Scholars Academic Journal of Biosciences (SAJB)
Sch. Acad. J. Biosci., 2014; 2(12C): 983-986
©Scholars Academic and Scientific Publisher
(An International Publisher for Academic and Scientific Resources)
www.saspublishers.com
ISSN 2321-6883 (Online)
ISSN 2347-9515 (Print)
DOI: 10.36347/sajb.2014.v02i12.027

Research Article

Quantitative trait locus detection associated with kernel length in maize

Changmin Liao[1,2*]
[1]Library, China West Normal University, Nanchong City, China
[2]College of Life Science, China West Normal University, Nanchong City, China

***Corresponding author**
Changmin Liao
Email: liaochangminlxh@aliyun.com

Abstract: Mo17 and Huanzaosi are two elite maize (*Zea mays* L.) inbred lines, and widely applied in breeding cultivation varieties and realizing genetic mechanism in China. In this presented study, a recombinant inbred line (RIL) population bred from the two maize materials as parents was used for quantitative trait locus (QTL) mapping for kernel length. The results showed that kernel length is a quantitative trait controlled by multiple genes according to its phenotypic investigation, but no QTLs controlling kernel length were identified via Interval Mapping and Composite Mapping methods, this could probably be caused from less markers included in the established map. The results are beneficial for us in realizing genetic basis of kernel length in maize breeding program.

Keywords: Maize (*Zea mays* L.), Quantitative trait locus (QTL), Kernel length, Recombinant inbred line (RIL) population.

INTRODUCTION

As well known, maize (*Zea mays* L.) is one of the most important crops throughout the world, and grain yield is always the target pursued by maize breeders. But the agronomic trait has complex genetic mechanism, and can be dissected into many secondary traits, such as plant number per hectare, ear number per plant, kernel number per ear, single-kernel weight, etc. Kernel length is an important trait, related to single-kernel weight and seed appearance. But to date, the study on genetic mechanism of kernel length was rarely reported from published literature.

Quantitative trait locus (QTL) mapping is an effective solution for understanding genetic mechanism of a trait, presently, a large number of QTLs were identified and mapped on different chromosomes in crops [1-3], but for maize, the studies on QTL detection are always focused on grain yield [4-6], plant morphology [7-9] disease resistance [10, 11], and so on. Whereas for kernel length trait, only limited reports were found in previous papers. Li et al. identified four QTLs for kernel length, on chromosomes 1, 4, 6, and 8 [12]. Four years later, Peng et al. identified seven QTLs for kernel length using two segregation populations, on chromosomes 1, 4, 5, 8 and 10 [13]. Lately, Zhang et al. and Liu et al. found total 10 QTLs associated with kernel length on four chromosomes [14, 15]. From these reports, it was easily found that different mapping population, genetic map or ecological conditions could leads to different results, including QTL number, location and genetic effects. Therefore, it is still significant that selecting a different segregation population from the previous to detect the QTLs controlling kernel length in maize.

In this experiment, an immortal recombinant inbred line (RIL) segregation population, derived from the cross between Mo17 and Huangzaosi, was used to detect the QTLs for kernel length, and the objectives were to understand the genetic basis of the trait more clearly, and to look for some molecular markers which can be applied in maize breeding project.

MATERIALS AND METHODS

Plant materials

The plant materials involved in this experiment included maize inbred lines Mo17 and Huangzaosi as parents, and an RIL population consisting of 239 RILs. The population was derived from the cross between Mo17 (female) and Huangzao4 (male).

Field experiment

According to randomized block design, the 241 individuals mentioned above were planted at the experiment field of Nanchong Agricultural Academy, Nanchong City, Sichuan Province, China, with three replicate for each individual and 20 plants per replicates.

Phenotypic observation and statistic analysis

After harvest, twenty kernels for each individual were measured the trait kernel length (mm) with an electronic digital caliper, then the mean of the twenty kernels was computed. For the population, descriptive statistics was analyzed using a statistical software named SPSS version 11.5, including minimum, maximum, range, mean, standard deviation (SD), coefficient of variation (COV), skewness and kurtosis.

QTL detection

Based upon an established marker linkage map [16], together with the kernel length data of the 239 RILs, the QTLs controlling kernel length were detected via the two methods interval mapping (IM) and composite interval mapping (CIM) within the QTL mapping software named Windows QTL Cartographer version 2.5 [17]. All controlling parameters were default settings during QTL scanning, and the logarithm of odds (LOD) threshold was set for the trait kernel length by randomly permuting 1,000 times at a significance level of P=0.05 [18].

RESULTS

Descriptive statistics

For the two parental lines, Mo17 and Huangzaosi had 9.34 mm and 8.69 mm, respectively. As to the segregation population, which parameter values were listed in Table 1, from the result, it was found that kernel length should be a quantitative trait controlled by multiple genes, and thus, the trait could be used for QTL mapping analysis.

Table 1: Descriptive statistics for the trait kernel length in RIL population

Trait	Minimum	Maximum	Range	Mean	CoV (%)	SD	Skewness	Kurtosis
Kernel length (mm)	5.72	12.00	6.28	8.22	11.92	0.98	0.178	0.311

SD: standard deviation; COV: coefficient of variation.

QTL detection

The results of 1000-time permutation test showed that the LOD threshold values should be higher than 2.0 for the two QTL mapping methods IM and CIM., and the QTL scanning results were shown in Figure 1 (IM method) and Figure 2 (CIM method). According to the LOD threshold values, it was easily found that no QTLs were identified. Nevertheless, the lager LOD values were found on chromosomes 2 and 4.

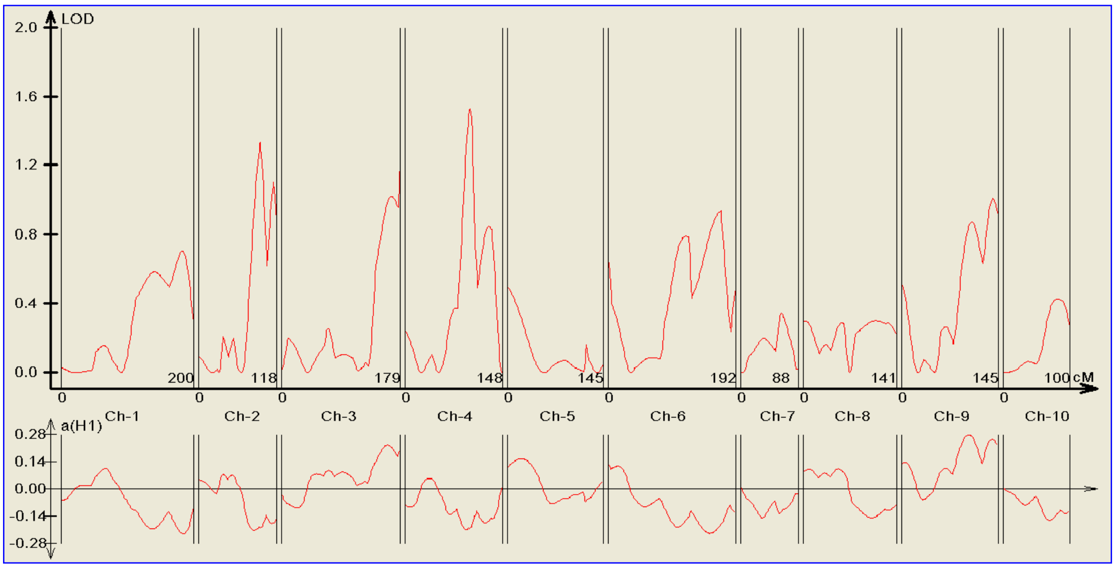

Fig-1: QTL scanning for kernel length via IM method. The maximum of LOD was showed on chromosome 4, but less than 2.0, so no QTL controlling kernel length was detected via IM method in this experiment.

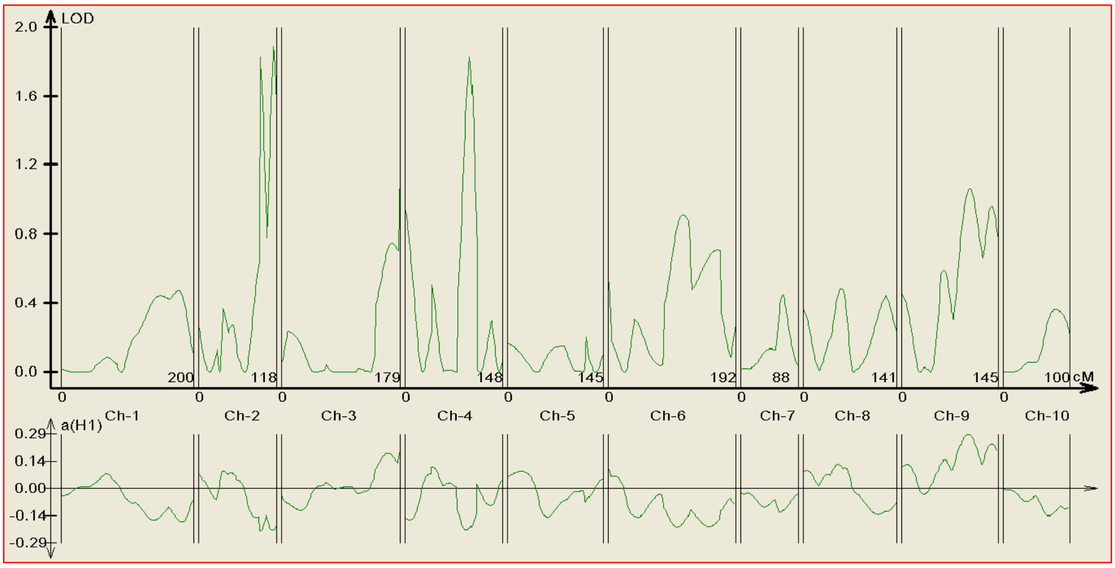

Figure 2: QTL scanning for kernel length via CIM method. Three high LOD values displayed on chromosomes 2 (two) and 4 (one), but all of them were obviously less than the LOD threshold value, thus, no QTLs for kernel length was identified via CIM method in this study.

DISCUSSION

In this experiment, an immortal RIL population was used to detect the QTLs for kernel length, and QTL scanning results showed that no QTL was identified. This was probably caused from the genetic map including fewer markers. Nevertheless, three higher LOD values were detected on within chromosomes 2 (two) and 4 (one) from the QTL scanning curves.

According to previous literatures, some QTLs were found on different chromosomes (Table 2). All the ten chromosomes include QTLs for kernel length, except for the seventh chromosome. Among the chromosomes identified QTLs for kernel length, the ninth chromosome possess the maximum QTLs, up to 5, followed by the fourth and fifth chromosomes, the third chromosome has the minimum in QTL number, only one. The different QTL mapping results were probably due to different mapping populations, genetic maps or environments. But to be mentioned, these results revealed that the agronomic trait kernel length was quantitative, and its phenotype was controlled by multiple genes.

Table 2: The QTLs for kernel length identified in different studies

References	**Parents**	**Number of QTLs**	**Chr. No.**									
			1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Li et al. [12]	Qi319×Huangzaosi	4	1			1		1		1		
Peng et al. [13]	Qi319×Huangzaosi	3	1			1						1
Peng et al.[13]	Ye478×Huangzaosi	4				1	1			1	1	
Zhang et al. [14]	Xu178×HuangC	4			1		2					1
Liu et al. [15]	V671×Mc	6		2							4	
This study	Mo17×Huangzaosi	0										

QTL: quantitative trait locus; Chr. No.: chromosome number

To identify some loci associated with kernel length in our study, more molecular markers must be added into the established genetic map, especially chromosomes 2 and 4, only in this way, we can find these markers that can be co-inherited with the QTLs for kernel length. Presently, this work was in process based on the constructed RIL segregation population.

ACKNOWLEDGMENT

This research supported by the Scientific Research Fund of Sichuan Provincial Education Department (#13ZA0012).

REFERENCES

1. Steele KA, Price AH, Witcombe JR, Shrestha R, Singh BN, Gibbons JM, Virk DS; QTLs associated with root traits increase yield in upland rice when

transferred through marker-assisted selection. Theor Appl Genet, 2013; 126: 101-108.

2. Guimaraes CT, Simoes CC, Pastina MM, Maron LG, Magalhaes JV, Vasconcellos RC, Guimaraes LJ, Lana UG, Tinoco CF, Noda RW, et al; Genetic dissection of Al tolerance QTLs in the maize genome by high density SNP scan. BMC Genomics, 2014; 15: e153.
3. Faris JD, Zhang Q, Chao S, Zhang Z, Xu SS; Analysis of agronomic and domestication traits in a durum × cultivated emmer wheat population using a high-density single nucleotide polymorphism-based linkage map. Theor Appl Genet, 2014; 127: 2333-2348.
4. Huang YF, Madur D, Combes V, Ky CL, Coubriche D, Jamin P, Jouanne S, Dumas F, Bouty E, Bertin P, Charcosset A, Moreau L; The genetic architecture of grain yield and related traits in Zea maize L. revealed by comparing intermated and conventional populations. Genetics, 2010; 186: 395-404.
5. Liu R, Jia H, Cao X, Huang J, Li F, Tao Y, Qiu F, Zheng Y, Zhang Z; Fine mapping and candidate gene prediction of a pleiotropic quantitative trait locus for yield-related trait in Zea mays. PLoS One, 2012; 7: e49836.
6. Semagn K, Beyene Y, Warburton ML, Tarekegne A, Mugo S, Meisel B, Sehabiague P, Prasanna BM; Meta-analyses of QTL for grain yield and anthesis silking interval in 18 maize populations evaluated under water-stressed and well-watered environments. BMC Genomics, 2013; 14: e313.
7. Sibov ST, de Souza CL Jr, Garcia AA, Silva AR, Garcia AF, Mangolin CA, Benchimol LL, de Souza AP; Molecular mapping in tropical maize (*Zea mays* L.) using microsatellite markers. 2. Quantitative trait loci (QTL) for grain yield, plant height, ear height and grain moisture. Hereditas, 2003; 139: 107-115.
8. Zhang ZM, Zhao MJ, Ding HP, Rong TZ, Pan GT; QTL mapping analysis of plant height and ear height of maize (Zea mays L.). Genetika, 2006; 42: 391-396.
9. Li Y, Dong Y, Niu S, Cui D; The genetic relationship among plant-height traits found using multiple-trait QTL mapping of a dent corn and popcorn cross. Genome, 2007; 50: 357-364.
10. Berger DK, Carstens M, Korsman JN, Middleton F, Kloppers FJ, Tongoona P, Myburg AA; Mapping QTL conferring resistance in maize to gray leaf spot disease caused by Cercospora zeina. BMC Genet, 2014; 15: e60.
11. Zambrano JL, Jones MW, Brenner E, Francis DM, Tomas A, Redinbaugh MG; Genetic analysis of resistance to six virus diseases in a multiple virus-resistant maize inbred line. Theor Appl Genet, 2014; 127: 867-880.
12. Li YX, Wang Y, Shi YS, Song YC, Wang TY, Li Y; Correlation analysis and QTL mapping for traits of kernel structure and yield components in maize. Scientia Agricultura Sinica, 2009; 42: 408-418.
13. Peng B, Li Y, Wang Y, Liu C, Liu Z, Zhang Y, Tan W, Wang D, Shi Y, Sun B, Song Y, Wang T, Li Y; Correlations and comparisons of quantitative trait loci with family per se and testcross performance for grain yield and related traits in maize. Theor Appl Genet, 213; 126: 773-789.
14. Zhang Z, Liu Z, Hu Y, Li W, Fu Z, Ding D, Li H, Qiao M, Tang J; QTL analysis of kernel-related traits in maize using an immortalized F2 Population. PLoS One, 2014; 9: e89645.
15. Liu Y, Wang L, Sun C, Zhang Z, Zheng Y, Qiu F; Genetic analysis and major QTL detection for maize kernel size and weight in multi-environments. Theor Appl Genet, 2014; 127: 1019-1037.
16. Liu XH, Tan ZB and Rong TZ; Molecular mapping of a major QTL conferring resistance to SCMV based on immortal RIL population in maize. Euphytica, 2009; 167: 229-235.
17. Wang S, Basten CJ and Zeng ZB; Windows QTL Cartographer 2.5. Department of Statistics, North Carolina State University, Raleigh, Available from http://statgen.ncsu.edu/qtlcart/WQTLCart.htm
18. Fu ZJ, Li WH, Zhang QB, Wang L, Zhang XX, Song GL, Fu ZY, Ding D, Liu ZH and Tang JH; Quantitative trait loci for mercury accumulation in maize (*Zea mays* L.) identified using a RIL population. PLoS One, 2014; 9: e107243.