Original Research Article

Comment [Rk1]: Avoid abbreviation in Title like CMS
Kindly submit the list of abbreviation used in throughout the manuscript

Assessment of genetic variability in CMS based wheat hybrid

Abstract

Present study was carried out to evaluate genetic variability and inheritance of yield contributing traits usingfifteen CMS based F1 hybrid of wheat involving fifteen CMS based lines and one restorer line received from IIWBR, Karnal and Division of Genetics, IARI under CRP on hybrid wheat programmealong withfivewheat checks.Experiment was conducted during *Rabi* 2019-20 in randomized block design with two replications in threedifferent sowingdatesat Seed Breeding Farm, JNKVV, Jabalpur. Analysis of variance revealed that, significant differences among the crosses for all the traits indicated that the presence of sufficient amount of genetic variability. High GCV% and PCV % accounted for the traits number of effective tillers/plantandnumber of ~~spikes/plant~~spikes/plants, thousand grain weight,spike weight and grain yield/plant in EI, EII, EIII and pooled environment. Genetic advance as percentage of meanestimate was highest for biological yield/plant(33.99%) andmean notedrespectivelynumber of effective tillers/plant, thousand grain weight, number of spikes/plant and grain yield/plant in different environment conditions. Hence,selection of these traits would be effective for further crop improvement programme. On the basis of mean and range, maximum mean value noted in respective CMS based hybrids *viz.*,grain yield/plant (CMS96A*Res-37), thousand grain weights and grains/ear(CMS86A*Res-37), harvest index (CMS85A*Res-37), number of effective tillers/plant (CMS95A*Res-37). These crosses contributed directly for yield improvement.

.

Keywords: Wheat, CMS lines and genetic variability, restorer line

UNDER PEER REVIEW

Introduction

Triticum aestivum, commonly known as wheat, is a cereal grass placed in family *poaceae* having chromosome number of 2n=42 hexaploid spp. and belief to originated in southeastern Asia. The genus *Triticum* includes many wheat species, notably *Triticum aestivum* and *Triticum durum*. It is the largest food crop to cover the earth's surface (218.54 million hectares in 2017) {FAO, 2017}. Wheat ranks second in world crop production and is a staple food for over 41% of the world's population and in more than 40 countries, So It is known as "King of cereals". During 2020-21, wheat production has reached an all-time record of 109.52 mt with an average national productivity of 3464 kg/ha. In Madhya Pradesh, area, production and productivity of wheat is 6.69 million hectare, 17.58 million tonnes and 2627 kg/ha, respectively (Anonymous, 2020-21).

A wide range of heritable variation has been reported in wheat germplasm, which indicates prospects of its improvement through selection following hybridization of superior genotypes. However, effectiveness of the selection depends upon the extent to which a particular trait is heritable. Variations, which prove heritable, are advantageous to the breeders giving opportunity of selection during early segregating generations with high selection efficiency and response to selection. Most of the polygenic traits, like grain yield/plant, are influenced by the environment and have low heritability. Thus, selection of such polygenic traits in early segregating populations becomes difficult. Study of statistical parameters like mean, variance, heritability, genetic advance, etc., is helpful to evaluate the performance of any particular genotype and also a measure to determine the effectiveness of selection for a particular trait in that genotype. Thus, the present study was designed to evaluate for genetic variability and inheritance of some yield and related traits and to select desirable CMS based wheat hybrid for future breeding strategies.

Material and Methods

Experiment comprised of newly developed fifteen CMS lines and one restorer lines, received from IIWBR, Karnal and Division of Genetics, IARI under CRP on hybrid wheat programme. The experiment was planted at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, J.N.K.V.V., Jabalpur (M.P.) during *Rabi* 2019-20.Recommended package and practice were followed to raise a healthy crop plant. A total of fifteen CMS lines and one restorer lines were mating design to generate 15 F1 hybrids, a total of 20entries (F1s and check) were evaluated in Randomized Complete Block Design with two replications in three date of sowing(EI-first date of sowing,EII-second date of sowing,EIII-third date of sowing). The observations were recorded on thirteen quantitative traits *viz.*, days to 50% heading, days to maturity, plant height, number of effective tillers/plant, number of spikes/plant, spike weight, spike length, number of spikelets/spike, number of grains/spike, thousand grain weight, biological yield/plant, harvest index and grain yield/plant. Observations were recorded on randomly selected five competitive plants from each line. These traits were used to assessgenetic

UNDER PEER REVIEW

parameters of variability *viz.*, mean, range, genotypic and phenotypic coefficient of variation, broad sense heritability and genetic advance as percentage of mean. The Genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were estimated by the formula suggested by Burton (1953). Heritability in broad sense was calculated according to the formula suggested by Hanson *et al.* (1956).Genetic advance by adopting the method of Johnson *et al.* (1955).

Table1 : List of genotypes used as experimental material

S. No.	Name of Entry	S. No.	Name of Entry	S. No.	Name of Entry
1	CMS 82A* Res-37	8	CMS 89A* Res-37	15	CMS 97A* Res-37
2	CMS 83A* Res-37	9	CMS 90A* Res-37	16	HI-1544
3	CMS 84A* Res-37	10	CMS 91A* Res-37	17	MP-3336
4	CMS 85A* Res-37	11	CMS 92A* Res-37	18	GW-322
5	CMS 86A* Res-37	12	CMS 94A* Res-37	19	Lok-1
6	CMS 87A* Res-37	13	CMS 95A* Res-37	20	MP-3382
7	CMS 88A* Res-37	14	CMS 96A* Res-37	**R line**	Res-37

Result and discussion:

Comment [Rk2]: Include Table 3 and Figure 1 also in result and discussion section like Table 2

Analysis of variance indicated that significant mean sum of squares is observed for all the characters under study which indicates presence of considerable amount of variability.The mean sum of square due to crosses were significant for all the characters except days to maturity, spike length and mean sum of square was maximum and highly significant for plant height, number of effective tillers/plant, number of spikes/plant, spike weight, number of spikelets/spike, number of grains/spike, thousand grain weight, biological yield/plant, harvest index and grain yield/plant in EI, EII, EIII and pooled environment. Hence, there is large scope for inclusion of these variable CMS based lines of wheat in breeding program for further improvement in yield and its attributing traits.

A wide range of genetic variation was observed for various quantitative traits (Table 2).Days to50%heading ranged from 73.5 to 84 with an overall mean performance of 80.97 days and maximum days to 50%heading was observed in cross CMS85A*Res-37 (84) in EI and this trait varied from 75 to 83.5 with grand mean of 79.5 days and maximum days to 50% heading

UNDER PEER REVIEW

were observed in cross CMS96A*RES-37 (83.5) in EII. Whereas, this trait showed variation from 71.5 to 81.5 with an overall mean performance of 77.5 days and maximum days to heading was observed in cross CMS83A*Res-37, CMS85A*Res-37, CMS94A*Res-37 and CMS97A*Res-37 (81.5) in EIII. Days to 50% heading ranged from 73.33 to 82.5 with an overall mean performance of 79.41 days and maximum days to heading was observed in cross CMS85A*Res-37 (82.5) in pooled environment. Days to maturity varied from 112.5 to 126.50 with grand mean of 122.18 days in EI, ranged from 109.50 to 124.50 with an average value of 119.88 days in EII, varied from 106.50 to 121.5 with an average value of 117.4 days in EIII and ranged from 109.5 to 124.17 with an average value of 119.82 days in Pooled analysis and maximum days to maturity was recorded in cross CMS87A*Res-37 in all above environmental conditions. Plant height ranged from 74.5 to 89.05 cm with mean value of 81.35 cm in EI, varied from 64.35 to 84 cm with mean of 74.5 cm in EII, varied from 66 to 83.25 cm with mean performance of 73.88 cm in EIII, varied from 70.6 to 83.45 cm with mean of 76.58 cm in pooled analysis. The average number of effective tillers/plant was 23.85 and it ranged from 11.8 to 32.65 (maximum in cross CMS95A*Res-37) in EI, while in EII ranged from 10.81 to 29.27 (in cross CMS97A*Res-37) with a mean value of 21.5. The average number of effective tillers/plant was 19.63 and it ranged from 9.5 to 28.66 (in cross CMS97A*Res-37) in EIII, whereas in pooled analysis ranged from 10.7 to 30.11 (in cross CMS95A*Res-37) with an average value of 21.66. The number of spikes/plant differed from 8.02 to 22.55 with grand mean of 15.99 and maximum number of spikes/plant was recorded in cross CMS89A*Res-37 (22.55) in pooled analysis. Spike length ranged from 9.32 to 13.43 cm with grand mean of 11.46 cm. Maximum spike length was recorded in cross CMS85A*Res-37 (13.43 cm) however spike weight ranged from 2.98 to 4.5 gm with mean performance of 3.71 gm in pooled analysis.The number of spikelets/spike varied from 16.09 to 24.13 with overall mean performance of 21.53 and maximum number of spikelets/spike was recorded in cross CMS85A*Res-37 (24.13) in pooled analysis.The number of grains/ear varied from 46.52 to 70.73 with a mean value of 62.69. Maximum number of grains/ear was noted in cross CMS86A*Res-37 (70.73) in pooled analysis. Thousand grain weights ranged from 39.38 to 58.09 gm with average test weight of 51.76 gm. The maximum test weight was recorded for cross CMS86A*Res-37 (58.09 gm) in pooled analysis. Biological yield/plant ranged from 80.93 to 130.25 gm with average mean of 94.75 gm, harvest index varied from 43.08 to 57.64 (in cross CMS85A*Res-37) with a grand mean of 47.97in pooled

UNDER PEER REVIEW

analysis. Grain yield/plant maximum in cross CMS96A*Res-37 and ranged from 34.72 to 60.2 with overall mean of 45.32. Similar results reported by Murad (2019), Biru and Negash (2020), Choudhary *et al*. (2020), Prasad *et al.* (2021), Chaudhary *et al.* (2022), Sharma *et al.* (2022).

High genotypic and phenotypic coefficient of variation was observed for number of effective tillers/plant (26.67 & 26.84) followed by number of spikes/plant (25.2 & 25.37) in EI. However, moderate GCV& PCV were recorded for grain yield/plant (17.83 & 18.58) followed by biological yield/plant (17.26 & 17.4), harvest index (14.41 & 15.26), thousand grain weight (13.9 & 14.12), spike weight (12.88 & 13.63), spike length (11.38 & 12.96) and number of spikelets/spike (10.76 & 11.16) and number of grains/spike (10.34 & 11.09) in EI. Whereas, High genotypic and phenotypic coefficient of variation was observed for number of effective tillers/plant (26.8 & 26.98) followed by number of spikes/plant (24.65 & 24.82) and grain yield/plant (20.75 & 20.86) in EII. High genotypic and phenotypic coefficient of variation was observed for number of spikes/plant (30.23 & 32.42) followed by number of effective tillers/plant (29.45 & 29.87) in EIII, High genotypic and phenotypic coefficient of variation was observed for number of effective tillers/plant (27.2 & 27.83) followed by number of spikes/plant (25.75 & 27.39) in pooled analysis. Similar results reported byMundiyara*et al.* (2014),Tiwari *et al.*(2016), Rajput (2019), Biru and Negash (2020), Choudhary *et al.* (2020), Prasad *et al.* (2021) and Sharma *et al.* (2022) andchaudhary*et al.* (2022).This result indicated that there was negligible variation in all different environmental conditions means these traits were show genotypic variation they would be used in hybridization programme for better crop improvement. These traits would be effective for selection.

High heritability % was noted for most of the trait under study *viz.*, number of effective tillers/plant (98.74) followed by number of spikes/plant (98.7), biological yield/plant (98.43), thousand grain weight (96.8), number of spikelets/spike (93.02), grain yield/plant (92.12), spike weight (89.24), harvest index (89.15), number of grains/spike (86.94) and spike length (77.17) in EI. The same traits also showed high heritability estimates in EII and EIII while only number of effective tillers/plant (95.5) followed by thousand grain weight (93.93) and number of spikes/plant (88.37) exhibited high heritability estimates in pooled analysis. Genetic advance as percentage of mean estimate was highest for biological yield/plant (33.99%) in EI, EII, EIII and pooled analysis. While high heritability coupled with medium genetic advance as percentage of

UNDER PEER REVIEW

mean was noted for grain yield /plant (16.36%) followed by thousand grain weight (15.43%), harvest index (13.58%), number of effective tillers/plant (13.02%) and number of grains/spike (13.01%) in EI, whereas similar traits also showed in EII, EIII and pooled analysis. Similar finding noted by Mecha*et al.* (2016), Yaqoob (2016), Arya *et al.* (2017), Chethana *et al.* (2017), Sabit*et al.* (2017), Bhanu *et al.* (2018), Gaur (2019), Choudhary *et al.* (2020), Prasad *et al.* (2021) and Sharma *et al.* (2022).

Conclusion:

Analysis of variance revealed that, presence of sufficient amount of genetic variability among the parental lines. High GCV% and PCV % accounted for the traits number of effective tillers/plant and number of spikes/plant while thousand grain weight, spike weight and grain yield/plant while, high heritability coupled with high genetic advance as percentage of mean noted for biological yield/plant whereas medium genetic advance exhibited by number of effective tillers/plant, thousand grain weight, number of spikes/plant and grain yield /plant in different environment conditions. Hence, these traits would be effective and suggested that selection of these traits could be practiced more effectively for further crop improvement programme. On the basis of maximum value of grain yield /plant (CMS96A*Res-37), thousand grain weights and grains/ear (CMS86A*Res-37), harvest index (CMS85A*Res-37), number of effective tillers/plant (CMS95A*Res-37). These crosses contributed directly for yield improvement. These diverse promising crosses, CMS based line and restorer line had desirable yield component traits under different sown conditions and prefer to selection and could be better exploit for future wheat hybridization programme.

Comment [Rk3]: Add commas,

UNDER PEER REVIEW

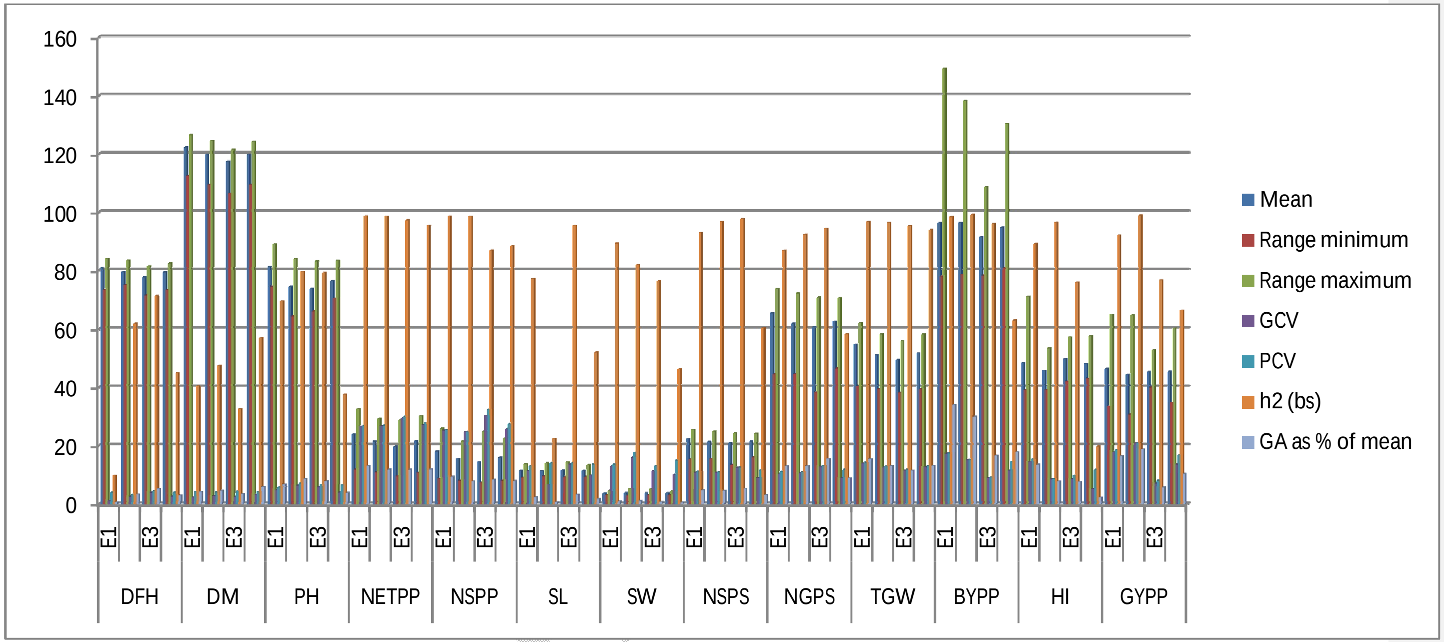

Figure1: Graphical presentation of genetic parameters of variability of CMS based wheat hybrid for quantitative traits

Table 2.Analysis of variance for quantitative traits in EI, EII and EIII environment in CMS based wheat hybrid lines

Env	Source of variation	DF	Mean sum of square												
			DFH	DM	PH	NETPP	NSPP	SL	SW	NSPS	NGPS	TGW	BYPP	HI	GYPP

EI	Replication	[1]	93.03**	225.63*	2.45	30.87**	21.23**	0.87	0.06	0.04	2.07	45.24**	1.43	47.68*	49.26**
	Genotype	[19]	10.92	23.86	37.44**	81.45**	41.61**	3.90**	0.48**	11.94**	98.61**	117.76**	557.45**	103.48**	142.74**
	Error	[19]	8.97	28.47	6.72	0.52	0.27	0.5	0.03	0.43	6.89	1.91	4.4	5.93	5.85
EII	Replication	[1]	32.40**	93.03*	2.26	28.58**	21.68**	1.85	0.50*	0.1	8.25	49.48**	23.93**	29.53**	54.78**
	Genotype	[19]	10.63**	33.57*	49.70**	66.85**	29.61**	3.07	0.80**	10.69**	89.42**	84.69**	425.64**	30.63**	170.07**
	Error	[19]	2.51	11.97	5.63	0.45	0.21	1.95	0.08	0.18	3.52	1.53	1.6	0.55	0.9
EIII	Replication	[1]	193.60**	722.50**	9.03	26.03**	5.51	0.07	0.62**	0.12	4.45	50.02**	16.23*	0.35	2.72
	Genotype	[19]	21.82**	35.51	42.04**	67.83**	40.56**	5.13**	0.41**	13.69**	123.97**	66.66**	138.20**	41.89**	23.67**
	Error	[19]	3.65	18.03	4.87	0.95	2.82	0.12	0.05	0.15	3.58	1.62	2.76	5.72	3.12

***significant at 5%, ** highly significant at 1%**

EI-first date of sowing, EII-second date of sowing, EIII-third date of sowing

Table3.Genetic parameters for quantitative traits of CMS based wheat hybrid lines in EI, EII, EIII and Pooled analysis

Characters	**Environment**	**Mean**	**Range**		**GCV**	**PCV**	**h^2(bs)**	**GA as % of mean**
			Mini	Maxi				
DFH	E1	80.97	73.5	84	1.22	3.89	9.79	0.64
	E2	79.5	75	83.5	2.54	3.22	61.86	3.27
	E3	77.75	71.5	81.5	3.88	4.59	71.32	5.24

UNDER PEER REVIEW

	Pool	79.41	73.33	82.5	2.63	3.93	44.87	2.89
DM	E1	122.18	112.5	126.5	2.35	4.19	40.45	4.12
	E2	119.88	109.5	124.5	2.74	3.98	47.43	4.66
	E3	117.4	106.5	121.5	2.52	4.41	32.65	3.48
	Pool	119.82	109.5	124.17	3.16	4.19	56.82	5.88
PH	E1	81.35	74.5	89.05	4.82	5.78	69.58	6.74
	E2	74.5	64.35	84	6.3	7.06	79.64	8.63
	E3	73.88	66	83.25	5.84	6.56	79.23	7.91
	Pool	76.58	70.6	83.45	3.95	6.45	37.55	3.82
NETPP	E1	23.85	11.8	32.65	26.67	26.84	98.74	13.02
	E2	21.5	10.81	29.27	26.8	26.98	98.66	11.79
	E3	19.63	9.5	28.66	29.45	29.87	97.24	11.75
	Pool	21.66	10.7	30.11	27.2	27.83	95.5	11.86
NSPP	E1	18.04	8.7	25.9	25.2	25.37	98.7	9.3
	E2	15.55	8.05	21.59	24.65	24.82	98.59	7.84
	E3	14.37	7.3	24.91	30.23	32.42	86.98	8.35
	Pool	15.99	8.02	22.55	25.75	27.39	88.37	7.97
SL	E1	11.45	9.1	13.75	11.38	12.96	77.17	2.36
	E2	11.33	9.5	14	6.62	13.98	22.39	0.73
	E3	11.58	9.2	14.3	13.67	13.99	95.43	3.19
	Pool	11.46	9.32	13.43	9.85	13.65	52.02	1.68
SW	E1	3.68	3.03	4.65	12.88	13.63	89.24	0.92
	E2	3.74	2.85	5.29	16.03	17.7	82	1.12
	E3	3.71	3.08	5.11	11.36	12.99	76.46	0.76
	Pool	3.71	2.98	4.5	10.17	14.95	46.28	0.53
NSPS	E1	22.29	15.3	25.45	10.76	11.16	93.02	4.77
	E2	21.37	15.54	24.91	10.73	10.91	96.69	4.64
	E3	20.91	13.46	24.26	12.44	12.58	97.81	5.3
	Pool	21.53	16.09	24.13	8.98	11.55	60.44	3.1
NGPS	E1	65.51	44.43	73.75	10.34	11.09	86.94	13.01

UNDER PEER REVIEW

	E2	61.84	44.45	72.22	10.6	11.02	92.43	12.98
	E3	60.71	38.34	70.88	12.78	13.16	94.39	15.53
	Pool	62.69	46.52	70.73	8.97	11.76	58.18	8.83
TGW	E1	54.77	40.4	62.09	13.9	14.12	96.8	15.43
	E2	51.03	39.5	58.16	12.64	12.87	96.45	13.05
	E3	49.47	38.25	55.84	11.53	11.81	95.25	11.47
	Pool	51.76	39.38	58.09	12.66	13.06	93.93	13.08
BYPP	E1	96.33	78	149.21	17.26	17.4	98.43	33.99
	E2	96.45	78.57	138.21	15.1	15.15	99.25	29.88
	E3	91.46	78.21	108.65	9	9.18	96.08	16.62
	Pool	94.75	80.93	130.25	11.5	14.48	62.99	17.81
HI	E1	48.48	39.1	71.13	14.41	15.26	89.15	13.58
	E2	45.68	39.06	53.33	8.49	8.64	96.49	7.85
	E3	49.76	41.97	57.28	8.55	9.81	75.96	7.63
	Pool	47.97	43.08	57.64	5.17	11.68	19.64	2.27
GYPP	E1	46.39	33.53	65.03	17.83	18.58	92.12	16.36
	E2	44.33	30.7	64.64	20.75	20.86	98.95	18.85
	E3	45.25	39.92	52.78	7.08	8.09	76.73	5.78
	Pool	45.32	34.72	60.2	13.66	16.76	66.36	10.39

DH - days to 50% heading, DM- days to maturity, PH- plant height, NTPP - number of tillers per plant, NSPP - number of spike per plant, SL - spike length, SW -spike weight, NSPS - number of spikelets per spike, NGPS - number of grains per spike, TGW - 1000-grain weight, BYPP - biological yield per plant, HI- harvest index, GYPP - grain yield per plant

UNDER PEER REVIEW

References:

Anonymous. 2020-21. Project director report, DWR, Karnal, pp:1

Arya VK, Singh J, Kumar L, Kumar R, Kumar P and Chand P. 2017. Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.). Indian J. Agric. Res. 51(2): 128-134.

Bhanu AN, Arun B and Mishra VK (2018). Genetic Variability, Heritability and Correlation Study of Physiological and Yield Traits in Relation to Heat Tolerance in Wheat (*Triticum aestivum* L.).*Biomed. J. Sci. & Tech. Res.* 2; ISSN: 2574-1241.

Chaudhary H, Jaiswal J P, Kumar A and Joshi S. 2022. Determination of genetic variability and diversity in bread wheat for yield and Yield contributing traits. *International Journal of Plant & Soil Science 34(19): 16-23*

Choudhary, L., Goyal, V.K., Pandey, S., Moitra, P.K. and Shukla, R.S., 2020. Assessment of genetic variability in advance breeding lines of wheat. *The Pharma Innovation Journal*, *9*(5), pp.239-244.

Murad J, Ahmed R, Azam M, Saeed M, Dost K, Ahmed B, Naeem M, Khan S (2019). Phenotypic association and heritability analysis in bread wheat (*Triticum aestivum* L.) genotypes. *International Journal of Biosciences*. 14 (6); 71-77.

Naresh, V., Yamini, K. N., Rajendrakumar, P. and Dinesh Kumar, V. 2009. EST-SSR Marker-based Assay for the Genetic Purity Assessment of Safflower Hybrids. Euphytica, 170: 347–353.

Rajdeep Mundiyara, Kerkhi SA, Jakhar ML, Mishra S. Genetic variability, correlation and path analysis in Wheat (*Triticum aestivum*L.). Journal of Plant Science Research. 2014; 30(1):39-47.

Rajput RS (2019). Path Analysis and Genetic Parameters for Grain Yield in Bread Wheat (*Triticumaestivum* L.). *Annual Research & Review in Biology*. 31(3): 1-8.

Sabit Z, Yadav B and Rai PK. 2017. Genetic variability, correlation and path analysis for yield and its components in f5 generation of bread wheat (Triticum aestivum L.). Journal of Pharmacognosy and Phytochemistry 6(4): 680687.

Sharma R, Rana V, Verma S, Gupta C, Priyanka, Rana A, Dwivedi Aparajita, Sharma Akriti and Sood VK. 2022. Genetic Variability Studies in Bread Wheat (*Triticum aestivum*L.) under

UNDER PEER REVIEW

Multi-Environment Trials in Northern Hills Zone. *Biological Forum – An International Journal* 14(2): 307-313.

Shukla RS and Moitra PK .2013. Genetic analysis of CIMMYT based bread wheat genotypes for yield and its contributing traits. JNKVV Research Journal 47(3): 255-259.

Singh M, Mishra DK, Shukla RS and Samaiya RK. 2015. Variation and heritability for some quality characteristics and grain yield in bread wheat (*Triticum aestivum* L.). Trends in Biosciences 8(1): 68-70.

Tiwari A, Mishra DK, Shukla RS, Choudhary P. Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat. Green Farming. 2016; (6):1296-1300.

UNDER PEER REVIEW