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Genetic variability and correlation of stalk yield-related traits and sugar concentration of stalk juice in a sweet sorghum (*Sorghum bicolor* L. Moench) population

Guihua Zou[1], Song Yan[1], Guowei Zhai[1], Zhipeng Zhang[2], Jianqiu Zou[2], Yuezhi Tao[1]

[1]State Key Laboratory Breeding Base for Zhejiang Sustainable Pest and Disease Control, Institute of Crop and Nuclear Technology Utilization, Zhejiang Academy of Agricultural Sciences, Hangzhou 310021, China
[2]Chinese National Sorghum Improvement Center, Liaoning Academy of Agricultural Sciences, Shenyang 110161, China

***Corresponding author: taoyz@zaas.org**

Abstract

The productivity of sweet sorghum (*Sorghum bicolor* L. Moench)，a raw material for ethanol production，is mainly determined by stalk yield and sugar content. To understand inherent differences and relationship between stalk yield related traits and sugar concentration of stalk juice, a large recombinant inbred (RI) population derived from a grain sorghum × sweet sorghum was grown in three different trials. Seven stalk yield related traits including heading date (HD), plant height (PH), harvested stem length (HSL), number of nodes (NN), stem diameter (SD), panicle length (PL) and panicle neck length (PNL), along with sugar concentration (SC) of stalk juice were evaluated. Significant differences among genotypes were observed for all measured traits. A large proportion of the phenotypic variance for PH, HSL, PL and SC was attributed by genotypic variance. Highest ratio of genotype × environment (G × E) interaction variance to phenotypic variance was observed for SD. Moderate proportion of phenotypic variances for HD, NN and PNL were explained by genotypic variances. Both the magnitude and direction of correlation coefficients among the traits measured were varied in different trials. PH, HSL and NN had consistently positive and significant correlation with SC. PNL had no significant correlation with SC in all three trials. HD, SD and PL had no consistently significant correlations with SC in three trials. Information obtained from this study is very helpful to further understand the genetic mechanism of stalk yield related traits and sugar concentration of stalk juice in this RI population.

Keywords: Correlation; Genetic variability; Recombinant inbred population; *Sorghum bicolor* L. Moench; Stalk yield related traits; Sugar concentration; Sweet sorghum.
Abbreviations: E- Environment; G- Genotype; G × E- Genotype × environment; HSL- Harvested stem length; HD- Heading date; NN- Number of nodes; PL- Panicle length; PNL- Panicle neck length; PH- Plant height; RI- Recombinant inbred; SC- Sugar concentration; SD- Stem diameter

Introduction

Sweet sorghum, a specific type of *Sorghum bicolor* L. Moench, has been considered a potentially valuable source for biofuel production because of its high energy convert efficiency (Roman et al., 1998; Woods, 2001; Dolciotti et al., 1998; Reddy et al., 2003, 2005). Many characteristics such as green stalk yield, stalk sugar content, stalk juice extractability and grain yield have been proved as major contributors to its economic superiority (Bala et al., 1996; Almodares et al., 2006, 2008). However, these traits are quantitatively and polygenically inherited in nature and very difficult to be manipulated directly in breeding procedure. Therefore, to successfully improve these complex traits, they need to be dissected into smaller morphological, physiological and genetical components, which are easily analyzed and evaluated. Cultivar development is, however, firstly based on the exploitation of genetic variability of the genotypes with the traits of interest (Makanda et al., 2009). Therefore, establishing the genotypic variability available for stalk yield associated traits and sugar concentration of stalk juice in a sorghum population is very important in determining the feasibility of developing elite sweet sorghum varieties. The consequences of the phenotypic variation depend largely on the environment. This variation is further complicated by the facts that all genotypes do not respond to environmental changes in a similar way and no two environments are exactly the same. Multi-environmental trials have been used to estimate genetic variability in their sorghum germplasm (Abu-Gasim and Kambal, 1985; Aba et al., 2001; Ali et al., 2009, 2011). Furthermore, correlations between the traits are of great importance for success in selections to be conducted in breeding programs. Significantly positive correlations show that the changes of two variables are in the same direction, while negative correlations indicate their inverse relationships with each other. For example, stalk yield has significantly positive correlations with plant height, stem diameter and juiciness (Audilakshmi et al., 2010). Therefore, selection for stalk yield should be focusing on both plant height and stem diameter. Total sugar content could be calculated from the Brix because of a significant linear correlation between Brix and total sugar content of the juice (Ma et al., 1992). The negative and highly significant correlation between grain yield and stem biomass suggested that the presence of a yield penalty as biomass is improved

(Makanda et al., 2009). The genetic variability and correlation of bio-fuel related traits have been studied in several different RI populations (Ritter et al., 2008; Murray et al., 2008; Srinivas et al., 2009; Shiringani et al., 2010). In order to study the genetic mechanisms of stalk yield related traits and sugar concentration of stalk juice, a specific RI population has been developed from a cross between grain and sweet sorghum lines in our laboratory. To further understand the genetics and relationship of stalk yield related traits and sugar concentration of stalk juice in the population, we investigated stalk yield related traits and sugar concentration of stalk juice in three different trials. The objectives of this study were: (1) to evaluate their variability for stalk yield related traits and sugar concentration of stalk juice; (2) to estimate heritability for these traits and (3) to assess the strength of associations between stalk yield related traits and sugar concentration of stalk juice.

Results

Trait performances of the parents and RI lines

The phenotypic values of the traits in the recombinant inbred lines showed continuous distribution, which approximately fitted normality with skewness less than 1.1, indicating that all measured traits were quantitatively inherited (Table 1 and Fig 1). Highly significant differences were observed among the lines for all the traits. The range of variability in the recombinant inbred lines for all traits was much higher than the differences between two parents. A clearly transgressive segregation in both directions for all traits was observed from the performance of the recombinant inbred lines, indicating that both parents transmitted favorable alleles for each trait. The data on average heading date of the parents and the recombinant inbred lines varied within and across locations (Table 1). The temperature and photoperiod at SY (short-day length) significantly differed from those at HZ and HN (long-day length), which distinctly hastened the heading time. Therefore, less time was required to heading at SY than at HZ and HN for both parents and the recombinant inbred lines. 654 took significantly more eleven days to heading than LTR108 at SY but opposite at HZ and HN, suggested that LTR108 was more sensitive to photoperiod than 654. Although the longitude and latitude were similar at HZ (30°26′ N, 120°16′ E) and HN (30°53′ N, 120°69′ E), HD of the parents and the recombinant inbred lines at HZ was shorter than at HN. PH was also significantly affected by modified growth environments. Similarly, PH of two parents and recombinant inbred lines at SY were significantly shorter than at HZ and HN, and the plants at HZ were shorter than at HN. However, differed from HD, PH of 654 was consistently shorter than LTR108 at three environments. Similar trend was observed for HSL. Likewise HD, PH and HSL, the two parents and the recombinant inbred lines at SY displayed less NN than at HZ and HN. The recombinant inbred lines at HN produced more NN than at HZ, although NN of the two parents kept mostly constant at these two environments. There was non-significant difference between two parents at SY, while the opposite occurred at HZ and HN. As like HD, SD had similar trend. Plants at SY produced thinner stem than at HZ and HN. SD of the parents and the recombinant inbred lines at HZ was thinner than at HN, although the mean SD of the recombinant inbred lines was the same. SD of 654 was thicker than LTR108 at SY while the opposite occurred at HZ and HN. PNL of 654 was longer than LTR108 at all three environments. Average values of PNL of the two parents and the recombinant inbred lines were significantly longer at SY than at HZ and HN. PNL of the parents and the recombinant inbred lines at HZ was longer than at HN. PL of 654 was longer than LTR108 at all three environments. Average values of PL of the two parents and recombinant inbred lines were significantly longer at HZ than at HN and SY. The recombinant inbred lines at HN produced longer PL than at SY, although PL of the two parents kept mostly constant at these two environments. Significant differences of SC between two parents were observed at all three environments. Average values of SC of the two parents and the recombinant inbred lines were significantly higher at SY than the ones at HZ and HN. The average value of SC generated from the recombinant inbred lines at HN was higher than that at SY, although the values of the two parents were relatively stable at these two environments.

Variance components and heritability of traits

The effects of G, E and G × E interaction caused by variation from calculated variance components over three environments of eight characteristics were presented in Table 2. As the fact that the population was derived from two extremely diverse parents, significantly genotypic mean squares ($P < 0.0001$) were observed for all traits across three environments. G × E interaction mean squares and E mean squares were also highly significant. Of three variance components, E mean squares were consistently much larger than those of G and G × E interaction mean squares for all traits. The values of genotypic and phenotypic variances, and the ratios of G (h^2), G × E interaction, and E variances to phenotypic variance were presented in Table 3. PH had the highest h^2 at 74.9%, followed by HSL (72.7%), PL (68.8%), SC (62.9%), PNL (57.6%), NN (54.8%) and HD (45.8%), whereas SD had the lowest h^2 at 21.0%. The proportion of G × E interaction was as high as 52.7% in SD, followed by HD (40.6%). HSL had the smallest E effect (2.7%), followed by PH (3.5%). For SC, 7.3% and 29.8% of the phenotypic variance was attributed to E effects and G × E interaction effects, respectively. A large proportion of the genotypic variance contained in the phenotypic variance (high h^2) indicated that genetic effects explained large proportion of total phenotypic variance for these traits, while E effects and G × E interaction effects accounted for a smaller proportion of the phenotypic variation. The improvement of a trait with high h^2 could be brought into appropriate selection programs. SD had the lowest h^2, indicating that this trait was more easily affected by environment than traits such as PH and HSL. Consequently, selection for this trait would be ineffective because the E variation or G × E interaction variation was so great that it may mask the genetic variation.

Table 1. The mean phenotypic values of parental lines, and minimum, maximum and mean phenotypic values of the recombinant inbred population for different traits in HZ (Hangzhou), HN (Haining) and SY (Sanya).

Trait	Environment	654	LTR108	Recombinant inbred population		Mean	Std	Skewness
				Minimum	Maximum			
HD (days)	HZ	70a	90b	49	129	81	23	0.6
	HN	87a	104b	70	134	100	15	0.1
	SY	63a	52b	50	81	68	4	-0.7
PH (cm)	HZ	178a	324b	100	510	295	68	-0.3
	HN	205a	344b	104	498	335	78	-0.4
	SY	150a	218b	95	295	205	40	-0.9
HSL (cm)	HZ	105a	268b	51	439	241	71	-0.2
	HN	140a	297b	54	423	273	75	-0.5
	SY	77a	154b	27	215	137	37	-1.0
NN (no. Plant^{-1})	HZ	14a	19b	9	32	17	4	1.1
	HN	15a	19b	11	32	20	4	0.6
	SY	9a	10a	6	14	9	1	0.1
SD (cm)	HZ	1.5a	1.9b	1.2	3.2	2.1	0.3	0.4
	HN	1.9a	2.3b	1.3	3.0	2.1	0.3	0.3
	SY	1.5a	1.3b	0.9	2.0	1.4	0.2	0.3
PNL (cm)	HZ	43a	34.3b	10.0	56.8	32.2	8.2	0.1
	HN	38a	26.5b	6.8	57.5	35.4	8.6	-0.2
	SY	46a	43.3b	23.0	64.7	42.9	7.9	0.3
PL (cm)	HZ	30.4a	21.5b	16.0	49.8	27.5	5.2	0.2
	HN	27.0a	20.5b	13.0	40.5	26.4	4.6	0.5
	SY	27.5a	20.0b	13.5	47.0	25.2	3.8	0.6
SC (Brix)	HZ	8.1a	15.3b	0	20.6	13.5	4.2	-1.1
	HN	8.3a	14.2b	0	22.1	13.8	3.6	-1
	SY	10.4a	17.6b	0	22.1	14.0	4.3	-1.1

HD, Heading date; PH, Plant height; HSL, Harvested stem length; NN, Number of nodes; SD, Stem diameter; PNL, Panicle neck length; PL, Panicle length; SC, Sugar concentration. Std, standard deviation; a and b, indicate significant difference of the trait mean values between two parents.

Phenotypic correlation

Correlations of sugar concentration of stalk juice and stalk yield related traits from HZ, HN and SY were presented in Table 4. Differences were observed in the correlation coefficients in terms of the magnitude and direction under different environments. SC had positively and significantly correlated with PH, HSL and NN at three environments. SC had a positive and significant correlation with HD at HN (r=0.314***), while no significant correlation with HD at HZ and SY. SD and PL had negative and significant correlations with SC at HN (r=-0.136**) and HZ (r=-0.117*), respectively. No significant correlation was found between SC and PNL. Among other correlations, HD was positively correlated with HSL, NN, and SD at all locations. HD was positively and significantly correlated with PH at HZ and HN, but negatively and significantly correlated with PNL at HZ and SY. HD had negatively and significantly correlated with PL at HZ, while no significant correlation with PL at other two locations. PH was positively correlated with HSL, NN, PNL and PL at all environments. Correlations between PH and SD were varied in different environments, positive and significant correlation at HZ, but negative and non-significant correlation at HN (r=-0.018) and significant and negative correlation at SY (r=-0.114*), respectively. HSL was positively correlated with NN at three environments, and also for SD at HZ, PNL and PL at HN and SY. NN was positively correlated with SD, but negatively correlated with PNL at SY and PL at HZ, respectively. SD was negatively

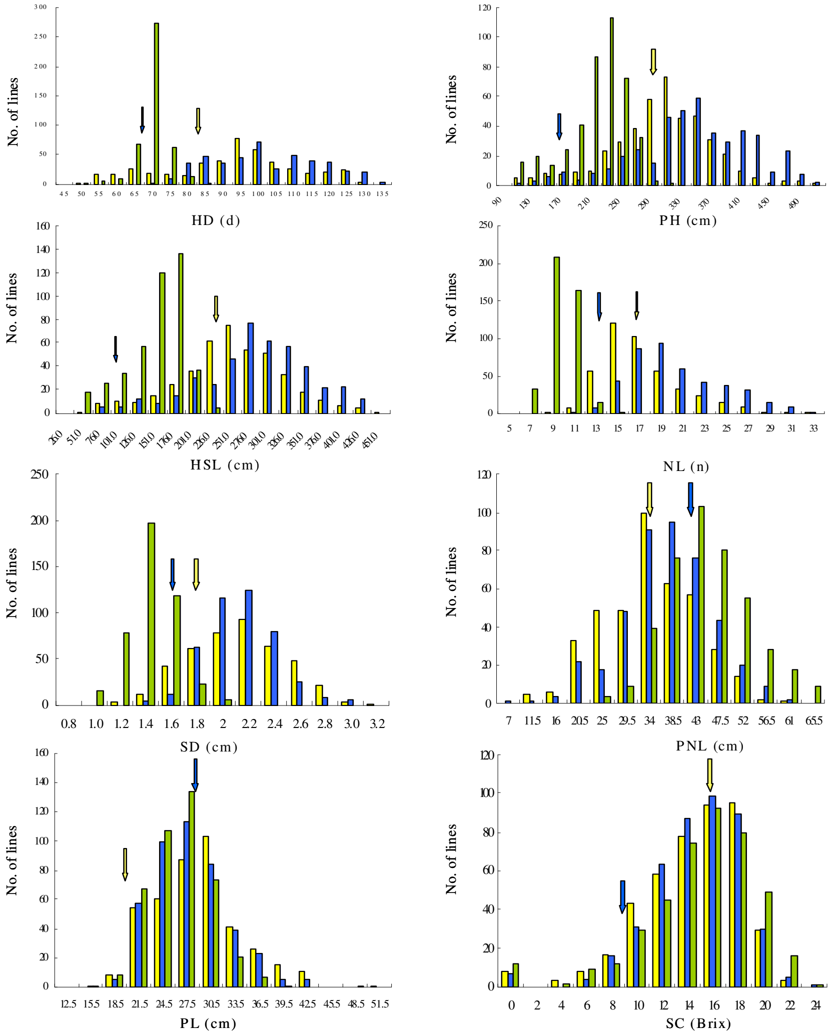

Fig 1. Frequency distributions of the recombinant inbred population for eight traits under three environments. Mean values of 654 (blue arrow) and LTR108 (yellow arrow) across three environments were shown above. Yellow, blue and green columns represent traits evaluation in HZ (Hangzhou), HN (Haining) and SY (Sanya), respectively.

and significantly correlated with PNL, and positively correlated with PL at SY. PNL was positively correlated with PL at all environments.

Discussion

Recently, breeding for improving various biofuel-related characteristics (i.e. fiber, sugar, juice, and biomass) is becoming an important breeding objective for sweet sorghum breeders to meet the rapidly increased demand for biofuel production worldwide. It is well known that progress in plant breeding depends on the extent of genetic variability existed in a population. Ritter et al. (2008) reported that the genetic variances within a RI population (184 lines, F_6) from R9188 and R9403463-2-1 were 5.32 for sugar content (Brix), 34 cm for plant height and 7 days for heading time, respectively. Murray et al. (2008) found that the variances of these three traits within the RI population (176 lines, $F_{4:5}$) from BTx623 and Rio were 11.3 for Brix, 157 cm for plant height and 23.5 for days flowering time, respectively. Sromvas et al. (2009) studied agronomically important traits in a RI population (168 lines, F_7) from 296B and IS18551. The variances were 124 cm for plant height, 25 days for days to anthesis, 5 no. plant^{-1} for total number of leaves and 24 cm for panicle length, respectively. And, Shiringani et al. (2010) investigated another RI population (188 lines, $F_{5:6}$) from SS79 and M71, the variances were 7.9 for Brix, 182 cm for plant height, 51 days for heading time and 0.93 cm for stem diameter, respectively. Because of small population, low generations and similar phenological pattern between the parents, only limited variances were observed in these four reports. In the present study, since the population was derived from two

Table 2. Mean squares values for eight traits measured in the recombinant inbred lines across HZ (Hangzhou), HN (Haining) and SY (Sanya).

Source of variation	df	HD	PH	HSL	NN	SD	PNL	PL	SC
G	435	371.2***	15921***	13764***	36.3***	0.15***	192.43***	64.14***	51.79***
E	2	289162.9***	3451143***	3870268***	23821.6***	116.45***	20156.94***	872.52***	72.42***
Rep	1	7.6 ns	2101 ns	490 ns	220.02***	0.67***	112.84 ns	16.95 ns	0.04 ns
G×E	870	201.1***	3994***	3751***	16.43***	0.12***	81.56***	20.01***	19.21***
Error	1308	50.3	557	369	4.08	0.04	34.56	11.39	3.76

HD, Heading date; PH, Plant height; HSL, Harvested stem length; NN, Number of nodes; SD, Stem diameter; PNL, Panicle neck length; PL, Panicle length; SC, Sugar concentration. G, genotype; E, environment; G × E, genotype × environment; df, degree of freedom; ns, not significant. *, level of significance (* significant at 95%; **, Significant at 99%; ****, Significant at 99.99%).

extremely diverse parents and in a larger size and more advanced generation (436 lines, F_8), all measured traits exhibited extensive variability. The ratios of G to phenotypic variance were moderate or high except stem diameter and heading date, indicating that expressions of these traits were genetic and could be exploited in breeding programs, such as high sugar concentration, early maturity, large panicle and short stalk. Photoperiodic control of flowering allows plants to coordinate their reproductive phase with the environment and other members of the species (Childs et al., 1997). Most sorghums are sensitive to photoperiod and classified as short day plants, which means that the plant requires short days (or long nights) before proceeding to the reproductive stage (Ferraris and Stewart, 1979). Large genotypic differences in day length requirements for floral initiation resulted in the variance of maturity among sweet sorghum cultivars (Miller et al., 1968; Ferraris and Stewart, 1979). It had been reported that the plants flowered at different times and differed in leaf number and size under the 10 hour nights of the summer (Quinby, 1972), and also that leaf number tend to increase with increasing temperature and day length (Hesketh et al., 1969). In this study, heading date, plant height, harvested stem length, number of nodes, stem diameter, panicle length, panicle neck length, and sugar concentration of stem juice were all significantly influenced by photoperiod. Taking advantage of a great variability on response to photoperiod existed in this population; breeders are able to develop varieties with higher biomass by selecting the genotypes with longer vegetative growth phase. On the other hand, genotypes with early maturity can be also developed for the areas where the growing season is limited by rainfall, temperature or other environmental factors. Additionally, the regrowth potential will help early maturing types to maximize grain and biomass yield, because a compromise can be reached between earliness and yielding. It is a continuous process that breeding elite sweet sorghum cultivars with high sugar concentration of stalk juice. This is generally achieved by crossing genotypes with desirable traits followed by selection. Knowledge of correlation is required to obtain the expected response of other characters when selection is applied to a particular character of interest in a breeding programme. Population with a variable combination of agronomically important traits was used to estimate the correlation of the traits in our study. It was found that the magnitude and direction of correlation coefficients of measured traits were varied under different environments. Of seven stalk yield related traits, three (plant height, harvested stem length and number of nodes) were positively and significantly correlated with sugar concentration of stalk juice under three environments consistently, suggesting that genetic improvement in these three traits could improve the total biomass and sugar content. Taller plants having more stem biomass and juice and higher stem sugar content could produce more sugar yield per hectare ultimately. The similar correlations between most of the interesting traits and biofuel production were also observed by other report (Murray et al., 2008). There was no significant correlation between panicle neck length and sugar concentration under different environments, meaning that panicle neck length did not affect sugar accumulation. Similar result was reported by Janssen et al. (1930). Other traits (heading date, stem diameter and panicle length) had no consistent correlations with sugar concentration of stalk juice under three environments, suggesting the need to ascertain their interrelationships over different environments across years before crop improvement practice.

Materials and methods

Genetic materials

A large and advanced population with 436 recombinant inbred lines derived from a cross between the parental lines 654 (grain sorghum) and LTR108 (sweet sorghum) was used for this study. 654, an early maturing and elite grain sorghum male parent widely used in sorghum breeding programs in China, had short internodes, a few nodes, thin and low-sweet juicy stem. LTR108, a sweet sorghum restorer line developed by Chinese National Sorghum Improvement Center, had long internodes, lots of nodes, thick and sweet juicy stems.

Experimental design

Three field trials were carried out at the experimental stations of Zhejiang Academic of Agricultural Sciences located in Hangzhou (HZ), Haining (HN), and Sanya (SY) in 2009, respectively. HZ was established on 29 April, HN on 6 May and SY on 18 November, respectively. A randomized complete block design (RCBD) was used with two replications of all progeny lines in each trial. The plot size was 7 rows of 4 m length with inter-row and intra-raw spacing of 0.75 m × 0.40 m. Each plot was oversown by hand and later thinned to 1 plant per hole after 3-4 weeks. 100 kg ha^{-1} composite fertilizer was applied into experimental plots during sowing. Regular irrigation, fertilizer, pesticides, insecticides and other crop cultural management practices were applied to raise a successful crop.

Table 3. Genotypic and phenotypic variances, and ratios of genotypic variance, genotypic × environment interaction to phenotypic variance for eight traits.

Trait	σ^2_p	σ^2_g	σ^2_{ge}	σ^2_e	σ^2_g/σ^2_p	$(\sigma^2_{ge}/n)/\sigma^2_p$	$(\sigma^2_e/nr)/\sigma^2_p$
HD	61.867	28.350	75.400	50.300	0.458	0.406	0.136
PH	2653.500	1987.833	1718.500	557.000	0.749	0.216	0.035
HSL	2294.000	1668.833	1691.000	369.000	0.727	0.246	0.027
NN	6.052	3.313	6.175	4.080	0.548	0.340	0.112
SD	0.026	0.005	0.040	0.040	0.210	0.527	0.263
PNL	32.072	18.478	23.500	34.560	0.576	0.244	0.180
PL	10.689	7.355	4.308	11.390	0.688	0.134	0.178
SC	8.632	5.430	7.726	3.756	0.629	0.298	0.073

HD, Heading date; PH, Plant height; HSL, Harvested stem length; NN, Number of nodes; SD, Stem diameter; PNL, Panicle neck length; PL, Panicle length; SC, Sugar concentration. σ^2_p=phenotypic variance; σ^2_g=genotypic variance; σ^2_{ge}=genotypic × environment; σ^2_e=error variance; n=number of environments; r=number of replicates; h^2, broad-sense heritability.

Table 4. Correlation coefficients of eight traits at HZ (Hangzhou), HN (Haining) and SY (Sanya).

Traits		HD	PH	HSL	NN	SD	PNL	PL
PH	HZ	0.660^{***}						
	HN	0.563^{***}						
	SY	0.091						
HSL	HZ	0.707^{***}	0.957^{***}					
	HN	0.586^{***}	0.991^{***}					
	SY	0.140^{**}	0.960^{***}					
NN	HZ	0.815^{***}	0.649^{***}	0.688^{***}				
	HN	0.771^{***}	0.601^{***}	0.630^{***}				
	SY	0.327^{***}	0.446^{***}	0.540^{***}				
SD	HZ	0.640^{***}	0.218^{***}	0.302^{***}	0.325^{***}			
	HN	0.109^{*}	-0.018	0.009	0.206^{***}			
	SY	0.305^{***}	-0.114^{*}	-0.089	0.274^{***}			
PNL	HZ	-0.334^{***}	0.206^{***}	0.073	-0.031	-0.326^{***}		
	HN	-0.011	0.327^{***}	0.212^{***}	-0.039	-0.276^{***}		
	SY	-0.123^{*}	0.371^{***}	0.144^{**}	-0.265^{***}	-0.228^{***}		
PL	HZ	-0.152^{**}	0.133^{**}	0.038	-0.105^{*}	-0.025	0.158^{**}	
	HN	0.052	0.267^{***}	0.189^{**}	0.042	0.07	0.247^{***}	
	SY	0.07	0.316^{***}	0.161^{**}	-0.009	0.202^{***}	0.363^{***}	
SC	HZ	0.042	0.143^{**}	0.159^{**}	0.105^{*}	0.003	-0.06	-0.117^{*}
	HN	0.314^{***}	0.385^{***}	0.403^{***}	0.294^{***}	-0.136^{**}	0.004	-0.008
	SY	0.053	0.159^{**}	0.188^{**}	0.193^{**}	-0.076	-0.051	-0.089

HD, Heading date; PH, Plant height; HSL, Harvested stem length; NN, Number of nodes; SD, Stem diameter; PNL, Panicle neck length; PL, Panicle length; SC, Sugar concentration. *, level of significance (* significant at 95%; **, Significant at 99%; ***, Significant at 99.9%).

Phenotypic measurements

The plants were harvested manually by cutting the stem at the base with a scissor in all three trials. Three uniform plants from each plot were selected for all data collection. Heading date (HD) was recorded when 50% of plants in the plot had 50% flowering (which occurs when anthers have burst on more than 50% of the panicle). Each line was harvested at hard dough stage to guarantee the plots at the same physiological stage in which sugar accumulation reached to an optimum level (Bian et al., 2006; Zhao et al., 2009). Plant height (PH) was measured from the ground surface to the panicle tip. Stem diameter (SD) was measured using venier caliper at middle internode per plant. Harvested stem length (HSL) was measured from the ground to the node of the panicle peduncle for each plot. Number of nodes (NN) was counted from the top to the base. Panicle length (PL) was defined as the length from panicle neck node to the uppermost grain tip and panicle neck length (PNL) was the length from the base of the flag leaf sheath to the panicle neck node. Sugar concentration (SC) of stalk juice was determined by Brix readings which were measured with hand refractometer (Atago, Japan) at physiological maturity from a composite juice sample obtainer from the one-above mid internode of stalks.

Statistical analysis

Analysis of variance (ANOVA) was performed for each measured trait using the multi-factor ANOVA procedure in order to compare the relative importance of main model terms: environment (E), replicate, genotype (G) and genotype × environment (G × E) interaction. The locations of different experiments were considered as different environments in this study. Broad-sense heritability (h^2) of each trait was estimated based on recombinant inbred lines according to the following equation:

$$h^2 = \sigma_g^2 / \sigma^2_p$$

Where σ_g^2 is the variance component of genotypes (recombinant inbred lines); σ^2_p, phenotypic variance among genotypes grown in r replicates and n environments can be expressed as $\sigma_g^2 + \sigma_{g1}^2/n + \sigma_e^2/nr$; σ_{g1}^2, the variance component of the interaction genotype × environment; σ_e^2, the error (Gao, 1986). Descriptive statistics and phenotypic correlations of the traits obtained from the experiment were computed using the genotypic means. All the statistical analyses were performed by using S-Plus V6.1 (Insightful Corporation 2001) for Windows.

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