

Comparison of selection indices using different weights in maize (*Zea mays* L.) for different biometrical characters

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ABSTRACT

The data on six different biometrical characters of fifty seven genotypes/hybrids of maize were collected from Main Maize Research Station (MMRS), A.A.U., Godhara during *Rabi* season of the year 2015-16 for the present study entitled "Comparison of selection indices using different weights in maize (*Zea mays* L.) for different biometrical characters". The experiment was conducted in randomized block design with three replications. Six characters grain yield per plant, cob height, cob length, number of grains per row, number of rows per cob and 100 kernel weight were used. The selection index technique was employed to study the crop improvement using different characters giving different weights to each character. Selection index for all possible combination of six characters can be calculated and the combination which provides the higher relative efficiency is selected. Selection index for all possible combination of six characters which provides the high percent relative efficiency (PRE) is selected. For this present investigation, three different weights i.e. equal weight, genotypic correlation and phenotypic correlation were given to different characters to construct selection indices to select the optimum index in maize. Total 63 selection indices were constructed for each weight method. In general higher per cent relative efficiency (PRE) was observed for equal weight method among all three weight methods. The selection index (I_{12346}) having grain yield per plant, cob height, cob length, number of grains per row and 100 kernel weight had the highest per cent relative efficiency (PRE) among all the combinations of selection indices in equal weight, genotypic correlation coefficient and phenotypic correlation coefficient weight methods. The rank correlation among different methods for selection index values were found positive and highly significant indicating agreement with all methods except equal weight. Therefore index based on equal weight taken is considered better than all other indices. The selection index without grain yield $I_{2346} = 0.492 X_2 + 2.275 X_3 + 0.649 X_4 + 1.125 X_6$ is the best indices.

Where, X_2 = cob height (cm), X_3 = cob length (cm), X_4 = number of grains per row and X_6 = 100 kernel weight (g)

Keywords: selection index, genotype, equal weight, genotypic correlation, phenotypic correlation

The data of large scale varietal trial having fifty seven genotypes/hybrids of maize were collected from Main Maize Research Station (MMRS), A.A.U., Godhara during *Rabi* season of the year 2015-16 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 per plant (X_1), cob height (X_2), cob length (X_3), number of grains per row (X_4), number of rows per cob (X_5) and 100 kernel (X_6) were used for this analysis.

MATERIALS AND METHODS

List of genotypes studied with their name

Sr. No.	Genotypes	Name of genotype
1	S3-25-1	P1
2	S4-06-1	P2
3	S4-22-5	P3
4	S4-44-5	P4
5	S4-70-1	P5
6	S4-70-2	P6
7	S3-17-1	P7
8	LM-5	P8
9	HKI-163	P9
10	CLQ-47	P10

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Let us assume that economic value of a plant is determined by different variables and the merit of a plant is H. Then

$$H = a_1G_1 + a_2G_2 + a_3G_3 + \dots + a_nG_n = \sum_{i=1}^n b_i X_i$$

$$I = b_1x_1 + b_2x_2 + b_3x_3 + \dots + b_nx_n \dots (1)$$

$$H = a_1G_1 + a_2G_2 + a_3G_3 + \dots + a_nG_n \dots (2)$$

These I and H were estimated in such way that regression of I on H was maximized.

Thus, $b = X^{-1} \times G \times a$

Selection index was calculated by substituting value of the character and b_i values in following equation

$$I = b_1x_1 + b_2x_2 + b_3x_3 + \dots + b_nx_n$$

Selection index for all possible combination of six characters 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 is selected

The expected genetic advance is calculated as

$$= (Z/P) / ((\sum a_i b_i G_i) / (\sum \sum b_i b_j p_{ij}))^{1/2}$$

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

Percent Relative efficiency (PRE)

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

Equal weight

In equal weight, a value of 1 was assigned for all characters to construct selection indices.

$$a_1 = a_2 = a_3 = \dots = a_n = 1$$

Genotypic and phenotypic correlation coefficient

The genotypic correlation and phenotypic correlation were worked out between different yield contributing characters and yield as per suggested by Hazel *et al.* (1943) using SPAR1 software. These correlation coefficients were used as weight for selection index.

Genotypic correlation coefficient	Phenotypic correlation coefficient
$r_{gi} = \frac{\hat{\sigma}_{gij}}{\sqrt{\hat{\sigma}_{gi}^2 \times \hat{\sigma}_{gj}^2}}$	$r_{pij} = \frac{\hat{\sigma}_{pij}}{\sqrt{\hat{\sigma}_{pi}^2 \times \hat{\sigma}_{pj}^2}}$

Where,

r_{gij} and r_{pij} = Genotypic and phenotypic correlation coefficient between i^{th} and j^{th} character. $\hat{\sigma}_{gi}^2$ and $\hat{\sigma}_{gj}^2$ = Genotypic variances of i^{th} and j^{th}

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

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

RESULTS AND DISCUSSION

Mean, range and coefficient of variation

The results presented in Table 1 revealed that the highest grain yield per plant was recorded by genotype/hybrid S4-22-5(P3) X CLQ-47 (P10) and it was highly significant compared to other genotypes. The value of broad sense heritability was 92.75 % which was second highest after 100 kernel weight. The maximum cob height was recorded for the genotype S4-70-2 (P6) X LM-5 (P8). The maximum cob lengths were recorded for genotype S4-44-5(P4) X S3-17-1(P7) and S3-25-1(P1) X S4-06-1(P2). The maximum number of grains per row were found for the genotype S4-22-5(P3) X CLQ-47 (P10). The highest number of rows per cob were recorded for genotype S3-25-1(P1) X S4-70-1 (P5) and S4-70-1(P5) X HKI-163 (P9). The maximum 100 kernel weight was recorded for genotype S4-22-5 (P3) X HKI-163 (P9). These results are in accordance with Hussain *et al.* (2016) and Ferdoush *et al.* (2017) in maize.

Genotypic and Phenotypic correlation coefficients

The correlation coefficients between grain yield per plant and its component traits among themselves were estimated at genotypic and phenotypic levels. The results of genotypic and phenotypic correlation coefficients between grain yield per plant and its components are given in Table 2.

Positive and significant genotypic correlation between grain yields with all the characters was observed. 100 kernel weights had the highest genotypic correlation with grain yield followed by number of grain per row. Similar trend was also observed for phenotypic correlation with yield. Cob height had also significant genotypic correlation with number of grains per row (0.3238), number of rows per cob (0.3557) and cob length (0.4292). Significant and positive phenotypic correlation of grain yield was found with all the character except cob height (0.1898). Cob height was found phenotypically non significant with all the character. The results of remaining characters observed that positive and significant correlation of cob length with number of grain per row, number of rows per cob and 100 kernel weight, while number of grain per row with 100 kernel

Table 1 Mean, range and coefficient of variation for different characters of maize

Sr No.	Genotypes	Grain yield per plant (g)	Cob height (cm)	Cob length (cm)	Number of grains per row	Number of rows per cob	100 kernel weight(g)
1.	P1	54.79	121.00	18.67	28.33	15.33	10.70
2.	P2	68.10	96.67	16.00	29.33	13.33	16.07
3.	P3	93.40	66.67	17.00	31.67	15.33	18.60
4.	P4	134.57	115.67	17.33	39.00	14.67	21.15
5.	P5	72.86	112.67	19.33	39.33	15.33	11.60
6.	P6	124.65	116.33	18.67	40.00	14.67	18.63
7.	P7	71.23	101.00	16.33	29.33	14.67	15.40
8.	P8	124.90	95.67	17.33	33.33	14.67	24.60
9.	P9	73.71	100.33	14.67	26.00	12.67	19.80
10.	P10	74.42	101.00	15.67	27.00	14.00	19.24
11.	P1 X P2	68.53	114.33	21.00	28.67	14.00	15.90
12.	P1 X P3	54.87	100.00	17.33	29.33	16.67	9.90
13.	P1 X P4	58.53	106.33	20.00	27.67	16.00	12.60
14.	P1 X P5	63.34	106.00	17.67	28.00	18.00	11.63
15.	P1 X P6	58.57	105.00	15.33	27.33	14.67	13.20
16.	P1 X P7	86.38	89.00	18.67	28.00	16.00	19.27
17.	P1 X P8	48.54	87.00	15.00	26.67	16.00	10.00
18.	P1 X P9	78.12	86.00	17.33	29.33	13.33	17.37
19.	P1 X P10	66.83	79.67	17.67	27.67	16.67	13.46
20.	P2 X P3	52.07	86.00	15.67	30.67	13.33	10.73
21.	P2 X P4	36.46	99.00	12.67	17.00	14.00	12.73
22.	P2 X P5	61.91	82.33	13.33	29.33	14.00	13.07
23.	P2 X P6	87.13	86.33	18.00	30.33	13.33	18.50
24.	P2 X P7	77.65	79.00	18.00	32.67	15.33	14.20
25.	P2 X P8	67.24	80.67	15.67	31.67	13.67	14.10
26.	P2 X P9	29.99	96.00	13.00	17.00	12.00	13.73
27.	P2 X P10	71.00	83.33	15.33	26.67	14.67	16.53
28.	P3 X P4	81.96	93.67	17.33	33.00	14.00	16.00
29.	P3 X P5	78.79	92.00	17.00	33.00	14.00	15.93
30.	P3 X P6	45.19	95.67	15.67	32.33	13.33	9.26
31.	P3 X P7	38.28	79.33	16.67	30.00	10.67	10.67
32.	P3 X P8	125.78	105.33	17.33	33.67	13.33	26.20
33.	P3 X P9	148.49	99.00	19.67	39.33	13.33	26.60
34.	P3 X P10	182.18	113.33	19.00	41.33	17.33	23.37
35.	P4 X P5	80.53	115.67	16.33	30.00	16.00	14.90
36.	P4 X P6	86.17	119.33	19.33	31.00	13.33	20.07
37.	P4 X P7	93.01	107.33	21.00	41.00	13.33	16.20
38.	P4 X P8	95.67	119.67	16.67	36.00	15.33	15.33
39.	P4 X P9	65.62	125.00	15.00	28.33	14.67	14.47
40.	P4 X P10	73.88	105.67	15.67	27.67	16.67	14.63
41.	P5 X P6	51.10	122.33	15.33	30.33	11.33	13.56
42.	P5 X P7	136.29	105.33	18.33	34.33	15.33	25.58
43.	P5 X P8	102.72	116.00	17.00	37.33	15.33	16.70
44.	P5 X P9	158.05	119.33	20.00	40.33	18.00	21.10
45.	P5 X P10	140.61	116.67	18.33	34.33	16.00	23.27
46.	P6 X P7	67.31	130.67	18.00	30.00	15.33	13.47

47.	P6 X P8	111.13	134.67	20.00	33.00	14.67	19.65
48.	P6 X P9	109.98	117.00	19.33	36.33	14.67	20.37
49.	P6 X P10	80.85	120.33	16.67	30.33	16.00	15.47
50.	P7 X P8	73.08	113.67	18.00	29.00	15.33	15.23
51.	P7 X P9	71.58	105.33	19.00	30.00	14.67	15.50
52.	P7 X P10	67.40	96.00	20.00	30.00	14.00	15.20
53.	P8 X P9	79.94	106.00	17.33	32.67	14.67	16.77
54.	P8 X P10	77.87	104.33	14.67	33.00	13.33	16.53
55.	P9 X P10	63.52	107.33	19.33	26.00	13.33	17.27
56.	GAYMH1	83.08	113.33	16.67	29.33	15.33	16.50
57.	HQPM 1	37.56	113.33	14.67	29.00	13.33	12.47
Mean		81.88	103.61	17.23	31.11	14.60	16.33
S. Em.±		7.20	7.40	0.81	2.00	0.88	0.92
Range		29.99 -	66.67 -	12.67 -	17.00 -	10.67 -	9.26 -
		182.18	134.67	21.00	41.33	18.00	26.60
C.D. (5%)		20.17	20.74	2.27	5.60	2.46	2.56
C.V. (%)		15.22	12.37	8.16	11.12	10.43	9.71
Broad sense heritability (%)		92.75	70.14	78.23	79.05	60.89	93.19

Table 2 Genotypic and phenotypic correlation coefficients between different characters in maize.

Character		GY	CH	CL	NOGPR	NORC	100KW
GY	rg	1.0000	0.3404**	0.5594**	0.7795**	0.4055**	0.8929**
	rp	1.0000	0.1898	0.4092**	0.7222**	0.3215*	0.7891**
CH	rg	-	1.0000	0.4292**	0.3238*	0.3557**	0.1908
	rp	-	1.0000	0.1531	0.1961	0.0773	0.1186
CL	rg	-	-	1.0000	0.6871**	0.3437**	0.4089**
	rp	-	-	1.0000	0.3988**	0.2348	0.2783*
NOGPR	rg	-	-	-	1.0000	0.2714	0.5032**
	rp	-	-	-	1.0000	0.1368	0.3841**
NORC	rg	-	-	-	-	1.0000	0.0700
	rp	-	-	-	-	1.0000	0.0053
100 KW	rg	-	-	-	-	-	1.0000
	rp	-	-	-	-	-	1.0000

r_g = genotypic correlation r_p = phenotypic correlation

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

Where, GY: Grain yield per plant, CH: Cob height, CL: Cob length, NOGPR: Number of grains per row, NORC: Number of rows per cob, 100 KW: 100 kernel weight

weight was also found highly significant and positive at genotypic and phenotypic level.

Positive and significant genotypic and phenotypic correlation between grain yield and cob height was observed by Hussain *et al.* (2016), Prasad and Shivani (2017). Similarly positive and significant genotypic and phenotypic association of grain yield with number of grains per row, number of rows per cob and 100 kernel weight were observed by Bocanski *et al.* (2009), Rani *et al.* (2017), Prasad and Shivani (2017), Bisen *et al.* (2018) and Varalakshmi

et al. (2018) in maize.

Selection indices using different weights

Selection indices were worked out taking six biometrical characters and were constructed taking all possible combinations of the characters. Total 63 selection indices were constructed using equal weight (W1), genotypic correlation coefficients (W2) and phenotypic correlation coefficients (W3) for all characters. The expected genetic gain and percent relative efficiency (PRE) of different indices were worked out and the results are given in Table 3 to 8.

Table 3 Selection indices, expected genetic gain and per cent relative efficiency (PRE) for single character by using differential weight methods

Sr. No.	Equations	Genetic Gain	PRE
1	Equal weight (W1)		
I_1	$I=0.86X1$	59.09	100.00
I_2	$I=0.492X2$	18.22	30.83
I_3	$I=0.612X3$	2.84	4.82
I_4	$I=0.625X4$	7.27	12.31
I_5	$I=0.371X5$	1.46	2.48
I_6	$I=0.869X6$	7.82	13.24
2	Genotypic correlation taken as weight (W2)		
I_1	$I=0.86X1$	59.09	100.00
I_2	$I=0.167X2$	6.20	10.50
I_3	$I=0.342X3$	1.59	2.69
I_4	$I=0.487X4$	5.66	9.59
I_5	$I=0.15X5$	0.59	1.01
I_6	$I=0.775X6$	6.98	11.82
3	Phenotypic correlation taken as weight (W3)		
I_1	$I=0.86X1$	59.09	100.00
I_2	$I=0.093X2$	3.45	5.85
I_3	$I=0.25X3$	1.16	1.97
I_4	$I=0.451X4$	5.25	8.89
I_5	$I=0.119X5$	0.47	0.80
I_6	$I=0.685X6$	6.17	10.45

Table 4 Selection indices, expected genetic gain and per cent relative efficiency (PRE) for possible combinations of two characters by using differential weight methods

Sr. No.	Equations	Genetic Gain	PRE
1	Equal weight (W1)		
I_{12}	$I=0.92X1+0.579X2$	70.51	119.32
I_{13}	$I=0.846X1+1.493X3$	61.31	103.75
I_{14}	$I=0.978X1-0.171X4$	65.76	111.28
I_{15}	$I=0.884X1-0.59X5$	60.04	101.60
I_{16}	$I=0.696X1+2.567X6$	67.55	114.32
I_{23}	$I=0.485X2+1.897X3$	21.19	35.86
I_{24}	$I=0.494X2+0.888X4$	22.70	38.41
I_{25}	$I=0.496X2+1.434X5$	19.65	33.26
I_{26}	$I=0.489X2+1.143X6$	21.87	37.02
I_{34}	$I=1.049X3+0.628X4$	10.27	17.39
I_{35}	$I=0.676X3+0.377X5$	3.78	6.40
I_{36}	$I=0.692X3+0.923X6$	9.71	16.44
I_{45}	$I=0.646X4+0.495X5$	8.02	13.59
I_{46}	$I=0.6X4+1.05X6$	13.74	23.25
I_{56}	$I=0.45X5+0.885X6$	8.17	13.84
2	Genotypic correlation taken as weight (W2)		
I_{12}	$I=0.873X1+0.271X2$	62.66	106.04
I_{13}	$I=0.841X1+1.257X3$	60.38	102.19
I_{14}	$I=0.969X1-0.269X4$	64.31	108.84
I_{15}	$I=0.88X1-0.787X5$	59.53	100.75
I_{16}	$I=0.693X1+2.493X6$	66.74	112.94

I ₂₃	$I=0.169X2+0.775X3$	7.69	13.01
I ₂₄	$I=0.176X2+0.572X4$	10.19	17.25
I ₂₅	$I=0.17X2+0.512X5$	6.75	11.43
I ₂₆	$I=0.17X2+0.867X6$	10.58	17.92
I ₃₄	$I=0.702X3+0.47X4$	7.40	12.53
I ₃₅	$I=0.368X3+0.157X5$	1.95	3.30
I ₃₆	$I=0.427X3+0.8X6$	7.99	13.52
I ₄₅	$I=0.493X4+0.251X5$	5.96	10.09
I ₄₆	$I=0.471X4+0.915X6$	11.52	19.50
I ₅₆	$I=0.222X5+0.782X6$	7.10	12.02
3	Phenotypic correlation taken as weight (W3)		
I ₁₂	$I=0.862X1+0.2X2$	61.08	103.37
I ₁₃	$I=0.839X1+1.177X3$	60.07	101.66
I ₁₄	$I=0.966X1-0.294X4$	63.94	108.20
I ₁₅	$I=0.88X1-0.815X5$	59.46	100.63
I ₁₆	$I=0.69X1+2.422X6$	65.95	111.61
I ₂₃	$I=0.096X2+0.489X3$	4.50	7.63
I ₂₄	$I=0.104X2+0.495X4$	7.52	12.73
I ₂₅	$I=0.096X2+0.32X5$	3.86	6.54
I ₂₆	$I=0.096X2+0.736X6$	7.88	13.34
I ₃₄	$I=0.593X3+0.426X4$	6.56	11.12
I ₃₅	$I=0.271X3+0.123X5$	1.45	2.46
I ₃₆	$I=0.328X3+0.701X6$	6.89	11.67
I ₄₅	$I=0.456X4+0.213X5$	5.48	9.28
I ₄₆	$I=0.435X4+0.815X6$	10.40	17.60
I ₅₆	$I=0.182X5+0.69X6$	6.26	10.60

Table 5 Selection indices, expected genetic gain and relative efficiency (%) for possible combination of three characters by using different weight methods

Sr. No.	Equations	Genetic Gain	PRE
1	Equal weight (W1)		
I ₁₂₃	$I=0.88X1+0.575X2+2.464X3$	73.28	124.01
I ₁₂₄	$I=1.048X1+0.607X2-0.279X4$	77.15	130.56
I ₁₂₅	$I=0.93X1+0.59X2+0.152X5$	71.51	121.01
I ₁₂₆	$I=0.791X1+0.591X2+2.222X6$	78.09	132.14
I ₁₃₄	$I=0.955X1+2.144X3-0.246X4$	68.23	115.46
I ₁₃₅	$I=0.87X1+1.646X3-0.77X5$	62.31	105.44
I ₁₃₆	$I=0.668X1+1.726X3+2.642X6$	69.75	118.03
I ₁₄₅	$I=1.017X1-0.253X4-0.844X5$	66.74	112.94
I ₁₄₆	$I=0.771X1+0.267X4+2.462X6$	73.82	124.92
I ₁₅₆	$I=0.703X1+0.484X5+2.543X6$	68.28	115.54
I ₂₃₄	$I=0.491X2+2.253X3+0.7X4$	26.31	44.53
I ₂₃₅	$I=0.494X2+1.799X3+1.132X5$	22.39	37.90
I ₂₃₆	$I=0.485X2+1.922X3+1.022X6$	24.94	42.21
I ₂₄₅	$I=0.499X2+0.861X4+1.47X5$	24.11	40.81
I ₂₄₆	$I=0.493X2+0.814X4+1.216X6$	27.18	45.99
I ₂₅₆	$I=0.493X2+1.513X5+1.155X6$	23.23	39.31
I ₃₄₅	$I=1.092X3+0.647X4+0.386X5$	11.05	18.70
I ₃₄₆	$I=1.093X3+0.596X4+1.049X6$	16.38	27.72
I ₃₅₆	$I=0.738X3+0.439X5+0.933X6$	10.21	17.29
I ₄₅₆	$I=0.614X4+0.586X5+1.059X6$	14.30	24.20

2	Genotypic correlation taken as weight (W2)		
I_{123}	$I=0.846X1+0.267X2+1.536X3$	64.10	108.48
I_{124}	$I=0.988X1+0.295X2-0.34X4$	67.94	114.98
I_{125}	$I=0.888X1+0.277X2-0.547X5$	63.09	106.76
I_{126}	$I=0.713X1+0.285X2+2.404X6$	70.05	118.54
I_{134}	$I=0.945X1+1.818X3-0.364X4$	65.80	111.34
I_{135}	$I=0.86X1+1.386X3-0.951X5$	60.86	103.00
I_{136}	$I=0.659X1+1.486X3+2.567X6$	68.05	115.15
I_{145}	$I=1.003X1-0.349X4-1.032X5$	64.80	109.65
I_{146}	$I=0.756X1+0.181X4+2.394X6$	71.61	121.19
I_{156}	$I=0.689X1+0.331X5+2.523X6$	67.03	113.44
I_{234}	$I=0.177X2+1.105X3+0.49X4$	12.25	20.73
I_{235}	$I=0.173X2+0.745X3+0.412X5$	8.16	13.82
I_{236}	$I=0.171X2+0.84X3+0.832X6$	12.10	20.49
I_{245}	$I=0.179X2+0.561X4+0.579X5$	10.72	18.15
I_{246}	$I=0.177X2+0.539X4+0.969X6$	15.18	25.70
I_{256}	$I=0.171X2+0.581X5+0.872X6$	11.02	18.65
I_{345}	$I=0.717X3+0.478X4+0.167X5$	7.70	13.04
I_{346}	$I=0.751X3+0.45X4+0.904X6$	13.00	22.00
I_{356}	$I=0.439X3+0.208X5+0.805X6$	8.15	13.80
I_{456}	$I=0.472X4+0.33X5+0.921X6$	11.73	19.86
3	Phenotypic correlation taken as weight (W3)		
I_{123}	$I=0.838X1+0.196X2+1.298X3$	62.13	105.15
I_{124}	$I=0.974X1+0.224X2-0.357X4$	65.99	111.67
I_{125}	$I=0.879X1+0.206X2-0.69X5$	61.45	103.98
I_{126}	$I=0.693X1+0.215X2+2.391X6$	67.82	114.77
I_{134}	$I=0.942X1+1.715X3-0.397X4$	65.10	110.16
I_{135}	$I=0.858X1+1.302X3-0.974X5$	60.48	102.35
I_{136}	$I=0.654X1+1.403X3+2.495X6$	66.96	113.31
I_{145}	$I=1X1-0.374X4-1.058X5$	64.35	108.90
I_{146}	$I=0.748X1+0.168X4+2.33X6$	70.47	119.26
I_{156}	$I=0.684X1+0.32X5+2.462X6$	66.19	112.01
I_{234}	$I=0.104X2+0.814X3+0.435X4$	9.06	15.33
I_{235}	$I=0.099X2+0.477X3+0.264X5$	4.87	8.25
I_{236}	$I=0.098X2+0.556X3+0.718X6$	8.91	15.08
I_{245}	$I=0.106X2+0.49X4+0.393X5$	7.90	13.37
I_{246}	$I=0.105X2+0.47X4+0.844X6$	12.25	20.73
I_{256}	$I=0.098X2+0.381X5+0.74X6$	8.15	13.80
I_{345}	$I=0.605X3+0.432X4+0.135X5$	6.80	11.51
I_{346}	$I=0.636X3+0.408X4+0.8X6$	11.51	19.49
I_{356}	$I=0.337X3+0.168X5+0.705X6$	7.02	11.88
I_{456}	$I=0.435X4+0.283X5+0.82X6$	10.57	17.90

Expected genetic gain and relative efficiency (%) for single character

The selection indices were constructed for single character separately. Total six selection indices were constructed for each weight methods (W1, W2 and W3). The selection indices with their expected genetic advance and per cent relative efficiency are presented in Table 3. The genetic gain in maize grain yield per plant (59.09) 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 selection of single character for different methods. Per cent relative efficiency (PRE) for selection index of biometrical characters ranged from 2.48 to 100, 1.01 to 100.00, 0.80 to 100.00 for W1, W2 and W3 respectively. The highest PRE were observed for grain yield per plant in equal weight methods. The lowest PRE were

Table 6 Selection indices, expected genetic gain and per cent relative efficiency (PRE) for possible combinations of four characters by using differential weight methods

Sr. No.	Equations	Genetic Gain	PRE
1	Equal weight (W1)		
1 ₂₃₄	$I=1.009X1+0.6X2+3.157X3-0.438X4$	80.24	135.79
1 ₂₃₅	$I=0.893X1+0.586X2+2.543X3-0.148X5$	74.30	125.74
1 ₂₃₆	$I=0.731X1+0.586X2+2.659X3+2.352X6$	80.85	136.81
1 ₂₄₅	$I=1.067X1+0.62X2-0.317X4-0.126X5$	78.15	132.25
1 ₂₄₆	$I=0.912X1+0.612X2+0.006X4+1.958X6$	84.45	142.91
1 ₂₅₆	$I=0.765X1+0.602X2+1.127X5+2.388X6$	79.03	133.73
1 ₃₄₅	$I=0.999X1+2.376X3-0.369X4-1.158X5$	69.30	117.28
1 ₃₄₆	$I=0.738X1+2.225X3+0.205X4+2.528X6$	76.25	129.03
1 ₃₅₆	$I=0.682X1+1.757X3+0.306X5+2.568X6$	70.49	119.29
1 ₄₅₆	$I=0.797X1+0.225X4+0.255X5+2.345X6$	74.55	126.16
2 ₃₄₅	$I=0.5X2+2.154X3+0.703X4+1.131X5$	27.49	46.52
2 ₃₄₆	$I=0.492X2+2.275X3+0.649X4+1.125X6$	30.70	51.96
2 ₃₅₆	$I=0.493X2+1.795X3+1.211X5+1.051X6$	26.08	44.14
2 ₄₅₆	$I=0.498X2+0.772X4+1.582X5+1.248X6$	28.50	48.24
3 ₄₅₆	$I=1.119X3+0.613X4+0.47X5+1.053X6$	16.99	28.76
2	Genotypic correlation taken as weight (W2)		
1 ₂₃₄	$I=0.96X1+0.288X2+2.111X3-0.458X4$	69.59	117.77
1 ₂₃₅	$I=0.862X1+0.272X2+1.64X3-0.744X5$	64.56	109.26
1 ₂₃₆	$I=0.672X1+0.28X2+1.749X3+2.492X6$	71.50	121.00
1 ₂₄₅	$I=1.016X1+0.303X2-0.408X4-0.816X5$	68.40	115.76
1 ₂₄₆	$I=0.798X1+0.3X2+0.059X4+2.233X6$	74.99	126.90
1 ₂₅₆	$I=0.698X1+0.289X2+0.555X5+2.5X6$	70.39	119.11
1 ₃₄₅	$I=0.984X1+2.023X3-0.481X4-1.324X5$	66.36	112.29
1 ₃₄₆	$I=0.726X1+1.892X3+0.092X4+2.436X6$	73.08	123.67
1 ₃₅₆	$I=0.663X1+1.496X3+0.171X5+2.55X6$	68.34	115.65
1 ₄₅₆	$I=0.763X1+0.173X4+0.151X5+2.366X6$	71.91	121.69
2 ₃₄₅	$I=0.18X2+1.073X3+0.492X4+0.417X5$	12.69	21.47
2 ₃₄₆	$I=0.178X2+1.146X3+0.463X4+0.928X6$	17.05	28.86
2 ₃₅₆	$I=0.174X2+0.793X3+0.468X5+0.843X6$	12.49	21.14
2 ₄₅₆	$I=0.179X2+0.521X4+0.664X5+0.983X6$	15.63	26.45
3 ₄₅₆	$I=0.752X3+0.456X4+0.236X5+0.907X6$	13.22	22.39
3	Phenotypic correlation taken as weight (W3)		
1 ₂₃₄	$I=0.948X1+0.217X2+1.844X3-0.468X4$	67.22	113.76
1 ₂₃₅	$I=0.855X1+0.2X2+1.409X3-0.862X5$	62.53	105.81
1 ₂₃₆	$I=0.655X1+0.209X2+1.512X3+2.469X6$	68.89	116.58
1 ₂₄₅	$I=1.004X1+0.231X2-0.433X4-0.956X5$	66.39	112.36
1 ₂₄₆	$I=0.767X1+0.229X2+0.078X4+2.247X6$	72.39	122.50
1 ₂₅₆	$I=0.681X1+0.219X2+0.448X5+2.469X6$	68.08	115.21
1 ₃₄₅	$I=0.98X1+1.916X3-0.513X4-1.343X5$	65.58	110.99
1 ₃₄₆	$I=0.719X1+1.782X3+0.069X4+2.364X6$	71.62	121.20
1 ₃₅₆	$I=0.656X1+1.408X3+0.165X5+2.49X6$	67.19	113.71
1 ₄₅₆	$I=0.75X1+0.169X4+0.161X5+2.325X6$	70.71	119.66
2 ₃₄₅	$I=0.107X2+0.799X3+0.437X4+0.272X5$	9.38	15.87
2 ₃₄₆	$I=0.105X2+0.852X3+0.413X4+0.813X6$	13.58	23.00
2 ₃₅₆	$I=0.101X2+0.531X3+0.311X5+0.725X6$	9.16	15.51
2 ₄₅₆	$I=0.107X2+0.459X4+0.466X5+0.854X6$	12.55	21.24
3 ₄₅₆	$I=0.635X3+0.412X4+0.196X5+0.803X6$	11.69	19.79

Table 7 Selection indices, expected genetic gain and per cent relative efficiency (PRE) for possible combinations of five characters by using differential weight methods

Sr.No.	Equations	Genetic Gain	PRE
1	Equal weight (W1)		
I ₁₂₃₄₅	$I=1.038X1+0.613X2+3.308X3-0.521X4-0.594X5$	81.31	137.59
I ₁₂₃₄₆	$I=0.861X1+0.604X2+3.23X3-0.138X4+2.031X6$	87.48	148.04
I ₁₂₃₅₆	$I=0.72X1+0.597X2+2.642X3+0.843X5+2.435X6$	81.77	138.37
I ₁₂₄₅₆	$I=0.895X1+0.622X2+0.054X4+0.751X5+2.045X6$	85.35	144.44
I ₁₃₄₅₆	$I=0.793X1+2.318X3+0.084X4-0.112X5+2.26X6$	77.01	130.33
I ₂₃₄₅₆	$I=0.5X2+2.148X3+0.642X4+1.233X5+1.158X6$	31.82	53.85
2	Genotypic correlation taken as weight (W2)		
I ₁₂₃₄₅	$I=0.994X1+0.296X2+2.289X3-0.564X4-1.149X5$	70.13	118.67
I ₁₂₃₄₆	$I=0.763X1+0.293X2+2.181X3-0.051X4+2.276X6$	76.62	129.65
I ₁₂₃₅₆	$I=0.666X1+0.284X2+1.74X3+0.365X5+2.532X6$	71.83	121.56
I ₁₂₄₅₆	$I=0.792X1+0.305X2+0.076X4+0.291X5+2.263X6$	75.32	127.46
I ₁₃₄₅₆	$I=0.761X1+1.95X3+0.011X4-0.205X5+2.262X6$	73.39	124.19
I ₂₃₄₅₆	$I=0.181X2+1.096X3+0.461X4+0.492X5+0.941X6$	17.43	29.49
3	Phenotypic correlation taken as weight (W3)		
I ₁₂₃₄₅	$I=0.984X1+0.223X2+2.03X3-0.58X4-1.258X5$	67.70	114.56
I ₁₂₃₄₆	$I=0.736X1+0.221X2+1.908X3-0.028X4+2.281X6$	73.61	124.56
I ₁₂₃₅₆	$I=0.651X1+0.213X2+1.506X3+0.281X5+2.498X6$	69.15	117.01
I ₁₂₄₅₆	$I=0.764X1+0.232X2+0.089X4+0.219X5+2.266X6$	72.64	122.93
I ₁₃₄₅₆	$I=0.75X1+1.832X3-0.001X4-0.193X5+2.213X6$	71.86	121.61
I ₂₃₄₅₆	$I=0.108X2+0.823X3+0.412X4+0.336X5+0.821X6$	13.85	23.44

Table 8 Selection indices, expected genetic gain and per cent relative efficiency (PRE) for possible combinations of six characters by using differential weight methods

Sr. No.	Equations	Genetic Gain	PRE
1	Equal weight (W1)		
I ₁₂₃₄₅₆	$I=0.893X1+0.615X2+3.282X3+0.207X4+0.163X5+1.877X6$	88.39	149.59
2	Simple correlation coefficients taken as weight (W2)		
I ₁₂₃₄₅₆	$I=0.764X1+0.225X2+1.947X3-0.093X4-0.162X5+2.144X6$	73.85	124.97
3	Genotypic correlation taken as weight (W3)		
I ₁₂₃₄₅₆	$I=0.791X1+0.298X2+2.226X3-0.118X4-0.127X5+2.135X6$	76.95	130.23

observed for number of rows per cob in all weight methods. Among the different characters under study, the highest per cent relative efficiency was observed (100) for grain yield per plant by all the methods. Grain yield per plant had equal PRE (100) in, equal weight, genotypic correlation coefficients and phenotypic correlation coefficients taken as weight because their weights were the same. In general the percent relative efficiency was higher in equal weight method as compared to other methods. This result in accordance with Al-Obaidy *et al.* (2015) in maize. Habib *et al.* (2007), Akteret *et al.* (2010), Anuradha & Rao (2015) and Chaudhary *et al.* (2017)

also found the similar result in rice

Expected genetic gain and relative efficiency (%) for combination of two characters

All possible combinations of two characters were used to construct selection indices using different weights (W1 to W3). Total 15 selection indices in each weight method were constructed and the indices with their per cent relative efficiency are given in Table 4.

The genetic gain for grain yield (single character) with equal weight method (59.0959) was considered as base and the efficiency was worked out for all

Table 9 Top three ranking selection indices in different weight methods with maize grain yield per plant

Combinations	Top Rank	Equal Wt.[W1]	GC Wt. [W2]	PC Wt. [W3]
Combinations of two characters	1	I_{12} (119.32)	I_{16} (112.94)	I_{16} (111.61)
	2	I_{16} (114.32)	I_{14} (108.84)	I_{14} (108.20)
	3	I_{14} (111.28)	I_{12} (106.04)	I_{12} (103.37)
Combinations of three characters	1	I_{126} (132.14)	I_{146} (121.19)	I_{146} (119.26)
	2	I_{124} (130.56)	I_{126} (118.54)	I_{126} (114.77)
	3	I_{146} (124.92)	I_{136} (115.15)	I_{136} (113.31)
Combinations of four characters	1	I_{1246} (142.91)	I_{1246} (126.90)	I_{1246} (122.50)
	2	I_{1236} (136.81)	I_{1346} (123.67)	I_{1346} (121.20)
	3	I_{1234} (135.79)	I_{1456} (121.69)	I_{1456} (119.66)
Combinations of five characters	1	I_{12346} (148.04)	I_{12346} (129.65)	I_{12346} (124.56)
	2	I_{12456} (144.44)	I_{12456} (127.46)	I_{12456} (122.93)
	3	I_{12356} (138.37)	I_{13456} (124.19)	I_{13456} (121.61)

Table 10 Rank correlations between different weight methods based on best selection index of respective weight methods including maize grain yield per plant

Weight	Equal wt.	GC Wt.	PC Wt.
Equal Wt.	1.0000**	0.9793**	0.9713**
GCWt.	0.9793**	1.0000**	0.9983**
PCWt.	0.9713**	0.9983**	1.0000**

selection indices of all possible combinations of six characters for different weights. PRE ranged between 6.40 (cob length and number of rows per cob) to 119.32 (Grain yield and cob height) for equal weight method, 3.30 (cob length and number of rows per cob) to 112.94 (grain yield and 100 kernel weight) for genotypic correlation weight method and 2.46 (cob length and number of rows per cob) to 111.61 (grain yield and 100 kernel weight) for phenotypic correlation weight method.

Expected genetic gain and relative efficiency (%) for combination of three characters

Out of six (biometrical characters) characters all possible combinations of three characters were taken at a time to construct selection indices using different weights. Total 20 indices consisting different combinations of characters were constructed. Different indices with their genetic gain and per cent relative efficiency for different weight method are given in Table 5.

The genetic gain for grain yield per plant (59.09) alone with equal weight method was used as base to workout per cent relative efficiency for all selection indices. Per cent relative efficiency ranged from

17.29 (cob length, number of rows per cob and 100 kernel weight) to 132.14 (Grain yield per plant, cob height and 100 kernel weight) for equal weight, 13.04 (cob length, number of grains per row and number of rows per cob) to 121.19 (grain yield per plant, number of grains per row and number of rows per cob) for genotypic correlation weight, 8.25 (cob height, cob length and number of rows per cob) to 119.26 (grain yield per plant, number of grains per row and 100 kernel weight) for phenotypic correlation.

Expected genetic gain and relative efficiency (%) for combination of four characters

There were fifteen different possible combinations of four characters and were used to selection indices with different weights. Selection indices, their genetic gain and their percent relative efficiency are given in Table 6.

The results revealed that PRE ranged from 28.76 (I3456) [cob length, number of grains per row, number of rows per cob and 100 kernel weight] to 142.91 (I1246) [Grain yield per plant, cob height, number of rows per cob and 100 kernel weight] for equal weight, 21.14 (I2356) [cob height, cob length, number of rows per cob and 100 kernel weight] to 126.90 (I1246) [Grain yield per plant, cob height, number of rows per cob and 100 kernel weight] for simple correlation, 15.51 (I2356) [cob height, cob length, number of rows per cob and 100 kernel weight] to 122.50 (I1246) [Grain yield per plant, cob height, number of rows per cob and 100 kernel weight] for phenotypic correlation.

It was reported that the higher per cent relative efficiency was observed in equal method as compared to the rest of the weight methods as the numerical value of weight was higher as compared to all methods. Index (I1246) gave highest PRE in equal weight (142.91), genotypic correlation as weight (126.90) and phenotypic correlation as weight gave (122.50).

Expected genetic gain and relative efficiency (%) for five characters

Out of six characters all possible combinations of five different characters were taken at a time to construct selection indices using different weight methods. Six different indices were constructed for each weight methods so total 18 indices were constructed using this method. Different indices with their genetic gain and per cent relative efficiency for different weight method are presented in Table 7. The genetic gain for grain yield per plant (59.09) alone with equal weight method was used as base to workout per cent

relative efficiency for all the selection indices.

Per cent relative efficiency ranged from 53.85 (I23456) [cob height, cob length, number of grains per row, number of rows per cob, 100 kernel weight] to 148.04 (I12346) [Grain yield per plant, cob height, cob length, number of grains per row and 100 kernel weight] for equal weight, 29.49 (I23456) [Grain yield per plant, cob height, cob length, number of grains per row and 100 kernel weight] to 129.65 (I12346) [Grain yield per plant, cob height, cob length, number of grains per row and 100 kernel weight] for genotypic correlation, 23.44 (I23456) [Grain yield per plant, cob height, cob length, number of grains per row and 100 kernel weight] to 124.56 (I12346) [Grain yield per plant, cob height, cob length, number of grains per row and 100 kernel weight] for phenotypic correlation

Expected genetic gain and relative efficiency (%) for six characters

Combinations of all six biometrical characters were used to construct selection indices using different weights. The selection indices with their per cent relative efficiency are presented in Table 8. The genetic gain for grain yield alone (59.09) with equal weight was considered as 100 PRE. Per cent relative efficiencies were 149.59, 130.23 and 125.00 to equal weight, genotypic correlation and phenotypic correlation, respectively.

Comparison of three ranking selection indices

The results presented in Table 9 showed that the selection index (I_{12346}), which was combination of grain yield per plant, cob height, cob length, number of grains per rows and 100 kernel weight possessed highest PRE for all the weight method. Thus, based on this results taking of equal weight method the per cent relative efficiency was highest and one can use equal weight (W_1) of characters for construction of selection indices to achieve higher genetic gain followed by genotypic correlation (W_2) and phenotypic correlation (W_3).

Selection score with rank for twenty one genotypes based on different indices

The index score values were worked out for all three weight methods in all genotypes with respect to 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 (Table 10) were positive and highly significant indicating agreement with all methods.

CONCLUSION

The selection index (I_{12348}), which was combination of grain yield per plant, cob height, cob length, number of grains per rows and 100 kernel weight possessed highest PRE for all weight methods. Thus, based on this results taking of equal weight method, the per cent relative efficiency was highest and one can use equal weight (W_1) of characters for construction of selection indices to achieve higher genetic gain followed by genotypic correlation (W_2) and phenotypic correlation (W_3).

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