



QTL mapping for ear tip-barrenness in maize

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Abstract

Barren tip on corn ear is an important agronomic trait in maize, which is highly associated with grain yield. Understanding the genetic basis of tip-barrenness may help to reduce the ear tip-barrenness in breeding programs. In this study, ear tip-barrenness was evaluated in two environments in a $F_{2:3}$ population, and it showed significant genotypic variation for ear tip-barrenness in both environments. Using mixed-model composite interval mapping method, three additive effects quantitative trait loci (QTL) for ear tip-barrenness were mapped on chromosomes 2, 3 and 6, respectively. They explained 16.6% of the phenotypic variation, and no significant QTL \times Environment interactions and digenic interactions were detected. The results indicated that additive effect was the main genetic basis for ear tip-barrenness in maize. This is the first report of QTL mapped for ear tip-barrenness in maize.

Additional key words: quantitative trait loci; *Zea mays* (L.); mixed-model composite interval mapping; SSR.

Abbreviations used: MCIM (mixed-model composite interval mapping); QTL (quantitative trait loci).

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Introduction

Barren tip on corn ear, which shows abortive kernels on the tip of cob tissue, often causes potential yield loss at different ratios (Wang, 2001). Previous studies reported that environmental factors, especially environmental stress at pollination or during grain filling stage, played important roles in the formation of barren tips in maize. For example, stresses like drought, high or low temperature and nutrient deficiency may limit pollination or cause abortive tip kernels after pollination (Zhang *et al.*, 1998; Edreira *et al.*, 2011). Wang *et al.* (1996) and Zhang *et al.* (1999) reported a relation between abortive tip kernels and dynamic changes of hormone components. A few studies on the inheritance of resistance to barren tip have been reported in maize, and the mode of inheritance seems to be polygenic (Meng *et al.*, 2007; Li *et al.*, 2008; Cai *et al.*, 2015). However, only limited genetic information is available at the molecular level. In the present study, we report

QTL mapping of the barren tip trait for the first time in maize.

Material and methods

A sample of 225 $F_{2:3}$ families derived from the cross Zheng58 \times Chang7-2 was used for QTL mapping. Zheng58 and Chang7-2 are the parental lines of the elite Chinese maize hybrid Zhengdan958. The $F_{2:3}$ families and parents were planted in 2010 at two experimental stations of Henan Agricultural University, namely Jiyuan and Zhengzhou. The experiment was a randomized complete block design with three replications in each location. Lines were grown in single rows of 3 m, spaced 0.67 m apart with planting density of 45,000 plants/ha. Nitrogen (170 kg/ha) was applied before sowing and standard cultural practices were used throughout the growing season. At maturity, eight ears in the middle of each plot were harvested and the barren tips were meas-

Table 1. Means of barren tips length (in centimetres) for parental lines and the $F_{2.3}$ population, variance components and broad sense heritability (H) at Jiyuan and Zhengzhou locations.

| Location | Chang7-2 | Zheng58 | $F_{2.3}$ families | | Variance components | | | H |
|-----------|-----------|-----------|--------------------|-----------|---------------------|-----------------|--------------|------|
| | Mean±SD | | Mean±SD | Range | σ_g^2 | σ_{ge}^2 | σ_e^2 | |
| Jiyuan | 0.42±0.24 | 1.58±0.32 | 1.35±0.39 | 0.50-2.49 | 0.44** | | | |
| Zhengzhou | 0.31±0.13 | 1.37±0.40 | 1.22±0.37 | 0.38-2.41 | 0.44** | | | |
| Combined | 0.37±0.20 | 1.45±0.38 | 1.30±0.35 | 0.40-2.27 | 0.27** | 0.13** | 0.12** | 0.81 |

**Significant at $p < 0.01$.

ured. The length of ear tip barrenness was referred to the distance from the bottom of the first round of shrunken kernels to the ear top (Meng *et al.*, 2007).

Standard analysis of variance was performed using the Proc GLM procedure of SAS (SAS Inst., 1999) to determine variation of barren tips among the $F_{2.3}$ families in Jiyuan and Zhengzhou locations. The components of variance were estimated using a complete random effects model and broad sense heritability was calculated as defined by Knapp *et al.* (1985).

Detailed information on the construction of the genetic map was reported previously (Ding *et al.*, 2011). Briefly, all the 225 $F_{2.3}$ families were used for genetic map construction, which included 180 polymorphic SSR markers evenly distributed on 10 chromosomes. The genetic map spanned a total length of 1987.7 cM with an average distance of 11.0 cM between markers. For QTL analysis, a full QTL model was selected to detect the effects and locations of multiple QTL by using the software QTLNetwork 2.0 (Yang *et al.*, 2007). The proportion of phenotypic variation explained by a single QTL was calculated by the square of the partial correlation coefficient, and the general contribution for each QTL was calculated from the relative contributions of all the putative QTL involved.

Results and discussion

The average performance and the descriptive statistics for barren tip of $F_{2.3}$ families as well as the two

parents are given in Table 1. Both parents, Chang7-2 and Zheng58, were consistently different in the length of barren tips: Zheng58 had longer barren tip than Chang7-2 in both locations. The means of $F_{2.3}$ families for barren tip were close to the parental line Zheng58. The analysis of variance revealed that the genotypic components of variance (σ_g^2) were significant ($p < 0.01$) for the $F_{2.3}$ families. The broad sense heritability was relatively high ($H = 0.81$), which indicates that much of the phenotypic variance was genetically controlled and suitable for further QTL mapping.

The search for QTL for barren tip followed the method of mixed model composite interval mapping (MCIM). In total, three additive effects of QTL for barren tip were found on chromosomes 2, 3 and 6, respectively (Table 2). Among them one QTL (bin 3.02), the barren tip increasing allele, was contributed by short barren tip parent Chang7-2, and the other two QTL (bin 2.04/05 and 6.06/6.07) had the barren tip increasing allele coming from long barren tip parent Zheng58. Since the means of $F_{2.3}$ families usually underestimate dominance by a factor of 1/2, only one QTL (bin 6.06/6.07) was detected with significant dominant effect. In combination, all the QTL explained 16.6% of the phenotypic variation, whereas each QTL individually accounted for between 4.0% and 8.5% of the phenotypic variation. No significant QTL \times Environment interactions and digenic interactions were detected.

Ear tip barrenness is an undesirable trait in maize breeding programs, which is usually caused by abortive kernels and unfertilized florets. Previous studies

Table 2. Estimated additive and dominance effect of QTL detected by the MCIM method for barren tips across two locations (Jiyuan and Zhengzhou).

| Bin | Flanking markers | Additive ^[a] (cm) | Dominance ^[b] (cm) | Var (%) ^[c] |
|---|------------------|------------------------------|-------------------------------|------------------------|
| 2.04/05 | umc2030-nc131 | 0.13*** | — | 4.1 |
| 3.02 | bnlg1325-umc2369 | -0.21*** | — | 8.5 |
| 6.06/07 | umc1424-phi123 | 0.11** | 0.11** | 4.0 |
| General contributions to variation: 16.6% | | | | |

^[a]Additive effect; positive values of the additive effect indicate that the Zheng58 alleles increase the barren tip of ear. ^[b]Dominance effect; positive values of the dominance effect indicate that the heterozygotes have higher phenotypic values than the respective means of two homozygotes. ^[c]Percentage of genotypic variation explained by each QTL. **significant at $p < 0.01$; *** significant at $p < 0.001$.

have pointed at environmental factors that affect tip barrenness (Zhang *et al.*, 1998; Edreira *et al.*, 2011). However, there is limited information about the molecular genetic mechanism in maize. In the present study, we provide evidence of QTL responsible for genetic control of tip barrenness in maize. Both additive and dominant effects QTL were identified for barren tip in maize, which further confirmed that the trait of tip barrenness is a polygenic quantitative character (Meng *et al.*, 2007; Li *et al.*, 2008; Cai *et al.*, 2015).

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