

Association and diversity studies in wheat

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ABSTRACT : The 169 wheat genotypes including checks *viz.*, DWR 162 and Kalyansona evaluated for 11 traits. The correlation studies revealed that grain yield per plot was positive and significantly associated with days to 50 per cent flowering and negatively significant with plant height, peduncle length and protein content. The maximum direct effect on grain yield was exhibited, by days to 50 per cent flowering followed by number of tillers per meter length. Hence, dwarf varieties are preferred, as they could withstand lodging, this association could be used advantageous for development of dwarf varieties. Following the cluster analysis all the 169 genotypes showed that the genotypes were grouped into twelve clusters, with the variable number of genotypes in each cluster. The inter cluster distance was found to be highest between cluster VIII and XI; hence accessions from these clusters are suggested to obtain improvement in seed yield of wheat.

Key Words : Wheat, Correlation, Path analysis, Genetic divergence, Cluster

How to cite this paper : Kolakar, Shashikala S., Hanchinal, R.R. and Nadukeri, Sadashiv (2012). Association and diversity studies in wheat, *Adv. Res. J. Crop Improv.*, **3** (2) : 79-83.

Paper History : Received : 28.05.2012; Revised : 10.08.2012; Accepted : 05.10.2012

Wheat (*Triticum aestivum* L.) is an important cereal crop of cool climates, and plays an important role in the food and nutritional security of India. Wheat, a cereal grass of the *Graminae* (*Poaceae*) family and of the genus *Triticum*, is the world's largest cereal crop.

India's productivity and the prominent position, it holds in the international food grain trade. Yield is one such character that results due to the actions and interactions of various component characters (Grafius, 1960). It is now realized that sustaining as well as increasing productivity may be essential. The knowledge of factors responsible for high yields has been rendered difficult as yield is a complex character.

Therefore, attaining higher yield levels, the breeder is required to deal the complex situation through handling of the yield components. The studies of characters association provide information about the estimates of interrelationship of various yield components in manifestation of yield. Path analysis focussed direct and indirect effect of component traits on yield. With this objective the present investigation has been taken in the wheat genotypes. Knowledge of genetic diversity in a crop species is fundamental to its improvement. Evaluation of genetic diversity levels among adapted, elite germplasm can provide predictive estimates of genetic variation among segregating progeny for pure-line cultivar development.

According to Franco *et al.* (2001) the study of phenotypic and genotypic diversity to identify groups with similar genotypes is important for conserving, evaluating and utilizing genetic resources; for studying the diversity of pre-breeding and breeding germplasm; and for determining the uniqueness and distinctness of the phenotypic and genetic constitutions of genotypes with the purpose of protecting a breeders intellectual property rights.

RESEARCH PROCEDURE

The material for the present investigation consisted of 169 wheat genotypes along with checks DWR 162 and Kalyansona, collected from Directorate of wheat research, Karnal. The experiment was laid out in an Simple lattice design with two replications. Each genotype in each replication was grown in a plot of 3 rows of 2 meter length each with a spacing of 23 cm between rows, at Wheat Improvement Project, Main agricultural Research station Dharwad, during 2004-05. All the agronomic practices were followed during the crop growth period. Observations were recorded on five randomly selected competitive plants for eleven characters days to 50 per cent flowering(X_1), days to maturity(X_2), plant height(X_3), peduncle length (X_4), number of productive tillers per meter(X_5), spike

length(X_6), number of spike lets per spike(X_7), number of grains per spike (X_8), 1000 grain weight(X_9), protein content (X_{10}) and grain yield per plot (X_{11}).

Genotypic and phenotypic correlations were calculated by using the formula given by Weber and Moorthy (1952), path coefficient analysis was carried out to know the direct and indirect effects on yield as suggested by Wright (1921), Mahalanobis (1936) D^2 – statistic was used for assessing the genetic divergence between genotypes, as illustrated by Dewey and Lu (1959).

RESEARCH ANALYSIS AND REASONING

The results obtained from the present investigation have been discussed below:

Correlation co-efficient analysis:

A close view of result (Table 1) indicated the grain yield per plot exhibited significant association in positive direction with days to 50 per cent flowering only at genotypic level and at phenotypic level no such association was noticed indicating influence of environment on association. This result was in confirmation with the report of Khan *et al.* (1999) and Nayem *et al.* (2003), respectively. Wherein, they observed positive and significant association of grain yield with days to 50 per cent

flowering. None of the traits other than days to 50 per cent flowering exhibited significant association with grain yield per plot except the traits such as plant height, peduncle length, protein content exhibited negative significant association with grain yield per plot.

The plant height and peduncle length had shown significant negative association with grain yield. These results are in confirmation with the Mahammad and Shahid *et al.* (2002) who reported strong negative association for plant height, Naik (2000) and Gautam and Sethi (2002) has reported significant negative and negative association respectively for peduncle length. Further, plant height exhibited positive significant association with peduncle length, 1000 grain weight, protein content and positive association with grains per spike indicating selection of genotypes through these characters could be effective.

Path co-efficient analysis:

Among the various traits studied (Table 2 and 3) days to 50 per cent flowering had high positive direct effect followed by productive tillers per meter length and 1000 grain weight at both genotypic and phenotypic levels on grain yield. Out of these traits all the traits had shown significant association except days to 50 per cent flowering which had significant association only at genotypic level. The results of high direct

Table 1 : Phenotypic and genotypic correlation coefficient among yield, yield components and protein content in wheat

		X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
X_1	P	1.000	0.788**	-0.128	-0.170*	-0.227**	0.173*	0.408**	0.138	0.063	-0.086	0.146
	G	1.000	0.794**	-0.131	-0.188*	-0.240**	0.183*	0.445**	0.154*	0.089	-0.104	0.169*
X_2	P		1.000	0.001	-0.131	-0.182*	0.235**	0.370**	0.108	0.061	-0.006	0.041
	G		1.000	0.000	-0.140	-0.189*	0.245**	0.409**	0.118	0.077	-0.011	0.044
X_3	P			1.000	0.477**	0.088	0.001	-0.113	0.040	0.167*	0.166*	-0.250**
	G			1.000	0.527**	0.095	-0.004	-0.137	0.061	0.210**	0.184*	-0.295**
X_4	P				1.000	0.100	-0.217**	-0.249**	-0.157*	0.143	-0.098	-0.160
	G				1.000	0.103	-0.241**	-0.306**	-0.188*	0.188*	-0.145	-0.195*
X_5	P					1.000	0.056	-0.018	-0.081	0.015	0.083	0.078
	G					1.000	0.053	-0.028	-0.102	0.012	0.092	0.087
X_6	P						1.000	0.312**	0.096	-0.131	0.065	0.008
	G						1.000	0.374**	0.106	-0.187*	0.077	-0.008
X_7	P							1.000	0.257**	-0.120	0.027	0.124
	G							1.000	0.300**	-0.154*	0.012	0.136
X_8	P								1.000	-0.139	0.041	0.020
	G								1.000	-0.184*	0.054	0.027
X_9	P									1.000	-0.137	0.094
	G									1.000	-0.174*	0.096
X_{10}	P										1.000	-0.330**
	G										1.000	-0.381**
X_{11}	P											1.000
	G											1.000

* and ** indicate significance of values at P=0.05 and 0.01, respectively

P-Phenotypic and G- Genotypic

Table 2 : Phenotypic path of different yield components and protein content on grain yield in wheat

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	rp
X ₁	0.166	-0.088	0.018	0.021	-0.034	-0.004	0.031	0.002	0.006	0.027	0.146
X ₂	0.131	-0.111	0.000	0.016	-0.027	-0.005	0.028	0.002	0.006	0.002	0.041
X ₃	-0.021	0.000	-0.141	-0.058	0.013	0.000	-0.009	0.001	0.016	-0.052	-0.250**
X ₄	-0.028	0.015	-0.067	-0.122	0.015	0.005	-0.019	-0.003	0.014	0.031	-0.160*
X ₅	-0.038	0.020	-0.012	-0.012	0.149	-0.001	-0.001	-0.001	0.001	-0.026	0.078
X ₆	0.029	-0.026	0.000	0.026	0.008	-0.022	0.024	0.002	-0.012	-0.020	0.008
X ₇	0.068	-0.041	0.016	0.030	-0.003	-0.007	0.076	0.004	-0.011	-0.009	0.124
X ₈	0.023	-0.012	-0.006	0.019	-0.012	-0.002	0.020	0.016	-0.013	-0.013	0.020
X ₉	0.010	-0.007	-0.024	-0.017	0.002	0.003	-0.009	-0.002	0.095	0.043	0.094
X ₁₀	-0.014	0.001	-0.023	0.012	0.012	-0.001	0.002	0.001	-0.013	-0.313	-0.330**

* and ** indicate significance of values at P=0.05 and 0.01, respectively

X₁-Days to 50% flowering

X₂-Days to maturity

X₃-Plant height

X₄-Peduncle length

X₅-Productive tillers per meter length

X₇-Number of spikelets per spike

X₈-Number of grains per spike

X₉-1000grain weight

X₁₀-Protein content

X₁₁-Yield per plot

X₆-Spikelength

Table 3 : Genotypic path of different yield components and protein content on grain yield in wheat

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	rg
X ₁	0.193	-0.102	0.018	0.034	-0.043	-0.008	0.027	0.005	0.008	0.038	0.169*
X ₂	0.153	-0.128	0.000	0.025	-0.034	-0.011	0.024	0.003	0.007	0.004	0.044
X ₃	-0.025	0.000	-0.139	-0.094	0.017	0.000	-0.008	0.002	0.020	-0.067	-0.295**
X ₄	-0.036	0.018	-0.073	-0.179	0.019	0.011	-0.018	-0.006	0.017	0.052	-0.195*
X ₅	-0.046	0.024	-0.013	-0.018	0.179	-0.002	-0.002	-0.003	0.001	-0.033	0.087
X ₆	0.035	-0.031	0.001	0.043	0.010	-0.045	0.022	0.003	-0.017	-0.028	-0.008
X ₇	0.086	-0.052	0.019	0.055	-0.005	-0.017	0.060	0.009	-0.014	-0.004	0.136
X ₈	0.030	-0.015	-0.008	0.034	-0.018	-0.005	0.018	0.029	-0.017	-0.020	0.027
X ₉	0.017	-0.010	-0.029	-0.034	0.002	0.008	-0.009	-0.005	0.093	0.063	0.096
X ₁₀	-0.020	0.001	-0.026	0.026	0.016	-0.003	0.001	0.002	-0.016	-0.362	0.381**

* and ** indicate significance of values at P=0.05 and 0.01, respectively

X₁-Days to 50% flowering

X₂-Days to maturity

X₃-Plant height

X₄-Peduncle length

X₅-Productive tillers per meter length

X₆-Spikelength

X₇-Number of spikelets per spike

X₈-Number of grains per spike

X₉-1000grain weight

X₁₀-Protein content

X₁₁-Yield per plot

Table 4: Intra (diagonal) and inter cluster distances for 11 characters in wheat genotypes

	Grp1	Grp2	Grp3	Grp4	Grp5	Grp6	Grp7	Grp8	Grp9	Grp10	GRP11	Grp12
Grp1	6.494	750.96	577.43	744.43	748.04	751.47	740.57	1037.34	501.68	422.32	1189.08	606.45
Grp2		188.95	830.56	909.04	864.36	951.21	938.87	1181.43	796.32	652.54	1301.03	435.22
Grp3			157.64	853.92	815.37	776.01	786.08	1020.66	620.45	598.74	1255.92	719.22
Grp4				174.98	934.79	912.99	851.58	1154.81	695.48	723.42	505.42	843.82
Grp5					141.41	904.81	901.27	1125.86	693.77	360.57	1282.29	759.74
Grp6						205.49	937.01	349.52	772.56	728.42	1258.19	873.87
Grp7							169.57	1158.30	323.29	726.57	1226.21	827.98
Grp8								0.000	1030.51	997.42	1450.95	1120.04
Grp9									0.000	468.293	1112.92	659.49
Grp10										0.000	1139.82	526.43
GRP11											0.000	1238.56
Grp12												0.000

positive effect of days to 50 per cent flowering on grain yield at both genotypic and phenotypic levels supported by work of Chaturvedi and Gupta (1995) and Halloli (1997). So direct selection of genotypes for grain yield through days to 50 per cent flowering could be effective.

Plant height and peduncle length had shown negative direct effects on grain yield per plot hence, dwarf varieties are preferred, as they could withstand lodging; this association could be used advantageous for development of dwarf varieties.

Cluster analysis:

Based on D^2 values 169 wheat genotypes were grouped into twelve clusters. Among the clusters, cluster III was largest consisting of 28 genotypes followed by cluster II, IV, V, VI and VII with 26 genotypes while the cluster I had 6 genotypes. The remaining clusters VIII, IX, XI and XII were solitary with the single genotype. This revealed the presence of divergent genotypes with in different clusters, the formation of solitary clusters may be due to total isolation preventing the gene flow or intensive natural/human selection for diverse adaptive complexes. The inter cluster D^2 values also ranged widely with minimum value of 323.29 between cluster VII and IX and maximum value of 1450.95 between clusters VIII and XI indicated high diversity among the genotypes (Table 4). Cluster VIII and XI with single genotype each were the most divergent groups

with a maximum inter cluster distance (1450.95). The genotype HI 8381 (cluster VIII) had higher grain yield per plot, days to 50 per cent flowering, days to maturity. Whereas, the genotype HB208 in cluster XI had low plant height, peduncle length and higher 1000 grain weight. It is desirable to select accessions from clusters showing high inter cluster distance (cluster VIII and cluster XI) and also with high grain yield as parents in recombination breeding programmes for obtaining desirable segregants. In conformity with this result earlier Sharma *et al.* (1998) also reported that the genotypes of heterogenous origin/ place of release and of different ploidy levels often grouped together in the same cluster, suggesting some degree of ancestral relationship between the genotypes. But, Murthy and Arunachalam (1966) were of the opinion that the wide adaptability would be possible due to factors like heterogeneity, genetic architecture of populations, past selection history, developmental traits and degrees of general combining ability. It appeared that varieties having same geographical origin differed and possessed wide divergence factors, since rapid ecotype differentiation was taking place even in the absence of reproductive isolation (Bennet, 1970).

Hybridization between genotypes of divergent clusters will lead to accumulation of favourable genes in a single varieties involving large number of divergent lines instead of closely related ones.

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