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Discriminant function analysis for yield improvement in bread wheat (*Triticum aestivum* L.)

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Abstract
Wheat is a crop that is grown in a range of ecosystems and has a big importance globally. It is an important cool-climate cereal crop with a crucial role to play in the world's food and nutritional security. The polygenic system that controls yield is greatly influenced by environmental changes. Hence, choosing a plant simply based on its yield would often not be particularly reliable. The discriminant-function technique was used to construct selection indices in 102 genotypes of bread wheat (*Triticum aestivum* L.). Eight characters were employed to formulate selection indices between grain yield and its attributing characters. Ninety-two selection indices were made between these eight characters ranging from single character-based selection indices to eight character-based selection indices. Out of these eight characters, five were found to have significant positive correlation at both genotypic and phenotypic levels with grain yield and six characters were found to have positive direct effect on grain yield genotypically as well as phenotypically. The preferential use of numbers of productive tillers/plants, spike length, weight of spike, numbers of grains/spike, weight of grains/spike and biological yield/plant are suggested over grain yield alone for the effective and fruitful multiple character combinations based indirect selection for the desired yield improvement in wheat.

Keywords: Selection indices, discriminant-function, grain yield, wheat, traits

Introduction

Wheat (*Triticum aestivum* L.) is the third-largest cultivated crop species worldwide after maize and rice and is the second-largest consumer food crop after rice (Garcia-Ruiz *et al*., 2021; Tiwari *et al*., 2017) [12, 55]. It is the staple food for a large part of the world population (Grote *et al*., 2021) [15] including India (Yadav *et al*., 2021) [62]. Wheat is one of the major crops and occupies an essential position in agricultural production, providing around 20% of calories and protein in the human diet (Shewry and Hey, 2015) [44]. Global wheat production is approximately 761 Mt in 2020 (Guarin *et al*., 2022) [16]. In order to meet the expected global grain demand by 2050, wheat production must be improved continuously in the context of climate change (Del *et al*., 2016; Yadav *et al*., 2021) [8, 62].Wheat grain is considered primarily as a source of energy, but it also supplies protein and vitamins, mainly B vitamins. Wheat grain is also an important source of bioactive substances with health-promoting properties, such as dietary fiber which contains arabinoxylans, oligosaccharides, lignin, phytates, and a wide range of phenolic compounds (Gooding and Shewry, 2022) [14].

Several desired plant characteristics have been taken into consideration when choosing a genotype, with various traits receiving varying degrees of weight in the decision-making process (Regmi *et al.*, 2021; Popovic *et al.*, 2020; Muhammad *et al.*, 2021; Ahmed *et al.*, 2022; Tiwari *et al*., 2012; Bafra *et al*., 2017; Makwana *et al*., 2021; Asati *et al*., 2022; Mandloi *et al*., 2022; Tomar *et al*., 2022; Tripathi *et al*., 2022; Rajpoot *et al*., 2023; Yadav *et al*., 2023) [38, 31, 28, 1, 54, 4, 21, 3, 22, 56, 58, 36, 66]. The best strategy to take advantage of genetic linkages with numerous qualities that have substantial heritability is to build an index that includes information on all the traits linked to yield (Geyer *et al.,* 2022; Kumar *et al.,* 2019; Mishra *et al*., 2020; Rajpoot *et al*., 2020; Choudhary *et al*., 2021; Mishra *et al*., 2021; Mishra *et al*., 2022a; Sharma *et al*., 2021; Shyam *et al*., 2021; Shyam *et al*., 2022; Sharma *et al*., 2023) [13, 18, 24, 35, 7, 24, 25, 42, 47, 48, 43]. This suggests employing a selection index that appropriately weights each of the two or more characters to be considered. The variability in the environment has a significant impact on yield, which is controlled by a polygenic system (Brinton and Uauy, 2019; Yadav *et al*., 2005; Tripathi *et al*., 2015; Shyam *et al*., 2020; Pramanik *et al*., 2021; Verma *et al*., 2021; Mishra *et al*., 2022b; Mishra *et al*., 2022c; Yadav *et al*. 2022a;

Yadav *et al*. 2022b; Yadav *et al*. 2022c; Ningwal *et al*., 2023; Shrivastava *et al*., 2023) [6, 61, 57, 46, 31, 59, 26, 65, 63, 64, 65, 30, 45]. Because of this, selecting a plant solely based on its yield is frequently not particularly reliable. Most researchers appreciate the significance of the component approach to selecting breeding methods. An application of discriminant function developed by Fisher (1936) [11] and first applied by Smith (1936) [52] helps to identify important combinations of yield component useful for selection by formulating suitable selection indices. In order to inadvertently increase the yield in various crop plants, selection indices were developed to identify the most value genotype and the most compatible combinations of features.

The genetic advancement that can be made using selection index compared to the corresponding genetic gain that can be made using direct selection for grain yield alone is employed to determine the effect of selection index (Allard, 1960) [2]. The most common application of a selection index is the simultaneous selection of numerous features. For the enhancement of wheat, several researchers, including Siahpoosh *et al*. (2001) [49], Singh *et al*. (2003) [51] and Kemelew (2011) [17] employed selection index and discriminant function analysis. By using both direct and indirect selection of the various traits, plant breeders are more successful when using the index selection to encourage the anticipated genetic development (Smith *et al*., 1981; Weyhrich *et al*., 1998 [53, 60]. Many studies have been done so far in order to determine the factors influencing wheat growth and development and to disclose the relationship between yields and other related variables (Zhang *et al*., 2020; Farokhzadeh *et al*., 2020) [67, 9]. With the simultaneous inclusion of each character, the relative effectiveness of the subsequent index consistently increased. However, in practice, the plant breeder might be interested in maximum gain with applying minimum numbers of characters. So, in the present investigation, six traits *viz*., numbers of tillers/plant, spike length, weight of spike, numbers of grains/spike, weight of grains/spike and biological yield/plant have been considered for selection index that might be advantageously exploited in the wheat breeding programmes. Thus, the present study was conducted to determine discriminant analysis of morpho-physiological data to assess the efficiency of selection index in wheat.

Materials and Method

The experiment was conducted with 102 diverse advance breeding lines of wheat (*Triticum aestivum* L.) during *Rabi* 2018-2019 in a Randomized Block Design (RBD) with two replications at Research Farm, Department of Genetics & Plant Breeding, College of Agriculture, Rajmata Vijayaraje Scindia Agricultural University, Gwalior, M.P., India (Table 1). Each genotype was consisting of SPS (single plant selection) and advanced breeding lines were sown in2.5 m length with a spacing of 20 cm. The morpho- physiological observations on different characters were recorded from five competitive plants were selected randomly for each genotype in each replication and their averages were employed for statistical analysis.

Statically analysis

a. Discriminant function analysis

Characters of economics value like yield are highly influenced by non-heritable variation and therefore the expected genetic advance for any character has been found to be greater, when the selection pressure is applied with the help of discriminant function technique, than when it is directly on the observed characters**.** The phenotypic and genotypic variance and co-variance used to compute the correlation provide the basic for constructing the selection index. The following model suggested by Robinson *et al*. (1951) [3] was used through the set of simultaneous equation of selection indices and development of a require discriminant function.

$$b_1p_{11} + b_2p_{12} + b_3p_{13} + b_4p_{14} + b_5p_{15} = g_{15}$$

$$b_1p_{12} + b_2p_{22} + b_3p_{23} + b_4p_{24} + b_5p_{25} = g_{25}$$

$$b_1p_{13} + b_2p_{23} + b_3p_{33} + b_4p_{34} + b_5p_{35} = g_{35}$$

$$b_1p_{14} + b_2p_{24} + b_3p_{34} + b_4p_{44} + b_5p_{45} = g_{45}$$

$$b_1p_{15} + b_2p_{25} + b_3p_{35} + b_4p_{45} + b_5p_{55} = g_{55}$$

Where

1. p_{11}, p_{22}, p_{33}, p_{44} and p_{55} represent the estimate of phenotypic variance for the characters numbering x_1, x_2, x_3, x_4 and x_5 respectively.
2. P_{12}, p_{13}, p_{14}, p_{15} represent the phenotypic co-variances of the different combinations of x_1, x_2, x_3, x_4, and x_5 respectively.
3. g_{15}, g_{25}, g_{35}, g_{45}, g_{55} represent genotypic co-variance of x_1, x_2, x_3, x_4, x_5 (grain yield) and g_{55} represents genotypic variance of character x_5 (grain yield).

The 'b' values computed from the above formulas indicated the phenotypic weights to be assigned to each of the various characters considered in selection indices. These obtained 'b' values were used for the construction of selection index in the following formulas.

$$Z = b_1x_1 + b_2x_2 + b_3x_3 \ldots\ldots + b_nx_n$$

Where

Z = Selection index

X_1, X_2, X_3 ………X_n represents the phenotypic values of n traits

b_1, b_2, b_3, ……. b_n represents phenotypic weights assigned to each of the n characters.

In such a way election indices were constructed for one character, two characters, three characters, four characters, five, six, seven and eight characters.

b. Expected genotypic advance (EGA) of selection index

The expected genotypic advance from several selection indexes was estimated by the following formulas suggested by Robinson *et al*. (1951) [3].

$$EGA = \frac{Z}{P}\sqrt{b_1g_1y + b_2g_2y + b_3g_3y \ldots\ldots + b_ng_ny}$$

Where

$\frac{Z}{P}$ = K, represents selection differential in standard units. Its value being 2.06 at 5% intensity of selection.

b_1, b_2, b_3 ……… b_n, represents phenotypic weight of corresponding n characters in the selection indices.

g_1y, g_2y, g_3y …….g_ny, represents genotypic co-variance of n characters with the depended character which is grain yield and g_{ny} represent genotypic variance.

c. Relative efficiency of selection indices as compared to the straight selection for yield

Relative efficiency of selection index was computed by comparing its expected genetic advance with expected genetic advance for yield and it is always expressed in percentage. The efficiency of selection for yield is assumed to be 100 percent and used as a basis for comparison of relative efficiency from use of various selection indices (Robinson *et al.*, 1951) [3].

Construction of selection indices, the character with higher and significant genetic correlation coefficient and sizable direct effect on grain yield were considered. In this context, eight characters *viz*. numbers of productive tillers/plant (X_5), spike length (X_6), weight of spike (X_7), number of grains/spike (X_8), weight of grains/spike (X_9), biological yield/plant (X_{10}), harvest index (X_{11}) and grain yield/plant (X_{12}) were employed to formulate selection indices between grain yield and its attributing traits. The selection indices were constructed with various character combinations as per method suggested by Robinson *et al.* (1951) [3]. Ninety-two selection indices were made between these eight characters ranging from single character-based selection indices to eight character-based selection indices. Their respective genetic advance was calculated as per the formula suggested by Robinson *et al.* (1951) [3] and relative efficiency of different discriminant functions in relation to straight selection for grain yield was assessed and compared, assuming the efficiency of selection for seed yield as 100%.

Results and Discussion

The selection for a single trait is not anticipated to adequately explain the genotypic variance for grain yield because grain yield is a quantitative character and the result of numerous qualities that contribute to yield. So, when two or more single trait-based selection indices are combined, the projected genetic progress and the selection efficiency of the resulting selection index are superior than utilising each of the single traits separately. The use of selection indices is more effective than direct selection for grain yield alone, and the estimation of the best possible trait combinations depends on the identification of easily measurably traits with greater precision under both field and laboratory conditions, as well as over the possible estimation of genotypic and phenotypic variances and covariance parameters for the optimisation of any selection index. Any selection index must have accurate estimates of variance and covariance that are specific to the breeding populations, season, and location in order to be reliable.

The cumulative influence of two or more correlated and co-heritable yield components determines whether any selection index is successful in predicting outcomes. This means that the direction and strength of the correlation between the traits utilized in the selection index and grain yield will determine how far one or more qualities in the selection index are employed for indirect selection. Hence, the ineffectiveness of the selection based on single variables may be related to poor genetic correlation coefficients, heritability, or both of each trait with grain yield. The negative correlation between the characteristics and grain yield accounts for the reduction in grain yield caused by the adoption of selection index. Which, when such features are combined, results in a negative correlated response.

Eight characters *viz.*, numbers of productive tillers/plant, spike length, weight of spike, numbers of grains/spike, weight of grains/spike, biological yield/plant, harvest index and grain yield/plant were employed to formulate selection indices between grain yield and its attributing characters. Out of these eight characters, five were found to have significant positive correlation at both genotypic and phenotypic levels with grain yield and six characters were found to have positive direct effect on grain yield genotypically as well as phenotypically. Ninety-two selection indices were made between these eight characters ranging from single character-based selection indices to eight character-based selection index and presented in Table 2.

To determine the characteristic combinations that contribute the most to the effectiveness of any selection index, each component trait was optimally analysed. To evaluate the relative selection efficacy of single character-based selection indices, grain yield and other selection indices built with all feasible combinations of yield-contributing features were evaluated. According to Roy *et al.* (2017) [40], selection based on the quantity of spikelets per panicle improved grain yield more effectively. All the indices that also displayed high heritability, high GCV, and a direct impact on grain yield per plant were shown to be essential for this trait. The most effective selection indices for improving grain yield were growth rate, spikelets per panicle, and grain yield since they combined the relative efficacy of selection and genetic advancement. The highest genetic progress and selection efficiency for direct selection were seen for grain yield among the single character-based selection indices, with values of 6.50 and 100%, respectively. Raiyani *et al.* (2015) [33] and Raghuwanshi *et al.* (2015) [34] also suggested that the efficiency of selection increased with the inclusion of a greater numbers of characters in the index. However, in case of two character-based selection indices, the genetic advance and selection efficiency increased up to 8.87 and 136.50% respectively for the selection index based on numbers of grains/spike + biological yield/plant. In this case the genetic advance and the selection efficiency increased upon the increase in the numbers of traits from one to two. In case of three, four, five and six characters-based selection indices the expected genetic advance and selection efficiency increased up to 8.87 and 136.50% respectively, indicating that the inclusion of more characters. While, constructing selection indices resulted in an overall enhancement of relative selection efficiency as well the genetic advance and hence the use of multiple traits combinations in the form of selection indices is preferred for effective indirect selection over the direct selection based on grain yield. Bergale *et al.* (2002) [5] also suggested that the numbers of spikes per plant, grainper spike and harvest index must be given preferencein selection along with optimum plant height and days to flowering to select the superior wheat genotypes. Singh *et al.* (2015) [50] advised that the plant height, numbers of tillers per plant, numbers of sparklets per paniclea long with grain yield per plant are useful to select the superior rice genotypes. Fredous *et al.* (2010) [10], Kemelew (2011) [17] and Shah *et al.* (2016) [41] were similarly with the opinion that an increase in characteristics resulted in an increase in genetic gain and that the selection indices improve the efficiency than the straight selection for grain yield per plant.

The preferred character combination over grain yield alone on the basis of present investigation are X9X11 (numbers of grains/spike + biological yield/plant) in case of two characters based selection indices, X7X9X11 (weight of spike + numbers of grains/spike + biological yield/plant) and X9X10X11 (numbers of grains/spike + weight of grains/spike + biological yield/plant) in case of three traits based selection indices, X6X7X9X11 (spike length + weight of spike + numbers of grains/spike + biological yield/plant) and X7X9X10X11 (weight of spike + numbers of grains/spike + weight of grains/spike + biological yield/plant) in case of four characters depended selection indices, X5X6X7X9X11 (numbers of productive tillers/plant + spike length + weight of spike + numbers of grains/spike + biological yield/plant) and X6X7X9X10X11 (spike length + weight of spike + numbers of grains/spike + weight of grains/spike + biological yield/plant) in case of five characters founded selection indices, X5X6X7X9X10X11 (numbers of productive tillers/plant + spike length + weight of spike + numbers of grains/spike + weight of grains/spike + biological yield/plant) and in case of six parameters depended selection index. So, the preferential use of numbers of productive tillers/plant, spike length, weight of spike, numbers of grains/spike, weight of grains/spike and biological yield/plant is suggested over grain yield alone for the effective and fruitful multiple characters combinations based indirect selection for the desired yield improvement in wheat (Table 2). Findings of the present study are in confirmation with the outcome of the research work done by Kemelew *et al.* (2011) [17], Rathod *et al.* (2013) [37], Raiyani *et al.* (2015) [33], Kumar *et al.* (2016) [19] and Nikita *et al.* (2018) [29].

The preferred characters for fabricating selection indices based on the present study were numbers of tillers/plant, spike length, weight of spike, numbers of grains/spike, weight of grains/spike and biological yield/plant that could be further employed for increasing grain yield in wheat.

Table 1: Detail of experimental material with their parentage / source used in present investigation

Advance Line No.	Pedigree	Advance Line No.	Pedigree
1	PW635 X (DSP-4/RAJ1555)	52	CW38 X UAS295
2	C306 X PHS 1104	53	DD-11-1353
3	C306 X (DSP-4/RAJ1555)	54	DD-11-1382
4	AKAW 4731 X SAWSN 3029	55	DDS-12-1419
5	DL803-3 X RAJ-1555D	56	DDS-12-1427
6	MACS6222 X GW173	57	DDS-12-1428
7	GW190 X HD 2932	58	DDS-12-1460
8	GW322 X RAJ1555	59	DDS-12-1461
9	DDS-14-1594	60	DDS12-1468
10	DDS-14-1603	61	DDS12-1470
11	DDS-14-1604	62	DDS-12-1475
12	DDS-14-1610	63	DDS-12-1480
13	DDS-14-1633	64	HPW-296 X SONALIKA
14	DDS-14-1641	65	RAJ4185 X LOK-1
15	DDS-14-1644	66	RAJ4188 X HW5205
16	DDS-14-1602	67	RAJ4188 X HW5205
17	DDS-14-1603	68	GW1244 X 994444/VL-998
18	DDS1-4-1606	69	VL 922 X MP 4010
19	DDS-14-1608	70	VL 907 / PHS 1103
20	DDS-14-1608	71	VL 907 / PHS 1103
21	DDS-14-1610	72	VL 907 / PHS 1103
22	DDS-14-1614	73	VL 907 / PHS 1103
23	DDS-14-1614	74	VL 907 / PHS 1103
24	DDS-14-1614	75	VL 907 / PHS 1103
25	DDS-14-1614	76	PW 612 / MP 4010
26	DDS-14-1614	77	GW 2007-77 (D) / MP 4010
27	DDS-14-1615	78	GW 2007-77 (D) / MP 4010
28	DDS1-4-1619	79	SBWON-17-0084
29	DDS-14-1619	80	SBWON-17-0118
30	DDS-14-1635	81	SBWON-17-0119
31	DDS-14-1635	82	SBWON-17-0121
32	DDS-14-1637	83	3rd SAWYT 304
33	DDS-14-1637	84	23rd SAWYT 340
34	DDS-14-1637	85	33th SAWSN 3190
35	DDS-14-1637	86	33th SAWSN 3020
36	DDS-14-1640	87	33th SAWSN 3080
37	DDS-14-1640	88	48th IBWSN 1299
38	DDS-14-1641	89	7th HLBSN 25
39	DDS-14-1641	90	DWAP 1532
40	DDS-14-1641	91	LOK 1
41	DDS-14-1644	92	DWAP 1538
42	DDS-14-1646	93	GW 2014-580

Advance Line No.	Pedigree	Advance Line No.	Pedigree
43	DDS-14-1646	94	HI 1609
44	DDS-14-1650	95	RAJ 4478
45	DDS-14-1652	96	UP 2971(UP2762/2572)
46	DDS-14-1652	97	HUW661(Sr9+11+Lr10+13+YrA+K)
47	DDS-14-1658	98	GW 455(Sr7 +Yr2)
48	DDS-14-1659	99	HUW 661 (Sr30+Lr1+2a+10+23+Yr2+L+K)
49	DDS-14-1659	100	HI 1605(TS-IR-CZ)
50	DDS-14-1659	101	KRL 77-1(K Resistance)
51	DDS-14-1660	102	RAJ 4188XHW5205

Table 2: Selection indices for grain yield, their discriminant functions, expected genetic advance and relative efficiency in wheat genotypes

Selection index	Discriminant function	EGA	SE (%)
X5 (Numbers of tillers)	1.510X5	3.66	56.31
X6 (Spike length)	0.432X6	1.02	15.75
X7 (Weight of spike)	1.196X7	1.74	26.86
X9 (Numbers of grains per spike)	0.071X9	1.69	29.10
X10 (Weight of grains per spike)	1.462X10	1.89	29.16
X11 (Biological yield per plant)	0.149X11	3.54	54.54
X12 (Harvest index)	0.055X12	2.55	39.23
X14 (Grain yield per plant)	0.915X14	6.50	100
X5.X6	1.508X5 + 0.425X6	3.57	55.64
X5.X7	1.533X5 + 1.953X7	4.18	64.43
X5.X9	0.326X5 + 0.997X9	6.48	99.70
X5.X10	1.495 X5 + 1.410X10	3.92	60.45
X5.X11	1.073X5 + 0.104X11	4.09	63.05
X5.X12	1.566X5 + 0.101X12	3.61	55.68
X5.X14	-0.031X5 + 0.921X14	6.21	95.66
X6.X7	0.143X6 + 1.104X7	1.82	28.03
X6.X9	0.135X6 + 0.066X9	6.48	99.70
X6.X10	0.135X6 + 01.366X10	1.91	29.52
X6.X11	0.160X6 +0.146X11	3.44	53.07
X6.X12	0.416X6 +0.047X12	1.11	17.20
X6.X14	0.027X6 + 0.913X14	6.21	95.66
X7.X9	0.800X7 +0.044X9	4.23	65.20
X7.X10	0.161X7 +1.28X10	1.89	29.21
X7.X11	0.758X7 +0.139X11	3.60	55.48
X7.X12	1.218X7 +0.065X12	1.91	29.39
X7.X14	0.173X7 +0.904X14	0.59	8.76
X9.X10	0.041X9 +1.045X10	1.56	24.13
X9.X11	1.765X9 +64.299X11	8.87	136.50
X9.X12	0.073X9 +0.067X12	2.35	36.25
X9.X14	0.009X9 +0.905X14	6.21	95.66
X10.X11	0.903X10 +0.137X11	3.61	55.61
X10.X12	1.489X10 +0.066X12	2.00	30.90
X10.X14	0.138X10 +0.907X14	0.573	8.82
X11.X12	0.150X11 +0.067X12	3.49	53.77
X11.X14	0.004X11 +0.905X14	5.94	92.52
X12.X14	0.010X12 +0.913X14	5.62	91.52
X5.X6.X7	1.523X5 +0.121X6 +1.160X7	3.95	60.78
X5.X6.X9	1.153X5 +0.213X6 +0.047X9	6.48	99.70
X5.X6.X10	1.495X5 +0.140X6 +1.312X10	3.94	60.63
X5.X6.X11	1.096X5 +0.244X6 +0.098X11	4.13	63.63
X5.X6.X12	1.559X5 +0.392X6 +0.093X12	3.73	57.43
X5.X6.X14	0.028X5 +0.025X6 +0.919X14	5.94	91.52
X6.X7.X9	0.031X6 +0.789X7 +0.043X9	6.48	99.70
X6.X7.X10	0.132X6 +0.096X7 +1.265X10	1.91	29.54
X6.X7.X11	-0.0299X6 +0.776X7 +0.139X11	3.60	55.49
X6.X7.X12	0.110X6 +1.147X7 +0.062X12	1.92	29.61
X6.X7.X14	-0.016X6 +0.183X7 +0.904X14	5.95	91.59
X7.X9.X10	-0.137X7 +0.042X9 +1.185X10	1.56	24.13
X7.X9.X11	0.460X7 +0.034X9 +0.137X11	8.87	136.50
X7.X9.X12	0.812X7 +0.045X9 +0.069X12	2.35	36.25
X7.X9.X14	0.124X7 +0.005X9 +0.902X14	6.21	95.66
X9.X10.X11	0.033X9 +0.575X10 +0.135X11	8.87	136.50

Selection index	Discriminant function	EGA	SE (%)
X9.X10.X12	0.043X9 +1.060X10 +0.070X12	2.35	36.25
X9.X10.X14	0.008X9 +0.061X10 +0.903X11	6.21	95.66
X10.X11.X12	0.930X10 +0.138X11 +0.073X12	3.68	56.72
X10.X11.X14	0.113X10 +0.016X11 +0.877X14	5.96	91.69
X11.X12.X14	0.005X11 +0.011X12 +0.902X14	5.95	91.54
X5.X6.X7.X9	1.502X5 +0.078X6 +1.038X7 +0.016X9	6.48	99.70
X5.X6.X7.X10	1.512X5 +0.116X6 +0.709X7 +0.564X10	3.96	60.63
X5.X6.X7.X11	1.153X5 +0.018X6 +0.939X7 +0.087X11	4.32	66.56
X5.X6.X7.X12	1.585X5 +0.062X6 +1.238X7 +0.110X12	4.09	63.03
X5.X6.X7.X14	-0.002X5 + -0.016X6 +0.182X7 +0.905X14	5.95	91.53
X6.X7X.X9.X10	0.024X6 +-0.144X7 +0.041X9 +1.183X10	1.56	24.13
X6.X7.X9.X11	-0.126X6 +0.504X7 +0.037X9 +0.138X11	8.87	136.50
X6.X7.X9.X12	-0.012X6 +0.816X7 +0.046X9 +0.069X12	2.35	36.25
X6.X7.X9.X14	0.033X6 +0.137X7 +0.006X9 +0.902X14	6.21	95.66
X7.X9.X10.X11	0.045X7 +0.033X9 +0.528X10 +0.136X11	8.87	136.50
X7.X9.X10.X12	0.541X7 + -0.053X9 +1.434X10 +0.061X12	2.35	36.25
X7.X9.X10.X14	1.100X7 + -0.093X9 + -0.181X10 +0.947X14	6.21	95.66
X9.X10.X11.X12	0.035X9 +0.589X10 +0.136X11 +0.075X12	2.35	36.25
X9.X10.X11.X14	0.008X9 +0.056X10 +0.004X11 +0.895X14	6.21	95.66
X10.X11.X12.X14	0.140X10 +0.004X11 +0.012X12 +0.896X14	5.95	91.58
X5.X6.X7.X9.X10	1.492X5 +0.075X6 +0.609X7 +0.016X9 +0.542X10	1.56	24.13
X5.X6.X7.X9.X11	-0.128X5 +0.084X6 +0.037X7 +0.536X9 +0.137X11	8.87	136.50
X5.X6.X7.X9.X12	1.561X5 +0.009X6 +1.093X7 +0.019X9 +0.112X12	4.11	63.30
X5.X6.X7.X9.X14	-0.009X5 + -0.033X6 +0.134X7 +0.006X9 +0.904X14	6.21	95.66
X6.X7.X9.X10.X11	-0.651X6 + -125.376X7 +0.139X9 +160.487X10 + -0.209X11	8.87	136.50
X6.X7.X9.X10.X12	-0.020X6 + -0.133X7 +0.044X9 +1.20X10 +0.070X12	2.35	36.25
X6.X7.X9.X10.X14	-0.031X6 +0.403X7 +0.006X9 +-0.341X10 +0.905X14	6.21	95.66
X7.X9.X10.X11.X12	0.043X7 +0.035X9 +0.544X10 +0.136X11+0.075X12	2.35	36.25
X7.X9.X10.X11.X14	0.395X7 +0.006X9 + -0.351X10 +0.004X11 +0.897X14	6.21	95.66
X9.X10.X11.X12.X14	0.008X9 +0.060X10 + -0.004X11 +0.013X12 +0.892X14	6.21	95.66
X5.X6.X7.X9.X10.X11	1.122X5+-0.034X6+0.568X7+0.019X9 +0.286X10 +0.087X12	8.87	136.50
X5.X6.X7.X9.X10.X12	1.550X5+0.005X6+0.655X7 +0.019X9 +0.553X10 +0.112X12	2.35	36.25
X5.X6.X7.X9.X10.X14	-0.007X5+-0.031X6+0.400X7+0.007X9+-0.340X10 +0.907X14	6.21	95.66
X6.X7.X9.X10.X11.X12	-0.180X6+0.098X7+0.040X9+0.556X10+0.138X11+0.080X12	2.35	36.25
X6.X7.X9.X10.X11.X14	-0.036X6+0.406X7+0.007X9+-0.348X10+0.004X11+0.896X14	6.21	95.66
X7.X9.X10.X11.X12.X14	0.393X7+0.006X9+-0.344X10+0.004X11+0.013X12+0.893X14	6.21	95.66
X5.X6.X7.X9.X10.X11.X12	1.183X5+-0.1016X6+0.614X7+0.022X9+0.300X10+0.086X11+0.109X12	2.35	36.25
X5.X6.X7.X9.X10.X11.X14	-0.016X5 + -0.037X6 +0.400X7 +0.007X9 + -0.347X10 +0.005X11 +0.899X14	6.21	95.66
X6.X7.X9.X10.X11.X12.X14	-0.046X6 +0.407X7 +0.007X9 + -0.340X10 +0.005X11 +0.014X12 +0.892X14	6.21	95.66
X5.X6.X7.X9.X10.X11.X12.X14	0.001X5 + -0.046X6 +0.407X7 +0.007X8 + -0.340X9 + 0.005X10 + 0.014X11 + 0.892X12	6.21	95.66

Conclusion

Comparing various selection indices can only be done in practice; using computed criteria to compare them is only theoretical since these indices only evaluate expected results. Application of these indices is therefore required to validate the outcomes. The present study showed consistent increase in the relative efficiency of the succeeding index with simultaneous inclusion of each character. Therefore, improvements of grain yield through these selection indices are suggested. However, in practice, the plant breeder might be interested in maximum gain with inclusion of minimum number of characters. The preferred characters for fabricating selection indices were numbers of tillers/plant, spike length, weight of spike, numbers of grains/spike, weight of grains/spike and biological yield/plant as they could be advantageously exploited in the wheat breeding programmes. The present study also revealed that the discriminant function method of making selection in plant appears to be the most useful than the straight selection for grain yield alone and hence, due weightage should be given to the important selection indices while making selection for grain yield advancement in wheat breeding programme.

References

1. Ahmed HGM, Zeng Y, Raza H, Muhammad D, Iqbal M, Uzair M, *et al*. Characterization of wheat (*Triticum aestivum* L.) accessions using morpho-physiological traits under varying levels of salinity stress at seedling stage. Frontiers in Plant Science. 2022;13:953670.
2. Allard RW. Principles of Plant Breeding. J. Wiely, New York. 1960. p. 95-115.
3. Asati R, Tripathi MK, Tiwari S, Yadav RK, Tripathi N. Molecular breeding and droughttolerance in chickpea. Life. 2022;12:1846. https://doi.org/10.3390/life12111846
4. Barfa D, Tripathi MK, Kandalkar VS, Gupta JC, Kumar G. Heterosis and combining ability analysis for seed yield in Indian mustard [Brassica Juncea (L) Czern& Coss]. 2017. p. 75-83.
5. Bergale S, Billore M, Holkar AS, Ruwali KN, Prasad SVS. Pattern of variability, character association and path analysis in wheat (*Triticum aestivum* L.). Agril. Sci. Digest. 2002;22(4):258-260.
6. Brinton J, Uauy C. A reductionist approach to dissecting grain weight and yield in wheat. Journal of integrative plant biology. 2019;61(3):337–358.

7. Choudhary ML, Tripathi K, Tiwari S, Pandya RK, Gupta N, Tripathi N, *et al*. Screening of pearl millet [Pennisetum glaucum (L.) R. Br.] germplasm lines for drought tolerance based on morpho-physiological traits and SSR markers. Current J of Applied Sci. and Tech. 2021;40:46-63.
8. Del PA, Yáñez A, Matus IA, Tapia G, Castillo D, Sanchez-JL, *et al*. Physiological traits associated with wheat yield potential and performance under water-stress in a Mediterranean environment. Front. Plant Sci. 2016;7:987.
9. Farokhzadeh S, Shahsavand-Hassani H, Zinati Z, Rajaei M. Evaluation of triticale lines compared to wheat cultivars in terms of agronomic traits using supervised learning methods and multivariate statistics. Philipp Agric Sci. 2022;105(4):369-389.
10. Ferdous MF, Shamsuddin AKM, Hasna D, Bhuiyan MMR. Study on relationship and selection index for yield and yield contributing characters in spring wheat. J Bangladesh Agril. Univ. 2010;8:191-194.
11. Fisher RA. The use of multiple measurements in taxonomic problems. Ann. Eugen. 1936;7:179.
12. Garcia-Ruiz H, Szurek B, Van den Ackerveken G. Stop helping pathogens: engineering plant susceptibility genes for durable resistance. Curr. Opin. Biotechnol. 2021;70:187-195.
13. Geyer M, Mohler V, Hartl L. Genetics of the Inverse Relationship between Grain Yield and Grain Protein Content in Common Wheat. Plants (Basel, Switzerland). 2022;11(16):2146.
14. Gooding MJ, Shewry PR. Wheat: environment Food and Health, Wiley. 2022. DOI:10.1002/9781119652601.
15. Grote U, Fasse A, Nguyen TT, Erenstein O. Food Security and the Dynamics of Wheat and Maize Value Chains in Africa and Asia. Front. Sustain. Food Syst. 2021;4:617009. doi: 10.3389/fsufs.2020.617009.
16. Guarin JR, Martre P, Ewert F, Webber H, Dueri S, Calderini D, *et al*. Evidence for increasing global wheat yield potential. Environ. Res. Lett. 2022;17:124045.
17. Kemelew M. Selection index in durum wheat (Triticum turgidum var. durum) variety development. Academic J Pl. Sci. 2011;4:77-83.
18. Kumar A, Mantovani EE, Simsek S, Jain S, Elias EM, Mergoum M. Genome wide genetic dissection of wheat quality and yield related traits and their relationship with grain shape and size traits in an elite × non-adapted bread wheat cross. PloS one. 2019;14(9):e0221826.
19. Kumar MA, Indu, Monpara BA, Raghuwanshi SS. Selection Indices for Yield improvement in bread wheat (*Triticum aestivum* L.). Journal of Pure and Applied Microbiology. 2016;10(4);2801-2805.
20. Lan Y, Chawade A, Kuktaite R, Johansson E. Climate Change Impact on Wheat Performance-Effects on Vigour, Plant Traits and Yield from Early and Late Drought Stress in Diverse Lines. International Journal of molecular sciences. 2022;23(6):3333.
21. Makwana K, Tiwari S, Tripathi MK, Sharma AK, Pandya RK, Singh AK. Morphological characterization and DNA finger printing of pearl millet (Pennisetum Glaucum (L.) germplasms. Range Management and Agroforestry. 2021;42(2):205-211.
22. Mandloi S, Tripathi MK, Tiwari S, Tripathi N. Genetic diversity analysis among late leaf spot and rust resistant and susceptible germplasm in groundnut (*Arachis hypogea* L.). Isr. J Plant Sci. 2022. doi: https://doi.org/10.1163/22238980-bja10058.
23. Mishra N, Tripathi MK, Tiwari S, Tripathi N, Trivedi HK. Morphological and Molecular Screening of Soybean Genotypes against yellow mosaic virus disease. Legume Research. DOI:10.18805/LR-4240
24. Mishra N, Tripathi MK, Tiwari S, Tripathi N,Gupta N, Sharma A. Morphological and physiological performance of Indian soybean [*Glycine max* (L.) Merrill] genotypes in respect to drought. Legume Research an International Journal. 2021. DOI: 10.18805/LR-4550
25. Mishra N, Tripathi MK, Tiwari S, Tripathi N, Sikarwar RS. Evaluation of qualitative trait based variability among soybean genotypes. The Pharma Innovation. 2022a;11(9):1115-1121.
26. Mishra N, Tripathi MK, Tripathi N, Tiwari S, Gupta N, Sharma A. Screening of soybean genotypes against drought on the basis of gene-linked microsatellite markers. In book: Innovations in Science and Technology. 2022b;3:49-61. DOI: 10.9734/bpi/ist/v3/2454C
27. Mishra N, Tripathi MK, Tiwari S, Tripathi N, Gupta N, Sharma A, *et al*. Characterization of soybean genotypes on the basis of yield attributing traits and SSR molecular markers.In book: Innovations in Science and Technology. 2022c;3:87-106. DOI: 10.9734/bpi/ist/v3/2471C
28. Muhammad A, Li J, Hu W, Yu J, Khan SU, Khan MHU, *et al*. Uncovering genomic regions controlling plant architectural traits in hexaploid wheat using different GWAS models. Scientific reports. 2021;11(1):6767.
29. Nikita S, Raval LJ, Shah SH. Selection Indices in Bread Wheat (*Triticum aestivum* L.) Under Very Late Sown Condition: International Journal of Pure and Applied Biosciences. 2018;6(5):426-429.
30. Ningwal R, Tripathi MK, Tiwari S, Yadav RK, Tripathi N, Solanki RS, *et al*. Assessment of genetic variability, correlation and path coefficient analysis for yield and its attributing traits in chickpea (*Cicer arietinum* L.) The Pharma Innovation Journal. 2023;12(3):4851-4859
31. Popović V, Ljubičić N, Kostić M, Radulović M, Blagojević D, Ugrenović V, Popović D, Ivošević B. Genotype × Environment Interaction for Wheat Yield Traits Suitable for Selection in Different Seed Priming Conditions. Plants. 2020;9(12):1804.
32. Pramanik A, Tiwari S, Tripathi MK, Mandloi S, Tomar RS. Identification of groundnut germplasm lines for foliar disease resistance and high oleic traits using SNP and gene-based markers and their morphological characterization. Legume Research. 2021. DOI: 10.18805/LR-4666
33. Raiyani GD, Patel Komal, Javia RM, Bhatiya VJ, Ramani VV. Selection indices for yield improvement in bread wheat under late sown condition, Asian Journal of Bio Science. 2015;10(2):148-152.
34. Raghuwanshi SS, Kachadia VH, Vachhani JH, Jivani LL, Malav Kumar A, Singh BS. Selection indices in groundnut (*Arachis hypogaea* L.): Electronic Journal of Plant Breeding. 2015 Sep;6(2):140-44.
35. Rajpoot NS, Tripathi MK, Tiwari S, Tomar RS, Kandalkar VS. Characterization of Indian mustard germplasm on the basis of morphological traits and SSR markers. Curr J Appl Sci Technol. 2020;39:300-311.

36. Rajpoot P, Tripathi MK, Solanki RS, Tiwari S, Tripathi N, Chauhan S, *et al*. Genetic variability and multivariate analysis in pearl millet (*Pennisetum glaucum* (L.) R. Br.) germplasm lines. The Pharma Innovation Journal. 2023;12(4):216-226.
37. Rathod VB, Mehta DR, Solanki HV, Raval LJ. Selection Indices in Indian Mustard (*Brassica juncea* (L.): Electronic Journal of Plant Breeding. 2013;4(4):1344-1347.
38. Regmi S, Poudel B, Ojha BR, Kharel R, Joshi P, Khanal S, *et al*. Estimation of Genetic Parameters of Different Wheat Genotype Traits in Chitwan, Nepal. International Journal of Agronomy. 2021. Article ID 6651325
39. Robinson HF, Comstock RE, Harvey PH. Genotypic and phenotypic correlation in corn and their implication in selection. Agron. J. 1951;43:282-287.
40. Roy C, Verma JS. Identification of morphological traits using Smith index for grain yield improvement in oat (*Avena sativa* L.), Agricultural Research Journal. 2017;54(1):11-15.
41. Shah S, Mehta DR, Raval LJ. Selection indices in bread wheat (*Triticum aestivum* L.). Electronic J Plant Breed. 2016;7:459-463.
42. Sharma A, Tripathi MK, Tiwari S, Gupta N, Tripathi N, Mishra N. Evaluation of soybean (*Glycine max* L.) genotypes on the basis of biochemical contents and anti-oxidant enzyme activities. Legume Res. 2021;44:LR-467.
43. Sharma A, Mishra N, Tripathi N, Nehra S, Singh J, Tiwari S, *et al*. Qualitative trait based variability among soybean genotypes. Acta Scientific Agriculture. 2023;7(1):02-13.
44. Shewry PR, Hey SJ. The contribution of wheat to human diet and health. Food and energy security. 2015;4(3):178–202.
45. Shrivastava A, Tripathi MK, Solanki RS, Tiwari S, Tripathi N, Singh J, *et al*. Genetic Correlation and Path Coefficient Analysis of Yield Attributing Parameters in Indian Mustard. Current Journal of Applied Science and Technology. 2023;42(7):42-58. DOI: 10.9734/CJAST/2023/v42i74079
46. Shyam C, Tripathi MK, Tiwari S, Tripathi N, Ahuja A. Molecular characterization and identification of Brassica genotype(s) for low and high erucicacidcontent using SSR markers. Global J Bio sci Biotechnol. 2020;9(2):56-66.
47. Shyam C, Tripathi MK, Tiwari S, Tripathi N. Genetic components, and diversity analysis inIndian mustard [Brassica juncea (Linn.) Czern &Coss] based on different morpho-physiological traits. Current Journal of Applied Science and Technology. 2021;40(20):34-57. DOI: 10.9734/CJAST/2021/v40i2031462
48. Shyam C, Tripathi MK, Tiwari S, Tripathi N, Sikarwar RS. Morpho-physiological variations and genetic components analysis in Brassica juncea (Linn.) Czern& Coss. In book: Research Developments in Science and Technology. 2022;1:98-126. DOI: 10.9734/bpi/rdst/v1/6009F
49. Siahpoosh MR, Assad MT, Emam Y, Saidi A. Implication of four selection indices in wheat cultivar (*Triticumaestivum* L.) for increasing the grain yield. Ind. J Genet. 2001;32:219-236.
50. Singh RS, Kachadia VH, Vachhani JH, Jivani LL, Malav AK, *et al*. Selection indices in groundnut (*Arachis hypogaea* L.): Electronic Journal of Plant Breeding. 2015;6(2):140-44.
51. Singh T, Balyan HS. Relative efficiency of various single plant selection criteria and F3 generation yield testing in wheat (*Triticum aestivum* L.). Ind. J Genet. 2003;63:24-29.
52. Smith HF. A discriminant function for plant selection. Ann. Eugen. 1936;7:240-250.
53. Smith OS, Hallauer AR, Russel WA. Use of index selection in recurrent selection programs in maize. Euphytica. 1981;20:611-618.
54. Tiwari S, Tripathi MK, Kumar S. Improvement of soybean through plant tissue culture and genetic transformation: A review. JNKVV Res. J. 2012;45(1):1-18.
55. Tiwari S, Tomar RS, Chand SC, Tripathi MK, Singh AK, Tomar SMS. Molecular breeding approaches for improving rust resistance in wheat: (*Triticum aestivum* L.): marker assisted gene pyramiding. Indian Res. J. Genet. & Biotech. 2017 Aug;9(3):382-396.
56. Tomar YS, Tiwari S, Tripathi MK, Solanki RS. Genetic diversity assessment and cluster analysis of morphological yield attributing traits of groundnut (*Arachis hypogaea* L. The Pharma Innovation Journal. 2022;11(6):1444-1450
57. Tripathi MK, Tomar SS, Tiwari VK, Awasthi D, Gupta JC. Heterosis in Indian mustard [*Brassica juncea* (L) Czern and Coss]. Prog. Res. 2015;10(4):3376-3379.
58. Tripathi N, Tripathi MK, Tiwari S, Payasi DK. Molecular breeding to overcomebiotic stresses in soybean: Update. Plants (Basel). 2022 Jul 28;11(15):1967.
59. Verma K, Tripathi MK, Tiwari S, Tripathi N. Analysis of genetic diversity among Brassica juncea genotypes using morpho-physiological and SSR markers. Int J Curr Microbiol App Sci. 2021;10(01):1108-1117.
60. Weyhrich RA, Lamkey KR, Hallauer AR. Response to seven methods of recurrent selection in the BS11 maize population. Crop Sci. 1998;38:308-321.
61. Yadav LN, Tripathi MK, Sikarwar RS, Mishra AK. Heterosis in sesame. Sesame & Safflower Newsl. 2005;20:6-10.
62. Yadav PK, Tiwari S, Kushwah A, Tripathi MK, Gupta N, Tomar RS, *et al*. Morpho-physiological characterization of bread wheat genotypes and their molecular validation for rust resistance genes Sr2, Sr31 and Lr24. Proc. Indian Natl. Sci. Acad. 2021;87:534-545. https://doi.org/10.1007/s43538-021-00049-y
63. Yadav PK, Singh AK, Tripathi MK, Tiwari S, Rathore J. Morpho-physiological characterization of maize (*Zea mays* L.) genotypes against drought. Biological Forum. 2022a;14(2):573-581.
64. Yadav PK, Singh AK, Tripathi MK, Tiwari S, Yadav SK, Tripathi N. Morpho-physiological and molecular characterization of maize (*Zea Mays* L.) genotypes for drought tolerance. European Journal of Applied Sciences. 2022;10(6):65-87.
65. Yadav PK, Singh AK, Tripathi MK, Tiwari S, Yadav SK, Solanki R, *et al*. (Assessment of maize (*Zea mays* L.) genotypes on the basis of biochemical contents in respect to drought. The Pharma Innovation Journal. 2022c;11(6):1996-2002
66. Yadav RK, Tripathi MK, Tiwari S, Tripathi N, Asati R, Patel V, *et al*. Breeding and genomic approaches towards

development of Fusarium wilt resistance in chickpea. Life. 2023;13:988. https://doi.org/ 10.3390/life13040988
67. Zhang PP, Zhou XX, Wang ZX, Mao W, Li WX, Yun F, *et al*., Using HJ-CCD image and PLS algorithm to estimate the yield of field-grown winter wheat. Sci Rep. 2020;10:5173.