



ISSN (E): 2277-7695  
ISSN (P): 2349-8242  
NAAS Rating: 5.23  
TPI 2022; SP-11(10): 716-718  
© 2022 TPI  
[www.thepharmajournal.com](http://www.thepharmajournal.com)  
Received: 21-07-2022  
Accepted: 24-08-2022

**Bhawna Nagar**

Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, MPUAT, Udaipur, Rajasthan, India

**Dr. Hemlata Sharma**

Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, MPUAT, Udaipur, Rajasthan, India

**Sarita Chaudhary**

Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, MPUAT, Udaipur, Rajasthan, India

**Rohinee**

Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, MPUAT, Udaipur, Rajasthan, India

## To study genetic variability for yield and its contributing traits in bread wheat

**Bhawna Nagar, Dr. Hemlata Sharma, Sarita Chaudhary and Rohinee**

### Abstract

In the present investigation, F<sub>2</sub> population of three crosses viz., HD 2967 × Raj 4120, DBW 173 × Raj 3777 and GW 451 × Raj 4120, their six parents and check HI 1544 were evaluated under Randomized Complete Block Design with three replication at Instructional Farm, Rajasthan College of Agriculture, MPUAT, Udaipur during Rabi 2021-2022. Analysis of variance indicated that the mean sum of square due to genotypes was found significant for all of the characters under this investigation showing that there is enough variability among genotypes for different traits. The estimates of Phenotypic Coefficient of Variation (PCV) were little higher than their corresponding Genotypic Coefficient of Variation (GCV) pointing out that the environment had minor effect on the expression of the different traits. Higher estimates for GCV and PCV were revealed for grain yield per plant followed by total chlorophyll content estimation, number of effective tillers per plant, length of awns, spike length and harvest index. The characters had high heritability along with high genetic gain were total protein content in grains, number of effective tillers per plant, grain yield per plant and length of awns.

**Keywords:** Wheat, genetic variability, heritability and genetic gain

### Introduction

Wheat [*Triticum aestivum* L.] is most important food crop in the world which belongs to genus *Triticum* and family poaceae. Wheat is a self-pollinated, monocotyledonous plant that had originated from South West Asia. The genus *Triticum* is composed of diploid, tetraploid and allohexaploid species. So, polyploidy has played a dominant role in wheat evolution. There are different species of wheat, out of which only three *Triticum* species are mostly cultivated throughout the world. These are *Triticum aestivum* (bread wheat), *Triticum durum* (macroni wheat) and *Triticum dicoccum* (emmer wheat).

The most widely grown crop in the world and a staple food for 40% of the world's population, wheat (*Triticum aestivum* L. and *Triticum durum* L.) supplies 20% of all dietary calories. With 12.1% protein, 1.8% fats, 1.8% ash, 2.0% reducing sugars, 59.2% starch, 70% total carbohydrate, and 314 K calories per 100 g, it has a decent nutritional profile. Together with the minerals zinc and iron, it provides a good source of vitamins including thiamine and vitamin B.

For each crop development effort, knowledge of the genetic variability in the genetic system of a certain crop is required. Wheat grain yield is a complex characteristic that depends on its constituent features. Selection must therefore take advantage of the variety that exists within each component characteristic in order to maximise grain production. Utilizing genetic metrics like variance, genotypic coefficient of variation, heritability and genetic progress as a basis for choosing certain exceptional genotypes from the current genotypes, the genetic variability in a population can be classified into heritable and non-heritable variation (Tsegaye *et al.* 2012) [12].

### Materials and Methods

The experimental material consisted of F<sub>2</sub> population of three crosses viz., HD 2967 × Raj 4120, DBW 173 × Raj 3777 and GW 451 × Raj 3777, their six parents and check HI 1544 were tested using Randomized Complete Block Design with three replications at Instructional Farm, RCA, Maharana Pratap University of Agriculture and Technology, Udaipur. The F<sub>2</sub> population was grown in 20 rows of 2 m length, while parents in 4 rows of 2 m length. All the recommended package of practices were followed to raise a good and healthy crop. The observations were recorded on ten randomly selected competitive plants for characters, viz., plant height (cm), number of effective tillers per plant, spike length (cm), number of spikelets per plant, length of awns (cm), number of grains per spike, flag leaf area (cm<sup>2</sup>), 1000- grain

**Corresponding Author:**

**Bhawna Nagar**

Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, MPUAT, Udaipur, Rajasthan, India

weight (g), biological yield per plant (g), grain yield per plant (g), harvest index (%), total protein content in grains (%) and total chlorophyll content estimation (mg/g), while the data on days to 50% flowering and days to 75% maturity were recorded on the whole plot basis. The analysis of variance was worked out separately for each character as per the method suggested by Panse and Sukhatme (1985) [10] in order to test the difference among the genotypes. The coefficient of genotypic and phenotypic variation was calculated by using the formula suggested by Burton (1952) [5]. Estimates of heritability (bs) was calculated as per the formula suggested by Burton and Devane (1953) [6]. Genetic advance and genetic gain was computed as per the formula described by Johnson *et al.* (1955) [8].

## Result and Discussion

The analysis of variance for fifteen characters revealed the genotypes showed highly significant differences for all the traits under study *viz.*, days to 50% flowering, days to 75% maturity, plant height, number of effective tillers per plant, spike length, number of spikelets per plant, length of awns, number of grains per spike, flag leaf area, 1000-grain weight, biological yield per plant, grain yield per plant, harvest index, total protein content in grains and total chlorophyll content estimation. Selection of these characters is useful for wheat improvement programme. Similar finding for such yield related traits have been reported by Farshadfar and Estehghari (2014) [7] and Bhutto *et al.* (2016) [4].

The parameters of genetic variability *viz.*, mean, range, phenotypic and genotypic coefficient of variation (%), heritability (%) in broad sense, genetic advance and genetic gain as per cent of mean (genetic gain) for each trait are presented in Table 1. In this study, the phenotypic coefficient of variation (PCV) is slightly higher than the genotypic coefficient of variation (GCV) for most of the traits indicating little effect of environmental variations on the characters. The magnitude of genotypic coefficient of variation (GCV) was recorded highest for the character *viz.*, total chlorophyll content (59.90%) followed by number of effective tillers per plant (29.39%), total protein content in grains (21.98%), grain yield per plant (15.93%), length of awns (10.44%). While moderate GCV was recorded for length of spike (9.57%), harvest index (8.97%), days to 50% flowering (8.59%), flag leaf area (7.83%), number of grains per spike (7.9%), biological yield per plant (6.53%). GCV was found low for 1000-grain weight (5.95%), number of spikelets per plant (5.65%), plant height (3.21%) and Days to 75% maturity (2.23%).

Similar findings were reported by Mishra *et al.* (2011) [9] and Potdukhe *et al.* (2013) [11].

High magnitude of PCV was observed for total chlorophyll content (59.93%) followed by number of effective tillers (29.99%), total protein content in grains (22.43%), grain yield per plant (18.53%), length of awns (12.15%), spike length (11.37%) and harvest index (11.11%). The characters *viz.*, flag leaf area (9.89%), number of grains per spike (9.80%), biological yield per plant (8.96%) and days to 50% flowering (8.93%) exhibited moderate magnitude of phenotypic coefficient of variation. Low magnitude of PCV was observed for days to 75% maturity (2.59%), plant height (4.60%), number of spikelets per plant (8.28%) and 1000 grain weight (8.62%). The results showed that phenotypic coefficient of variation is slightly higher than their corresponding genotypic coefficient of variation for all the traits indicates negligible

effect of environment on the expression of traits and selection may be effective. Similar findings were reported by Kareem *et al.* (2011) [1].

Broad sense heritability was estimated for all the traits under study. Presence of high heritability is an important aspect for choosing the suitable trait for selection. The majority of the characters had high heritability and it was recorded highest for the total chlorophyll content estimation (99.92%) followed by total protein content in grains (96.07%), number of effective tillers (95.98%), days to 50% flowering (92.64%), days to 75% maturity (74.29%), grain yield per plant (73.84%), length of awns (73.80%), spike length (70.86%) and harvest index (65.12%) while moderate heritability was observed for flag leaf area (62.76%), number of grains per spike (59.94), biological yield per plant (53.19), plant height (48.85), 1000 grain weight (47.58) and number of spikelets per plant (46.64). High heritability was observed for most of the characters under study indicating the strong genetic base. Similar findings were reported by Yadav *et al.* (2011) [3] and Wahid and Shahla (2014) [2].

The maximum genetic advance was recorded for number of spikelets per plant (12.54%) followed by days to 50% flowering (11.19%), number of grains per spike (7.83%) and harvest index (5.70%). The characters *viz.*, total chlorophyll content estimation (1.30%), length of awns (1.35%) and length of spike (1.84%) exhibited low genetic advance. Present findings are in accordance with the findings of Mishra *et al.* (2011) [9] and Potdukhe *et al.* (2013) [11].

The maximum genetic advance as per cent of mean *i.e.* genetic gain was recorded for number of effective tillers per plant (59.31%) followed by total protein content in grains (44.38%) and grain yield per plant (28.19%), while it was observed low for days to 75% maturity (3.96%), plant height (4.63%) and number of spikelets per plant (7.95%), 1000 grain weight (8.45) and biological yield per plant (9.82%). Present findings are in accordance with the findings of Farshadfar and Estehghari (2014) [7].

**Table 1:** Variability parameters

SN	Characters	GCV	PCV	h <sup>2</sup>	GA	GG
1	Days to 50% Flowering	8.59	8.93	92.64	11.19	17.04
2	Days to 75% maturity	2.23	2.59	74.29	4.51	3.96
3	Plant height	3.21	4.60	48.85	4.31	4.63
4	No. of effective tillers per plant	29.39	29.99	95.98	5.06	59.31
5	Spike length	9.57	11.37	70.86	1.84	16.60
6	No. of spikelets per plant	5.65	8.28	46.64	12.54	7.95
7	Length of awns	10.44	12.15	73.80	1.35	18.48
8	No. of grains per spike	7.59	9.80	59.94	7.63	12.10
9	Flag leaf area	7.83	9.89	62.76	5.13	12.78
10	1000 grain weight	5.95	8.62	47.58	3.20	8.45
11	Biological yield per plant	6.53	8.96	53.19	3.71	9.82
12	Grain yield per plant	15.93	18.53	73.84	3.00	28.19
13	Harvest index	8.97	11.11	65.12	5.70	14.91
14	Total protein content in grains	21.98	22.43	96.07	4.10	44.38
15	Chlorophyll content	59.90	59.93	99.92	1.30	12.33

## Conclusion

Analysis of variance indicated that there is a presence of huge amount of variability among the materials under study. The estimated values of Phenotypic Coefficient of Variation (PCV) were in general little higher than their corresponding Genotypic Coefficient of Variation (GCV) pointing out that the environment had minor effect on the expression of the different traits. High heritability coupled with high genetic gain was observed for the traits like grain yield per plant,

length of awns, number of effective tillers per plant and total chlorophyll content estimation indicating that all these traits are regulated by additive gene action and the direct selection of these traits are expected to show genetic improvement in bread wheat.

## References

1. Abdel El-Kareem THA, El-Saidy AEA. Evaluation of yield and grain quality of some bread wheat genotypes under normal irrigation and drought stress conditions in calcareous soils. *J Biol. Sci.* 2011;11:156-164.
2. Abdul Wahid Baloch, Shahla Karim Baloch, Siraj Ahmed Channa, Abdul Majeed Baloch M, Ali Masood Ahmed Junejo, Gul Muhammad Baloch. Character association and heritability analysis in elite bread wheat cultivars. *International Journal of Applied Biology and Pharmaceutical Technology.* 2014;5(4):15-18.
3. Yadav AK, Maan RK, Kumar S, Kumar P. Variability, heritability and genetic advance for quantitative characters in hexaploid wheat (*Triticum aestivum* L.). *Electronic Journal of Plant Breeding.* 2011;2:405–408.
4. Bhutto A, Rajpar A, Kalhor S, Ali A, Kalhor F, Ahmed M, *et al.* Correlation and Regression Analysis for Yield Traits in Wheat (*Triticum aestivum* L.) *Natural Science.* 2016;8:96-104.
5. Burton GW. Quantitative inheritance in grasses. *Proc. 6<sup>th</sup> International Grassland Congress.* 1952;1:277-283.
6. Burton GW, Devane DE. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal.* 1953;45:478-481.
7. Farshadfar E, Estehghari MR. Estimation of genetic architecture for agro-morphological characters in common wheat. *International Journal of Bioscience.* 2014;5(6):140-147.
8. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. *Agronomy Journal.* 1955;47:14-318.
9. Mishra AK, Yadav VK, Tiwari RK. Character association and path analysis in bread wheat (*Triticum aestivum* L.). *Environment and Ecology.* 2011;29(4A):1983-1985.
10. Panse VG, Sukhatme PV. *Statistical Methods for Agricultural Workers*, ICAR New Delhi; c1985.
11. Potdukhe, Nilkanth Ramachandra, Nukasani V, Swati Bharad, Deshmukh S, Shinde SM. Genetic variability, correlation and path analysis in wheat. *J Wheat Res.* 2013;5(2):48-51.
12. Tsegaye D, Dessalegn T, Dessalegn Y, Share G. Genetic variability, correlation and path analysis in durum wheat germplasm. *Agricultural Economics Research Review.* 2012;1(4):107-112.