Gene Effects for Sugar Content, Green Cane Yield and its Component Traits in Sweet Sorghum [*Sorghum bicolor* (L.) Moench]

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Generation mean analysis was carried out to estimate the nature and magnitude of gene effects for sugar content, green cane yield and its component traits in sweet sorghum [*Sorghum bicolor* (L.) Moench]. Six generations *viz.,* P_1, P_2, F_1, F_2, BC_1 and BC_2 of a cross derived from two parents *viz.,* 27 B and NSSV 13, which are contrasting for the trait of interest *i.e.,* grain quality and yield traits of grain sorghum and juiciness of sweet sorghum were evaluated in *summer* 2012. The scaling tests as well as chi square test from joint scaling test were highly significant for all the fourteen quantitative characters, indicating inadequacy of simple additive - dominance model and justifying the use of six parameter model for the detection of gene interactions. Both additive and dominance gene effects were highly significant for all the traits barring stem girth, grain yield, total biomass and fresh stalk yield where only dominance component is predominant in first two traits, while additive in later two traits. Among non allelic interactions, dominance × dominance (I) gene interaction was of greater magnitude than main gene effects for all the characters under study indicating the importance of heterosis breeding to utilize non additive gene effects.

Key words: Sweet sorghum, Generation mean analysis, Scaling test, Additive - dominance model, Sugar yield.

Sweet sorghum being one of the many kinds of sorghum bestowed with high sugar content besides good grain yield. Having rapid growth, high sugar accumulation and high biomass production potential, sweet sorghum has the ability to grow in most inhospitable environments and offers comparable grain yields (*Reddy et al.* 2008). The economic superiority is attributed to traits such as stalk yield, stalk sugar content (Brix per cent), stalk juice extractability, content of non-reducing and reducing sugars and grain yield (*Bala Ravi et al.* 1996). The feasibility of converting stalk sugars to ethanol, jaggery on or near farms, syrup and the adaptability of sorghum to a wide range of environments prompted researchers to evaluate the potential of sweet sorghum as an alternative crop for ethanol production (*Daniel et al.* 1991). Eventually, sweet sorghum is widely recognized as a potential source of biofuel. The sweet sorghums have not been a major focus of commercial breeding programmes; though hybrids have been developed between grain sorghum and sweet sorghum, usually for fodder or dual purpose use (grain and fodder). Thus, increasing stalk sugar and green cane yield is becoming an important objective in sweet sorghum breeding (*Murray et al.* 2009). Genetic enhancement of the crop for increased sugar and green cane yield is very critical to make sweet sorghum more remunerative to the farmers and the industry, while sustaining grain yield, juice volume, plant height, plant girth and other important components. The choice of an efficient breeding programme depends to a large extent on knowledge of the type of gene action involved in the expression of the trait in question. The knowledge on nature of gene action for sugar yield, green cane yield and its component traits like brix per cent and juice content in the breeding material can provide useful information for selecting suitable breeding method for future genetic enhancement. The literature regarding inheritance of the traits under study and their genetic interactions in sweet sorghum is scanty. Keeping this in view, an attempt has been made to understand the gene action controlling sugar yield, green cane yield and its component traits through generation mean analysis.

Materials and Methods

A grain sorghum line 27B and a sweet sorghum line, NSSV13 were chosen as female and male parents, respectively. The female parental line is widely used in breeding programme because of its good grain quality, high yielding and good combining ability. Male parent NSSV 13, is a sweet stalked type with high sugar content, biomass and brix content. Six generations *viz.,* P_1, P_2, F_1, F_2, BC_1 and BC_2 of this inter-varietal cross (27 B × NSSV 13) were developed and raised in randomized block design with three replications at Directorate of Sorghum Research, Hyderabad during *summer* 2012. In the experimental plot, parents and F_1 were raised in 5 rows each, whereas, back crosses and F_2 families by 15 and 20

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rows, respectively per block. A uniform inter and intra row spacing of 45 cm and 15 cm with row length of 4 m was maintained. Observations were recorded on five randomly selected plants from the parents and F_1; on 50 competitive plants from each back cross progenies and in 200 competitive plants from every F_2 in each block and analysed on single plant basis. Data were recorded on days to 50 *per cent* flowering, days to maturity, plant height (cm), number of nodes per plant, stem girth (cm), total biomass (g / plant), fresh stalk yield (g / plant), grain yield (g / plant), brix per cent, juice yield (g / plant), juice extraction per cent, total soluble sugars (%), sugar yield (g / plant) and bioethanol yield (ml / plant).

The adequacy of simple additive - dominance model to explain the gene action of characters was tested by applying the joint scaling test of *Cavalli* (1952). Since the joint scaling test was positive, indicating the presence of interactions attempts were made to test the digenic epistatic model of Hayman (1958) as out lined by Mather and Jinks (1977). Successive mean effects [m] followed by one or more of the additive [d], dominance [h], additive ×

additive [i], additive × dominance [j] and dominance × dominance [l] effects were fitted by the weighted least squares procedure and tested for goodness of fit. The chi-square value was compared with table χ^2 at (6 - 3) degrees of freedom. The significance of estimates of genetic parameters was tested by t-tests. The model showing the least mean residual sum of squares from the observed generation means was chosen for genetic interpretation of the data.

Results and Discussion

Analysis of six generations was carried out to know the real genetic worth of the individual. A perusal of these generation means indicated that, the F_2 means were lesser than the F_1 means in respect of most of the traits (Table 1) except days to 50 per cent flowering, days to maturity, nodes per plant, brix per cent, juice extraction per cent, total soluble sugars and bioethanol yield indicating high degree of inbreeding depression for most of the traits. These results revealed predominant role of non-additive gene action, which includes both dominance as well as epistatic interactions.

Table 1. Generation mean for 14 characters in the cross '27 B × NSSV 13' of sweet sorghum

Character	Generations					
	P_1	P_2	F_1	F_2	BC_1	BC_2
Days to 50% flowering	78.00 ± 0.68	85.00 ± 0.48	77.00 ± 0.47	82.49 ± 0.20	77.72 ± 0.25	82.88 ± 0.37
Days to maturity	118.00 ± 0.68	125.00 ± 0.48	117.00 ± 0.47	122.49 ± 0.20	117.72 ± 0.25	122.88 ± 0.37
Plant height (cm)	126.83 ± 0.79	245.00 ± 1.23	222.67 ± 1.11	184.72 ± 2.49	145.20 ± 2.65	223.74 ± 2.48
Nodes per plant	9.53 ± 0.22	14.33 ± 0.12	10.33 ± 0.19	12.34 ± 0.12	7.24 ± 0.13	8.74 ± 0.13
Stem girth (cm)	1.27 ± 0.02	1.81 ± 0.03	1.67 ± 0.04	1.54 ± 0.01	1.63 ± 0.04	1.64 ± 0.04
Total biomass (g / plant)	222.00 ± 3.72	617.67 ± 4.88	758.67 ± 4.65	446.44 ± 12.46	253.62 ± 14.14	497.82 ± 25.57
Fresh stalk yield (g / plant)	118.00 ± 2.67	479.00 ± 2.96	506.33 ± 2.72	270.25 ± 9.62	111.64 ± 6.49	288.89 ± 15.88
Grain yield (g / plant)	44.00 ± 1.38	46.33 ± 1.39	91.00 ± 1.28	76.36 ± 1.07	41.04 ± 2.99	47.04 ± 3.02
Brix per cent	14.20 ± 0.13	19.90 ± 0.22	17.47 ± 0.30	18.00 ± 0.17	9.77 ± 0.26	15.31 ± 0.36
Juice yield (g / plant)	22.33 ± 0.77	184.00 ± 2.22	186.00 ± 1.66	117.64 ± 4.89	30.58 ± 2.94	89.42 ± 5.94
Juice extraction per cent	18.87 ± 0.29	38.40 ± 0.31	36.73 ± 0.17	40.94 ± 0.93	25.40 ± 1.48	30.59 ± 1.09
Total soluble sugars (%)	12.57 ± 0.12	17.55 ± 0.19	15.43 ± 0.26	15.89 ± 0.15	8.70 ± 0.22	13.54 ± 0.32
Sugar yield (g / plant)	2.81 ± 0.11	32.27 ± 0.32	28.68 ± 0.49	20.08 ± 0.94	2.65 ± 0.27	12.18 ± 0.86
Bioethanol yield (ml / plant)	6692.69 ± 61.97	9346.79 ± 102.11	8213.75 ± 140.92	8582.47 ± 84.70	4630.87 ± 119.28	7209.54 ± 168.51

The adequacy of simple additive - dominance model was tested by application of A, B, C and D scaling tests of Mather (1949) and joint scaling test of Cavalli (1952), which were highly significant for all the characters (Table 2), indicating inadequacy of simple additive - dominance model justifying the use of six parameter model for detection of interaction. This Joint scaling tests (Table 3) revealed that both additive and dominance gene effects were highly significant for all the traits; stem girth, grain yield, total biomass and fresh stalk yield where only dominance component is predominant for first two traits while additive for later two traits. However, all the traits were associated with negative sign confirming the combination of genes from both the parents did not add up to the improvement oft the characters. Importance of both additive and non-additive gene effects for sugar traits of sorghum was revealed in previous studies by Ramalingam and Rangasamy

(1987); Saxena *et al.* (1999); Audilakshmi *et al.* (2010) and Sudhir Kumar *et al.* (2011). Further, dominance component [h] of generation mean observed was greater in magnitude than additive gene effect [d] for most of the traits, which strengthens the fact that dominance component played a major role in the inheritance of all these traits.

The predominant role of non-additive gene action for plant height, stem girth, total soluble solids (Brix %), stalk yield and juice yield in sweet sorghum was earlier reported by Sankarapandian *et al.* (1994). Similarly, Vemanna *et al.* (2013) and Gupta and Baliwal (1976) reported non additive gene action for days to 50 per cent flowering and total soluble solids (Brix %), respectively. The negative sign found associated with the additive and dominance effect for most of the traits indicate the additive and dominance effect for decreasing alleles as it reduced the trait value in hybrid combinations in which it was close

Table 2. Scaling tests for 14 characters in the cross '27 B × NSSV 13' of sweet sorghum

Character	Scaling tests			
	A	B	C	D
Days to 50% flowering	0.44 ± 0.96	3.76** ± 1.00	12.96** ± 1.48	4.38 ± 0.60
Days to maturity	0.44 ± 0.96	3.76** ± 1.00	12.96** ± 1.48	4.38 ± 0.60
Plant height (cm)	-59.10** ± 5.48	-20.19** ± 5.22	-78.31** ± 10.30	0.49 ± 6.16
Nodes per plant	-5.39** ± 0.39	-7.19** ± 0.34	4.83** ± 0.64	8.70 ± 0.30
Stem girth (cm)	0.31** ± 0.09	-0.20* ± 0.09	-0.26* ± 0.10	-0.19 ± 0.06
Total biomass (g / plant)	-473.43** ± 28.90	-380.69** ± 51.57	-571.24** ± 51.05	141.44 ± 38.39
Fresh stalk yield (g / plant)	-401.06** ± 13.52	-407.55** ± 32.02	-528.69** ± 39.07	139.96 ± 25.78
Grain yield (g / plant)	-52.93** ± 6.27	-43.25** ± 6.32	33.11** ± 5.35	64.64 ± 4.75
Brix per cent	-12.12** ± 0.61	-6.75** ± 0.82	2.96** ± 0.95	10.91 ± 0.56
Juice yield (g / plant)	-147.17** ± 6.16	-191.16** ± 12.19	-107.79** ± 19.96	115.27 ± 11.81
Juice extraction per cent	-4.79 ± 2.98	-13.95** ± 2.22	33.02** ± 3.76	25.88 ± 2.62
Total soluble sugars (%)	-10.60** ± 0.53	-5.90** ± 0.71	2.59** ± 0.83	9.55 ± 0.49
Sugar yield (g / plant)	-26.19** ± 0.73	-36.58** ± 1.81	-12.11** ± 3.90	25.33 ± 2.08
Bioethanol yield (ml / plant)	-5644.70** ± 283.92	-3141.47** ± 379.31	1862.91** ± 456.61	5324.54 ± 267.07

* Significant at P = 0.05   **Significant at P = 0.01

to their lower parent. Contrary to this, Dangi *et al.* (1978) reported predominant role of additive gene action for days to 50 per cent flowering as well as for plant height and stem thickness, while Umakanth *et al.* (2012) noticed additive gene action for fresh stalk yield, juice yield, brix content, total sugar yield and computed bioethanol yield.

Among the digenic interactions, dominance × dominance (l) interaction was positive for all characters except stem girth. It was found that magnitude of l (dominance × dominance) was significant and higher than both i (additive × additive) and j (additive × dominance) components revealing the presence of associated pair of genes for all the traits.

Opposite signs of dominance [h] and dominance × dominance (l) gene effects revealed duplicate epistasis for all the traits except plant height and total biomass. The negative sign associated with dominance [h] and positive sign associated with dominance × dominance (l) component in majority of traits indicate positive dominance gene action consisted of positive dominance digenic interaction whereas, the balance of the dominance gene effects of the genes controlling these traits were negative.

In a nut shell, generation mean analysis of the cross, 27 B × NSSV 13 in the present study has unraveled the presence of epistasis for all the 14 quantitative characters under study. The presence

Table 3. Gene effects for 14 quantitative characters in the cross '27 B × NSSV 13' of sweet sorghum

Character	Gene effects						Type of epistasis	χ²value
	m	$\hat{d}$	$\hat{h}$	$\hat{i}$	$\hat{j}$	$\hat{l}$		
Days to 50% flowering	82.49** ± 0.20	-5.16** ± 0.45	-13.26** ± 1.34	-8.76** ± 1.19	-1.66** ± 0.61	4.56* ± 2.31	D	120.04**
Days to maturity	122.49** ± 0.20	-5.16** ± 0.45	-13.26** ± 1.34	-8.76** ± 1.19	-1.66** ± 0.61	4.56* ± 2.31	D	120.04**
Plant height (cm)	184.72** ± 2.49	-78.54** ± 3.63	35.77** ± 12.39	-0.98 ± 12.32	-19.46** ± 3.70	80.27** ± 17.80	C	174.19**
Nodes per plant	12.34** ± 0.12	-1.50** ± 0.18	-19.00** ± 0.63	-17.40** ± 0.59	0.90** ± 0.22	29.97** ± 0.98	D	1017.20**
Stem girth (cm)	1.54** ± 0.02	-0.02 ± 0.06	0.52** ± 0.13	0.38** ± 0.13	0.25** ± 0.06	-0.49* ± 0.25	D	30.73**
Total biomass (g / plant)	446.44** ± 12.46	-244.20** ± 29.22	55.95 ± 76.99	-282.88** ± 76.79	-46.37 ± 29.38	1137.00** ± 127.52	C	427.38**
Fresh stalk yield (g / plant)	270.25** ± 9.62	-177.25** ± 17.15	-72.10 ± 51.67	-279.93** ± 51.56	3.25 ± 17.27	1088.54** ± 78.96	D	1175.50**
Grain yield (g / plant)	76.36** ± 1.07	-6.00 ± 4.25	-83.46** ± 9.64	-129.29** ± 9.51	-4.84 ± 4.36	225.47** ± 17.81	D	190.69**
Brix per cent	18.00** ± 0.17	-5.54** ± 0.44	-21.41** ± 1.17	-21.83** ± 1.12	-2.69** ± 0.46	40.70** ± 2.01	D	567.04**
Juice yield (g / plant)	117.64** ± 4.89	-58.84** ± 6.63	-147.71** ± 23.70	-230.54** ± 23.61	21.99** ± 6.73	568.87** ± 33.18	D	802.71**
Juice extraction per cent	40.94** ± 0.93	-5.19** ± 1.84	-43.67** ± 5.24	-51.76** ± 5.23	4.58* ± 1.85	70.50** ± 8.27	D	121.82**
Total soluble sugars (%)	15.89** ± 0.15	-4.84** ± 0.39	-18.73** ± 1.02	-19.09** ± 0.98	-2.35** ± 0.40	35.59** ± 1.76	D	567.29**
Sugar yield (g / plant)	20.08** ± 0.94	-9.54** ± 0.90	-39.52** ± 4.20	-50.66** ± 4.17	5.19** ± 0.91	113.42** ± 5.30	D	1492.29**
Bioethanol yield (ml / plant)	8582.47** ± 84.70	-2578.67** ± 206.46	-10455.06** ± 555.63	-10649.07** ± 534.13	-1251.62** ± 214.92	19435.24** ± 943.66	D	585.70**

* Significant at P = 0.05; **Significant at P = 0.01;
D = Duplicate type of interaction C = Complementary type of interaction

of epistasis has important implications for any plant breeding endeavor. It is due to the fact that, magnitude of heterosis is influenced by non-allelic interactions and these non-allelic interactions are known to either reduce or enhance the extent of heterosis depending upon their direction and magnitude of gene action. The results of the present investigation may be applicable to the genotypes under study,

the identification of dominance and epistatic effects suggest that complimentary research is needed to further advance the sweet sorghum breeding. Confounding epistatic effects it suggested that inheritance of these traits is complex and polygenic (Warnock *et al.,* 1998). Higher magnitude of dominant gene effects and dominant gene interactions could not be exploited for heterosis breeding due to the

presence of duplicate epistasis in the present inter varietal cross, as it minimizes the manifestation of heterosis (Kearsy and Pooni, 1996). Hence, selection for high sugar yielding genotypes would be effective only if dominance and epistatic effects were first reduced only by few generations of selfing. Then biparental mating followed by intermating of selected progeny and selection in subsequent segregating generation or population by improved methods may possibly serve the purpose of developing high sugar yielding genotypes of sweet sorghum.

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