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## Genetic variability, heritability and genetic advance in durum wheat (*Triticum durum* Desf.) genotypes

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### Abstract

The current examination was laid out using 57 durum wheat genotypes at Instructional Farm, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur during Rabi, 2019-2020 in augmented randomized block design with four replication of checks only. Analysis of variance manifested significant difference between genotypes for many character studied, indicating sufficient genetic variability among the genotypes. Phenotypic Coefficient of Variation (PCV) was somewhat higher than the respective Genotypic Coefficient of Variation (GCV) for all the character reflecting that the environment had little effect on the characters. GCV was found higher for the Number of grains per spike, sedimentation value, number of effective tillers per plant and 1000-grain weight while higher values of PCV was recorded for the number of effective tillers per plant, number of grains per spike, sedimentation value and grain yield per plant. High heritability (broad sense) coupled with the high genetic gain was recorded for the traits like sedimentation value (ml), days to 50% heading, number of grains per spike and 1000-grain weight.

**Keywords:** Durum wheat, genetic variability, GCV, PCV, heritability, genetic advance

### Introduction

Durum wheat (*Triticum durum* Desf;  $2n = 4x = 28$ ), be a member of Poaceae family, is one of the most common staple food amongst major cereals of the world. It covers 17 percent (one-sixth) of global cropland, feeds about 40% of the world's population, and accounts for 20% of overall food calories and protein in human nutrition. Wheat is a self-pollinated, monocotyledonous plant that had originated from South West Asia. There are different species of wheat, out of which only three *Triticum* species are mostly cultivated throughout the world. These are *Triticum aestivum* (bread wheat), *Triticum durum* (macaroni wheat) and *Triticum dicoccum* (emmer wheat).

Globally, wheat (*Triticum spp.*) is grown in about 224.09 million hectares holding the position of highest acreage among all crops with annual production hovering around 794.44 million metric tones (USDA, 2021) [19]. In India, it is grown in an area of 31.76 million hectares (14.17% of the global area) with a production of 108.75 million metric tones (13.68% of world production) and productivity of 3424 kg/ha. In Rajasthan, it is grown in an area of 3.02 mha with a production and productivity of 10.57 mt and 3501 kg/ha respectively (Anonymous, 2020). Wheat is mostly grown in the districts of Shri Ganganagar, Hanumangarh, Bharatpur, Churu, Jaipur, Kota, Baran, Alwar, Bundi, and other parts of Rajasthan.

Durum wheat (*Triticum durum* Desf.) is second most cultivated species of wheat both globally and nationally, after bread wheat. The typical durum wheat grain is very hard, vitreous and amber-colored with rich in protein content. The composition of durum wheat is comparable to that of ordinary wheat. In durum wheat kernel starch and lipids have about equal amounts but protein content is a little more to bread wheat. The mineral distribution in the kernel is one of the most noticeable difference. This difference may have a role in the higher cooking quality of durum wheat pasta (Matsuo, 1994) [14]. This crop has a lot of genetic variation, and that diversity applies to the many common ways of eating it, including spaghetti, couscous, bourghul, *gofio*, and semolina, to name a few.

The world's durum wheat acreage and production is concentrated in West Asia, North Africa, Canada, Mexico, India and Mediterranean Europe. Durum is pre-dominantly spring wheat, although winter durum is also grown to a limited extent. Worldwide, durum wheat is grown approximately over 13 million hectares with an approximate annual production of 30 million tones (Kadkol and Sissons, 2016) [11] which contributes less than 5% of the world's wheat

production.

A crop improvement programme requires information of genetic variability in the genetic system of a specific crop. The plant breeder's key goal is to develop the genotype in order to increase yield. Grain yield in wheat is a complex character and is dependent on its component traits. Therefore, to enhance grain yield, selection must exploit the variability existing within each component trait. Correlation and path coefficient analysis together provide a clear-cut picture of the inter-relationships and relative contributions of independent characters to the dependent variable, allowing a plant breeder to apply appropriate selection procedures for crop improvement. The use of Mahalanobis D<sup>2</sup> statistics to determine the extent of divergence and the relative contribution of various components to overall divergence aids in the identification of divergence parameters for hybridization and yield improvement in wheat.

### Material and Method

The 52 durum wheat genotypes along with 05 checks evaluated in this experiment were obtained from the AICRP on Wheat and Barley, Department of Genetics and Plant Breeding, RCA, MPUAT, Udaipur. The experiment was conducted at RCA, MPUAT, Udaipur. It is situated at an elevation of 582.17 meters above mean sea level in southeast of Rajasthan on latitude of 24° 35' N and longitude of 37° 42'. The research field's soil texture was clay loam with a pH of 7.6. All the 52 genotypes along with 05 checks were grown in Augmented Randomized Block Design, in which only checks were replicated. Genotypes were sown in two rows of 2.5 m row length with row-to-row and plant-to-plant spacing of 23 cm and 5 cm respectively. The experiment was sown on November 16, 2019. To raise a good crop, agronomic practices and plant protection measures were adopted. Five competitive plants from each genotype were chosen at random to be observed for all of the traits under investigation. However, observation for days to 50% heading and days to maturity were recorded on the basis of plant population of each genotype.

**Statistical analysis:** To test the difference among the genotypes, the analysis of variance was performed individually for each character as per method suggested by Federer (1956)<sup>[8]</sup>. Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were calculated as per the standard formula suggested by Burton (1952)<sup>[5]</sup>.

$$GCV (\%) = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

#### Where

$\sigma^2_g$  = Genotypic variance  
 $\bar{X}$  = General mean

$$PCV (\%) = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100$$

#### Where

$\sigma^2_p$  = Phenotypic variance  
 $\bar{X}$  = General mean

Heritability ( $h^2$ ) was calculated in broad sense by using the following formula given by Johnson *et al.*, (1955)<sup>[10]</sup>.

$$h^2_{bs} (\%) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

#### Where

$\sigma^2_g$  = Genotypic variance  
 $\sigma^2_p$  = Phenotypic variance  
 $h^2_{(bs)}$  = Heritability in broad sense

Genetic gain (GG) is the genetic advance expressed as percent of mean. It was estimated by using the formula of Lush (1945) and Johnson *et al.*, (1955)<sup>[10]</sup>.

$$GG (\%) = \frac{GA}{\bar{X}} \times 100$$

$$GA = H_{(bs)} \times k \times \sigma_p$$

#### Where

$\bar{X}$  = General mean  
 GA = Genetic advance  
 $\sigma_p$  = Phenotypic standard deviation  
 k = Selection intensity (k = 2.06 at 5% selection intensity)

### Results and Discussion

The analysis of variance (ANOVA) indicated that the mean sum of square due to genotypes were highly significant for the character, such as days to 50% heading, days to maturity, number of grains per spike, 1000 grain weight (g) and Sedimentation value (ml) indicating, existence of ample amount of genetic variation among all the genotypes. The mean sum of square due to block was found significant for protein content (%) only, Table 1.

It was found that GCV was found higher for the number of grains per spike (15.81%) followed by sedimentation value (14.97%), number of effective tillers per plant (13.28%), 1000 grain weight (11.30%) and Grain weight per spike (10.87%) while it was lower for the character *viz.*, protein content (4.53%), harvest index (4.87%), days to maturity (5.01%), plant height (5.70%), days to 50% heading (6.73%) and number of spikelets per spike (6.99%).

For all of the characters studied, the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation. The highest PCV was recorded for number of effective tillers per plant (18.34%) followed by number of grains per spike (17.48%), Sedimentation value (15.31%) and 14.63% for Grain yield per plant, while it was found lower for the character as days to maturity (5.14%) followed by protein content (5.57%) and days to 50% heading (96.95%), Table No. 2

For all of the characters under investigation, broad sense heritability was estimated. The majority of the characteristics had a high heritability and it was recorded highest for the sedimentation value (95.66%) followed by days to maturity (95.14%), 1000 grain weight (94.85%) and 93.82% for days to 50% heading. However, length of main spike (31.39%) and harvest index (43.17%) showed lowest heritability. The highest genetic advance as per cent of mean (genetic gain) was recorded for sedimentation value (30.17%) followed by number of grain per spike (29.44%) and number of effective tillers per plant (19.81%) while, it was found lower for the character harvest index (6.60%) followed by protein content (7.58%) and plant height (8.57%). Table No. 2

In this study, the phenotypic coefficient of variation (PCV) is

slightly higher than the genotypic coefficient of variation (GCV) for all of the traits, indicating that environmental variations have almost no effect on the characters. The Number of grains per spike, sedimentation value, number of effective tillers per plant and 1000-grain weight showed moderate (10-20%) genotypic coefficient of variation whereas the harvest index, days to maturity, plant height and days to 50% heading exhibited lower (<10%) genotypic coefficient of variation. Moderate phenotypic coefficient of variation (10-20%) was observed for number of effective tillers per plant followed by number of grains per spike, sedimentation value and grain yield per plant while lowest phenotypic coefficient were found for days to maturity followed by protein content. The similar findings were reported by Dhakar *et al.*, (2012) [7], Tambe *et al.*, (2013) [17], Wolde *et al.*, (2016) [20] and

Malbhave *et al.*, (2020) [13].

The heritability estimates (broad sense) for most of the characters were very substantial, suggesting a strong genetic nature for all of the traits studied. Because of the higher heritability, selection for the majority of the traits could be effective in this group of genotypes. Estimates of high heritability coupled with the high genetic gain for the traits like sedimentation value (ml), days to 50% heading, number of grains per spike and 1000-grain weight indicated that all these characters are regulated by additive gene action and the direct selection be expected to show improvement in such traits. The results were similar to those reported by Tsegaye *et al.*, (2012) [18], Wolde *et al.*, (2016) [20], Adhikari *et al.*, (2018) [1], Zemede *et al.*, (2019) [21] and Alemu *et al.*, (2020) [3].

**Table 1:** Analysis of variance for yield and its contributing traits in durum wheat

S. No.	Character	Block	Treatment	Check	Germplasm	C v/s G	Error
		[3]	[56]	[4]	[51]	[1]	[12]
1.	Days to 50% heading	1.12	34.37**	51.18**	33.56**	8.72	2.07
2.	Days to maturity	0.85	37.89**	11.68**	40.63**	2.93	1.98
3.	Plant height (cm)	15.93	44.71	9.80	47.53	40.53	22.17
4.	No. of effective tillers per plant	1.08	1.68	0.99	1.76	0.39	0.84
5.	Length of main spike (cm)	0.23	0.93	1.33	0.91	0.03	0.63
6.	Number of spikelets per spike	1.11	3.27	3.00	3.24	6.29	1.40
7.	Number of grains per spike	29.89	155.46**	58.96	128.36**	1923.59**	23.38
8.	Grain weight per spike (g)	0.30	0.34*	0.64*	0.29	1.60**	0.13
9.	1000 grain weight (g)	0.68	26.75**	32.66**	23.68**	159.78**	1.22
10.	Biological yield per plant (g)	1.88	30.58*	58.43*	28.99	0.30	12.41
11.	Grain yield per plant (g)	1.41	5.43	7.16	5.40	0.15	2.90
12.	Harvest Index (%)	4.19	7.20	2.39	7.68	1.90	4.37
13.	Sedimentation Value (ml)	0.05	18.11**	11.20**	18.45**	28.62**	0.80
14.	Protein (%)	0.64*	0.72**	2.80**	0.54*	1.56*	0.18

**Table 2:** Genetic variability parameters for yield and its contributing traits in durum wheat

S. No.	Character	Mean	Range		GCV (%)	PCV (%)	H <sup>2</sup> (%)	GA	GG
			Min.	Max.					
1	Days to 50% heading	83.33	70.00	93.00	6.73	6.95	93.82	11.20	13.44
2	Days to Maturity	124.00	112.00	138.00	5.01	5.14	95.14	12.49	10.07
3	Plant height (cm)	88.42	74.00	100.70	5.70	7.80	53.36	7.58	8.57
4	Number of effective tillers per plant	7.23	5.20	9.40	13.28	18.34	52.43	1.43	19.81
5	Length of main spike (cm)	7.47	5.80	9.80	7.17	12.79	31.39	0.62	8.27
6	Number of spikelets per spike	19.35	15.80	23.00	6.99	9.30	56.59	2.10	10.84
7	Number of grains per spike	64.83	43.80	88.30	15.81	17.48	81.78	19.09	29.44
8	Grains weight per spike (g)	3.70	2.31	5.16	10.87	14.59	55.56	0.62	16.70
9	1000 grain weight (g)	41.95	33.60	53.40	11.30	11.60	94.85	9.51	22.67
10	Biological yield per plant (g)	42.47	32.40	55.20	9.59	12.68	57.20	6.34	14.94
11	Grain yield per plant (g)	15.88	11.25	20.20	9.95	14.63	46.27	2.21	13.95
12	Harvest Index (%)	37.38	30.24	41.82	4.87	7.42	43.17	2.47	6.60
13	Sedimentation Value (ml)	28.06	18.00	38.00	14.97	15.31	95.66	8.46	30.17
14	Protein content (%)	13.06	11.70	15.00	4.53	5.57	66.03	1.00	7.58

GCV- Genotypic coefficient of variation, PCV-Phenotypic coefficient of variation, H<sup>2</sup> -Heritability, GG-Genetic Gain

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