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Research Article

Genetic Variability, Correlation and Path Analysis in Durum Wheat (*Triticum durum* L.)

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ABSTRACT

The experiment was carried out at the Agriculture Research Station, S. D. Agricultural University, Ladol using thirty-five genotypes of durum wheat. All genotypes were sown and evaluated under timely sown condition during rabi 2019-2020, in a simple randomized block design (RBD) with four replications. In the present experiment, 10 morphological and 2 biochemical characters were studied. The analysis of variance showed significant variation among the genotypes for all the studied characters indicating the presence of adequate amount of variability among thirty-five genotypes. High heritability associated with high genetic advance as per cent of mean were found for the characters viz., number of effective tiller per meter, grain yield per plot and biological yield per plot which indicated that the characters were simply inherited in nature and controlled by few major genes or possessed additive gene effects. Grain yield per plot revealed highly significant and positive correlation with days to heading, days to maturity, spike length, number of effective tiller per meter, number of grain per spike, 1000 grain weight, biological yield per plot and harvest index at genotypic as well as phenotypic level. The path coefficient analysis showed that the biological yield per plot recorded highest direct effect towards grain yield per plot followed by harvest index, sedimentation value, 1000 grain weight, spike length and days to heading. On the basis of this experiment, for the improving grain yield in durum wheat more attention should be emphasized to biological yield per plot, harvest index, sedimentation value, 1000 grain weight, spike length and days to heading while making selection for developing high yielding durum wheat genotypes.

Keywords: *Durum wheat, Variability, Heritability, Correlation and Path coefficient analysis.*

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INTRODUCTION

Wheat is the second most important staple food next to rice, consumed by nearly 35 per cent of the world population. It is known for its remarkable adoption to a wide range of environments and its role in world economy. The total area and production of durum wheat is about 20 million hectares and 30 million metric tons globally (Kahrizi et al., 2010). As reported by Central Statistics Authority (CSA, 2011), the average world productivity of durum wheat is 25 q/ha. In India wheat occupies an area of 29.58 million hectares under irrigation with production of 107.86 million tonnes and productivity is 3371 Kg/ha (Directorate of Economics & Statistics, DAC & FW 2019-20). While, In Gujarat wheat occupies an area of 1.381 million hectares with production of 4.505 million tonnes and productivity is 3260.78 Kg/ha (Directorate of Agriculture, Gujarat State 2019-20).

Analysis of variability among the traits and the correlation of a particular character with other traits contributing to yield of a crop would be great importance in planning a successful breeding programme (Mary & Gopalan, 2006). The choice of parents is prior importance in breeding programme. For effective selection, information on nature and proportion of variation in population, association of character with yield and among themselves and the extent of environmental influence on the expression of these characters are necessary (Yagdi, 2009).

Correlation studies along with path analysis provide a better understanding of the association of different characters with grain yield. Correlation is useful in disclosing measure and direction of the relationship between various yield contributing traits and yield. While path coefficient analysis measures the direct effect of a predictor variable upon its response variable and the second component being the indirect effects of a predictor variable (Dewey & Lu, 1959).

Yield is the complex quantitative character and depends on various components. Various biometrical techniques are extensively used for the estimation of relative magnitude of the different components of genetic variation, out of which techniques developed by Hayman (1958); Jinks and Jonse (1958) and Mather (1949) require less number of families and are comprehensive, easy and equally informative.

MATERIALS AND METHODS

Plant materials

The experimental material for present study comprised 35 wheat genotypes. These genotypes were received from the Wheat Research Station, S. D. A. U, Vijapur (Table 1).

Field experiment

The experimental material consisting 35 genotypes of durum wheat which were grown in randomized block design (RBD) with four replications. The experimental material was sown in field during rabi in the year 2019-20 at ARS, SDAU, Ladol. In each genotype consist of double rows of 3.0 m length with a spacing of 22.5 cm between two rows. The genotypes were randomly allocated to the plots in each replication. All the suggested agronomical practices along with required plant protection measures were followed timely for the successful raising of the crop. Twelve characters viz., days to heading (N), days to maturity (N), plant height (cm), number of effective tiller per meter, spike length (cm), number of grain per spike, biological yield per plot (g), harvest index (%), 1000 grain weight (g), protein content (%), sedimentation value (ml) and grain yield per plot (g) were studied.

Statistical analysis

The mean performance of each genotype was subjected to statistical analysis. Analysis of variance to test the significance for each character was carried out as per the methodology given by Panse and Sukhatme (1985). The phenotypic and genotypic correlations worked out as per procedure suggested by Hazel (1943). Heritability in broad sense ($h^2_{b.s.}$) and genetic advance as percentage of mean were estimated using the formula given by Allard (1960). Correlation and path coefficient were estimated as per the method suggested by Al-Jibouri et al. (1958) and Dewey and Lu (1959) respectively.

RESULTS AND DISCUSSION

The result revealed highly significant differences among the tested genotypes for all the characters viz., days to heading, days to maturity, plant height, number of effective tiller per meter, spike length, number of grain per spike, biological yield per plot, harvest index, 1000 grain weight, protein content, sedimentation value and grain yield per plot. This indicated the presence of adequate genetic variability among the genotypes for various characters.

Genotypic and Phenotypic coefficient of variation (GCV and PCV)

The estimates of genotypic and phenotypic coefficient of variability indicated that the values of phenotypic coefficient of variation were slightly higher than that of genotypic coefficient of variation for most of the traits studied, indicating less effect of environment on the expression of characters studied.

The values of PCV were found higher than the GCV for all the traits studies indicating the influence of environment on the expression of these characters although the differences were small. High estimated of GCV (17.23 %) and PCV (21.53 %) for grain yield per plot. Low estimated of GCV (2.22 %) and PCV (2.87 %) for days to maturity. The highest GCV and PCV for grain yield per plot was also observed by Dwivedi et al. (2002), Singh and Sharma (2007) and Ali et al. (2008).

Heritability and genetic advance expressed as percentage of mean

Heritability in broad sense and genetic advance as per cent of mean are direct selection parameters that provide an index of transmissibility of traits which indicates the effectiveness of selection in improving the characters. The heritability of a character describes the extent to which it is transmitted generation after generation. The genetic advance is the further estimation of expected gain resulting from selection pressure in breeding material. High heritability associated with high genetic advance for different yield components has a better scope for selection of high yielding genotypes.

High heritability (64.09 %) associated with high genetic advance as per cent of mean (28.42 %) was found for grain yield per plot which indicated the dominance of additive gene action, and therefore selection would be rewarded for improvement of these characters. Moderate estimate of heritability (34.2 %) associated with the value of genetic advance (4.11 %) was low for protein content. High heritability associated with high genetic advance as per cent of mean was found for grain yield per plot which was observed by Dagade et al. (2020) and Vaghela et al. (2021).

Correlation coefficients

The correlation coefficients were estimated among twelve (12) phenotypic and quality traits to find out association between grain yield per plot and its component at genotypic (rg) and phenotypic (rp) levels. The genotypic correlation coefficients were higher than their phenotypic correlation coefficients. This indicated that a high degree of association between two variables at genotypic levels; its phenotypic expression may deflect by the influence of the environment.

The correlation coefficient provides a symmetrical measurement of degree of association between two variables or traits to help plant breeder to understand the nature and magnitude of association among grain yield or economic yield and yield components. grain yield per plot had highly significant and positive correlation with days to heading (rg = 0.394 and rp= 0.288), days to maturity (rg = 0.486 and rp = 0.373) spike length (rg = 0.429 and rp = 0.346), number of effective tiller per meter (rg = 0.727 and rp = 0.400), number of grain per spike (rg = 0.835 and rp = 0.505), biological yield per plot (rg = 0.711 and rp = 0.617), 1000 grain weight (rg = 0.994 and rp = 0.720) and harvest index (rg = 0.554 and rp = 0.567) at both the genotypic and phenotypic levels, that indicated that these attributing traits were more influence on the grain yield in durum wheat. It had non-significant and positive correlation with plant height (rg = 0.131 and rp= 0.067) at genotypic and phenotypic level. It had non-significant and negative correlated with protein content (rg = -0.081 and rp = -0.225) and sedimentation value (rg = -0.100 and rp = -0.220) at genotypic level and highly significant and negative correlated with both trait at phenotypic level. Similar results were obtained by Meles et al. (2017), Kumar et al. (2018) and Dagade et al. (2020).

Path coefficient analysis

Path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effects. The characters which had shown significant genotypic correlation with grain yield per plot were considered for path coefficient analysis. Every component character will have a direct effect on yield and their effects are called as direct effects. The effects of an independent character on the dependent one via other independent traits are known as indirect effects. Residual effect measures the role of other possible independent variables that were not included in the study on the dependent variable. In path analysis, a line diagram that is constructed with the help of a simple correlation coefficient among various characters included under study is referred to as path diagram.

The characters which had shown significant genotypic correlation with grain yield per plot were considered for path coefficient analysis. The Residual effect (0.00016) in path coefficient analysis was considerably low indicating a high contribution of independent traits to the dependent trait.

The overall path analysis based on genotypic correlation revealed that biological yield per plot (0.839) showed highest positive direct effect followed by harvest index, sedimentation value, 1000 grain weight, spike length and days to heading. The characters days to maturity, plant height, number of grain per spike, number of effective tiller per meter and protein content had shown negative direct effect on grain yield per plot at genotypic level.

Table 1: List of genotypes used in the present study along with place of material received

Sr. No.	Name of Genotype	Sr. No.	Name of Genotype
1.	GW 1139	19.	HI 8704
2.	GW 1246	20.	HI 8708
3.	GW 1247	21.	HI 8713
4.	GW 1286	22.	HI 8737
5.	GW 1328	23.	HI 8774
6.	GW 1329	24.	HI 8783
7.	GW 1332	25.	HI 8810
8.	GW 1338	26.	HI 8813
9.	GW 1339	27.	DDW 47
10.	GW 1348	28.	MPO 1262
11.	GW 1351	29.	MPO 1343

12.	GW 1352	30.	UAS 428
13.	GW 2014 – 566	31.	UAS 460
14.	GW 2015 – 675	32.	NIDW 842
15.	GW 2016 – 796	33.	NIDW 1158
16.	GW 2016 – 797	34.	JD 2013-4
17.	HI 8498	35.	GDW 1255
18.	HI 8691		

Material received from the Wheat Research Station, S. D. A. U, Vijapur

Table 2: Genetic parameters of variation for grain yield and its contributing characters in durum wheat

Sr. No.	Characters	GCV (%)	PCV (%)	h^2(b.s) (%)	GA (%)
1	Days to heading	4.89	5.23	87.62	9.43
2	Days to maturity	2.22	2.87	59.73	3.54
3	Plant height	4.09	6.66	37.67	5.17
4	Number of effective tiller per meter	12.65	16.36	59.76	20.14
5	Spike length	6.51	8.86	54.04	9.86
6	Number of grain per spike	9.49	11.78	64.92	15.75
7	Biological yield per plot	15.15	18.89	64.30	25.03
8	Harvest index	12.44	17.81	48.80	17.90
9	1000 grain weight	10.02	10.88	84.79	19.00
10	Protein content	3.41	5.84	34.20	4.11
11	Sedimentation value	4.06	6.17	43.36	5.51
12	Grain yield per plot	17.23	21.53	64.09	28.42

Table 3: Genotypic correlation and phenotypic correlation coefficient for different characters in durum wheat

		DH	DM	PH	TIL/M	SL	NGS	BYP	HI	TGW	PC	SV	GYP
DH	r_g	1											
	r_p	1											
DM	r_g	0.548**	1										
	r_p	0.454**	1										
PH	r_g	0.093	0.143	1									
	r_p	0.119	0.180*	1									
TIL/M	r_g	0.491**	0.227**	0.051	1								
	r_p	0.348**	0.095	0.040	1								
SL	r_g	0.383**	0.346**	0.301**	0.300**	1							
	r_p	0.294**	0.355**	0.101	0.106	1							
NGS	r_g	0.387**	0.396**	0.332**	0.524**	0.737**	1						
	r_p	0.283**	0.253**	0.109	0.331**	0.434**	1						
BYP	r_g	0.555**	0.530**	0.185*	0.679**	0.351**	0.567**	1					
	r_p	0.424**	0.385**	0.091	0.402**	0.246**	0.349**	1					
HI	r_g	-0.120	0.049	0.014	0.212*	0.212*	0.513**	-0.189*	1				
	r_p	-0.091	0.058	-0.005	0.074	0.175*	0.268**	-0.287**	1				
TGW	r_g	0.201*	0.366**	0.034	0.531**	0.368**	0.738**	0.645**	0.634**	1			
	r_p	0.163	0.273**	-0.025	0.340**	0.271**	0.534**	0.451**	0.398**	1			
PC	r_g	-0.224**	0.154	-0.280**	-0.239**	-0.331**	-0.391**	-0.148	0.031	-0.132	1		
	r_p	-0.151	0.028	-0.256**	-0.044	-0.137	-0.166	-0.177*	-0.080	-0.052	1		
SV	r_g	-0.028	0.354**	-0.228**	-0.195*	-0.320**	-0.322**	0.071	-0.258**	-0.148	0.899**	1	
	r_p	-0.031	0.098	-0.197*	-0.030	-0.171*	-0.175*	-0.077	-0.186*	-0.094	0.861**	1	
GYP	r_g	0.394**	0.486**	0.131	0.727**	0.429**	0.835**	0.711**	0.554**	0.994**	-0.081	-0.100	1
	r_p	0.288**	0.373**	0.067	0.400**	0.346**	0.505**	0.617**	0.567**	0.720**	-0.225**	-0.220**	1

*, ** significant at 0.05% and 0.01% level of significance, respectively

Table 4: Direct and indirect effects of yield component on grain yield in durum wheat

	DH	DM	PH	TIL/M	SL	NGS	BYP	HI	TGW	PC	SV	Genotypic Correlation with GYP
DH	**0.037**	-0.029	-0.001	-0.003	0.016	-0.042	0.466	-0.094	0.013	0.037	-0.005	0.394**
DM	0.020	**-0.053**	-0.002	-0.002	0.014	-0.043	0.445	0.039	0.024	-0.025	0.069	0.486**
PH	0.004	-0.008	**-0.011**	-0.0003	0.012	-0.036	0.155	0.011	0.002	0.046	-0.044	0.131
TIL/M	0.018	-0.012	-0.001	**-0.007**	0.012	-0.057	0.570	0.166	0.035	0.039	-0.038	0.727**
SL	0.014	-0.018	-0.003	-0.002	**0.041**	-0.080	0.295	0.166	0.024	0.054	-0.062	0.429**
NGS	0.014	-0.021	-0.004	-0.003	0.030	**-0.109**	0.476	0.401	0.049	0.064	-0.062	0.835**
BYP	0.021	-0.028	-0.002	-0.004	0.014	-0.062	**0.839**	-0.147	0.042	0.024	0.014	0.711**
HI	-0.004	-0.003	-0.0002	-0.001	0.009	-0.056	-0.158	**0.782**	0.042	-0.005	-0.050	0.554**
TGW	0.007	-0.020	-0.0004	-0.004	0.015	-0.080	0.541	0.496	**0.066**	0.022	-0.029	0.994**
PC	-0.008	-0.008	0.003	0.002	-0.014	0.042	-0.124	0.025	-0.009	**-0.164**	0.174	-0.081
SV	-0.001	-0.019	0.002	0.001	-0.013	0.035	0.059	-0.202	-0.010	-0.147	**0.194**	-0.100

DH = days to heading (N), **DM =** days to maturity (N), **PH =** plant height (cm), **TIL/M =** number of effective tiller per meter, **SL =** spike length (cm), **NGS =** number of grain per spike, **BYP** = biological yield per plot (g), **HI =** harvest index (%), **TGW** = 1000 grain weight (g), **PC =** protein content (%), **SV =** sedimentation value (ml) and **GYP =** grain yield per plot (g)

CONCLUSION

The analysis of variance revealed highly significant differences among the tested genotypes for all the traits. This indicated the presence of considerable genetic variability among the genotypes for various characters. High heritability associated with high genetic advance as per cent of mean was found for the characters viz., grain yield per plot and biological yield per plot which indicated the dominance of additive gene action, so that selection would be rewarded for improvement of these characters. Study of correlations showed that days to heading, days to maturity, spike length, number of effective tiller per meter, number of grain per spike, 1000 grain weight, biological yield per plot and harvest index were highly significantly and positively correlated with grain yield per plot at both phenotypic and genotypic levels among the characters studied. Path analysis studies revealed that positive and direct effect towards grain yield per plot was observed by days to heading, spike length, biological yield per plot, harvest index, 1000 grain weight and sedimentation value. Hence, characters viz., days to heading, spike length, biological yield per plot, harvest index, 1000 grain weight and sedimentation value turned out to be the major components traits for grain yield per plot and direct selection for these traits by plant breeder will be rewarded for improvement of yield and its attributing traits.

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