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Comparative study of selection indices based on different weights in forage sorghum [*Sorghum bicolor* (L.) Moench]

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ABSTRACT

Selection indices are constructed using different weights viz. equal weight, genotypic correlation, phenotypic correlation and path coefficient (direct effects) with all possible combination of traits in forage sorghum (Sorghum bicolor (L.)Moench.) based on six biometrical characters viz. plant height at 50 % flowering (cm), number of tillers per plant, number of leaves per plant, leaf length (cm), leaf width (cm) and green fodder yield per plant (g plant^{-1}*) along with their genetic gain and percent relative efficiency relative to fodder yield. The data were collected from a set of forty genotypes of sorghum grown in randomized complete block design with three replications at Main Forage Research Station, Anand Agricultural University, during kharif 2013. Higher relative efficiency of selection indices is observed when equal weight is assigned to the biometrical characters. The index (I134) consisting of plant height at 50% flowering, number of leaves and leaf length has the highest relative efficiency in all the weight methods. Rank correlations between different weight methods in construction of selection index without green fodder yield per plant are highly significant and positive. Also, the genotypes are ranked on the basis of their selection score value. Rank correlations between different weight methods without green fodder yield per plant were highly significant and positive. Thus, they indicated that the ranking of genotypes based on the selection index I134 with highest percent relative efficiency with using equal weight, genotypic correlation, phenotypic correlation and path coefficients taken as weight were more or less similar for all the genotypes on an average. The index with equal weight is finally suggested I134 = 1.0761* X_1 *-0.6539* X_3 *+ 6.5097* X_4 *Where,* X_1*= plant height at 50% flowering,* X_3*= number of leaves per plant and* X_4*= leaf length.*

Keywords: Forage sorghum, genotypic and phenotypic correlation, path analysis, relative efficiency, selection index

Like green revolution, India is contemplating for white revolution, which is possible only with adequate supply of nutritious feeds and fodders. Chellapandian *et al*. (2016) stimated that the 60-70 percent of total cost in livestock production is due to feed and fodder. Due to limited allocation of land ,In India hardly 5.23 per cent (Kumar, 2016) of the cropped area is utilized to grow fodder. Sorghum [*Sorghum bicolor* (L.) Moench] is the fifth most important crop in the world. Sorghum ranks first (GOI, 2014) among the cereal fodder crops because of its growing ability in poor soil, faster growth habit, higher yield, palatability and nutritious quality. The average fodder yield of sorghum in India is low because major area is covered by local and out-dated varieties (Kour and Pradhan, 2016). As there is little scope of increasing area under cultivation of fodder crops due to urbanization, industrialization and traditional inclination among farmers. The only optional strategy to meet fodder requirement is to exploit crop productivity through better yielding varieties and efficient agronomic management.

One of the most important components in bringing improvement in metric traits both in plant breeding is selection. It is all the more important when genes act additively and as such it is the appropriate method for changing the gene constitution of a population. Selection here means breeding from best individuals whatever best may be. However, in practical, selection is not confined to one character but applied to several characters simultaneously. This is usually termed as multitrait selection and can be implemented by various selection strategies. The selection index method as developed by Hazel (1943) is based on simultaneous selection of all components characters along with their relative weights attached to their phenotypic value in such a manner that the correlation between compounded phenotypic score and corresponding compounded genetic score is maximum. Former score would then discriminate, in the best possible manner, those individuals with greatest genetic score. The relative weights depend on their economic importance, heritability and genetic and phenotypic correlation. The selection index procedure is used to select superior genotypes for further breeding programme so as to achieve higher genetic gain. Biswas *et al*. (2001) constructed 31 selection indices on five characters using 33 genotypes of sorghum (*Sorghum bicolor* L.). The highest relative efficiency over straight selection on grain yield alone was realized. Jain and Patel (2012) observed that fodder yield in sorghum was positively and significantly correlated with number of leaves per plant, leaf length, leaf width and panicle length. Vemanna *et al*. (2013) constructed sixty-three different selection indices by discriminant function

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analysis based on the data of a population of 800 F_2 plants.

However, if the aim is to have improvement in the particular trait then still the selection index methodology can be used by manipulating economic weights of characters. The rate of genetic improvement in a quantitative character can be increased if the variation in this trait due to one or more auxiliary trait, particularly at environmental level is minimized. In such case, selection can be made on the bases of an index expressed as a deviation of the phenotypic value of the trait from the expected value predicted with the help of partial regression equation of the auxiliary traits. Such an index is called as phenotypic index and was developed by Narain and Mishra (1975). In practical, situation breeders are interested to know the relative contribution of individual traits in the overall genetic progress for a defined aggregate genotype. This can be studied by constructing a reduced index by deleting the traits and comparing the efficiency of reduced index relative to that of original index, by means of their correlation with aggregate genotype. A faster and simple method is proposed by Cunningham (1969) for comparing the relative efficiency of selection indices and various reduced indices obtained by ignoring some source of information. Through this methodology, one can study the relative contribution of the individual traits on the overall improvement. This procedure is very useful in judging the contribution of a particular trait without going through the entire computational procedure of fitting selection index.

In this paper selection indices are constructed based on different weights. Also reduced selection indices are constructed for different combination of characters. The details of statistical methods used are discussed in material and method section. Again, the relative efficiency is calculated for all indices. The genotypes are ranked based on the selection score values. The genotypes are selected based on ranks obtained in different weight methods in selection index and the details of the analysis are discussed in result and discussion part.

MATERIALS AND METHODS

The present investigation was conducted at Main Forage Research Station, A.A.U., Anand, during *kharif* season of the year 2013. Anand is situated at 22º35´ North Latitude and 72º55´ East longitude and 45.11 m above the mean sea level. The soil of experimental field is sandy loam, which is locally known as "Goradu Soil." It is alluvial in origin, deep, well drained and has fairly good moisture holding capacity. It is poor in organic matter, medium in available phosphorous and rich in available potash. It responds well to irrigation and nitrogen application. The experimental material for present investigation comprised of 40 diverse genotypes of forage purpose sorghum obtained from the germplasm maintained at Main Forage Research Station, A.A.U., Anand.

The experiment was conducted in RBD with three replications and 30 x 10 cm inter and intra row spacing respectively during *kharif* 2013. Data on six biometrical characters viz. X_1 - plant height at 50 % flowering (cm), X_2 -number of tillers plant^{-1}, X_3 - number of leaves plant^{-1}, X_4 - leaf length (cm), X_5 - leaf width (cm) and Y- green fodder yield plant^{-1} (g plant^{-1}) were used. The data were statistically analyzed as per standard statistical process. The genotypic correlation is chiefly caused by pleiotrophy and linkage action of gene and was estimated as suggested by Hazel *et al*. (1943). The genotypic and phenotypic correlation coefficients were worked out for all possible pairs and were tested against standardized tabulated significant values as per the procedure suggested by Fisher and Yates (1943).

The cause and effect, interrelationship between two variables cannot be estimated from correlation coefficient analysis. The genotypic correlations are free from environmental influence and hence, it's the path analysis suggested by Wright (1921) was followed in order to partition genotypic correlation of different variables with fodder yield into direct and indirect effects of these variables on yield. The path coefficients were obtained by solving simultaneous equations which represent the basic relationship between correlation and path coefficient.

$$\begin{bmatrix} r_{x_1 y} \\ r_{x_2 y} \\ \vdots \\ r_{x_6 y} \end{bmatrix} = \begin{bmatrix} r_{x_1 x_1} & \cdots & r_{x_1 x_6} \\ \vdots & \vdots & \vdots \\ r_{x_6 x_1} & \cdots & r_{x_6 x_6} \end{bmatrix} \begin{bmatrix} a \\ b \\ c \\ d \\ e \\ f \end{bmatrix}$$

Name the above matrices in terms of A, B and C and then proceed A = B * C ’!C = B^{-1}A, provided B is non-singular matrix. Where A is correlation vector of traits with yield, B is the correlation matrix and C is the path coefficients.

Selection index first adopted by Smith (1936) and then used by Hazel and Lush (1942) and Hazel (1943). This procedure uses the concept of linear discriminant function given by Fisher (1936) to derive a linear equation based on observable characteristics as the best available guide to the genetic value of each individual in the population. The method for constructing selection index and working out of genetic gain is as under.

Let P_i be the phenotypic value of ith character and G_i and E_i represent genetic and environmental values of the same character respectively. It can be written that

Table 1: Genotypic and phenotypic correlation coefficients between different characters in sorghum Tables should be formatted as per the format of the journal; for details visit www.cropandweed.com

Characters		X_1	X_2	X_3	X_4	X_5	Y
X_1	Rg	1.000	-0.495**	-0.561**	-0.242	0.326*	0.253
	Rp	1.000	-0.432**	-0.494**	-0.203	0.248*	0.220
X_2	Rg		1.000	0.355 *	0.192	-0.232	-0.247
	Rp		1.000	0.332**	0.147	-0.150	-0.224
X_3	Rg			1.000	0.403*	-0.076	0.117
	Rp			1.000	0.398**	-0.052	0.106
X_4	Rg				1.000	0.436**	0.612**
	Rp				1.000	0.388**	0.552**
X_5	Rg					1.000	0.750**
	Rp					1.000	0.616**
Y	Rg						1.000
	Rp						1.000

*Note: *, ** significant at P = 0.05 and 0.01 levels, respectively*

Table 2: Genotypic path coefficients (direct and indirect effects) of causal variables on green fodder yield per plant in sorghum

Sr. No.	**Characters**	**X_1**	**X_2**	**X_3**	**X_4**	**X_5**	**Geno. Corr.with Y**
1	X_1	0.207	0.086	-0.088	-0.104	0.153	0.253
2	X_2	-0.102	-0.174	0.056	0.082	-0.108	-0.247
3	X_3	-0.116	-0.062	0.158	0.172	-0.036	0.117
4	X_4	-0.050	-0.033	0.064	0.427	0.204	0.612**
5	X_5	0.067	0.040	-0.012	0.187	0.468	0.750**

Note:, ** significant at P = 0.05 and 0.01 levels, respectively.*

Table 3: Top three selection indices in different weight methods

All possible Combinations of Traits.	Rank	**Different Weights**			
		Equal	**Rg**	**Rp**	**Path**
Two	1	I_{15}(50.17)	I_{14} (14.48)	I_{14} (11.57)	I_{15} (10.55)
	2	I_{12}(49.15)	I_{15} (14.31)	I_{15} (11.29)	I_{12}(10.38)
	3	I_{14}(47.57)	I_{12} (13.98)	I_{12} (11.05)	I_{14}(10.37)
Three	1	I_{134}(116.03)	I_{134} (33.64)	I_{134}(103.68)	I_{134}(26.64)
	2	I_{125}(49.78)	I_{145} (13.97)	I_{125} (11.57)	I_{145} (10.88)
	3	I_{145}(48.53)	I_{124} (13.27)	I_{126} (11.29)	I_{125} (10.68)
Four	1	I_{1245}(48.13)	I_{1245} (14.08)	I_{1245} (12.33)	I_{1245} (10.96)
	2	I_{1235}(46.25)	I_{1234} (13.09)	I_{1234} (11.50)	I_{1234}(10.16)
	3	I_{1234}(44.32)	I_{1235} (12.79)	I_{1235} (11.09)	I_{1235}(10.12)
Five	1	I_{1234}(45.27)	I_{12345}(13.89)	I_{12345} (12.17)	I_{12345}(10.66)

Note: Figures in the parentheses are represent percentage relative efficiency
R_g – Genotypic correlation ; R_p – Phenotypic correlation.

Table 4: Selection score values with rank of forty genotypes of sorghum

Rank	Genotypes with score value for different weight			
	Equal	**Rg**	**Rp**	**Path**
1	PB-19	GFS-3	PB-19	GFS-3
	251.40	231.81	91.11	184.55
2	DSIS-8731	CHITRA	GFS-3	CHITRA
	245.26	229.21	88.66	182.62
3	PB-215	PB-19	CHITRA	PB-19
	240.85	228.28	87.70	182.48
4	PB-266	PB-181	PB-181	PB-181
	237.64	219.06	85.68	174.88
5	DSIS-243	PB-215	DSIS-243	PB-215
	237.18	216.36	85.27	172.84
6	PB-79	DSIS-243	PB-215	DSIS-243
	234.93	215.82	85.06	172.43
7	ASFS-5	ICRISAT-700	AMRUTA	ICRISAT-700
	234.54	214.55	84.46	171.25
8	PB-181	GUNDRI	PB-266	GUNDRI
	234.52	214.50	84.37	170.99
9	PIPER-83	PB-266	GUNDRI	PB-266
	232.29	213.55	83.91	170.63
10	ICRISAT-700	AMRUTA	AFS-14	AMRUTA
	229.25	212.20	83.86	169.46
11	IS-3367	PB-23	ICRISAT-700	PB-23
	228.28	210.31	83.72	167.92
12	DSIS-1005	COFS-29	PB-23	COFS-29
	227.67	209.64	83.07	167.25
13	SS-96-785	AFS-14	COFS-29	AFS-14
	226.37	205.84	82.75	164.64
14	CHITRA	DSIS-5535	GFS-5	ASFS-5
	224.93	203.98	82.58	163.00
15	PIPER-56	ASFS-5	ASFS-5	DSIS-5535
	224.61	203.86	80.99	162.96
16	DSIS-5535	GFS-5	DSIS-5535	GFS-5
	223.37	203.67	80.64	162.85
17	PB-23	DSIS-1005	DSIS-8731	DSIS-1005
	218.40	202.70	80.33	161.95
18	AFS-14	PIPER-83	PIPER-83	PIPER-83
	217.81	202.17	80.08	161.62
19	AMRUTA	AFS-28	DSIS-1005	AFS-28
	216.57	199.59	79.80	159.11
20	IS 685-14	IS KMR-8	PB-79	IS KMR-8
	215.54	198.86	79.16	158.75
21	GFS-5	SS-96-785	SS-96-785	SS-96-785
	214.20	197.76	78.72	158.13
22	PB-78	PB-79	AFS-28	PB-79
	213.32	197.27	78.50	157.88

Contd.

Table 4 Contd.

Rank	**Genotypes with score value for different weight**			
	Equal	**Rg**	**Rp**	**Path**
23	GFS-3	DSIS-8731	SSG 59-3	DSIS-8731
	211.19	196.71	78.27	157.66
24	IS KMR-8	UP-CHARI	IS KMR-8	SSG 59-3
	207.91	195.12	78.16	155.76
25	S-1049	SSG 59-3	MP-CHARI	UP-CHARI
	205.80	195.00	77.54	155.67
26	COFS-29	AFS-15	UP-CHARI	MP-CHARI
	202.08	193.72	76.99	154.69
27	IS-3347	MP-CHARI	AFS-15	AFS-15
	201.58	193.60	76.90	154.66
28	MP-CHARI	IS 685-14	S-10497	IS 685-14
	200.83	190.43	6.84	152.18
29	IS-3353-1	PB-78	AFS-26	PB-78
	199.42	189.86	75.94	151.68
30	GUNDRI	IS-3367	IS-336	IS-3367
	198.82	189.07	775.87	151.34
31	IS-3192	PIPER-56	IS 685-14	PIPER-56
	194.87	188.77	75.15	151.00
32	AFS-15	S-1049	PIPER-56	S-1049
	194.64	187.80	75.03	150.30
33	AFS-26	AFS-30	PB-78	AFS-30
	194.40	187.11	74.58	149.17
34	SSG 59-3	IS-3353-1	AFS-30	IS-3353-1
	194.37	185.40	73.41	147.95
35	IS-3214	AFS-26	IS-3353-1	AFS-26
	193.42	179.85	71.91	144.16
36	UP-CHARI	IS-3347	IS-334	IS-3347
	188.26	174.58	770.30	139.69
37	IS 686	C-10-2	C-10-2	C-10-2
	184.62	170.83	69.56	136.66
38	C-10-2	IS 686	IS-3192	IS-3214
	183.15	165.19	66.18	132.13
39	AFS-28	IS-3214	IS-3214	IS 686
	179.84	165.15	66.16	131.96
40	AFS-30	IS-3192	IS 686	IS-3192
	173.04	164.47	64.94	131.63

Table 5: Rank correlation between different methods based on (I_{134})

	Eql. Wt.	**Gen.cor.Wt**	**Phe.cor. Wt.**	**Path coeff.Wt**
Eql.Wt.	1.00	0.6019**	0.6375**	0.6107**
Gen.cor.Wt		1.00	0.9733**	0.9959**
Phe.cor. Wt.			1.00	0.9803**
Path coeff.Wt				1.00

*Note: *, ** significant at P = 0.05 and 0.01 levels, respectively.*

$P_i = G_i + E_i$

Let, $H = \sum_{i=1}^{n} a_i G_i$ be a linear function of genetic value and a_i as corresponding economic value. As G_i cannot be measured, H cannot be used as a criterion for selection. For overcoming this problem, an index is constructed which is based on phenotypic value Pi and bi. The bi's are obtained in such way that correlation between H and I is maximized, *i.e.*

On maximizing r_{HI}, the solution for bi can be obtained in matrix notation from

Pb = Ga

Or, $b = P^{-1}G\ a$

Where P is the phenotypic variance-covariance matrix, G is denoted as genetic variance-covariance matrix and a as vector or economic weights.

The expected genetic advance is then calculated as,

$$\Delta H = i\sqrt{a'GP^{-1}Ga}$$

$$= \frac{z}{q}\sqrt{a'GP^{-1}Ga}$$

Where q is denoted as the percentage saved by selection and z is the ordinate value corresponding to q value of normal integral table. Z/P = Selection intensity *i.e.* 2.06 at 5 per cent level of significance.

Also, the percentage relative efficiency were calculated as,

$$\text{Percentage relative efficiency} = \frac{\text{Genetic gain of an selection index}}{\text{Genetic gain of fodder yield}} \times 100$$

RESULTS AND DISCUSSION

The variations among genotypes for different traits were found highly significant. The correlation coefficients between green fodder yield per plant and its component traits among themselves were estimated at genotypic and phenotypic levels. The results of genotypic correlation coefficient (Rg) and phenotypic correlation coefficients (Rp) between yield and its yield components are given in table 1.

Green fodder yield plant^{-1} is the result of direct and indirect effects of several yields contributing traits. To know the contribution of various characters towards green fodder yield, the genotypic correlation of different characters with green fodder yield plant^{-1} were partitioned into their direct and indirect effects by using the path analysis. This will provide more valuable information for the selection of important characters. Direct and indirect effects of five traits on green fodder yield plant^{-1} are given in table 2.

From the table it reveals that, plant height has positive and non-significant genotypic correlation with green fodder yield plant^{-1}. However, its direct effect was positive on green fodder yield plant^{-1}. It has positive indirect effect on green fodder yield plant^{-1} via leaf width and number of tillers plant^{-1}. While, indirect effects via other traits were negative with lower magnitude. Negative and non-significant genotypic correlation was observed between number of tillers plant^{-1} and green fodder yield plant^{-1} and its direct effect was also negative on green fodder yield plant^{-1}. While it's indirect effect through plant height and leaf width were negative whereas, indirect effect through leaf length and number of tillers plant^{-1} were positive. In similar way, we can conclude for other characters from the table 2.

Selection indices were constructed taking all six biometrical traits. The selection indices were constructed taking all possible combinations of Traits. Total 63 selection indices were constructed using equal weight, genotypic correlation coefficients and phenotypic correlation coefficients and path coefficients as weight. Also the expected genetic gain obtained from selection index of green fodder yield with equal weight was considered 100 per cent to work out percent relative efficiency of different indices. Among all possible combinations, the top three ranking selection indices with respect to their percentage relative efficiency in different methods without green fodder yield per plant are given in table 3. From the table, it revealed that the highest percent relative efficiency was observed with index I_{134} (116.03) which consist of plant height at 50% flowering, number of leaves plant^{-1} and leaf length with equal weights. It was also highest for the same index taking genotypic correlation coefficient (33.64), phenotypic correlation coefficient (103.68) and path coefficient (26.64) taken as weight. Thus, taking equal weight, the percent relative efficiency was highest and one can use equal weight of variables for construction of selection indices to achieve higher genetic gain. So the selection index consisting of plant height at 50% flowering, number of leaves and leaf length (I_{134}) was considered more reliable as it was commonly having highest relative efficiency in all methods.

The index score values were worked out for all four weight methods for all genotypes and the genotypes are ranked based on their index score in table 4. Genotype PB-19 ranked first in equal weight method followed by DSIS-8731 as second and PB-215 as third. GFS-3 ranked first followed by Chitra as second and PB-19 as third for genotypic correlation and genotypic path coefficient taken as weight, genotype PB-19 ranked first in phenotypic correlation followed by GFS-3 as second and

Chitra as third. Genotype PB-19 was selected as top-ranking genotype followed by GFS-3, Chitra, PB-215 and PB-181 for future breeding programme. The top thirteen ranks for genotypes remain same when genotypic correlation and path coefficients are taken as weight. The equal weight method performs better than other three methods as it has highest selection score value in all ranks as compare to others. A rank correlation study also conducted between different weights and its results are presented in table 5. Rank correlation study between different weight methods indicated that all correlation coefficients among different weight methods were more than 0.60. Thus, they indicated that the ranking of genotypes based on the selection index consisting of three variables (X_1, X_3 and X_4) with highest percent relative efficiency with using different weights were more or less similar for all the genotypes on an average.

Rank correlations between different weight methods without green fodder yield plant^{-1} were highly significant and positive. Thus, they indicated that the ranking of genotypes based on the selection index I134 with highest percent relative efficiency with using equal weight, genotypic correlation, phenotypic correlation and path coefficients taken as weight were more or less similar for all the genotypes on an average. In general, one can use any weight under study. Green fodder yield data are available after harvest therefore selection index I_{134} is most reliable to select biometrical characters in plant breeding programmes for the improvement of fodder yield in forage sorghum. The following index with equal weight is finally suggested $I_{134} = 1.0761\ X_1 - 0.6539\ X_3 + 6.5097\ X_4$ Where, X_1= plant height at 50% flowering, X_3= number of leaves plant^{-1} and X_4= leaf length.

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