Exploitation of genetic variability and trait association analysis for diverse quantitative traits in bread wheat (*Triticum aestivum* L.)

ABSTRACT

The present investigation was conducted using 102 wheat genotypes at Research Farm, College of Agriculture, Gwalior during *Rabi* 2018-2019 in randomized block design with two replications. A set of 102 wheat genotype were used to estimate genetic variability, correlation coefficients and path coefficients for fourteen yield and its accrediting attributes. A wide range of variation was observed for important yield components. GCV and PCV was recorded highest for biological yield/plant. High heritability accompanied with higher genetic advance for numbers of productive tillers/plants, spike length, weight of spike, numbers of grains/spike, weight of grains/spike, biological yield/plant, grain yield/plant, harvest index and test weight. Genotypic correlation coefficients were found to be higher in magnitude than that of phenotypic correlation coefficients for most of the traits under investigation, which clearly indicated the presence of inherent association among various characters. The genotypic correlation analysis in the present study observed significant positive association for grain yield with five yield contributing characters *viz*., numbers of productive tillers/plant, biological yield/plant, weight of grains/spike, weight of spike and numbers of grain/spike.Thus, selection for these characters would be directly follow the immediate improvement of the grain yield for wheat crop. Analysis of phenotypic path coefficient for various traits on grain yield disclosed highest positive direct effect on grain yield for numbers of productive tillers/plant tracked by biological yield/plant, weight of grains/spike, test weight, harvest index, numbers of grains/spike and numbers of spikelets/spike. Whilst, highest positive indirect effect on grain yield was documented for biological yield per plant *via* numbers of productive tillers/plants. Henceforward, these traits must be given weightage in selection for the improvement of wheat in future breeding programmes.

Keywords: Wheat, GCV (Genotypic coefficient of variance), PCV (Phenotypic coefficient of variance), Heritability, Correlation, Path coefficient analysis

INTRODUCTION

Wheat (*Triticum aestivum* L., 2n=6x=42) is a monocot plant, belongs to the tribe *triticeae*, under the grass family *poaceae*. Wheat, a cereal grass of the Gramineae (Poaceae) family and of the genus (*Triticum aestivum.* Emm. L) with 17 species, out of which only three species *viz. Triticum aestivum* (bread wheat), *Triticum durum* (macroni/pasta wheat) and *Triticum dicalcium* (emmer wheat) are mainly cultivated throughout the world [1]. Wheat is a monoecious plant with perfect flowers, reproducing sexually as an autogamous crop although limited (3%) cross pollination is possible. Wheat grain has a high nutritional value with 70-75% starch, 14% water, 8-20% proteins, 2-3% non-starch polysaccharides, 2% lipids, 1.6% minerals, antioxidants *etc.* and is main staple food crop for a huge world population [2-3]. It has a higher protein level than either maize or rice.It is the dominant source of cereal and vegetable protein in human meals worldwide. After considering maize's greater use in animal feeds, it currently surpasses rice and maize as the principal crop used to provide food for humans in terms of total production tonnes [4].

Globally, wheat (*Triticum spp.*) is grown in about 220.83 million hectares holding the position of highest acreage among all crops with annual production hovering around 769.31 million tones[5].India is the world's second-largest producer of wheat, trailing China. While the state of M.P.'s estimated annual wheat is cultivated in 29.55 million hectares29.55 million hectares with 101.20 million tonnes production with a record average national productivity of 3424 kgha^{-1}for the year 2019–20 [6]. The estimated annual wheat production in India is estimated at 108.75 million tonnes with a national productivity of 3424 kgha^{-1}[7].

Grain yield is a complex trait and highly influenced by many genetic factors and environmental fluctuations. In plant breeding programme, direct selection for yield as such could be misleading [8-10]. A successful selection depends upon the information on the genetic variability and association of morpho-agronomic traits with grain yield [11-16]. Analyzing the genotypic, phenotypic, and yield components of several crop genotypes, a breeder may be able to ascertain the amount to which the environment affects yield [17-23]. Breeders can pick desired features and obtain the greatest genetic increase with the least amount of time and resources by using an accurate allocation of resources based on heritability estimates [24]. At present different molecular markers most widely used to detect variability present among genotypes in most of the crops including wheat [25-33].

Correlation studies along with path analysis provide a better understanding of the association of different characters with grain yield. The correlation coefficient measures the mutual relationship between various plant characters and determine the component character on which selection can be based for improvement of yield [34-35]. Path coefficient analysis separates the direct effects from the indirect effects through other related characters by partitioning the correlation coefficient [36].The information obtained by path coefficient analysis helps in indirect selection for genetic improvement of yield because direct selection is not effective for low heritable trait like yield. Thus, the estimation of heritability and genetic advance is essential for a breeder which helps in understanding the magnitude, nature and interaction of genotype (s) and environmental variation of the traits. Hence, in this investigation, exotic as well as local genotypes were used and an attempt was made to generate information on inheritance, relationships of yield and its components and their implication in selection of better genotypes of wheat for the development or improvement of cultivars and germplasm as well.

MATERIALS AND METHODS

The experimental material constituted 102 wheat genotypes (single plant selections and advanced breeding lines) acquiredfromAICRP on Wheat, Department of Genetics&Plant Breeding, College of Agriculture, Rajmata Agricultural University, Gwalior, Madhya Pradesh, India (Table 1). These genotypes were sown in Randomized Complete Block Design with two replications. The sowing was done by dibbling seeds in rows with spacing of 20 cm apart and 4-6 cm within a row on November 21st in timely sown environment in the year 2018-19. The recommended packages of practices were adopted for optimum crop growth.Five competitive plants per genotype in each replication were selected randomly and observations were recorded on fourteen different characters as per the DUS guideline and their average values were employed for statistical analysis.

Statistical Analysis

The mean values of each genotype were employed for statistical analysis. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was estimated as per the formula suggested by Burton [37].Heritability percent in broad sense was estimated by formula given by Singh and Chaudhary [38]. Genetic advance (GA) and genetic advance as per cent of mean (GAPM) were calculated by Johnson *et al*. [39]. Phenotypic and genotypic correlation coefficient between characters were computed utilized respective components of variance and co-variance, by following formula suggested by Miller et al. [40]. The proportion of direct and indirect contribution of various characteristics to the total correlation coefficients with grain yield per plant was estimated through path coefficient analysis as suggested by Wright [41,42] and elaborated by Dewey and Lu [43].

RESULTS AND DISCUSSION

Analysis of Variance

Analysis of variance revealed that all the 102 genotypes differed significantly for all the 14 character *viz.* days to heading, days to maturity, grain filling period, plant height, numbers of productive tillers/plants, spike length, weight of spike, numbers of spikelets/spike, numbers of grains/spike, weight of grains/spike, biological yield/plant, harvest index, test weight and grain yield/plant (Table 2).This outcome of the present investigation exhibited similarity with earlier research work conducted by Bozhidar *et al.*[44](2015), Tabassum *et al* . [45] (2017)and Khairnar et al.[46] (2018).

Estimation of Genetic parameters

The genetic characteristics for the characters under study, including mean, range, PCV and GCV, heritability estimates, and genetic advance as a percentage of mean are shown in Table 3 and Fig 1. In the present investigation, large differences in mean values for all the traits were observed. The trait day to heading ranged from 78.00 to 90.50, days to maturity between 130.50 to 140.50, grain filling periods from 44.50 to 58.50, plant height 80.97 to 139.75 cm, numbers of tillers/ plant ranged between 3.73 to 9.45, spike length from 7.39 to 13.97 cm, weight of spike from 1.92 to 5.93g, numbers of spikelets/spike from 17.40 to 27.20, numbers of grains/spike from 31.57 to 88.10, weight of grains/spike ranged from 1.33 to 4.73 g, biological yield/plant from 13.20 to 63.00 g, grain yield/plant from 3.73 to 17.86 g, harvest index from 23.68 to 53.20 and test weight ranged between 32.20 to and 53.30g. The experimental material had a wide range of variability and favorable mean performance for most of the traits studied.

Estimates of genotypic and phenotypic variance

Variability plays an important role in crop breeding. The development of an effective plant breeding programme depends on genetic variability. The total variation present in a population arises due to genotypic and environmental effect presence of genetic variability in the breeding materials is essential for a successful plant breeding programme [9-13]. The efficiency of selection largely depends on the magnitude of genetic variability present in plant population.Variability was measured by estimation of mean value, coefficient of variation (genotypic and phenotypic), heritability, genetic advance, and genetic gain [14-16].

Estimation of PCV (σ^2p) and GCV (σ^2g) were obtained for different characters (Table 3, Fig. 1). A wide range of variance was documented for all the characters.The estimates of PCV were higher than their respective GCV for all the traits. A proximity between GCV and PCV values for almost all the characters revealed less influence of the environment on expression of the characters [47]. Phenotypic variance was higher than genotypic variance for most of the yield and yield contributing characters indicating that these characters are influenced to a greater extent by the environment and hence large magnitude of variations for these characters are because of environment only. PCV and GCV was recorded highest for biological yield/plant (g)followed by grain yield per plant (g).High value indicates that heritability may be due to higher contribution of genotypic components. Tesfaye *et al.* [48], Chethana *et al.* [49], Khairnar *et al.* [46] and Pachauri *et al.* [50] also reported similar results for high heritability estimates.Whilst moderate PCV and GCV were recorded for the traits plant height (cm), numbers of productive tillers/plant, spike length (cm), weight of grains/spike (g), numbers of spikelets/spike, numbers of grains/spike, weight of grains/spike (g), harvest index and test weight (g). Present findings are in confirmation with results of Meles*et al.* [51],Balkan[52], Dabi *et al.* [53] and Nimbal and Naik *et al.* [54]. Whereas low PCV and GCV was found for grain filling period and test weight. Dabi *et al.* [53], Taneva *et al.* [55] and Regmi *et al.* [56]have also been reported earlier similar finding. This indicates the environmental factors had more influence on the expression of these characters than the genetic factors, suggesting the limited scope for improvement of these traits through direct selection for better-performing genotypes.

Heritability (in broad sense) and genetic advance as percent of mean

The estimates of heritability measure the degree of inheritance of any particular trait. Although high heritability suggests high component of heritable portion of variation that can be exploited by breeders in the selection of superior genotypes [57]. Heritability predicts the transmission of characters from parents to offspring while genetic advance clarifies the involvement of the type of gene action in the expression of any trait. High heritability coupled with higher genetic advance is an indication of the involvement of additive gene action in the transmission as well in the expression of any trait and the selection may be effective in such a case.

The estimates of broad sense heritability varied from 39.17 to 99.13 % (Table 3). In the present study high heritability accompanied with higher genetic advance was documented for numbers of productive tillers/plants, spike length, weight of spike, numbers of grains/spikes, weight of grains/spike, biological yield/plant, grain yield/plant, harvest index and test weight. However, high heritability coupled with moderate genetic advance was recorded for grain filling period, plant height and numbers of spikelets/spike indicating the lesser influenced by environment and are governed by both additive as well non-additive gene action. While days to heading and days to maturity showed low genetic advance. These findings are in confirmation with the outcome of the research workconducted by Lone *et al.*[58], Adhikari *et al.*[59], Gite *et al.* [60], Hossain *et al.*[61] Ibrahim *et al.*[62] and Jaiswal *et al.*[63] .

Estimates of phenotypic and genotypic correlation coefficients

Estimates of genotypic and phenotypic correlation coefficients were calculated among all characters under investigation (Tables 4).Phenotypic correlation is the observable correlation between two variables, including both genotypic and environmental effects and genotypic correlation is the inherent heritable association between two variables, hence genotypic correlation is of greater importance to the plant breeder as compared to phenotypic correlation for the genetic improvement of any one character by selecting the other character which is genetically correlated with the selected trait. Inthe present investigation, genotypic correlation coefficientswere found to be higher in magnitude than that of phenotypic correlation coefficients for most of the traits under study, which clearly indicated the presence of inherent association among various characters. Many earlier research findings also reported lesser magnitude of phenotypic correlation coefficients than the genotypic correlation coefficients [35, 53] that revealed the presence of inherent genetic relationships among various characters and the phenotypic expression of these traits were less influenced by the environment.

In the present study the analysis of genotypic and phenotypic correlation disclosed a significant positive correlation of grain yield/plantwith numbers of productive tillers/plant, weight of spike, numbers of grains/spike, weight of grains/spike and biological yield/plant. Whilstdays to heading displayed significant positive correlation with days to maturity and numbers of spikelets/spike. Whereas days to maturity had a significant positive correlation with harvest index. Plant height exhibited significant positive correlation with harvest index and test weight. Numbers of tillers/plant disclosed significant positive correlation with biological yield/plant. Spike length presented significant positive correlation with weight of spike, numbers of spikelets/spike, numbers of grains/spike, weight of grains/spike and biological yield/plant. However, weight of spike exhibited significant positive correlation with numbers of spikelets/spike, numbers of grains/spike, weight of grains/spike, biological yield/plant, and spike length. Spike length is positively correlated with weight of spike per plant, numbers of spikelets per spike, numbers of grains per spike, weight of grains per spike and biological yield per plant. Weight of spike per plant significantly correlated with numbers of spikelets per spike, numbers of grains per spike and biological yield. Whilst numbers of spikelets/spike had positive correlation with numbers of grains/spike and weight of grains/spike. Weight of grains per spike significantly and positivelycorrelated with spike length, weight of spike and numbers of spikelets per spike. Whereas weight of grains/spike positively correlated with spike length, weight of spike, numbers of spikelets/spike and numbers of grains/spike. While biological yield/plantshowed significant positive correlation with numbers of productive tillers/plant, spike length, weight of spike and weight of grains/spike. Harvest indexexposed significant positive correlation with days to maturity and plant height. Test weight disclosed significant positive correlation with plant height.The interrelationship among yield components would help in increasing the yield levels and therefore, more emphasis should be given to these components while selecting better types in wheat.Likewise, the association of grain yield with either one or more than one traithas also been reported by Desheva [64], Phougat *et al.* [65]Arya *et al.* [66], Abdul*et al.* [67], Madić *et al.* [68],Negash*et al.* [69], Ashish *et al.* [70] and Aklilu *et al.*[71].

Path analysis

This technique was first used for plant selection.The path coefficient analysis is the simply a standardized partial regression coefficient which split the correlation coefficient into the measure of direct and indirect effects. According to Singh *et al.* [35] (2012) and Gelalcha and Hanchinal [72], path analysis not measure the direct effect of one variable, but also partition both direct and indirect effects and also measure the residual effect of all those passively independent variables which are not taken into consideration during the study, this assist plant breeder to identify traits that are useful as selection criteria to improve yield.

Analysis of genotypic path coefficients is present in Table5. It is disclosed that the highest positive direct effect on grain yield was recorded for numbers of productive tillers/plant tracked by biological yield/plant, test weight, weight of grains/spike, harvest index, numbers of grains/spike and numbers of spikelets/spike, whereas it was recorded lowest for days to heading.Similar findings were also addressed byWahidy *et al.* [73], Desheva [64] (2016), Phougat *et al.* [65],Arya*et al.* [66] and Ashish *et al.*[70] 2020 in bread wheat.

Positive indirect effect of various characters was recorded *via* other traits on grain yield which are prominent for days to heading showed a positive indirect effect on grain yield *via* numbers of spikelets/spike, harvest index, biological yield/plant, and numbers of grains per spike. Days to maturity exhibited positive indirect effect on grain yield *via* days to heading and harvest index. Whilst grain filling period exhibited positive indirect effect on grain yield *via* test weight, numbers of productive tillers/plant, harvest index. Whereas plant height revealed a positive indirect effect on grain yield *via* test weight, harvest index. Numbers of productive tillers/plant exhibited a positive direct effect on grain yield and a positive indirect effect on grain yield *via* biological yield/plant, numbers of grains/spike and days to maturity. Spike length had a positive indirect effect on grain yield *via* weight of grains/spike, biological yield/plant, numbers of grains/spike, numbers of spikelets/spike and harvest index. Weight of spike showed positive indirect effect on grain yield *via* weight of grains/spike, numbers of grains/spike, biological yield/plant, numbers of spikelets/spike and test weight. Numbers of spikelets/spike exposedpositive direct effect on grain yield and a positive indirect effect on grain yield via numbers of grains/spike, weight of grains/spike andbiological yield/plant. Numbers of grains/spike had a positive indirect effect on grain yield *via* weight of grains/spike, biological yield/plant, numbers of productive tillers/plant and numbers of spikelets/spike. Weight of grains/spike had a positive indirect effect on grain yield *via* biological yield/plant, numbers of grains/spike, numbers of spikelets/spike and numbers of productive tillers/plant. Biological yield exhibited a positive indirect effect on grain yield *via* numbers of productive tillers/plant, weight of grains/spike and numbers of grains/spike. Test weight exhibited a positive indirect effect on grain yield via harvest index. Harvest index exhibited a positive indirect effect on grain yield *via* test weight and days to maturity.The residual path effect value found to be 0.6269 indicated that contribution of characters included in this study explained almost all the variation for grain yield as shown in Table 5.These findings are in confirmation with the outcome of the research work done by Mecha *et al.*[74], Adhikari *et al.*[59]) and Saleh *et al.*[75].

Analysis of phenotypic path coefficient for various traits under study on grain yield disclosed as the highest positive direct effect on grain yield was recorded for numbers of productive tillers/plant tracked by biological yield/plant, weight of grains/spike, test weight, harvest index, numbers of grains/spike, numbers of spikelets/spike, whereas it was recorded lowest for days to maturity.

Highest positive indirect effect on grain yield was recorded for biological yield per plant *via* numbers of productive tillers/plant tracked by weight of spike *via* weight of grains/spike, numbers of productive tillers/plant *via* biological yield/plant and numbers of grains/spike *via* weight of grains/spike. Whereas days to heading displayeda positive indirect effect on grain yield *via* numbers of spikelets and harvest index. Days to maturity had a positive indirect effect on grain yield *via* harvest index. Grain filling period showeda positive indirect effect on grain yield *via* test weight, numbers of productive tillers/plant and harvest index.Whilst plant height disclosed positive indirect effect on grain yield *via* test weight and harvest index. Numbers of productive tiller/plant displayedpositive indirect effect on grain yield *via* biological yield/plant and numbers of grains/spike. Spike length had s positive indirect effect on grain yield *via* weight of grains/spike, biological yield/plant, numbers of grains/spike and numbers of spikelets/spike. Weight of spike exhibited a positive indirect effect on grain yield *via* weight of grains/spike, biological yield/plant, grains/spike, numbers of spikelets/spike and test weight. Numbers of spikelets/spike had a positive indirect effect on grain yield *via* weight of grains/spike, numbers of grains/spike and biological yield/plant. Numbers of grains/spike displayedpositive indirect effect on grain yield *via* weight of grains/spike, numbers of productive tillers/plant, biological/plant and numbers of spikelets/spike.While weight of grains/spike had a positive indirect effect on grain yield *via* biological yield/plant, numbers of grains/spike and numbers of spikelets/spike.Biological yield had a positive indirect effect on grain yield *via* numbers of productive tillers/plant, weight of grains/spike, numbers of grains/spike. Harvest index exhibited a positive direct effect on grain yield and a positive indirect effect on grain yield *via* test weight. Test weight exhibited a positive indirect effect on grain yield *via* harvest index. The residual path effect value found to be 0.6558. The residual path effect value found to be 0.6558 indicated that contribution of characters included in this study explained almost all the variation for grain yield as shown in Table 5. These results are in confirmation with the outcome of the research work done by Sharma *et al.* [76] *and* Pooja *et al.*[77].

CONCLUSION

Significant variability was observed among 102 wheat genotypes for all the traits studied indicating the need for effective selection. High heritability coupled with higher genetic advance was recorded for numbers of tillers/plant, spike length, weight of spike, numbers of grains/spike, weight of grains/spike, biological yield/plant, grain yield/plant, harvest index and test weight (1000 - seeds) indicating that these characters are governed by additive gene action and hence direct selection for these traits will give more effective results for increasing the grain yield through genetic improvement in wheat. Significant positive correlation was reported for grain yield/plant with five characters *viz.* numbers of tillers/plant, biological yield/plant, weight of grains/spike, weight of spike and numbers of grains/spike. Hence selection for these characters may be followed for the improvement of grain yield in wheat. Outcome of the path analysis disclosed higher positive and direct effect of numbers of tillers/plant, biological yield/plant, test weight, weight of grains/spike, harvest index, numbers of grains/spike and numbers of spikelets/spike over grain yield whereas other characters exhibited prominent positive indirect effect over grain yield through other characters. Hence, these traits must be given weightage in selection for the improvement of wheat in future breeding programmes.

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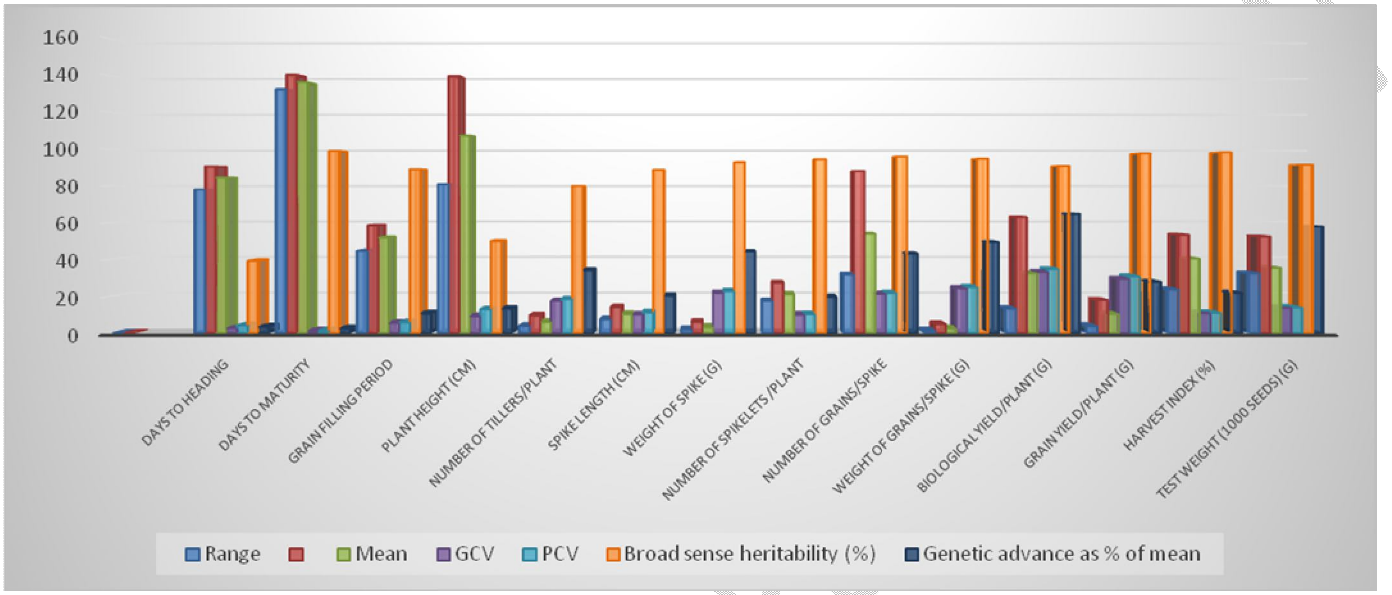

Fig. 1 Components of variance and genetic parameters present among various traits of wheat genotypes

Table 1 Detail of experimental material with their parentage / source used in present investigation

Advance Line No.	Pedigree	Advance Line No.	Pedigree
1	PW635 X (DSP-4/RAJ1555)	52	CW38 X UAS295
2	C306 X PHS 1104	53	DD-11-1353
3	C306 X (DSP-4/RAJ1555)	54	DD-11-1382
4	AKAW 4731 X SAWSN 3029	55	DDS-12-1419
5	DL803-3 X RAJ-1555D	56	DDS-12-1427
6	MACS6222 X GW173	57	DDS-12-1428
7	GW190 X HD 2932	58	DDS-12-1460
8	GW322 X RAJ1555	59	DDS-12-1461
9	DDS-14-1594	60	DDS12-1468
10	DDS-14-1603	61	DDS12-1470
11	DDS-14-1604	62	DDS-12-1475
12	DDS-14-1610	63	DDS-12-1480
13	DDS-14-1633	64	HPW-296 X SONALIKA
14	DDS-14-1641	65	RAJ4185 X LOK-1
15	DDS-14-1644	66	RAJ4188 X HW5205
16	DDS-14-1602	67	RAJ4188 X HW5205
17	DDS-14-1603	68	GW1244 X 994444/VL-998
18	DDS1-4-1606	69	VL 922 X MP 4010
19	DDS-14-1608	70	VL 907 / PHS 1103
20	DDS-14-1608	71	VL 907 / PHS 1103
21	DDS-14-1610	72	VL 907 / PHS 1103
22	DDS-14-1614	73	VL 907 / PHS 1103
23	DDS-14-1614	74	VL 907 / PHS 1103
24	DDS-14-1614	75	VL 907 / PHS 1103
25	DDS-14-1614	76	PW 612 / MP 4010
26	DDS-14-1614	77	GW 2007-77 (D) / MP 4010
27	DDS-14-1615	78	GW 2007-77 (D) / MP 4010
28	DDS1-4-1619	79	SBWON-17-0084
29	DDS-14-1619	80	SBWON-17-0118
30	DDS-14-1635	81	SBWON-17-0119
31	DDS-14-1635	82	SBWON-17-0121
32	DDS-14-1637	83	3rd SAWYT 304
33	DDS-14-1637	84	23rd SAWYT 340
34	DDS-14-1637	85	33th SAWSN 3190
35	DDS-14-1637	86	33th SAWSN 3020
36	DDS-14-1640	87	33th SAWSN 3080
37	DDS-14-1640	88	48th IBWSN 1299
38	DDS-14-1641	89	7th HLBSN 25
39	DDS-14-1641	90	DWAP 1532
40	DDS-14-1641	91	LOK 1
41	DDS-14-1644	92	DWAP 1538

Advance Line No.	**Pedigree**	**Advance Line No.**	**Pedigree**
42	DDS-14-1646	93	GW 2014-580
43	DDS-14-1646	94	HI 1609
44	DDS-14-1650	95	RAJ 4478
45	DDS-14-1652	96	UP 2971(UP2762/2572)
46	DDS-14-1652	97	HUW661(Sr9+11+Lr10+13+YrA+K)
47	DDS-14-1658	98	GW 455(Sr7 +Yr2)
48	DDS-14-1659	99	HUW 661 (Sr30+Lr1+2a+10+23+Yr2+L+K)
49	DDS-14-1659	100	HI 1605(TS-IR-CZ)
50	DDS-14-1659	101	KRL 77-1(K Resistance)
51	DDS-14-1660	102	RAJ 4188XHW5205

Table 2Analysis of variance for yield and its attributing traits in wheat genotypes

Source	**DF**	**Days to heading**	**Days to maturity**	**Grain filling period**	**Plant height**	**Numbers of tillers /plant**	**Spike length**	**Weight of spike /plant**	**Numbers of spike lets /spike**	**Numbers of grains /spike**	**Weight of grains /spike**	**Biological yield /plant**	**Grain yield /plant**	**Harvest index**	**Test weight**
Replication	1	107.37**	22.67*	38.83**	42.03**	0.04	0.78*	4.90**	4.35**	70.82**	0.04	31.23	0.21	5.92	126.65**
Genotypes	101	21.38**	5.78*	23.95**	198.81**	2.35**	2.43**	1.02**	8.95**	269.87**	0.77**	236.95**	19.07**	72.05**	49.63**
Error	101	4.49	3.99	2.75	3.80	0.15	0.15	0.04	0.25	5.61	0.02	11.42	0.85	2.99	2.95

*** Significant at 5% and 1% level respectively

Table 3 Estimation of components of variance and genetic parameters for 14 quantitative characters in wheat genotypes

Characters	Range		Mean	GCV	PCV	Broad sense heritability (%)	Genetic advance as % of mean
	Min.	Max.					
Days to heading	78.00	90.50	84.62	2.60	4.14	39.17	3.35
Days to maturity	132.50	140.50	136.3	1.19	1.20	99.13	2.45
Grain filling period	44.50	58.50	51.7	5.44	5.76	88.99	10.56
Plant height (cm)	80.97	139.75	107.4	9.08	12.85	49.85	13.20
Numbers of tillers/plants	3.73	9.45	6	17.40	18.56	80.02	33.96
Spike length (cm)	7.39	13.97	10.2	10.00	11.09	88.69	20.38
Weight of spike (g)	1.92	5.93	3.2	21.88	22.75	92.88	44.19
Numbers of spikelets /plants	17.40	27.20	21.2	9.87	10.12	94.46	19.69
Numbers of grains/spike	31.57	88.10	53.8	21.37	21.81	95.93	43.09
Weight of grains/spike (g)	1.33	4.73	2.5	24.33	24.98	94.70	49.27
Biological yield/plant (g)	13.20	63.00	32.21	32.97	34.60	90.80	64.70
Grain yield/plant (g)	3.73	17.86	10.29	29.33	30.65	97.65	27.68
Harvest index (%)	23.68	53.20	40.4	10.71	10.80	98.32	21.88
Test weight (1000 -seeds) (g)	32.20	52.30	35.2	13.59	13.75	91.51	57.81

Table 4Genotypic correlation (Above diagonal) and phenotypic (below diagonal) correlation coefficients of wheat genotypes

Characters	**DTH**	**DTM**	**GFP**	**PH**	**NT**	**SL**	**WS**	**SPKL**	**GPS**	**WGS**	**BY**	**HI**	**TW**	**GY**
DTH	1	0.5946**	-0.2921**	0.0399	-0.1532	-0.0821	-0.0102	0.3736**	0.0798	0.0284	0.0599	0.1442	-0.3836**	-0.0199
DTM	0.3711**	1	0.0149	-0.1064	-0.2972**	-0.1109	-0.113	0.0423	-0.1221	-0.1628	-0.0199	0.2583**	-0.0607	-0.1548
GFP	-0.1307	0.0138	1	0.0678	0.0455	-0.0709	-0.0124	-0.2531*	-0.0682	-0.0242	-0.0869	0.0863	0.1946	-0.0045
PH	-0.0864	-0.0648	0.0401	1	-0.0768	0.0782	-0.0797	-0.1423	-0.2285*	-0.0571	-0.0533	0.2267*	0.2432*	-0.0215
NT	-0.1151	-0.2786**	0.0276	-0.051	1	0.0103	-0.0034	-0.1147	0.1318	0.0209	0.4240**	-0.1428	-0.074	0.5961**
SL	-0.0482	-0.1033	-0.0888	0.0488	0.005	1	0.4532**	0.5992**	0.4699**	0.4350**	0.2090*	0.0879	-0.0192	0.1728
WS	-0.0028	-0.1075	-0.0097	-0.0644	-0.0178	0.4072**	1	0.3761**	0.5876**	0.9699**	0.2245*	-0.0537	0.0693	0.2996**
SPKL	0.2261*	0.0402	-0.2188*	-0.0762	-0.1059	0.5495**	0.3585**	1	0.5900**	0.3497**	0.0986	0.0209	-0.3552**	0.0895
GPS	0.0356	-0.1166	-0.0545	-0.1009	0.1131	0.4348**	0.5541**	0.5826**	1	0.5539**	0.1851	-0.0684	-0.2720**	0.2852**
WGS	-0.0039	-0.1566	-0.0182	-0.0083	0.0192	0.3917**	0.9293**	0.3449**	0.5325**	1	0.2450*	-0.0579	0.0227	0.3134**
BY	0.0146	-0.0184	-0.0637	-0.0341	0.4206**	0.1894	0.2054*	0.0963	0.1679	0.2294*	1	-0.0318	-0.0333	0.5789**
HI	0.0943	0.2559**	0.0823	0.158	-0.1261	0.0825	-0.0523	0.0222	-0.0638	-0.0539	-0.0334	1	0.1678	0.0907
TW	-0.2621**	-0.0571	0.1827	0.1722	-0.0705	-0.0168	0.0717	-0.3400**	-0.2629**	0.0247	-0.0289	0.1641	1	0.127
GY	-0.089	-0.1477	-0.0036	-0.0121	0.5926**	0.1595	0.2611**	0.0776	0.2549**	0.2913**	0.5638**	0.0767	0.121	1

*, ** significant at 5% and 1% level respectively

Where is; **DTH –** Days to heading, **DTM –** Days to maturity, **GFP –** Grain filling period, **PH –** Plant height, **NT –** Numbers of tillers per plant, **SL–** Spike length, **WS –** Weight of spike per plant, **SPKL –** Numbers of spikelets per spike, **GPS –** Numbers of grains per spike, **WGS –** Weight of grains per spike, **BY –** Biological yield per plant, **GY –** Grain yield per plant, **HI –** Harvest index, **TW –** Test weight per 1000 seeds.

Table 5 Genotypic path and phenotypic path coefficient matrix of direct and indirect effects of different traits on grain yield in wheat genotypes

Characters		DTH	DTM	GFP	PH	NT	SL	WS	SPKL	GPS	WGS	BY	HI	TW	GY
DTH	G	**0.0701**	-0.0264	0.0018	-0.0004	-0.0743	0.0074	0.0005	0.0356	0.0102	0.0058	0.0196	0.0228	-0.0926	-0.0199
	P	**-0.0331**	0.0024	0.0033	0.0013	-0.0551	0.0031	0.0001	0.0188	0.0039	-0.0008	0.0047	0.0132	-0.051	-0.089
DTM	G	0.0417	**-0.0444**	-0.0001	0.0012	-0.1441	0.01	0.0059	0.004	-0.0156	-0.033	-0.0065	0.0408	-0.0147	-0.1548
	P	-0.0123	**0.0066**	-0.0004	0.001	-0.1333	0.0066	0.0054	0.0033	-0.0126	-0.0308	-0.0059	0.0358	-0.0111	-0.1477
GFP	G	-0.0205	-0.0007	**-0.0061**	-0.0008	0.0221	0.0064	0.0006	-0.0241	-0.0087	-0.0049	-0.0285	0.0136	0.047	-0.0045
	P	0.0043	0.0001	**-0.0256**	-0.0006	0.0132	0.0057	0.0005	-0.0182	-0.0059	-0.0036	-0.0205	0.0115	0.0355	-0.0036
PH	G	0.0028	0.0047	-0.0004	**-0.0111**	-0.0373	-0.0071	0.0042	-0.0136	-0.0292	-0.0116	-0.0175	0.0358	0.0587	-0.0215
	P	0.0029	-0.0004	-0.001	**-0.015**	-0.0244	-0.0031	0.0032	-0.0063	-0.0109	-0.0016	-0.011	0.0221	0.0335	-0.0121
NT	G	-0.0107	0.0132	-0.0003	0.0009	**0.4850**	-0.0009	0.0002	-0.0109	0.0169	0.0042	0.1391	-0.0226	-0.0179	0.5961
	P	0.0038	-0.0018	-0.0007	0.0008	**0.4785**	-0.0003	0.0009	-0.0088	0.0123	0.0038	0.1356	-0.0177	-0.0137	0.5926
SL	G	-0.0058	0.0049	0.0004	-0.0009	0.005	**-0.0904**	-0.0237	0.0572	0.0601	0.0881	0.0686	0.0139	-0.0046	0.1728
	P	0.0016	-0.0007	0.0023	-0.0007	0.0024	**-0.0640**	-0.0205	0.0456	0.0471	0.0771	0.0611	0.0116	-0.0033	0.1595
WS	G	-0.0007	0.005	0.0001	0.0009	-0.0017	-0.041	**-0.0523**	0.0359	0.0751	0.1964	0.0737	-0.0085	0.0167	0.2996
	P	0.0001	-0.0007	0.0002	0.001	-0.0085	-0.0261	**-0.0504**	0.0297	0.06	0.1829	0.0662	-0.0073	0.0139	0.2611
SPKL	G	0.0262	-0.0019	0.0015	0.0016	-0.0556	-0.0541	-0.0197	**0.0954**	0.0754	0.0708	0.0324	0.0033	-0.0858	0.0895
	P	-0.0075	0.0003	0.0056	0.0011	-0.0507	-0.0352	-0.0181	**0.0830**	0.0631	0.0679	0.0311	0.0031	-0.0661	0.0776
GPS	G	0.0056	0.0054	0.0004	0.0025	0.0639	-0.0425	-0.0308	0.0563	**0.1279**	0.1122	0.0607	-0.0108	-0.0657	0.2852
	P	-0.0012	-0.0008	0.0014	0.0015	0.0541	-0.0278	-0.0279	0.0483	**0.1083**	0.1048	0.0541	-0.0089	-0.0511	0.2549
WGS	G	0.002	0.0072	0.0001	0.0006	0.0101	-0.0393	-0.0508	0.0334	0.0708	**0.2025**	0.0804	-0.0091	0.0055	0.3134
	P	0.0001	-0.001	0.0005	0.0001	0.0092	-0.0251	-0.0468	0.0286	0.0577	**0.1968**	0.074	-0.0076	0.0048	0.2913
BY	G	0.0042	0.0009	0.0005	0.0006	0.2056	-0.0189	-0.0118	0.0094	0.0237	0.0496	**0.3281**	-0.005	-0.0081	0.5789
	P	-0.0005	-0.0001	0.0016	0.0005	0.2013	-0.0121	-0.0104	0.008	0.0182	0.0452	**0.3224**	-0.0047	-0.0056	0.5638
HI	G	0.0101	-0.0115	-0.0005	-0.0025	-0.0693	-0.0079	0.0028	0.002	-0.0087	-0.0117	-0.0104	**0.1579**	0.0405	0.0907
	P	-0.0031	0.0017	-0.0021	-0.0024	-0.0604	-0.0053	0.0026	0.0018	-0.0069	-0.0106	-0.0108	**0.1401**	0.0319	0.0767
TW	G	-0.0269	0.0027	-0.0012	-0.0027	-0.0359	0.0017	-0.0036	-0.0339	-0.0348	0.0046	-0.0109	0.0265	**0.2414**	0.127
	P	0.0087	-0.0004	-0.0047	-0.0026	-0.0338	0.0011	-0.0036	-0.0282	-0.0285	0.0049	-0.0093	0.023	**0.1944**	0.121

Genotypic Residual effect: 0.626992, Phenotypic Residual effect:0. 655828
Where; G**- Genotypic, P- Phenotypic**
DTH – Days to heading, **DTM –** Days to maturity, **GFP –** Grain filling period, **PH –** Plant height, **NT –** Numbers of tillers per plant, **SL–** Spike length, **WS –** Weight of spike per plant, **SPKL –** Numbers of spikelets per spike, **GPS –** Numbers of grains per spike, **WGS –** Weight of grains per spike, **BY –** Biological yield per plant, **GY –** Grain yield per plant, **HI –** Harvest index, **TW –** Test weight per 1000- seeds.

* Bold and underlined figures indicate the direct effect of each attributing trait on grain yield/plant