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Upasna Mishra
Department of Genetics & Plant Breeding, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya, Gwalior, Madhya Pradesh, India

Shailja Chauhan
Department of Genetics & Plant Breeding, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya, Gwalior, Madhya Pradesh, India

VS Kandalkar
Department of Genetics & Plant Breeding, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya, Gwalior, Madhya Pradesh, India

AK Sharma
Department of Genetics & Plant Breeding, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya, Gwalior, Madhya Pradesh, India

Corresponding Author:
Upasna Mishra
Department of Genetics & Plant Breeding, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya, Gwalior, Madhya Pradesh, India

Genotypic and phenotypic correlation coefficients, path-coefficients and the implication of discriminant selection index for genetic improvement in advance wheat (*Triticum aestivum* L.) cultivars

Upasna Mishra, Shailja Chauhan, VS Kandalkar and AK Sharma

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Abstract

Selection indices were derived using discriminant function analysis in Thirty-six genotypes of bread wheat (*Triticum aestivum* L.) of relative economic importance of the various characters. Discriminant function technique provided genetic correlation with total of 36 selection indices having high heritability to construct an index based on grain yield per plant and its components. Genotypic coefficient of correlation was calculated and it was found that there was a high significant positive correlation between the yield and the 1000 grains weight. Thus, the genotypic path coefficient analysis disclosed a positive direct effect of 1000 grain weight and days to maturity on grain yield while at phenotypic level, it was for 1000 grain weight only. Among these characters; days to heading, 1000 grains weight, days to maturity were much similar to GCV and PCV that is least influenced by the environment whereas grain yield and plant height yielded a higher PCV than that of GCV where large variation of these characters are environment dependent. The estimate of heritability was high and genetic gains were high in 1000 grain weight, plant height, days to heading and grain yield which showed better efficiency of selection which improved these traits. A discriminant of plant height, days to heading, 1000 grain weight, days to maturity and grain yields showed the optimum selection procedure of grain yields with a heritableness of 3.72 and acceptable genetic improvement of 135.98 percent. The indices are recommended during the selection of high performing bread wheat genotypes.

Keywords: Correlation coefficient, path analysis, discriminant analysis, biometrical genetics, variance, selection indices, relative efficiency

Introduction

Wheat (*Triticum* spp.) is a principal cereal crop belonging to the family Poaceae (Gramineae), cultivated globally as a major staple for human nutrition. The genus *Triticum* includes several economically significant species, among which *Triticum aestivum* (bread wheat), *Triticum durum* (macaroni or pasta wheat), and *Tritium compactum* (club wheat) are the most commercially important. The domestication of wheat dates back to the Fertile Crescent, in particular, the Levantine and Ethiopian areas where the early agricultural cultures started breeding the ancestral diploid and tetraploid species. In the Indian subcontinent, species such as *Triticum dicoccum* (Khapli or Emmer wheat) and *Triticum durum* have been cultivated since prehistoric times. These crops, especially *T. aestivum* have been the backbone of the wheat economy of India. Wheat has the largest area of cultivation of cereal crops around the globe with a total of 220.7 million hectares or 2023 being expected to grow. The worldwide production was recorded at approximately 799 million tonnes, with major contributions from China (136.6 Mt), India (110.6 Mt), and Russia (104.2 Mt). The Food and Agriculture Organization (FAO) projects a modest increase in global wheat output in 2025, reaching up to 805 million tonnes. France and Germany have been known to be productive in that the average tonnes that they produce per hectare are 6.99 tonnes and 7.58 tonnes respectively. India has been ranked as the countries that are second in terms of wheat production globally with an average acreage under cultivation of 31.83 million and an estimated production project of 117.5 million tonnes by 2025-26. Despite being the largest in terms of area under wheat cultivation, India's national average yield (~3.59 t/ha) lags behind several high-input regions in Europe.

The subcontinent continues to grow multiple crop species on a commercial scale, including sugarcane, rice (paddy), and oil palm, though wheat occupies a dominant share in the Rabi season cropping pattern. It is also important to learn the factors that affect the production of wheat to improve the production. In this analysis, the coefficient of variation in the available agronomic traits and the phenotypic, as well as the genotypic correlation, would be evaluated to evaluate a direct and indirect impact of different characters to the grain yield. The discriminant function model proposed by Robinson *et al.* (1951) and for plant selection was first proposed by Smith in 1936 is employed to select key yield-contributing traits through appropriate selection indices. Furthermore, path coefficient analysis (Dewey and Lu, 1959) is used to partition correlation coefficients into direct and indirect effects, thereby offering insight into the relative contribution of each trait toward final yield formation. This practice helps in development of specific breeding programs since it is able to determine traits that have the greatest effect in genetic improvement and stability of yields in a broad range of agro-climatic environments.

Objectives

The study in question was conducted with the view of the following specific objectives:

- In a quest to determine the strength and the direction of relationship between grain yield and contributing traits; to estimate the correlation coefficients between the various traits and grain yield.
- Conducting path coefficient analysis in order to measure the Direct and Indirect effects of individual yield factors in the determination of Grain Yield and thus explain why the associations exist.
- In order to use discriminant function analysis in the development and testing of selection indices, as a means of identifying the relative performance of various traits in enhancing grain yield by means of selection.

Materials and Methods

This study was developed with the purpose of knowing the nature of grain yield inheritance and the characteristics that contribute to grain yield in wheat. A total of 36 test genotypes (details provided in Table 1) were evaluated during the Rabi season of 2014-2015 at the Research Farm, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya (RVSKVV), Gwalior, Madhya Pradesh. The experimental site is situated in the Agro-climatic Zone No. 6, wheat-pearl millet cropping zone. The experimental design followed was a Randomized Complete Block Design (RCBD) with two replications. All the genotypes were planted under similar agronomic settings to limit the implications of environmental variation and to provide an accurate determination of genetic aspects. During the period of growing of the crop, the standard cultural practices to be adopted in the wheat cultivation in the region were observed. Recordings were recorded on grain yield and other characters contributing to yield with an aim of determining their variability between each other as well as genetic relationship. Collected data were analysed statistically to obtain an estimate of correlation coefficients, path coefficients, and discrimination function indices to establish traits which have high influence on the grain yield. The primary objective was to study the mode of inheritance of grain yield and its yield determining characters across 36 wheat genotypes (Table 1).

The texture of soil in the experimental field was sandy loam, which has been characterized as follows: N Nitrogen available: LOW, Available phosphorus: Medium, Potash available: high, Soil pH-8.5. The experiment was laid out in a Randomized Complete Block Design (RCBD) with two replications. It was sowed in 21st November 2014 in timely sown environment by dibbling method given row to row spaces 20 cm and plant to plant spacing 4-6 cm. The local best possible agronomy practices and crop management measures were also applied according to the standard package practices of wheat crop cultivation in order to provide best possible crop growth and yield.

The plants of each application (five at random in each replication) were measured on the following characters: Days to heading (DAS), Days to maturity (DAS), Plant height (cm), 1000-grain weight (g) and Grain yield (kg/plot).

These traits were selected because of their significance in determining the final grain yield and carried out statistical algorithms to estimate genetic correlation, path coefficients and selection indices.

Table 1: Data pertaining to the cultivars subjected to the investigation.

Sl. No.	Cultivar name	Source	Sl. No.	Cultivar name	Source
1	DBW 170	IIWBR, Kernal	19	RVW 4232	RVSKVV, Gwalior
2	DBW 169	IIWBR, Kernal	20	UAS 369	UAS, Dharwad
3	UAS 372	UAS, Dharwad	21	MP 3440	JNKVV, Power kheda
4	HI 1610	Delhi	22	NIAW 2595	MPKV, Rahuri
5	UP 2909	GB Pant nagar	23	NIAW 2495	MPKV, Rahuri
6	HI 1608	Delhi	24	GW 473	Vijapur, Gujrat
7	GW 468	Vijapur, Gujrat	25	AKAW 4798	PDKV, Akola
8	JWS 147	Sagar	26	UAS 371	UAS, Dharwad
9	MACS 6671	ARI Pune	27	MACS 6668	ARI Pune
10	DBW 168	IIWBR Kernal	28	GW 471	Vijapur, Gujrat
11	MP 1309	JNKVV, Power kheda	29	MP 1311	JNKVV, Power kheda
12	HI 1607	IARI, Indore	30	NIAW 2539	MPKV, Rahuri
13	RAJ 4424	Durgapura	31	PBW 732	PAU, Punjab
14	UAS 370	UAS, Dharwad	32	GW 469	Vijapur, Gujrat
15	WH 1109	Checks	33	GW 470	Vijapur, Gujrat
16	HI1909	Delhi	34	CG 1016	IGKV, Raipur
17	HP 1960	CSKHPKV, Palampur	35	MACS 6222 C	ARI Pune
18	MP 1310	JNKVV, Powarkheda	36	HI 1544 C	IARI, Indore

The two variance-covariance matrices needed to compute the genotypic and phenotypic correlation coefficients as well as for estimating the coefficients $b_1, b_2, .., b_n$ which are used for discriminant function analysis, were derived from the mean squares and mean cross products of genotypes and of errors for different characters measured across replicated trials. Separate ANOVA (Analysis of covariance) for individual character and for all of the combined five traits and ANOVA independently performed for all possible pair wise combinations of the five characters, using data from 36 wheat genotypes under investigation.

1. Analysis of variance (ANOVA): It is used to determine significant different mean values of each character were computed and subjected to analysis of variance (ANOVA) following the method outlined by Panse and Sukhatme, 1967 [20] appropriate for a Randomized Complete Block Design (RCBD). This method used to assess the variability among genotypes and to partition the total variation into genotypes (treatments), replications, and experimental error.

a) The statistical analysis for the randomized complete block design (RCBD) is computed as follows:

$$y_{il} = \mu + g_i + b_j + e_{ij}$$

Where,

y_{il} = Observed value of the *i*th genotype in the *j*th replication

μ= Overall mean effect

g_i= Effect of the i^{th} genotype

b_j= Effect of j^{th}replication over the genotype

e_{ij}= Random error term with i^{th} observation, which is supposed to have normal and independent distribution having mean zero and a constant variance

With regards to testing the significance of genotypic variation, the ANOVA was conducted on a trait by trait basis so as to identify the significance of the measure of variation of the five measured traits. The analysis was useful in determining the extent to which there existed variations in the 36 genotypes across the characters under analysis.

Table 2: ANOVA for 36 genotypes under Randomized complete block design

Sources of variation	Degrees of freedom (df)	Mean squares (MSS)
Replications (r)	r-1	MSS_r
Treatment (t)	t-1	MSS_t
Errors	(r-1) (t-1)	MSS_e
Total	rt-1	

Where, r = number of replications, t = number of treatments

MSS_r = Mean sum of squares for the replications, MSS_t = Mean sum of squares for the treatments (genotypes), MSS_e = Mean sum of squares for the error.

In this table, this indicated the arrangement of the layout randomized block design concerning the efficacy of 36 wheat genotypes. Mean squares that were computed using ANOVA were also used to provide estimates of genotypic and phenotypic variation as well as determine significance of variation between genotypes of the traits analyzed.

(b) Statistical analysis of Standard error of mean, critical difference and coefficient of variation

The Standard error of mean (S.E.m±): To calculate the Standard error of mean the stated equation was used,

Standard error of the mean

$$\text{S.E. (m)}\pm= \frac{\sqrt{\text{MSSe}}}{\text{r}}$$

Where,

MSSe = Mean sum of squares for the error and r = Number of replications

Standard error of difference (S.E.d±): it was computed as:

$$\text{S.E(d)} \pm = \sqrt{\frac{2 \times \text{MSSe}}{\text{r}}}$$

Where,

S E (d)±= Standard error of difference

MSSe = Error mean sum of squares

r = Number of replications

Critical difference (C.D. at 5%): It was calculated as formula given as:

C. D. (5%) = Standard error difference × ’t’value at 5% level of significance

Coefficient of variation (CV%): It was computed as mentioned bellow:

$$\text{cv (\%)} = \frac{\sqrt{\text{MSSe}}}{\bar{x}} \times 100$$

Where,

C V (%) = Coefficient of variation in percent,

MSS_e = mean sum of square for the error

$\bar{x}$ = Sample mean of given observations

Computation of phenotypic and genotypic coefficients of variation: the coefficient of variation calculated as per the following formulae proposed by Burton (1952) [4]:

$$\text{PCV (\%)} = \frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100,$$

$$\text{GCV (\%)} = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$$

Where,

PCV = Phenotypic coefficient of variation,

GCV = Genotypic coefficient of variation,

$\sigma^2 g$ = Genotypic variance, this is a measure of the genetic variability within a population for a specific trait,

σ^2p = Phenotypic Variance, This represents the total variation in a trait, considering both genetic and environmental influences,

Mean ($\bar{X}$): This is the average value of the trait being measured.
The coefficient of variation was proposed by Sivasubramanian and Madhava Menon (1973):

0-10% = Low variability, 10-20% = Moderate variability and >20% = High variability

(2) Estimation of correlations: Phenotypic and genotypic correlation coefficient between characters was computed using respective components of variance and covariance by using the standard procedure suggested by Miller *et al.* (1958) [18]. These correlations help in understanding the degree of direction between traits of both the phenotypic and genotypic levels:

$$r_{XY} = \frac{Cov._{X,Y}}{\sqrt{V_X.V_Y}}$$

Where,
r_{XY} = Correlation coefficient between character X and Y,
Cov_{XY} = Covariance between characters X and Y,
V_X = Variance of character X,
V_Y = Variance of character Y

The magnitudes of phenotypic and genotypic correlation coefficients were tested for significance by comparing with the estimated values against the tabular values of Fisher and Yates (1936) [8] at n-2 d.f. using both probabilities, 5% and 1%.

(3) Path coefficient analysis: Path coefficient analysis is an extension of the correlation analysis through dividing correlation coefficients into direct and indirect effects through mediating variables. In this process standardized partial regression coefficients are estimated and are used to measure the direct effect of one variable to the other and at the same time capturing the effect of other variables that may be indirect. Originally articulated by Wright (1921, 1934), the method was subsequently elaborated and applied to plant breeding by Dewey and Lu (1959). Path coefficient analysis has been used in this current study in order to define the direct and indirect effects of yield components characters on the grain yield per plant.
In this regard, a set of simultaneous equations was created and solved:

$$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \cdots + r_{1i}P_{iy}$$
$$r_{2y} = r_{2y}P_{1y} + P_{2y} + r_{23}P_{3y} + \cdots + r_{2i}P_{iy}$$
$$r_{iy} = r_{i1}P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \cdots + P_{iy}$$

Where,
r_1y to r_iy = Correlation between causal factor 1 to *i* and dependent variable
r_{12} to r(i−1,i) = Inter-correlation among independent variables
P_1y to P_iy = Direct effects (path coefficients) of independent variables 1 to *i* on grain

(a) Residual effect: It was calculated to determine the proportion of variability in grain yield that is not explained by the included independent variables in the path analysis model. It was computed the following formula:

$$\text{Residual effect}(P_{RY}) = \sqrt{1 - R^2}$$

Where,

$$R^2 = \sum_{iy} P^2{}_{iy} + 2\sum_{\substack{i\neq j \\ i>j}} P_{iy}P_{jy}r_{ij}$$

(4) Discriminant function analysis: The tabular and numerical data show that social characters of economic value, including yield, depend on non-heritable variation. Therefore, the predicted response to selection is greater if selection is done based on discriminant function technique than if selection is carried on observed characteristics. The basic idea to construct selection index lies in phenotypic and genotypic variances and covariances between them which are being utilized in determining repeatability.
The model proposed by Robinson *et al.* (1951) [18] was used through the set of simultaneous equation for the construction of selection indices and the development of the required discriminant function.

b1 p11 + b2 p12 + b3 p13 + b4 p14 + b5 p15 = g15
b1 p12 + b2 p22 + b3 p23 + b4 p24 + b5 p25 = g25
b1 p13 + b2 p23 + b3 p33 + b4 p34 + b5 p35 = g35
b1 p14 + b2 p24 + b3 p34 + b4 p44 + b5 p45 = g45
b1 p15 + b2 p25 + b3 p35 + b4 p45 + b5 p55 = g55

Where,

- p_{11}, p_{22}, p_{33}, p_{44} and p_{55} are the estimate of phenotypic variance of the characters numbering x_1, x_2, x_3, x_4 and x_5 respectively.
- p_{12}, p_{13}, p_{14}, p_{15} are the phenotypic co-variances of the various combinations of x_1, x_2, x_3, x_4, and x_5 respectively.
- 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 calculated values of the b as performed in the above expression were the phenotypic weights that ought to be assigned to each of the various characters considered in selection indices.

These obtained b values were used in construction of selection index as follows

$Z = b_1x_1 + b_2x_2 + b_3x_3 + b_4x_4 + b_5x_5$

Where,
Z = Selection index
X_1, X_2, X_3, X_4 and X_5 is the phenotypic values of traits X_1, X_2, X_3, X_4 and X_5, respectively.
b_1, b_2, b_3, b_4 and b_5 is the phenotypic weights of the characters i.e. X_1, X_2, X_3, X_4 and X_5, respectively.

These indices on way selection were made upon one character, two characters, three characters, four characters, and five characters.

(a) Expected genotypic advance (EGA) of various selection indices: It was calculated following the methodology proposed by Robinson *et al*. (1951) [18]. This method measures how many grains more of grain yield will be obtained by indirect selection on the basis of several traits correlated with each other in the selection index.

The EGA was calculated as the following:

$$\text{EGA} = \frac{Z}{P}\sqrt{b_1 g_{15} + b_2 g_{25} + b_3 g_{35} + b_4 g_{45} + b_5 g_{55}}$$

Where,

$\frac{Z}{P}$ = represents selection differential in standard units denoted as K. For a selection intensity of 5%, its value is 2.06.

b_1 to b_5 = phenotypic weights of the corresponding characters included in the selection indices.

g_{18} to g_{55} = genotypic co-variance of characters x_1 to x_4 with grain yield x_5 and

g_{55} = genotypic variance of grain yield x_5.

(b) Relative efficiency of selection indices compared to direct selection for yield: During the comparative assessment of alternative selection indices, the relative efficiency of how each of them can result to improvement in grain yield is one of the benchmark criterions. This measure is calculated as a percentage, and it is calculated as below

Relative Efficiency (%) = (EGA index/EGA yield) x 100

Robinson *et al*., (1951) [18] establish that direct selection for grain yield constitutes the baseline (100%) against which the other indices are compared. A relatively more efficient index implies that a better performance is achieved in case grain yield is aimed indirectly through the index.

Results

Correlation coefficients of genotypic and phenotypic Pearson between grain yield and that of related traits are as shown below

- **Genotypic correlation coefficient:** The positive relationship with grain yield was found in 1000-grain weight at an insignificant level, Table 3 showed that the correlation coefficient 0.4881 between 1000-grain weight and grain yield was significant. It implies that grain yield has been accompanied by parallel increases in weight of 1000 grains, and this means that it is a good option among a selection criterion of yield-increasing in wheat. They were negative for other traits, such as, for days to heading it was (-0.5876) and for plant height it was (-0.4529). Each of them was a statistically significant correlation. In addition to this, days to heading was highly correlated with days to maturity at 0.5568. This denotes that the earlier flowering genotypes, in fact, mature faster translated as the correlation between the phenological features of the analysed genotypes is high.
- **Phenotypic correlation coefficient:** It is represented in Table 3 represented that days to heading highest, negative and significant correlation with grain yield (-0.3778). This suggests that genotypes with delayed heading tend to have lower grain yields. It was also positively significant correlated with days to maturity (0.3881) indicating that early-heading genotypes generally matured earlier as well.

Table 3: Matrix of Genotypic (upper diagonal) and phenotypic (lower diagonal) correlation coefficients of various traits of wheat genotypes

Characters	Plant height (PH)	Days to heading (DAH)	1000 grain weight (GW)	Days to maturity (DM)	Grain yield (GY)
Plant height (PH)	-	0.2359	0.2632	0.1077	-0.4529**
Days to heading (DAH)	0.1696	-	-0.1152	0.5568**	-0.5876**
1000 grain weight (GW)	0.1931	-0.1069	-	-0.1364	0.4881**
Days to maturity (DM)	0.2156	0.3881*	-0.0620	-	-0.2298
Grain yield (GY)	-0.1798	-0.3778*	0.2759	-0.2812	-

*, ** represent as significance at 5% and 1% respectively.

Table 4 Path analyses at genotypic level: Direct effects on grain yield mentioned diagonally and indirect effects (all other values).

Intimated from the path analysis was highest negative direct effect of plant height (-0.5095) on grain yield. However, the study also had positive indirect effects on grain yield through days to maturity (0.0200), and 1000-grain weight (0.1551); this showed that the dwarf plants produce high grain yields. Days to heading indicated a direct negative path coefficient (-0.5027) on grain yield but an overall positive though less significant indirect impact on grain yield through days to maturity (0.1032). As a result genotypes that head early yields more grains. Thus 1000-grain weight had the highest direct positive impact on grain yield at 0.5896, and also had a positive impact on grain yield through days to heading, though minimal at 0.0579. As for the direct effect, days to maturity were a positive value of 0.1854 while control treatment had a negative value of-0.2204. The result of the residual effects was pegged at 0.4782.

Table 4: Genotypic Path Coefficient Matrix Showing Direct and Indirect Effects of Yield-Related Traits on Grain Yield in Wheat Genotypes

Characters	Plant height (PH)	Days to heading (DAH)	1000 grain weight (GW)	Days to maturity (DM)	Genotypic correlation with Grain yield (GY)
Plant height (PH)	-0.5095	-0.1186	0.1551	0.0200	-0.4529**
Days to heading (DAH)	-0.1202	-0.5027	-0.0679	0.1032	-0.5876**
1000 grain weight (GW)	-0.1341	0.0579	0.5896	-0.0253	0.4881**
Days to maturity (DM)	-0.0549	-0.2799	-0.0804	0.1854	-0.2298

Residual effect was 0.4782. Dark values indicate direct effects.

(b) Phenotypic path analysis: Direct (diagonal) and indirect effect of various traits on grain yield:

Plant height exhibited a negative direct effect on grain yield and its estimate was-0.1586. But it was positively and significantly related to grain yield through 1000-grain weight with an indirect effect of 0.0520. Days to heading showed a negative direct effect on grain yield which were-0.2740. However, we found that 1000-grain weight had a positive direct impact on grain yield worth 0.2695, and positive indirect effects through days to heading (0.0293) days to maturity (0.0077). On the other hand, days to maturity revealed a negative direct effect on grain yield, with the value of-0.1240. In this study, the residual factor value that stands for other effects on grain yield which are not accounted for by the various factors was estimated to be 0.8711. These results focus on the interactions between the traits, where first-order and second-order effects are used to partition the total variation in the grain yield.

Table 5: Phenotypic Path coefficient matrix estimated the direct and indirect effects due to varying traits on grain yield of the wheat genotypes

Character	Plant height (PH)	Days to heading (DAH)	1000 grain weight (GW)	Days to maturity (DM)	Phenotypic correlation with Grain yield (GY)
Plant height (PH)	-0.1586	-0.0465	0.0520	-0.0267	-0.1798
Days to heading (DAH)	-0.0269	-0.2740	-0.0288	-0.0481	-0.3778*
1000 grain weight (GW)	-0.0306	0.0293	0.2695	0.0077	0.2759
Days to maturity (DM)	-0.0342	-0.1063	-0.0167	-0.1240	-0.2812

Discriminant function analysis

Expected genetic advance calculated for different selection indices functions for yield, and traits contributing to yield have been presented in table 5. Discriminant functions consisting five indices of single characters, four indices of two characters, six indices of three characters, three indices of four and one index of five characters were calculated and result have been described below.

The genetic advance was 274.15 for grain yield which assumed 100 percent efficiency in selection indices. Among the single character indices, days to heading showed highest genetic advance of 258.64, followed by those of 1000 grain weight, plant height and days to maturity 189.01, 160.57 and 79.14, respectively. Among the two character indices days to heading + grain yield showed highest genetic advance of 321.26, followed by those of 1000 grain weight + grain yield, plant height + grain yield and days to maturity + grain yield 298.45, 296.58 and 274.16, respectively. Among the three character indices days to heading + 1000 grain weight +grain yield showed highest genetic advance of 342.06, followed by those of plant height + days to heading + grain yield, plant height + 1000 grain weight +grain yield, days to heading + days to maturity + grain yield, 1000 grain weight +days to maturity + grain yield and plant height + days to maturity + grain yield 335.02, 333.30, 325.73, 298.48 and 297.12 respectively. Among the four character indices plant height + days to heading + 1000 grain weight + grain yield showed highest genetic advance of 365.86, followed by those of days to heading + 1000 grain weight + days to maturity + grain yield and plant height + 1000 grain weight + days to maturity + grain yield337.09 and 334.06 respectively. The all five character index showed genetic advance of 372.80. Among all the results the following index turned out to be resulting into best genetic advance, that is 372.80 and it was five character index with the following combination: plant height + days to heading + 1000 grain weight + days to maturity + grain yield; followed by four character indices those of plant height + days to heading + 1000 grain weight + grain yield and days to heading + 1000 grain weight + grain yield, 365.86 and 342.06 respectively.

The relative efficiency (%) was assumed 100 percent for grain yield in section indices. Among the single character indices revealed that days to heading followed by 1000 grain weight, plant height and day to maturity showed highest relative efficiency of 94.34, 68.94, 58.57 and 28.87 respectively. Among the two characters indices days to heading + grain yield showed highest relative efficiency of 117.18 followed by those of1000 grain weight + grain yield, plant height + grain yield and days to maturity + grain yield, 108.86, 108.18 and 100 respectively. Among the three character indices days to heading + 1000 grain weight +grain yield showed highest relative efficiency of 124.77, followed by those of plant height + days to heading + grain yield, plant height + 1000 grain weight +grain yield, days to heading + days to maturity + grain yield, 1000 grain weight +days to maturity + grain yield and plant height + days to maturity + grain yield 122.20, 121.57, 118.8, 108.87 and 108.38 respectively. Among the four character indices plant height + days to heading + 1000 grain weight + grain yield showed highest relative efficiency of 133.45, followed by those of days to heading + 1000 grain weight + days to maturity + grain yield and plant height + 1000 grain weight + days to maturity + grain yield 122.96 and 121.85 respectively. The five character indices revealed plant height + days to heading + 1000 grain weight + days to maturity + grain yield showed relative efficiency of 135.98. Among all the results the following index turned out to be resulting into best relative efficiency that is 138.98 and it was a five character index with the following combination: plant height + days to heading +1000 grain weight + days to maturity + grain yield; followed by four character indices those of plant height + days to heading + 1000 grain weight + grain yield and days to heading + 1000 grain weight + grain yield, 133.45 and 124.77 respectively.

Table 6: Different selection indices for grain yield, expected genetic advance and their relative efficiency of bread wheat genotypes

Sl. No.	Selection index	Discriminant function	Expected genetic Advance	Relative Efficiency (%)
(1)	(2)	(3)	(4)	(5)
1	x1 (PH)	-10.00X1	160.57	58.57
2	x2 (DAH)	-9.00X2	258.64	94.34
3	x3 (GW)	-8.00X3	189.01	68.94
4	x4 (DM)	-7.00X4	79.14	28.87
5	x5 (GY)	-6.00X5	274.15	100.00
6	x1.x5	-7.16X1 + 0.33X5	296.58	108.18
7	x2.x5	-24.12X2 + 0.27X5	321.26	117.18
8	x3.x5	19.53X3 + 0.31X5	298.45	108.86
9	x4.x5	-0.44X4 + 0.36X5	274.16	100.00
10	x1.x2.x5	-6.05X1 +-22.58X2 + 0.25X5	335.02	122.20
11	x1.x3.x5	-9.72X1 + 26.05X3 + 0.26X5	333.30	121.57
12	x1.x4.x5	-7.36X2 + 3.78X4 + 0.34X5	297.12	108.38
13	x2.x3.x5	-37.31X2 + 19.40X3 + 0.18X5	342.06	124.77
14	x2.x4.x5	-41.43X2 + 18.48X4 + 0.24X5	325.73	118.8
15	x3.x4.x5	-84.94X3 +-22.89X4 + 0.55X5	298.48	108.87
16	x1.x2.x3.x5	-8.56X +-21.88X2 + 25.20X3 + 0.19X5	365.86	133.45
17	x1.x3.x4.x5	-9.44X1 + 104.49X3 +-113.82X4 + 0.09X5	334.06	121.85
18	x2.x3.x4.x5	26.43X2 + 133.18X3 +-164.39X4 + 0.16X5	337.09	122.96
19	x1.x2.x3.x4.x5	-9.27X1 +-25.18X2 + 25.45X3 + 15.83X4 + 0.20X5	372.80	135.98

Where
PH = Plant height
DAH = Days to heading
GW = 1000 grain weight
DM = Days to maturity
GY = Grain yield

Discussion

On the basis of the present study, genotypic correlation coefficient analysis revealed that the association between yield and yield contributing characters were found positive and significant only for 1000 grain weight (0.4881). Present finding are confirmed with Ashraf *et al.* (2014) [1], Bagrei *et al.* (2015) [2] and Nasri *et al.* (2014) [19]. Phenotypic correlation coefficient analysis revealed that grain yield was significantly but negatively correlated with days to heading. Among the components traits days to heading was significantly positively correlated with days to maturity.

In genotypic path analysis, relationship between yield and yield contributing characters were studied in details through path coefficient analysis. Path coefficient analysis performed to disclose the causes and effects of chain relationships of different yield contributing characters with yield (Majumder *et al*. 2008) [16]. Path coefficient analysis at genotypic level revealed that only two character, 1000 grain weight (0.5896) and days to maturity (0.1854) showed positive direct effect on grain yield and also1000 grain weight recorded positive indirect effect via days to heading (0.0579) on grain yield. Remaining two characters *viz*., plant height (-0.5095) and days to heading (-0.5027) exhibited negative direct effect on grain yield but these characters recorded positive indirect effect *viz*., plant height via 1000 grain weight (0.1551) and days to maturity (0.0200), days to heading via days to maturity (0.1032) on grain yield. The residual factor value was relatively high indicating some other characters which have not been studied. Similar results have been reported by Bhushan *et al.* (2013) [3], Hama *et al.* (2016) [11], Iftikhar *et al.* (2012) [14], Khan *et al.* (2013) [15], Khokhar *et al*. (2009) [24] and Majumadar*et al*. (2008) [16].

Path analysis at phenotypic level revealed that only one character 1000 grain weight (0.2695) showed positive direct effect on grain yield. Remaining three characters *viz*., days to heading (-0.2740), plant height (-0.1586) and days to maturity (-0.1240) showed negative direct effect on grain yield but these characters recorded positive indirect effect *viz*., plant height (-0.1586) via 1000 grain weight (0.0520), 1000 grain weight via days to heading (0.0293) and days to maturity (0.0077). The residual factor value was found high thereby indicating that some more characters may be considered in future study. Present finding are conformed to those of Bagrei and Bybordi (2015) [2].

Of all the bivariate techniques the discriminant function developed by Fisher (1936) [8] and adopted for plant selection by Smith (1936) is helpful in improvement in yield through characters combination. When considering only yield as a parameter for selection, index selection is far better for the purpose of enhancing yield. Hence discriminant function based on important characters for selection has given very useful direction in plant and exceedingly helpful to eliminate undesirable genotype on the basis of the performance. Hazel & Lush (1943) [12] established that selection which is undertaken using such an index is more efficient than selection done on the individual characters. The foundation on which the selection indices could have been developed has been given by Smith (1936), Hazel (1943) [12] and Robinson *et al.* (1951) [18]. According to Hazel and Lush (1943) [12], superior selection based on index rises with the number of characters involving in selection indices. McVetty and Evan (1980) [17], Esheghi *et al*. (2011) [6] also mentioned that selection indices were found to be superior to direct selection in wheat.

A strait selection index for grain yield and various indirect selection indices comprising of component traits in addition to grain yield were developed and compared to determine their combined efficiency for selection of high yielding genotypes. The discussion was done on the basis of expected genetic gain and relative efficiency for different selection indices. The highest genetic advance (GA) and relative efficiency for single character direct selection index of grain yield were 274.15 and considered as percentage 100, respectively. The two character combinations i.e., (days to heading + grain yield) showed enhanced genetic advance 321.26 and relative efficiency 117.18 percent. Genetic advance rose with three character blends, like day to heading, 1000 grain weight, and grain yield up to 342.06 percent, and relative efficiency up to 124.77per cent with four character blends of plant height and day to heading, 1000 grain weight and grain yield were 365.86 percent and 133.45 percent respectively. Here genetic advance and relative efficiency enhanced to an even greater extent when estimation of selection index involved two or more characters with increase in the number of character combinations.

Last of all five character combination index (plant height + days to heading + 1000 grain weight + days to maturity + grain yield) also had the highest genetic advance 372.80 and relative efficiency 135.98 percent. There was also an increase in the characters and the efficiency obtained by the selection indices was higher than those of the simple selection on grain yield alone. This conclusion harmonized with the findings of Ferdous *et al*. (2011) [7].

Summary

Path-coefficients, discriminant function, genotypic and phenotypic correlations of wheat-studies reveal that:

- Genotypic wise correlation analysis revealed positive and significant correlation of yield with some yield attributing characters only when the yield weighed in term of 1000 gram.With these characters,%26quot respectively it is possible to directly select the wheat crop to improve the yield.
- From the genotypic path coefficient analysis it was found that the components having positive direct effect on grain yield were 1000 grain weight (0.5896) and days to maturity (0.1854) while at phenotypic level only 1000 grain weight (0.2695).
- The total number of the indirect influences at both the genotypic and phenotypic level have been proved to contribute to the small unpredictable percentage hence, does not needed to be discussed any further, yet they contribute though in a small proportion.
- Optimum efficiency in selection of grain yield was obtained with discriminant function as plant height, days to heading, 1000 grain weight, days to maturity and grain yield in it and representing genetic advance of 372.80 and relative efficiency of 135.98 percent.

Conclusion

The regression equation implied that there was a positive correlation between yield and 1000 grain weight and the correlation was extremely significant and, therefore, it could boost selection of the character to improve wheat yield. The path analysis confirmed that 1000 grain weight and days to maturity were the traits that have genotypic positive direct impact on grain yield, because of this we should take into accounts both the component traits when selecting wheat breeding programme in coming years. It is also apparent in the present study that the discriminant function technique of selection in plant appears more practical over the other classical breeding tools; and thus the promising selection indices on grain yield improvement of wheat breeding programme could be given due consideration to. Better genotype HI 1610 in terms of grain yield was the best of all genotype hence can be used as parents in future breeding improvement programme. The five characters discriminant function; (plant height + days to heading + 1000 grain weight + days to maturity + grain yield) may be used to greater advantage to increase the genetic advance and relative efficiency of selection than grain yield alone.

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