



Tailoring Variability for Yield and Quality Traits in Bread Wheat (*Triticum aestivum* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The present research was carried out at the Breeder Seed Production Unit, JNKVV, Jabalpur, Madhya Pradesh using twenty-one sets of bread wheat genotypes. These were sown and evaluated under the timely sown condition in a randomized complete block design with three replication during post-rainy season 2021- In the present investigation thirteen morphological and one biochemical trait were analyzed. The analysis of variance indicated the occurrence of significant variation among the genotypes for all the traits. The present results indicate that the estimates of PCV were in general slightly elevated than their corresponding GCV for most of the traits studies which indicated that the variability for these traits in the genotypes was not much affected by the environments for the expression of these traits. High heritability with high genetic advance was observed for flag leaf length, grains yield per plant, biological yield per plant, and tiller per plant, and high heritability (narrow sense) coupled with the moderate genetic advance in percent of mean was observed for flag leaf width, grains per spike, plant height, and spikelet per spike. It can be summarized that constructive variability in parents and progenies was developed through hybridization which can be appropriately utilized for the selection of suitable genotypes to obtain high protein and high yield potential in bread wheat.

Keywords: *Wheat; variability; heritability; genetic advance.*

1. INTRODUCTION

Wheat (*Triticum aestivum* L.) is a member of the family *Poaceae* and one of the essential cereal crops for the world's population. Because of its trouble-free cultivation, ecological suitability, and wider adaptability to agro-climatic conditions, it is very popular among growers. Wheat being a widely consumed cereal staple crop, it may be exploited as a suitable target for protein and yield attributing traits for minimizing the nutritional gaps in cereal diet-based nations. It is however a difficult job for the plant breeders to increase the level of crop production as the up-and-coming population of the world, especially in developing countries like India. Worldwide, primarily in Asia and the African region, nearly 2 billion people have suffered from malnutrition caused by a cereal-based diet [1]. It is forecasted that the situation will be even more severe than expected soon if no implementation of imperative remedial strategies is done, as the global population is escalating alarmingly. All kinds of malnutrition remain a global challenge. It was estimated that in 2020, 22.0% (149.2 million) of children aged under 5 years were suffering from stunting, 6.7% (45.4 million) were affected by wasting, and 5.7% (38.9 million) were overweight. However, the actual figures are probably more than estimated (FAO, WHO, WFP, UNICEF and IFAD, 2021) [2].

Since It is not feasible to increase the cultivated area under production. therefore, there is a need to increase productivity by budding high-yielding varieties along with high protein content to deal with severe malnutrition conditions. The development of high-yielding and high protein-containing varieties depends upon the existence of genetic variability present in the wheat germplasm. As a result, analysis of genetic variation among the genotypes plays a vital role ahead of crafting any breeding program Although the accomplishment of genetic enhancement in any yield traits and quality depends upon the nature of variability there in the characters. For this reason, an idea of the degree of variability present in the gene pool of a particular crop species is extremely essential to a plant breeder for a preliminary plant breeding program Generally, in a crop improvement program genetic component of variation is important in view of the fact that only this component is transmitted to the offspring or the next generation. Nevertheless, when we are trading with initial generations, the genetic variance consists of additive as well as dominance

components only if, we neglect the epistatic component. Ever since in self-pollinated crops such as wheat where the dominance component has almost no contribution to the phenotype of homozygous lines derived from a particular population due to selfing. As a result, in such cases, simply the additive component of the genetic variance is significant. Therefore, for the F_1 generation, the relative amount of additive component of variance to the total phenotypic variance is a much more suitable evaluation of heritability.

Heritability along with estimates of genetic advance facilitates the understanding of the kind of gene action involved in the expression of various quantitative characters. Since the high and low values of genetic advance are suggestive of additive and non-additive gene action respectively. Hence, it will not be an accurate measure to select parents on the basis of phenotypic performance only as phenotypically superior lines may capitulate to poor recombinants. It is, therefore, very crucial that the parents ought to be selected on the basis of their genetic worth. In the outlook of the above, an attempt has been made in the present research to assess a set of twenty one genotypes of bread wheat. The goal of this study is to investigate genetic variability, heritability, and genetic advance and to estimate the component of variances for protein, yield, and its attributing traits.

2. MATERIALS AND METHODS

2.1 Plant Material and Experimental Design

For the present investigation, a field experiment was conducted at Breeder Seed Production Unit, Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur, M.P situated at an elevation of about 306.06 m above sea level. The experimental materials consisted of six well-adapted varieties of wheat, viz., JW-1203, WB-02, GW-322, HI-1633, HI-1634 and MP-3382, and their 15 F_1 's. Parental lines were grown and all possible single crosses (excluding reciprocals) were made in a half-diallel fashion (6 x 6) during Rabi 2020-2021. The experiment was conducted using a randomized complete block design with three replications during 2021-2022, seeds of six parents and their 15 F_1 'S were sown by hand dibbling method and the length of each row was kept 1m long by maintaining row to row and plant to plant distances of 22.5 cm and 10 cm, respectively.

2.2 Data Collection

Data were recorded on five randomly selected plants in each replication on the following characters: Days to 50% heading, plant height, days to maturity, spike length, spikelet per spike, grains per spike, tiller per plant, flag leaf length, flag leaf width, thousand kernel weight, biological yield per plant, harvest index, grain yield per plant. Days to 50% and days to maturity were measured on a plot basis, while plant height, spike length, spikelet per spike, grains per spike, tiller per plant, flag leaf length, and flag leaf width were measured on five representative plants in field condition before harvesting. Whereas, thousand kernel weight, biological yield per plant, and grain yield per plant on five representative plants after harvesting. The harvest index of all the plants was calculated by dividing the grain yield per plant by the biological yield per plant.

$$HI(\%) = \frac{\text{Economic yield(g)}}{\text{Biological yield (g)}} \times 100$$

2.3 Total Protein Content Determination

Total protein content in the present investigation is determined by the method developed by Kjeldahl, Johann in 1883 [3]. A 1 gm of flour is digested with a strong acid so that it releases nitrogen which can be determined by a suitable titration technique. The amount of

protein present is then calculated from the nitrogen concentration of the sample by multiplying it by a conversion factor of 5.70.

2.4 Statistical Analysis

Data were subjected to Analysis of Variance (ANOVA) using for loop function for RCBD design through R statistical package (version 4.2.1), a free open source software available at <https://cran.r-project.org/bin/windows/base/>. Analysis of variance for the design of the experiment was computed as recommended by Panse and Sukhatme [4] whereas heritability in a narrow sense by Kempthorne and Curnow [5] and genetic advance by Johnson et al. [6].

3. RESULTS AND DISCUSSION

Analysis of variance had shown high significant differences among the genotypes used in the present examination for protein, yield, and yield attributing traits which further shows the existence of the broad range of genetic variability. The mean squares for all are presented in Table 1. Such kind of results was also reported by Mohammad Imran et al. [7], Kumar et al. [8] and Singh et al. [9]. The results indicated that constructive variability in offspring and parents was developed in the course of hybridization, which could be suitably utilized for selection and further bread wheat improvement program.

Table 1. Analysis of variance for the traits for 21 sets of genotypes during the post-rainy season (2021-2022)

	Replication	Treatments	Error
Degree of freedom	2	20	40
Days to 50% Flowering	12.333	18.605***	2.417
Plant Height(cm)	7.520	103.14***	2.770
Days to Maturity	21.330	24.65***	5.100
Spike length(cm)	0.448	0.7294***	0.048
Spikelet/spike	2.102	4.032***	0.568
Grains/Spike	25.750	72.52***	10.120
Tiller /plant	1.063	3.254***	0.813
flag leaf length(cm)	0.310	58.48***	1.470
Flag leaf width(cm)	0.017	0.10931***	0.005
1000 Kernel weight(g)	1.307	4.008*	1.923
Biological yield/plant(g)	84.340	232.57***	13.190
Harvest index(%)	42.000	100.67*	48.810
Grains yield / plant(g)	17.030	147.08***	12.820
Total protein (%)	0.132	1.891***	0.422

Where, *, **, *** are significant at 0.1, 0.05 and 0.001%

Table 2. Variability amongst all the traits during the post-rainy season (2021-2022)

S. No	Traits	Mean	Range		CV		H%	GAM%
			Min.	Max.	PCV	GCV		
1	Days to 50% Flowering	66.10	60.00	73.00	4.23	3.51	69.07	6.02
2	Plant Height (cm)	92.47	79.12	102.24	6.51	6.25	92.34	12.38
3	Days to Maturity	117.14	110.00	124.00	2.91	2.18	56.1	3.36
4	Spike length (cm)	9.67	8.48	11.03	5.42	4.93	82.55	9.22
5	Spikelet/spike	17.52	14.23	19.56	7.49	6.13	67.01	10.34
6	Grains/Spike	44.90	31.26	54.67	12.39	10.16	67.27	17.16
7	Tiller /plant	6.49	4.00	9.00	19.65	13.89	50	20.24
8	Flag leaf length (cm)	22.86	16.10	33.15	19.79	19.07	92.83	37.84
9	Flag leaf width (cm)	1.85	1.21	2.10	10.72	10.07	88.14	19.47
10	1000 Kernel weight (g)	42.61	39.18	46.26	3.8	1.96	26.55	2.08
11	Biological yield/plant (g)	32.97	14.60	56.49	28.18	25.94	84.72	49.18
12	Harvest index (%)	70.31	48.01	85.69	11.56	5.91	26.15	6.23
13	Grains yield / plant (g)	23.28	10.12	42.26	32.6	28.74	77.73	52.19
14	Total protein (%)	12.42	10.05	14.88	7.69	5.64	53.72	8.51

The values of GCV and PCV were presented in Table 2 along with the mean and range for all the fourteen traits. A broad range of variability at hand in any crop always provides a better likelihood of selecting the desired type [10]. The accomplishment of crop improvement depends on vigilant management of variability and techniques to be used in any case will depend upon a clear understanding of the degree and nature of variability. Nevertheless, screening of the materials considered under this investigation induced ample variability for all fourteen characters. Similar results on variability have been reported by Mohammad Imran et al. [7]. Kumar et al. [11], for various yield and quality components in wheat. In the midst of GCV & PCV, the present results revealed that the estimates of the phenotypic coefficient of variation were in general slightly elevated than their corresponding genotypic coefficient of variation for all the traits which indicated that the variabilities for these traits in the genotypes were not much affected by the environments for the expression of these traits. A similar finding has been reported by Dhananjay et al. [12], Singh et al. [9], and Kumar and Kumar [13] for days to flowering, days to maturity, plant height, tillers per plant spike length, grains per spike, thousand-grain weight, biological yield per plant, grain yield per plant, harvest index, protein content, flag leaf area, in wheat.

In the present investigation, very high estimates of heritability (>30%) in a narrow sense were

observed for flag leaf length (92.83), plant height (92.34), flag leaf width (88.14), biological yield (84.72), spike length (84.55), and grain yield per plant (77.73). High (>50%) for days to 50% flowering (69.07), spikelet per spike (67.01), grains per spike (67.27), days to maturity (56.1), total protein (53.72). Whereas, moderate (30-50%) heritability for tiller per plant (50), while low (0-30%) heritability for harvest index (26.15) and thousand kernel weight (26.55). High heritability indicates the possibility of genetic improvement of these traits through selection. Similar results were reported by Kumar et al. [10]. High heritability estimates were also reported by Panwar and Singh [11] and Asif et al. [12] for plant height. High heritability estimates for these traits indicated it might be due to the presence of additive and additive x additive type of gene effects. This indicates that, if these traits may be subjected to mass or progeny or family selection, aimed at exploiting additive (fixable) genetic variance, a widely tailored genotype could be developed possessing good productivity and with better protein in wheat.

Genetic advance is the improvement in the mean genotypic value of selected plants over the parental population Johnson et al. [6]. Characters exhibiting high heritability may not be necessarily given high genetic advance. Johnson et al. [6] showed that high heritability should be accompanied by high genetic advance to arrive at a more reliable conclusion. The breeder should be cautious in making selections based

on heritability as it includes both additive and non-additive gene effects. A high estimate of expected genetic advance expressed as a percentage of the mean (> 20%) was observed high for grain yield per plant (52.19), biological yield per plant (49.18), flag leaf length (37.84), and tiller per plant (20.24), whereas, Moderate (10-20%) estimate of genetic advance was recorded for flag leaf width (19.47), grains per spike (17.16), plant height (12.38) and spikelet per spike (10.34). Whereas all remaining traits recorded low genetic advance. Similar findings were also reported by Mohammad Imran et al. [7] for grain yield per plant and its contributing characteristics in wheat.

High heritability with high genetic advance was observed for flag leaf length, grains yield per plant, biological yield per plant, and tiller per plant, and high heritability (narrow sense) coupled with the moderate genetic advance in percent of mean was observed for flag leaf width, grains per spike, plant height, and spikelet per spike [13,14]. Indicated that there is the least influence of the environment in the expression of these traits and the selection of desirable plants could be easily made on the basis of these traits. High heritability along with the low genetic advance in percent of mean was observed for days to 50% flowering days to maturity, and total protein content indicated the presence of non-additive gene action [15,13]. Similar findings were also reported earlier by Kumar et al. [10], Singh et al. [9] and Yadawad et al. [16] for grain yield and its contributing traits in spring wheat.

4. CONCLUSION

The panorama for increasing global food and nutrition security needs the cultivation of high-yielding and high-quality wheat in the framework of sustainable agriculture to achieve the sustainable development goal. However, from our investigation, it is clear that the variability can be created by utilizing the suitable resources and germplasm in wheat, to make it much more nutritive and productive. Our results indicated that useful variability in parents and progenies was developed through hybridization which can be properly utilized for the selection of suitable genotypes based on genetic parameters to obtain high protein and high yield potential in bread wheat.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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