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Genetic Variability and Character Association Analysis in Wheat (*Triticum aestivum* L.) in Saline Water Condition

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ABSTRACT

The study was conducted to evaluate eight germplasms/varieties of wheat during the *rabi* season (November-April, 2022–23) using a randomized block design with three replications at the research farm of Agricultural Research Sub-Station (ARSS), Nagaur (Rajasthan), India to estimate the variability parameters and characters association for nine characters. The results were revealed that mean sum of squares due to genotypes showed significant differences for all the nine characters under study, suggested that the genotypes were genetically divergent. The phenotypic coefficient of variation values was higher than genotypic coefficient of variation values for all the nine traits which reflect the influence of environment on the expression of traits. Spike length and number of spikelets were showed higher PCV and medium GCV. High heritability estimates were recorded for all the nine characters. High genetic advance as percentage of mean along with high heritability was observed for number of spikelets, spike length, number of effective tillers plant^{-1}, seed yield and number of grains spike^{-1}. This indicated the existence of lesser environmental influence and prevalence of additive gene action in their expression and these traits possessed high selective value. These characters could be further improved through individual plant selection. Grain yield had highly significant and positive genotypic and phenotypic correlations with plant height, number of effective tillers plant^{-1}, spike length, number of spikelets and number of grains spike^{-1}. These characters can be considered as criteria for selection for higher grain yield as these were mutually and directly associated with grain yield.

KEYWORDS: Character association, genetic variability, heritability, saline water and wheat

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Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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1. INTRODUCTION

Wheat (*Triticum aestivum* L.) is a globally cultivated allopolyploid crop, bread wheat has been shaped for success by multiple steps of domestication and polyploidization (Pont and Salse, 2017). Bread wheat is an allohexaploid species, composed of 21 chromosome pairs organized in three sub genomes, A, B and D, Genome AABBDD, 2n=6x=42 (Belova, 2014). The three genomes of bread wheat (A, B and D) are derived from three diploid wild ancestors (Marcussen et al., 2014; El-Baidouri et al., 2017). Wheat is cultivated during winter season from mid-October to April (except in higher hills of north India where the harvesting of wheat is done in the month of May). Sowings of wheat are initiated when the average of day-night temperatures is equal to 23°C (Gupta et al., 2023). It is primarily grown in temperate region, higher altitude and also at medium altitude of tropical climate. However, it is cultivated widely around the world due to wide adaptation and greater role in human nutrition as well as in agricultural economy (Meles et al., 2017). In India, wheat is the second most important crop after rice occupying 30.47 million hectares, with production of 106.84 mt with an average productivity of 3507 kg ha^{-1} (Anonymous, 2022). Uttar Pradesh, Madhya Pradesh and Punjab are important states from the point of both area and production. Currently, about 95% of the wheat grown worldwide is hexaploid bread wheat mostly used for bread making with the remaining 5% being tetraploid wheat used for pasta making (Shewry, 2009). Wheat is the dominant crop on arable land, but its productivity is hindered by several environmental stresses, especially salinity stress, which is common in arid and semiarid regions. Wheat is a moderately salt-tolerant crop, but high salinity levels can reduce its yield by more than 50% (Tao et al., 2021). Therefore, cultivating wheat in saline conditions is challenging without implementing practices to mitigate the negative effects of salinity stress on its growth and yield. Grain yield is the principal trait of a cereal crop. This is a complex quantitative trait, which is influenced by a number of yield contributing traits. Therefore, the selection for desirable types should not only be based on yield, the other yield components should also be considered. Direct selection for yield is often misleading in wheat because wheat yield is polygenically controlled. For effective utilization of the genetic stock in crop improvement, information of mutual association between yield and yield components is necessary (Majumder et al., 2008). It is, therefore, necessary to know the correlation of various component characters with yield and among themselves. The study of character associations among various traits is useful to breeders in selecting genotypes possessing groups of desired traits (Ali et al., 2008). Hence, in this investigation, an effort has been made to evaluate a set of wheat genotypes with the objectives, to estimate the GCV, PCV, heritability, genetic advance as percentage of mean for yield, character association and their implication in selection of better genotypes of wheat for the development or improvement of cultivars and germplasm as well.

2. MATERIALS AND METHODS

Eight germplasms/varieties of wheat were obtained from the ARS (Agricultural Research Station) Jodhpur, Rajasthan. During *Rabi* season (November-April, 2022–23), the genotypes of wheat were assessed using a randomized block design with three replications at the research farm of Agricultural Research Sub-Station, Nagaur, Rajasthan, India. The ground water of the experimental site was saline with a PH of 7.8, electrical conductivity of 5.7 ds m^{-1} and TDS 4500 mg l^{-1}. The soil of the experiment site was sandy loam (sand 49.1%, silt 29.6% and clay 21.3%) with a PH of 7.1. It contained 0.55% organic carbon. Each genotype was planted in a 4.0×2.25 m^2 plot with ten rows that were 22.5 cm apart from one another. Plants were kept 10 cm apart from one another. Ten plants were chosen at random from each genotype and replication to record observations at various stages of crop growth on characteristics such as plant height, number of effective tillers plant^{-1}, spike length, number of spikelets, number of grains spike^{-1} and seed yield. However, observations on days to heading, days to maturity and 1000 grain weight were recorded on a plot-by-plot basis. All the recommended package of practices for wheat was followed to raise a healthy crop. The data were subjected to analysis of variance (Panse and Sukhatme, 1985) to determine genotypic and phenotypic coefficients of variation (Burton and De vane, 1953), broad sense heritability (Hanson et al., 1956). The genotypic and phenotypic correlation coefficients were calculated as described by Singh and Choudhary (1985) and as per formula given by Johnson et al. (1955).

3. RESULTS AND DISCUSSION

3.1. Genetic variability parameters

The mean sum of squares due to genotypes showed significant differences for all the nine characters under study, suggested that the genotypes were genetically divergent (Table 1). This indicates that there is ample scope for selection of promising lines from the present gene pool for grain yield and its components. Thus, it indicates ample scope for selection for different quantitative characters for wheat improvement. Similar results were also observed by Asif et al. (2004), Kumar et al. (2009) and Azene et al. (2020) for grain yield and its component characters in wheat. The genetic variability parameters such as genotypic coefficient of variation, phenotypic coefficient of variation,

Table 1: Analysis of variance for nine metric traits in wheat

Source of Variation	d.f	Days to heading	Mean sum of squares							
			Days to maturity	Plant height (cm)	No. of effective tillers plant^{-1}	Spike length (cm)	No. of spikelets	No. of grains spike^{-1}	1000 grain weight (g)	Grain yield (kg ha^{-1})
Replications	2	0.66	2.00	2.42	0.04	0.11	0.25	0.66	1.29	8767.40
Genotypes	7	14.75^{**}	28.37^{*}	150.78^{**}	4.09^{**}	10.20^{**}	21.79^{**}	88.24^{**}	28.20^{**}	917255.03^{**}
Error	14	1.95	6.71	3.75	0.01	0.14	0.14	1.41	0.54	8191.81

*Significant at p=0.05 and **Significant at p=0.01

heritability and genetic advance as percentage of mean for nine characters are presented in Table 2. The phenotypic coefficient of variation values was higher than genotypic coefficient of variation values for all the nine traits which reflect the influence of environment on the expression of traits. The estimates of GCV and PCV were low for days to heading, days to maturity, plant height and 1000-grain weight; medium for number of effective tillers plant^{-1}, number of grains spike^{-1} and seed yield. Spike length and number of spikelets were showed higher PCV and medium GCV. High heritability estimates were recorded for all the nine characters. Sachan and Singh (2003) also reported high heritability estimates for grain yield, number of spikelets spike^{-1}, number of seeds spike^{-1}, plant height, 1000-seed weight and number of tillers plant^{-1} which support the present findings. The highest genetic advance as percentage of mean was observed for number of spikelets, spike length, number of effective tillers plant^{-1}, seed yield and number of grains spike^{-1}. The characters viz., plant height and 1000-grain weight showed moderate genetic advance as percentage of mean. Similar findings have been reported in wheat by Arega et al. (2011) and Meles et al. (2017). In the present investigation, high genetic advance as a percentage of mean along with high heritability was observed for number of spikelets, spike length, number of effective tillers plant^{-1}, seed yield and number of grains spike^{-1}. This indicated the existence of lesser environmental influence and prevalence of additive gene action in their expression and these traits possessed high selective value. These characters could be further improved through individual plant selection.

Table 2: Estimation of genetic variability parameters for different traits in wheat

Characters	Range	Mean	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Heritability (%)	Genetic advance as percentage of mean
Days to heading	74.33-80.33	77.21	2.68	3.23	68.61	4.57
Days to maturity	120.33-129.67	124.13	2.17	3.01	51.82	3.21
Plant height (cm)	71.50-89.00	81.64	8.58	8.90	92.88	17.02
No. of effective tillers plant^{-1}	5.23-8.73	6.39	18.25	18.37	98.63	37.33
Spike length (cm)	7.60-12.40	9.28	19.73	20.15	95.93	39.82
No. of spikelets	10.63-17.50	13.52	19.87	20.07	98.00	40.53
No. of grains spike^{-1}	35.43-51.37	42.18	12.76	13.06	95.34	25.65
1000 grain weight (g)	41.47-49.22	45.55	6.67	6.86	94.44	13.35
Grain yield (kg ha^{-1})	2784.67-4344.33	3320.88	16.57	16.80	97.37	33.69

1.2. Correlation coefficient analysis

The phenotypic and genotypic correlation coefficients for grain yield and its components characters are presented in Table 3. Grain yield had highly significant and positive genotypic and phenotypic correlations with plant height, number of effective tillers plant^{-1}, spike length, number of spikelets and number of grains spike^{-1}. These characters can be considered as criteria for selection for higher grain yield as these were mutually and directly associated with grain yield. Days to heading showed significant and positive association with days to maturity. Number of effective tillers plant^{-1} had highly significant and positive genotypic and phenotypic correlations with plant height, spike length, number of spikelets, number of grains spike^{-1}, 1000-grain weight and grain yield. Spike length had highly significant and positive genotypic and phenotypic correlations with

Table 3: Genotypic and phenotypic correlation coefficients between different traits in wheat

Characters		Days to heading	Days to maturity	Plant height (cm)	No. of effective tillers plant^{-1}	Spike length (cm)	No. of spikelets	No. of grains spike^{-1}	1000 grain weight (g)	Grain yield (kg ha^{-1})
Days to heading	rg	1	0.574^{*}	0.504^{*}	-0.246	-0.206	-0.098	-0.109	-0.691^{**}	-0.195
	rp	1	0.457^{*}	0.437^{*}	-0.245	-0.159	-0.097	-0.089	-0.518^{**}	-0.192
Days to maturity	rg		1	0.051	-0.158	-0.235	-0.440^{*}	-0.285	0.615^{**}	-0.284
	rp		1	0.024	-0.113	-0.215	-0.355	-0.211	0.488^{*}	-0.176
Plant height (cm)	rg			1	0.619^{**}	0.537^{**}	0.533^{**}	0.581^{**}	0.057	0.582^{**}
	rp			1	0.600^{**}	0.515^{*}	0.508^{*}	0.560^{**}	0.055	0.535^{**}
No. of effective tillers per plant	rg				1	0.966^{**}	0.877^{**}	0.972^{**}	0.446^{*}	0.954^{**}
	rp				1	0.934^{**}	0.867^{**}	0.939^{**}	0.418^{*}	0.936^{**}
Spike length (cm)	rg					1	0.958^{**}	0.989^{**}	0.356	0.884^{**}
	rp					1	0.921^{**}	0.948^{**}	0.317	0.849^{**}
No. of spikelets	rg						1	0.933^{**}	0.183	0.767^{**}
	rp						1	0.899^{**}	0.166	0.738^{**}
No. of grains spike^{-1}	rg							1	0.245	0.937^{**}
	rp							1	0.250	0.906^{**}
1000 grain weight (g)	rg								1	0.295
	rp								1	0.287

*Significant at p=0.05 and **Significant at p=0.01

plant height, number of effective tillers plant^{-1}, number of spikelets, number of grains spike^{-1} and grain yield. Number of spikelets had highly significant and positive genotypic and phenotypic correlations with plant height, number of effective tillers plant^{-1}, spike length, number of grains spike^{-1} and grain yield. Number of grains spike^{-1} had highly significant and positive genotypic and phenotypic correlations with plant height, number of effective tillers plant^{-1}, spike length, number of spikelets and grain yield. The significant positive correlation of tillers plant^{-1} and ear length with yield plant^{-1} have been reported by Mondal et al. (1997) and that of number of grains spike^{-1} and number of spikelets spike^{-1} by Raut et al. (1995). Similar findings were also observed by many researchers such as Diyali et al. (2015) for number of spike plant^{-1}, number of spikelets spike^{-1}, number of grain spike^{-1}, weight of grain spike^{-1}, flag leaf area and 1000 grain weight; Ahmad et al. (2018) for spike length; Shehrawat and Kumar (2021) for biological yield, 1000 grain weight, harvest index, grains spike^{-1}, spike length, peduncle length and tillers plant^{-1}; Akbarzai et al. (2022) for spike length, spike weight, number of grains spike^{-1}, number of spikelets spike^{-1}, 1000 grain weight and biological yield plot^{-1}; Ezici et al. (2022) for test weight, days to heading and plant height; Akbarzai et al. (2023) for spike length, spike weight, number of grains spike^{-1}, number of spikelets spike^{-1}, 1000 grain weight, biological yield plot^{-1} and number of productive tillers meter^{-1} and Hussain et al. (2023) for grain weight spike^{-1}, grain length and number of grain plant^{-1}.

4. CONCLUSION

Grain yield had highly significant and positive genotypic and phenotypic correlations with plant height, number of effective tillers plant^{-1}, spike length, number of spikelets and number of grains spike^{-1}.

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