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CHARACTER ASSOCIATION AND PATH ANALYSIS FOR YIELD AND ITS CONTRIBUTING TRAITS IN F_2 SEGREGATING POPULATION OF BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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ABSTRACT

The present studywas conducted in *Rabi* 2021-2022 at Instructional Farm, of the Rajasthan College of Agriculture, MPUAT, Udaipur to determine the association among yield components and their direct and indirect influence on grain yield of bread wheat. The genotypes showed highly significant differences for all the traits under study showing that there is enough variability among genotypes for different traits. Association study revealed that the grain yield per plant had a positive and significant correlation with number of effective tillers per plant, spike length, number of spikelets per plant, length of awns, number of grains per spike, flag leaf area, 1000-grain weight, biological yield per plant, total protein content in grains and total chlorophyll content estimation at both genotypic and phenotypic level. The path coefficient analysis showed that the maximum positive direct effect on grain yield per plant was exerted by biological yield per plant, the number of grains per spike, number of spikelets per plant and flag leaf area. So these characters can be considered as selection criteria in improving the grain yield.

Key words: Bread wheat, variability, correlation, path coefficient, grain yield

Introduction

Wheat [*Triticum aestivum* L.] is the majoritykey food crop in the world which belongs to genus *Triticum* and family poaceae. Wheat is a self-pollinated, monocotyledonous plant that had originated from South West Asia. The genus *Triticum* is composed of diploid, tetraploid and allohexaploid species. So, polyploidy has played a dominant role in wheat evolution. There are different species of wheat, out of which only three *Triticum* species are mostly cultivated throughout the world. These are *Triticum aestivum* (bread wheat), *Triticum durum* (macroni wheat) and *Triticum dicoccum* (emmer wheat). Wheat (*Triticum aestivum* L. and *Triticum durum* L.) is the world's largest cultivated crop and world-wide staple food; provide 20% of total food calories to about 40% of the world population. It has excellent nutritional value with 12.1 percent protein, 1.8 percent lipids, 1.8 percent ash and 2.0 percent reducing sugars, 6.7 percent pentose, 59.2 percent starch, 70

percent total carbohydrate and 314 K cal/100 g food. It is also good source of vitamins as thiamine and vitamin B along with minerals which is zinc and iron.

Grain yield is a complex trait and is strongly influenced by many genetic and environmental factors. Thus, direct selection for yield can mislead and decelerate the pace of breeding program. Successful selection of high yielding genotypes depends on information available for genetic variability and the association of morpho-agronomic traits with grain yield. The degree of association between two or more variables is estimated by the correlation coefficient (r). Correlation and path coefficient analysis, when combined, provide a clearpicture of the inter-relationship and relative contribution of independent characters to the dependent variable, allowing a plant breeder to apply appropriate selection procedures for crop improvement. Correlation coefficients are commonly used in breeding studies to determine the relationship between grain yield and yield components, which aids in

selection to improve yield and its contributing characters at the same time. It is necessary to consider the implications of the inter-relationships of multiple characteristics, as well as path coefficients in order utilize the best combination of yield contributing characters in a single genotype.

Material and Method

Experimental Details

The experiment was conducted in randomized complete block design (RCBD) with three replications at Instructional Research Farm, Rajasthan College of Agriculture, Udaipur, during *Rabi* 2021-22. The experimental material consisted of F_2 population of three crosses *viz*; HD2967 × DBW 173, DBW 173 × Raj 4120 and Raj 3777 × Raj 4120, their six parentsand check HI 1544. These crosses were chosen on the basis of good GCA, SCA and heats us ceptibility index in F_1 generation. The F_2 population was grown in 20 rows of 2m length, while parents in 4 rows of 2m length by maintaining row to row spacing of 22cm. All the recommended package of practices was adopted to raise the healthy crop.

Data Collection

The observations were recorded on 100 plants from F_2 generation and 10 randomly selected competitive plants from parents plot in each replication for characters, *viz.,* plant height (cm), number of effective tillers per plant, spike length (cm), number of spikelets per plant, length of awns (cm), number of grains per spike, flag leaf area (cm^2), 1000-grain weight (g), biological yield per plant (g), grain yield per plant (g), harvest index (%), total protein content in grains (%) and total chlorophyll content estimation (mg/g), while days to 50% flowering and days to 75% maturity was recorded on plot basis.

Statistical Analysis

Correlation coefficient analysis:

The analysis of variance was worked out as per the method suggested by Panse and Sukhatme (1985). The phenotypic and genotypic correlation coefficients were computed from the phenotypic and genotypic variance and co-variances as according to Searle (1961).

Genotypic correlation coefficients between character X and Y

$$rxy(g) = \frac{Cov._{xy}(g)}{\sqrt{\sigma^2 g(x).\sigma^2 g(y)}}$$

Phenotypic correlation coefficients between character X and Y

$$rxy(p) = \frac{Cov._{xy}(p)}{\sqrt{\sigma^2 p(x).\sigma^2 p(y)}}$$

Where,

$r_{xy(g)}$ and $r_{xy(p)}$ denote genotypic and phenotypic correlation coefficients between X and Y characters, respectively.

$Cov_{xy(g)}$ and $Cov_{xy(p)}$ denote genotypic and phenotypic co-variances between X and Y characters, respectively.

$V_{x(g)}$ and $V_{x(p)}$ denote genotypic and phenotypic variances for characters X, respectively.

$V_{y(g)}$ and $V_{y(p)}$ denote genotypic and phenotypic variances for characters Y, respectively.

Test of significance

The significance of correlation coefficient was tested by the 't' test given by W.S. Gosset (1908).

Path coefficient analysis

The direct and indirect effects were estimated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). The following

Table 1: Analysis of variance for 15 characters in bread wheat.

S No.	Characters	Replication [2]	Genotype [9]	Error [18]
1	Days to 50% flowering	6.10	145.78**	2.14
2	Days to 75% maturity	1.30	194.24**	3.56
3	Plant height	11.03	188.62**	3.61
4	Number of effective tillers per plant	2.51	22.59**	1.05
5	Spike length	4.68	13.54**	1.45
6	Number of spikelets per plant	129.34	945.77**	73.62
7	Length of awns	1.98	10.04**	0.63
8	Number of grains per spike	3.08	146.88**	7.68
9	Flag leaf area	1.37	35.11**	4.07
10	1000-grain weight	1.81	29.76**	6.48
11	Biological yield per plant	4.74	225.06**	4.86
12	Grain yield per plant	2.48	114.39**	2.82
13	Harvest index%	26.70	237.01**	19.54
14	Total protein content in grains	0.04	6.95**	0.07
15	Total chlorophyll content in plants	0.01	0.37**	0.01
*, ** Significant at 5% and 1%, respectively				

Table 2: Genotypic (rg) correlation coefficient and Phenotypic (rp) correlation coefficient for different characters in bread wheat

SN	Character	R	DF	DM	PH	NET	SL	SPLP	LA	NGP	FLA	TW	BYPP	GYPP	HI	TPC	TCC
1	DF	rg		0.31		-0.73**	-0.72**	-0.76**	-0.87**	-0.40	-0.37	-0.86**	-0.72**	-0.38	0.15	-0.34	-0.44
		rp		0.28		-0.67**	-0.58**	-0.67**	-0.81**	-0.34	-0.29	-0.58**	-0.69**	-0.37	0.12	-0.32	-0.45
2	DM	rg			0.38	-0.25	0.31	-0.41	-0.24	-0.42	-0.55*	-0.43	-0.14	-0.31	-0.43	-0.13	-0.64**
		rp			0.35	-0.22	0.23	-0.34	-0.23	-0.37	-0.49*	-0.27	-0.11	-0.27	-0.35	-014	-0.60**
3	PH	rg				-0.49	-0.31	-0.71**	-0.55*	-0.94**	-0.94**	-0.57*	-0.60**	-0.95**	-0.98**	-0.85**	-0.89**
		rp				-0.46	-0.25	-0.62**	-0.49*	-0.83**	-0.85**	-0.47*	-0.57**	-0.90**	-0.86**	-0.81**	-0.86**
4	NET	rg					0.78**	0.85**	0.88**	0.53*	0.45	0.62*	0.89**	0.70**	0.16	0.75**	0.63**
		rp					0.67**	0.75**	0.69**	0.49*	0.42	0.52**	0.82**	0.67**	0.21	0.72**	0.54*
5	SL	rg						0.74**	0.84**	0.47	0.31	0.75**	0.95**	0.60*	-0.04	0.70**	0.37
		rp						0.64**	0.66**	0.30	0.26	0.45*	0.80**	0.55**	0.02	0.60**	0.28
6	SPLP	rg							0.98**	0.86**	0.84**	1.06**	0.96**	0.87**	0.45	0.74**	0.90**
		rp							0.81**	0.69**	0.66**	0.73**	0.81**	0.80**	0.46*	0.65**	0.78**
7	LA	rg								0.82**	0.76**	1.02**	0.92**	0.79**	0.35	0.73**	0.77**
		rp								0.62**	0.56**	0.62**	0.77**	0.67**	0.26	0.65**	0.70**
8	NGP	rg									1.08**	0.82**	0.71**	0.98**	0.92**	0.77**	0.97**
		rp									0.84**	0.70**	0.62**	0.84**	0.73**	0.73**	0.84**
9	FLA	rg										0.87**	0.67**	0.94**	0.90**	0.74**	1.02**
		rp										0.60**	0.50*	0.83**	0.83**	0.64**	0.84**
10	TW	rg											0.93**	0.84**	0.44	0.54	0.87**
		rp											0.64**	0.56**	0.27	0.39	0.59**
11	BYPP	rg												0.85**	0.33	0.81**	0.68**
		rp												0.80**	0.24	0.76**	0.65**
12	GYPP	rg													0.78**	0.91**	0.90**
		rp													0.77*	0.86**	0.85**
13	HI	rg															0.66**	0.84**
		rp															0.58**	0.71**
14	TPC	rg																0.76**
		rp																0.71**

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

equations were solved for estimating the various direct and indirect effects.

$$r_{1y} = P_{1y} + r_{12}P_{2y} + \ldots\ldots\ldots + r_{1p}P_{py}$$

$$r_{2y} = r_{21}P_{1y} + P_{2y} + \ldots\ldots\ldots + r_{2p}P_{py}$$

$$\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots$$

$$\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots$$

$$R_{py} = r_{p1}P_{1y} + r_{p2}P_{2y} + \ldots\ldots\ldots + P_{py}$$

Where,

P_{1y}, P_{2y} ……………P_{py} are direct effects of character 1,2, ………..p on Y and r_{1y}, r_{2y}…………r_{py} denote correlation coefficient between independent characters 1,2…….p and dependent character 'Y'.

Residual effect was calculated using the following formula:

$$1 = P^2Ry + SP_{iy}R_{iys}$$

$$P_{Ry} = \sqrt{1 - (P_{1y}r_{1y}) - (P_{2y}r_{2y}) \ldots\ldots\ldots (P_{iy}r_{iy})}$$

Where,

P_{Ry} is the residual effect

Y is the seed yield

Results and Discussions

ANOVA

The analysis of variance for fifteen characters are presented in Table 1. The genotypes showed highly significant differences for all the traits under study. Selection of these characters is useful for wheat improvement program.

Correlation Coefficient Analysis

During present investigation, genotypic and phenotypic correlation coefficient was worked out for different characters including grain yield. The genotypic correlation coefficient was generally higher than the respective phenotypic correlation coefficient. Similar results were also reported by Upadhayay *et al*., (2020) and Sharma *et al*., (2018).

The grain yield per plant had positive and significant correlation with flag leaf area, number of effective tillers per plant, spike length, number of spikelets per plant, length of awns, number of grains per spike, 1000-grain weight, biological yield per plant, harvest index, total protein content in grains and total chlorophyll content at both genotypic and phenotypic levels. Similar findings were also reported by Sabit *et al*., (2017) Sharma *et al*., (2018), Baye *et al*., (2020) and vagela *et al*., (2021).

Days to 50% flowering showed negative and significant correlation with number of effective tillers per

plant, spike length, number of spikelets per plant, length of awns, 1000-grain weight and biological yield per plant at both genotypic and phenotypic level. Similar findings were also reported by Wani *et al*., (2018) and Vagela *et al*., (2020). Days to 75 % maturity showed negative and significant correlation with flag leaf area and total

Table 3: List of genotypic correlation among various characters in Bread Wheat.

S No.	Characters	Significantly positive correlation	Significantly negative correlation
1	Days to 50% flowering		NET, SL, BYPP
2	Days to 75% maturity		SL, NGP, TW
3	Plant height (cm)		SPLP, NGP, GYPP
4	Number of effective tillers per plant	SPLP, LA, TW, TPC	
5	Spike length (cm)	LA, TE, BYPP, GYPP	
6	Number of spikelets per plant	NGP, FLA, TW, TPC, TPP	
7	Length of awns (cm)	NGP, FLA, TW	
8	Number of grains per spike	FLA, TW, BYPP, TCC	
9	Flag leaf area (cm²)	TW, BYPP, GYPP, TCC	
10	1000-grain weight (g)	BYPP, GYPP, TPC, TCC	
11	Biological yield per plant (g)	GYPP, TPC, TCC	
12	Grain yield per plant (g)	HI, TPC, TCC	
13	Harvest index (%)	TPC, TCC	
14	Total protein content in grains (%)	TCC	

DF- Days to flowering; DM- Days to 75% maturity; PH-Plant height (cm); NET -Number of effective tillers per plant; SL-Spike length (cm); SPLP: Number of spikelets per plant; LA: Length of awns (cm); NGP: Number of grainsper spike; FLA: Flag leaf area (cm²); TW= Test weight; BYPP = Biological yield per plant (g); GYPP: Grain yield per plant (g); HI: Harvest index; TPC: Total protein content ingrains(%); TCC: Totalchlorophyllcontentin plants (mg/g).

Table 4: Genotypic path analysis for Grain yield per plant in bread wheat.

S. No.	Character	Days to 50% flowering	Days to 75% maturity	Plant height	No. of effective tillers per plant	Spike length	No. of spikelets per plant	Length of awns	No. of grains per spike	Flag leaf area	Test weight	Biological yield per plant	Total protein content	Total chlorophyll content	r with grain yield per plant
1	Days to 50% flowering	-0.2895	-0.0336	-0.0751	0.0456	0.0135	-0.1624	0.0432	-0.1573	-0.0624	0.2614	-0.3683	0.0646	0.3450	-0.3752
2	Days to 75% maturity	-0.0898	-0.1083	-0.3711	0.0153	-0.0058	-0.0869	0.0117	-0.1648	-0.0943	0.1294	-0.0697	0.0246	0.5014	-0.3083
3	Plant height	-0.0220	-0.0407	-0.9878	0.0304	0.0058	-0.1520	0.0271	-0.3683	-0.1603	0.1725	-0.3096	0.1608	0.6968	-0.9474**
4	No. of effective tillers per plant	0.2127	0.0267	0.4834	-0.0621	-0.0145	0.1813	-0.0433	0.2064	0.0771	-0.1889	0.4586	-0.1427	-0.4937	0.7012*
5	Spike length	0.2095	-0.0339	0.3054	-0.0481	-0.0187	0.1578	-0.0418	0.1840	0.0535	-0.2291	0.4859	-0.1314	-0.2893	0.6039
6	No. of spikeletes per plant	0.2192	0.0439	0.7000	-0.0525	-0.0137	0.2145	-0.0484	0.3368	0.1431	-0.3218	0.4912	-0.1401	-0.7035	0.8686**
7	Length of awns	0.2528	0.0255	0.5422	-0.0543	-0.0158	0.2099	-0.0495	0.3218	0.1291	-0.3084	0.4726	-0.1374	-0.6000	0.7887**
8	No. of grains per spike	0.1165	0.0457	0.9308	-0.0328	-0.0088	0.1848	-0.0407	0.3909	0.1839	-0.2477	0.3639	-0.1455	-0.7587	0.9822**
9	Flag leaf area	0.1057	0.0597	0.9269	-0.0280	-0.0058	0.1797	-0.0374	0.4208	0.1708	-0.2636	0.3454	-0.1391	-0.7953	0.9397**
10	Test weight	0.2491	0.0461	0.5610	-0.0386	-0.0141	0.2273	-0.0502	0.3189	0.1483	-0.3037	0.4786	-0.1016	-0.6761	0.8450**
11	Biological yield per plant	0.2078	0.0147	0.5961	-0.0555	-0.0177	0.2053	-0.0455	0.2772	0.1150	-0.2832	0.5131	-0.1535	-0.5273	0.8465**
12	Total protein content	0.0990	0.0141	0.8403	-0.0469	-0.0130	0.1590	-0.0359	0.3009	0.1257	-0.1633	0.4167	-0.1890	-0.5955	0.9121**
13	Total chlorophyll content	0.1279	0.0695	0.8818	-0.0393	-0.0069	0.1933	-0.0380	0.3799	0.1740	-0.2630	0.3466	-0.1442	-0.7805	0.9012**

Residual effect = 0.483

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

chlorophyll content at both genotypic and phenotypic level. Similar findings were also reported by Vagela *et al*., (2020).

The plant height showed negative and significant correlation with number of spikelets per plant, length of awns, number of grains per spike, flag leaf area, 1000-grain, biological yield per plant, grain yield per plant, harvest index, total protein content in grains and total chlorophyll content estimation at both genotypic and phenotypic level. Similar findings were also reported by Vagela *et al*., (2020) and Singh *et al*., (2021).

Path Analysis

The correlation analysis provides information which is incomplete in the sense that they do not through light on the underlying causes that are operative for the various inter-relationship. The path coefficient analysis breaks the correlation coefficient into direct and indirect effects and thus provides the causal basis of various inter-relationships. Path coefficient analysis was performed to assess the direct and indirect effects of different characters on grain yield per plant.

Direct Effect

The path coefficient analysis showed that the maximum positive direct effect on grain yield per plant was exerted by biological yield per plant, the number of grains per spike, number of spikelets per plant and flag leaf area. Similar findings were also reported by Ayer *et al*., (2017), Tabassum *et al*., (2018) and Singh *et al*., (2021).

However, traits like plant height, total chlorophyll content estimation, 1000-grain weight, days to 50% flowering, total protein content in grains, days to 75% maturity, number of effective tillers per plant, length of awns and spike length exhibited negative direct effect on grain yield per plant. Similar findings were also reported by Patel *et al*., (2020), Singh *et al*., (2021) and Vagela *et al*., (2021).

Indirect effect

The maximum positive indirect effect was noted by number of grains per spike through plant height followed by flag leaf area via plant height, total chlorophyll content through plant height, total protein content in grains through plant height and number of spikelets per plant via plant height. Present findings are in accordance with the findings of Ibrahim *et al*., (2019) and Baye *et al*., (2020).

Residual effect

The residual effect (R= 0.483) indicated that 51.7% variability was demonstrated by the traits considered for path study.

Conclusion

Based on the above-mentioned findings, it may concluded that number of spikelets per plant, number of grains per spike, flag leaf area and biological yield per plant exerted positive direct effect along with positive and significant correlation on grain yield per plant. These characters must be given preference in selection while selecting the superior genotypes. Therefore, these particular traits should be considered for enhancing yields in the wheat breeding program.

Acknowledgement

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