

Tailoring variability for protein and yield in bread wheat (*Triticum aestivum* L.)

Abstract

The present research was carried out at the Breeder Seed Production Unit, JNKVV, Jabalpur, Madhya Pradesh using twenty one set of bread wheat genotypes. These were sown and evaluated under timely sown condition, in a randomized complete block design with three replication during post-rainy season 2021-22. In present investigation thirteen morphological and one biochemical traits were analyzed. The analysis of variance indicated the occurrence of significant variation among the genotypes for all the traits. The present results publicized that the estimates of PCV were in general slightly elevated than their corresponding GCV for most of the traits studies which indicated that the variabilities 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 were observed for flag leaf length, grains yield per plant, biological yield per plant and tiller per plant, and high heritability (narrow sense) coupled with moderate genetic advance in percent of mean were 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 selection of suitable genotypes to obtained 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 family poaceae and one of the essential cereal crop for the world's populations. Because of its trouble-free cultivation, ecological suitability and wider adaptability in agro-climatic conditions, it is very popular amongst the growers. Wheat being widely consumed cereal staple crop, it may be exploited as an suitable target for protein and yield attributing traits for minimizing the nutritional gaps in cereal diet-based nations. It is however a difficult job to the plant breeders to augment the level of crop production as the up-and-coming population of the world, especially in the 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 (Grew, 2018)^[4]. It is forecasted that the situation will be even more severe than expected soon if no any implementation of imperative remedial strategies is done, as the global population is escalating alarmingly. All kinds of malnutrition remains a global challenge. It was estimated that in 2020, 22.0% (149.2 million) 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 to be more than the estimated (FAO, WHO, WFP, UNICEF and IFAD, 2021)^[3].

Since, It is not feasible to increase the cultivated area under the production. therefore, there is need to increase the productivity by budding high yielding varieties along with high protein content to deal with the severe malnutrition conditions. The development of high yielding and high protein containing varieties is depend upon the existence of genetic variability present in the wheat germplasm. As a result, analysis of genetic variation amongst the genotypes plays a vital role ahead of crafting the any breeding programme. 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 an extremely essential to a

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plant breeder for preliminary plant breeding programme. Generally, in crop improvement programme, 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 have 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 initial generation, the relative amount of additive component of variance to the total phenotypic variance is much more suitable evaluation of heritability.

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Heritability along with estimates of genetic advance facilitate in understanding the kind of gene action involved in the expression of various quantitative characters. Since, the high and low values of genetic advance are suggestive to additive and non-additive gene action respectively. Hence, it will not be a accurate measure to select parents on the basis of phenotypic performance only as phenotypically superior lines may capitulate poor recombinants. It is, therefore, very crucial that the parents ought to be selected on the basis 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 the genetic variability, heritability, genetic advance and to estimate the component of variances for protein, yield and its attributing traits.

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2. Materials and Methods

2.1 Plant materials

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For the present investigation, field experiment was conducted at Breeder Seed Production Unit, Jawaharlal Nehru Krishi Vishwa Vidhyalaya, Jabalpur, M.P situated at an elevation of about 306.06 m above from 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 F1'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 randomized complete block design with three replications during 2021-2022, seeds of six parents and their 15 F1'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 Agronomic traits

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Data were recorded on five randomly selected plants in each replications 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 karnel weight, biological yield per plant, harvest index, grain yield per plant, total protein content.

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2.2 Total protein content determination

Total protein content in the present investigation is determined by the method developed by Kjeldahl, Johann in 1883^[7]. 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.

2.3 Statistical Analysis

Results 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 experiment was computed as recommended by Panse and Sukhatme (1985)^[12] whereas heritability in narrow sense by Kempthorne and Curnow (1961)^[6] and genetic advance by Johnson *et al.* (1955)^[5].

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3.Result and Discussion

Analysis of variance had shown high significant differences amongst 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 yield and protein are presented in Table 1. Such kind of result were also reported by Mohammad Imran *et al.* (2018)^[11], Kumar *et al.* (2013)^[10], Singh *et al.* (2013)^[14]. 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 programme.

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Table 1. Analysis of variance for the traits for 21 set of genotypes during post-rainy season (2021-22)

	Replication	Treatments	Error
Degree of freedom	2	20	40
Days to 50% Flowering	12.333	18.605***	2.417
Plant Height	7.520	103.14***	2.770
Days to Maturity	21.330	24.65***	5.100
Spike length	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	0.310	58.48***	1.470
Flag leaf width	0.017	0.10931***	0.005
1000GW	1.307	4.008*	1.923
Biological yield/plant	84.340	232.57***	13.190
Harvest index	42.000	100.67*	48.810
Grains Yield / plant	17.030	147.08***	12.820
Total protein	0.132	1.891***	0.422

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The values of GCV and PCV were presented in Table 2, along with mean and range for all the fourteen traits. A broad range of variability at hand in any crop always provides the better likelihood of selecting desired type (Vavilov, 1951)^[15]. The accomplishment of crop improvement depends on vigilant management of variability and techniques to be used in any case will depend upon clear understanding of degree and nature of variability. Nevertheless, screening of the materials considered under this investigation publicized ample variability for all the fourteen characters. Similar results on variability have been reported by Mohammad Imran *et al.* (2018)^[11], Kumar *et al.* (2016)^[8], for various yield and quality components in wheat. In the midst of GCV & PCV, the present results revealed that the estimates of phenotypic coefficient of variation were in general slightly elevated than their corresponding

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genotypic coefficient of variation for all the traits studies which indicated that the variabilities for these traits in the genotypes was not much affected by the environments for the expression of these traits. Similar finding has been reported by Dhananjay *et al.* (2012)^[2], Singh *et al.* (2013)^[14], Kumar *et al.* (2014)^[9] for days to flowering, days to maturity, plant height, tillers per plant spike length, grains per spike, thousand grain weight, biological yield per plant, gain yield per plant, harvest index, protein content, flag leaf area, in wheat.

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Table 2. Variability amongst all the traits during post-rainy season (2021-22)

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	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	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	22.86	16.10	33.15	19.79	19.07	92.83	37.84
9	Flag leaf width	1.85	1.21	2.10	10.72	10.07	88.14	19.47
10	1000 Kernal weight	42.61	39.18	46.26	3.8	1.96	26.55	2.08
11	Biological yield/plant	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	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

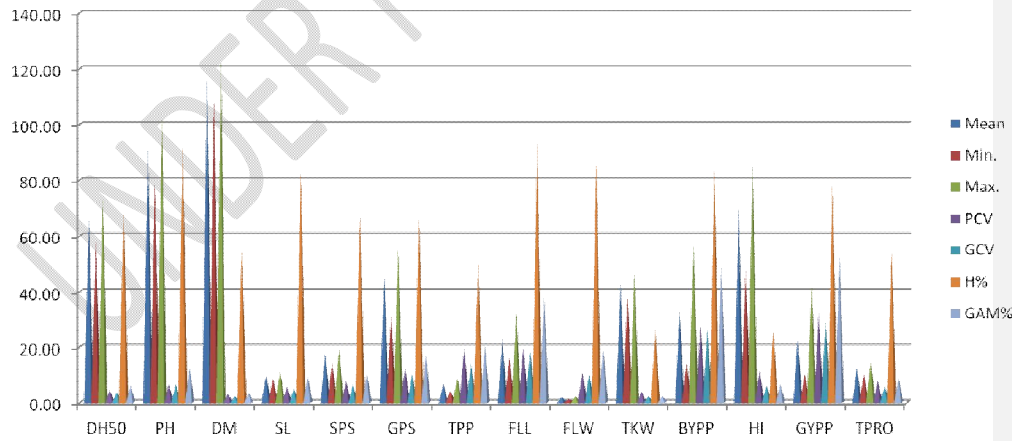
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Figure 1. Histogramical representation of traits distribution over mean, range coefficient of variance, heritability and genetic advance as percent of mean during post-rainy season 2021-22



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Where, DH50: Days to 50% flowering, PH: Plant height, DM: Days to maturity, SL: Spike length, SPS: Spikelet per spike, GPS: Grains per spike, TPP: Tiller per plant, FLL: Flag leaf length, FLW: Flag leaf width, TKW: Thousand kernal weight, BYPP: biological yield per plant, HI: Harvest index, GYPP: Grain yield per plant, TPRO: Total protein

In the present investigation, very high estimates of heritability (>30%) in 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.* (2016)^[8]. High heritability estimates were also reported by Panwar and Singh (2000)^[13] and Asif *et al.* (2004)^[11] 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.*(1955)^[5]. Characters exhibiting high heritability may not be necessarily give high genetic advance. Johnson *et al.* (1955)^[5] showed that high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion. The breeder should cautious in making selection based on heritability as it includes both additive and non-additive gene effect. High estimate of expected genetic advance expressed as percentage of 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.* (2018)^[11] for grains yield per plant and its contributing characters in wheat.

High heritability with high genetic advance were observed for flag leaf length, grains yield per plant, biological yield per plant and tiller per plant, and high heritability (narrow sense) coupled with moderate genetic advance in percent of mean were observed for flag leaf width ,grains per spike, plant height, and spikelet per spike. indicated that there is least influence of environment in expression of these traits and selection of desirable plants could be easily made on the basis of these traits.. High heritability along with 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.. Similar findings were also reported earlier by Kumar *et al.* (2016)^[8]; Singh *et al.*(2013)^[14]; Yadawad *et al.*(2015)^[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 utilizing the suitable resources and germplasm in wheat, so as to make it much more nutritive and productive. Protein is not only essential but also its deficiency cause kwashiorkor and marasmus disorders. Hence, inculcating protein content in wheat along with developing high yielding varieties must be focused in recent time. Our results indicated that useful variability in parents and progenies was developed through hybridization which can be

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properly utilized for selection of suitable genotypes on the basis of genetic parameters to obtained high protein and high yield potential in bread wheat.

6. References

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