Dhairya V Makwana
Department of Genetics and
Plant Breeding, N.M.C.A.,
Navsari Agricultural University,
Navsari, Gujarat, India

Prashant K Jagtap
Niger Research Station, Navsari
Agricultural University,
Vanarasi, Gujarat, India

Himani P Vadodariya
Department of Genetics and
Plant Breeding, N.M.C.A.,
Navsari Agricultural University,
Navsari, Gujarat, India

Divya S Patel
Department of Genetics and
Plant Breeding, B.A.C.A., Anand
Agricultural University, Anand,
Gujarat, India

Chirag P Chandramaniya
Department of Genetics and
Plant Breeding, B.A.C.A., Anand
Agricultural University, Anand,
Gujarat, India

Study of genetic variability, heritability and genetic advance in wheat [*Triticum aestivum* L.] germplasms

Dhairya V Makwana, Prashant K Jagtap, Himani P Vadodariya, Divya S Patel and Chirag P Chandramaniya

Abstract
The present investigation was carried out during *rabi,* 2021 at Niger Research Station, Navsari Agricultural University, Varanasi. A total of 40 wheat genotypes are included in this study which were evaluated in a Randomized Block Design (RBD) with three replications and observations were recorded for twelve characters. The analysis of variance revealed significant mean sum of squares values for all the twelve traits in forty genotypes indicating a sufficient amount of variability present among them. The values of PCV were observed slightly higher than GCV for all twelve characters indicating minor influence of environmental factors. Genotypes exhibited moderate values of Genotypic Coefficient of Variation (GCV) for effective tillers per plant, spike length, grains per spike, filled grains per spike, test weight, grain yield per plant and gluten content. This result indicated the presence of inherent variation for these characters and its further improvement is possible by applying judicious selection to the individual traits. High heritability was observed for all the traits thus showing least environmental influence. High heritability coupled with high genetic advance as percent mean showed by filled grains per spike, grain yield per plant, grains per spike, gluten content, test weight and effective tillers per plant which suggested that for desired genetic improvement, selection for these characters would be more effective.

Keywords: Wheat, variability, heritability and genetic advance

1. Introduction
Wheat [*Triticum aestivum* (L.), 2n = 6x = 42] is the world's second most important cereal staple food crop after rice, which dominates all other cereal crops in area and production and also providing around 20 percent of total food calories to the world's population. It belongs to the genus Triticum of the Poaceae family and also a self pollinated crop. Hexaploid wheat (AABBDD), accounts for over 95 percent of all wheat farmed today and it is used to make bread and other baked goods (Debasis and Khurana, 2001) [6]. Wheat cultivation in India started 5000 years ago (Feldman, 2001) [7].

The availability of sufficient genetic variability is of crucial role in a crop improvement programme. As per the information on the nature and magnitude of variation at population level, the interaction among the various traits with grain yield and among themselves are essential for effective selection. Additionally, extent of environmental influence on the expression of these characters are also required for effective selection (Yagdi, 2009) [15]. Wide variability, high heritability along with the high genetic advance will lead to the successful selection of genotypes. As a result, it is important for a breeder to measure variability using parameters such as phenotypic coefficient of variation, genotypic coefficient of variation, heritability, and genetic advance which provide information about the availability of genetic variability for various traits in germplasm.

Hence, the study of the variability of yield and its relevant traits among different genotypes creates the way for selecting desirable lines, which will further helps in improvement of grain yield and other agronomic characteristics.

2. Materials and Methods
2.1 Experimental site and experimental design
This experiment was carried out at Research Farm of Niger Research Station, Navsari Agricultural University, Varanasi, during *rabi*, 2021-22. A total of 40 wheat genotypes used in this study *viz*;VA-1819, LOK-175, VA-1733, VA-1802, LOK-77, VA-1822, VA-1828, J-1830, J-1813, VA-1933, VA-1921, VA-1920, VA-1928, VA-1922, VA-1919, VA-1917, GS

Corresponding Author:
Dhairya V Makwana
Department of Genetics and
Plant Breeding, N.M.C.A.,
Navsari Agricultural University,
Navsari, Gujarat, India

-6025, GS-1007, GS-5013, GS-4049, GS-9036, GS-6027, GS-7005, GS-7042, ESWYT-118, ESWYT-143, SAWYT-309, SAWYT-323, GS-1003, GS-1005, GS-1006, GS-1007, GS-1010, GS-1018, GS-1024, GS-1041, LOK-1, GW-173, GW-11, HD-2932. The source of seeds is the Wheat Research Station, Bardoli, Navsari Agricultural University, Navsari. These genotypes were evaluated in a randomized block design with three replications. All genotype was shown in two row of 2.7 m row length with row to row spacing of 22.5 cm in each replication. All the recommended agronomic practices were performed to raise a healthy crop.

2.2 Characters studied
The data were recorded from five randomly selected plants from each genotype on twelve different morphological traits *viz.*, days to heading, plant height (cm), effective tillers per plant, spike length (cm), grains per spike, filled grains per spike, days to maturity, test weight (g), grain yield per plant (g), straw yield per plant (g), harvest index (%) and gluten content (%).

2.3 Statistical analysis
A statistical analysis was performed on the overall mean values of the various characters. The data were subjected to the statistical procedure on randomized block design (RBD) as explained by Panse and Sukhatme (1954) [11] in order to perform an analysis of variance. Using Burton's (1952) [4] method, the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated.

$$GCV\ (\%) = \frac{\sqrt{Vg}}{\bar{x}} \times 100$$

Where,
Vg = genotypic variance
$\bar{x}$ = general mean of the character under investigation

$$PCV\ (\%) = \frac{\sqrt{Vp}}{\bar{x}} \times 100$$

Vp = phenotypic variance
$\bar{x}$ = general mean of the character under investigation

Heritability in broad sense was estimated by the method as suggested by Johanson *et al.* (1955) [10].

$$h^2_{bs}\ (\%) = \frac{Vg}{Vp} \times 100$$

Where, h^2 = Heritability in broad sense
Vg = Genotypic variance
Vp = Phenotypic variance

The expected genetic advance (GA) expressed in percentage of mean were calculated by using the method suggested by Johanson *et al.* (1955) [10].

$$GA\ as\ percent\ of\ mean = \frac{GA}{\bar{x}} \times 100$$

Where,
GA = Expected genetic advance
$\bar{x}$ = Mean of the character under study

3. Result and Discussion
3.1 Analysis of variance
The analysis of variance (ANOVA) was calculated to test the significant differences among genotypes for all the twelve traits under study and presented here in Table 1. The results shown here depicted that the mean sum of square due to genotypes were highly significant for all the quantitative and qualitative characters which indicated that presence of considerable amount of genetic variability among all genotypes under study for various traits. This show that there is a ample scope to generate early and high yielding materials by applying a judicious selection pressure for specific traits. Similar results for most of characters were also found by Vaghela *et al.* (2021) [14], Chauhan *et al.* (2022) [5] and Shankar *et al.* (2022) [13].

The mean values of different genotypes for all the twelve characters studied, showing wide range for the days to heading (46.00 to 58.00 days), plant height (55.33 to 87.44 cm), effective tillers per plant (2.52 to 4.95), spike length (6.04 to 10.93 cm), grains per spike (24.33 to 54.00), filled grains per spike ranged (21.67 to 44.67), days to maturity (90.67 to 114 days), test weight (31.00 to 55.33 g), straw yield per plant (13.20 g to 27.94 g), harvest index (28.50 to 38.35%), Wet gluten (23.54 to 41.91%) and grain yield per plant (5.27 g and 17.41 g). The SAWYT-323 (17.41 g) was found to be the highest yielding genotype, while GS-1041 (5.27 g) was found to be the lowest yielding genotype, with a mean value of 13.07 g (Table 2).

3.2 Genotypic and Phenotypic variability
The estimates of mean, range and variances due to Genotype and Phenotype, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for various characters studied are shown in Table 2. The higher and closer values of phenotypic coefficient of variation (PCV) than the respective genotypic coefficient of variation (GCV) for all the twelve traits under study showed the inherent connection between genotypes and phenotypic expression of the traits under study. Moderate GCV and PCV values were observed for the traits *viz.*, effective tillers per plant, spike length, grains per spike, filled grains per spike, test weight, grain yield per plant and gluten content, which indicated the presence of extensive inherent variation for these characters and its further improvement is possible by applying judicious selection to the individual traits. The same result was depicted by work of Vaghela *et al.* (2021) [14] for effective tillers per plant, spike length and grains per spike, Ali *et al.* (2008) [2] and Chauhan *et al.* (2022) [5] for test weight, Vaghela *et al.* (2021) [14] and Roy *et al.* (2021) [12] for grain yield per plant and Arya *et al.* (2017) [3] for gluten content.

However, days to heading, days to maturity, straw yield per plant and harvest index recorded lower value of GCV indicating a narrow range of variability for these traits and restricting the scope of selection. This result was in accordance with findings of Ibrahim *et al.* (2019) [9], Roy *et al.* (2021) [12] and Chauhan *et al.* (2022) [5] for days to heading and days to maturity.

3.3 Heritability and expected genetic advance
Thes result of this are presented in Table 2. High heritability

was observed for all the characters including gluten content (88.67%), harvest index (87.80%), days to maturity (87.27%), grain yield per plant (78.3%), test weight (76.67%), days to heading (71.26%), spike length (68.32%), straw yield per plant (65.59%), grains per spike (65.28%), filled grains per spike (64.39%), effective tillers per plant (63.73%), plant height (62.93%). Similar results were reported by Gaur *et al.* (2019) [8], Roy *et al.* (2021) [12] for grains per spike, test weight, grain yield per plant and harvest index, Vaghela *et al.* (2021) [14] for days to heading, effective tillers per plant, grains per spike, test weight, spike length and grain yield per plant and Chauhan *et al.* (2022) [5] for days to heading, days to maturity, plant height, effective tillers per plant, grains per spike, test weight, harvest index and grain yield per plant.
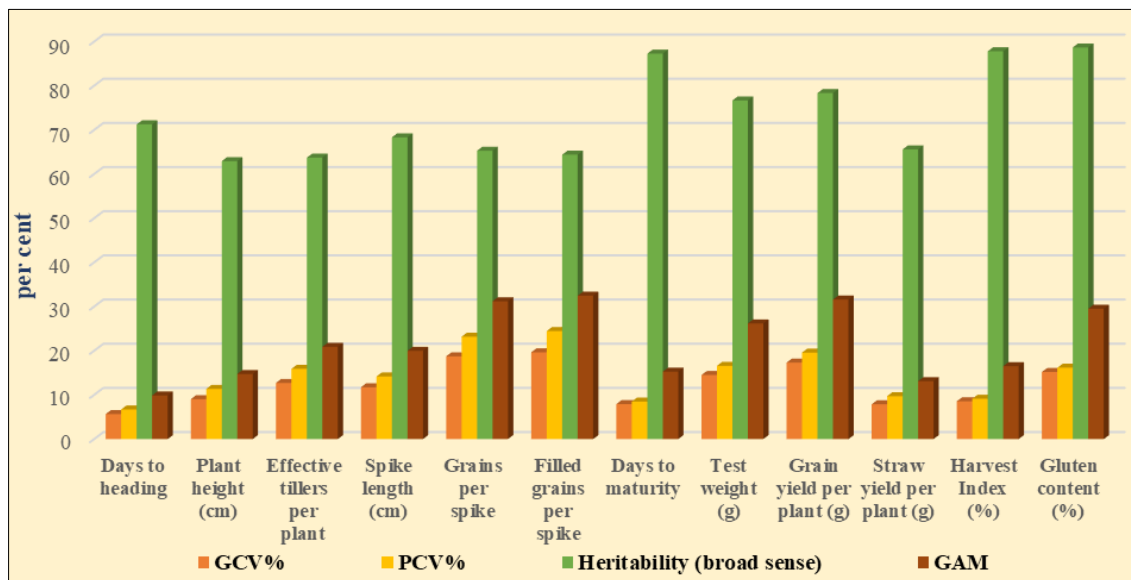
GCV (%) = Genotypic coefficient of variation PCV (%) = Phenotypic coefficient of variation GAM = Genetic Advance as percent of mean (%)

Fig 1: GCV, PCV, Heritability (broad sense) % and GAM for twelve characters in wheat

The estimates of genetic advance expressed as percent of mean were found high for filled grains per spike (32.47%) followed by grain yield per plant (31.59%), grains per spike (31.19%), gluten content (29.52%), test weight (26.18%) and effective tillers per plant (20.88%). Similar results obtained by Vaghela *et al.* (2021) [14] for effective tillers per plant, grains per spike and grain yield per plant, Chauhan *et al.* (2022) [5] for effective tillers per plant, grains per spike, test weight and grain yield per plant. In case of spike length (19.99%), harvest index (16.51%), days to maturity (15.27%), plant height (14.74%) and straw yield per plant (13.12%) medium genetic advance was observed. Same results showed by Vaghela *et al.* (2021) [14] and Chauhan *et al.* (2022) [5] for plant height and spike length. Days to heading (9.86%) showed low genetic advance and also supported by Abinasa *et al.* (2011) [1], Ibrahim *et al.* (2019) [9] and Roy *et al.* (2021) [12]. Higher heritability coupled with high genetic advance as percent mean is observed for filled grains per spike, grain yield per plant, grains per spike, gluten content, test weight and effective tillers per plant. This confirmed a role of additive gene action and thus improvement in these traits could be brought about by direct phenotypic selection over the genotypes. These findings were similar to results by Vaghela *et al.* (2021) [14] for effective tillers per plant, grains per spike and grain yield per plant, Chauhan *et al.* (2022) [5] for effective tillers per plant, grains per spike, test weight and grain yield per plant and Shankar *et al.* (2022) [13] for test weight, grain yield per plant and grains per spike.

Higher heritability with medium genetic advance as percent mean is observed in spike length, harvest index, days to maturity, plant height and straw yield per plant, while higher heritability coupled with low genetic advance observed in case of days to heading indicating that the effect of non-additive gene action and there is a limited scope of improvement through direct phenotypic selection for these traits. Similar results were observed by Ibrahim *et al.* (2019) [9] for days to heading and Chauhan *et al.* (2022) [5] for plant height and spike length.

Table 1: Analysis of variance of experimental design for yield and yield contributing characters in wheat

Source	d.f.	DTH	PH	ETP	SL	GPS	FGPS	DTM	TW	GYPP	SYPP	HI	GC
Replication	2	2.425	28.33	0.37	1.12	19.51	7.56	11.43	3.675	1.88	1.23	1.92	17.49
Genotypes	39	30.27**	129.98**	0.82**	2.88**	173.24**	131.02**	210.24**	105.11**	16.83**	14.20**	25.93**	70.67**
Error	78	21.32	0.13	0.38	26.08	20.38	3.58	9.74	9.67	1.42	2.11	1.14	2.89
S.Em	-	2.67	0.20	036	2.94	2.60	1.09	1.80	1.79	0.68	0.84	0.61	0.98
CD @ 5%	-	7.50	0.58	1.01	8.30	7.33	3.07	5.07	5.05	1.93	2.36	1.74	2.76
CD @ 1%	-	9.95	0.78	1.33	11.00	9.73	4.08	6.72	6.70	2.56	3.13	2.30	3.66
CV%	-	6.92	9.58	7.99	13.66	14.60	3.60	3.03	8.00	9.10	5.69	3.18	5.43
*, ** significant at 5% and 1% levels, respectively													

Table 2: Measures of variability parameters of twelve characters in wheat

		DTH	PH	ETP	SL	GPS	FGPS	DTM	TW	GYPP	SYPP	HI	GC
Range	Minimum	46	53.33	2.52	6.04	24.33	21.67	90.67	31.00	5.27	13.20	28.50	23.54
	Maximum	58	87.44	4.95	10.93	54.00	44.67	144.00	55.33	17.41	27.94	38.35	41.91
Grand Mean		52.57	66.69	3.78	7.76	37.36	30.91	102.96	38.85	13.07	25.52	33.59	31.23
Genotypic Variance		8.89	36.21	0.23	0.83	49.05	36.88	66.83	31.81	5.13	4.02	8.26	22.59
Phenotypic Variance		12.48	57.54	0.36	1.21	75.13	57.26	76.57	41.48	6.55	6.14	9.40	25.48
Environmental Variance		3.58	21.32	0.13	0.38	26.08	20.38	9.74	9.67	1.41	2.11	1.14	2.88
GCV (%)		5.67	9.02	12.70	11.74	18.74	19.64	7.93	14.51	17.32	7.87	8.55	15.21
PCV (%)		6.72	11.37	15.91	14.20	23.19	24.47	8.50	16.57	19.57	9.71	9.12	16.16
ECV (%)		3.60	6.92	9.58	7.99	13.66	14.60	3.03	8.05	9.10	5.69	3.18	5.43
Heritability in broad sense (h^2_{bs}) (%)		71.26	62.93	63.73	68.32	65.28	64.39	87.27	76.67	78.35	65.59	87.80	88.67
Genetic Advance (% Mean)		9.86	14.74	20.88	19.99	31.19	32.47	15.27	26.18	31.59	13.12	16.51	29.52

Where,

DTH = Days to heading PH = Plant height (cm) ET = Effective tillers per plant SL = Spike length (cm) GPS = Grains per spike GC = Gluten content (%)

FGPS = Filled grains per spike DTM = Days to maturity TW = 1000 grain weight (g) SYPP = Straw yield per plant (g) HI = Harvest Index (%) GYPP = Grain yield per plant (g)

GCV (%) = Genotypic coefficient of variation PCV (%) = Phenotypic coefficient of variation ECV (%) = Environmental coefficient of variation

4. Conclusion

Based on the current investigation, it can be concluded that the majority of the traits had sufficient genetic variability in the experimental material. In order to effectively respond to yield enhancement, consideration should be given to the traits with moderate to high variability and genetic advance. When alleles with additive gene action accumulate, stabilizing selection should be used. It may be suggested to select and hybridize genotypes with high heritability, genetic advance, and genotypic coefficient of variation in order to further increase bread wheat yield in a particular region.

5. Acknowledgement

6. References

1. Abinasa M, Ayana A, Bultosa G. Genetic variability, heritability and trait associations in durum wheat (*Triticum turgidum* (L.) var. durum) genotypes. African Journal of Agricultural Research. 2011;6(17):3972-3979.
2. Ali Y, Atta BM, Akhter J, Monneveux P, Lateef Z. Genetic variability, association, and diversity studies in wheat (*Triticum aestivum* L.) germplasm. Pakistan Journal of Botany. 2008;40(5):2087-2097.
3. Arya VK, Singh J, Kumar L, Kumar R, Kumar P, Chand P. Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.). Indian Journal of Agricultural Research. 2017;51(2):128-134.
4. Burton GW, DeVane. Estimation of heritability in tall Festuca (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953;45:478-479.
5. Chauhan S, Tyagi SD, Gupta A, Singh S. Genetic variability, correlation, path coefficient, and cluster analysis in bread wheat (*Triticum aestivum* L.) under rainfed conditions. The Pharma Innovation Journal. 2022;11(11):818-823.
6. Debasis P, Khurana P. Wheat biotechnology: A mini review 2001. EJB ISSN. 0717-3458.
7. Feldman M. Origin of cultivated wheat. The world wheat book: a history of wheat breeding. 2001;3-53.
8. Guar SC. Genetic improvement through variability, heritability and genetic advance for grain yield and its contributing traits in Wheat [*Triticum aestivum* (L.) em. Thell]. International Journal of Pure and Applied Bioscience. 2019, 7(1):368-373.
9. Ibrahim AU. Genetic variability, correlation and path analysis for yield and yield components in F6 generation of Wheat (*Triticum aestivum* Em. Thell.). IOSR Journal of Agriculture and Veterinary Science. 2019;12(1):17-23.
10. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47:314-318.
11. Panse VG, Sukhatme PV. Statistical Methods for Agricultural Workers. ICAR Publication. 1978;87-89.
12. Roy A, Kumar A, Singh A, Mandi A, Barman M. Analysis of genetic diversity and correlation studies on grain yield and its component characters in bread wheat (*Triticum aestivum* L. em Thell) genotypes. Pharma Innovation Journal. 2021;10:341-345.
13. Shankar S, Singh G, Prasad BK. Estimation of genetic variability, correlation and path coefficient analysis for yield and its attributes in wheat (*Triticum aestivum* L.). Journal of Emerging Technologies and Innovative Research. 2022;9:107-118.
14. Vaghela GK, Patel JM, Rahevar P. Assessment of genetic variability and character association for morpho-chemical traits in bread wheat (*Triticum aestivum* L.). Emergent Life Sciences Research. 2021;7:14-20.
15. Yagdi K. Path coefficient analysis of some yield components in durum wheat (*Triticum durum* Desf.). Pakistan Journal of Botany. 2009;41(2):745-751.