Short communication

Genetic analysis of sugarcane biomass yield and its component traits using ADAA model

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Abstract

This paper analyzes the genetics of sugarcane biomass yield and heterosis of stalk number and weight using the additive, dominance and additive × additive epistasis model. Results indicate that stalk number is controlled by additive and dominance effects, stalk weight by dominance, epistasis, and their interaction with environment, and biomass yield by additive, dominance, dominance × environment, and epistasis × environment effects. Accessions ROC20, ROC24, and ROC25 had high general combining ability with other lines for stalk number. Yuetang 81/3254, Yuetang 85/177, Yuetang 79/177, and Yuetang 80/101 were good female lines with ROC20 and ROC25 as male lines and Yuetang 85/177 × ROC25 was the only superior cross combination.

Sugarcane (*Saccharum officinarum* L.) is an important industrial crop that provides raw material for the production of white sugar and alcohol, but shows complex polyploidy (Zhou et al., 2005a). In China, the cultivated area of sugarcane has reached 1,106 km^2 in 2004 (Qi and Jiang, 2006). Yield is one of the most important and complex traits (Cox et al., 1994) and in recent decades, increase in sugar yield has been achieved by increasing cane biomass rather than sugar content (Jackson, 2005). In order to evolve a selection strategy to improve biomass yield, estimating the additive and epistatic effects for agronomic traits involved in yield performance is important. The partitioning of genetic variance in intercrossed population would provide estimates of additive and epistatic additive × additive variances. Zhu (1992) proposed a method for predicting genotypic values and heterosis with an additive, dominance, and additive × additive epistasis (ADAA) model, formulated in accordance with the general

genetic model (Cockerham, 1980). Data from diallel crossing experiments or incomplete diallel crossing experiments could be evaluated in this manner (Xu et al., 1998). In this paper, we analyze two-year data on biomass yield per clump and its two component traits from an incomplete diallel cross of 5×6 sugarcane lines following the method of Zhu (1992). Although such analysis is typically done with data on three generations, since F_1 generation in sugarcane was vegetatively produced, it is unnecessary to conduct the predictive analysis on the heterosis of F_2 generation.

Five female lines, Yuetang 81/3254 (P_1), Yuetang 85/177 (P_2), Yuetang 72/426 (P_3), Yuetang 79/177 (P_4), and Yuetang 80/101 (P_5), and six male lines, ROC16 (P_6), ROC20 (P_7), ROC22 (P_8), ROC23 (P_9), ROC24 (P_{10}), and ROC25 (P_{11}) were used to produce 30 crosses of F_1s. The lines were selected because they are widely used in the main production area of Southern China.

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The parents and their F_1s were planted at Zhanjiang Sugarcane Research Center, Guangdong Province during 2000 and 2001. The experimental design was completely randomized block with three replications. The plots had three rows, 4 m long and 1 m wide. Standard cultivation practices were adopted (Li et al., 2000). Twenty samples were collected from each plot before harvesting for determining the stalk number per clump, stalk weight, and biomass yield per clump. Genetic ADAA model (Zhu, 1992) with genotype × environment interaction for agronomic traits was applied in the analysis of inheritance for each trait. Variance and covariance components were estimated by MINQUE (0/1) method (Zhu and Weir, 1996) and quantitative genetic analysis using the software package QGA Station 1.0 (Chen and Zhu, 2003).

Table 1 indicates that stalk number per clump of female lines was rather small, but the stalk weight was greater than that of the male accessions. Mean biomass yield per clump was similar for both categories. Likewise, stalk number per clump for F_1 was comparable to that of the parents with high values. The results indicate that heterosis is expected for stalk number and the means were similar in 2000 and 2001. Stalk number and weight as well as biomass yield are determined by factors such as the general genetic effect, genotype × environment interaction effect, and residual effect (Table 2). Biomass yield per clump was significantly influenced by the additive, dominance × environment and additive × additive × environment interaction effects. Previous studies also showed that inheritance of biomass is determined by additive gene effects (Zhou et al., 2005b).

Average genotypic values (ì+G) and general heterosis of 30 F_1 crosses for three traits are listed in Table 3. F_1 genotypic value was similar to population mean for stalk number per clump, although the reverse was true for stalk weight and biomass yield per clump. Heterosis

Table 1. Means and standard errors calculated on biomass and its components of six females, five male lines, and 30 crosses of sugarcane in Southern China over two years.

Generation	2000			2001		
	SN	SW	BY	SN	SW	BY
Female	2.727±0.081	1.237±0.059	3.369±0.185	2.633±0.078	1.317±0.057	3.456±0.134
Male	3.150±0.136	1.080±0.031	3.398±0.169	3.033±0.131	1.209±0.070	3.630±0.119
F1	3.193±0.074	0.999±0.023	3.174±0.092	3.006±0.077	1.061±0.019	3.163±0.081

SN=stalk number per clump, SW=stalk weight (kg), BY=biomass yield per clump (kg).

Table 2. Proportion of estimated variance components to phenotypic variance for three sugarcane yield traits in Southern China.

Proportion	SN		SW		BY	
	Estimate	Standard error	Estimate	Standard error	Estimate	Standard error
V_A/V_P	0.453**	0.010	0.000	0.000	0.374**	0.020
V_D/V_P	0.407**	0.028	0.273**	0.070	0.446**	0.017
V_{AA}/V_P	0.000	0.000	0.321*	0.107	0.000	0.000
V_{AE}/V_P	0.007	0.010	0.000	0.000	0.000	0.000
V_{DE}/V_P	0.000	0.000	0.160*	0.051	0.076	0.041
V_{AAE}/V_P	0.000	0.000	0.103*	0.046	0.032*	0.014
V_R/V_P	0.133**	0.023	0.143**	0.027	0.073**	0.013

SN=stalk number per clump, SW=stalk weight (kg), BY=biomass yield per clump (kg). V_A=additive variance, V_D=dominance variance, V_{AA}=additive-additive variance, V_{AE}= additive-environment variance, V_{DE}=dominance-environment variance, V_{AAE}= Additive-additive-Environment variance, V_R= residual variance, V_P= phenotypic variances. * and ** indicates statistical significance at $p < 0.05$ and 0.01 levels of probability respectively.

Table 3. Predicted genotypic values and general heterosis for three sugarcane yield traits in Southern China.

Traits	SN		SW		BY	
	Predictor	Standard error	Predictor	Standard error	Predictor	Standard error
Predicted	3.128	0.042	1.107[**]	0.007	3.127[**]	0.029
Hpm	0.115[**]	0.013	–0.234[**]	0.001	–0.134[**]	0.010
Hpb	0.032	0.022	–0.306[**]	0.010	–0.195[**]	0.014

SN=stalk number per clump, SW=stalk weight (kg), BY=biomass yield per clump (kg). Predicted= predicted genotypic values of F_1, Hpm = predicted general heterosis over the mid-parent of F_1, Hpb = predicted general heterosis over the better-parent of F_1. ** indicates statistical significance at *p* < 0.01.

for stalk number per clump over mid-parent was 11.5%. Significant negative general heterosis over mid-parent and better parent on stalk weight and the biomass yield per clump were noted in F_1. Similar phenotypic variations (4% to 10%) have also been reported earlier (Aitken et al., 2008).

As can be seen from Table 4, the predicted genotypic values of F_1 were significant. There were 23 crosses for stem number, 13 crosses for stem weight, and 21 for biomass yield. This implies that genotype × environment interaction is important for biomass yield per clump and its two component traits. As for predicted general heterosis over the mid-parent values of F_1, the promising crosses for stem number were $P_1 \times P_7$, $P_2 \times P_7$, $P_2 \times P_{11}$, $P_4 \times P_7$, $P_4 \times P_{11}$, and $P_5 \times P_{11}$, while for biomass yield, the crosses were $P_2 \times P_{11}$, $P_4 \times P_{10}$, and $P_5 \times P_{11}$. All crosses for stem weight showed negative heterosis. $P_2 \times P_{11}$ was the only promising cross for biomass yield having heterosis over better parent.

In conclusion, this paper demonstrated that P_1, P_2, P_4, and P_5 were good female lines with P_7 and P_{11} as male lines and $P_2 \times P_{11}$ was the only one superior cross combination with respect to biomass yield. The genetic divergence investigated presently would be helpful for selecting the characters critical to biomass yield as well as for determining the genetic variability and contribution of morphological traits to biomass yield. The information would be useful for evolving suitable strategies to develop commercial clones of sugarcane for different ecoclimatic zones.

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Table 4. Genotypic values and heterosis of 30 crosses of sugarcane for three yield traits in Southern China.

Cross	SN			SW			BY		
	Predicted	Hpm	Hpb	Predicted	Hpm	Hpb	Predicted	Hpm	Hpb
$P_1 \times P_6$	2.630*	–0.013	–0.078	0.883*	–0.542**	–0.646**	1.659**	–0.573**	–0.580**
$P_1 \times P_7$	3.916**	0.305**	0.136**	1.178**	–0.229**	–0.369**	3.751*	0.018	–0.029
$P_1 \times P_8$	2.209**	–0.085*	–0.085*	1.254**	–0.219**	–0.299**	2.786**	–0.255**	–0.278**
$P_1 \times P_9$	2.192*	–0.088	–0.091	0.930**	–0.477**	–0.600**	1.430**	–0.538**	–0.650**
$P_1 \times P_{10}$	3.127	0.076	–0.063	1.068	–0.316**	–0.472**	2.947	–0.250**	–0.318**
$P_1 \times P_{11}$	3.289	0.125	–0.019	1.141	–0.224**	–0.404**	3.399	–0.100	–0.156
$P_2 \times P_6$	2.430*	–0.072	–0.144	1.038	–0.280**	–0.292**	2.185**	–0.345**	–0.405**
$P_2 \times P_7$	4.272**	0.429**	0.253**	0.947*	–0.328**	–0.352**	3.325	–0.047	–0.160*
$P_2 \times P_8$	2.622*	0.056	0.050	1.267**	–0.091	–0.127	3.432	0.010	–0.079
$P_2 \times P_9$	2.020**	–0.138*	–0.141*	1.031	–0.266**	–0.274**	1.747**	–0.374**	–0.420**
$P_2 \times P_{10}$	3.845*	0.318*	0.173	1.114	–0.157**	–0.197**	3.924**	0.116*	–0.017
$P_2 \times P_{11}$	4.063**	0.385**	0.235*	1.182**	–0.070	–0.134*	4.396**	0.273**	0.151*
$P_3 \times P_6$	2.158**	–0.163*	–0.233*	1.446**	0.001	–0.086	3.233	–0.134*	–0.185**
$P_3 \times P_7$	3.861*	0.292*	0.118	1.127	–0.260**	–0.383**	3.836**	–0.001	–0.003
$P_3 \times P_8$	2.655*	0.066	0.061	1.133	–0.314**	–0.377**	3.207	–0.171**	–0.193**
$P_3 \times P_9$	2.249*	–0.065	–0.066	1.067	–0.332**	–0.438**	2.195**	–0.347**	–0.505**
$P_3 \times P_{10}$	4.074*	0.392*	0.248	0.989	–0.372**	–0.511**	3.852*	–0.017	–0.040
$P_3 \times P_{11}$	3.541	0.212*	0.064	1.141*	–0.207*	–0.369**	3.957**	0.027	0.016
$P_4 \times P_6$	2.433**	–0.144**	–0.146**	0.961*	–0.390**	–0.416**	1.782**	–0.550**	–0.571**
$P_4 \times P_7$	4.581**	0.457**	0.355*	0.910*	–0.401**	–0.463**	3.231	–0.157*	–0.189**
$P_4 \times P_8$	2.374*	–0.098	–0.165	1.083	–0.300**	–0.302**	2.470**	–0.367**	–0.375**
$P_4 \times P_9$	2.496	–0.055	–0.125*	1.148	–0.196*	–0.242*	2.318**	–0.279**	–0.406**
$P_4 \times P_{10}$	3.932*	0.274*	0.201	1.230*	–0.087	–0.166	4.257**	0.138*	0.085
$P_4 \times P_{11}$	4.400**	0.422**	0.345*	1.073	–0.210*	–0.312**	4.103**	0.102	0.061
$P_5 \times P_6$	2.255*	–0.155	–0.201*	1.128	–0.168**	–0.208**	2.484**	–0.297**	–0.313**
$P_5 \times P_7$	4.181*	0.373*	0.223	1.042	–0.212**	–0.216**	3.803	0.056	–0.013
$P_5 \times P_8$	2.558	0.009	–0.010	1.253	–0.076*	–0.141*	3.505	–0.011	–0.056
$P_5 \times P_9$	1.984**	–0.176*	–0.199*	1.121	–0.154**	–0.175**	2.139**	–0.296**	–0.386**
$P_5 \times P_{10}$	3.503	0.180	0.061	1.218**	–0.032	–0.044*	4.203*	0.159	0.069
$P_5 \times P_{11}$	3.999**	0.338**	0.214**	1.095	–0.122*	–0.158**	4.238**	0.181*	0.103

SN=stalk number per clump, SW=stalk weight (kg), BY=biomass yield per clump (kg). Predicted = predicted genotypic values of F_1, Hpm= predicted general heterosis over the mid-parent values of F_1, Hpb = predicted general heterosis over the better-parent values of F_1. * and ** indicates the statistical significance at $p < 0.05$ and 0.01 respectively.

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