Tailoring variabilityfor protein and yield in bread wheat (*Triticumaestivum*L.)

Abstract

The present research was carried out at the Breeder Seed Production Unit, JNKVV, Jabalpur, Madhya Pradesh using twenty one set of breadwheat 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 forflag 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.

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Keywords: Wheat, Variability, Heritability, Genetic advance

1. Introduction

Wheat (*Triticumaestivum*L.) is a member of family poaceae and one of the essential cereal crop for the world's populations. Because of itstrouble-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, adifficult job to the plant breeders to augment thelevel of crop production as the up-and-coming population ofthe 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].

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Since,Itis notfeasible to increase the cultivated area under theproduction. therefore, there is need to increase theproductivity by budding high yielding varieties along with high protein content to deal with the severe malnutritton conditions. The development of high yielding and high protein containing varieties isdepend upon the existence of genetic variability present in the wheat germplasm. As a result, analysis of genetic variation amongst the genotypes playsa vital role ahead ofcrafting theany breeding programme. Although the accomplishment of genetic enhancement in any yield traits and quality depends upon the nature ofvariability there in the characters. For this reason, an idea of the degree of variability present in the gene poolof a particular crop species is an extremely essential to a plantbreeder

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forpreliminary plant breeding programme. Generally, in crop improvement programme, genetic component of variation is important in view of the fact that only thiscomponent 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 componentsonly 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 intialgeneration, the relative amount of additive componentof variance to the total phenotypic variance ismuch more suitableevaluation of heritability.

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Heritability along with estimates of genetic advance facilitate in understanding the kind of gene actioninvolved in the expression of various quantitativecharacters. 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 thebasis of phenotypic performance onlyas phenotypically superior lines may capitulate poor recombinants. It is,therefore, very crucial that the parents oughtto be selected on thebasis their genetic worth. In the outlook of the above, an attempt has been made in the present research to assess aset oftwenty one genotypes of bread wheat. The goal ofthis study is to investigate the genetic variability, heritability,genetic advance and to estimate the component of variancesfor protein, yield and its attributing traits.

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2. Materials and Methods

2.1 Plant materials

For the present investigation, field experiment was conducted at Breeder Seed Production Unit, Jawaharlal Nehru KrishiVishwaVidhyalaya, 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. 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 functionfor RCBD design throughR 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 significantdifferences amongst the genotypes used in the presentexamination for protein, yield and yield attributing traitswhich further shows the existence of the broadrange of genetic variability. The mean squaresfor yield and protein are presented in Table1. Suchkind of result were also reported by Mohammad Imran *et al.* (2018)[11], Kumar *et al* (2013)[10], Singh *etal* (2013)[14]. The results indicated that constructive variability in offspring and parents was developed in the course ofhybridization, which could be suitably utilized for selection and further bread wheat improvement programme..

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Table1.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
Mean Sums of Square	**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

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.inthe midst of GCV & PCV, the present results revealed that the estimates of phenotypic coefficient of variation were in general slightly elevated than their corresponding genotypic coefficient of variation for all the traits studies which indicated that the variabilityfor 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

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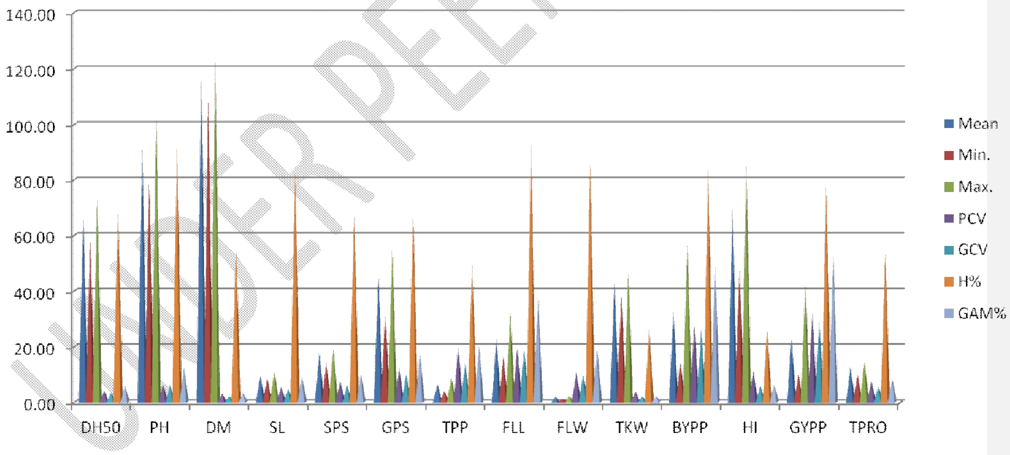
Table 2. Variability amongst all the traits during post-rainy season (2021-22)

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	**1000Karnel 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

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



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 karnel 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 karnel weight(26.55). High heritabilityindicates the possibility of genetic improvement of these traitsthrough selection.Similarresults 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)[1] for plant height. High heritability estimates forthese traits indicated it might be due to the presenceof additive and additive x additive type of gene effects.This indicates that, if these traits may be subjected tomass or progeny or family selection, aimed at exploiting additive (fixable) geneticvariance, a widely tailored genotype could be developedpossessing good productivity and with better protein inwheat.

Genetic advance is theimprovement in the mean genotypic value of selected plants over the parental populationJohnson *et al.*(1955)[5]. Characters exhibiting highheritability may not be necessarily give high genetic advance.Johnson *et al.* (1955)[5] showed that high heritability should beaccompanied by high genetic advance to arrive at more reliableconclusion. The breeder should cautious in making selection basedon heritability as it includes both additive and non-additive geneeffect. High estimate of expected genetic advanceexpressed as percentage of mean (> 20%) was observedhigh 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. Similarfindings were also reported by Mohammad Imran *et al.* (2018)[11]for grains yield per plant and itscontributing characters in wheat.

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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 advancein percent of mean were observed forflag leaf width ,grains per spike, plant height, and spikelet per spike.indicated that thereis least influence of environment in expression of thesetraits and selection of desirable plants could be easilymade on the basis of these traits.. Highheritability along with low genetic advance in percent ofmean was observed for days to 50% flowering days to maturity, and total protein content indicated the presence of non-additive gene action.. Similarfindings were also reported earlier by Kumar *et al.* (2016)[8];Singh *et al.*(2013)[14];Yadawad*et al.*(2015)[16] forgrain yield and its contributing traits in spring wheat.

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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 kwashiorkorandmarasmus 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 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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