Descriptive statistics and correlation analysis of agronomic traits in a maize recombinant inbred line population

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ABSTRACT. Maize (*Zea mays* L.) is one of the most important crops in the world. In this study, 13 agronomic traits of a recombinant inbred line population that was derived from the cross between Mo17 and Huangzao4 were investigated in maize: ear diameter, ear length, ear axis diameter, ear weight, plant height, ear height, days to pollen shed (DPS), days to silking (DS), the interval between DPS and DS, 100-kernel weight, kernel test weight, ear kernel weight, and kernel rate. Furthermore, the descriptive statistics and correlation analysis of the 13 traits were performed using the SPSS 11.5 software. The results providing the phenotypic data here are needed for the quantitative trait locus mapping of these agronomic traits.

Key words: Maize (*Zea mays* L.); Agronomic traits;
Descriptive statistics; Correlation analysis

INTRODUCTION

Quantitative trait locus (QTL) mapping depends on a segregating population. Although there are many types of maize segregating populations, F_2 and backcross are the most widely applied populations in maize (*Zea mays* L.) breeding. The 2 populations are not time-consuming and have a low cost. However, in QTL mapping no continuous plants are used for phenotypic investigations and DNA extraction; thus, the 2 population types have the deficiency named temporality (Pilet et al., 2001). Comparatively, recombinant inbred line (RIL) populations are immortal and can be utilized in different regions and times because of their homogeneous individuals. Of course, these populations are associated with longer time commitments and higher costs for population construction than F_2 and backcross populations (Wan et al., 2008). Currently, the studies using an RIL as a mapping population are focused on a few crops, including rice (Wan et al., 2006), soybean (Fu et al., 2006), and wheat (Ma et al., 2007). Only limited reports were found in maize in the literature (Bouchez et al., 2002; Ordas et al., 2008), especially in China (Ding et al., 2008).

Maize is one of the most important crops throughout the world. The studies on QTL mapping of maize agronomic traits have been reported frequently and include traits that are related to plant phenotype (Ribaut et al., 1997), yield (Guo et al., 2008), and flower period (Liu et al., 2010). Nevertheless, the number, location, and genetic effects of QTL for some traits demonstrate differences in different experiments. These results are influenced to some extent by different mapping parents, population types, and genetic maps.

Therefore, an RIL population that was derived from the 2 elite inbred lines Mo17 and Huangzao4 was used as experimental material, and 13 important agronomic traits were investigated and analyzed. The objective of this study was to provide phenotypic data for further QTL mapping of these traits.

MATERIAL AND METHODS

Plant materials

The experimental materials included parental lines Mo17 and Huangzao4 and an RIL population consisting of 221 RILs. Mo17 and Huangzao4 belong to Lancaster (USA) and Tangsipingtou (China) heterotic groups, respectively; the RIL population was derived from the cross between Mo17 and Huangzao4.

Experimental methods

All 223 lines were sown in a completely randomized design with 6 replicates at the experiment field (Shanxi Academy of Agricultural Sciences, Xinzhou City, Shanxi Province, China) that had single-row planting for each replicate, 20 plants per row, 67 cm as the row interval, and 25 cm as the plant interval within a row. During florescence, the middle 10 plants of every replicate of each line were individually investigated for the 13 traits: ear diameter (ED), ear length, ear axis diameter (EAD), ear weight, plant height, ear height, days to pollen shed (DPS), days to silking (DS), the interval between DPS and DS (IPS), 100-kernel weight (KW), kernel test weight, ear kernel weight, and kernel rate. In total, 60 plants per line were

used to compute the mean. Based on the statistical means, descriptive statistics and relation analysis were performed using the SPSS11.5 software (www.spss.com).

RESULTS AND DISCUSSION

Descriptive statistics for parents and population

For the parents, the average values from Mo17 were higher than those from Huangzao4 for all 13 traits except KW, ED, and EAD (Table 1). With regard to the population, the results of phenotypic statistics, including mean, skewness, kurtosis, minimum, maximum, and coefficient of variation (CoV), are shown in Table 2. The 5 parameters including mean, skewness, kurtosis, minimum, and maximum could not be compared between the 13 traits. However, the CoV can be used to reflect the variation extent of different RILs in the population. The CoV value of IPS was the highest (up to 36.38%), followed by KW (33.84%); the lowest was DS (3.25%).

From these statistical values, it was concluded that the 13 agronomic traits were quantitative and were controlled by multiple genes.

Table 1. Descriptive statistics for parental lines Mo17 and Huangzao4.

Genotypes	KW (g)	KR (%)	KTW (g)	EGW (g/L)	DPS (days)	DS (days)	IPS (days)	EH (m)	PH (m)	EL (cm)	ED (cm)	EW (g)	EAD (cm)
Mo17	23.48	82.66	194.93	60.06	91.00	95.75	4.75	0.86	2.13	11.73	3.69	71.22	2.56
Huangzao4	27.85	81.84	193.30	46.62	88.83	93.00	4.17	0.69	1.79	10.66	4.02	56.43	2.84

KW = 100-kernel weight; KR = kernel rate; KTW = kernel test weight; EGW = ear kernel weight; DPS = days to pollen shed; DS = days to silking; IPS = the interval between days to pollen shed and days to silking; EH = ear height; PH = plant height; EL = ear length; ED = ear diameter; EW = ear weight; EAD = ear axis diameter.

Table 2. Descriptive statistics on 13 agronomic traits for the population derived from Mo17 x Huangzao4.

Traits	Mean	Skewness	Kurtosis	Minimum	Maximum	CoV (%)
ED (cm)	3.87	-0.06	0.92	2.87	5.09	8.79
EL (cm)	13.07	0.18	0.20	6.03	19.36	17.75
EAD (cm)	2.75	0.30	1.41	1.95	3.66	9.09
EW (g)	71.49	0.45	0.16	12.40	166.93	31.71
PH (m)	1.94	0.32	0.61	1.39	2.76	11.65
EH (m)	0.71	0.53	0.56	0.40	1.25	21.35
DPS (d)	92.53	0.13	-0.43	85.17	100.17	3.49
DS (d)	98.27	-0.03	0.00	88.67	106.25	3.25
IPS (d)	5.80	0.57	1.07	0.83	14.75	36.38
KW (g)	25.21	2.86	9.98	10.90	69.48	33.84
KTW (g)	194.35	-0.50	0.18	167.45	215.40	4.55
EGW (g/L)	58.85	0.23	0.99	11.60	128.74	33.20
KR (%)	80.57	-2.44	11.62	34.41	98.43	9.06

CoV = coefficient of variation; ED = ear diameter; EL = ear length; EAD = ear axis diameter; EW = ear weight; PH = plant height; EH = ear height; DPS = days to pollen shed; DS = days to silking; IPS = the interval between DPS and DS; KW = 100-kernel weight; KTW = kernel test weight; EGW = ear kernel weight; KR = kernel rate.

Correlation analysis of the population

Correlation analysis was carried out among the 13 traits for the experimental popula-

tion, and the results are listed in Table 3. The correlation between different agronomic traits could be classified into 5 types among the 78 correlation combinations: 0.01 level-positive correlation, 0.05 level-positive correlation, 0.01 level-negative correlation, 0.05 level-negative correlation, and no correlation (Table 4). Their statistic values were 28, 3, 11, 1, and 35, respectively.

Table 3. Correlation analysis between different traits for the population derived from Mo17 x Huangzao4.

Traits	KR	KTW	EGW	DPS	DS	IPS	EH	PH	EL	ED	EW	EAD
KW	0.052	0.205**	0.158*	-0.007	-0.036	-0.036	0.105	0.086	0.207**	0.096	0.152*	0.096
KR		0.091	0.547**	-0.219**	-0.463**	-0.341**	-0.038	-0.016	0.233**	0.304**	0.434**	0.04
KTW			0.057	0.002	0.044	0.041	0.074	-0.001	-0.043	-0.096	0.044	0.039
EGW				-0.064	-0.298**	-0.348**	0.278**	0.268**	0.688**	0.511**	0.980**	0.296**
DPS					0.785**	-0.268**	0.523**	0.346**	-0.042	-0.082	-0.034	-0.032
DS						0.363**	0.336**	0.242**	-0.128	-0.256**	-0.250**	-0.057
IPS							-0.283**	-0.163*	-0.124	-0.232**	-0.322**	-0.038
EH								0.740**	0.256**	0.058	0.305**	0.092
PH									0.254**	0.067	0.285**	0.039
EL										0.212**	0.711**	0.153*
ED											0.521**	0.561**
EW												0.336**

KW = 100-kernel weight; KR = kernel rate; KTW = kernel test weight; EGW = ear kernel weight; DPS = days to pollen shed; DS = days to silking; IPS = the interval between DPS and DS; EH = ear height; PH = plant height; EL = ear length; ED = ear diameter; EW = ear weight; EAD = ear axis diameter. **Correlation significant at the 0.01 level (two-tailed). *Correlation significant at the 0.05 level (two-tailed).

Table 4. Statistical values of different correlation types among the 13 agronomic traits.

Correlation types	Significant levels	No.
Positive	0.01 (**)	28
	0.05 (*)	3
Negative	0.01 (**)	11
	0.05 (*)	1
No correlation		35
Sum		78

**Correlation significant at the 0.01 level (two-tailed). *Correlation significant at the 0.05 level (two-tailed).

CONCLUSIONS

In this study, 13 agronomic traits were investigated in an RIL population that was derived from Mo17 x Huangzao4 and its parents. According to the values of descriptive statistics of the parents and population and correlation analysis among the 13 traits in the population, it was concluded that these traits were quantitative and were controlled by multiple genes. The obtained data here could be further used for the QTL mapping of these traits in maize.

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