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Genetic variability, association and diversity studies in wheat (*Triticum* spp. L.)

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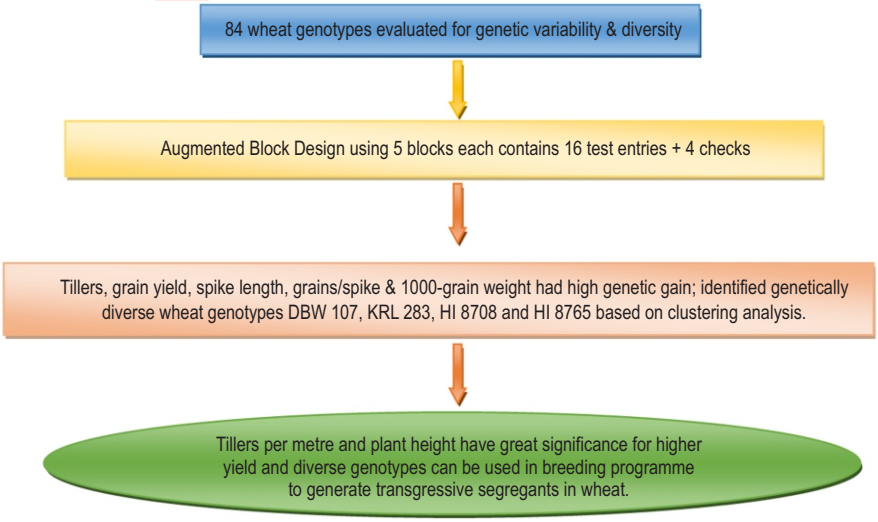
Abstract

Aim: The present study was aimed to assess the genetic variability and diversity in wheat genotypes and identification of elite lines for future genetic improvement.

Methodology: Eighty-four wheat (*Triticum* spp. L.) genotypes were evaluated in Augmented Block Design with 5 blocks wherein each block contains 20 genotypes including 16 test entries and 4 checks (randomly allocated). Each genotype was sown in double rowed plot of 2.5 m.

Results: High GCV and high genetic gain was observed for the traits like tillers/meter row length, grain yield per plot, spike length, grains per spike and 1000-grain weight showing predominance of additive genetic effect for these traits. Grain yield per plot had positive and significant correlation with plant height and tillers number per meter row length. Therefore, these characters should be emphasized more during selection for yield traits and thereby yield improvement in wheat. The cluster analysis identified DBW 107, KRL 283 among bread wheat and HI 8708 and HI 8765 among durum wheat as genetically most diverse genotypes.



Interpretation: Greater emphasis should be given on tillers per meter row length and plant height traits while selecting for higher yield. Diverse genotypes identified by multivariate methods can be used in breeding program to generate transgressive segregants in wheat.

Key words: Association, Genetic variability, Heritability, Path analysis, Principal component analysis, Wheat

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Introduction

Bread wheat (*Triticum species* L.) is one of the major staple cereals crop grown to feed nearly 2.5 billion of world population and provides almost half of all calories requirements. It is one of the most valuable sources of protein in least developed and middle-income countries. Wheat is cultivated as winter and spring types in the world of which Indian wheat belongs to spring type (Ramadas *et al.,* 2019). Wheat acreage in India is about 31.76 million hectares (14 % of global area) to produce the all time highest output of 109.52 million tons of wheat (13.64 % of world production) with an average productivity of 3448 kg ha^{-1} (MoA&FW, 2021). In India, three wheat species namely bread wheat (*T. aestivum* L .em Thell), durum wheat or kathia wheat (*T. durum*) and dicoccum or khapli wheat (*T. dicoccum*) are grown for consumption; out of which bread wheat occupies more than 85 % area and production. Bread wheat [*Triticum species* (L.) em. Thell], is an allohexaploid species with 2n=6X=42 chromosomes whereas durum and dicoccum kinds of wheat are allotetraploid species with 2n=4X=28 chromosomes.

The nutritional value of wheat is significant as it is one of the few crops that is widely cultivated as a staple food source. The importance of wheat is mainly due to the fact that its seed can be ground into flour, semolina, etc., which form the key ingredients of chapattis, breads, cakes, biscuits, pasta and a variety of hot ready-to-eat breakfast foods. It is a major source of energy/starch and it also provides good amount of health promoting components *viz.,* proteins, nutrients, vitamin B complex, dietary fiber and phytochemicals. Dietary fiber of wheat offers reduced risk of cardio-vascular disease, different types of cancers, especially colo-rectal cancer and type 2 diabetes (Shewry and Hey, 2015). Knowledge of inherent diversity is needed for the development of high reproductive cultivars and genetic variation in the germplasm lines which play an important role in formulating a tangible and successful breeding programme. If there is enough genetic heterogeneity in the population, superior genotypes can be identified by selection, which provides the foundation for further improvement and ensures better chances of evolving desired plant types. The variability expressed in terms of phenotypic and genotypic coefficients of variability are indicative of heritable genetic effects and non-heritable environmental effects that provide baseline information for traits to be emphasized during selection of promising progenies.

The knowledge of other genetic parameters *viz.,* heritability and genetic advance is useful for predicting accurate genetic progress in breeding programmes and developing efficient breeding strategies. Genetic diversity is indispensable to convene the diversified target of plant breeding such as breeding for yield enhancement, wider adaptation, desirable quality, pest and disease resistance (Hailegiorgis *et al.,* 2011). Plant genetic diversity is crucial component for improvement to enhance production levels (Mohibullah *et al.,* 2013). Hybridization and subsequent selections are one of the most successful approaches adopted for wheat breeding (Bhatt, 1973) which depends primarily on the target trait and subsequent choice of parents to be utilized. Transgressive segregation may be exploited in such cases when parents used in hybridization are genetically dissimilar (Rieseberg *et al.,* 2003) which is directly proportional to the extent of heterosis observed in progenies (Cheres *et al.,* 2000). The interaction of different component characters with the environment determines yield as a complex character. Correlation studies help quantify and evaluate the proportion of phenotypic correlation associated with genetic backgrounds, investigate whether the selection for a particular character affects more traits, scrutinize indirect gains due to selection on correlated traits and dissect the complexity of traits. Assessment of mutual relationships among various characters contributing to the yield and partitioning these associations into direct and indirect effects through path coefficient analysis aid in selection in order to increase the yield and its contributing characters simultaneously (Kumar *et al.,* 2018).

Genetic diversity available in the existing germplasm determines the success of any crop improvement programme through combination breeding. Using multivariate method like cluster analysis the genotypes can be classified based on a set of measured variables into different groups so that similar genotypes are placed in the same group. This method sorts the genotypes into clusters or groups in such a way that the degree of association may be strong between members of the same cluster and weak between members of different clusters. The cluster analysis is performed using Euclidean distance and a measure of similarity levels (Everitt, 1993; Eisen *et al.,* 1998). Principal Component Analysis (PCA) is most frequently used method to assess genetic diversity while securing relative basic differences between genotypes. Moreover, the analysis is characterized by the fact that it includes the total variance of variables, explains maximum of variance within a data set and is a function of primary variables (Birhanu *et al.,* 2017). Therefore, considering the above facts, extent of genetic variability, heritability, correlation, path analysis and genetic advancement for yield and different yield attributing traits in 84 diverse wheat genotypes were investigated.

Materials and Methods

The experimental material comprised of 80 wheat genotypes along with 4 checks were studied. The genotypes included in the study were taken from National Genetic Stock Nursery (NGSN) constituted at ICAR-IIWBR, Karnal. This nursery, commonly known as 'Suggested Crossing Block', included bread wheat, durum wheat, dicoccum wheat and Triticale genotypes which are categorized as agronomic bases, genetic stocks for various traits, disease resistant sources and elite germplasm lines. The parentage and source information of genotypes included in the study is being provided in the Table 6. The investigation was done at Agronomy Farm, RCA, MPUAT, Udaipur during 2019-20 adopting Augmented Block Design with 5 blocks, each with 16 test entries and 4 checks (with random allocation) with the total of 20 genotypes per block. Genotype was sown in 2.5 m long two rows plot with a 20 cm line to line spacing

and plant to plant was 5 cm, respectively. Improved and recommended packages of practices were followed to raise a healthy crop. For traits *viz.,* plant height (PH in cm), tillers / meter row length (TPMR), Grains spike^{-1} (GPS), spike length (SL in cm) and TGW (1000-grain weight in g), all data was collected on five randomly chosen competitive plants from each genotype in each block while for days to 50 % heading (DH), days to 75 % maturity (DM) and grain yield plot^{-1} (GYPP), the data was recorded on a whole plot basis. The analysis of variance was done as per Federer (1956) and the Phenotypic and genotypic coefficients of variation (PCV and GCV) (Burton, 1952), genetic advance (Johnson *et al.,* 1955), heritability in broad sense (Burton and Devane, 1953), correlation coefficients (Al Jibouri *et al.,* 1958) and path coefficients (Dewey and Lu, 1959) calculated accordingly. Cluster analysis and PCA were performed using ClustVis web tool (Metsalu and Vilo, 2015).

Results and Discussion

For all traits, except TGW, the analysis of variance revealed substantial variations among genotypes, demonstrating significant variability in the experimental materials (Table 1). The mean, range, genotypic and phenotypic coefficient of variation (GCV and PCV), broad sense heritability (h^2), genetic advance and genetic gain for various characters were also estimated as presented in Table-2. A wide range was observed for all the traits studied, indicating wider variability for these traits. It was observed that the genotypes performed beyond the range of checks for all the traits. It provides more opportunity to select best performing genotypes in desirable direction. A similar trend was also observed for mean values where genotypic mean was better as compared to checks for all the traits in the desired direction.

Trait specific variability was estimated in the form of phenotypic (PCV) and genotypic (GCV) coefficients of variation. PCV scores were generally greater than GCV values because of the effect of the environment on the expression of trait. The highest GCV value was observed for TPMR (28.08 %) followed by GYPP (25.79 %), SL (17.75 %), GPS (17.19 %) and TGW (12.15 %). Among these traits, TPMR and GYPP showed high GCV whereas moderate GCV values were observed for PH, GPS, TGW and SL. Similarly, high PCV was observed for TPMR, GYPP and SL whereas moderate PCV was observed for PH, GPS and TGW. A low GCV as well as PCV value was observed for DH and DM which indicated less variability among genotypes for these traits. The PCV and GCV estimations indicated the presence of

Table 1: ANOVA using ABD (Augmented Block Design) for various traits in wheat

Trait	Block	Treatment	Check	Genotype	C v/s G	Error
	[4]	[83]	[3]	[79]	[1]	[12]
Days to Heading	2.25	21.38**	4.85	21.97**	24.01**	1.52
Days to Maturity	7.05*	15.15**	9.92**	15.42**	9.61*	1.42
Spike length	5.32	5.44*	1.65	5.43*	17.64*	2.03
Grains spike^{-1}	9.92	152.75**	335.52**	147.48**	20.70	31.39
Plant Height	83.82**	149.39**	118.73**	134.79**	1395.02**	11.03
Tillers/ meter row	87.45	977.77**	273.13	1009.39**	592.92	153.72
TGW	11.37	55.65*	162.34**	52.30	0.41	22.17
Grain yield plot^{-1}	16166.88**	17203.73**	6994.58*	17798.73**	826.56	1997.71

Figure in parenthesis is degree of freedom; *, ** represent significant at P=0.05 and P=0.01, respectively

Table 2: Variability parameters for several traits in wheat

Trait	Range		Mean		GCV (%)	PCV (%)	h^2 (%)	GA (%)	GG (%)
	Genotypes	Checks	Genotypes	Checks					
Days to Heading	69.00-91.00	84.80-87.00	85.03	86.25	5.32	5.51	93.10	8.99	10.57
Days to Maturity	116.00-132.00	125.20-128.60	126.28	127.05	2.96	3.11	90.81	7.35	5.82
Spike length (cm)	6.00-18.00	8.60-9.80	10.40	9.35	17.75	22.41	62.73	3.01	28.96
Grains spike^{-1}	35.00-99.00	50.20-68.80	62.69	61.55	17.19	19.37	78.72	19.69	31.41
Plant Height (cm)	68.00-132.00	84.00-94.80	97.24	87.90	11.44	11.94	91.82	21.96	22.58
Tillers/ meter row	35.00-200.00	87.40-104.40	104.19	98.10	28.08	30.49	84.77	55.48	53.25
TGW (g)	34.40-70.20	38.92-50.70	45.19	45.03	12.15	16.00	57.61	8.58	18.99
Grain yield plot^{-1} (g)	260.00-795.00	431.00-522.00	487.44	480.25	25.79	27.37	88.78	243.98	50.05

GCV=Genotypic Coefficient of Variation; PCV=Phenotypic Coefficient of Variation; h^2=heritability in broad sense; GA=Genetic Advance; GG=Genetic Gain

Table 3: Genotypic (rg) and Phenotypic (rp) correlation coefficients between various characters in wheat

Character		Days to Heading	Days to Maturity	Plant Height	Tillers/ meter row	Grains spike^{-1}	TGW	Spike length	Grain yield plot^{-1}
Days to Heading	rg	1.00	0.90**	-0.14	-0.23*	0.24*	-0.02	0.09	0.11
	rp	1.00	0.86**	-0.15	-0.18	0.18	-0.08	-0.01	0.10
Days to Maturity	rg		1.00	-0.08	-0.26*	0.24*	-0.02	0.10	0.08
	rp		1.00	-0.10	-0.20	0.15	-0.07	-0.00	0.01
Plant Height	rg			1.00	0.22*	0.12	-0.12	0.13	0.22*
	rp			1.00	0.14	0.11	-0.03	0.07	0.24*
Tillers/ meter row	rg				1.00	-0.01	-0.20	0.04	0.32**
	rp				1.00	-0.05	-0.17	0.03	0.24*
Grains spike^{-1}	rg					1.00	-0.28*	0.33**	-0.12
	rp					1.00	-0.30**	0.29**	-0.03
TGW	rg						1.00	-0.58**	0.05
	rp						1.00	-0.17	0.11
Spike length	rg							1.00	-0.21
	rp							1.00	-0.14
Grain yield plot^{-1}	rg								1.00
	rp								1.00

*, ** represent significant at P=0.05 and P=0.01, respectively

Table 4: Path coefficient analysis indicating direct and indirect effects of different component characters on grain yield in wheat

Character	Days to Heading	Days to Maturity	Plant Height	Tillers/ meter row	Grains spike^{-1}	TGW	Spike length	Genotypic correlation coefficient with grain yield
Days to Heading	0.29	-0.02	-0.03	-0.08	-0.03	0.00	-0.02	0.11
Days to Maturity	0.26	-0.02	-0.02	-0.09	-0.03	0.00	-0.03	0.08
Plant Height	-0.04	0.00	0.23	0.07	-0.02	0.00	-0.03	0.22*
Tillers /meter row	-0.07	0.01	0.05	0.34	0.00	0.01	-0.01	0.32**
Grains spike^{-1}	0.07	-0.01	0.03	-0.00	-0.13	0.01	-0.08	-0.12
TGW	-0.01	0.00	-0.03	-0.07	0.04	-0.03	0.15	0.05
Spike length	0.03	-0.00	0.03	0.01	-0.04	0.02	-0.25	-0.21

Residual effect= 0.8614

significant level of variation. Dhakar *et al.* (2012) also reported highest GCV and PCV for grain yield per plant, number of effective tillers, length of spikes and number of seeds per spike. Similarly, Tambe *et al.* (2013) observed high GCV and PCV for grain yield per plant, number of effective tillers per plant, spike length and 1000-grain weight while studying genetic variability in 28 diverse genotypes of durum wheat. Further, Joshi *et al.* (2018) reported highest coefficient of variability for grain yield during study of 184 wheat germplasm accessions. Dashora *et al.* (2020) also noticed highest value of GCV and PCV among 59 durum wheat accessions for grain yield per plot, tillers per meter row length, spike length, grains per spike and test grain weight.

The existence of high GCV and PCV values in the present study suggests that selection for these traits may be beneficial in wheat improvement. The heritability in broad sense was estimated for all the traits and the percentage of heritability was described as low, medium and high according to Robinson *et al.* (1949). Heritability ranged from 57.6 % for TGW to 93.1 % for DH. High heritability was observed for DH (93.1 %), PH (91.8 %), DM (90.8 %), GYPP (88.8 %) and TPMR (84.8 %). Similarly, high genetic advance as per cent of mean (genetic gain) was observed for TPMR (53.25 %), GYPP (50.05 %), GPS (31.41 %), SL (28.96 %), PH (22.58 %) whereas moderated values were observed for TGW (18.99 %) and DH (10.57 %). The combined perusal of high heritability and genetic gain indicated preponderance of additive gene effects for GYPP, TPMR, GPS and PH which also showed moderate to high GCV and therefore, selection of these traits may be advocated in wheat improvement programmes.

Based on *per se* performance, promising genotypes showing better performance than trait wise best checks were identified for all the traits studied. The promising genotypes HIKK 09, HW 3631, DHTW 60, TL 3006 (T) for early days to heading; HIKK 09, HIKK 05, HW 3631, DHTW 60, TL 3006 (T), HIKK 06 for early maturity; MP 3336, KBRL 79-2, HI 8759 (d), FLW 16, DBW 93 for dwarf stature; HIKK 09, WH 1127, WH 1063 for more tiller numbers, WH 1080, HD 3043, AKAW 4927, HD 3171, DBW 88,

Table 5: Percentage of variance, cumulative variance and coefficients of indices in the first and second main components

PC	% of variance for each PC	Cum.% of variance for each PC	Days to heading	Days to maturity	Plant height	Tillers per meter row	Grains per spike	TGW	Spike length	Grain yield per plot
1	0.98	0.98	-2.46	0.29	-1.72	-1.36	-3.93	-5.11	-7.41	21.70
2	0.01	0.99	-0.13	0.29	0.07	1.82	-0.41	-0.54	-0.74	-0.35
3	0.01	1.00	-0.46	-1.29	-0.50	0.72	-0.12	0.31	0.98	0.36
4	0.00	1.00	-0.19	-0.25	0.28	0.01	0.62	-0.38	-0.08	0.00
5	0.00	1.00	-0.18	-0.14	0.61	-0.06	-0.33	0.09	0.01	-0.01
6	0.00	1.00	0.16	0.01	0.03	-0.02	-0.10	-0.27	0.19	0.00
7	0.00	1.00	0.11	-0.08	0.01	0.00	0.00	0.02	-0.06	0.00
8	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

WH 1127, HS 627, HTW 11 for more grain number/spike, MACS 5044 (dic.), DDK 1051 (dic.), DWAP 1531, PDW 344 (d) for 1000-grains weight, GRU-2010-18/7, BRW 3723 for longer spikes and GRU-2010-18/7, AKAW 3717, WH 1105, HI 8737(d), HI 8751 (d) for grain yield per plot. These genotypes may be used as trait specific donors. In addition, eleven bread wheat genotypes namely, FLW 22, DBW 187, DBW 107, DBW 150, HI 1620, NIAW 1994, PBW 757, WH 1310, HIKK09, KBRL 79-2, KBRL 82-2 were identified as promising genotypes for multiple yield component traits which can be extensively utilized in wheat improvement programmes for yield enhancement and disease resistance.

As yield is the result of several inter-connected traits, selection should be based on these component traits after determining their association with yield. Correlation coefficient at phenotypic and genotypic levels were estimated using eight characters in eighty-four genotypes of wheat to study the degree of mutual relationship between yields and its component traits (Table 3). The results demonstrated that the values of GCV were greater than the PCV values, implying a strong intrinsic link between the traits tested. Results indicated significantly positive association of GYPP with PH and TPMR both at genotypic and phenotypic level. Similar trend of significantly positive trait association at both the levels was also observed between SL with GPS and DH with DM whereas significant but negative correlation was observed between TGW and GPS. For other trait combinations, non-significant phenotypic associations were estimated. However, GPS showed significantly positive genotypic correlation with DH and DM similarly,TPMR showed significant genotypic correlation with PH in positive direction but significantly negative correlation with DH and DM. Significant but negative genotypic correlation was also observed between SL and TGW. Therefore, traits with strong positive correlations with yield should be explored, while selecting traits for wheat yield improvement. The other significantly positive associations may be exploited in trait improvement. In earlier study by Abdul *et al.* (2014) with 20 wheat accessions indicated positive and significant association of grain yield per plant with productive tillers per plant, spike length, spikelets per spike, grains per spike, seed index, total biomass and harvest index while in the study of Dashora *et al.* (2020), grain yield was positively and significantly correlated with plant height, grains per spike and spike length which are corroborated with our findings especially for PH and TPMR. A thorough selection for these traits (PH and TPMR) will automatically improve seed yield in wheat because the yield contributing traits are associated among themselves, selection in one of the traits will wholly result in the improvement of the other traits. As the association study is insufficient to explain meaningful association for an effective modulation of the traits, path coefficients were estimated to split yield and trait relationship into direct and indirect effects (Table 4). Direct effects provide ample scope of yield improvement by selecting respective trait whereas indirect effects provide opportunity for yield improvement through other associated traits.

The results revealed that significantly positive genotypic correlation of GYPP with TPMR and PH is due to their direct effects on yield. The highest direct effect on GYPP was showed by TPMR (0.34). Although non-significant genotypic correlation of DH was observed with GYPP, which showed high direct effect (0.29). High direct effects of TPMR and PH have suggested selection of these traits for yield maximization in wheat. These findings are in agreement with the study of Nukasani *et al.* (2013) where they also noticed that tiller number per metre had maximum positive direct effect on grain yield.The residual effect value (0.8614) suggests that there may be some more components that should not be overlooked during the selection process. Crossing the genotypes is a basic breeding method to create variation for further selection. For making a cross selection of parents is extremely important based on the existing genetic variation. Clustering and PCA analysis are important tool for grouping the genotypes that helps breeder to select suitable parents for crossing program. Cluster analysis was conducted to assess the quantum of genetic diversity within and between the distinct groups based on the index of similarity and dissimilarity as indicated by the genetic distance between them.

Distance coefficient between individuals was calculated using the Euclidean square distance method along with cluster analysis Ward method. Ward method is more efficient in grouping the genotypes which can be further cross-validated by using discriminate analysis. Based on the dendrogram and heat map (Fig. 1), all wheat genotypes were broadly classified into 2 distinct clusters based on an index of similarity and dissimilarity of attributing traits. Cluster-I has 65 genotypes which was further

Table 6: Details of genotypes along with parentage/sources

SN	Genotypes	Parentage	Sources	Year	Zone/State
A.	**Agronomic basis**				
G1	AKAW 4901	WRHT-5/WH 730//AKAW 4320-2-16	PDKV, Akola	2018	Test entry NGSN
G2	AKAW 4927	DL157-5/AKW619	PDKV, Akola	2018	
G3	BRW 3723	ACHYUT/BL1887	BAU, Sabour	2017	RF-TS-BH
G4	CG 1013	GW 322/KYZ 0285	IGKVV, Bilaspur	2018	IR-TS-CG
G5	DBW 39	ATTILA/HUI	IIWBR, Karnal	2014	IR-TS-NEPZ
G6	DBW 71	PRINIA/UP 2425	IIWBR, Karnal	2015	IR-LS-NWPZ
G7	DBW 88	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES	IIWBR, Karnal	2016	IR-TS NWPZ
G8	DBW 93	WHEAR/TUKURU/WHEAR	IIWBR, Karnal	2015	RI-TS-PZ
G9	DBW 107	TUKURU/INQLAB	IIWBR, Karnal	2015	IR-LS-NEPZ
G10	DBW 110	KIRITATI/4/2*SERI*2/3/KAUZ*2/BOW//KAUZ	IIWBR, Karnal	2015	RI-TS-CZ
G11	DBW 173	KAUZ/AA//KAUZ/PBW602	IIWBR, Karnal	2017	IR-LSNWPZ
G12	DBW 187	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KACHU/6/KACHU	IIWBR, Karnal	2019	IR-TS-NEPZ
G13	GJW 463	GW496/KLP010	JAU, Junagadh	2017	TS-IR-Guj
G14	HD 3043	PJN/BOW/OPATA*2/CROC_1/AeSq(224)//OPATA	IARI, Delhi	2015	TS-RI-NWPZ
G15	HD 3086	DBW14/HD2733//HUW468	IARI, Delhi	2014	IR-TS-NWPZ
G16	HD 3171	PBW 343/HD2879	IARI, Delhi	2017	RF-TS-NEPZ
G17	HI 1609	W15.92/4/Pastor/HXL7573/2*BAU/3/WBLL1	IARI-RS, Indore	2014	Test entry NIVT 2
G18	HI 1612	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES	IARI-RS, Indore	2018	RI-TS-NEPZ
G19	HI 1620	(NAC/TH.AC//3*PVN/3/MIR LO/BUC/4/2*PASTOR/5/KA CHU/6/KACHU)	IARI-RS, Indore	2019	RI-TS-NWPZ
G20	HUW 669	ALTR84/HUW206/MILAN	BHU, Varanasi	2018	TS-RF-UP
G21	HW 5207	HW3029//V763 - 2312(Yr15)	IARI-RS, Wellington	2017	TS-RI-TN
G22	K 1006	PBW343/HP1731	CSAUAT, Kanpur	2014	IR-TS-NEPZ
G23	K 1317	K0307/K9162	CSAUAT, Kanpur	2018	TS-RI-NEPZ
G24	KRL 283	CPAN3004/ KHARCHIA65//PBW343	CSSRI, Karnal	2018	Salinity- UP
G25	MP 3336	HD2402/GW 173	JNKVV, Jabalpur	2016	IR-LS-CZ
G26	MP 3382	CHOIX/STAR/3/HE1/3*CNO79//2*SERI/4/GW273	JNKVV, Jabalpur	2016	IR-TS-MP
G27	NIAW 1994	NIAW 34/PBW 435	MPKV, Niphad	2016	IR-TS-MH
G28	PBW 752	(PBW621/4/PBW343//YR10 /6*AVOCET/3/3*PBW 343/5 /PBW621)	PAU, Ludhiana	2018	IR-LS-NWPZ
G29	PBW 757	(PBW550/YR15/ 6*AVOCET/3/2*PBW550/4/PBW 568+YR36/3*PBW550)	PAU, Ludhiana	2018	IR-VLS-NWPZ
G30	UAS 334	SITE/MO/4/NAC/TH. AC//3*PVN/3/MIRL O/BUC	UAS, Dharwad	2018	IR-TS- Karnataka
G31	UAS 375	UAS 320/GW 322// Lok 62	UAS, Dharwad	2018	TS-RI-PZ
G32	WH 1105	MILAN/S87230//BABAX	CCSHAU, Hisar	2014	IR-TS-NWPZ
G33	HI 8708 (d)	HG 822/HI 8498	IARI-RS, Indore	2014	INGR 14042
G34	HI 8737(d)	HI 8177/HI 8158//HI 8498	IARI-RS, Indore	2014	IR-TS-CZ
G35	HI 8777 (d)	B93/HD 4672//HI 8627	IARI-RS, Indore	2018	PZ- RF-TS
G36	MACS 3949 (d)	STOT//ALTAR84/AL D/3/THB/CEP7780// 2*MUSK_4	ARI, Pune	2017	IR-TS-PZ
B. Disease resistant lines					
G37	HS 626	CHEN/Ae.Sq(TAUS)/BCN/3/BAV92/4/BERKUT	IARI-RS, Shimla	-	Resistant to all 3 types of rusts
G38	HS 627	69-1776/663//2*BCN/4/PARUS/PASTOR	IARI-RS, Shimla	-	
G39	PBW 725	PBW621//GLUPR O/3*PBW 568/3/ PBW 621	PAU, Ludhiana	2016	
G40	PBW 756	PBW55O/6/HPO/TAN//VEE/3/2*PGO/4/MILAN/5/SSERII	PAU, Ludhiana	-	
G41	PBW 760	YR15+YR24/6*AVOCET//2*BAXTER/3/3*PBW 343+Lr24+LR28/4/PBW343*6/KBRL22	PAU, Ludhiana	-	
G42	WH 1216	WAXWING*2/VIVITSI	CCSHAU, Hisar	-	
G43	WH 1310	WHEAR/SOKOLL	CCSHAU, Hisar	-	
G44	HI 8759 (d)	HI8663/HI8498	IARI-RS, Indore	2017	
G45	TL 3006 (T)	T2969/T2987	PAU, Ludhiana	-	
G46	TL 3007 (T)	T2938/T2969	PAU, Ludhiana	-	

Table continued

SN	Genotypes	Parentage	Sources	Year	Zone/State
G47	DBW 220	PBN142/DBW30	IIWBR, Karnal	-	Resistant to stripe
G48	PDW 344 (d)	GREEN/RXD-130	PAU, Ludhiana	-	& leaf rusts
G49	UAS 459 (d)	UAS415/HI8663//NDW295	UAS, Dharwad	-	
G50	PBW 719	UP2556/PBW543	PAU, Ludhiana	-	Resistant to
G51	DDK 1051 (dic.)	DDK1025/HW1095//DDK1038	UAS, Dharwad	-	stem& leaf rusts
G52	MACS5044(dic.)	MACS2956/DDK1029	ARI, Pune	-	
C. Genetic stocks					
G53	DBW 129	PFAU/Milan/5/CHEN/Ae.Sq (TAUS)//BCN/3/VEE#7/BOW/4/Pastor	IIWBR, Karnal		Disease resistance
G54	FLW 10	WH542/Moro	IIWBR-RS, Shimla	2017	
G55	FLW 16	UP2338/T. spelta album	IIWBR-RS, Shimla	2017	
G56	FLW 22	WH542/CS2DMLr28//WH542/China-84-40022	IIWBR-RS, Shimla	2017	
G57	HI 8751	HD4685/HI8634	IARI-RS, Indore	2017	
G58	HI 8765	HI8504/CPAN6206//HI8627	IARI-RS, Indore	2017	
G59	HIKK 05	NP4*6/RL6010	IARI-RS, Indore	2016	
G60	HIKK 06	NP4*6/RL6004	IARI-RS, Indore	2016	
G61	HIKK 09	NP4*6/RL6092	IARI-RS, Indore	2016	
G62	HW 3631	WH147*3/Cook*6//C80-1	IARI-RS, Wellington	2013	
G63	KBRL 79-2	CMH77.308/6* WH542	PAU, Ludhiana	2015	
G64	KBRL 82-2	HP1531/6*WH542	PAU, Ludhiana	2015	
G65	PBW 703	PBW343+Lr24+LR28/AVOCET + Yr10//AVOCET+Yr15	PAU, Ludhiana	2015	
G66	DBW 246	KACHU//SAUAL/8/ATTILA*2/PBW65/6/PVN //CAR422ANA/5/BOW/CROW//BUC/PVN/3/ YR/4/TRAP#1/7/ATTILA/2*PASTOR	IIWBR, Karnal	2018	
G67	AKAW 3717	HW2035/NI5439	PDKV, Akola	2010	Heat tolerance
G68	DBW 150	DBW16/GW322	IIWBR, Karnal	2017	
G69	DHTW 60	IC36761A	IIWBR, Karnal	2015	
G70	HTW 6	IC29007A	IIWBR, Karnal	2011	
G71	HTW 9	Raj 3765/P11632	IIWBR, Karnal	2011	
G72	HTW 11	IC35117	IIWBR, Karnal	2011	
G73	WH730	CPAN2O92/IMPROVED LOK1)	CCSHAU, Hisar	2006	
G74	WH 1063	Selection from BARBET1	CCSHAU, Hisar	2010	Quality traits
G75	WH 1080	PRL/2*PASTOR	CCSHAU, Hisar	2010	
G76	WH 1127	RL6043/4/NAC/PASTOR/3/BABAX	CCSHAU, Hisar	2015	
D. Elite lines					
G77	DWAP 1530	Yield component line	IIWBR, Karnal	-	Yield traits
G78	DWAP 1531	Yield component line	IIWBR, Karnal	-	
G79	GRU-2010-18/7	Yield component line	IIWBR, Karnal	-	
G80	UASD DT-6	Yield component line	UAS, Dharwad	-	
E. Checks					
G81	Sonalika (C1)	II54.338/AN/3/Y/T54/N 10B/LR 64	IARI, N Delhi	1969	NWPZ
G82	HD 2967 (C2)	ALD/COC//URES/HD2160M/HD2278	IARI, N Delhi	2011	NWPZ
G83	HI 8713 (d)(C3)	HD 4672/PDW 233	IARI-RS, Indore	2012	CZ
G84	RAJ 4079 (C4)	UP 2363/WH 595	SKRAU, Durgapura	2011	Rajasthan

divided into two sub-clusters, *viz.,* sub-cluster IA and sub-cluster IB. There were 41 genotypes accommodated in sub-cluster IA which makes it largest sub-cluster whereas sub-cluster IB contained 24 genotypes. On the other hand, Cluster-II had significant distance with cluster-I and accommodated only 19 genotypes. Based on cluster analysis, genotype KRL 283 (G 24) from cluster IA and DBW 107 (G 9) from cluster II were identified as genetically most diverse bread wheat genotypes whereas HI 8708 (G 33) from cluster IA and HI 8765 (G 58) from cluster II were the most distantly related durum wheat genotypes. These genotypes exhibited highly desirable and significant genetic diversity with respect to diverse morphological and yield attributing traits. Similar findings on clustering pattern in wheat genotypes were also reported by Amin *et al.* (2014) where they grouped 50 wheat lines into 4 different clusters using Mahalanobis's D^2 and PCA for fourteen traits. Dotlacil *et al.* (2000)

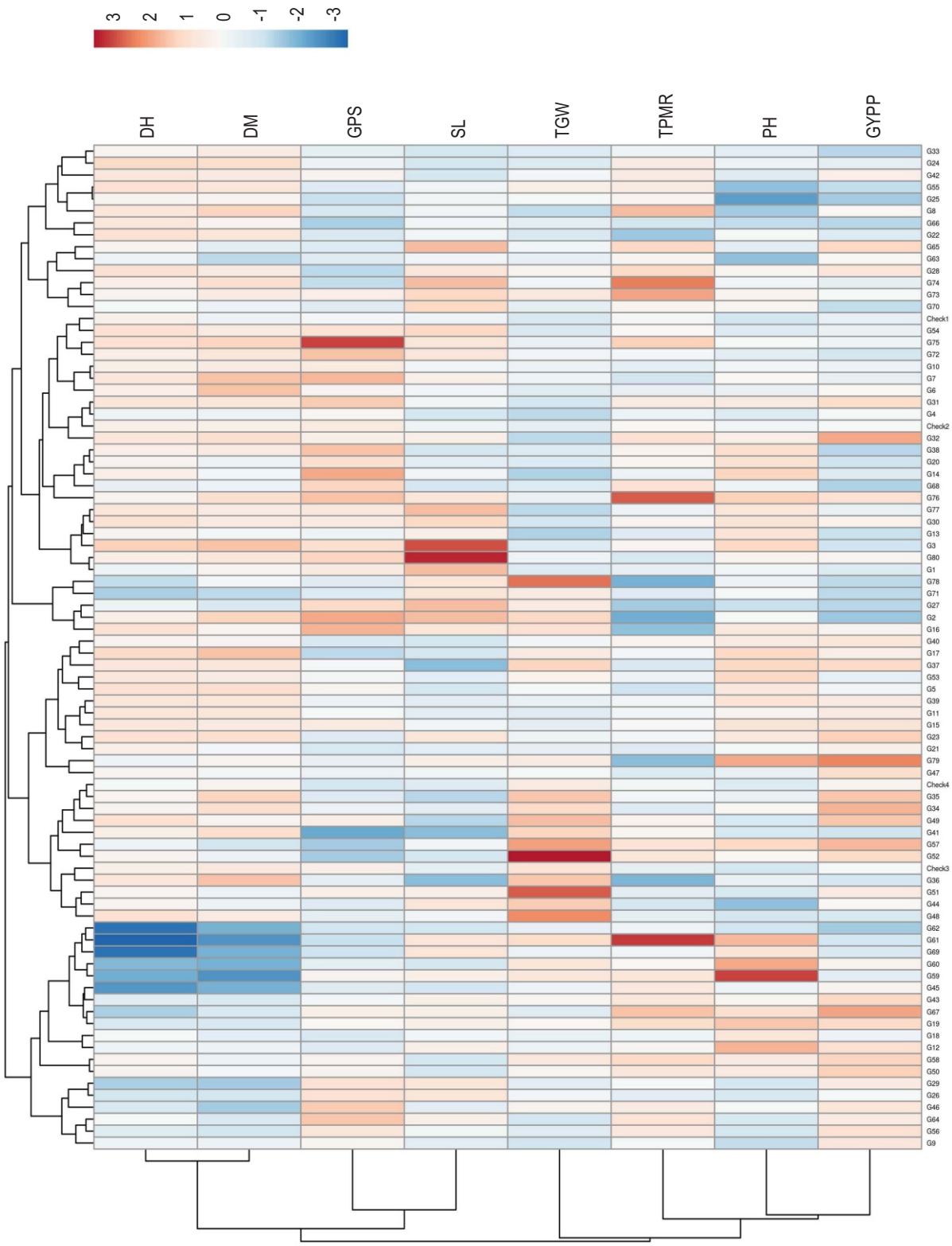

Fig. 1: Clustering pattern of 84 wheat genotypes under study (DH – Days to heading, DM – Days to maturity, GPS – Grains per spike, SL – Spike length, TGW – Test grain weight, TPMR – Tillers per meter row, PH – Plant height and GYPP – Grain yield per plot).

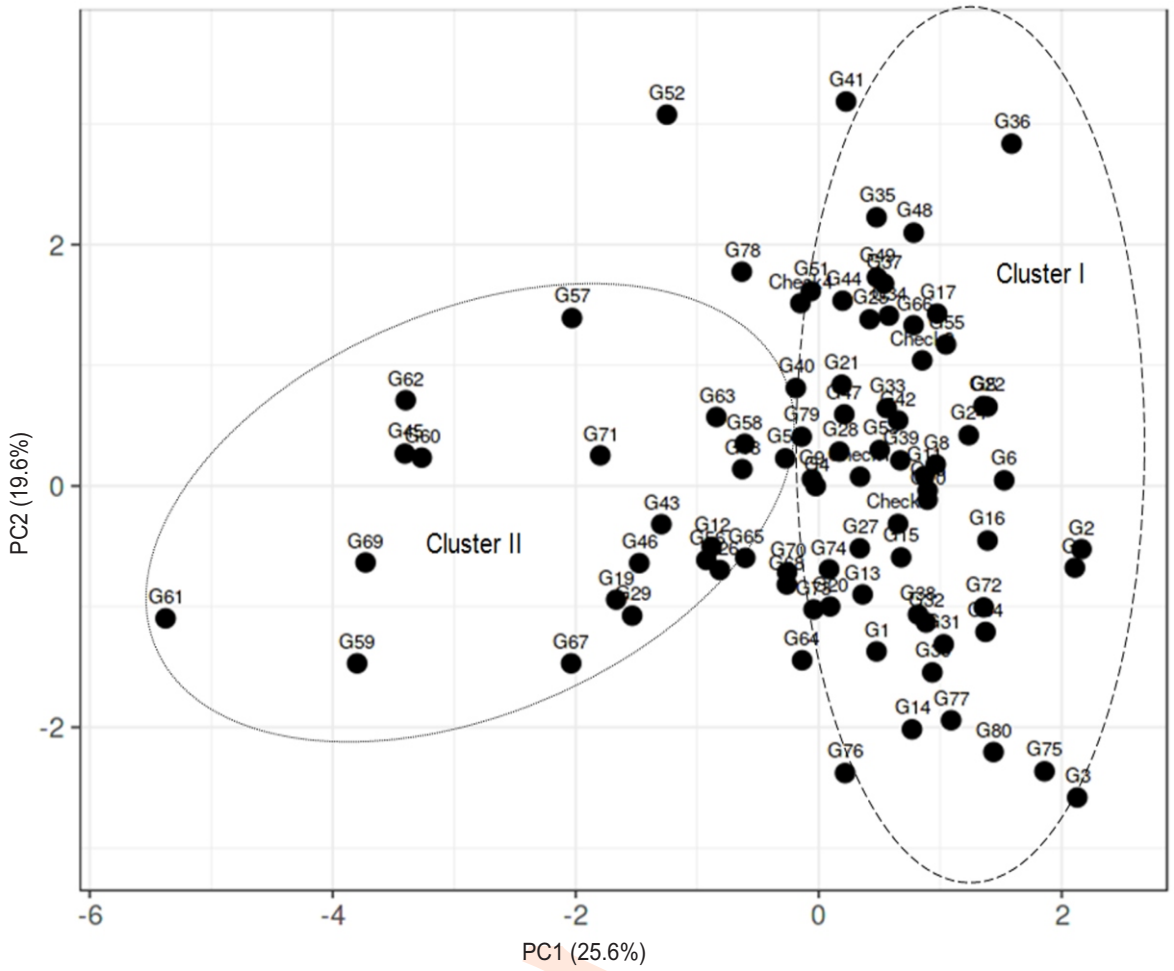

Fig. 2: PCA for the quantitative traits (yield attributing traits).

have also reported meaningful cluster analysis for 380 accessions of wheat landraces including durum wheat, cultivated emmer and cultivated einkorn. Hailegiorgis *et al.* (2011) used cluster analysis method to group 49 genotypes of bread wheat into 22 different clusters and further from cluster mean values they selected parents from diverse clusters to directly use as parents in hybridization program to develop high yielding wheat varieties.

Multivariate analysis has been used as an important mean to study genetic diversity in wheat germplasms by earlier workers. Aharizad *et al.,* 2012 reported cluster analysis based on all the traits under study using Ward's algorithm and squared Euclidean distances that assigned 94 bread wheat recombinant inbred lines into three groups. The first group lines were superior with respect to grain yield. Similarly, Ajmal *et al.* (2013) used multivariate techniques to study 50 wheat genotypes for 07 quantitative traits and sequestrated all genotypes into 5 clusters based on Ward's method. In our study also we have reported three different clusters for 84 wheat genotypes based on Ward's algorithm and squared Euclidean distances. It is interesting to mention that both the triticale genotypes TL 3006 and TL 3007 were placed in cluster II whereas both the dicoccum genotypes DDK 1051 and MACS5044 were placed in sub-cluster IB. All the durum genotypes, except HI 8708 (G33) were accommodated in sub-cluster IB. Bread wheat genotypes were distributed in all the clusters and sub-clusters. This clustering pattern may be further utilized in selection of distinct parents in hybridization programme for accumulation of more diverse gene combinations for wheat improvement and production of transgressive segregants in minimum period of time. Similarly, Wani *et al.* (2018) estimated the extent of genetic diversity in 24 bread wheat genotypes and clustered all genotypes into 4 distict group based on an index of similarity and dissimilarity of attributing traits. Group I and II have one genotype each whereas third group had 6 genotypes. The fourth group had two sub-groups. The first sub-group had five genotypes and the second sub-group had eight genotypes. In this study also, we observed 2 major clusters *viz.,* cluster I (65 genotypes) and cluster II (19 genotypes) where cluster I had 2 sub-clusters (IA and IB) and suggested that diverse parents can be identified with a scope in generating transgressive segregants

for prospective breeding strategies in the improvement of wheat crop using multivariate methods. In the present study, Fig.1 also showed clustering of traits based on their similarity. It is worth mentioning that the GYPP showed closeness with TPMR and PH which is also supported by their significantly positive correlations. Similar trend was also observed between DH and DM and other yield component traits with each other.

The principal component analysis, by summarizing the first-order correlated variables in the form of independent and finite components, enables the grouping of individuals in a two-dimensional or three-dimensional space (Falconer, 1960). In the present investigation, principal component 1 and principal component 2 explained 25.6 % and 19.6 % of the total variance, respectively. In the two-dimensional diagram, which is based on the data derived from the principal component analysis, the effect of traits on the grouping of genotypes as different vectors and the location of each genotype is also shown based on the selected component type. Fig. 2 represents the PCA analysis of standardized log transformed and significantly correlated (at 0.001 level) quantitative phenotypic traits for 84 wheat genotypes that indicated two main clusters namely cluster I containing 65 genotypes and cluster II containing 19 genotypes. It was also observed that GYPP has major contribution in PC 1 whereas TPMR contributed most for PC 2 component. This pattern of principal component analysis is in accordance to the clustering pattern of wheat genotypes and it may be useful for identifying diverse genotypes which can be further utilized for future breeding programmes. Categorization of wheat genotypes into different clusters was also reported by Ahmad *et al.* (2014) where they grouped nineteen genotyopes into three clusters on the basis of average linkage and PCA analysis and observed maximum Total variance percentage in PC-I (39.17) followed by PC-II and PC-III which was same (21.89). In this study also 25.6 % and 19.6 % of the total variance in PC I and PC II, respectively.

It may be concluded that there exist a wide range of variability among bread wheat and durum wheat genotypes which can be exploited in bread as well as durum wheat improvement. The character associations of TPMR and PH with GYPP and their high direct effects on yield have ample scope for combined utilization of these characters for wheat improvement. The developmental programme is further augmented and aided by identifying desirable parents possessing significant genetic diversity for yield and yield attributing traits. The clustering and PCA analysis categorized genotypes into three distinct groups and explained total phenotypic variation and distantly related promising genotypes for use as donor parents for future wheat improvement programmes.

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Add-on Information

Authors' contribution: A. Dashora: Execution, data analysis and manuscript preparation; **R. Mehta:** Collection of literature related to present study; **D. Singh:** Cluster and PCA analysis and its interpretation; **Urmila:** Field preparation for conducting experiment and collection of morphological data; **S.K. Singh:** Categorized and supplied the study material and editing the manuscript.

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