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Research Article

Comparison of selection indices using different weights for biometrical characters in bajra crop

Kalola A. D., D. J. Parmar, G. N. Motka And P. R. Vaishnav
B. A. College of Agriculture, Anand Agricultural University, Anand- 388 110

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Abstract

The data on different biometrical characters of large scale varietal trial having 21 genotypes of bajra were collected from regional research station, Anand for present study. The experiment was conduct in a Randomized Block Design with three replications. The characters for grain yield (kg/plot) (X1), 1000 seed weight (gm) (X2), ear head length (cm) (X3), ear head girth (cm) (X4) and effective tillers/plant (X5) were used for this analysis. The selection index technique was employed to study the crop improvement using different characters giving different weights to each character. Selection index for individual character, combination of two characters, three characters and so on can be calculated and the combination which provides the higher relative efficiency is selected. Selection index for single or combination of characters which provides the high per cent relative efficiency (PRE) is selected. The genotypic correlation and phenotypic correlation were worked out between yield and yield contributing characters. Selection indices were worked out taking five biometrical characters and were constructed taking all possible combinations of the characters. Total 31 selection indices were constructed using equal weight (W1) for all characters. The genotypic correlation coefficients (W2), phenotypic correlation coefficients (W3), direct effects of biometrical characters based on genotypic (W4) and phenotypic correlations (W5) as weight for different characters. The expected genetic gain and PRE of different indices were calculated. The results indicated that in general PRE with equal weight was higher than rest of the weights in all combinations of indices. The rank correlation among different methods for selection score values were positive and highly significant indicating agreement with all methods except equal weight. Therefore index based genotypic correlation taken as weight is considered better than all other indices.

Keywords
Bajra, selection index, rank correlation, relative efficiency

Introduction

The bajra is one of the most important food grain crops of India and cultivated in 6.98 million hectares area with 8.06 million tones production and productivity of 1154 kg/ha. The bajra crop occupied 0.39 million hectares of area producing 0.79 million tones with productivity of 2004 kg/ha in Gujarat (Anonymous, 2017). The aim of most of the breeding programmes is simultaneous improvement of several characters. It has been recognized that most rapid improvement in the economic value is expected from selection applied simultaneously to all the characters which determine the economic value of a plant, when appropriate weights are assigned to each character according to their relative economic importance. There is no standard procedure to assign weights to the biometrical characters in selection index. The data of large scale varietal trial having 21 bajra genotypes evaluated in a Randomized Complete Block Design with three replications at Regional Research Station, Anand during the summer-2013 and selection index technique was employed to study the crop improvement using different characters giving different weights to each character. The data on grain yield (kg/plot), 1000 seed weight (gm), ear head length (cm), ear head girth (cm) and effective tillers/plant were used for statistical analysis.

Materials and Methods

Selection index for individual character, combination of two characters, three characters and so on can be calculated and the combination which provides the higher relative efficiency is selected. Genetic gain and percent relative efficiency (PRE) were calculated by using the following formulae. Selection index for single or combination of characters which provides the high PRE was selected.

The expected genetic advance is calculated as

$$= (Z/P)((\sum\sum a_i b_i G_{ij}) / (\sum\sum b_i b_j p_{ij})^{½})$$

Where Z/P = Selection intensity i.e. 2.06 at 5% level of significance.

Percent Relative efficiency (PRE) is calculated as follows.

$$\text{PRE} = \frac{\text{Genetic gain of selection index}}{\text{Genetic gain of grain yield}} \times 100$$

The genotypic correlation and phenotypic correlation were worked out between yield and yield contributing characters suggested by Hazel *et al*. (1943) using SPAR1 software.

Genotypic correlation coefficient Phenotypic correlation coefficient

$$\mathrm{r}_{\mathrm{gigj}} = \frac{\hat{\sigma}_{gigj}}{\sqrt{\hat{\sigma}^2{}_{\mathrm{gi}} \ \mathrm{x} \hat{\sigma}^2{}_{\mathrm{gj}}}} \quad \mathrm{r}_{\mathrm{pipj}} = \frac{\hat{\sigma}_{pipj}}{\sqrt{\hat{\sigma}^2{}_{\mathrm{pi}} \ \mathrm{x} \hat{\sigma}^2{}_{\mathrm{pj}}}}$$

Where,

r_{gigj} and r_{pipj}=Genotypic and phenotypic correlation coefficient between i^{th} and j^{th} character.

$\hat{\sigma}^2{}_{gi}$ and $\hat{\sigma}^2{}_{gj}$ = Genotypic variances of i^{th} and j^{th} character

$\hat{\sigma}^2{}_{pi}$ and $\hat{\sigma}^2{}_{pj}$ = Phenotypic variances of i^{th} and j^{th} character, respectively.

σ_{gigj} and σ_{pipj} = Genotypic & Phenotypic covariance between i^{th} and j^{th}character.

These correlation coefficients were used as weight for selection index. Selection index proposed by Smith (1936) based on discriminant function of Fisher (1936) was used to calculate genetic worth (H, economic value) of genotypes using different biometrical characters of bajra.

Path analysis will be carried as suggested by (Wright,1921). The direct effects of respective characters were taken as weight for selection index.P_{yx1}, P_{yx2} and P_{yx3} represent path coefficients (direct effect) from cause X_1, X_2 and X_3, respectively, The path coefficient for path from X_1 to Y is defined as

$$P(\mathrm{y} \ \leftarrow \mathrm{x}_1) = P_{yx1} = \frac{\sigma_{yx1}}{\sigma_y}$$

Results and Discussion

The variation among genotypes for different characters for were found significant. The results of mean performance are given in Table 1(I). The result of grain yield per plot was significantly highest observed in GHB-953 (5.400 kg) followed by GHB-935 (5.121 kg).The result of test weight was recorded significantly highest for the genotype GBH-941 (8.935gm). The genotype GHB-1032 had significantly highest ear head length (35.47 cm) and ear head girth (11.93 cm). The effective tillers/plant was found significant and it ranged from 2.3(GHB-1107) to 4.4 cm (GHB-984).The highest genotypic coefficient of variation (GCV%) were observed for grain yield (17.96%) followed by ear head length (15.33%) and effective tillers per plant (11.56 %). The effective tillers per plant had highest PCV % (24.65%) followed by grain yield per plot (22.86%) which indicated higher influence of environment on these characters. The broad sense heritability was highest for test weight (82.9%) followed by ear head length (76.3%) while the lowest heritability was 22.0% in effective tillers per plant. (Habib *et al* , 2007), (Kole *et al.*, 2008), Akinwale *et al.*, 2011), and (Rao *et al.*,2011).

The correlation coefficients between grain yield per plot and its component traits among themselves were estimated at genotypic and phenotypic levels. The results of genotypic and phenotypic correlation coefficients between yield and its components are given in Table 2. Effective tillers per plant had positive and highly significant genetic correlation (r_g= 0.818) with grain yield per plot, while for rest of the characters it was non-significant. Positive and significant correlation (r_g=0.626) between ear head length and ear head girth was observed at genotypic level. None of the characters had significant correlation with grain yield per plot at phenotypic level, while test weight (r_p=0.333) and ear head length (r_p=0.453) had positive and significant correlations with ear head girth at phenotypic level. Effective tillers per plant had positive and significant (r_g=0.818) genotypic correlation with grain yield per plot and its direct effect was also positive and higher (0.836) on grain yield per plot followed by test weight (0.394) and ear head girth (0.175). In case of indirect effects, ear head girth had higher indirect effect on grain yield per plot via test weight. While, indirect effects of ear head length and girth via effective tillers per plant were negative with higher magnitude. (Table3). Significant and positive genotypic/ phenotypic correlations between fodder yield and leaf width of sorghum was observed as reported by (Yadav, *et al.*, 2003), (Iyanar *et al.*, 2010), (Jain and Patel, 2012) and (Kaour, 2013). (Chaudhary *et al.*, 2017b).

The direct effect of phenotypic path coefficients, test weight (0.283), effective tillers per plant (0.257) and ear head girth (0.236) were having the high direct effect on grain yield per plot. Indirect effect of ear head length (0.107) was observed higher on grain yield per plot via ear head girth but its direct effect was negatively higher on grain yield per plot.(Table 4)

Selection indices were worked out taking five biometrical characters and were constructed taking all possible combinations of the characters. Total 31 selection indices were constructed using equal weight (W1) for all characters. The genotypic correlation coefficients (W2), phenotypic correlation coefficients (W3), direct effects of biometrical characters based on genotypic (W4) and phenotypic correlations (W5) as weight for different characters. The expected genetic gain and percent relative efficiency (PRE) of different indices were worked out and the results are given in Table 5 to 9.

The genetic gain for grain yield (3.656) with equal weight was considered as a base in all single as well as combinations of characters. Relative to this, the efficiency was worked out for all selection index with different weights. PRE for selection of biometrical characters other than grain yield ranged from 6.79% to 688.02%, 0.69% to 181.64%, 1.73% to 151.36%, 5.67% to 118.34% and 1.75% to 238.74for W1, W2, W3, W4 and W5, respectively (Table 5).The lowest PRE were observed for effective tillers per plant in all weight methods except genotypic correlation coefficient taken as weight while the highest PRE was observed for ear head length in all weight methods. The highest relative efficiency (688.02) was observed for ear head length relative to grain yield with equal weight followed by the method of phenotypic path coefficient taken as weight, genotypic correlation coefficient taken as weight, phenotypic correlation coefficient taken as weight and genotypic path coefficient taken as weight for the same character.

Possible combinations of two characters of five yield and yield attributing characters were used to construct selection indices using different weights (W1 to W5) as mentioned above. Total 10 indices in each weight method were constructed and best three indices with their percent relative efficiency are selected (Table6). PRE ranged from 10.03% (ear head girth and effective tillers per plant in genotypic path coefficient as taken weight) to 823.91% (ear head length and girth in equal weight). In equal weight method, the highest PRE was observed for combination of ear head length and ear head girth characters (I_{34}) while combination of grain yield and ear head length (I_{13}) gave higher PRE in rest of the methods.

Different indices with their genetic gain and PRE for different weight method are given in Table7. The highest PRE (874.82%) was observed for combination of test weight, ear head length and ear head girth ($I_{234)}$) in equal weight methods whereas combination of three characters (grain yield, ear head length and effective tillers per plant) had higher PRE in all methods (I_{135}) except equal weight method.

There were five possible combinations of four characters and selection indices were worked out with different weights (Table8).Thus, total 25 indices with their genetic gain and their percent relative efficiency are given in Table 8. The results revealed that PRE ranged from 127.14 (test weight, ear head length, ear head girth and tillers per plant (I_{2345}) in genotypic path coefficient taken as weight) to 856.91(I_{1234}) (grain yield, test weight, ear head length and ear head girth in equal weight methods) with equal weight. Among other than equal methods, higher PRE was observed for combination of four characters (grain yield, test weight, ear head length and tillers per plant) except genotypic correlation taken as weight, in which combination of grain yield, ear head length and ear head girth and tillers per plant had higher PRE (I_{1235}).

Combinations of all five biometrical characters were used to construct selection indices using different weights. The selection indices with their percent relative efficiency are given in Table 9. Percent relative efficiencies were 842.61, 305.41, 230.71, 247.48 and 297.93% respectively for W1,W2,W3,W4 and W5.

Among all methods, the highest percent relative efficiency was observed to be 842.61 in equal weight methods relative to grain yield followed by the method of genotypic correlation coefficient, phenotypic path coefficient, genotypic path coefficient and phenotypic correlation coefficient taken as weight for the combination of all five characters. (Ferdous, *et al*., 2010; Chaudhary, A. P., 2017).

Results presented in Table 10 indicated that the highest percent relative efficiency was observed with index I_{234} (874.82) consisting of test weight, ear head length and ear head girth with equal weights but in other methods, the highest PRE was observed with the index I_{1345} (297.04) in the method of genotypic correlation coefficient taken as weight and in rest of methods, Index I_{1235}showed highest PRE. Therefore, one can use equal weight of variables for construction of selection indices to achieve higher genetic gain. The selection index consisting of test weight, ear head length and ear head girth (I_{234}) with equal weight was considered more reliable as it was commonly having highest relative efficiency in all methods.Green fodder yield and grain yield of sorghum have to be simultaneously improved through selection was reported by (Biswas, *et al.*2001).

The index score values were worked out for all five weight methods for all genotypes in respect of highest PRE given by different combination of characters. The results indicated that in general PRE with equal weight was higher than rest of the weights in all combinations of indices. The rank correlation among different methods for selection score values were positive and highly significant indicating agreement with all methods except equal weight. Looking to the overall results it was observed that selection index with equal weight had highest PRE but rank correlation between grain yield rank and score value rank of equal weight was non-significant whereas rank of other methods had significant positive correlation with grain yield rank. Therefore, the following index based genotypic correlation taken as weight is considered better than all other indices. (Kaour, 2013).

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Table 1. (I) Mean performance of twenty one genotypes for yield and yield attributing characters in bajra crop

Sr. No.	Genotypes	Grain yield (kg/Plot) (GYP)	1000 seed wt. (gm) (T_WT)	Ear head length (cm) (EHL)	Ear head girth (cm) (EHG)	Effective tillers/Plant (ETP)
1	GHB-935	5.121	7.622	22.23	9.13	3.9
2	GHB-939	3.673	8.042	27.73	9.77	3.1
3	GHB-941	3.776	8.935	20.63	9.57	2.5
4	GHB-952	4.940	7.425	21.63	9.13	3.6
5	GHB-953	5.400	7.169	19.90	9.43	3.2
6	GHB-961	3.441	7.947	22.80	9.97	3.2
7	GHB-964	3.334	6.743	24.77	8.60	4.3
8	GHB-965	3.340	7.802	23.87	8.20	2.8
9	GHB-966	3.028	7.521	25.20	9.30	3.1
10	GHB-984	3.981	6.879	18.93	8.50	4.4
11	GHB-993	3.959	7.010	22.30	9.27	2.7
12	GHB-996	3.661	8.227	27.93	8.90	2.8
13	GHB-997	2.936	6.362	26.37	7.93	3.2
14	GHB-1000	4.784	7.844	24.17	9.20	3.9
15	ABH-09-04	4.146	7.852	31.20	10.23	3.0
16	GHB-1026	4.056	7.975	28.10	9.37	3.3
17	GHB-1107	2.405	6.113	23.33	8.73	2.3
18	GHB-1032	3.867	8.107	35.47	11.93	3.3
19	GHB-558 (c)	3.926	7.828	21.03	9.57	3.9
20	GHB-538 (c)	4.755	8.229	23.23	7.83	3.8
21	GHB-732 (c)	4.943	7.801	22.97	8.60	4.0
	S.Em.	0.320	0.170	1.27	0.37	0.4
	CD (P=0.05)	0.928	0.489	3.45	1.05	1.2

(II) Variability: CV,GCV, PCV and h^2 for different characters of bajra

Sr. No.	Varibility	Grain yield (kg/Plot) (GYP)	1000 seed wt. (gm) (T_WT)	Ear head length (cm) (EHL)	Ear head girth (cm) (EHG)	Effective tillers/Plant (ETP)
1	CV %	14.15	3.90	8.54	6.90	21.77
2	GCV %	17.96	8.60	15.33	8.81	11.56
3	PCV %	22.86	9.44	17.55	11.19	24.65
4	h^2 %	61.70	82.90	76.30	62.00	22.00

* Significant ‘r’ value at 0.05 level of probability =0.433

Table 2. Genotypic (upper diagonal values) and phenotypic (lower diagonal values) correlation coefficients between different characters in bajra

Characters	Grain yield (kg/Plot)	1000 seed wt. (gm)	Ear head Length (cm)	Ear head girth (cm)	Effective tillers/Plant
Grain yield (kg/Plot)	1.000	0.369	-0.264	-0.006	0.818**
1000 seed wt. (gm)	0.271	1.000	0.217	0.416	-0.071
Ear head Length (cm)	-0.220	0.202	1.000	0.626**	-0.343
Ear head girth (cm)	0.141	0.333*	0.453**	1.000	-0.284
Effective tillers/Plant	0.255	-0.079	-0.141	-0.122	1.000

*, ** Significant at P<0.05 and <0.01 level, respectively

Table 3. Genotypic path coefficients (direct and indirect effects) of causal characters on grain yield per plot of bajra

Characters	T_WT	EHL	EHG	ETP	Genotypic correlation with GYP
T_WT	0.394	-0.037	0.073	-0.060	0.369
EHL	0.085	-0.172	0.110	-0.287	-0.264
EHG	0.164	-0.108	0.175	-0.237	-0.006
ETP	-0.028	0.059	-0.050	0.836	0.818**

*, ** Significant at P<=0.05 and 0.01 level, respectively

Table 4. Phenotypic path coefficients (direct and indirect effects) of causal variables on grain yield per plot of bajra

Characters	T_WT	EHL	EHG	ETP	Genotypic correlation with GYP
T_WT	0.283	-0.07	0.079	-0.02	0.271
EHL	0.057	-0.347	0.107	-0.036	-0.220
EHG	0.094	-0.157	0.236	-0.031	0.141
ETP	-0.022	0.049	-0.029	0.257	0.255

Table 5. Selection indices, expected genetic gain and relative efficiency (%) for single character by using different weight methods

Sr. No.	Equations	Genetic Gain	% Relative efficiency
	Equal weight		
I_1	$I=0.390X_1$	3.656	100.00
I_2	$I=0.693X_2$	4.833	132.20
I_3	$I=0.591X_3$	25.154	688.02
I_4	$I=0.393X_4$	4.176	114.23
I_5	$I=-0.026X_5$	0.248	6.79
	Genotypic correlation coefficients as weight		
I_1	$I=0.390X_1$	3.656	100.00
I_2	$I=0.256X_2$	1.784	48.78
I_3	$I=-0.156X_3$	6.641	181.64
I_4	$I=-0.002X_4$	0.025	0.69
I_5	$I=-0.022X_5$	0.203	5.55
	Phenotypic correlation coefficients as weight		
I_1	$I=0.390X_1$	3.656	100.00
I_2	$I=0.188X_2$	1.310	35.83
I_3	$I=-0.13X_3$	5.534	151.36
I_4	$I=0.055X_4$	0.589	16.11
I_5	$I=-0.007X_5$	0.063	1.73
	Genotypic Path coefficients as weight		
I_1	$I=0.390X_1$	3.656	100.00
I_2	$I=0.273X_2$	1.904	52.09
I_3	$I=-0.102X_3$	4.327	118.34
I_4	$I=0.069X_4$	0.731	19.99
I_5	$I=-0.022X_5$	0.207	5.67
	Phenotypic Path coefficients as weight		
I_1	$I=0.390X_1$	3.656	100.00
I_2	$I=0.196X_2$	1.368	37.42
I_3	$I=-0.205X_3$	8.728	238.74
I_4	$I=0.093X_4$	0.986	26.96
I_5	I=-0.007X5	0.064	1.75

Table 6. Selection indices, expected genetic gain and relative efficiency (%) for possible combination of two characters by using different weight methods

Sr. No.	Equations	Genetic Gain	% Relative Efficiency (PRE)
	Equal weight		
I_{23}	I=0.872X2+0.587X3	26.824	733.68
I_{34}	I=0.594X3+0.875X4	30.122	823.91
I_{35}	I=0.562X3-0.234X5	24.260	663.57
	Genotypic correlation coefficients as weight		
I_{13}	I=0.402X1-0.169X3	8.767	239.79
I_{34}	I=-0.142X3-0.153X4	6.829	186.79
I_{35}	I=-0.175X3+0.020X5	7.455	203.90
	Phenotypic correlation coefficients as weight		
I_{13}	I=0.397X1-0.143X3	7.759	212.22
I_{23}	I=0.148X2-0.128X3	5.359	146.59
I_{35}	I=-0.135X3+0.033X5	5.795	158.51
	Genotypic Path coefficients as weight		
I_{12}	I=0.376X1+0.453X2	5.256	143.77
I_{13}	I=0.393X1-0.115X3	6.695	183.13
I_{15}	I=0.563X1+0.116X5	5.557	152.00
	Phenotypic Path coefficients as weight		
I_{13}	I=0.409X1-0.218X3	10.722	293.27
I_{23}	I=0.133X2-0.203X3	8.495	232.35
I_{35}	I=-0.210X3+0.058X5	9.000	246.16

Table 7. Selection indices, expected genetic gain and relative efficiency (%) for possible combination of three characters by using different weight methods

Sr. No.	Equations	Genetic Gain	% Relative Efficiency
	Equal weight		
I_{134}	I=0.04X1+0.565X3+0.877X4	28.906	790.65
I_{234}	I=0.836X2+0.591X3+0.875X4	31.984	874.82
I_{345}	I=0.57X3+0.831X4-0.22X5	29.154	797.44
	Genotypic correlation coefficients as weight		
I_{123}	I=0.387X1+0.408X2-0.174X3	9.142	250.06
I_{134}	I=0.489X1-0.139X3-0.277X4	9.158	250.50
I_{135}	I=0.556X1-0.177X3+0.158X5	10.354	283.20
	Phenotypic correlation coefficients as weight		
I_{123}	I=0.376X1+0.353X2-0.149X3	8.104	221.66
I_{134}	I=0.466X1-0.108X3-0.201X4	7.558	206.72
I_{135}	I=0.425X1-0.143X3+0.19X5	8.411	230.07
	Genotypic Path coefficients as weight		
I_{123}	I=0.375X1+0.446X2-0.121X3	7.395	202.26
I_{125}	I=0.554X1+0.401X2+0.14X5	6.701	183.29
I_{135}	I=0.554X1-0.124X3+0.14X5	8.444	230.96
	Phenotypic Path coefficients as weight		
I_{123}	I=0.394X1+0.331X2-0.222X3	10.868	297.27
I_{134}	I=0.498X1-0.168X3-0.253X4	10.210	279.27
I_{135}	I=0.434X1-0.217X3+0.213X5	11.319	309.59

Table 8. Selection indices, expected genetic gain and relative efficiency (%) for possible combination of four characters by using different weight methods

Sr. No.	Equations	Genetic Gain	% Relative efficiency
	Equal weight		
I_{1234}	I=-0.003X1+1.203X2+0.553X3+0.825X4	31.3288	856.91
I_{1345}	I=0.083X1+0.585X3+0.953X4-0.221X5	30.5305	835.08
I_{2345}	I=0.849X2+0.567X3+0.83X4-0.175X5	31.0346	848.87
	Genotypic correlation coefficients as weight		
I_{1234}	I=0.467X1+0.484X2-0.144X3-0.301X4	9.5653	261.63
I_{1235}	I=0.545X1+0.375X2-0.181X3+0.179X5	10.6792	292.10
I_{1345}	I=0.671X1-0.14X3-0.347X4+0.12X5	10.8596	297.04
	Phenotypic correlation coefficients as weight		
I_{1234}	I=0.433X1+0.452X2-0.115X3-0.231X4	8.0748	220.86
I_{1235}	I=0.397X1+0.367X2-0.149X3+0.212X5	8.7605	239.62
I_{1345}	I=0.501X1-0.108X3-0.209X4+0.16X5	8.2161	224.73
	Genotypic Path coefficients as weight		
I_{1234}	I=0.42X1+0.545X2-0.088X3-0.188X4	7.3318	200.54
I_{1235}	I=0.54X1+0.41X2-0.128X3+0.163X5	9.0092	246.42
I_{1345}	I=0.638X1-0.083X3-0.231X4+0.106X5	8.2650	226.07
	Phenotypic Path coefficients as weight		
I_{1234}	I=0.463X1+0.471X2-0.175X3-0.285X4	10.5521	288.62
I_{1235}	I=0.412X1+0.349X2-0.222X3+0.234X5	11.4829	314.08
I_{1345}	I=0.531X1-0.168X3-0.261X4+0.173X5	10.8124	295.74

Table 9. Selection indices, expected genetic gain and relative efficiency (%) for all five characters by using different weight methods

Sr. No.	Equations	Genetic Gain	% Relative efficiency
	Equal weight		
I_{12345}	I=0.201X1+1.376X2+0.546X3+0.71X4+0.085X5	30.806	842.61
	Genotypic correlation coefficients as weight		
I_{12345}	I=0.708X1+0.491X2-0.147X3-0.409X4-0.217X5	11.166	305.41
	Phenotypic correlation coefficients as weight		
I_{12345}	I=0.55X1+0.456X2-0.117X3-0.29X4-0.301X5	8.435	230.71
	Genotypic Path coefficients as weight		
I_{12345}	I=0.661X1+0.559X2-0.092X3-0.296X4-0.196X5	9.048	247.48
	Phenotypic Path coefficients as weight		
I_{12345}	I=0.586X1+0.474X2-0.178X3-0.347X4-0.326X5	10.893	297.93

Table 10. Different combinations of characters in top three ranking selection indices in different methods

Combination	Rank	Equal Wt.	Geno. Corr. Wt.	Pheno. Corr. Wt.	Geno. Path coeff. Wt	Pheno path wt.
Combination of two characters	1	I_{34} (823.91)	I_{13} (239.79)	I_{13} (212.22)	I_{13} (183.13)	I_{13} (293.27)
	2	I_{23} (733.68)	I_{35} (203.9)	I_{35} (158.51)	I_{15} (152)	I_{35} (246.16)
	3	I_{35} (663.57)	I34 (186.79)	I_{23} (146.59)	I_{12} (143.77)	I_{23} (232.35)
Combination of three characters	1	I_{234} (874.82)	I_{135} (283.2)	I_{135} (230.07)	I_{135} (230.96)	I_{135} (309.59)
	2	I_{345} (797.44)	I_{134} (250.5)	I_{123} (221.66)	I_{123} (202.26)	I_{123} (297.27)
	3	I_{134} (790.65)	I_{123} (250.06)	I_{134} (206.72)	I_{125} (183.29)	I_{134} (279.27)
Combination of four characters	1	I_{1234} (856.91)	I_{1345} (297.04)	I_{1235} (239.62)	I_{1235} (246.42)	I_{1235} (314.08)
	2	I_{2345} (848.87)	I_{1235} (292.1)	I_{1345} (224.73)	I_{1345} (226.07)	I_{1345} (295.74)
	3	I_{1345} (835.08)	I_{1234} (261.63)	I_{1234} (220.86)	I_{1234} (200.54)	I_{1234} (288.62)

Table 11. Rank correlation between different methods based on (I_{234})

	gyp	equal	Geno corr	Pheno corr	Geno path	Pheno path
gyp	1.000	-	-	-		
equal	-0.242	1.000	-	-	-	-
Geno corr	0.673*	-0.725*	1.000	-	-	-
Pheno corr	0.447*	-0.499*	0.826*	1.000	-	-
Geno Path	0.506*	-0.392	0.782*	0.969*	1.000	-
Pheno path	0.417*	-0.613*	0.844*	0.984*	0.938*	1.000

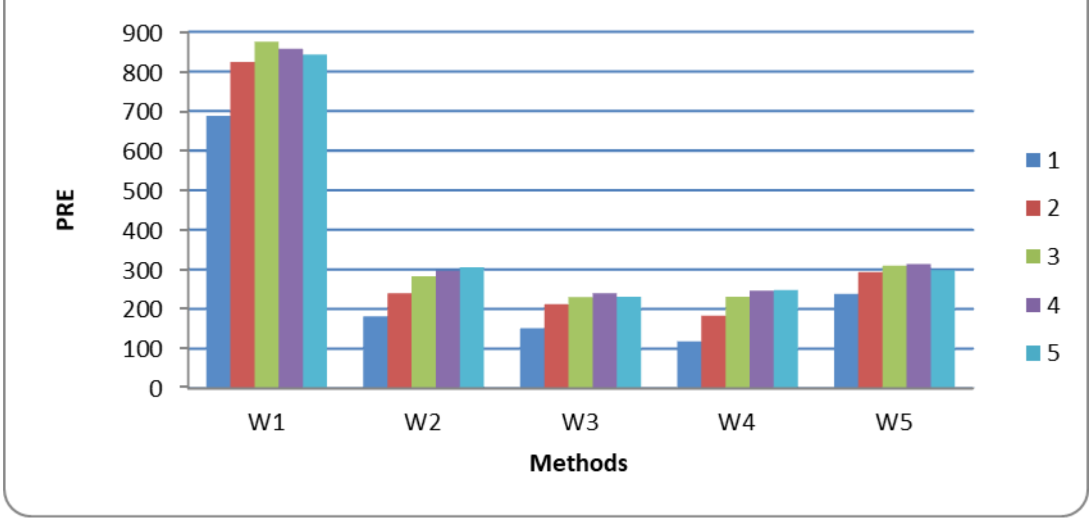

Fig.1 : PRE for different combination of characters in different methods