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Research Article

Genotypic Variability for Protein, Phytic Acid and Mineral Contents of Grain and Yield Contributing Traits in Advanced Breeding Lines of Bread Wheat

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Abstract

The present investigation was undertaken to assess genetic variability existing among the newly developed twenty-one advance lines and nine released bread wheat varieties. The experiment was conducted during *rabi* 2016-17 in Randomized Complete Block Design (RCBD) with three replications at Agricultural Research Station, Niphad, Mahatma Phule Agricultural University, Maharashtra. The analysis of variance (ANOVA) showed that the mean sum of squares were highly significant for all the characters. In general, the phenotypic coefficients of variation were higher than the respective genotypic coefficients of variation for all the traits under study. The GCV of various characters ranged from 4.387 to 25.55 while the PCV varied from 4.458 to 28.624. Higher estimates of heritability in broad sense were observed for all the characters studied. The higher estimates of genetic advance as percent of mean were observed for grain yield per running meter, phytic acid content of grains, number of productive tillers per running meter and Zn content of grains. High heritability estimates coupled with high estimates genetic advance as per cent mean were observed for Coleoptile length, number of productive tillers per meter, number of grains per spike, Grain yield per running meter, Phytic acid and Zn content of grains. Direct selections for these characters may contribute in the improvement in yield of wheat crop or in the development of new genotypes.

Keywords: Bread wheat, Variability, phytic acid, protein, Zn and Fe

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Introduction

Common wheat or bread wheat (*T. aestivum*) is a hexaploid species, the most widely cultivated in the world which covers 90 per cent area of the total area under wheat. Wheat is a C_3 plant and as such it thrives in cool environments but it has a wide adaptation due to the complex nature of the genome of the species, which provides great plasticity to the crop [1].

Wheat is the second most important food crop of the world after, rice in terms of both area and production. India contributes 12 per cent to the total world wheat production. India achieved spectacular progress in wheat grain production following the largest producer China. The significant increase in growth of wheat production was attributed to the enhanced productivity of semi dwarf wheat varieties and investment of input like fertilizer and irrigation. During 2016-17 area under wheat cultivation was 30.72 mha with the production of 97.44 mt with an average productivity of 31.72 q/ha, while it occupied an area of 10.73 lakh ha in Maharashtra State with production of 16.72 lakh tones with an average productivity of 15.58 q/ha.

Wheat compares well with other cereals in nutritive value. It has good nutrition profile with 12.1 per cent protein, 1.8 per cent lipids, 1.8 per cent ash, 2.0 per cent reducing sugars, 59.2 per cent starch, 70 per cent total carbohydrates and provides 314K cal/100g of food. It is also a good source of minerals and vitamins *viz*., calcium and iron, with 37 mg/100g and 4.1 mg/100g, respectively [2].

Genetic variability in any crop is the core of plant breeding because proper utilization of variability can produce desired permanent gain in the performance. Estimates of the magnitude of variation within genotypes for traits contributing towards grain yield enables breeders to exploit genetic variability more efficiently and to determine the amount of progress to be made by selection. However, the existence of variation alone in the population is not sufficient to improve desirable characters. High heritability is prerequisite to have better opportunity for direct selections for the characters of interest.

In view of these facts, an effort has been made to estimate the genetic variability for yield, yield contributing traits and micronutrient content of grains.

Materials and Methods

A field experiment was conducted during *rabi* 2016-17, at Agricultural Research Station, Niphad, Dist. Nasik, Maharashtra State, India. The experimental material for the present investigation consisted of 19 advance genotypes and 11 released varieties of bread wheat (*Triticum aestivum* L.). The list of genotypes along with pedigree is given in **Table 1**.

Table 1 Genotypes included in the studies

S.No.	Genotype	Pedigree
1.	NIAW 3245	NIAW-917 X RAJ-4083
2.	NIAW 3386	BECARD/QUAIU #1
3.	NIAW 3423	CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/ WEAVER /5/2*JANZ/6/SKAUZ/BAV92
4.	NIAW 3433	BAJ #1/TECUE #1
5.	NIAW 3442	TOB/ERA//TOB/CNO67/3/PLO/4/VEE#5/5/KAUZ/6/FRET2/7/MINO
6.	NIAW 3270	NIAW-917 X NIAW-1415
7.	NIAW 3390	BECARD/CHYAK
8.	NIAW 3500	WBLL1*2/CHAPIO*2//MURGA
9.	NIAW 3309	DBW-14 X RAJ-4083
10.	NIAW 3340	CHIBIA//PRLII/CM65531/3/FISCAL/4/SUP152
11.	NIAW 3354	FRET2*2/BRAMBLING//MESIA/3/BECARD
12.	NIAW 3523	WBLLl *2/KURUKU/ /HEllO
13.	NIAW 3525	CS/TH.SC//3*PVN/3/MIRlO/BUC/4/URES/JUN//KAUZ/5/HUITES/6/YANAC / 7/ CS/TH.SC//3
14.	NIAW 3212	BAJ#1*2/WHEAR
15.	NIAW 3161	ROLF07*2/5/FCT/3/GOV/AZ//MUS/4/DOVE/BUC
16.	NIAW 3170	SKOLL/ROLF07
17.	NIAW 3033	LOK 62 / NIAW 1415
18.	NIAW 3217	ND643/2*WBLL 1//2*BAJ#1
19.	GW 322	PBW 173/GW 196
20.	DBW 168	SUNKU/CHIBIA
21.	NI 5439	NI 8883/MP 1055
22.	NI 9947	MRL "S"/BUL "S"
23.	NIAW 34	CNO79/PRL'S'
24.	NIAW 301*	SERI 82/3/MRS/JUP/HORK'S'
25.	NIAW 917**	GW 244/BOB WHITE
26.	NIAW 1415$^{\#}$	GW 9506/PRL//PRL
27.	NIAW 1994 $^{\#\#}$	NIAW 34/PBW 435
28.	MACS 6222	HD 2189*2/MACS 2496
29.	HD 2932	KAUZ/STAR//HD2643
30.	HD 2189	HD 1963/HD 1931

* = Trimbak, ** = Tapovan, $^{\#}$ = Netravati and $^{\#\#}$ = Phule Samadhan

The experiment was laid out in a randomized block design with three replications. Each genotype was represented by two rows of 5 m length spaced at 20 cm. A basal dose of 60 kg N, 60 kg P_2O_5, 40 kg K_2O per ha was applied at the time of sowing. Seeds were directly sown by dibbling. The remaining dose of 60 kg N was applied before application of first irrigation *i.e.* after 21 days after sowing. Recommended package of practices for cultivation of wheat was adopted to grow the crop.

Five plants were selected at random from each genotype in each replication. The randomly selected plants were tagged for recording observations on various morphological characters and harvested separately to record post harvest observations. Observations on thirteen characters *viz.*, days to 50 percent heading, days to maturity, coleoptile length(cm), plant height (cm), length of peduncle (cm), no. of productive tillers per meter, number of grains per spike, thousand grain weight (g), grain yield per meter (g), Protein (%), phytic acid, iron and Zink content of grains(mg/kg).

Estimation of protein content

Seed samples from selected plant were ground in a grinder and 0.2 g of sample was analyzed for protein content. Per cent crude protein of the wheat sample was estimated by determining total nitrogen content of seeds by adopting

Micro-Kjeldhal distillation method. The per cent protein in seeds was calculated by multiplying per cent nitrogen in sample by 6.25 representing the common factor for material used.

Estimation of Phytic acid content (mg/kg)

For estimation of Phytic acid, finely ground 35 to 40 mg flour per sample per replication was taken in 1.5 ml centrifuge tube and extraction buffer (0.75N HCl) was added and kept overnight on rocker. Samples were centrifuged at 10,000 rpm for 10 min. at room temperature (25^0C). Supernatant was transferred to another tube to which 0.1 g NaCl was added and vortexed. Samples were kept at -20^0C for 20 min and then centrifuged at 10,000 rpm for 10 min. The supernatant was collected and diluted to 1:24 with glass distilled water. Thereafter, to 750 µl of the diluted supernatant, 250 µl of Wade reagent (0.03% $FeCl_3.6H_2O$ + 0.3% sulfosalicylic acid) was added. Calorimetric determination of phytic acid phosphate (PAP) was done as per the procedure described [3] with appropriate modifications [4]. Observations were recorded at 500 nm using spectrophotometer.

Estimation of iron and zinc

Iron and zinc contents were determined by Atomic Absorption Spectrophotometry (AAS). Samples were digested by proper procedure as suggested [5]. One gram of finely powdered wheat seeds were taken in 100 ml conical flask and 20 ml of mixture of concentrated nitric acid and perchloric acid (5:1) was added and kept overnight. Next day, the samples were digested on hotplate at 200^0C. Samples were then allowed to cool and volumes were made up to 50 ml using glass distilled water. The diluted samples were filtered through Whatman No. 42 filter paper and filtrate was used for the estimation of iron and zinc using atomic absorption spectrophotometer.

Statistical Analysis

The mean values of five randomly selected observational plants for 13 different traits were used for statistical analysis. The analysis of variance was done as suggested by [6]. The phenotypic and genotypic variance were calculated by utilizing the respective means square values from the Variance Table [7]. The genotypic and phenotypic coefficient of variation [8], Heritability percentage in broad sense [9] and Genetic advance [7] were calculated by the formulae as suggested earlier.

Results and Discussion

Analysis of Variance

The analysis of variance for 13 characters is presented in **Table 2**. Analysis of variance that there were highly significant differences among the genotypes for all the characters under study, indicating wide range of variation in 30 genotypes of wheat.

Table 2 Analysis of variance for 13 characters in wheat

S. No.	Character	Mean Sum of Square		
		Replications (2)	**Genotypes (29)**	**Error (58)**
1	Days to 50 % heading	0.700	84.405**	0.643
2	Days to maturity	0.411	81.746**	0.882
3	Coleoptile length (cm)	0.063	1.396**	0.006
4	Plant height (cm)	8.525	95.161**	1.654
5	Length of peduncle (cm)	1.056	46.959**	1.834
6	Number of productive tillers per meter	212.800	1190.239**	68.915
7	Number of grains per spike	3.475	104.114**	1.855
8	Thousand grain weight (g)	0.916	29.606**	1.032
9	Grain yield per meter (g)	258.488	5780.693**	296.657
10	Phytic acid content of grains (mg/kg)	2.305	10.561**	0.638
11	Protein content of grains (%)	0.805	3.032**	0.883
12	Fe content of grains (mg/kg)	2.232	30.144**	1.757
13	Zn content of grains (mg/kg)	1.171	66.658**	2.478

** significant at 5% probability and values in parenthesis indicate degrees of freedom

Genetic variability

The parameters of genetic variability *viz*., Mean, Range, PCV, GCV, heritability (b.s.), Genetic Advance and Genetic Advance as per cent of Mean are summarized in **Table 3**.

Table 3 Genetic variability parameters for 13 characters in 30 genotypes of wheat

Sr. No.	Characters	General mean	Range	GCV	PCV	Heritability % (bs)	Genetic advance	G.A. as % of mean
1	Days to 50 % heading	69.13	58-80.3	7.643	7.731	97.8	10.762	15.567
2	Days to maturity	118.36	106.7-126.7	4.387	4.458	96.8	10.524	8.892
3	Coleoptile length (cm)	4.90	4.02-6.83	13.901	13.989	98.8	1.393	28.457
4	Plant height (cm)	89.04	80.5-100.2	6.27	6.434	95.0	11.207	12.587
5	Length of peduncle (cm)	39.62	31-49.7	9.789	10.368	89.1	7.543	19.038
6	Number of productive tillers per running meter	111.27	78-156	17.376	18.91	84.4	36.595	32.89
7	Number of grains per spike	52.91	42.7-62.3	11.035	11.331	94.8	11.712	22.137
8	Thousand grain weight (g)	43.38	37.8-51.5	7.114	7.49	90.2	6.039	13.921
9	Grain yield per running meter (g)	161.03	89.6-284.1	25.55	28.624	86.0	81.696	50.732
10	Phytic acid content of grains (%)	7.369	4.88-11.36	24.682	26.956	83.8	3.431	46.554
11	Protein content of grains (%)	11.433	9.73-13.53	7.402	11.062	44.8	1.167	10.204
12	Fe content of grains (%)	40.010	29.87-44.93	7.688	8.372	84.3	5.82	14.545
13	Zn content of grains (%)	29.839	19.8-35.47	15.501	16.374	89.6	9.02	30.229

Mean performance and Range

Days to 50 % heading ranged from 58.0 to 80.3 days with mean value of 69.13 days while the mean value for Days to maturity was 118.36 days in the range of 106.7 to 126.7 days. Estimates of coleoptiles length ranged from 4.02 cm to 6.83 cm with mean coleoptile of length 4.90 cm., these results confirm earlier reports [10-12].

The genotypes under study exhibited Mean plant height of 89.04 cm in the range of 80.5 and 100.2 cm. The genotypes under study showed range of 31.0 to 49.7 cm for length of peduncle with mean peduncle length of 39.62 cm. The number of productive tillers per running meter ranged from 78.0 to 156.00 with mean of 111.27 productive tillers per meter. The number of grains per spike ranged from 42.7 to 62.3 with mean of 52.91 grains per spike. Thousand grain weight of genotypes under study ranged from 37.8 g to 51.5 g with the mean thousand grain weight of 43.38 g. The economical character, grain yield per meter had range between 89.6 g and 284.1 g with mean grain yield of 161.03 g**.**

Phytic acid content of grains of genotypes ranged from 4.88 mg/kg to 11.36 mg/kg with mean Phytic acid content of 7.369 mg/kg. The values for protein content of grains ranged from 9.73 % to 13.53 % for genotypes studied with mean protein content of 11.433 %.

The values for Fe content of grain ranged from 29.87 mg/kg to 44.93 mg/kg with mean Fe content of 40.010 mg/kg while the values for Zn content of grains ranged from 19.8 mg/kg to 35.47 mg/kg with mean Zn content of 29.839 mg/kg. The earlier reports [13] suggest several fold variations for nutrient concentrations and grain protein content among 150 genotypes bread wheat genotypes. Similar observations confirming the wide variation for Phytic Acid (4.97 mg/g to 15.02 mg/g), Fe(0.042 to 0.098 mg/g) and Zn(0.017 mg/g to 0.029 mg/g) content is documented [14] and another study [15] reported wide variation for Zn content (16.85 mg/kg to 60.77 mg/kg) and Fe (26.26 mg/g to 68.78 mg/kg).

Coefficient of variation

The magnitude of phenotypic coefficients of variation was greater than genotypic coefficients of variation. Highest phenotypic and genotypic coefficients of variation were exhibited by grain yield (28.624 and 25.55, respectively), while lowest by Days to maturity (4.458 and 4.387, respectively). These findings confirm the earlier reports for highest GCV for grain yield [16] and for number of grains spike-^{1} [17]. Earlier studies conducted [18-22] support the findings of present investigation for higher estimates of genetic genetic coefficient of variability for number of effective tillers plant-^{1}, number grains spike-^{1} and grain yield plant-^{1}. Findings of the present study confirm the earlier results documented [23] for higher estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for days to 50 % flowering and plant height. The results of the present study are similar to the earlier findings [24] and [25] for highest phenotypic coefficient of variance (PCV) for yield per plant, 1000 grain weight and number of grains per spike. Higher magnitude of GCV and PCV for productive tiller per plant whereas, least for days to maturity and days to 50 per cent flowering has been reported [26]. Very high genotypic coefficient of variation for Iron content is reported in earlier studies [14] whereas, lowest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for days to maturity and higher for grain yield per hectare observed earlier [27] were confirmed in the present study.

The magnitude of difference between phenotypic and genotypic coefficient of variation was highest for grain yield per meter length of row(3.074) followed by phytic acid content of grains (2.274) and number of productive tiller per meter (1.534) suggested that environmental effect was prominent for expression of these characters.

Heritability % (b.s.)

The proportion of variability inherited from parents to off spring is manifested by heritability [28]. In this context, the presence of additive gene effect and selection may be made for the improvement in the character recording higher estimates oh heritability. Heritability estimates in broad sense for traits under study ranged from 44.8 % to 98.8 %. Highest estimate of heritability was recorded for Coleoptile length (98.8) while lowest was recorded for Protein content (44.8 %). Very high estimates (> 83.6 %) of heritability was recorded for almost all the characters excluding Protein content of grains.

Higher estimates of heritability observed in the present investigation for various traits confirm the earlier reports [18] for number of effective tillers plant-^{1}, number grains spike-^{1} and grain yield plant-^{1} ; for plant height, number of grains spike^{-1}, 1000 grain weight and yield plant-^{1} [19] ; for plant height, grains spike-1, 1000 grain weight and grain yield [29]; for plant height and grains spike^{-1} however, low heritability was observed for grain yield plant^{-1} [30] ; for numbers of effective tillers plant-^{1} and grain yield plant^{-1} [20]; for grain yield plot^{-1} [31]; for plant height and grain yield [21]; for plant height, tillers m^{-1}, and grain yield m^{-1} [22] ; for number of effective tillers per plant, days to maturity, plant height at maturity, 1000 grain weight, number of grain per spike and grain yield per plant [32]; for grain yield plot^{-1} and days to heading [33]; for yield per plant, 1000 grain weight, grain per spike and plant height [24]; for plant height and 1000 seed weight [34]; for productive tillers per running meter, 1000 grain weight and grain yield per plant [26]; for Tillers per plant, Peduncle length, Days to maturity and grain yield per hectare [27].

Genetic advance

In the present study, estimates of Genetic advance ranged from 1.167 to 11.712. Highest estimate of Genetic advance was recorded for grain yield (81.696) while lowest Genetic advance was recorded for Protein content (1.167). Critical examination of estimates of Genetic advance revealed that number of productive tillers per meter and grain yield per running meter recorded higher estimates of genetic advance while Days to 50 % heading, Days to maturity, plant height and grains per spike recorded moderate estimates of genetic advance. Out of thirteen traits studied, lower estimates of Genetic advance was recorded for eight traits including phytic acid, protein, Fe and Zn content of grains.

Character or the traits showing high heritability may not be inevitable impart high genetic advance [7]. It can be find out with greater degree of accuracy when heritability coupled with genetic advance is studied [35]. Therefore, estimation of heritability along with genetic advance is more useful to understand the type of gene action involved in the expression of various polygenic characters. High heritability estimates coupled with high estimates genetic advance as per cent mean were observed for Coleoptile length, number of productive tillers per meter, number of grains per spike, Grain yield per running meter, Phytic acid and Zn content of grains.

The results of the present investigation confirm the earlier findings for higher heritability estimates coupled with high genetic advance as per cent of mean for grains spike^{-1} and grain yield [29]; for numbers of effective tillers plant-^{1} and grain yield plant^{-1} [20,21] ; for grains spike^{-1}[29]; for grain yield ha^{-1} and number of grain per spike[31]; for grain yield plot^{-1} [32] and for productive tillers per running meter and grain yield [26]. The findings indicated that substantial contribution of additive gene action in the expression of the characters hence, direct selection for such traits would be more effective. On the contrary [low heritability along with moderate genetic advance for grain yield plant^{-1} indicated that direct selection for grain yield may not be effective [29]. The earlier finding for traits plant height[22]; plant height, 1000 seed weight [33] and for plant height at maturity and days to maturity [31] are not supported by the results of present study. In the present investigation the character days to maturity exhibited high heritability along with low genetic advance suggested, predominance of non-additive gene action hence; direct selection for improvement in days to maturity would mislead the expected results.

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