



E-ISSN: 2618-0618

P-ISSN: 2618-060X

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2024; 7(5): 45-48

Received: 10-03-2024

Accepted: 19-04-2024

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# International Journal of Research in Agronomy

## Selection indices and character association studies in wheat (*Triticum aestivum* L.) under late sown condition

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DOI: <https://doi.org/10.33545/2618060X.2024.v7.i5a.686>

### Abstract

The discriminant-function technique was used to create selection indices for 29 wheat genotypes (*Triticum aestivum* L.) growing under late-sown condition. The discriminant function technique was used to create 31 selection indices based on grain yield (q/ha) and its four components. Increasing the amount of characters in the selection index improves selection efficiency. The selection index based on five characters, that is, grain yield (q/ha), harvest index (%), test weight (1000 kernel wt. in g), number of tillers per plant, and biological yield (q/ha), exhibited highest relative efficiency, with genetic advance of 2619.76% and 17.34, respectively. The correlation coefficient study demonstrated a substantial positive relationship between grain yield (q/ha) and key traits, including test weight (1000 kernel wt. in g), biological yield (q/ha), harvest index (%), flag leaf area (cm<sup>2</sup>), and number of tillers per plant. Path coefficient analysis further highlighted that harvest index (%), test weight (1000 kernel wt. in g), number of tillers per plant, and biological yield (q/ha) have a significant beneficial direct effect on grain yield.

**Keywords:** Selection indices, discriminant function, relative efficiency, correlation coefficient analysis, path coefficient analysis and wheat

### Introduction

Wheat is a staple food for a vast proportion of the world's population, including India. In India, wheat occupies an area of 31.86 million hectares with a total production of 110.55 million tonnes and a productivity of 36.24 q/ha, respectively. In Chhattisgarh wheat was grown on 146.40 ('000 hectares) area with a total production of 248 ('000 metric tonnes) and productivity of 1386 kg/ha during 2022-23 (Anon., 2023) <sup>[1]</sup>. Grain yield is a complex polygenic trait that is influenced by the actions and interactions of several factors. In many circumstances, genotype selection merely based on grain yield would be unreliable. Selection based on a proper selection index has been shown to be more effective than direct selection for grain production. Fisher (1936) invented the discriminant function, which was first used by Smith (1936) <sup>[10]</sup>, to help find significant combinations of yield components helpful for selection by establishing appropriate selection indices. As a result, the goal of this study was to develop and evaluate the efficacy of selection indices in bread wheat.

### Materials and Methods

During Rabi 2022-23, a field trial was conducted at the research cum instructional farm, B.T.C. College of Agriculture and Research Station (IGKV), Bilaspur, Chhattisgarh, using twenty-nine different wheat genotypes in a randomized block design (RBD) with two replications under late sown conditions. The characters evaluated were days to 50% heading, days to maturity, flag leaf area (cm<sup>2</sup>), plant height (cm), number of tillers per plant, spike length (cm), number of grains per spike, test weight (1000 kernel wt. in g), biological yield (q/ha), harvest index (%) and grain yield (q/ha). Characters with a positive and significant association and sizable positive direct effects on grain yield were used to generate the selection indices. In this context, grain yield (X1), number of tillers per plant (X2), test weight (X3), biological yield (X4), and harvest index (X5) were identified and considered in late sown condition. The model proposed by Robinson et al. (1951) <sup>[8]</sup> was utilized to construct selection indices and the required discriminant function. A total of 31 selection indices were produced utilizing five components.

The relevant genetic advance via selection was also computed using the formula proposed by Robinson *et al.* (1951) [8]. The relative efficacy of various discriminant functions for straight selection in grain production was evaluated and compared, with selection efficiency set at 100%.

### Results and Discussion

Selection indices for grain production and other parameters were created and tested to determine their relative effectiveness in selecting superior genotypes. Table 3 presents the findings for selection indices, discriminant functions, expected genetic gain, and relative efficiency. The results showed that when selection was based on component characters, the genetic advance and relative efficiency tested for different indices were higher than with straight selection, and it increased significantly when two or more characters were included. Selection indices are thus more practical for selecting suitable genotypes because they are developed by providing appropriate weightage to yield-related characteristics. In corn, Robinson *et al.* (1951) [8] found that when more characters were added to the index formula, the efficiency of selection indices increased. According to Hazel and Lush (1943) [4], as the number of characters under selection rises, the superiority of index-based selection improves and Reddy and Babariya (2020) [7], Shah *et al.* (2016) [9] and Eshoghi

*et al.* (2011) [2] also suggested that the selection index to be superior to direct selection in wheat. The highest relative efficiency with genetic advance was 2619.76% and 17.34 respectively was recorded, when all the five characters (grain yield, number of tillers per plant, test weight, biological yield and harvest index) were considered together. The maximum relative efficiency with genetic advance in single character discriminant function was 2160.27% and 14.301 respectively, was exhibited by test weight. However, it increased up to 2308.74% and 15.28 in two character combination (test weight and harvest index); 2370.50% and 15.69 in three character combination (grain yield, test weight and harvest index) and in case of four characters (grain yield, test weight, biological yield and harvest index), it was 2485.13% and 16.45. Fredous *et al.* (2010) [3], Kemelew (2011) [6], and Shah *et al.* (2016) [9] all concluded that increasing the number of characters resulted in more genetic gain and that selection indices were more efficient than simple selection for grain yield. Furthermore, it was discovered that straight selection for grain yield was not as profitable (GA = 0.662, RI = 100%) as it was through component characters or their combinations. The current investigation demonstrated a continuous increase in the relative efficiency of the subsequent index with the simultaneous inclusion of each character.

**Table 1:** Phenotypic (above diagonal) and Genotypic (below diagonal) correlation matrix

Traits	DH	DM	FLA	PH	TPP	SL	GPS	TW	BY	HI	GY
DH	1	0.235*	-0.095	-0.129	0.07	0.06	0.079	-0.053	-0.005	0.077	0.047
DM	0.606**	1	0.249*	-0.132	0.086	0.263*	0.128	-0.173	0.177	-0.021	0.170
FLA	-0.122	0.414**	1	0.081	-0.149	0.434**	-0.155	0.366**	0.056	0.436**	0.310*
PH	-0.166	-0.217*	0.125	1	0.162	0.245*	-0.218*	-0.026	-0.159	0.048	-0.087
TPP	0.081	0.327**	-0.127	0.182	1	-0.105	0.101	-0.004	0.387**	0.178	0.302*
SL	-0.018	0.461**	0.481**	0.298*	-0.137	1	-0.528**	-0.037	-0.098	0.057	-0.023
GPS	0.124	0.174	-0.161	-0.275*	0.109	-0.565**	1	0.069	0.125	-0.002	0.116
TW	-0.056	-0.212*	0.357*	-0.078	0.022	-0.016	0.065	1	0.353*	0.246*	0.623**
BY	0.136	0.475**	0.017	-0.305*	0.597**	-0.232*	0.137	0.367**	1	0.08	0.589**
HI	-0.105	0.140	0.546**	0.234*	0.280*	-0.008	0.075	0.304*	0.108	1	0.449**
GY	0.148	0.189*	0.323*	0.184	0.424**	-0.105	0.125	0.643**	0.592**	0.686**	1

\*\* Significant at 1% probability level and, \* significant 5% level of probability, respectively

**Note:** \*Significant at 5% probability level, \*\* Significant at 1% probability level, R critical value at 5% level of significance-  $\pm 0.1853$ , R critical value at 1% level of significance-  $\pm 0.2054$ , DH= days to 50% heading, DM= days to maturity, FLA= Flag leaf area (cm<sup>2</sup>), PH= plant height (cm), TPP= number of tillers per plant, SL= spike length (cm), GPS= number of grains per spike, TW= test weight (1000 kernel wt. in g), BY= biological yield (q/ha), HI= harvest index (%), GY= grain yield (q/ha)

**Table 2:** Genotypic path coefficient analysis showing direct (diagonal) and indirect effects (off diagonal)

Traits	DH	DM	FLA	PH	TPP	SL	GPS	TW	BY	HI	Genotypic correlation with GY
DH	-0.149	0.077	0.077	0.108	0.055	-0.001	-0.016	-0.013	0.075	-0.065	0.148
DM	-0.109	0.127	-0.035	0.124	0.079	0.010	-0.023	-0.090	0.039	0.087	0.189
FLA	0.030	0.052	-0.085	-0.071	-0.035	0.018	0.021	0.152	0.001	0.240	0.323**
PH	0.166	-0.027	-0.010	-0.132	0.051	0.011	0.036	-0.032	-0.025	0.146	0.184
TPP	-0.020	0.0418	0.011	-0.104	0.282	-0.005	-0.014	0.009	0.049	0.174	0.424**
SL	0.004	0.059	-0.041	-0.070	-0.038	0.038	0.074	-0.006	-0.019	-0.004	-0.105
GPS	-0.030	0.022	0.013	0.157	0.030	-0.021	-0.032	0.027	0.011	0.046	0.125
TW	0.013	-0.027	-0.030	0.044	0.006	-0.001	-0.008	0.425	0.030	0.189	0.643**
BY	-0.033	0.060	-0.001	0.174	0.168	-0.008	-0.018	0.156	0.082	0.011	0.592**
HI	0.026	0.017	-0.046	-0.134	0.079	-0.001	-0.009	0.129	0.001	0.623	0.686**

Residual are 0.15081

**Note:** \*Significant at 5% probability level, \*\* Significant at 1% probability level, Residual effect genotypic= 0.15081 DH= days to 50% heading, DM= days to maturity, FLA= flag leaf area (cm<sup>2</sup>), PH= plant height (cm), TPP= number of tillers per plant, SL= spike length (cm), GPS= number of grains per spike, TW= test weight (1000 kernel wt. in g), BY= biological yield (q/ha), HI= harvest index (%), GY= grain yield (q/ha)

**Table 3:** Phenotypic path coefficient analysis showing direct (diagonal) and indirect effects (off diagonal)

Traits	DH	DM	FLA	PH	TPP	SL	GPS	TW	BY	HI	Phenotypic correlation with GY
DH	-0.046	0.030	-0.018	0.076	0.012	-0.003	-0.001	-0.021	-0.001	0.019	0.047
DM	-0.011	0.128	0.048	0.023	0.015	-0.014	-0.002	-0.068	0.055	-0.005	0.170
FLA	0.004	0.031	0.195	-0.014	-0.127	-0.053	0.003	0.144	0.017	0.110	0.310**
PH	0.019	-0.016	0.015	-0.077	0.029	-0.013	0.004	-0.010	-0.050	0.012	-0.087
TPP	-0.003	0.0110	-0.029	-0.028	0.182	0.005	-0.002	-0.002	0.121	0.045	0.302*
SL	-0.002	0.0337	0.084	-0.043	-0.019	-0.054	0.010	-0.014	-0.031	0.014	-0.023
GPS	-0.004	0.016	-0.030	0.038	0.018	0.028	-0.018	0.027	0.039	-0.001	0.116
TW	0.002	-0.022	0.071	0.004	-0.001	0.002	-0.001	0.393	0.110	0.062	0.623**
BY	0.001	0.022	0.011	0.028	0.070	0.005	-0.002	0.139	0.314	0.001	0.589**
HI	-0.003	-0.002	0.085	-0.008	0.032	-0.003	0.001	0.096	0.001	0.253	0.449**

Residual are 0.26348

**Note:** \*Significant at 5% probability level, \*\* Significant at 1% probability level, Residual effect genotypic= 0.26348DH= days to 50% heading, DM= days to maturity, FLA= flag leaf area (cm<sup>2</sup>), PH= plant height (cm), TPP= number of tillers per plant, SL= spike length (cm), GPS= number of grains per spike, TW= test weight (1000 kernel wt. in g), BY= biological yield (q/ha), HI= harvest index (%),GY= grain yield (q/ha)

**Table 3:** Selection index, discriminant function, expected genetic advance in yield and relative efficiency from the use of different selection indices in bread wheat.

S. No.	Selection index	Discriminant function	Expected genetic advance	Relative efficiency (%)
1	X1 Grain Yield (q/ha)	0.4821X1	0.662	100
2	X2 Number of tillers per plant	0.877X2	1.67	252.27
3	X3 Test weight (1000 kernel wt. in g)	0.542X3	14.301	2160.27
4	X4 Biological yield (q/ha)	0.823X4	1.218	183.99
5	X5 Harvest index (%)	0.264X5	5.382	812.99
6	X1.X2	0.9831X1 + 1.1360X2	3.73	563.44
7	X1.X3	1.0958X1 + 0.9022X3	14.40	2174.77
8	X1.X4	1.1473X1 + 1.3049X4	5.23	790.15
9	X1.X5	2.8703X1 + 0.56609X5	6.17	932.22
10	X2.X3	0.9090X2 + 0.9017X3	14.40	2175.19
11	X2.X4	1.3699X2 + 1.1913X4	4.21	635.98
12	X2.X5	0.9899X2 + 0.5686X5	5.72	864.54
13	X3.X4	0.9021X3 + 0.7823X4	14.38	2171.72
14	X3.X5	0.9018X3 + 0.5665X5	15.28	2308.74
15	X4.X5	0.7606X4 + 0.5666X5	5.53	834.72
16	X1.X2.X3	0.9105X1 + 1.2239X2 + 0.9028X3	14.86	2244.57
17	X1.X2.X4	1.4006X1 + 0.9973X2 + 1.3780X4	7.44	1123.84
18	X1.X2.X5	0.6126X1 + 1.6446X2 + 0.5856X5	7.03	1061.59
19	X1.X3.X4	0.4547X1 + 0.9050X3 + 0.3781X4	14.49	2188.64
20	X1.X3.X5	3.2360X1 + 0.8956X3 + 0.5573X5	15.69	2370.50
21	X1.X4.X5	1.0639X1 + 1.5462X4 + 0.5802X5	7.92	1196.83
22	X2.X3.X4	1.3247X2 + 0.9017X3 + 1.2648X4	14.94	2256.23
23	X2.X3.X5	0.9948X2 + 0.9018X3 + 0.5689X5	15.41	2327.68
24	X2.X4.X5	1.5622X2 + 1.0350X4 + 0.5678X5	6.94	1047.73
25	X3.X4.X5	0.9022X3 + 0.7945X4 + 0.5669X5	15.36	2319.93
26	X1.X2.X3.X4	1.4037X1 + 0.9577X2 + 0.9011X3 + 1.4831X4	16.23	2451.30
27	X1.X2.X3.X5	0.5405X1 + 1.7319X2 + 0.9041X3 + 0.5865X5	16.01	2418.01
28	X1.X2.X4.X5	1.3130X1 + 1.0298X2 + 1.6024X4 + 0.5799X5	9.62	1453.73
29	X1.X3.X4.X5	1.0620X1 + 0.9021X3 + 1.5855X4 + 0.5805X5	16.45	2485.13
30	X2.X3.X4.X5	1.9904X2 + 0.9024X3 + 0.6936X4 + 0.5672X5	15.95	2410.09
31	X1.X2.X3.X4.X5	1.3158X1 + 0.9927X2 + 0.9013X3 + 1.6611X4 + 0.5802X5	17.34	2619.76

## Conclusion

The present findings indicate that additive gene action was operating for the number of grains per spike, test weight (g), number of tillers per plant, flag leaf area (cm<sup>2</sup>), spike length (cm), biological yield (q/ha), harvest index (%), and grain yield (q/ha). In addition, correlation, path coefficient analysis, and selection indices demonstrated the significance of these qualities. As a result, these qualities should be given adequate weight in the context of bread wheat genetic improvement. Direct selection of genotypes that outperform checks HI 1634, CG 1029, and HD 2932 in terms of many yield-related parameters should be an effective method for improving grain yield.

## Research Conflict

The research investigates selection indices for wheat genotypes under late sown condition. While some favor features like as test weight and number of tillers per plant for direct selection due to their significant yield contribution, others prefer qualities such as flag leaf area and spike length, which also have a major impact on yield. This conflict questions the prioritization of traits and the effectiveness of selection strategies. Resolving it requires understanding trait relevance under various circumstances and then construct integrated selection procedures. Investigating trait relationships and their genetic basis can refine selection criteria, improving wheat yield stability and resilience in late-sown condition.

### Acknowledgement

I extend my heartfelt gratitude to the Department of Genetics and Plant Breeding at B.T.C. College of Agriculture and Research Station (IGKV), Bilaspur, Chhattisgarh. Dr. Roshan Parihar, Assistant Professor and Chairperson, has been instrumental with unwavering support. Special thanks to Dr. A. P. Agarwal, Dr. H.P. Agarwal, and Dr. N. K. Chaure for their invaluable contributions. Thank you sincerely.

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