

Hierarchical Clustering, Association and Pedigree Analyses under Water Stress and Irrigated Environments in Wheat

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Abstract : Forty wheat varieties were evaluated under different moisture regimes to study water stress resilient genotypes with diversity, trait interrelationship and also looking for ancestral lines serving water stress tolerant genetic base of present day cultivars. The variety HS490 (4.80 g) exhibited the highest grain yield/plant under water stress environment followed by GW273 (4.26 g), DPW621-50 (4.18 g), Raj 3765 (4.07 g), Raj 3777 (4.07 g) etc. Under water limited environment, the promising genotypes Raj 3765, PBW 373 and Raj 4037 were grouped in same cluster, while the genotypes viz. HS 490, GW 273 and WR 544 were observed diverse and may be picked as one of the parents for water use efficiency breeding programmes. Under water stress, the highest significant positive genotypic correlation coefficients with grain yield were depicted by biological yield followed by spikelets/spike ($r = 0.69^{**}$) and spike length ($r = 0.58^{**}$), respectively. Path analysis suggested that directional selection for spike length, tiller/m and biological yield in water stress, while in addition to these grains/spike and 1000 grain weight would be helpful for grain yield enhancement. In pedigree analysis of DBW 16, Raj 3765, Raj 4037, WR544 etc. the ancestral lines HD 1962, E4870 and K65 were found as common while, for HS490 and PBW373 the parental lines Kalyansona and Bluebird were regarded as contributors for water stress resilience.

Keywords: Wheat, hierarchical clustering, heritability, GCV, pedigree analysis.

INTRODUCTION

Under changing climatic conditions with burgeoning population and shrinking natural resources, water stress is one of the most limiting factor for sustainable crop productivity and a key constraint to the global food security (Araus *et al.* 2002, Blum 2005, Chakraborty and Newton 2011, Smol 2012). Cluster analysis refers to grouping of the genotypes by maximizing the inter group variances and mainly performed using either distance or model based approaches (Mohammadi and Prasanna 2003). The distance based approach can be further divided into hierarchical or non-hierarchical methods. Hierarchical Ward's method (based on the sum of squares) using squared Euclidean distances is a good method and widely used for clustering different genotypes and preparing dendro grams for quick view of grouping of different genotypes (Mohammadi and Prasanna 2003). Wheat is an auto gamous crop and increasing effect genes and allelomorphs are distributed in the

form of multitude of pure lines (Ahlawat *et al.* 2008). The plant ideotype for drought stress breeding is always not perfect and inter relationship studies are in variably required to design fruitful breeding programmes (Blum 2005). In the breeding programmes to develop water stress resilience strains, it is better option to identifying the traits directly contributing towards grain yield under water stress and as well as under favourable environments. Inter relationship study reveals the association among the quantitative traits, which is quite useful in crop improvement programmes during selection for desirable plant types in field. The real multiplicative inter relationship can be concluded by further refinement of the genotypic correlation coefficients into direct and indirect effects in path coefficient analysis (Dewey and Lu 1959). In addition, the prior knowledge of clustering among genotypes is always helpful to design new breeding programmes with diverse sources of water stress

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resilience. The identified prominent sources were further traced back for their pedigree analysis to find out the common ancestors being contributors for hardness to water stress. Therefore, the present study was carried out to study the response of *elite* bread wheat varieties under different moisture regimes, while also generating information of clustering of prominent wheat varieties with interrelationship and pedigree analyses.

MATERIALS AND METHODS

During *rabi*, 2011-12, 40 *elite* wheat varieties of different zones were grown in three environments/moisture regimes, which were created by skipping irrigations at different crop growth stages. E1 was the main water stress environment, where single irrigation was applied at 23 days after sowing (DAS), while in E2 two irrigations were given at CRI and heading stages. The third environment (E3) was favourable environment, where recommended irrigations were followed. The genotypes were evaluated in randomized complete block design (RCBD) with two replications in paired rows of 2 meter length in each environment separately. The observations were recorded on eight quantitative traits *viz.* spike length (cm), peduncle length (cm), tillers/meter, spikelets/spike, grains/spike, 1000 grain weight (g), biological yield/plant (g) and grain

yield/plant (g). The analysis of variance (ANOVA) for experimental design was carried out as per standard procedures. Heritability ($h^2_{b.s.}$), phenotypic and genotypic coefficient of variation (PCV and GCV), genetic advance (GA at 5 per cent, $K = 2.06$) and correlation coefficients were computed as per standard procedures (Falconer 1989, Singh and Chaudhary 1985). Interrelation studies were further refined using path coefficient analysis considering grain yield as the resultant variable of multiplicative interactions per the method described by Dewey and Lu (1959). The hierarchical cluster analysis was performed using Ward's method (Ward 1963).

RESULTS AND DISCUSSION

ANOVA and *per se* Performances

Analysis of variance revealed significant differences ($p < 0.01$) for all the characters indicating substantial genetic variation among the genotypes under different environments. The variety HS 490 (4.80 g) depicted the highest grain yield/plant under water stress environment E1 followed by GW 273 (4.26 g), DPW621-50 (4.18 g), Raj 3765 (4.07 g), Raj 3777 (4.07 g) etc. Whereas, in E2, the genotypes WR544, Raj 4037, PBW373, DBW16, UP2338 etc. were top five high yielders. Under irrigated conditions the genotype HD 2967 (10.40 g) was high yielder followed by DPW 621-50 (10.31 g), DBW 17 (10.18 g), GW273

Table 1
(PCV and GCV %), GA and broad sense heritability ($h^2_{b.s.}$) estimates in bread wheat

Genetic parameters	Spike length	Peduncle length	Tillers/m	Spikelets /spike	Grains /spike	1000 grain wt.	Biological yield/plant	Grain yield/plant
<i>Environment 1</i>								
PCV (%)	14.49	26.61	13.20	13.88	15.45	8.06	18.29	17.30
GCV (%)	10.19	25.65	11.00	12.21	13.14	6.94	12.55	12.43
GA (K = 2.06)	1.37	6.30	17.16	3.24	10.28	3.71	1.64	0.65
$h^2_{(b.s.)}$	0.50	0.93	0.69	0.77	0.72	0.74	0.47	0.51
<i>Environment 2</i>								
PCV (%)	12.35	23.05	15.19	12.19	12.57	4.90	12.88	11.55
GCV (%)	9.45	21.10	13.65	10.65	8.78	3.86	9.04	8.12
GA (K = 2.06)	1.61	5.52	28.27	3.01	7.06	2.18	2.14	0.73
$h^2_{(b.s.)}$	0.58	0.83	0.81	0.76	0.48	0.62	0.49	0.49
<i>Environment 3</i>								
PCV (%)	9.38	21.34	15.75	11.64	12.28	3.65	10.14	8.83
GCV (%)	6.94	20.62	14.92	10.74	11.29	2.71	7.91	7.54
GA (K = 2.06)	1.26	6.23	39.08	3.46	14.32	1.58	3.01	1.18
$h^2_{(b.s.)}$	0.55	0.93	0.89	0.85	0.85	0.55	0.61	0.73
<i>Pooled</i>								
PCV (%)	12.50	23.35	14.11	12.29	12.44	5.07	11.67	10.06
GCV (%)	9.55	22.16	12.67	10.91	10.12	3.97	7.87	6.99
GA (K = 2.06)	1.60	5.98	26.34	3.15	9.47	2.20	1.79	0.62
$h^2_{(b.s.)}$	0.58	0.90	0.81	0.79	0.66	0.62	0.46	0.48

(9.95 g), Raj 4037 (9.93 g) etc. The pooled mean spike and peduncle lengths were exhibited as 10.68 cm and 13.80 cm, while average grains/spike, 1000 grain weight and biological yield/plant were depicted as 55.81, 34.30 g and 16.40 g, respectively. The highest pooled mean grain yield/plant was observed as 6.21 g, which ranged from 4.98 to 7.05 g.

Genetic Parameters

After perusal of data in Table 1, it could be assumed that the heritability estimates deviated more for the traits *viz.* tillers/m, spikelets/spike, grains/spike, 1000 grain weight and grain yield in different environments.

In general, the estimates of PCV were higher than GCV for all the characters, which revealed the influence of water stress on all the metric traits. The heritability estimates for spike length and grain yield in E1, E2 and E3 were exhibited as 0.51 and 0.50, 0.49 and 0.58 and 0.73 and 0.55, respectively (Table 1). The water stress played significant role for the expression of the characters namely spike length, tillers/m, 1000 grain weight, biological yield/plant and grain yield as the ratio of PCV and GCV showed linear increase from water stress to irrigated conditions. The highest pooled PCV per cents were observed for peduncle length (23.35) followed by tillers/meter (14.11), spike length (12.50) and grains/spike (12.44) (Table 1). Similarly, the highest GCV per cent were also depicted by peduncle length (22.16) followed by tillers/meter (12.67) and spikelets/spike (10.91).

Hierarchical Clustering

The non-hierarchical methods are based on partitioning of the samples, while the hierarchical methods are based on either agglomerative or divisive approaches (Zait and Messatfa 1997). Ward's method is based on the sum of squares between the two clusters, summed over all variables (Khodadadi *et al.* 2011). The perusal of dendrograms in environments E1, E2, E3 and on pooled basis depicted that the 40 bread wheat genotypes were grouped into major two clusters and further incisions revealed seven small sub-clusters in E1, E2 and E3 while on pooled basis the genotypes were grouped into eight small sub-clusters. The genotypes namely *viz.* HS 490, UP 2338 and GW 273 were grouped into same major cluster in all three environments and pooled basis (Fig. 1). For irrigated conditions, the mega wheat varieties of north western plain zone

(NWPZ) namely DBW17, HD2967, DPW621-50 etc. were grouped nearly and similarly central zone varieties *viz.* MP4010, HI1531 and Lok1 were also grouped in same cluster under irrigated conditions. The central zone varieties namely MP4010, HI1531 and Lok1 were also grouped closely under water limited environment (E1). Under water limited environment, the promising genotypes Raj3765, PBW373 and Raj 4037 were grouped in same cluster, while DBW16 and Raj 3777 were contained in same cluster. The other resilient genotypes *viz.* HS490, GW273 and WR544 were observed diverse and grouped in separate clusters. Genetic diversity is an essential phenomenon and crucial to obtain heterotic combinations with complementary gene action and dispersed genes among the parental lines (Kallesh *et al.* 2012, Singh *et al.* 2010).

Interrelationship Studies

The genotypic and phenotypic correlation coefficients among different yield components were largely affected by the moisture regimes. In E1, the highest significant positive genotypic correlation coefficients with grain yield were depicted by biological yield ($r = 0.93^{**}$) followed by spikelets/spike ($r = 0.69^{**}$) and spike length ($r = 0.58^{**}$), respectively. In E2, the highest significant and positive genotypic correlation coefficients with grain yield were registered by biological yield ($r = 0.96^{**}$) followed by spikelets/spike ($r = 0.60^{**}$), grains/spike ($r = 0.45^{**}$) and peduncle length ($r = 0.37^*$), respectively. In favourable environment E3, the genotypic correlation coefficients of the characters *viz.* biological yield, 1000 grain weight, grains/spike, spike length and spikelets/spike were significantly and positively associated with grain yield. These results are in agreement with Hassan *et al.* 2004, Kashif and Khaliq 2004, Singh *et al.* 2010 and Khan and Naqvi 2012. The highest pooled significant and positive genotypic correlation coefficients with grain yield were exhibited by biological yield ($r = 0.94^{**}$) followed by grains/spike ($r = 0.69^{**}$), spikelets/spike ($r = 0.65^{**}$), spike length ($r = 0.41^{**}$) and 1000 grain weight ($r = 0.36^*$), respectively. Genotypic correlations showed that the traits biological yield/plant and spikelets/spike were positively associated with grain yield under different environments. The character grains/spike was found associated under medium water stress and irrigated conditions, while 1000 grain weight was correlated under irrigated environment only.

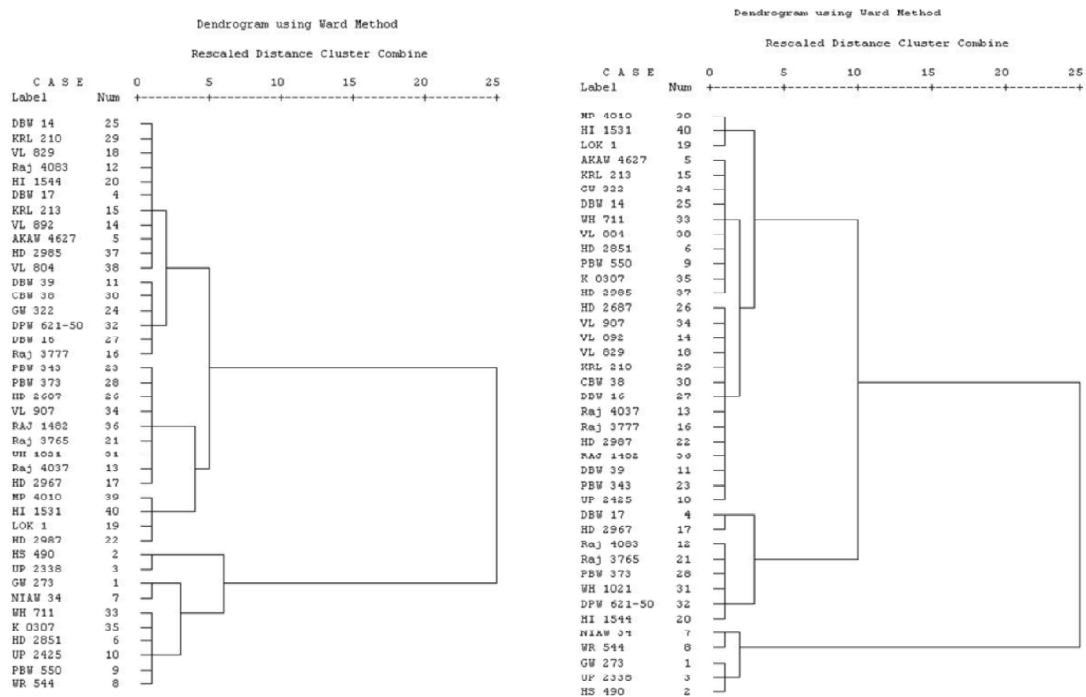


Figure 1: Ward’s dendrogram for water limiting (E1) and irrigated conditions (E3)

Table 2
List of water stress varieties with pedigree

Variety	Pedigree
DBW 16	RAJ3765/WR484//HUW468
GW 273	CPAN2084/VW205
HS 490	HS364/HPW114//HS240/HS346
PBW 373	ND/VG9144//KAL/BB/3/YCO”S’/4/VEE#S”S”
RAJ 3765	HD2402/VL639
RAJ 3777	RAJ3160/HD2449
RAJ 4037	DL788-2/RAJ3717
WR 544	KALYANSONA/HD1999//HD2204/DW38

In the lime light of established genotypic correlation coefficients, the association among the yield components were further refined in “standardized partial regression coefficient” (path coefficient)(Singh and Chaudhary 1985). For E1, the highest positive direct effects were exhibited by biological yield (1.31) followed by grains/spike (0.19), spike length (0.09) and tillers/m (0.02) on grain yield under water stress conditions. The character spikelets/spike showed negative direct effects (-0.35) and contributed through spike length, grains/spike, 1000 grain weight and biological yield/plant towards grain yield. The traits viz. tillers/m, spikelet/spike, 1000 grain weight and biological yield contributed positive direct effects in medium stress environment (E2), while grains/spike contributed through peduncle length, tillers/m, spikelets/spike, 1000

grain weight and biological yield. Under irrigated conditions spike length, 1000 grain weight, grain/spike and biological yield/plant were depicted positive direct effects. Naserian *et. al.* 2007, Kotal *et. al.* 2010 and Khan and Naqvi 2012 also reported high positive direct effect of grain/spike on grain yield/plant in favourable environments.

Pedigree Analysis

The genotypes HS490, GW273, Raj 3765, Raj 3777, Raj 4037, WR544 etc. were found with satisfactory performance for grain yield under water stress and medium water stress environments (Table 2). The wheat varieties DBW16 and PBW373 revealed their satisfactory performances under E1, E2 and E3 environments, respectively. Based on grain yield *per se* these potential wheat varieties with water stress resilience were also subjected to pedigree analysis. In pedigree analysis, it was observed that the variety DBW16 (Raj 3765/WR484//HUW468) has Raj 3765 as one of the parent and Raj 3765 was noticed with pedigree HD2402/VL639. The variety Raj 4037 (DL788-2/RAJ 3717) showed DL788-2 in its parentage and DL788-2 was having pedigree as K7537/HD2160/HD2278/L24/K4.14. The genotypes Raj 3777 (RAJ 3160/ HD2449) and WR544 (KALYAN SONA/HD1999//HD2204/DW38) were also having

parents *i.e.* HD2449 and HD1999 and HD2204, respectively in their parentage. It was assumed that probably the lines *viz.* HD2402, HD2204 and HD2278 may be the potential parents for water stress resilience performance for the considered *elite* wheat varieties.

These genotypes namely HD2402, HD2204 and HD2278 were further studied and were found with common parents *i.e.* HD1962, E4870 and K65 in pedigree analysis. Thus, it was hypothesized that the genotypes HD1962 (SL SIB/NP852), E4870 (PJ SIB/P14/ /KT54B) and K65 (TYPE9/8B/ /NP773) may be the common sources for water stress tolerance. Lauer *et al.* 2012 also emphasized that most of the parents of present day cultivars were developed under water limited conditions and drought tolerance genes already exist in these progenitors. Furthermore, for HS490 (HS364/HPW114/ /HS240/HS346), one of its parents HS240 was observed with parentage as AU/KAL-BB/ /WOP'S/PAVON'S and it was assumed that for HS490 and PBW373 (ND/VG9144/ /KAL/BB/3/YCO'S'/4/VEE#S'S'') the parental line Kalyansona (KAL = PJSIB/GB55) and Bluebird (BB = CNO SIB/ /SN64/KLRE/3/8156) were common and may be contributor for water stress resilience.

CONCLUSION

Therefore, from the present study it could be concluded that the genotypes namely HS490, Raj 3765, Raj3777, GW273, WR544 etc. exhibited water stress resilience with divergence and may be considered as one of the potential parents for future hybridization programmes aimed for higher water use efficiency. Directional selection for the traits *i.e.* spike length, tiller/m and biological yield in water stress conditions, while in addition to these grains/spike and 1000 grain weight under favourable environment would be fruitful for higher grain yield and breaking yield barriers. Spikelets/spike was also observed as an important parameter, which contributed majorly through spike length, grains/spike, 1000 grain weight and biological yield under water stress and irrigated conditions. The genotypes HD1962, E4870, K65, Kalyan sona and Bluebird were apparent as potential ancestors for water stress resilience performance under pedigree analysis. These parents would be further useful for the development of mapping populations for water use efficiency and delineating studies at molecular and genetic levels.

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