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Analysis of genetic variability, heritability and genetic advance for yield & yield associated traits in wheat

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Abstract

The present study was undertaken to explore the characters highly responsible for yield of wheat. Genetic variability, heritability and genetic advance for yield and yield associated characters were studied for 64 wheat genotypes and data were recorded on days to heading, days to maturity, plant height, flag leaf length, spike length, spike per plant, spikelet per spike, grains per spike, test weight and yield per plant. The experiment was carried out in Randomized block design with two replications. Spikes per plant, Grain yield per plant, Flag leaf length, Spike length, grains per spike, spikelet's per spike, Days to 50 percent heading showed relatively high Genotypic coefficient of variation (GCV) & Phenotypic coefficient of variation estimates (PCV). The PCV were higher than GCV for all ten traits showing that they all interacted with the environment to some extent. High heritability was obtained for Days to heading (96.8%), Flag leaf length (81.6%), Plant height (80%), Yield (76.3%) & Spike length (63.4) which indicates High heritable portion of variation. High to medium estimates of genetic advance were obtained for plant yield (41.15), Flag leaf length (27.34), Spike length (17.27), & Plant height (16.73) indicating the roles of additive gene action & a good scope of selection using their phenotypic performance. So it concluded that Flag leaf length, Spike length, Plant height may be targeted as selection criteria in wheat breeding programs.

Keywords: Variability, heritability, genetic advance, GCV, PCV, wheat

Introduction

Wheat (*Triticum aestivum*) is one of the world's most favoured cereal crop and belongs to the family Poaceae (Graminae) and genus *Tritium*. Wheat is a monocotyledonous angiosperm originated in South West Asia. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity and the significant position it holds in the international food grain trade. Wheat is the second most produced cereal crop grown on 30.42 million hectare of area with 98.38 million tons production in India in the current Rabi season of 2017-18. The ultimate aim of plant breeding is to improve the plant characteristics for agronomic and economic superiority. In this regard, a sound knowledge of nature and extent of genetic variability present in the genotypes or breeding materials helps the breeder for a better breeding programme. Genotypic variation is always prerequisite for based on this, two facts are more important. Firstly, selection acts primarily upon the heritable variation and secondly, selection never creates variability but acts only on existing variability. The basic objective of most of the crop improvement programmes is to realize a marked improvement in crop yield. Heritability plays a very important role in selection as it predicts the crop performance. Yield in wheat is a complex character, which is influenced by polygenic traits both through direct and indirect effects. Generally, direct selection is not more effective for yield due to its low heritability and it is desirable to select various component traits indirectly for crop improvement in plant breeding.

Materials and Methods

The experiment was carried out at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi during Rabi seasons 2016-17. The agriculture research farm is situated in South-Eastern part of Varanasi city at 25° 15' North latitude and 83° 03' East longitude at an elevation of 129.23 m above the mean sea level. Experimental materials for current study consist of 64 genotypes, which were grown under randomized block design (RBD) with two replications.

The observations were recorded on five plants of each genotype from two replication on 10 quantitative traits viz. days to heading, days to maturity, plant height, flag leaf length, spike

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length, spike per plant, spikelet per spike, grains per spike, test weight and yield per plant. Analysis of variance was done for partitioning the total variation into variation due to treatment and replication according to procedure given by Panse and Sukhatame (1967) [18]. In the present investigation Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated using formula

given by Burton (1952) [4]. Phenotypic and genotypic variances expressed in percentage is usually called as the broad sense heritability. This parameter was calculated utilizing the formula given by Johnson, Robinson and Comstock (1955). The estimates of genetic advance as per cent of mean were as obtained by Johnson *et al.* (1955).

Table 1: List of wheat genotypes used in present investigation

S. No.	Name of Genotype
1.	NIAW-34(C)
2.	GW-2015-669
3.	AKAW-4842
4.	SONALIKA(e)
5.	NIAW-2844
6.	DWAP-1408
7.	DBW-71(e)
8.	GW-2010-321
9.	RWP-2013-09
10.	DBW-14(e)
11.	GW-2014-619
12.	WS-1503
13.	WR-544-(e)
14.	GW-2015-667
15.	HD-2932 (e)
16.	GW-2015-668
17.	AKAW-5014
18.	DBW-14-(e)
19.	GW-2015-670
20.	WR-544-(e)
21.	GW-2015-671
22.	RWP-2015-15
23.	DBW-71-(e)
24.	LBP-2014-(e)
25.	AKAW-4127
26.	NIAW-34(e)
27.	RAJ-4486
28.	HD-2932-(e)
29.	UP-2973
30.	SONALIKA(e)
31.	RAJ-4482
32.	RWP-2014-19P
33.	HD-2932(e)
34.	RAJ-4484
35.	DBW-71(e)
36.	RAJ-4485
37.	NIAW-2874
38.	NIAW-34(e)
39.	RWP-2014-15
40.	GW-2012-475
41.	SONALIKA(e)
42.	RWP-2013-10
43.	DBW-14(e)
44.	RWP-2014-18
45.	WR-544(e)
46.	RAJ-4483
47.	RWP-2015-11
48.	CNM-15-2
49.	HD-2932-(e)
50.	RWP-2015-16
51.	WS-15-7
52.	DBW-14-(e)
53.	UP-2972
54.	RAJ-4358
55.	SONALIKA(e)
56.	UP-2974
57.	WS-2014-07

58.	NIAW-34-(e)
59.	WS-2015-01
60.	GW-2014-624
61.	DBW-71-(e)
62.	GW-2015-672
63.	RWP-2015-14
64.	RW-544-(e)

Data were recorded for Ten quantitative characters

The technique of random sampling was adopted for recording the observations on various quantitative characters of wheat. Five plants of each genotype from two replication were selected at random at the time of recording the data on 10 characters. Data of five plants were averaged entry wise in both replications and mean data were used for statistical analysis. Recommended agronomic package and practices were applied to raise a healthy crop.

Coefficient of variation

A measurement of variance which is independent of the unit of measurement is provided by the standard deviation expressed as percentage of mean. This is known as coefficient of variation (CV).

$$CV (\%) = \frac{\text{Standard deviation}}{\text{mean}} \times 100$$

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated using formula given by Burton (1952)^[4] as follows:

Genotypic coefficient of variation (GCV)

$$GCV (\%) = \frac{\text{Genotypic standard deviation}}{\text{mean}} \times 100$$

Phenotypic co-efficient of variation (PCV)

$$PCV (\%) = \frac{\text{Phenotypic standard deviation}}{\text{mean}} \times 100$$

Heritability (h²)

The proportion of phenotypic and genotypic variances expressed in percentage is usually called as the broad sense heritability. This parameter was calculated utilizing the formula given by Johnson, Robinson and Comstock (1955) as follows:

$$h^2 (\%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

h² = heritability (in broad sense)

$\sigma^2 g$ = Genotypic Variance

$\sigma^2 p$ = Phenotypic Variance

Genetic advance

Genetic advance was estimated using the following formula,

$$\text{Genetic advance (GA)} = h^2 \cdot K \cdot \sqrt{VP}$$

Where, \sqrt{VP} = Phenotypic standard deviation.

h² = Heritability

K = Selection differential at 5 selection intensity (k= 2.06, Lush 1947)

Genetic advance as percent of mean /Genetic Gain (%)

$$GA \text{ as percent of mean} = \frac{\text{Genetic advance}}{\text{mean}(x)} \times 100$$

Where

x = General mean of the characters

GA = Genetic advance

The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al.* (1955).

Low = Less than 10%

Moderate = 10-20%

High = More than 20%

Result and Discussions

Analysis of variance (ANOVA)

The result showed highly significant difference for three characters under study *viz.* Days to heading, plant height and flag leaf length due to genotypes for all the characters studied indicating presence of sufficient genetic variation among 64 genotypes. Some traits under study was found to be non-significant differences among the genotypes *viz.* Days to maturity, Length of spike, Spike per plant, Spikelet's per Spike, Grains per Spike, Test weight and Yield per plant., Table 2.

Table 2: Analysis of variance (ANOVA) for 10 characters in 64 wheat genotypes

Source of variation	Degree of freedom	Days to Heading	Days to Maturity	Plant Height	Flag Leaf Length	Length of Spike	Spike Per Plant	Spikelet's Per Spike	Grains Per Spike	Test Weight	Yield Per Plant
Replication	1	0.09	0.021	0.02	0.10	0.02	0.35	0.02	5.70	0.02	0.02
Treatment	63	35.29**	3.00	3.00**	11.24**	1.48	0.95	2.63	15.33	6.24	6.23
Error	63	0.57	1.17	1.17	1.14	0.33	0.67	0.69	7.73	1.81	1.81

** Significant at P≤ 0.01 level of significance

Table 3: Summary table of the range of variation, general mean, genotypic, phenotypic, error variance, heritability, genetic advance, phenotypic coefficient of variation, genotypic coefficient of variation and environmental coefficient of variation.

		DH	DM	PH	FLL	LPS/SL	SPP	SLPS	GPS	TW	YP
Range	Min	56.75	100.67	68.34	15.10	7.69	2.33	12.67	23.34	35.29	4.13
	Max	77.75	106.15	99.00	25.32	11.72	5.50	19.00	39.83	43.51	12.03
Grand mean		64.90	102.96	83.63	19.61	9.24	3.68	15.50	34.14	39.00	8.17
Genotypic variance		17.36	0.916	35.12	5.05	0.58	0.14	0.97	3.80	2.21	2.12
Phenotypic variance		17.93	2.09	43.91	6.19	0.91	0.81	1.66	11.53	4.02	2.78
Error variance		0.57	1.17	8.78	1.14	0.33	0.67	0.69	7.72	1.81	0.66
h ² (Broad Sense)%		96.8	43.8	80	81.6	63.4	17.1	58.4	33	55	76.3
Genetic advance as % of mean		16.67	1.62	16.73	27.34	17.27	11.00	12.81	8.66	7.46	41.15
PCV (%)		6.52	1.40	7.92	12.69	10.32	24.42	8.31	9.94	5.14	20.42
GCV (%)		6.42	0.93	7.09	11.46	8.22	10.09	6.35	5.71	3.81	17.84
ECV (%)		1.17	1.05	3.54	5.44	6.24	22.24	5.36	8.14	3.45	9.94

DH=Days to heading, DM=Days to maturity, PH=plant height, FLL=Flag leaf length, SL= Spike length, SPP=Spike per plant, SLPS=Spikelet per spike, GPS=Grains per spike, TW=Test weight, YP=Plant yield

The estimates of phenotypic coefficient of variation, genotypic coefficient of variation and environmental coefficient of variation are presented in table 3.

The results of phenotypic coefficient of variation (PCV) revealed that the character spike per plant showed highest phenotypic coefficient of variation (24.42%) followed by yield per plant (20.42%) and flag leaf length (12.69%). Phenotypic coefficient of variation for characters like Spike length, grains per spike, spikelet per spike, plant height, days to heading and test weight were estimated to be 10.32%, 9.94%, 8.31%, 7.92%, 6.52% and 5.14% respectively. Maximum value for genotypic coefficient of variation (GCV) was obtained for characters yield per plant i.e.17.84%, followed by flag leaf length (11.46%) and spike per plant (10.09%). Characters like spike length, plant height, days to heading, Spikelet per spike, grains per spike and test weight showed GCV of 8.22%, 7.09%, 6.42%, 6.35%, 5.71% and 3.81% respectively. Lower value of GCV (≤ 10) for a character indicates the lesser influence of the environment for the variation observed in that particular character.

Variability

The development of an effective plant breeding programme is dependent upon the presence of genetic variability and selection for yield improvement can only be effective if sufficient genetic variability is present in plant population (Ali *et al.*, 2008) [2].

The variance measure the variation within the trait but it does not provide the real measure for comparison of variation between different traits. The coefficient of variation truly provides a relative measure of variance among the different traits. In the present study, all the traits showed higher phenotypic coefficient of variation than the genotypic coefficient of variation. The characters like days to heading, days to maturity, plant height, flag leaf length, spike length, spike per plant, spikelet per spike, grains per spike, test weight and yield per plant exhibited high value of PCV than their respective GCV, which is in accordance with studies of Sharma and Garg (2002) [20], Yadav *et al.*, (2006)., and Navin *et al.*, (2014). Thus, the characters showing maximum PCV would be considered while making selection process in spite of environmental influence to a certain extent.

The maximum value of GCV was found for grain yield (17.84), flag leaf length (11.46), spike per plant (10.09), spike length (8.22), plant height (7.09), days to heading (6.42), spikelet per spike (6.35), grains per spike (5.71), test weight (3.81), days to maturity (0.98) respectively. Thus, the traits with high GCV are to be considered during selection.

Heritability and Genetic Advance

The maximum percentage of heritability was observed for days to heading (96.8%) and flag leaf length (81.6%) followed by plant height (80%) and yield per plant (76.3%). The least percent of heritability was observed for spike per plant (17.1%). The estimates of heritability in broad sense and genetic advance are presented in table 3. The estimates for genetic advance as a percent of mean was found maximum for yield per plant (41.15) followed by flag leaf length (27.34) and minimum in days to maturity (1.62). This suggests that these quantitative traits were governed by additive gene & selection could be effective. The graphical representation of phenotypic, genotypic and error coefficient of variation, genetic advance and heritability of yield components in 64 wheat genotypes are presented in fig 1.

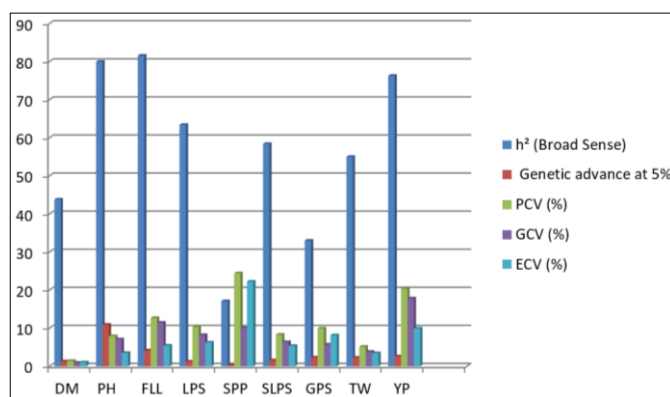


Fig 1: Histogram depicting estimates of phenotypic, genotypic and error coefficient of variation, genetic advance and heritability of yield components in 64 wheat genotypes.

The effectiveness of selection for a trait depends in the expression of phenotypic differences among the genotypes in population; this concept is referred to as heritability. The heritability of a character has major impact on the method chosen for entire population improvement.

The heritability is the measure of the fraction of phenotypic variation caused by various gene actions. In present study days to heading 96.8 per cent, flag leaf length 81.6 per cent, plant height 80 per cent, plant yield 76.3 per cent, spike length 63.8 per cent, spikelet per spike 58.4 per cent, test weight 55 per cent exhibited high heritability. Similar results were published by Ikramullah *et al.*, (2011) [18], kalimulah *et al.*, (2012), Iqbal *et al.*, (2017) [19].

The lowest heritability was exhibited by spike per plant 17.1 per cent. Since high heritability indicates least influence of

environment.

Only heritability provides no clear about the amount of genetic improvement that is expected to come out from selection of individual genotype in a population. High genetic advance as percent of mean indicated predominance of additive gene action. Hence, knowledge of genetic advance as percent of mean coupled with heritability is more useful in formulating selection procedure.

High heritability coupled with high genetic advance as percent of mean was recorded for plant yield (41.15), flag leaf length (27.34), plant height (16.73), days to heading (16.67) indicating effectiveness of selection for the improvement of these traits. These results show similarity with findings of Cheema *et al.*, (2006)^[6], Singh *et al.*, (2012)^[21], Desheva *et al.*, (2015)

However, some character like test weight showed low genetic advance along with high level of heritability which indicates presence of non additive gene action. This suggests that selection for such traits will be not be worthwhile.

Summary and Conclusion

Analysis of variance showed the significant differences among the genotypes for many characters under study indicating that there is sufficient scope for selection of promising genotypes for yield improvement.

From the variability studies, maximum PCV exhibited by spike per plant, plant yield and flag leaf length and GCV was found highest for plant yield. Further, high heritability coupled with high expected genetic advance as per cent of mean was observed for days to heading, plant yield, flag leaf length and spikelet per spike indicating the less influence of environmental variance in the inheritance of these traits.

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