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Research Article

Study on ear number per plant in maize RIL populating under two nitrogen regimes

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Abstract: Maize (*Zea mays* L.) is one of the most important crops in the world. Quantitative trait locus (QTL) mapping must depend on statistical analysis on phenotypic data of traits in a segregation population. In this presented study, a recombinant inbred line (RIL) population derived from the cross Mo17 × Huangzao4 were used to investigate the trait ear number per plant (ENPP) under two nitrogen regimes. Based on the phenotypic data of the two parental inbred lines and RIL population in the trait ENPP, SPSS version 11.5 software was selected to perform descriptive statistics, analysis of variance and correlation analysis. The results could be further used for QTL identification for the agronomic trait ENPP in maize breeding program.

Keywords: maize, recombinant inbred line, ear number per plant, statistical analysis.

INTRODUCTION

Carrying out quantitative trait locus (QTL) identification must depend on a population consisting of lots of individuals [1]. To this date, there were many types of population used for QTL mapping, among them, F_2 and backcross populations is the most widely applied in plant breeding [2-7]. The two populations have many merits, including less-time consuming, low cost and codominance. But there is a deficiency in QTL mapping, no continuous plants used for phenotypic investigation and DNA extraction, so the two kinds of populations are named temporal segregation populations [8]. Relatively, recombinant inbred line (RIL) population is immortal, and can be applied in different time and regions, owing to its homogenous individuals. Nevertheless, constructing this population will cost longer time and higher investments. Up to now, RIL population has been widely used for QTL mapping in many crops, including rice [9-11], wheat [12-14] and sorghum [15-17], but only limited reports were found in maize (*Zea mays* L.) [18-20]

It is generally known that maize is one of the most important crops in the world. From literature, it is easily found that many agronomic traits have been studied on QTL mapping, including yield [21-23], virus resistance [24-26], plant characteristics [27-29] related traits. But, the trait ear number per plant (ENPP) related to yield was hardly studied on QTL detection. Furthermore, the QTL number, location and genetic effects of same trait probably show differences in different studies by different researchers, caused by different mapping parents, genetic maps or segregation population types.

In our study, a RIL population derived from the two elite inbred lines Mo17 and Huangzao4 was selected to investigate and analyzed the trait ENPP. This objective is to provide some data which can be used for QTL mapping.

MATERIAL AND METHODS

Experimental Materials

The experimental materials involved in this study consisted of parental maize inbred lines Mo17 (a representative line in USA) and Huangzao4 (a representative line in China), and an F_9 RIL population composed of 221 RILs. The RIL population was bred from the cross between Mo17 and Huangzao4.

Field measurement and Statistical Analysis

The two parental lines and their RIL population were sown in a randomized complete block design with six replicates at the experimental farm of Shanxi Academy of Agricultural Sciences, Xinzhou City, Shanxi Province, China, with single-plant planting and 15 plants per row in one replicate, every line is designed three replicates under same nitrogen regime. Before harvest, the agronomic trait ENPP was observed. The data for the parents and RIL population were analyzed using Statistical Package for Social Scientists (SPSS) software version 11.5, including 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 higher than Huangzao4 under HNR, but 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 lower values than those under LNR for range, maximum, skewness and kertosis, while for mean, standard deviation (SD), coefficient of variation (CoV), there were reverse results. Minimum is a special parameter, same value was found under HNR and LNR. From the frequency distribution graphs of the RIL population (Figures 1 and 2), both of the two group data displayed normal distribution approximately, which suggested that the trait NBETP is a quantitative trait and its phenotypic value is controlled by multiple genes.

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

N regimes	Mo17	Huangzao4
HNR	1.33	1.10
LNR	1.11	1.33

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

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

N regimes	Range	Minimum	Maximum	Mean	SD	CoV (%)	Skewness	Kurtosis
HNR	0.87	0.93	1.80	1.11	0.17	15.32	1.85	3.31
LNR	1.02	0.93	1.96	1.10	0.16	14.55	2.25	6.09

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

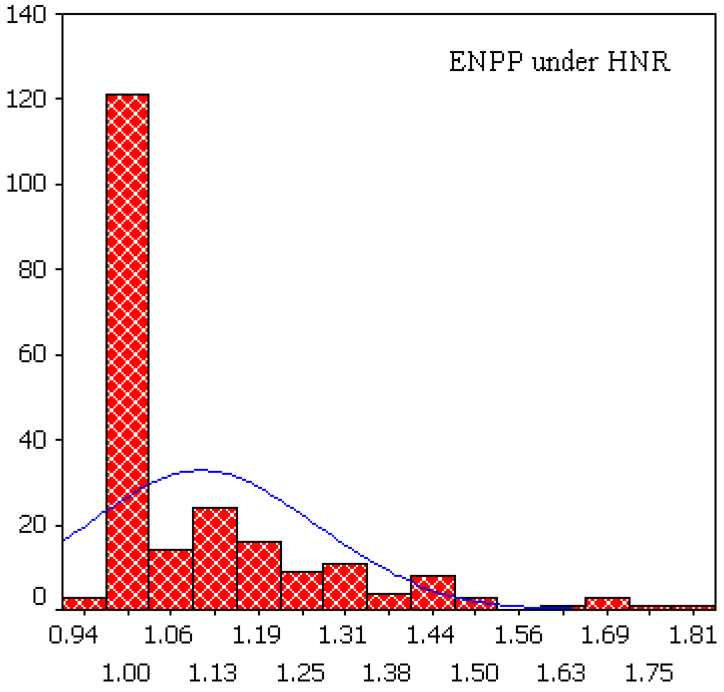

Figure 1. Frequency distribution of the RIL population under HNR for the trait ENPP. Lateral axis for the values of ENPP and vertical axis for the number of RILs.

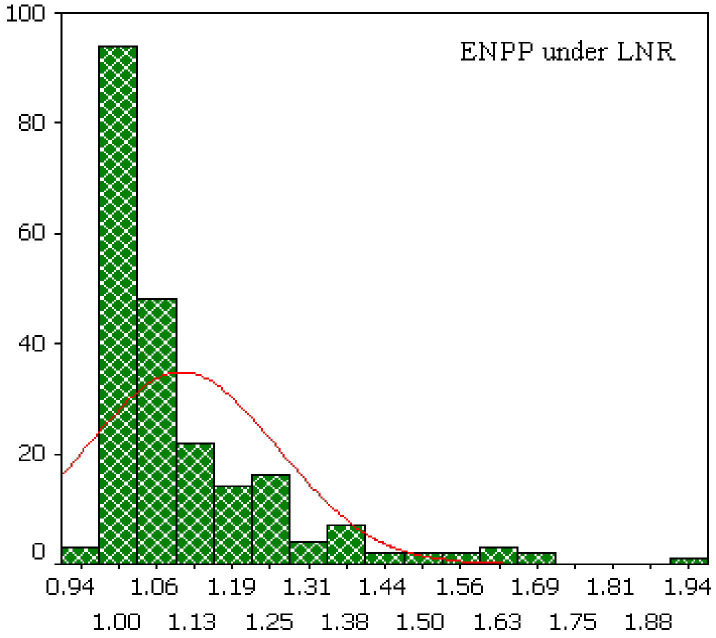

Figure 2. Frequency distribution of the RIL population under LNR for the trait ENPP. Lateral axis for the values of ENPP and vertical axis for the number of RILs.

ANOVA of the RIL population

The RIL population under two nitrogen environments was performed ANOVA according to the observed phenotypic values of ENPP for the 221 individuals. The results were indicated in table 3. According to the data in table 3, it was found that the 221 RILs under both N regimes presented significant differences between them in ENPP at 0.01 probability level (P < 0.001).

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

N regimes	Variation source	Sum of Squares	Df*	Mean Square	F	Sig.
HNR	Between Groups	15.505	219	0.071	2.721**	0.000
	Within Groups	10.721	412	0.026		
	Total	26.227	631			
LNR	Between Groups	15.853	219	0.072	2.656**	0.000
	Within Groups	11.176	410	0.027		
	Total	27.029	629			

*excluded missing data;
**significant difference at 0.01 probability level,
HNR = high nitrogen regime;
LNR = low nitrogen regime.

Correlation analysis of the RIL population between two nitrogen regimes

Based upon the observed values of every RIL of the population under two nitrogen regimes, correlation analysis was performed. The results provided that they were positively correlated at 0.01 probability level for the trait ENPP, and the value was up to 0.474.

CONCLUSIONS

The RIL population bred from Mo17 × Huangzao4 was investigated the trait ENPP in field together with their parental lines Mo17 and Huangzao4. According to the results of descriptive statistics, ANOVA and correlation analysis using SPSS11.5 software, it was concluded that the agronomic trait ENPP was quantitative and affected by multiple genes. The obtained data here could be used to map the QTLs for the trait and breed by marker-assisted selection.

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