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Studies on genetic variability, heritability and genetic advance for yield and yield attributing traits in wheat (*Triticum aestivum* L.)

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Abstract

In this study, a set of twenty genotypes of Wheat (*Triticum aestivum* L.) were evaluated over two years from 2015-16 to 2016-17 to assess the genetic analysis of these genotypes for yield and its contributing traits over years and environments. These were evaluated in randomized complete block with 3 replications and two dates of sowing i.e. 3rd week of November (timely sown) and 1st week of January (very late sown). Significant variability were found in all the environments for all the traits. Higher magnitude of both coefficients were observed for traits viz., number of dead tillers plant⁻¹, number of grains plant⁻¹, yield plant⁻¹ and number of effective tillers plant⁻¹/number of ears plant⁻¹ in all the sowing conditions. Traits viz., biological yield plant⁻¹, yield plant⁻¹, ear head length (cm), peduncle length, harvest index (%) and ear weight governed by additive gene action in all the environments. Therefore, selection for grain yield plant⁻¹ can be done through biological yield plant⁻¹, ear head length (cm), peduncle length, ear weight and harvest index (%).

Keywords: Genetic analysis, genotypic & phenotypic coefficients, additive gene action

Introduction

Wheat (*Triticum aestivum* L.) is the world's largest cereal crop, it is self-pollinated belong to *Poaceae* family and of the genus *Triticum*. It is estimated that more than 35 per cent of the world population depends on wheat [Borlaug, 1968, Johnson *et al.* 1978] [3]. India produced 94.88 million tonnes wheat on an area of 29.90 m. ha. with the productivity 3173.24 kg/ha. On the other hand, Madhya Pradesh is the third largest producer state of wheat with 16.10 million tonnes from the 5.40 million hectares area with the productivity 2959.00 kg/ha (Anonymous, 2014). The present study was carried out to resolve the potential and promising wheat genotypes with stable yield performance under different agro climatic situation. Furthermore, selection based on only yield is confusing. Thus, for valuable selection, information on nature and amount of variation in population on the idiom of these characters are necessary (Yagdi 2009; Tsegaye *et al.* 2012) [10]. The mission of breeder is to screen out genotypes planted at different interval enables the selection of those genotypes which are suitable for wide range of planting. Idea of phenotypic and genotypic and environmental variation, initiative of heritability and genetic advance is an important attribute of breeding programme.

Materials and Methods

The experiment was carried out at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture Tikamgarh, Jawaharlal Nehru Krishi Vishwa Vidhyalaya, Jabalpur (M.P.) under irrigated timely and very late sown conditions. The experimental area occupied was quite uniform in respect of topography and fertility. The experimental material comprised of 20 promising genotypes of wheat, procured from different Wheat Improvement Projects, research centers of India. Experiment was grown in a Randomized Complete Block Design with three replications. Each plot consists of three rows of 2.5 m length and 22.5 cm apart under irrigated normal sown and very late sown conditions during both experimental years. These observations viz., Days to 50% flowering, Days to maturity, Plant height (cm), No. of tillers plant⁻¹, No. of effective tillers plant⁻¹, No. of dead tillers plant⁻¹, No. of spikelet's ear⁻¹, No. of ears plant⁻¹, No. of grains ear⁻¹, No. of grains plant⁻¹, Ear head length (cm), Ear weight (g), Peduncle length (cm), 100 grain weight (g), Biological yield plant⁻¹ (g), Yield plant⁻¹ (g), Harvest index (%) was recorded on 5 randomly selected plant from each plot.

The genetic parameters of variability, estimation of heritability and genetic advance were computed according to the method suggested by Johnson *et al.*, 1955 [5]. The character association was estimated from variance and covariance components as given.

Result and Discussion

The analysis of variance revealed significant differences among the genotypes for almost all the characters in all the environments. [Table-1].

In pooled analysis of variance mean square due to varieties, Varieties x environment, and pooled deviation were significant for all the characters. Varieties were significant for all the characters (except number of dead tillers plant⁻¹, number of spikelets ear⁻¹, ear weight and peduncle length). Varieties x environment interaction was significant for all the characters (except plant height, number of dead tillers plant⁻¹, number of spikelets ear⁻¹, number of grains ear⁻¹, number of grains plant⁻¹, ear head length, ear weight, peduncle length, 100 grain weight, byp⁻¹ and harvest index). Pooled deviation was shown significant difference among all (except days to 50% flowering, number of tillers plant⁻¹, number of effective tillers plant⁻¹, number of ears plant⁻¹, ear weight and biological yield plant⁻¹).

This suggested that the genotypes selected were genetically variable and considerable amount of variability existed among them.

Variability: The values of phenotypic coefficient of variation for all the traits under study were found to be more than genotypic coefficient of variation. In first year high genotypic and phenotypic coefficient of variation were found for number of grains plant⁻¹ (E1), yield plant⁻¹ (E1/E2), peduncle length (E1), number of ears plant⁻¹ (E2) and number of effective tillers plant⁻¹ (E2). In second year high genotypic and phenotypic coefficient of variation were recorded for number of dead tillers plant⁻¹ (E3), number of grains plant⁻¹ (E3/E4), ear head length (E3) and yield plant⁻¹ (E3/E4). While in pooled analysis number of dead tillers plant⁻¹ followed by number of grains plant⁻¹, yield plant⁻¹, number of effective tillers plant⁻¹/ number of ears plant⁻¹, ear weight, number of tillers plant⁻¹ and harvest index showed high value of PCV and GCV. [Table-2]. The results indicate that the above traits offer a better opportunity for improvement through selection. Similar findings were reported by Preeti *et al.* (2018) [7], Pinki *et al.* (2018) [8], H.K. Rathwa *et al.* (2018) [9]. These values alone are not helpful in determining the heritable portion of variation.

Heritability and genetic advance (expressed as percentage of mean): High heritability coupled with high genetic advance (as percentage of mean) was recorded under both timely sown condition (E1 & E3) for biological yield plant⁻¹ and yield plant⁻¹. Whereas, high value of heritability with high genetic advance for ear head length (cm), peduncle length, harvest index (%) in E1 and ear weight in E3 only. Under both late sown condition (E2 & E4) high heritability coupled with high genetic advance was recorded for the traits *viz.*, biological yield plant⁻¹ and yield plant⁻¹ while number of grains plant⁻¹ in E4 only. High heritability coupled with moderate genetic advance were exposed by days to 50% flowering and 100 grain weight (g) in both the timely environments (E1 & E3), whereas plant height in E1 only. While under vary late sown condition plant height and 100 grain weight recorded in E2 only. High/ moderate heritability

coupled with high/moderate genetic advance was indicative of the presence of additive gene effects and the selection for such traits will be rewarding for further varietal improvement. [Table-2, 3]. Similar result was reported by Pradeep *et al.* (2016) [6], H. A. Avinash *et al.* (2017) [2]. Therefore it can be said that economically important traits like yield plant⁻¹, biological yield plant⁻¹, days to 50% flowering and 100 grain weight which exhibited high estimates for expected genetic advance accompanied with high heritability estimate can be improved by hybridization followed by selection.

Conclusion

To conclude the present investigation, significant variability in all the environments for all the traits indicates that the advanced genotypes could develop through hybridization whose have sufficient exploitable level of genetic variability to be utilized for breeding suitable genotypes for different environments. In the present study, higher magnitude of both coefficients were observed for traits *viz.*, number of dead tillers plant⁻¹, number of grains plant⁻¹, yield plant⁻¹ and number of effective tillers plant⁻¹/number of ears plant⁻¹ in all the sowing conditions. Traits *viz.*, biological yield plant⁻¹, yield plant⁻¹, ear head length (cm), peduncle length, harvest index (%) and ear weight governed by additive gene action in all the environments. Thus the above characters were given due importance.

Table 1: Pooled ANOVA over all the experimental years

Source of Variations	df	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of tillers plant ⁻¹	No. of effective tillers plant ⁻¹	No. of dead tillers plant ⁻¹	No. of spikelets ear ⁻¹	No. of ears plant ⁻¹	No. of grains ear ⁻¹
Replicate	2	0.158	22.589	26.486	5.79	4.448	0.090	2.374	4.448	23.151
Environments	3	1617.52***	6697.063***	3792.197***	290.122***	257.302***	1.071***	53.833***	257.302***	1578.119***
Interactions	6	13.68	25.422	165.126	5.827	6.417	0.163	7.129	6.417	104.882
Overall Sum	11	1631.357***	6745.074***	3983.809***	301.74***	268.168***	1.325	63.337*	268.168***	1706.151***
Treatments	19	3038.21***	3316.30***	5494.00***	194.388***	191.134***	2.647**	166.894***	191.134***	2369.467***
Error	209	782.16	2090.15	6444.021	227.905	238.877	14.033	541.924	238.876	5191.493

Pooled ANOVA over all the experimental years

Source of Variations	Df	No. of grains plant ⁻¹	Ear head length (cm)	Ear weight (g)	Peduncle length (cm)	100 grain weight (g)	Biological yield plant-1 (g)	Yield plant-1 (g)	Harvest index (%)
Replicate	2	10008.02	7.664*	0.431	3.916	0.178	5.388	1.761	6.771
Environments	3	403694.50***	81.31***	15.529***	694.201***	3.896***	6228.758***	1852.038***	2839.104***
Interactions	6	13942.88	9.263	0.647	8.508	0.156	36.276	23.542	173.501
Overall Sum	11	427645.439***	98.237***	16.608***	706.625***	4.229***	6270.423***	1877.341***	3019.376***
Treatments	19	456447.349***	115.528***	8.84***	270.162**	17.727***	2215.254***	959.831***	2053.881***
Error	209	791137.929	219.297	33.906	1361.477	9.306	2051.248	793219	5039.691

, * indicate level of significance at 5% and 1%, respectively.

Table 2: Pooled parameters of genetic variability for yield and its component traits in wheat genotypes for over both experimental year.

S. No.	Traits	Mean	Range		C.V.	PCV	GCV	ECV	h ² (Broad Sense)%	Gen. Adv as % of Mean 1%
			Minimum	Maximum						
1	Days to 50% flowering	66.569	61.346	71.983	2.906	6.133	5.400	2.906	77.55	9.797
2	Days to maturity	107.892	101.871	114.709	2.931	4.513	3.432	2.931	57.83	5.376
3	Plant height (cm)	91.232	79.981	97.883	6.086	7.931	5.086	6.086	41.11	6.717
4	No's of Tillers plant ⁻¹	8.304	6.487	10.319	12.575	16.388	10.509	12.575	41.13	13.884
5	No's of Effective tillers plant ⁻¹	7.094	5.320	9.216	15.068	19.356	12.149	15.068	39.40	15.710
6	No's of dead tillers plant ⁻¹	1.209	1.022	1.395	21.422	22.361	6.413	21.422	8.22	3.788
7	No's of Spikelets ear ⁻¹	17.167	15.283	18.627	9.379	10.271	4.184	9.379	16.59	3.511
8	No's of Ears plant ⁻¹	7.094	5.320	9.216	15.068	19.356	12.149	15.068	39.40	15.710
9	No's of Grains ear ⁻¹	43.030	35.867	49.061	11.582	13.383	6.704	11.582	25.10	6.918
10	No's of Grains plant ⁻¹	337.523	252.073	410.601	18.228	21.916	12.167	18.228	30.82	13.915
11	Ear head length (cm)	8.326	7.046	9.512	12.303	14.554	7.776	12.302	28.55	8.559
12	Ear weight (g)	2.444	2.121	2.828	16.477	17.713	6.501	16.477	13.47	4.915
13	Peduncle length(cm)	17.303	15.638	18.931	14.749	15.459	4.631	14.749	8.97	2.857
14	100 grain weight (g)	4.372	3.842	4.801	4.826	7.876	6.224	4.826	62.45	10.131
15	B. yield plant ⁻¹ (g)	32.824	28.624	38.887	9.544	13.178	9.087	9.544	47.55	12.909
16	Yield plant ⁻¹ (g)	13.426	10.758	17.281	14.510	20.653	14.697	14.510	50.64	21.544
17	Harvest index (%)	40.426	35.960	46.514	12.147	13.797	6.544	12.147	22.50	6.394

Table 3: Estimate of heritability and genetic advance under all the conditions

Traits	Timely sown				Very late sown				Pooled	
	E1		E3		E2		E4			
	h ²	GA	h ²	GA	h ²	GA	h ²	GA	h ²	GA
Days to 50% flowering	H	M	H	M	H	L	H	L	H	L
Days to maturity	H	L	H	L	H	L	H	L	M	L
Plant height (cm)	H	M	M	L	H	M	M	M	L	L
No. of tillers plant ⁻¹	M	H	M	H	M	H	M	H	L	M
No. of effective tillers plant ⁻¹	M	H	M	H	M	H	M	H	L	H
No. of dead tillers plant ⁻¹	L	H	L	H	L	M	M	H	L	L
No. of spikelets ear ⁻¹	M	H	M	M	L	L	M	L	L	L
No. of ears plant ⁻¹	M	H	M	H	M	H	M	H	L	H
No. of grains ear ⁻¹	L	M	L	M	M	M	M	M	L	L
No. of grains plant ⁻¹	M	H	L	H	M	H	H	H	L	M
Ear head length (cm)	H	H	M	H	M	H	L	M	L	L
Ear weight (g)	M	H	H	H	L	M	L	M	L	L
Peduncle length (cm)	H	H	M	H	L	M	M	H	L	L
100 grain weight (g)	H	M	H	M	H	M	M	M	M	M
Biological yield plant ⁻¹ (g)	H	H	H	H	H	H	H	H	L	M
Yield plant ⁻¹ (g)	H	H	H	H	H	H	H	H	M	H
Harvest index (%)	H	H	L	L	M	H	M	H	L	L

H- High M- Medium L - Low

Reference

- Anonymous. Project Directorates Report, DWR, Karnal, 2014, 1.
- Avinashe HA, Dubey Nidhi, Shukla RS. Genetic Analysis for Economic Traits in Wheat under Timely and Very Late Sown Conditions. International Journal of Pure & Applied Bioscience. 2017; 5(5):157-162.
- Borlaug NE. Wheat breeding and its impact on world food supply. Public lecture at the 3rd International Wheat Genetics Symposium, Australian Academy of Science, Canberra, Australia, 1968.
- Johansson H. Improvement of nutritional quality in barley and sprig wheat: A FAO/SIDA/SAREC project. Seed protein improvement by nuclear techniques, 1978, 85-90.
- Johnson HW, Robinson HF, Comstock RE. Estimate of genetic and environmental variability in soybean. Agron. J., 1955; 47:314-318.
- Kumar Pradeep, Singh Gyanendra, Kumar Sarvan, Kumar Anuj, Ojha Ashish. Genetic analysis of grain yield and its contributing traits for their implications in improvement of bread wheat cultivars. Journal of Applied and Natural Science, 2016; 8(1):350-357.
- Pachauri Preeti, Kandalkar VS, Satankar Navneet. Analysis of genetic variability and path coefficient for yield and yield contributing traits in cultivated and synthetic wheat and their interspecific crosses. Journal of Pharmacognosy and Phytochemistry; 2018, SP2:83-87.
- Pinki, Singh Vikram, Rohila Neha. Component of Variability for Protein Content and Yield Related Traits in Recombinant Inbred Lines (RILs) Population of Bread Wheat (*Triticum aestivum* L. Em. Thell) in Normal and Late Sown Environments Int. J Curr. Microbiol. App. Sci. 2018; 7(4):1539-1547.
- Rathwa HK, Pansuriya AG, Patel JB, Jalu RK, Genetic Variability, Heritability and Genetic Advance in Durum Wheat (*Triticum durum* Desf.). International Journal of Current Microbiology and Applied Sciences. 2018; 7(1):1208-1215.
- Tsegaye D, Dessalegn T, Dessalegn Y, Share G. Genetic variability, correlation and path analysis in durum wheat germplasm (*Triticum durum* desf). Agricultural Research and Reviews. 2012; 1(4):107-112.
- Yagdi K, Sozen E. Heritability, variance components and correlations of yield and quality traits in durum wheat (*Triticum Durum* Desf.). Pakistan Journal of Botany, 2009; 41(2):753-759.