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Simultaneous selection and stability under late planted commercial cane sugar

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Abstract

The modified form of selection index method utilizing simultaneous selection for yield (mean performance) and stability, Kang's rank sum method and Eberhart and Russell method were applied to a set of twenty sugarcane (*Saccharum* sp.) genotypes under late planted condition. The yield stability index method utilizing both stability variance statistic and mean performance of genotypes was found to be better than the Kang's rank sum method. The genotypes CoLk 9411, CoLk 9618, CoLk 9606 and CoLk 9216 were high yielding and stable with respect to CCS (t/ha).

Key Words: Sugarcane, genotype x environment interaction, late planting, simultaneous selection

Introduction

Stability of a genotype refers to its performance with respect to changing environmental factors over time within a given location. The selection of genotypes for a particular character depends upon their mean performance and stability parameters. The selected genotypes must have high mean value coupled with stable performance. In yield trials, the pooling of genotypic means over years or over environments is not desirable for genotypic selection without considering the stability parameters if genotype x environment interaction is significant. The genotypes selected under late planted condition should have high mean and stability over number of seasons in both plant and ratoon crop. The late planting of sugarcane refers to its planting after wheat harvest in the month of April and May which has gained a lot of importance in northern parts of India including Punjab, Haryana and Western Uttar Pradesh.

The rank sum method proposed by Kang [1] utilized stability variance statistic [2] for simultaneous selection of mean performance and stability. However, this method had a tilt towards mean performance as compared to stability parameters. Simultaneous selection for yield and stability [3] provided 3 different indices to mark the genotype performance with reference to both mean yield and stability. An attempt has been made in this study to mark high yielding, stable genotypes by utilizing the modified form of these indices in sugarcane and their applicability under late planted conditions for commercial cane sugar (CCS t/ha).

Materials and Methods

The experimental material comprised of seventeen genotypes of sugarcane (*Saccharum* sp. complex) along with three varieties (CoLk 8102, CoS 767 and CoJ 64). The genotypes belonged to both early and mid late groups (Table 1). Two plant crops were taken in second fortnight of April during 1998-99 and 1999-2000 while ratoon crop was initiated in 1999-2000. The experiment was conducted in three replications with plot size kept at 4 rows of 4 meters spaced 75 cm apart per genotype per replication. All recommended agronomic packages and practices were applied during the conduct of trial.

The millable canes from each plot were sampled randomly for cane juice quality. The brix % and pol % of cane juice were estimated and were utilized to estimate sugar yield as per Meade and Chen [4].

The data were subjected to analyses using Eberhart and Russell [5], Kang [1] and a modified form of stability index method [2].

Results and discussion

The genotypes differed significantly for commercial cane sugar at 10 months. Since the genotype x environment (linear) and pooled deviation are significant with respect to pooled error, it is required to test the significance of genotype x environment with respect to pooled deviation, which is non significant. The overwhelming portion of the G x E interaction is of non-linear type. Further testing of individual deviation of each genotype against pooled error was done to find out genotypes for which interaction was entirely linear. The regression (b_i) and deviation from regression of each genotype were tested for their significance (Table 2). The

Table 1. The genotypes used in the study and their parentage

S. No.	Genotypes	Parentage
(a) Early maturing		
1.	CoLk 91236	CoC 671 × Co 7717
2.	CoLk 91239	Co 6806 × Co 7117
3.	CoLk 9229	CoC 671 × Co 1148
4.	CoLk 9411	Bo 91 × Co 617
5.	CoLk 9412	Bo 91 × Co 1305
6.	CoLk 9414	Co 7717 × Co 775
7.	CoJ 64	Co 976 × Co 617
(b) Mid late		
8.	CoLk 9110	Co 1158 × IA 1548
9.	CoLk 9204	Co 6806 × CoS 510
10.	CoLk 9210	Co 62399 × Co 1148
11.	CoLk 9212	Co 449 × Co 1148
12.	CoLk 9216	Bo 91 × Co 617
13.	CoLk 9301	Co 62174 × Co 1148
14.	CoLk 9302	Co 6806 × Co 775
15.	CoLk 9606	Co 7224 × Poly cross
16.	CoLk 9617	Co 62399 × Bo 9l
17.	CoLk 9618	Co 62399 × Bo 91
18.	93-A-21	LG 72115 (Self)
19.	CoLk 8102	Co 1158 GC
20.	CoS 767	Co 419 × Co 313

genotypes CoLk 9411, CoLk 9216, CoLk 9606, CoLk 8102, CoS 767 and 93-A-21 were selected as they were having high mean (above over all mean), unit regression and least deviation from regression. Though the model is widely used, some weaknesses of the model must be considered before making final conclusions. The model depends upon the computation of environmental indices which are non-independent, the joint regression (environment (linear)) with 1 degree of freedom equals between environment sum of square with (s-1) degrees of freedom (s = number of environments) sum of squares. The model also assumes the homogeneity of individual deviations, which may not hold true. Moreover the model also accounts for only linear portion of G x E interaction where as in sugarcane large amount of non linear G x E interaction has been observed. To overcome some of these weaknesses and to apply simultaneous selection for yield and stability, the data were also subjected to analyses by Kang [1] and a modified form of Bajpai and Parbhakaran [3]. Kang 's method utilized adjusted yield ranks (CCS) and stability ratings to find out mean yield stability index (Ysi) value of each genotype (Table 3). The genotypes CoLk 9606, CoLk 9618, CoLk 9411, CoLk 9216, CoLk 9212 and CoLk 8102 were selected. In this approach some of the weaknesses of Eberhart and Russell method were corrected. Here both CCS and stability were given importance during genotype selection and a large portion of G x E interaction is accounted for by Shukla's stability variance statistic. There is a big risk for Kang's index weighing heavily in the direction of mean performance of the trait as compared to stable performance. Since the stability variance statistic is significant for most of the genotypes at 1% level of significance, a constant score of -8 is given for all of them. This means that the Ysi values

Table 2. Stability parameters of different genotypes for CCS Yield (t/ha)

S. No.	Genotypes	Mean	bi	Sd_i^2
1	CoLk 9110	9.05	1.76**	5.18
2	CoLk 91236	4.17	0.77	0.03
3	CoLk 91239	6.98	-0.22*	2.57
4	CoLk 9204	4.53	2.71	0.02
5	CoLk 9210	5.07	0.70	1.29
6	CoLk 9212	9.14	1.63**	2.75
7	CoLk 9216	9.93	3.52	0.56
8	CoLk 9229	5.19	2.88	0.54
9	CoLk 9301	7.30	–0.40**	8.11
10	CoLk 9302	6.95	–0.44	0.51
11	CoLk 9411	10.60	0.23	0.78
12	CoLk 9412	5.97	–1.89	0.04
13	CoLk 9414	5.96	–3.28**	6.24
14	CoLk 9606	9.74	–0.04	0.03
15	CoLk 9617	8.42	3.91**	2.15
16	CoLk 9618	10.82	1.96*	2.23
17	93-A-21	8.43	–2.13	0.01
18	CoLk 8102	9.06	5.23	1.01
19	CoS 767	8.73	4.46**	3.48
20	CoJ 64	4.49	–1.34	0.03

Table 3. Simultaneous selection of genotypes for CCS yield and stability (Kang's Procedure)

S. No.	Genotypes	Mean (t/ha)	Yield rank	Adjustment to rank		Sd_i^2	Stability rating	Ysi
1	CoLk 9110	9.05	14	3	17	8.91	–8	9+
2	CoLk 91236	4.17	1	–3	–2	–0.29	0	–2
3	CoLk 91239	6.98	9	–3	6		–8	–2
4	CoLk 9204	4.53	3	–3	0	1..		?
5	CoLk 9210	5.07	4	–3	1	1.82	–8	
6	CoLk 9212	9.14	16	3	19	4.49	–8	11+
7	CoLk 9216	9.93	18	3	21	5.58	–8	13+
8	CoLk 9229	5.19	5	–3	2	3.33	–8	–6
9	CoLk 9301	7.30	10	–1	9	14.69	–8	1
10	CoLk 9302	6.95	8	–3	5	2.10	–8	–3
11	CoLk 9411	10.60	19	3	22	1.45	–8	14+
12	CoLk 9412	5.97	7	–3	4	6.17	–8	–4
13	CoLk 9414	5.96	6	–3	3	24.40	–8	–5
14	CoLk 9606	9.74	17	3	20	0.52	–4	16+
15	CoLk 9617	8.42	11	3	14	9.87	–8	6+
16	CoLk 9618	10.82	20	3	23	4.11	–8	15+
17	93-A-21	8.43	12	3	15	7.28	–8	7+
18	CoLk 8102	9.06	15	3	18	15.65	–8	10+
19	CoS 767	8.73	13	3	16	14.58	–8	8+
20	CoJ 64	4.49	2	–3	–1	3.94	–8	–9

are based primarily on adjusted mean trait value grades. The role of stability is thus very limited as compared to mean performance. There is thus a need for a method of simultaneous selection for CCS and stability, which can rectify this lacuna.

Bajpai and Prabhakaran [3] constructed a number of indices in which the level of achievement by the genotype in performance and stability are quantified by expressing the individual achievements relative to mean achievement in the group of genotypes considered. The indices proposed were obtained as follows.

Table 4. CCS Stability Indices for different genotypes (Modified from Bajpai and Prabhakaran 2000)

S. No.	Genotypes	$\hat{\sigma}^2_i$	CCS Stability Index			
			$\alpha = 1$	$\alpha = .5$	$\alpha = .25$	$\alpha = .1$
1	CoLk 9110	8.91	43.66	47.98	53.02	54.20
2	CoLk 91236	–0.29	33.84	55.14	79.81	100.00
3	CoLk 91239	5.04	36.38	45.94	57.03	64.41
4	CoLk 9204	1.96	38.04	56.30	77.46	94.04
5	CoLk 9210	1.82	34.21	50.48	69.33	84.09
6	CoLk 9212	4.49	29.79	36.69	44.71	49.77
7	CoLk 9216	5.58	31.91	37.39	43.76	47.12
8	CoLk 9229	3.33	38.22	53.16	70.47	83.48
9	CoLk 9301	14.69	65.41	68.54	72.22	70.40
10	CoLk 9302	2.10	27.36	38.75	51.97	62.04
11	CoLk 9411	1.45	18.16	25.59	34.20	40.74
12	CoLk 9412	6.17	43.39	54.39	67.15	75.52
13	CoLk 9414	24.40	100.00	99.97	100.00	92.04
14	CoLk 9606	0.52	16.46	25.19	35.30	43.37
15	CoLk 9617	9.87	47.81	52.29	57.50	53.51
16	CoLk 9618	4.11	26.14	31.78	38.32	42-31
17	93-A-21	7.28	39.78	45.81	52.82	56.14
18	CoLk 8102	15.65	64.53	64.74	65.03	60.14
19	CoS 767	14.58	61.83	63.06	64.54	60.96
20	CoJ 64	3.94	44.48	61.70	81.67	96.64

l_i maximum (the genotype showing maximum l_i value or yield stability index taken as hundred). The minimum yield stability index thus signifies the most important while the maximum yield stability index (= 100) represents least important genotype considering both yield and stability simultaneously.

The stability indices were computed at four different levels of α (Table 5). At α = 1 (equal weight to CCS and stability), and (α = 0.5 (weight of CCS and stability were given in the ratio of 2:1), CoLk 9606, CoLk 9411, and CoLk 9618 emerged as top three entries. At lower levels of α, the trend is repeated. However the genotypes CoLk 9216 and CoLk 9212 takes either 4th or 5th position in both the cases (α = 0.25 and α = 0.1) due to their high yield ranks. A close look at Table 5 reveals that the rankings of genotypes based on extreme α values (α = 1 and α = 0.1) may not be liked by the breeders for genotype selection. The genotype CoLk 91236 ranked 7th at α = 1 and the genotype CoLk 9110 ranked 6th at α = 0.I get selected despite of there low CCS and stability respectively. Therefore, there is a need to go for a level of α either at 0.5 or 0.25 as perceived by the breeders under a particular situation. This method thus provides a lot of flexibility in the hands of breeders.

Table 5. Ranking of top 7 genotypes as per different approaches

Rank	CCS (t/ha)	Kang's rank sum method	Modified Bajpai and Prabhakaran			
			$\alpha = 1$	$\alpha = .5$	$\alpha = .25$	$\alpha = .1$
1	CoLk 9618	CoLk 9606	CoLk 9606	CoLk 9606	CoLk 9411	CoLk 9411
2	CoLk 9411	CoLk 9618	CoLk 9411	CoLk 9411	CoLk 9606	CoLk 9618
3	CoLk 9216	CoLk 9411	CoLk 9618	CoLk 9618	CoLk 9618	CoLk 9606
4	CoLk 9606	CoLk 9216	CoLk 9302	CoLk 9212	CoLk 9216	CoLk 9216
5	CoLk 9212	CoLk 9212	CoLk 9212	CoLk 9216	CoLk 9212	CoLk 9212
6	CoLk 8102	CoLk 8102	CoLk 9216	CoLk 9302	CoLk 9302	CoLk 9110
7	CoLk 9110	CoLk 9110	CoLk 91236	93-A-21	93-A-21	93-A-21

$$I = \bar{Y}_i / \bar{Y} + \alpha^* \frac{(1/\hat{\sigma}^2_i)}{1/n \sum (1/\hat{\sigma}^2_i)}$$

Where $Y_{i.}$ is the average performance by the ith genotype, Y.. the overall mean and α the weight to be attached to stability component of the index. (The value of α can be selected as per the requirement of breeder, for example, α = x means equal weight to yield and stability; α = x means weight for yield and stability in the ratio of 1: x).

In the present investigation, the indices proposed by Bajpai and Prabhakaran [3] were modified further to assign a single quantitative value of stability index of each genotype. The modified index l_i is as follows.

$$l_i = \frac{1/\bar{Y}_i}{1/n \sum_i (1/\bar{Y}_i)} + \alpha^* \frac{\hat{\sigma}^2_i}{(1/n \sum_i \hat{\sigma}^2_i)}$$

The l_i values corresponding to each genotype were transformed to obtain an index as proportion of

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