

Research Article

Investigation and analysis on the number of barren ear tip per plant in a maize RIL population

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Abstract: Maize (*Zea mays* L.) is one of the most important cereal crops in the world. In this present study, a recombinant inbred line (RIL) population derived from the cross between Mo17 and Huangzao4 were selected to be investigated the trait the number of barren ear tips per plant (NBETP) under two nitrogen regimes, an important agronomic trait related to yield. Based on the phenotypic values of the two parents and RIL population in the trait NBETP, SPSS 11.5 software was used to perform descriptive statistics, analysis of variance and correlation analysis. The results are useful for further quantitative trait locus mapping for the trait NBETP in maize breeding project.

Keywords: maize; the number of barren ear tip per ear; recombinant inbred line population; statistic analysis

INTRODUCTION

Quantitative trait locus (QTL) detection must depend on a segregating population consisting of large number of individuals. Currently, many types of population had already be used for QTL mapping, thereinto, F₂ population is the most widely applied in plant breeding [1-5]. The population has many merits, such as less-time consuming, low cost and codominance. But, there is a shortcoming in QTL mapping for F₂ population, which is to be no continuous plants used for phenotypic survey and DNA experiment, so this type of population is temporal [6]. Comparatively, recombinant inbred line (RIL) population is immortal, and can be utilized in different time and regions, because of its homogenous individuals. However, constructing this population will cost longer time and higher investment funds compared to F₂ population [7]. Presently, RIL population has been used for QTL mapping in many crops, including rice [8-10], soybean [11-13] and wheat [14-16], etc., but only limited reports were searched in maize (*Zea mays* L.) [17-20], especially in China [21-22].

As well known, maize is one of the most important crops throughout the world. According to previous literature, there were many studies on QTL mapping for maize agronomic traits [23-28], including plant phenotype [29-31], yield [32-34] and flower period [35-36] related traits. But, the number of barren ear tip per plant (NBETP), an important agronomic trait related to yield, was hardly studied on QTL identification. Additionally, the QTL number, location and genetic

effects of same trait demonstrate differences in different experiments to some extent, due to different mapping parents, population types or genetic maps.

Therefore in this present study, the trait NBETP of a RIL population derived from the two elite inbred lines Mo17 and Huangzao4 was investigated and analyzed. This objective is to obtain some important data that can be further used for QTL identification.

MATERIAL AND METHODS

Plant materials

The plant materials involved in this study was consisting of two parental inbred lines Huangzao4 and Mo17, and an F₉ RIL population consisting of 221 RILs. Huangzao4 and Mo17 are the representative lines of the Tansipingtou (China) and Lancaster (USA) heterotic groups, respectively. The RIL population was bred from the cross between the two parental lines.

Field Experiments and Statistical Analysis

Above 223 lines were sown under high nitrogen regime (HNR) and low nitrogen regime (LNR) in a complete randomized design with six replicates at Shanxi Academy of Agricultural Sciences, Xinzhou City, Shanxi Province, China, with single-plant planting and 15 plants per row in one replicate, of which three replicates were under high N regime (HNR) and another three replicates were under low N regime (LNR).

During harvest, the middle 10 plants of every replicate of each line were individually investigated the

trait NBETP. Based on the statistic means of every line in a replicate, Statistical Package for Social Scientists software version 11.5 (SPSS 11.5) was used to perform descriptive statistics, analysis of variance (ANOVA) and correlation analysis.

RESULTS AND DISCUSSION

Descriptive Statistics for Parents and Population

For parental materials, the average values of Mo17 were lower than Huangzao4 under HNR, while under LNR, the statistic result is adverse (Table 1). The results of descriptive statistics for the RIL population were shown in Table 2. The RIL population under HNR

possessed higher values than those under LNR for all the eight parameters except minimum and coefficient of variation (CoV). From the frequency distribution graphs of the RIL population (Figures 1 and 2), both of the two group data displayed normal distribution, which suggested that the trait NBETP is a quantitative trait and controlled by polygene.

There were some studies on descriptive statistics for segregation populations and their parents, but they cannot be compared with each other, owing to different parental lines or population types.

Table 1. Mean of the two parental lines in the trait NBETP

N regimes	Mo17	Huangzao4
HNR	1.11	1.26
LNR	1.25	1.09

HNR = high nitrogen regime;
LNR = low nitrogen regime.

Table 2. Descriptive statistics of the RIL population in the trait NBETP

N regimes	Range	Minimum	Maximum	Mean	SD	CoV (%)	Skewness	Kurtosis
HNR	4.48	0.00	4.48	1.25	0.79	63.20	0.99	1.57
LNR	3.79	0.00	3.79	1.12	0.75	66.96	0.83	0.47

SD = standard deviation;
CoV = Coefficient of variation;
HNR = high nitrogen regime;
LNR = low nitrogen regime.

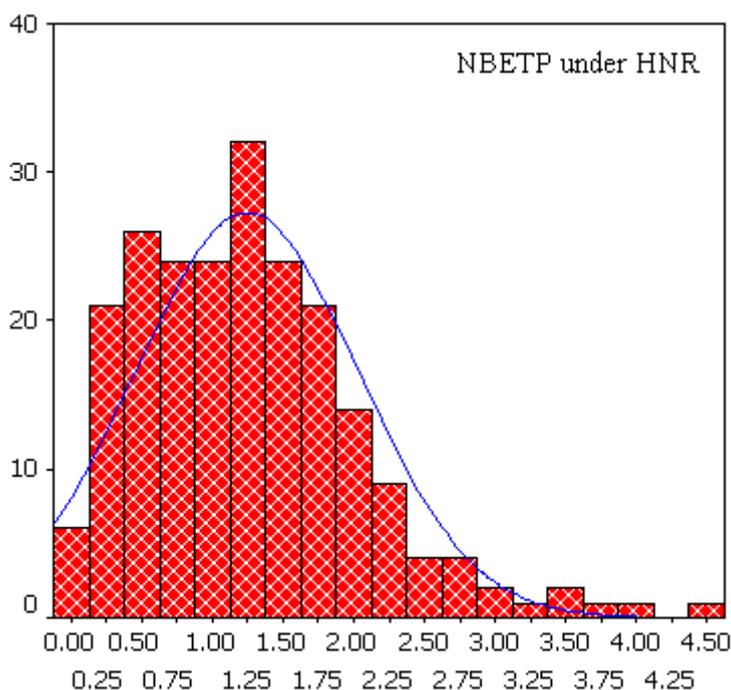


Figure 1. Frequency distribution of the RIL population under HNR for the trait NBETP. Lateral axis for the values of NBETP and vertical axis for the number of RILs.

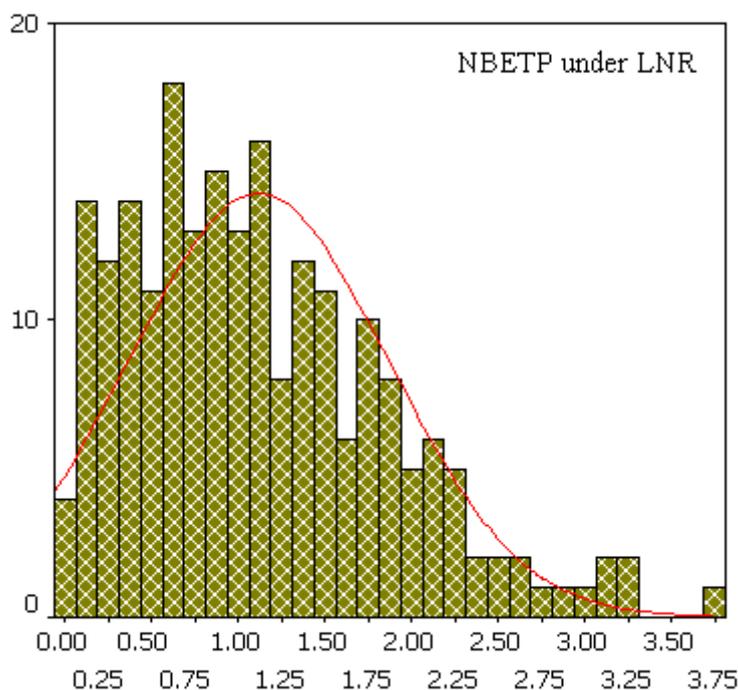


Figure 2. Frequency distribution of the RIL population under LNR for the trait NBETP. Lateral axis for the values of NBETP and vertical axis for the number of RILs.

ANOVA of the RIL population

The RIL population under two nitrogen regimes was performed ANOVA according to the investigated phenotypic values of NBETB for the 221 individuals with three replicates. The results were listed in table 3.

From the data in table 3, it was concluded that the 221 RILs under both N regimes provided significant differences between them in NBETP at 0.01 probability level ($P < 0.001$).

Table 3 ANOVA of the RIL population across two nitrogen regimes in NBETP.

<i>N regimes</i>		<i>Sum of Squares</i>	<i>Df</i> [*]	<i>Mean Square</i>	<i>F</i>	<i>Sig.</i>
HNR	Between Groups	372.643	216	1.725	4.803	0.000
	Within Groups	144.382	402	0.359		
	Total	517.025	618			
LNR	Between Groups	327.259	214	1.529	3.331	0.000
	Within Groups	173.099	377	0.459		
	Total	500.358	591			

* excluded missing data;
HNR = high nitrogen regime;
LNR = low nitrogen regime.

Correlation analysis of the RIL population between two nitrogen regimes

According to the phenotypic values of every RIL of the population under two nitrogen regimes, correlation analysis was performed. The results indicated they were positively correlated at 0.01 probability level, and the value was up to 0.631.

CONCLUSIONS

A RIL population derived from Mo17 × Huangzao4 were investigated the trait NBETP in field together with their parental inbred lines. According to the results of descriptive statistics, ANOVA and

correlation analysis, it was concluded that the trait was quantitative and controlled by multiple genes. The obtained data here could be further used for QTL detection associated with the trait in maize molecular breeding.

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