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Genetic variability, heritability and genetic advance among elite wheat [*Triticum aestivum* (L.)] genotypes

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Abstract

Bread wheat (*Triticum aestivum* L.), an allohexaploid (2n=6x=42), is the principal food crop of worldwide importance. It is also a crop where traditional plant breeding has paid rich dividend as epitomized by the Green Revolution. The present research work was conducted in *Rabi* season, 2021-2022 at Wheat and Maize Research Unit, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani. Sonalika, HD2967 and HI8713 were the three checks and 78 genotypes that made up the experimental materials for this investigation. These genotypes were assessed in an augmented block design and confermances were recorded for twelve characters *viz.* days to 50% anthesis, plant height, days to 50% heading, number of grains per spike, number of tillers per meter, test weight, biological yield, grain yield, days to maturirty, spike length, protein content and chlorophyll content. The data were documented on five randomly selected plants per entry and analyzed for variance, heritability, variability and genetic advance for quantitative characters. The variance was found to be topmost for number of grains per spike and least for grain yield per plot. The coefficient of variability was observed to be highest for days to 50% anthesis and lowest for days to maturity. Heritability in broad sense was upmost for biological yield per plot and undermost for chlorophyll content. Broadly speaking, Genetic advance as a percent of mean was topmost for biological yield per plot and least for chlorophyll content.

Keywords: Wheat, phenotype, genotype, character, heritability, variability and genetic advance

Introduction

Wheat (*Triticum aestivum*) is number one cereal of the world and is grown on the largest area. Wheat is grown on every continent in the world, unlike rice. Wheat's form and physiology were significantly impacted by domestication and the rise in ploidy (from diploid to tetraploid to hexaploid). According to Simmons (1987) [18], modern wheat has bigger leaves, a shorter tillering phase, fewer but heavier spikes, and nearly no shattering. Modern wheat relies more on photosynthates from leaves and stems for grain filling than on spikes, and the increased distribution of aboveground mass to grain is largely responsible for grain output. Jensen (1978) [8] also noted that decrease in plant was linked to dwarf Mexican wheat, whose introduction sparked the Green Revolution—in other words, the wheat revolution in India.

The cultivated wheat's of today constitute an alloploid series, diploids through hexaploids. It is evident from the examination of the physical similarities between tetraploid wheat (*T. turgidum* L.) and diploid wheat (*T. monococcum* L.) that *T. monococcum* is the source of the polyploidy wheat's gene "A." The diploid wheat that gave the "A" gene to the tetraploid was a wild variant, according to archeological data. *T. tauschi* is the source of the "D" gene in hexaploids. The donor of the "B" gene may be *T. speltoides*, Sarkar and Stebbins (1956) [15], or *T. longissimum*, Feldman (1970) [5], or *T. urartu*, Johnson (1975) [9] according to differing views.

Most wheat breeding and analysing programmes aim to stabilize cultivar perpetration for high grain production over a varying range of conditions and wide adaptation. Cultivars are usually tested in a variety of scenarios or site years to determine their potential yield during sporadic occurrences of both normal and extraordinary conditions. Due to time and budget constraints, the quantity and placement of testing sites are typically suboptimal. This could lead to the selection of subpar lines or the inappropriate promotion of genetic material.

To create an effective breeding strategy, one needs to understand the genetic makeup of genotypes. It is pivotal to determine the relative extent of genetic variations, both additive and non-additive, heritability, and genetic gain in relation to the breeder-important characteristics. The episodes in the systematic breeding map-out include building genetic variation, conducting genotype selection, and using those genotypes to develop promising cultivars. The quantity of genetic diversity among genotypes alters the wide spectrum of genetic variability in segregating populations, which dispenses superior selection opportunities. In order to fully take advantage of the future research predictions of wheat refinement, estimates of GCV, PCV, heritability, and genetic advance will be pivotal.

Materials and Methods

The present examination was carried to estimate genetic heritability, variability and genetic advance for quantitative characters at the Wheat and Maize Research Unit, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani during *Rabi* season of 2021-2022.

The exploratory material for the present investigation comprised of 78 germplasm accessions of wheat received from National Genetic Stock Nursery, Indian Institute of Wheat and Barley Research, Karnal and 3 prominent checks (Sonalika, HD2967 and HI8713) were planted in an Augmented Block Design, taking into consideration that each germplasm as a single plot, which consisted of 2 rows measuring 4m long with a spacing of 20 cm (row to row) and 10 cm (plant to plant). These genotypes were examined in an augmented block design and observations were recorded for twelve characters *viz*. days to 50% heading, days to maturity, days to 50% anthesis, plant height, spike length, number of grains per spike, number of tillers per plant, test weight, grain yield, biological yield, protein content and chlorophyll content.

The scrutiny of variance for augmented block design was determined by using the method given by Federer (1961) described by Federer and Ragavarao (1975) [4], and Petersen (1985) [14]. Genetic advance and Broad-sense heritability was estimated for all the traits using formula of Johnson *et al.*, (1955) [10].

Results and Discussion

The current study was conducted to estimate a number of genetic characteristics, including heritability, genetic advance (GA), genetic advance as a percentage of mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and variability estimation. Profound genetic variability among 81 lines was observed for characters are presented in (Table 1) under investigation. Analysis of variance revealed noteworthy differences. This suggested that there is a significant amount of genetic variation among genotypes and that all of the aforementioned traits have a lot of potential for use. The analysis of variance showed highly significant differences between the genotypes for number of tillers per meter and number of grains per spike and while, test weight, spike length, biological yield per plot and plant height exhibited significant differences for the genotypes. Number of grains per spike showed the highest variance followed by days to 50% heading, plant height, days to 50% anthesis and number of tillers per meter. Average amount of variance had been displayed by days to maturity, chlorophyll content and test weight. Least amount of variance had been exhibited by spike length, biological yield, protein content and grain yield per plot. These findings are in agreement with the studies Monpara (2009) [12], Vamshikrishna Nukasani *et al.* (2013) [19], Degewione *et al.* (2013) [3] and Yousaf Ali *et al.* (2008) [20].

Genetic and Phenotypic coefficient of variation, Heritability and Genetic advance

The traits under consideration were analysed for a number of factors, including heritability (broad sense), genotypic variance (GV), phenotypic variance (PV), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance (GA) and genetic advance as percent of mean (GAM). Improving a character requires a detailed assessment of genetic variability of the population. The likelihood of choosing the desired genotype is elevated when the experimental material comprises a wide range of variability. Table 2 displays the parameters. Breeders can choose the optimal breeding technique to achieve the desired result quickly by understanding genetic variability, genetic advancement, and heritability. This will help them determine the relative degree to which a trait will be passed down to the next generation. For crop improvement, it is crucial to comprehend the variability present in the experimental material. The selection process will be easier and the response to selection will be higher for a character with a higher heritability. The gene activity involved in the evolution of various polygenic traits is revealed when heritability and genetic advance estimates are compared, and this knowledge can be used as a trustworthy selection criterion.In this study, GCV was lower than PCV for all yield contributing traits, but there was minute difference between the phenotypic and genotypic coefficients of variation. These results are in agreement with Jagadish Prasad *et al.* (2020) [7], Shadi heidari *et al.* (2020) [16], Majumder *et al.* (2008) [11] and Navin Kumar *et al.* (2014) [13].

The high estimates of phenotypic coefficient of variation and genotypic coefficient of variation was observed for biological yield per plot (38.925 and 38.511) and grain yield per plot (36.733 and 34.487). These findings are in agreement with Yousaf Ali *et al.* (2008) [20], Vamsikrishna nukasani *et al.* (2013) [19], Anzer Ul islam *et al.* (2017) [2] and Jagadish Prasad *et al.* (2020) [7]. The moderate estimates of phenotypic coefficient of variation and genotypic coefficient of variation was observed for Number of tillers per meter (12.573 and 11.436), Spike length (12.881 and 11.821), Number of grains per spike (15.679 and 12.260), Test weight (16.628 and 13.344) and plant height (14.295 and 10.894).Similar findings were also reported by Yousaf Ali *et al.* (2008) [20], Monpara (2009) [12], Fikre *et al.* (2015) [6], Anzer Ul Islam *et al.* (2017) [2] and Alpay (2018) [1]. The low values of phenotypic coefficient of variation and genotypic coefficient of variation was observed for days to maturity (4.234 and 3.968), chlorophyll content (7.158 and 2.961) and protein content (8.198 and 7.127).Similar findings were reported by Shashikala *et al.* (2012) [17], Navin Kumar *et al.* (2014) [13] and Fikre *et al.* (2015) [6].

The degree of genetic variability and the degree to which it will be passed down from one generation to the next determine how effective selection is for any given trait. One cannot determine the percentage of total heritable variation just from the genotypic and phenotypic coefficients of variation. In this regard, the genetic advancement and heritability expressed as a percentage of mean estimations are more accurate indicators. It is suggested that, while estimating the extent of progress by selection, it is pivotal to examine both heritability and genetic advance as a percentage of the mean of characters instead of comprehending the characters individually (Johnson *et al.* 1955) [10]. Heritability estimates by themselves are less useful for calculating yield under phenotypic selection than heritability combined with high genetic advancement, given as a percentage of the mean. High heritability and high genetic advancement as a percentage of mean suggest that selection may be working and that additive gene influence is most likely the source of the heritability. Heritability ranged from 22.86 to 97.88. The characters; Number of tillers per meter, number of grains per spike, days to maturity, spike length, test weight, protein content, grain yield and biological yield were found to have high heritability in the current investigation.

The genotypic coefficient of variation alone cannot reveal the entire heritable fraction of variation. High heritability indicates the efficiency of selection based on phenotypic performance, but it does not imply the genetic gain under selection. Hence it is necessary to estimate the genetic gain under selection i.e., genetic advance. Heritability estimations in conjunction with genetic advancement are more helpful in forecasting the efficiency of selection than high heritability alone. High heritability combined with high genetic advancement shows the presence of additive gene action, which makes selection efficient; on the other hand, high heritability combined with low genetic advancement suggests the presence of non-additive gene action, making selection ineffective. Genetic advance as percent of mean ranged from 2.52 to 78.48. Number of tillers per meter, test weight, grain yield, spike length and biological yield recorded high genetic advance as percent of mean. The characters number of tillers per meter, spike length, biological yield, test weight and grain yield upheld high reckoned values of heritability associated with strong genetic advance as percent of mean indicating additive gene influence, As a result, selecting for these characters in genetically varied material would be fruitful for achieving desired genetic improvements. Similar results were reported by Yousaf Ali *et al.* (2008) [20], Navin Kumar *et al.* (2013) [13] and Vamshikrishna Nukasani *et al.* (2013) [19].

Table 1: Analysis of variance for different characters of 81 bread wheat genotypes.

Sl. No	Characters	Mean sum of squares		
		Block (2)	Check (2)	Error (4)
1	Days to 50% heading	53.444	301.445*	37.444
2	Days to 50% anthesis	43.004	307.000	45.498
3	Number of tillers per metre	36.646**	31.136	16.905
4	Spike length	0.218*	0.101*	0.243
5	Number of grains per spike	1092.73**	5575.020*	656.39
6	Days to maturity	6.752	18.023	2.668
7	Test weight	0.885*	11.947	16.056
8	Biological yield (kg/plot)	0.008*	0.241***	0.001
9	Plant height	50.253*	212.680	56.704
10	Chlorophyll content	0.998	15.239	8.631
11	Protein content	0.214	4.347	0.247
12	Grain yield (kg/plot)	0.001	0.028*	0.003

** Significant at 1% probability level

* Significant at 5% probability level

Degrees of freedom are indicated in paranthesis.

Table 2: Genotypic coefficient of variation, Phenotypic coefficient of variation, Heritability, Genetic advance and Genetic advance as percent of mean of different characters of wheat lines studied.

Sl. No	Characters	GCV%	PCV%	(h^2)	Genetic advance	Genetic advance as% of mean
1	Days to 50% heading	6.724	11.797	32.49	4.984	7.895
2	Days to 50% anthesis	5.267	11.016	22.86	3.616	5.187
3	Number of tillers per metre	11.436	12.573	82.73	16.86	21.428
4	Spike length	11.821	12.881	84.22	2.152	22.348
5	Number of grains per spike	12.26	15.679	61.14	51.762	19.747
6	Days to maturity	3.968	4.234	87.84	8.476	7.661
7	Test weight	13.344	16.628	64.4	8.908	22.058
8	Biological yield (kg/plot)	38.511	38.925	97.88	0.462	78.488
9	Plant height	10.894	14.295	58.08	13.917	17.104
10	Chlorophyll content	2.961	7.158	17.11	1.138	2.523
11	Protein content	7.127	8.198	75.58	1.568	12.763
12	Grain yield (kg/plot)	34.487	36.733	88.14	0.278	66.698

Conclusion

This research study stipulated presence of large amount of scope for a breeder in selecting superior genotypes for yield improvement in wheat after studying character association as this study recorded presence of large amount of variation for various yield and yield contributing traits. Thus, According to estimates of genetic parameters such as PCV, GCV, heritability, and genetic advancement, it is clear that the traits that exhibit the highest values for PCV, GCV, heritability, and genetic advance—namely, biological yield, grain yield, and number of tillers per meter—were deemed most valuable, and that selecting for these traits could be a more efficient way to increase the grain yield in wheat. Genotypes with these traits can be utilised for yield improvement aspects and play a major role in breeding for obtaining desired genotypes as well as advanced to next generation.

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