

Evaluating Top Vs. Bottom Segments Performance of Sugarcane Genotypes

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Abstract: The use of specific planting segments as sowing material can augment sustainable production of sugarcane. Therefore, to have a base-line information on the sustainable production of sugarcane (*Saccharum officinarum* L.), field trials were carried out on the growth and yield analysis of the crop on farmers' field at Dargai, Malakand Agency, Khyber Pakhtunkhwa-Pakistan during the spring cropping season of 2010-11 and 2011-12. Triplicate RCB, design was used with plot area of 67m². A total of 16 sugarcane genotypes, comprising 14 candidate and two check genotypes were used in the experiment. The data were collected on eight yield and yield contributing parameters. Combined ANOVA over years and segments revealed significant differences among sugarcane genotypes for germination, tillers, plant height, internode length, cane yield, millable canes and sugar yield. Significant ($p \leq 0.05$) segment x genotype interactions were observed for cane yield, sugar yield and millable canes. Mean results showed that highest germination (65.92 and 47.58%) and tillers (164.95 and 137.00) in top and bottom segments were exhibited by genotype MS91CP238, against the check genotypes. The maximum plant height (233.64 cm) for top segment was exhibited by genotype Hoth127, while the same for bottom segment (234.17cm) was recorded by genotype MS94CP15. The maximum nodes plant⁻¹ (20.22, 17.78) in top and bottom segments, respectively was recorded for genotypes Hoth127 and MS99HO388. Genotypes MS92CP979 and MS94CP15 exhibited maximum internode length (16.45 and 17.04cm) in top and bottom segments, respectively. The highest cane yield (59.72, 64.10 t ha⁻¹) and millable canes (127.26 and 95.81) in top and bottom segments were recorded for genotypes MS99HO388 and MS91CP238, respectively. Maximum sugar recovery (12.23 and 10.49%) in top and bottom segments, respectively was recorded for genotypes MS99HO93 and S97CP288. The highest sugar yield (7.05 and 5.96 t ha⁻¹) in top and bottom segments was recorded for genotypes MS99HO388 and MS91CP238, respectively. On the basis of overall combined over years performance, it can be concluded that genotypes MS99HO388, Hoth127, S96SP1215, MS91CP238 and MS99HO388 showed better performance in top segments regarding parameters germination, tillers, plant height, cane yield, millable canes, sugar recovery and sugar yield. On the contrary, genotypes MS94CP15, MS99HO388, MS91CP238 and CP89831 exhibited better performance in bottom segments for the same growth and yield attributes. Genotypes MS91CP238, MS99HO388, MS94CP15 and Hoth127 proved to be superior in both top and bottom segments for the studied traits.

Key words: Sugarcane genotypes • Top vs bottom segments performance • Cane yield • Sugar yield • Dargai

INTRODUCTION

Sugarcane (*Saccharum officinarum*) is the major cash crop of Pakistan in general and of Khyber Pakhtunkhwa in particular due to its area under cultivation, production and existing Sugar Mills. The area under sugarcane is gradually increasing but its local production is still poor and insufficient for smooth running of the existing Sugar

Mills. There are several limiting factors affecting the sugarcane production. Among these; one is the lack of proper environment that stimulate flowering in sugarcane for breeding activities. Therefore, in Pakistan most of the sugarcane varieties have been evolved through selection from introduced material. The introduced material is first sown in the nursery, followed by transplantation to fields. The screened material is then propagated by cuttings of

mature stalks with one or more buds, properly called as setts. The basis of a good crop is considered to be good bud development on planted cuttings, followed by satisfactory agronomic practices [1].

Among the various techniques for obtaining maximum sugarcane production, one is the use of apex (top) portion as sowing material for cultivation. Planting material (cane setts) in field is obtained from the top of cane to bottom. The common farmers use the middle, base and top portions for sowing purpose but the progressive farmers use mostly the top portions as planting material and use the middle and base portions to supplement the tops in areas where large acreage of lands are used for sugarcane cultivation. Due to the presence of very active primordial cells in young buds, the top and middle portions are preferred as sowing material. Moreover, as the top and middle portions contain enzymes that are easily activated under favorable environmental conditions [2], therefore, these differential cellular compositions may affect subsequent growth and development of the sugarcane seedlings. The objectives of the present study were to evaluate the growth performance of two segments of sugarcane stalk e.g., top and bottom segments and to identify the plant part more contributing to final yield.

MATERIALS AND METHODS

In order to study the relative performance of the top and bottom segments of the mature sugarcane stalks, this experiment was conducted using 16 promising sugarcane genotypes. The list of genotypes and their source is given in Table 1. This experiment was undertaken on

farmer's field at Dargai, Malakand Agency during the spring cropping seasons of 2010-11 and 2011-12. Sugarcane cuttings, top and bottom segments each with three buds (setts) were obtained from mature stalks of each genotype. Double setts of each portion were used as a sowing material. To get an unbiased true reflection of each clonal segment performance, both the top and bottom segments were planted in separate fields with triplicate RCB design. Each genotype was assigned to a separate block of seven rows. The central row consisted of 150 buds. Recommended dose of fertilizer was applied as N (150 Kg ha⁻¹), P (100 Kg ha⁻¹) and K (100 Kg ha⁻¹) from sulphate of potassium (SOP), diammonium phosphate (DAP) and Urea as 225.00 kg DAP ha⁻¹ at planting time and 250.00 kg SOP with 125 kg urea ha⁻¹ in May and June. Urea was additionally applied at 125.00 kg ha⁻¹ at the time of earthing up. Data were recorded on five randomly selected genotypes from central row on nine agronomic parameters i.e., germination %, number of tillers, plant height (cm), internode length (cm), cane yield (t ha⁻¹), number of millable canes, sugar yield (t ha⁻¹) and sugar recovery %.

Statistical Analysis: For the comparison of sugarcane top and bottom portions as planting material, the combined data over two years of each segment was statistically analyzed by using Fisher's analysis of variance technique and genotypes means were compared by using Least Significance Difference (LSD) test according to Steel and Torrie [3]. A combined ANOVA table was constructed for the genotypes mean comparisons of both top and bottom segments.

Table 1: List of 16 sugarcane genotypes and their source used for morphological characterization at SCRI, Mardan, during 2010-11

S.No	Genotypes	Source
1	MS91CP272	USDA-ARS stations at Canal Point, USA
2	MS94CP15	USDA-ARS stations at Canal Point, USA
3	MS91CP238	USDA-ARS stations at Canal Point, USA
4	MS92CP979	USDA-ARS stations at Canal Point, USA
5	MS99HO391	USDA-ARS stations, Houma, Louisiana, USA
6	S97CP288	USDA-ARS stations at Canal Point, USA
7	MS99HO317	USDA-ARS stations, Houma, Louisiana, USA
8	RS97N45	South African Research Institute, Natal (South Africa)
9	MS99HO388	USDA-ARS stations, Houma, Louisiana, USA
10	MS99HO675	USDA-ARS stations, Houma, Louisiana, USA
11	MS99HO93	USDA-ARS stations, Houma, Louisiana, USA
12	S96SP1215	São Paulo (Brazil)
13	Hoth127	USDA-ARS stations, Houma, Louisiana, USA and Sugarcane Research Institute, Thatta
14	CP89831	USDA-ARS stations at Canal Point, USA
15	CP77400 (Check-I)	USDA-ARS stations at Canal Point, USA
16	Mardan93 (Check-II)	USDA-ARS stations at Canal Point, USA

MS: Mardan Selection, Hoth: Houma-Thatta, SP: São Paulo, HO: Houma, N: Natal
 USDA-ARS: United States Department of Agriculture-Agriculture Research Service

RESULTS AND DISCUSSION

Germination: The combined over years means square results revealed highly significant differences ($p \leq 0.01$) among the genotypes for germination % (Table 2). Significant differences were also shown by years, segments, year x genotype interactions and year x segment interactions for this trait. Non-significant differences ($p \geq 0.05$) were observed for interactions of segment x genotype and year x segment x genotype.

Mean results exhibited that germination in sugarcane genotypes ranged from 24.00 to 65.92% in top segments vs. 20.25 to 47.58% in bottom segments (Table 3). Top segment exhibited significantly high percentage of buds germination as compared to bottom.

All sugarcane genotypes showed maximum buds germination in top segments than in bottom. The genotype MS91CP238 germinated highest buds (65.92 and 47.58%) compared to genotype S97CP288 (24 and 20.25%) in both top and bottom segments, respectively. Averaged over 16 sugarcane genotypes, germination in top and bottom segments were 47.04 and 33.50%, respectively. Our results are supported by the findings of Clements [4], who reported that top cuttings from the upper section of mature stalk germinated faster and with a higher percentage than did cuttings from the older basal portions of the stalks. Das [5] also reported that sets graded in order of ageing of buds showed gradual decline in germination percentages with an increase in age.

Table 2: Mean squares for germination, number of tillers, plant height, nodes plant⁻¹, internode length, cane diameter and cane yield in top vs bottom segments performance of 16 sugarcane genotypes at Dargai, during 2010-11 and 2011-12

SOV	df	Germination (%)	Tillers	P.H	I.L	C.Y	M.C	S.R (%)	S.Y
Years	1	17063.02**	38105.56**	177026.13**	124.66**	3581.12**	37664.49**	270.37**	205.14**
Segments	1	8788.55**	33513.77**	4.13 ^{ns}	0.90 ^{ns}	74.80 ^{ns}	19676.93**	156.93**	37.95**
Years x Segments	1	671.26*	21959.40**	475.49 ^{ns}	0.32 ^{ns}	17.80 ^{ns}	10774.52**	381.83**	70.06**
Reps (Segments x Years)	8	508.34	1309.07	2125.18	6.03	113.26	1042.15	2.29	3.26
Genotypes	15	746.99**	6137.81**	1915.93*	15.35**	431.40**	3688.27**	0.80 ^{ns}	4.31**
Genotypes x Years	15	716.57**	6093.49**	1334.68 ^{ns}	6.61 ^{ns}	343.62**	4295.17**	2.00 ^{ns}	3.76**
Genotypes x Segments	15	168.69 ^{ns}	741.71 ^{ns}	399.11 ^{ns}	2.11 ^{ns}	190.91**	877.59*	1.51 ^{ns}	2.48**
Genotypes x Years x Segments	15	105.54 ^{ns}	867.03 ^{ns}	444.30 ^{ns}	3.69 ^{ns}	170.11**	849.93*	1.36 ^{ns}	2.48**
Error	120	98.11	538.24	875.67	4.58	56.38	469.06	1.29	0.91
C. V%		24.60	23.20	14.37	15.22	15.55	30.56	10.59	18.23

*, **, Significant at 5% and 1% probability levels, ns = non-significant, P.H = Plant height, I. L= Inter node length, C.Y= Cane yield, M. C= Millialie cane, S. R= Sugar recovery, S. Y= Sugar yield

Table 3: Mean performance of top vs. bottom segments for germination % and tillers of 16 sugarcane genotypes evaluated at Dargai, during 2010-11 and 2011-12

Genotypes	Germination (%)			Tillers		
	Top segments	Bottom segments	Genotype mean	Top segments	Bottom segments	Genotype mean
MS91CP272	55.50	33.25	44.38	127.56	95.00	111.28
MS94CP15	45.25	30.84	38.04	98.71	88.26	93.48
MS91CP238	65.92	47.58	56.75	164.95	137.00	150.97
MS92CP979	49.84	47.50	48.67	116.17	118.69	117.43
MS99HO391	47.42	31.17	39.29	95.00	68.59	81.80
S97CP288	24.00	20.25	22.13	53.95	45.69	49.82
MS99HO317	50.67	29.58	40.12	117.35	73.09	95.22
RS97N45	51.09	27.34	39.21	107.06	59.56	83.31
MS99HO388	64.17	40.25	52.21	157.12	98.37	127.74
MS99HO675	48.92	32.92	40.92	111.37	83.54	97.45
MS99HO93	39.50	28.25	33.88	102.30	71.89	87.09
S96SP1215	46.17	32.83	39.50	118.87	87.71	103.29
Hoth127	38.59	33.00	35.79	89.52	74.82	82.17
CP89831	42.25	27.09	34.67	99.39	68.74	84.07
CP77400	40.00	37.33	38.67	104.21	93.06	98.63
Mardan93	43.34	36.92	40.13	106.00	82.72	94.36
Segment mean	47.04	33.50		110.59	84.17	
Genotype LSD (0.05)		8.01			2.83	
Segment LSD (0.05)		11.32			18.75	
G X S LSD (0.05)		6.63			26.52	

Ns = Non-significant, G X S = Genotype x segment

Further, they reported that the differences in germinability due to age of buds were statistically significant. Plana and Alvarez [6] observed that top sections of mature stalks have higher level of reducing sugars than the bottom sections and hence showed better germination and could explain the superiority of the top section in germination.

Number of Tillers: Number of tillers was recorded in 10 m long central row. Tillers are directly proportional to cane yield and therefore play a key role in enhancing the final yield of sugarcane. The analysis of variance results in Table 2 exhibited significantly high variations for number of tillers. Significant variations were also recorded for years, segments and year x genotype interactions and significant differences ($p \geq 0.05$) were observed for year x segment interactions. Non-significant differences ($p \geq 0.05$) were recorded for segment x genotype interactions and year x crop segment x genotype interactions.

Mean results exhibited that tillers in sugarcane genotypes ranged from 53.95 to 164.95 in top segments vs. 45.69 to 137.00 in bottom segments (Table 3). Top segments exhibited maximum number of tillers as compared to bottom. About 93.75% sugarcane genotypes showed maximum number of tillers in top segments than in bottom. Among the top segments, genotype MS91CP238 produced the highest tillers (164.95) while genotype S97CP288 produced the least (53.95). Similarly, among the bottom segments the same genotype MS91CP238 produced the maximum tillers (137.00), while the genotype S97CP288 produced the minimum (45.69). Averaged over 16 sugarcane genotypes, tillers in top and bottom segments were 110.59 and 84.17, respectively. Our results are in good agreement with the findings of Ahmed *et al.* [7], who conducted experiment on effect of planting parts and potassium rate on the productivity of sugarcane (*Saccharum officinarum*) and concluded that NCS 008 produced the highest number of tillers and was significantly ($P \leq 0.05$) higher than the number produced by Bida local for plant and ratoon crops. Further, they concluded that top parts gave the highest number of tillers, although there was no significant difference between middle and bottom parts for both plant and ratoon crops.

Plant Height: The analysis of variance results showed significant differences ($p \leq 0.05$) for plant height among the genotypes (Table 2). Significant

differences were observed for years while non-significant ($p \geq 0.05$) variations were observed for crop segment and interactions of year x segment, year x genotype, segment x genotype and year x segment x genotype.

Mean results showed that plant height in sugarcane genotypes ranged from 191.45 to 233.64cm in top segments vs. 175.95 to 234.17cm in bottom segments (Table 4). Bottom segment exhibited maximum plant height compared to the top. About 43.75% of sugarcane genotypes showed maximum plant height in top segments than in bottom. Among the top segments, genotype Hoth127 was the tallest (233.64 cm) while check genotype Mardan93 was the shortest (191.45 cm). Similarly, among the bottom segments, genotype MS94CP15 was the tallest whereas genotype MS99HO93 was shortest (175.95 cm). Averaged over 16 sugarcane genotypes, plant height in top and bottom segments were 205.84 and 206.13cm, respectively.

Internode Length: The internode length contributes positively to final cane yield. Highly significant variations ($p \leq 0.01$) were observed among the genotypes for internode length. Highly significant variations ($p \leq 0.01$) were also recorded for years while non-significant ($p \leq 0.05$) differences were noted for segments, interactions of year x segment, year x genotype, segment x genotype and year x segment x genotype (Table 2). Our results are in contrary with those obtained by Kolo *et al.* [8], who reported non-significant differences for internode length in evaluation of different portions (top, middle and bottom) of cane as sowing material. The possible reason for this discrepancy in results may be the use of only one variety of sugarcane by the researchers in their study while in the present experiment 16 different genotypes were used.

The mean results indicated that internode length ranged from 12.42 to 16.45cm in top segments vs. 12.14 to 17.04cm in bottom segments (Table 4). About 50% of the sugarcane genotypes had longer internode in top segments than in the bottom. Among the top segments, genotype MS92CP979 had the longest internode (16.45cm) whereas genotype MS99HO93 had the shortest (12.42cm). Similarly, among bottom segments, the genotype MS94CP15 produced the longest internode (17.04cm) whereas the genotype MS99HO317 produced the shortest (12.14 cm). Averaged over 16 sugarcane genotypes, internode length in top segments and bottom segments were 14.13 and 14.00 cm, respectively.

Table 4: Mean performance of top vs. bottom segments for plant height and nodes plant⁻¹ of 16 sugarcane genotypes evaluated at Dargai, during 2010-11 and 2011-12

Genotypes	Plant height (cm)			Internode length (cm)		
	Top segments	Bottom segments	Genotype mean	Top segments	Bottom segments	Genotype mean
MS91CP272	204.58	211.28	207.93	14.22	14.70	14.46
MS94CP15	224.79	234.17	229.48	16.61	17.04	16.83
MS91CP238	195.82	206.41	201.11	13.17	13.66	13.41
MS92CP979	217.54	221.31	219.42	16.45	15.18	15.81
MS99HO391	213.74	195.21	204.48	14.38	13.56	13.97
S97CP288	197.82	205.01	201.41	12.84	12.85	12.84
MS99HO317	198.74	190.12	194.43	13.89	12.14	13.01
RS97N45	193.85	201.79	197.82	14.17	14.67	14.42
MS99HO388	229.39	217.51	223.45	14.34	14.23	14.28
MS99HO675	198.35	199.28	198.82	14.64	14.45	14.54
MS99HO93	192.85	175.95	184.40	12.42	11.56	11.99
S96SP1215	204.40	200.79	202.59	13.98	13.48	13.73
Hoth127	233.64	221.02	227.33	14.11	13.20	13.65
CP89831	208.40	204.97	206.68	14.20	14.33	14.26
CP77400	188.04	208.33	198.18	13.53	15.00	14.27
Mardan93	191.45	204.97	198.21	13.22	13.94	13.58
Segment mean	205.84	206.13		14.13	14.00	
Genotype LSD (0.05)		23.92			8.46	
Segment LSD (0.05)		33.83			1.73	
G X S LSD (0.05)		0.61			2.45	

Ns = Non-significant, G X S = Genotype x segment

Table 5: Mean performance of top vs. bottom segments for cane yield and millable canes of 16 sugarcane genotypes evaluated at Dargai, during 2010-11 and 2011-12

Genotypes	Cane yield (t ha ⁻¹)			Millable canes		
	Top segments	Bottom segments	Genotype mean	Top segments	Bottom segments	Genotype mean
MS91CP272	47.41	49.72	48.56	94.41	66.00	80.21
MS94CP15	47.98	51.27	49.63	78.44	58.61	68.53
MS91CP238	56.66	64.10	60.38	119.16	95.81	107.48
MS92CP979	52.48	58.44	55.46	90.51	76.27	83.39
MS99HO391	48.73	49.99	49.36	73.31	59.39	66.35
S97CP288	29.99	32.40	31.19	33.42	29.33	31.37
MS99HO317	55.22	42.03	48.63	95.35	52.65	74.00
RS97N45	55.07	38.95	47.01	80.21	39.76	59.99
MS99HO388	59.72	42.91	51.31	127.26	67.47	97.37
MS99HO675	48.27	43.69	45.98	79.16	68.43	73.79
MS99HO93	47.37	49.88	48.62	76.54	55.37	65.95
S96SP1215	54.59	47.68	51.13	85.91	53.01	69.46
Hoth127	47.85	48.07	47.96	61.04	52.50	56.77
CP89831	42.88	46.44	44.66	52.07	52.66	52.37
CP77400	43.04	50.77	46.91	76.01	77.29	76.65
Mardan93	45.18	46.14	45.66	73.26	67.59	70.43
Segment mean	48.90	47.65		81.00	60.76	
Genotype LSD (0.05)		6.07			2.15	
Segment LSD (0.05)		8.58			17.51	
G X S LSD (0.05)		6.19			24.76	

Ns = Non-significant, G X S = Genotype x segment

Cane Yield: The analysis of variance results given in Table 2 revealed highly significant ($p \leq 0.01$) differences among the genotypes for cane yield. Highly significant ($p \leq 0.01$) differences were also recorded for years, interactions of year x genotype, segment x genotype and year x segment x genotype while non-significant differences ($p \leq 0.05$) were observed for segments and year x segment interactions. Our results are in contrary with those obtained by Kolo *et al.* [8], who reported non-significant results for the same parameter while evaluating different portions (top, middle and bottom) of cane as sowing material using two sugarcane cultivars. The difference in results could be due to the use of very limited population by the authors while in our experiment much diverse and comparatively larger number of sugarcane populations has been used.

Mean results highlighted that cane yield in sugarcane genotypes ranged from 42.88 to 59.72 t ha⁻¹ in top segments vs. 38.95 to 64.10 t ha⁻¹ in bottom segments (Table 5). Bottom segments produced the maximum cane yield compared to top ones. About 31.25% of sugarcane genotypes, produced highest cane yield in top segments than in bottom. Among the top segments, genotype MS99HO388 produced the highest cane yield (59.72 t ha⁻¹), while genotype CP89831 produced the lowest (42.88 t ha⁻¹). Similarly, among the bottom segments, genotype MS91CP238 produced maximum cane yield (64.10 t ha⁻¹), whereas genotype RS97N45 produced the lowest (38.95 t ha⁻¹). Averaged over 16 sugarcane genotypes, cane yield in top and bottom segments were 48.90 and 47.65 t ha⁻¹, respectively.

Number of Millable Canes: The mean squares combined over year analysis indicated highly significant variations ($p \leq 0.01$) for millable canes among the cultivars for years, segments, year x crop segment interactions and year x genotype interactions. Significant variations ($p \leq 0.05$) were observed for interactions of segment x genotype and year x segment x genotype (Table 2). These results suggested that highest number of millable canes were harvested from top segments as compared to bottom. Kolo *et al.* [8] also reported significant differences for same parameter.

Mean results indicated that millable canes in sugarcane genotypes ranged from 33.42 to 127.26 in top segments vs. 29.33 to 95.81 in bottom segments (Table 5). Top segment produced the maximum millable canes compared to bottom. About 87.50% of sugarcane genotypes used in this study produced highest millable

canes in top segments than in bottom. Among the top segments, genotype MS99HO388 produced the highest millable canes (127.26), while genotype S97CP288 produced the lowest (33.42). Similarly, among the bottom segments, genotype MS91CP238 produced the maximum millable canes (95.81) whereas genotype S97CP288 produced the minimum (29.33). Averaged over 16 sugarcane genotypes, millable canes in top and bottom segments were 81.00 and 60.76, respectively.

Sugar Recovery (%): Mean squares results showed non-significant variations ($p \geq 0.05$) among the genotypes for sugar recovery. Non-significant differences were also recorded for interactions of year x genotype, segment x genotype and year x crop segment x genotype whereas highly significant variations ($p \leq 0.01$) were observed for years, segments and year x crop segment for this parameter (Table 2).

Mean results revealed that sugar recovery in sugarcane genotypes ranged from 11.11 to 12.23% in top segments vs. 9.14 to 10.49% in bottom segments (Table 6). Top segments exhibited the maximum sugar recovery compared to bottom. All sugarcane genotypes had the highest sugar recovery in top segments compared to the bottom. Among the top segments, genotype MS99HO93 had the highest sugar recovery (12.23%), while genotype RS97N45 had the lowest (11.11%). Similarly, among the bottom segments, genotype S97CP288 showed the maximum sugar recovery (10.49%) whereas genotype MS99HO388 exhibited the lowest (9.14%). Averaged over 16 sugarcane genotypes, sugar recovery in top and bottom segments were 11.61 and 9.21%, respectively.

Sugar Yield: The analysis of variance revealed highly significant differences ($p \leq 0.01$) among the genotypes for sugar yield. Highly significant variations were also observed for years, segments, interactions of year x crop segment, year x genotype, crop segment x genotype and year x crop segment x genotype for this parameter (Table 2).

Mean results indicated that sugar yield in sugarcane genotypes ranged from 3.35 to 7.05 t ha⁻¹ in top segments vs. 3.58 to 5.96 t ha⁻¹ in bottom segments (Table 6). Top segment produced the maximum sugar yield compared to bottom. About 87.50% of sugarcane genotypes produced highest sugar yield in top segments than in bottom. Among the top segments, genotype MS99HO388 produced the highest sugar yield (7.05 t ha⁻¹), while genotype S97CP288 produced the lowest (3.35 t ha⁻¹).

Table 6: Mean performance of top vs. bottom segments for sugar recovery % and sugar yield of 16 sugarcane genotypes evaluated at Dargai, during 2010-11 and 2011-12

Genotypes	Sugar recovery (%)			Sugar yield (t ha ⁻¹)		
	Top segments	Bottom segments	Genotype mean	Top segments	Bottom segments	Genotype mean
MS91CP272	11.35	10.47	10.91	5.36	5.10	5.23
MS94CP15	11.74	10.32	11.03	5.61	5.38	5.50
MS91CP238	11.79	9.53	10.66	6.69	5.96	6.32
MS92CP979	11.72	10.05	10.89	6.10	5.88	5.99
MS99HO391	11.37	9.31	10.34	5.56	4.90	5.23
S97CP288	11.36	10.49	10.92	3.35	3.58	3.46
MS99HO317	11.54	9.24	10.39	6.40	4.31	5.35
RS97N45	11.11	9.98	10.54	6.09	4.29	5.19
MS99HO388	11.69	9.14	10.41	7.05	4.06	5.55
MS99HO675	11.98	8.75	10.36	5.80	3.99	4.90
MS99HO93	12.23	9.27	10.75	5.82	4.68	5.25
S96SP1215	11.25	9.72	10.49	6.14	4.61	5.37
Hoth127	11.64	9.97	10.80	5.47	4.98	5.22
CP89831	11.99	10.30	11.15	5.10	4.97	5.04
CP77400	11.76	10.04	10.90	5.02	5.05	5.03
Mardan93	11.29	10.29	10.79	5.11	4.71	4.91
Segment mean	11.61	9.80		5.66	4.78	
Genotype LSD (0.05)		Ns			0.77	
Segment LSD (0.05)		Ns			0.27	
G X S LSD (0.05)		Ns			1.09	

Ns = Non-significant, G X S = Genotype x segment

Similarly, among the bottom segments, genotype MS91CP238 produced the maximum sugar yield (5.96 t ha⁻¹) whereas genotype S97CP288 produced the minimum (3.58 t ha⁻¹). Averaged over 16 sugarcane genotypes, sugar yield in top and bottom segments were 5.66 and 4.78 t ha⁻¹, respectively.

CONCLUSIONS

It can be concluded that sugarcane genotypes planted from top segments performed better than bottom on the basis of germination, tillers, millable canes, sugar recovery % and sugar yield. This is considerably good for farmers with small land holding however, the farmers holding large acreage of land could use the bottom segments in addition to top and middle. Genotypes MS99HO388, Hoth127, S96SP1215, MS91CP238 and MS99HO388 showed better performance in top segments regarding germination, tillers, plant height, cane yield, millable canes, sugar recovery and sugar yield. Genotypes MS94CP15, MS99HO388, MS91CP238 and CP89831 displayed better performance in bottom segments regarding germination, tillers, plant height, internode length, cane yield, millable canes, sugar recovery and sugar yield. There were some genotypes (MS91CP238, MS99HO388, MS94CP15 and Hoth127) that proved to be superior in both top and bottom segments regarding the

above parameters. The performance of other genotypes was average to satisfactory.

Top segments are recommended to farmers as planting material based on results from this study. The genotypes that performed superior regarding both top and bottom segments should be recommended to farmers for cultivation. The average and poor performed genotypes should be tested further to obtain some conclusive results.

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