Genetic variability and correlation in quantitative characters in durum wheat (*Tritium durum* **L**)

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Abstract

The present investigation was carried out with 30 durum wheat genotypes during Rabi 2010-11 in RBD having three replications at Field Experiment Centre of Department of Genetics and Plant Breeding, Allahabad School of Agriculture, SHIATS. The data were recorded on 12 quantitative characters to study the variability, heritability, genetic advance and correlation. Analysis of variance revealed considerable variability among the genotypes for all characters. On the basis of mean performance highest grain yield per plant was exhibited by genotype NIDW-309(12.30g). A perusal of coefficient of variation showed that PCV was higher than GCV for all the characters studied indicating less effect of environment on the expression of these characters. The phenotypic and genotypic coefficient of variation (PCV and GCV) was high for grain yield per plant followed by biological yield per plant and test weight. High estimates of heritability were observed for plant height, number of grains per spike, grain yield per plant, test weight and days to 50% flowering. Moderate estimates of genetic advance were exhibited by biological yield per plant, flag leaf length, grain yield per plant and days to maturity. Genotype NIDW-29 was found best for grain yield per plant and other yield related characters. High estimates of genotypic and phenotypic coefficient of variation was observed for grain yield per plant, effective tillers per plant, biological yield and test weight along with high estimates of heritability. Further positive correlation of test weight and effective tillers per plant with grain yield, revealing the scope for improvement of durum wheat yield through selection for these traits.

Key word : durum wheat, correlation, variance, genetic advance, heritability.

Introduction:

Durum wheat is used in the production of pasta and biscuits, which are consumed extensively .All about 22 million tons of wheat is produced annually (**Anonymous, 2014**) .The study of genetic variability is the prerequisite for any crop improvement programmes success in recombination breeding depend on suitable exploitation of genotypes as parent of obtaining heterotic crosses and transgressive sergeants for the presence of genetic variability in base population in essential. The nature and extent of variability forms the basis for crop improvement according to (**Allard, 1960).** Yield is polyginetically controlled quantatives character and is highly influenced by the environment. Partition of observed variability into heritable and non-heritable component is very much essential to get a true indication of genetic co-efficient of variation as a useful measure of the magnitude for selection. The estimates of heritability helps plant breeder in determining characters for which selection would be rewarding. Heritability and genetic advance are other important selection parameters. Estimates of heritability help the plant breeder in determining the character for which selection would be rewarding. The breeders are interested in selection of superior genotypes based on their phenotypic expression. The major function of heritability estimates is to provide information on transmission of characters from the

parents to the progeny. Heritability estimates can anticipate improvement by selection of useful characters**.** *http://www.wikpedia.durumwheat.com* Maximum exploitation of the allelic source of economic species like wheat in minimum time is of paramount importance in keeping food production abreast with population growth. It is well known that all plant breeding programmes involve selection at one stage or other. Genetic variances serve as a basis for major plant breeding decision; they provide a greater array of genotypes among which selection can be practiced to develop still new varieties or breeding materials.

http://www.wikpedia.durumwheat.com.Durum wheat (*Triticum tergidum* durum) is the only tetraploid species of wheat widely cultivated. Today Durum is the hardest of all wheat. Its high protein content and gluten strength make durum good for pasta and bread durum has high gluten content. Grain yield is a complex character because it depends upon nicking ability of genes responsible for yield and yield contributing characters. There may not be genes for yield *per se* but for their components and the multiplicative interaction of which results in ultimate yield. Therefore, a successful and efficient crop improvement programme it would be desirable to have by systematic and detailed information on component characters and their relationship with yield. Improvement is any desirable traits are largely dependent upon the magnitude of genetic variability in for the targeted trait. Phenotypic variability arises due to glance type and environment interaction. High phenotypic variability does not necessarily mean high available genetic variation selection on the basis of phenotypic variation is not efficient and selection therefore, base on evaluation and utilization of genetic variability in a desi had direction is extremely important in any crop improvement programme in this regard it is necessary to find out association the various plant characters in the basic materials. As yield is a complex character, direct selection for this character as such becomes a difficult task without knowledge of relationship between yield and its various components similarly these characters are correlated, the change in one of the character may cause a series of change in other characters. This approach might be useful in character without sacrificing much in other characters. If association is significantly positive it will accelerate the rate of genetic gain; however if it is in negative direction than it was referred the genetic progress. Thus is any crop improvement programme evaluation of germplasm for identification of genetic variability in various quantitative traits and creating further variability through hybridization is of vital importance.

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Materials and Methods

The investigation was carried out at the Field Experimentation Centre of Department of Genetics and Plant Breeding, Allahabad School of Agriculture, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Deemed to be University, Allahabad (U.P)**.** The experimental materials consisted of 30 genotypes (28 parents+2checks) of durum wheat, which were obtained from wheat breeding programme, Directorate of Research, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Deemed to be University, Allahabad (U.P.). Grown under randomized block design (RBD) with three replications, during rabi 2010-11. The experimental material comprising of 30 diverse wheat genotypes, the experimental field was divided into 3 blocks of equal size and each block possesses 30 plots. Each genotype was accommodated in a two row of 2 meter length spaced at 25 cm with an approximate plant to plant distance of 5 cm. The observations were recorded on five randomly selected competitive plants in each entry of each replication for all the characters except for days to 50% flowering and days to maturity, which were recorded on plot basis. The data were recorded for following traits: Days to 50% flowering, Days to maturity, Number of tillers per plant, Flag leaf length (cm), Flag leaf width (cm), Plant height (cm), Spike length (cm), Biological yield (g),Number of grain per spike, Grain yield per plant (g)**,** Test weight (g)**,** Harvest Index **(%)** The value of harvest index was calculated from the following formula given by **(**Donald and Hamblin, 1976) **Statistical Analysis:** The data thus recorded were subjected to statistical and biometrical analysis as detailed below: 1 **Analysis of Variance**

Table 1: Estimation of components of variance and genetic parameters for different characters in durum wheat

Sr. No.	Characters	VG	VP	GCV	PCV	ECV	h^2 (bs)%	GA	GA as % of mean
1	Days to 50% Flowering	01.96	3.28	1.81	2.34	1.32	59.67	2.22	2.88
2	Days to maturity	06.12	7.97	2.08	2.38	1.85	76.80	4.46	3.76
3	Plant height	36.77	37.02	7.63	7.68	0.25	99.32	12.44	15.73
4	Flag leaf width	0.038	0.04	13.31	14.39	0.01	85.51	0.37	25.35
5	Flag leaf length	10.82	10.90	12.94	13.00	0.09	99.21	6.74	26.56
6	Spike length	01.48	1.49	15.61	15.68	0.01	99.18	2.50	32.04
7	Effective tiller/plant	09.57	10.87	30.81	32.85	1.30	87.99	5.97	59.54
8	Number of grains/spike	49.16	49.60	15.51	15.58	0.43	99.12	14.38	31.82
9	Test weight	14.30	14.37	13.41	13.18	0.08	99.46	7.76	27.01
10	Biological yield	169.26	170.44	31.51	31.62	1.18	99.31	26.70	64.69
11	Harvest Index	189.68	189.85	45.87	45.89	0.17	99.91	28.35	94.46
12	Grain yield/plant	10.00	10.29	29.81	30.24	0.29	97.17	6.42	60.54

- VG = Genotypic Variance, VP = Phenotypic Variance, GCV=Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation, ECV = environmental Coefficient of Variation, h^2 (bs) = Heritability (board sense), GA = Genetic Advance.

by **Panse and Sukhatme (1967)**.2 Coefficient of variation The formulae used to calculate PCV, GCV and ECV were given by **Burton (1952).**3 The estimates of genetic advance were obtained by the formula given by **Johnson *et al.* (1955).**And **Heritability (broad sense):4** It was calculated by the formula given **Burton** and **Devane (1953).**Correlation coefficient analyses are calculated by following formula given by **Al-Jibouri *et al.* (1958). 5 Test of significance:** To test the significance of correlation coefficient, the estimated values were compared with table values of correlation coefficient prescribed by **Fisher and Yates (1938)**,

Result and discussion

A perusal of per se performance revealed that higher grain yield were observed in genotype NIDW-29 (17.72) followed by RD-1093 (15.93), WR-1022 (14.62), HI-8645 (14.52) and DBY-01-11 (14.26).

Analysis of variance showed higher significant differences among the 30 genotypes for 12 quantitative characters under study, which indicates that there was considerable genetic variability present among the gene pool for future yield improvement of durum wheat. One of the important considerations in any crop improvement is the detailed study of genetic variability. Variability is a measure by estimation of phenotypic and genotypic variance, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic gain for different quantitative and qualitative traits.

These parameters deserve attention in selection for improvement in the concerned characters. The phenotypic variability, which is observable, includes both genotypic and environmental variation. It changes under different environmental conditions. Environmental variation is the non heritable variation, which is slowly due to environmental effects and varies under different environmental conditions.

The estimates of variance, coefficient of variation, heritability and genetic advance for all the twelve characters studied have been boxed in the Table 2 and explained here as under Wide range of phenotypic (VP or r^2p) and genotypic variance (Vg or r^2g) were observed in the experiential materials for all the

traits studied. The highest phenotypic and genotypic variances were recorded for Harvest index (189.85 and 189.68) followed by biological yield (170.44 and 169.26), number of grain per spikes (49.60 and 49.16), plant height (37.02 and 36.77) and Test weight (14.37 and 49.16), while moderate values were observed for Hag leaf length (10.90 and 10.82), effective tillers per plant (10.87 and9.57) and grain yield per plant (10.29 and 10.00). Whereas Hag leaf width (0.05 and 0.04), spike length (1.9 and 1.48) and Days to 50% flowering (3.28 and 1.96) showed low estimates of variance. Less difference in the estimates of genotypic and phenotypic variance and higher genotypic values compared to environmental variances for all the characters suggested that the variability present among the genotypes were mainly due to genetic reason with minimum influence of environment and hence heritable. The genotypic estimates of variability (VG, GCV) being the most important, help in the measurement of the contribution of the genotype to the expression of a particular character and gives clue to compare the genetic variability for different characters. These findings of genotypic and phenotypic variance for different quantitative characters in wheat are in accordance with the findings of **Singh *et al.* (2001), Sharma** and **Garg (2002), Yagdi and Sozen (2009) and Mohsin *et al.* (2009)**.

it is depicted from table 2 that in general, estimates of phenotypic coefficient of variation were found higher than their corresponding genotypic coefficient of variation, indicating that the little influence of environment on the expression of these characters. However, good correspondence was observed between genotypic coefficient of variation and phenotypic coefficient of variation in all the characters: The estimate of phenotypic coefficient of variation (PCV) observed for all the traits ranged from 2.30 (days to maturity) to 45.89 (grain yield per plant). Higher magnitude of PCV was recorded for Harvest index (45.89), effective tillers per plant (32.85), Biological yield (3.62) Grain yield per plant (30.24), spike length (15.68), number of grain per spike (15.50), flag leaf width (14.39), Test weight (13.18) , and while moderate estimate of PCV was depicted by number of plant height (7.68), days to maturity (2.38) and 50% flowering

Table 2: Estimation of genotypic (rg) & phenotypic (rp) correlation coefficient for different quantitative characters in durum wheat.

Sr. No.	Characters	r	Days 50% flowering	Days to maturity	Plant height	Flag leaf width	Flag leaf length	Spike length	Effectivr Tillers plant	Grain spikes	Test weight	Biological yield	Harvest index	Grain yield/plant
1	Days 50% flowering	rG	1.00	0.29	-0.21	-0.04	0.17	0.30	0.06	-0.09	0.22	-0.09	-0.26	-0.17
		rP	1.00	0.14	-0.21*	-0.04	0.13	0.22*	0.03	-0.06	0.17	-0.07	-0.20	-0.13
2	Days to maturity	rG		1.00	-0.11	-0.04	-0.020	0.26	0.14	-0.07	0.30	0.23	-0.09	0.40
		rP		1.00	-0.10	-0.06	-0.02	0.23*	-0.13	0.05	0.26*	0.20	-0.08	0.34***
3	Plant height	rG			1.00	0.19	0.17	0.22	-0.12	0.03	-0.15	0.11	-0.04	-0.13
		rP			1.00	0.18	0.17	0.22*	0.32	0.04	-0.15	0.11	-0.04	-0.13
4	Flag leaf width	rG				1.00	0.29	-0.04	0.28**	0.03	-0.11	0.10	-0.33	0.10
		rP				1.00	0.27	-0.04	-0.06	-0.02	-0.10	0.10	-0.31**	0.10
5	Flag leaf length	rG					1.00	0.03	-0.07	0-02	0.02	0.13	-0.23	0.13
		rP					1.00	0.03	0.09	0.35	0.02	0.13	-0.23*	0.26*
6	Spike length	rG						1.00	0.08	0.35**	0.09	0.33	0.26	0.27
		rP						1.00	1.00	0.14	0.09	0.33**	0.25*	0.27
7	Tillers plant	rG							1.00	0.13	-0.19	0.43	-0.47	0.41
		rP								1.00	-0.17	0.40***	-0.44***	0.38***
8	Grain spikes	rG								1.00	0.31	0.08	0.10	0.36
		rP								0.31**	0.09	0.10	0.33**
9	Test weight	rG									1.00	0.08	0.04	-0.13
		rP									1.00	0.08	0.04	-0.13
10	Biological yield	rG										1.00	-0..42	0.54
		rP										1.00	-0.42***	0.53***
11	Harvest index	rG											1.00	0.01
		rP											1.00	0.01
12	Grain yield/plant	rG												1.00
		rP												1.00

*and ** significant at 5% and 1% level of significant respectively.

(2.30) whereas, depicted least phenotypic coefficient of variation. A perusal of genotypic coefficient of variation (GCV) revealed that it ranged from 1.81 (50% flowering) to 45.87 (Harvest index). Higher magnitudes of GCV were recorded for Harvest index (45.87) followed by effective tillers per plant (30.81), grains yield per plant (29.81), spike length (15.61), number of grains per spike (15.51), flag leaf width (13.31), flag leaf length (12.94), plant height (7.63), days to maturity (2.08) biological yield (31.62), test weight (13.14) and days to 50% flowering (1.81) exhibited moderate estimates and exhibited least genotypic coefficient of variation. On an average, the higher magnitude of GCV and PCV were recorded for harvest index, biological yield, grain yield per plant, tillers per plant, spike length, flag leaf length, test weight, number of effective and number of grain per spike suggesting sufficient variability and thus scope for genetic improvement through selection for these traits. Relatively low magnitudinal difference was observed between GCV and PCV for all the traits studied. This indicated less environmental influence on the expression of all the attributes. These findings are in agreement with those of **Dwivedi *et al.* (2002), Yagdi and Sozen (2009) and Mohsin *et al.* (2009),** who have also observed the PCV values, were higher than GCV values for different quantitative characters in wheat.

Heritability is a measure of the extent of phenotypic variation caused by the action of genes. For making effective improvement in the character for which selection is practiced, heritability has been adopted by large number of workers as a reliable indicator. Heritability in broad sense according to **Lush (1949)** is the ratio of total genotypic variance to phenotypic variance, expressed in percentage. The estimates of heritability are more advantageous when expressed in terms of genetic advance**. Johnson *et al.* (1955)** suggested that without genetic advance the estimates of heritability will not be of practical value and emphasized the concurrent use of genetic advance along with heritability. **Hanson (1963)** stated that heritability and genetic advance are two complementary concepts.

Heritability and genetic advance have been worked out for all the twelve quantitative characters and are presented in Table 2.

High estimates of heritability (above 75%) in broad sense were recorded for all the twelve characters studied. The highest heritability was recorded for Harvest index (99.91 percent) followed by number of test weight (99.46 percent), plant height (99.32), biological yield (99.31 percent), flag leaf length (99.21 percent), spike length (99.18), grain per spike (99.12 percent), grain yield per plant (97.17), effective tillers per plant (87.99 percent), flag leaf width (85.51 percent), days to maturity (76.80 percent), days to 50% flowering(59.67 percent) number of and High values indicate that heritability may be due to higher contribution of genotypic component. High heritability estimates were also reported by **Amin *et al.* (1990)** and **Phadnawis *et al.* (2002)** for 1000 grain weight, **Panwar and Singh. (2000)** and **Asif *et al.* (2004)** for plant height, **Joshi** and **Mahal (2004),** and **Rasal *et al.* (2008)** has also observed high value of heritability for grain yield and its components in wheat.

A perusal of genetic advance (table 2) revealed that it was highest to low for Harvest index (28.35), biological yield (26.71), number of grains per spike (14.38), plant height (12.45), test weight (7.77), flag leaf length (6.75), grain yield per plant (6.42), number of effective tillers per plant (5.99), days to maturity (4.47), spike length (2.50), days to 50% flowering (2.23) and flag leaf width (0.37).The heritability estimates coupled with expected genetic advance indicate the mode of gene action in the expression of traits which helps in choosing an appropriate breeding methodology. High heritability along with high genetic advance was registered for plant height (98.96, 15.31), test weight (97.80, 12.33), harvest index (97.28, 11.43), number of grain per spike (98.41, 11.41), days to 50% flowering (97.71, 8.83) suggesting predominance of additive gene action in the expression of these traits. High heritability along with moderate genetic advance was registered for grain yield /plant (97.17, 6.42) suggesting predominance of additive and non additive gene action in the expression of these traits therefore, these characters can be improved by mass selection and other breeding methods based on progeny testing. Similar results in wheat have been also reported by **Pawar *et al.* (2002), Yagdi and Sozen (2009) and Mohsin *et al.* (2009).**However, characters like effective

tillers per plant (89.99, 5.58), days to maturity (76.80, 4.46), day to 50% per flowering (59.67, 2.22) possessed high heritability with low genetic advance, suggesting non-additive gene action in the expression of these traits.The high heritability of these traits was due to favorable influence of environment rather than genotypic and selection for these traits may not be rewarding. Similar results were reported by **Yagdi and Sozen (2009) and Mohsin *et al.* (2009),Navin et al (2014)** for plant height, number of tillers exhibited higher heritability.

The inherent or heritable association between two variables is known as genotypic correlation. This type of correlation may be either due to phenotypic action of genes or due to linkage or more likely both. The main genetic cause of such correlation is pleiotropy, which refers to manifold effects of a gene **(Falconer, 1981)**. This type of correlation is more stable and is of paramount importance for a plant breeder to bring about genetic improvement in one character by selecting the other character of a pair that is genetically correlated. Table 3 depicts phenotypic and genotypic correlation coefficients computed from the estimation of variance an co-variance for all possible combination of the characters studied. In the present investigations the genotypic correlation coefficients are in general higher than the corresponding phenotypic correlation coefficients. That is why the environmental affect covering, the total expression of genotype altering the phenotypic expression. High genotypic correlations also suggest that there is inherent relationship between the characters studied. This was supported by the findings of **Gupta *et al*. (2002).** Character wise phenotypic and genotypic correlation is presented here as under: characters *viz* : harvest index (0.06**), flag leaf width (0.09) and flag leaf length (0.13) showed positive but non significant correlation biological yield (0.53*), number of effective tillers per plant (0.38**), days to maturity (0.34**) and grain per spike (0.33**), showed positive significant correlation with grain yield which indicates strong association of these characters with yield. Therefore, by increasing the value of these components trait, yield may easily be pushed up suggesting the selection for these characters will be useful in improving seed yield. These

results are in agreement with the work of **Dwivedi *et al.* (2002), Biljana and Marija (2006), Yagdi and Sozen (2009)** who also observed significant and positive association of yield per plant with biological yield per plant. While other characters like days to 50% flowering (-0.13), Plant height (-0.13*) and test weight (0.13) day to maturity exhibited negative significant correlation with grain yield at phenotypic level. Negative and significant association indicates that selection on the basis of these characters will not be beneficial as increase in one character will decrease the other .Days to 50% flowering exhibited positive significant association with flag leaf test weight (0.17**), days to maturity (0.14**), and flag leaf width (0.13**). Whereas rest of all the characters like spike length (-0.22*) showed negative non significant and plant height (-0.21**), grain yield per plant (-0.13**), harvest index (-0.20**), biological yield (-0.07**), grains/spikes (-0.06), flag leaf width (-0.04cm) and effective tillers per plant (-0.03**), showed negative significant correlation with days to 50% flowering at phenotypic level. These results of correlation are in general agreement with the result of **Dwivedi *et al.* (2002), Mohsin *et al.* (2009).**Days to maturity showed significant negative correlation with grain yield per plant (-0.34***),test weight (0.26*),biological yield (0.20),effective tillers per plant (0.12),flag leaf width (0.06) and grains per spikes (0.05) and showed negative significant spike let length (-0.23*) and showed negative non significant flag leaf length (-0.02) and plant height (-0.10) with days to maturity at phenotypic level. Plant height exhibited positive association but no/n significant association with spike length (0.22**), flag leaf width (0.18cm), flag leaf length (0.17),biological yield (0.11) and grains/ spikes. Showed negative grains yield /plant (-0.13), effective tillers/ plat (-0.12), test weight (0.15gm) and harvest index (-0.04).Spike length exhibited positive but non significant association with number of grains per spike (0.18), biological yield per plant (0.02), harvest index (0.007), days to maturity (0.09) and grain yield per plant (0.005). However rest of the characters like flag leaf length (0.34**), flag leaf width (0.42**) and test weight (0.38**) showed positive significant correlation with spike length at phenotypic level. Flag leaf width showed

positive but non significant association with number of effective tillers/plant (0.28), flag leaf length (0.27cm), biological yield (0.10), grain yield/ plant (0.10) and grains/spike (0.03) showed positive significant correlation while harvest index (-0.31), test weight (-0.10) and spike length (-0.04) showed significant negative correlation with flag leaf length at phenotypic level. Flag leaf length showed positive but non significant association with Biological yield (0.13). However, rest of the characters like grain yield/plant (0.13) and spike length (0.03) and test weight (0.02), showed significant negative correlation and harvest index (-0.23*), effective tillers/plant (-0.7) and grains spikes (-0.2) showed non significant negative correlation with flag leaf length at phenotypic level.Number of effective tillers per plant showed positive but non significant association with biological yield (0.40), Grain yield/plant (0.38). However rest of the characters like number of grain per spike (0.13*) showed significant negative correlation and Harvest index (-0.23), Effective tillers/plant (-0.7) and grain/spikes (0.2) showed non significant negative correlation with number of effective tiller per plant at phenotypic level. Number of grains per spike exhibited non-significant positive correlation with Grain yield/plant (0.33) and test weight (0.30). While rest of the characters like harvest index (0.10) and biological yield (0.08) showed positive significant correlation. Test weight revealed significant positive correlation with biological yield (0.08) while harvest index 0.04) showed significant negative correlation with grain yield spike (-0.13) at phenotypic level. Biological yield per plant exhibited significant positively correlation with grain yield/spike (0.53**) showed negative non significant correlation with harvest index (-0.42). These results are in agreement with the results of **Dwivedi *et al.* (2002) and Mohsin *et al.* (2009).**Harvest index exhibited significant positive correlation with grain yield per plant (0.01) showed negative significant correlation with harvest (0.41) and grain per spikes (0.14) and negative association with was observed harvest index (-0.47),test weight (-0.19) at genotypic level. Flag leaf length showed positive association with biological yield (0.13),grains yield per plant (0.13) spike length (0.03) and test weight (0.02) showed positive

index at phenotypic level. Table 3 depicts the estimates of genotypic correlation coefficient. The present investigation suggested that grain yield per plant was positively correlated with plant height (0.40), number of effective tillers per plant (0.40), biological yield (0.53), grain per spikes (0.33),spike length (0.27),flag leaf length (0.13), flag leaf width (0.10), and harvest index (0.01) with grain yield per plant whereas plant height (-0.13),test weight (-0.13) and days to 50% flowering (-0.17) exhibited negative correlation with grain yield per plant at genotypic level. Mutual correlation between the components characters revealed those days to 50% flowering was and positively correlated with test weight (0.22) and days to maturity (0.29). Days to 50% flowering had negative correlation with spike length (-0.30), plant height (-0.27), harvest index (-0.26), biological yield (-0.09), effective tillers per plant (-0.06),flag leaf width (-0.04), grain yield per plant (-0.17) negative association at genotypic level.

Days to maturity showed positive association with grain yield per plant (0.40),test weight (0.30),biological yield (0.23),effective tiller per plant (0.14),grains per spike (0.07) and flag leaf width (0.04) and negative association spike length (-0.26),plant height (-0.11),harvest index (-0.09) and flag leaf length (-0.02) at a genotypic level.Plant height showed positive association with spike length (0.22), flag leaf width (0.19), flag leaf length (0.17), biological yield (0.10), grains per spike (0.04). Plant height showed negative association with test weight (-0.15), grain yield per plant (-0.13), effective tiller per plant (-0.13), biological yield (-0.11) and harvest index (-0.04) at genotypic level. Spike length showed positive association with grain per spikes (0.35), biological yield (0.34), grains yield per plant (0.27) harvest index (0.26) test weight (0.09) and effective tillers per plant (0.08) at genotypic level.

Number of effective tillers per plant was positive correlation with biological yield (0.36), grain yield per plant correlation while harvest index (-0.23),effective tiller per plant (-0.06) and grain spikes (-0.02) at genotypic level. Flag leaf width showed positive association with effective tillers per plant (0.32) flag leaf length (0.29),biological yield (0.01), grain yield per plant (0.01)and grains per spike (0.03) showed

positive correlation while harvest index (-0.33),test weight (-0.11) and spike length (-0.04) showed negative association with flag leaf width at genotypic level. Number of grains per spike showed positive association with grain yield per plant (0.34), test weight (0.31), harvest index (0.10) and biological yield (0.08) showed positive association with number of grains per spike at genotypic level. Biological yield showed positive association with grain yield per plant (0.54) showed positive association and harvest index (-0.42) showed negative correlation at genotypic level. Harvest index showed positive association with grain yield per plant (0.01) and positive association with harvest index at genotypic level. Test weight showed positive association with biological yield (0.08), harvest index (0.04) and negative association with grain yield per plant (-0.13) showed negative association with test weight at genotypic level. The correlation studies

facilitate the assessment of the chance for mutual improvement of two traits by common selection. In other words the estimates of correlation coefficient gives a clear picture of the extent of association between a pair of traits and indicated whether simultaneous improvement of the correlated traits may be possible or not. Thus association analysis suggested that the yield in durum wheat could possibly be improved by increasing grains per spike and 1000 grain weight. As these characters are significantly and positively correlated with yield. Increase in the length of the spike and plant height will results in the increase in number of grains per spike but will show any enhancement in grain yield due to the positive correlation of these characters with yield. Similar findings in durum wheat have also been reported by **Biljana and Marija (2006), Mohsin *et al.* (2009) and Yagdi and Sozen (2009).**

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