 Mb of physical distance. The gene was successfully cloned and its function was verified in *Arabidopsis* [20]. The discovery of these branching genes can help increase yield and enhance ornamental effects. The weeping trait is a unique ornamental trait in woody plants, and is considered to be a completely recessive quality trait controlled by a single gene in *Prunus mume* Sieb. et Zucc. [21,22]. However, these studies are far from enough to study the plant architecture of woody plants.

*Lagerstroemia* is an important woody ornamental plant in the world, which has beautiful tree postures, bright flowers and extremely long flowering periods [23]. In addition, there are various plant architectures in *Lagerstroemia*. The predecessors first carried out molecular marker development [24–28] and genetic diversity analyses [29]. He et al. (2014) used 192 F<sub>1</sub> progenies of *L. caudate* Chun et How ex S. Lee et L. Lau × *L. indica* Linn. “Xiang Xue Yun” to construct the first genetic map of *Lagerstroemia* using amplification fragment length polymorphisms (AFLP) and simple sequence repeats (SSR) markers. The map focuses on flower traits, contains 20 linkage groups and covers 1162.1 cm with a mean distance of 10.69 cm between adjacent markers.

Ye et al. (2017) [30] investigated the inheritance of plant height, internode length, and primary lateral branch height traits of *Lagerstroemia* by using a mixed major gene plus polygene inheritance model, internode length is a one additive-dominance major gene plus additive-dominance epistasis polygene genetic model. Plant height and primary lateral branch height are two additive-dominance-epistasis major genes plus additive-dominance-epistasis polygene genetic models. Internode length was mainly controlled by genetic factors with a low effect of environmental factors. Plant height and primary lateral branch height are mainly controlled by environmental factors. Through the development of SNP molecular markers, two markers highly related to internode length and one marker highly related to primary lateral branch height were found, which can be applied to marker-assisted selection [26]. Plant height is highly correlated with internode length, internode length was explained mainly by cell number, and secondarily by cell length and reveals the

key role of auxin in cell division in the shoot apical meristem, implying that the interaction between auxin and GA4 regulates the internode length of *Lagerstroemia* [31]. In terms of branching, the *LfiDAD2* gene may be related to the branching pattern of *Lagerstroemia* [3]. GA synthesis and signal transduction pathways play a role in weeping traits. When virus-induced gene silencing (VIGS) reduces the expression level of *LfiGRAS1*, a negative element of the GA signal, new branches grow in the infected plant in a negatively geotropic manner [8].

The variable plant architecture of *Lagerstroemia* is an ideal material for studying plant architecture traits of woody plants, however, there are few reports on QTL mapping of plant architecture traits, which makes it difficult to carry out more systematic and complete research. In this study, a population of 188 BC<sub>2</sub> progenies with obvious strain segregation were selected as the mapping population and three molecular markers of AFLP, g-SSR, and EST-SSR were used to construct a genetic linkage map. In addition, QTL mapping of the plant architecture traits of *Lagerstroemia*, including plant height, crown width, primary lateral branch height and internode length, aims to provide a basis for the directional cultivation of *Lagerstroemia*.

## 2. Materials and Methods

### 2.1. Plant Materials

The F<sub>1</sub> progenies came from a *L. fauriei* × *L. indica* “Pocomoke” cross in 2011. *L. fauriei* was an arbor (>3 m) with long internodes (internode length of new branches > 4 cm), and “Pocomoke” was a dwarf shrub (0.3–0.6 m) with short internodes (internode length of new branches < 1.8 cm). One progeny in F<sub>1</sub> population was selected to backcross with “Pocomoke” to produce the BC<sub>1</sub> population in 2013. One non-dwarf progeny in the BC<sub>1</sub> population was used to cross with “Pocomoke” and produced 188 BC<sub>2</sub> progenies in 2015. All the BC<sub>2</sub> progenies were cultivated at China National Engineering Research Center for Floriculture (CNERCF) in Beijing (40°020' N, 115°500' E).

### 2.2. Phenotypic Data Collection

At the end of the vegetative stage, four traits, including plant height, crown width, primary lateral branch height, internode length were measured in 2017. Three traits (plant height, crown width and primary lateral branch height) were measured once for each individual, the methods refer to Ye et al. [26]. Plant height refers to the vertical distance between the highest point of the plant and the ground level. Primary lateral branch height refers to the vertical distance between the first branch point of the plant and the ground level. We evaluated internode length for each individual from three different orientations and selected annual branches. The crown width was measured twice and the average value of the east–west and north–south directions was taken. Data were processed using software SPSS 20.0 (SPSS, Chicago, IL, USA), and histograms of frequency were drawn.

### 2.3. DNA Extraction and Molecular Marker Development

The FastDNA kit (Tiangen Biotech, Beijing, China) was used to extract total genomic DNA for AFLP and SSR analysis from fresh young leaves in accordance with the manufacturer’s protocol. DNA quality and concentration were measured by 1% agarose gel electrophoresis (Gel red with 0.1 mg/mL 1× TAE buffer), and the bands were observed under ultraviolet light [32].

AFLP was performed according to the method described by He et al. (2014) [33]. A total of 921 SSR primers were synthesized based on published papers [24,25,27,34–36]. SSR was performed according to the method described by Ye et al. [28].

### 2.4. Data Analysis and Map Construction

The ABI 3730 DNA automatic sequencer was used to detect the amplified products of AFLP and SSR. GeneMarker Version1.71 (Applied Biosystems) software was used for data

collection and processing. AFLP data were scored as “1” or “0” in Excel format, while SSR data were exported in fragment sizes.

The genetic map was constructed according to the operation guide of Joinmap 4.1. After importing the encoded data, the model of the drawing group was selected as the cross pollinator group, and the group command was used in the toolbar to divide all the obtained marks into different linkage groups. Linkage between two markers was declared significant in two-point linkage analyses with an LOD threshold of 2.0. The map distance was calculated using the Kosambi mapping function [37], and MapDraw was used to draw the map [38].

### 2.5. QTL Analysis

QTL analysis was performed using composite interval mapping (CIM) using Windows QTL Cartographer 2.5. The LOD threshold significant value was obtained using 1000 permutations of the phenotyping data. The QTL naming rules in this study are: “q” + “target traits” + “-” + “chromosome number or linkage group code” + “QTL number”. The full name of the QTL is usually presented in italics, such as *qPH-4-1*, indicating the first in the fourth linkage group related to plant height QTL.

## 3. Results

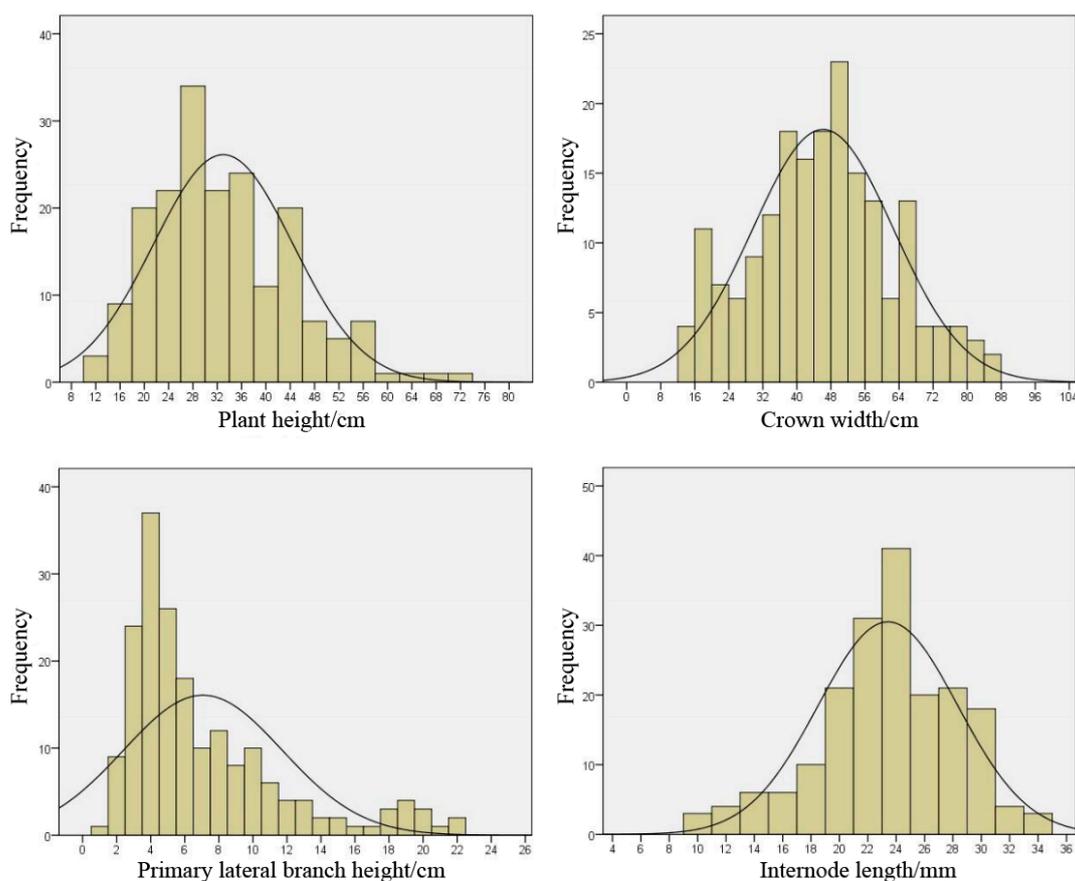
### 3.1. Phenotype Data Analysis

The phenotypic data statistics of 188 mapping progenies are shown in Table 1. The average plant height is 31.1 cm, the maximum is 72.0 cm, the minimum is 8.1 cm, the SD is 11.4, the variance is 130.8, the kurtosis is 0.7, the skewness is 0.39, and the CV is 36.7%. The average crown width is 44.1 cm, the maximum is 86.0 cm, the minimum is 10.3 cm, the SD is 16.6, the variance is 274.1, the kurtosis is 0.1, the skewness is −0.4, and the CV is 37.6%. The average primary lateral branch height is 6.5 cm, the maximum is 22.0 cm, the minimum is 0.2 cm, the SD is 4.6, the variance is 21.2, the kurtosis is 1.47, the skewness is 1.74, and the CV is 70.8%. The average internode length is 22.5 mm, the maximum is 34.6 mm, the minimum is 8.0 mm, the SD is 5.1, the variance is 26.0, the kurtosis is −0.24, the skewness is 0.41, and the CV is 22.7%.

**Table 1.** Descriptive statistics of the four traits in the mapping population.

Trait	Mean	Max	Min	SD	Variance	Skewness	Kurtosis	CV
Plant height/cm	31.1	72.0	8.1	11.4	130.8	0.39	0.7	36.70%
Crown width/cm	44.1	86.0	10.3	16.6	274.1	−0.4	0.1	37.6%
Primary lateral branch height/cm	6.5	22.0	0.2	4.6	21.2	1.74	1.47	70.80%
Internode length/mm	22.5	34.6	8.0	5.1	26.0	0.41	−0.24	22.70%

Combining the frequency distribution of the four traits (Figure 1), it can be seen that the distributions of plant height, crown width, and primary lateral branch height are all left skewed, and only the distribution area of internode length tilts to the right. Therefore, the skewness of the internode length is negative, and the skewness of the other three traits is positive. From the perspective of the skewness value, the height of the primary lateral branch height is the largest, and the distribution curve is severely inclined to the left, indicating that there is a certain degree of skewness segregation for this trait in the population. The more symmetrical the distribution, the more evenly distributed the trait is in the population.



**Figure 1.** Frequency distribution of plant height, crown width, primary lateral branch height and internode length.

Comprehensive phenotypic trait data statistics and frequency histogram, the differences among the four trait traits are significant, the degree of separation is high, and they show continuous changes, which are in line with the characteristics of normal distribution, suitable for QTL positioning research.

### 3.2. Polymorphisms Revealed by Molecular Markers

Of the 384 AFLP primer combinations tested, 46 AFLP primer combinations showed highly repeatable polymorphisms, which were subsequently used to evaluate 188  $F_1$  progenies. In AFLP analysis, the size of the AFLP fragment is between 48 and 496 bp. These 46 primer combinations produced 958 amplification products that were polymorphic, accounting for 23% of the total. Chi-square ( $\chi^2$  test, d.f. = 1) was used to detect the segregation of each locus. Among all loci, there were 708 that met Mendel's 1:1 segregation ratio and 3:1 segregation ratio, accounting for 74%. The rest of the sites did not meet the chi-square test, these represent partial segregation markers and were no longer used in subsequent map construction.

SSR polymorphisms were screened for the parents and four progenies, and 118 primers were obtained with good polymorphisms. The chi-square test found that 100 pairs of primers met Mendel's expected segregation ratio ( $\chi^2 < 0.01$ ), and 18 primers had a partial segregation, the ratio was 15%. A total of 330 polymorphic sites were amplified by 118 SSR primers, with an average of 2.8 per primer.

### 3.3. Linkage Analysis and Map Construction

A total of 808 markers (708 AFLP and 100 SSR) were used to construct linkage maps. A total of 234 loci (198 AFLP and 36 SSR) were mapped into 22 genetic linkage groups, and the remaining 574 markers were not mapped to the link map (Figure 2, Table 2). The map

covers a total genome length of 1272 cm, the longest linkage group reaches 167.2 cm, the smallest is 15.6 cm, the average linkage group length is 57.8 cm, the maximum spacing between each marker is 28.30 cm, and the minimum spacing is 0.40 cm. The average distance between them is 6.8 cm. Among all the linkage groups, four linkage groups are larger, 12 linkage groups are smaller, and there are four triplets and two diads. There are 66 markers on the largest linkage group, and only two markers on the smallest linkage group. The average number of markers in each linkage group is 11.

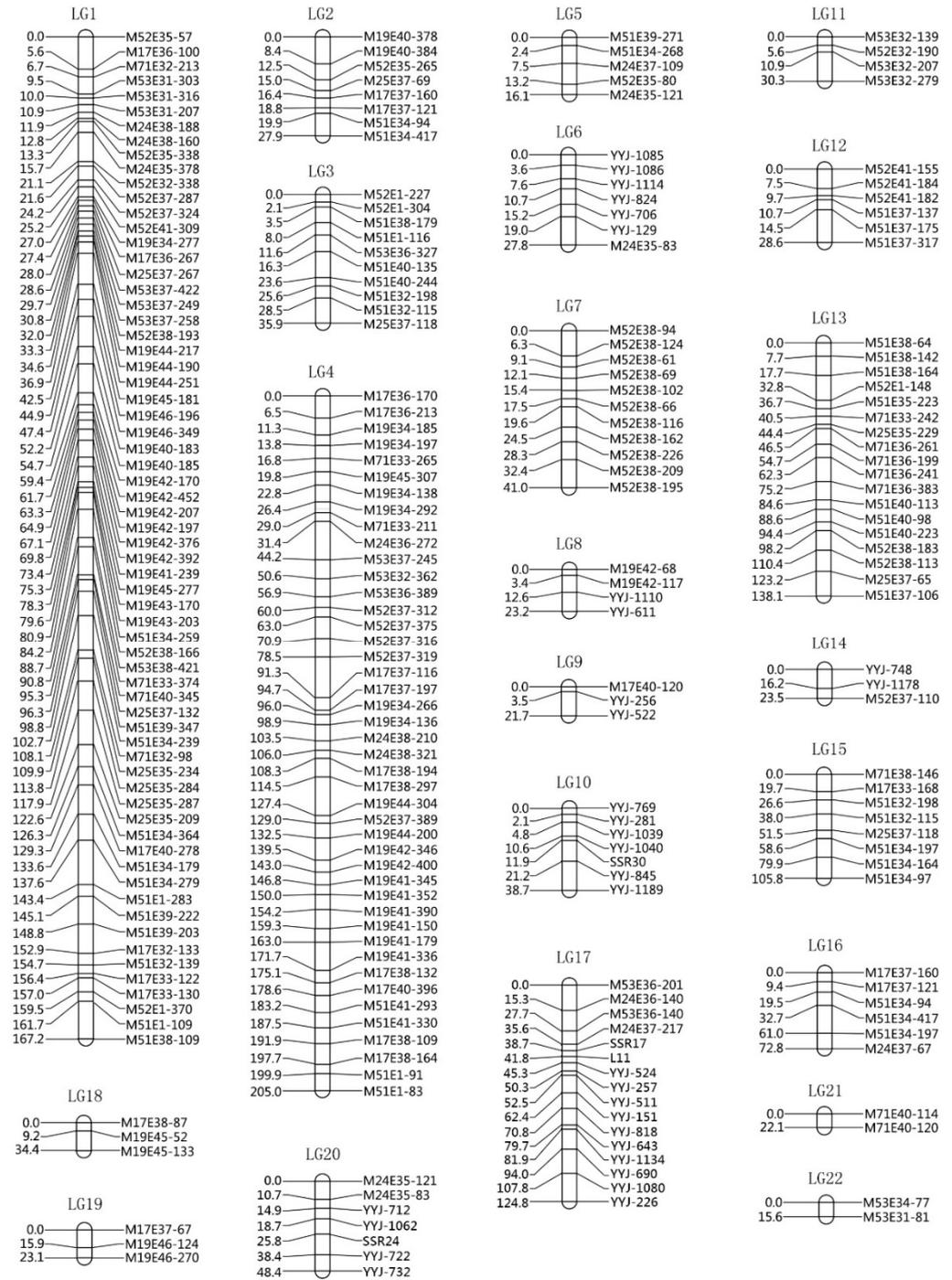


Figure 2. The genetic linkage map of Lagerstroemia derived from the BC<sub>2</sub> populations. Map distances are shown in cm on the left of each linkage group and molecular markers are on the right side of each linkage group.

**Table 2.** Markers on the different linkage of the genetic maps in *Largerstroemia*.

Linkage Group	Markers Number	Number of Gaps Greater than 20 cm	Total (cm)	Max (cm)	Min (cm)	Average (cm)
LG1	66	0	167.2	5.8	0.4	2.53
LG2	8	0	27.9	8.4	1.1	3.49
LG3	10	0	35.9	7.4	1.4	3.59
LG4	44	0	205.0	12.9	1.3	4.66
LG5	5	0	16.1	5.7	2.4	3.22
LG6	7	0	27.8	8.8	3.1	3.97
LG7	11	0	41.0	8.6	2.1	3.73
LG8	4	0	23.2	10.6	3.4	5.80
LG9	3	0	21.7	18.2	3.5	7.23
LG10	7	0	38.7	17.5	1.3	5.53
LG11	4	0	30.3	19.4	5.3	7.58
LG12	6	0	28.6	14.1	1.0	4.77
LG13	18	0	138.1	15.1	2.1	7.67
LG14	3	0	23.5	16.2	6.9	7.83
LG15	8	1	105.8	25.9	7.38	13.23
LG16	6	1	72.8	28.3	9.4	12.13
LG17	16	0	124.8	17.0	2.2	7.80
LG18	3	1	34.4	25.2	9.2	11.47
LG19	3	0	23.1	15.9	7.2	7.70
LG20	7	0	48.4	12.6	3.9	6.91
LG21	2	1	22.1	22.1	22.1	11.05
LG22	2	0	15.6	15.6	15.6	7.80
Average	11	0.75	57.8	15.1	5.1	6.80

### 3.4. QTL Mapping

Using the composition interval mapping method and setting the LOD value to 2.0, a total of eight QTL sites were detected (Table 3, Figure 3).

**Table 3.** QTLs controlling the four traits examined by composite interval mapping.

Trait	QTL Loci	Linkage Group	Marker Interval	Position	LOD Threshold	Variation Explained
Plant height	<i>qPH-1-1</i>	LG1	M19E44-251-M19E45-181	38.2	4.2	32.36
	<i>qPH-4-1</i>	LG4	M52E37-319-M17E37-116	84.6	3.2	16.18
	<i>qPH-17-1</i>	LG17	YYJ-1134-YYJ-690	83.2	2.9	12.73
Crown width	<i>qCW-4-1</i>	LG4	M19E34-138-M19E34-292	23.1	3.6	18.07
Primary lateral branch height	<i>qPLBH-1-1</i>	LG1	M19E44-251-M19E45-181	40.9	3.4	20.59
	<i>qPLBH-7-1</i>	LG7	M52E38-116-M52E38-162	20.7	2.9	15.34
Internode length	<i>qIL-1-1</i>	LG1	M25E35-209-M51E34-364	123.8	3.1	14.86
	<i>qIL-20-1</i>	LG20	YYJ-1062-SSR24	22.6	2.5	9.87

Three QTLs related to plant height were located, namely *qPH-1-1*, *qPH-4-1* and *qPH-17-1*. Among them, *qPH-1-1* was located between the LG1 linkage group M19E44-251-M19E45-181 markers, the marker spacing is 38.2 cm, the LOD value is 4.2, and the phenotypic

variation rate is 32.36%; *qPH-4-1* was located between the LG4 linkage group M52E37-319-M17E37-116 markers, the marker spacing is 84.6 cm, the LOD value is 3.2, and the phenotypic variation rate is 16.18%; *qPH-17-1* was located in the LG17 linkage group between YYJ -1134-YYJ-690 markers, the marker spacing is 83.2 cm, the LOD value is 2.9, and the interpretable phenotypic variation rate is 12.73%.

The *qCW-4-1* related to crown width was located, which was located between the LG1 linkage group M19E34-138-M19E34-292 markers, the marker spacing is 23.1 cm, the LOD value was 3.6, and the phenotypic variability was explained 18.07%.

Two QTLs related to the primary lateral branch height were located, namely *qPLBH-1-1* and *qPLBH-7-1*. Among them, *qPLBH-1-1* was located between the LG1 linkage group M19E44-251-M19E45-181 markers, the marker spacing is 40.9 cm, the LOD value is 3.4, and the interpretable phenotypic variation rate is 20.59%; *qPLBH-7-1* was located between LG52 linkage group M52E38-116-M52E38-162 markers, with a marker spacing of 20.7 cm, an LOD value of 2.9, and an interpretable phenotypic variation rate of 15.34%.

Two QTLs related to internode length were located, namely *qIL-1-1* and *qIL-20-1*. Among them, *qIL-1-1* is located between LG1 linkage group M25E35-209-M51E34-364 markers, the marker spacing is 123.8 cm, the LOD value is 3.1, and the phenotypic variation rate is 14.86%; *qIL-20-1* was located between the LG20 linkage group YYJ-1062-SSR24, the marker spacing is 22.6 cm, the LOD value is 2.5, and the interpretable phenotypic variation rate is 9.87%.

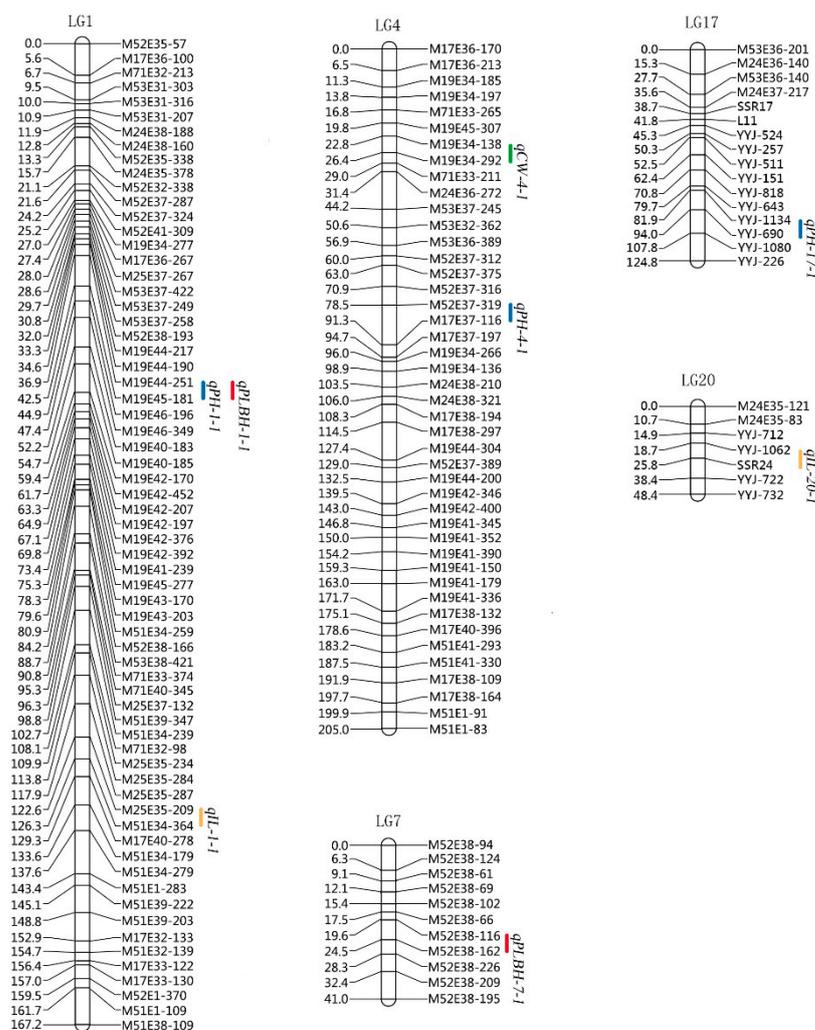


Figure 3. The results of the QTL test for the plant architecture traits. The right side shows the QTL name.

## 4. Discussion

### 4.1. Genetic Mapping Is an Effective Way of Gene Mapping

With the continuous development of gene sequencing technology, biological research has entered the whole genome era, but genetic linkage maps and QTL mapping are still important bridges between genes and phenotypes, and they have irreplaceable application value. A genetic linkage map is different from GWAS in that it needs to construct a mapping population. Although it takes a long time, it is more targeted for the study of traits and is an important research method for precise positioning.

In rice, the QTL controlling rice grain length and grain weight was preliminarily located through genetic maps [39], and it was located within the 7.9 Kb range of the third chromosome, and finally, the *GS3* gene was located [40]. In peach, by constructing a genetic map, the candidate gene *PpeMYB25* was found to control the hair of the fruit [41]. Since Peltier et al. [42] first constructed a genetic map of *petunia hybrida* using RAPD molecular markers and morphological markers in 1994, various ornamental plants have successively been used for research on genetic linkage maps. Abe et al. [43] used RAPD and ISSR to construct the first Asiatic hybrid lily genetic map; Sun et al. [44] constructed a genetic map of plum, with 129 SSRs and 1484 SNP markers; Yu et al. [45] constructed a genetic linkage map of tetraploid rose with the largest population so far; Fu et al. [46] developed a large number of SNPs and constructed a genetic map of *Gerbera hybrida*, with 20 QTLs being detected.

It can be seen that both genetic linkage and QTL mapping are effective methods for gene mapping. However, it is difficult to build populations of woody plants due to their large size, slow growth, and difficulties associated with asexual reproduction. Asexual reproduction in woody plants takes a long time, and therefore, the application of this in woody plant research is limited. *Lagerstroemia* is easy to hybridize, grows quickly, and has a high survival rate of asexual reproduction. It is an ideal material for genetic research on woody plant populations.

### 4.2. Mapping Population and Molecular Markers

The construction of a genetic linkage map must consider the genetic background of the parent material, the size of the segregating population and the characteristics of the selected molecular markers. The selection of parents of the mapping group and the size of the group play a decisive role in the mapping results. It is difficult for woody plants to construct RIL groups, such as crops and vegetables in the short term, and they are heterozygous, so the double pseudo-testcross mapping strategy is adopted for group construction.  $F_1$  [34] was constructed using *L. fauriei* and *L. indica* "Pocomoke". After SSR molecular marker evaluation, the parents were found to be highly polymorphic at the molecular level. On this basis, high type progenies were selected as the female parent and backcrossed with *L. indica* "Pocomoke" to obtain the  $BC_1$  population, and then high type  $BC_1$  progenies were selected as the female parent and backcrossed with *L. indica* "Pocomoke" to obtain 188  $BC_2$  progenies.

SSR markers are considered to be extremely reliable molecular markers and can be integrated with information anchor points from previously generated genetic linkage maps. Most of these markers exist in non-coding regions. AFLPs can generate more polymorphic markers without any prior knowledge of DNA sequence, and restriction sites are often distributed in the expression region of genes. Two effective polymorphic markers—due to the different mutation rates and uneven linkage disequilibrium (LD)—can capture the distribution of different genome characteristics between chromosomes, resulting in the map markers being more evenly distributed [45,47].

However, the repeatability of AFLP technology is not good, and this can easily result in partial segregation [48,49]. The emergence of this phenomenon has been widely reported, and the reasons behind it are mainly due to biological factors (population size, marker type, DNA quality, selection effect of gametes or sporophytes, free-riding effect, environmental factors, etc.) and statistical bias or errors in genotyping and scoring [45,50,51]. In this

study, the segregation ratio of AFLP markers reached 26%, and the markers in the final figure of the genetic map filtered out the segregation markers, in line with the Mendelian segregation ratio.

#### 4.3. Genetic Linkage Map

This map is the second genetic linkage map of *Lagerstroemia*, and the first time QTL mapping has been used to produce a genetic map for *Lagerstroemia*. He et al. (2014) constructed an F<sub>1</sub> population with *L. caudata* and *L. indica* “Xiang Xue Yun”, which have large differences in floral traits, and used AFLP and SSR as markers to construct a genetic linkage with 173 markers and a distance of 1162.1 cm.

The difference with the first genetic map of *Lagerstroemia* is that our map focuses on the characteristics of plant architecture. *Lagerstroemia* covers most of the plant architecture characteristics of woody plants, including low shrubs of 0.3 m and large shrubs of more than 3 m. Therefore, we used it as a research material for studying the architecture characteristics of woody plants. Finally, a genetic linkage map with 234 markers and a length of 1272 cm was obtained. QTL mapping for plant height, primary lateral branch height, crown width and internode length was carried out, laying the foundation for the study of plant architecture traits.

#### 4.4. QTL Mapping for Plant Architecture Traits

Research on plant architecture varies according to the characteristics of the plant itself, and these often determine its economic value. For example, tiller in rice can increase its yield [5], a reasonable ratio of plant height to ear height in corn can increase its yield [52], apple branch number and plant height affect its yield and harvest [53], plant height and the weeping trait of plum can increase its ornamental value [54]. Plant architecture research has different directions in different plants.

The progenies of the population have great differences in phenotype. The coefficient of variation of plant height, crown width, primary lateral branch height and internode length all exceed 20%, which is a trait with a high degree of variation. In addition, the frequency distributions of the four traits all show continuous changes, and there is a certain skewness on the histogram, which is approximately in line with the characteristics of the normal distribution. We believe that the reason for the skewness is that the traits of the BC<sub>2</sub> population are more similar to those of the backcross parents.

The *qPH-1-1* and *qPLBH-1-1* are located in the same interval, which is consistent with the mechanism of plant height traits, that is, plant height is positively correlated with internode length [31]. This indicates that in the interval between M19E44-251 and ME19E45-181, there may be a regulatory factor that can regulate plant height by regulating the length of internodes.

Plant architecture traits are gradually formed during plant development, so they cannot be viewed from a static perspective alone. In particular, in plant height research, dynamic QTL can locate regulatory genes at different developmental stages of plants, aiding understanding the development process of plants [55]. This research will continue in this regard, and guide plant cultivation by understanding the QTL regulation of plant height dynamics.

In this study, a preliminary QTL location was carried out. In future studies, the gene location can be further accurately located by combining GWAS, BSA or encrypting the target gene interval.

## 5. Conclusions

Plant architecture is an important woody plant trait, but related research is still insufficient. In this study, using 188 BC<sub>2</sub> progenies as materials, a genetic map of *Lagerstroemia* was constructed using AFLP and SSR markers, and the QTLs of four key plant architecture traits (plant height, crown width, primary lateral branch height and internode length) were analyzed. The genetic map contains 22 linkage groups, including 198 AFLP markers and

36 SSR markers. The total length of genome covered by the map is 1272 cM, and the average distance between markers is 6.8 cM. On this basis, further gene function verification and analysis of its molecular mechanisms are necessary.

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