

Association of Indian bread wheat genotypes under different moisture regimes

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Abstract

Forty *elite* bread wheat genotypes were assessed under different moisture regimes to ascertain the extent of genetic diversity and were grouped in to eight clusters. In irrigated conditions, the inter cluster distances ranged from 1.66 (cluster IV to VIII) to 9.47 (cluster II to VII), whereas the range of inter cluster distances under water stress conditions obtained was from 1.98 to 9.10. On pooled basis, the clusters II, III and IV had the most divergent genotypes with high inter cluster distances. The genotype GW 273 performed well in severe water stress, while WR 544 and Raj 4037 were found promising under water stress at grain filling stage.

Key words: Genetic divergence, water stress, cluster analysis, bread wheat

Water stress is one of the most severe abiotic stresses faced by the sustainable crop productivity, which globally reduces crop yield drastically [3, 5, 10, 14]. In India, out of 78 m ha net sown area, 55 per cent is under rainfed agriculture, which accounts for 40 per cent food production [2, 6]. During 2011-12, the annual wheat production in India was 93.90 million tonnes and global wheat production was estimated at 704.08 million tonnes [8, 13]. Wheat consumption worldwide is estimated to surpass 817 million tonnes by 2030 and production would need increase from the current production level to meet the estimated consumption demand [19].

Cluster analysis refers to grouping of the genotypes based on their similar performances (homogenous *per se*) and minimize the intra

constellation variance and maximize the inter group variance [16]. Hence, the present study was undertaken to grouping 40 *elite* bread wheat genotypes under different moisture regimes. The identified genetically distant genotypes would be gainfully utilized in future hybridization programmes and are likely to give rise superior high yielding and water stress resilient transgressive segregants.

The experiments were conducted at New Experimental Farm, Directorate of Wheat Research, Karnal, during *rabi* 2011-12. Forty *elite* bread wheat genotypes were selected on the basis of their area of adoption, pedigree and production conditions. Three environments/moisture regimes were created by skipping irrigations at different crop growth stages. In the first environment (E1) single irrigation was applied at 23 days after sowing and crop plants faced the severe water stress at tillering, heading and grain filling stages. In second environment (E2), two irrigations were provided at CRI and heading stages, while third environment (E3) was favourable environment. The genotypes were grown in paired rows of two meter row length in Randomized Complete Block Design (RCBD) with two replications in each environment. 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 data were recorded on ten randomly selected competitive plants for each character (except tillers/

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m) and analysis of variance was performed as per SAS Institute, 9.3 [18]. The cluster analysis was performed as per Mahalanobis and Rao [15, 17].

The analysis of variance revealed significant differences ($p < 0.01$) indicating presence of adequate genetic variation among the genotypes. The 40 bread wheat genotypes were grouped in to eight clusters under different environments, while on pooled basis the genotypes were grouped into five clusters (Table

1). In environment E1, the clusters I, II and III contained two genotypes each and the highest number of genotypes (11) were grouped into VIII cluster (Table 1). In medium water stress environment (E2) and under irrigated conditions (E3), the cluster V and II and had single genotype LOK 1 and WH 1021, respectively. On pooled basis cluster I and IV occupied the highest number (16) of genotypes, while the cluster V contained only single genotype.

Table 1. Clustering of bread wheat genotypes under different moisture regimes

Cluster	Environment	No. of genotypes	Genotypes
I	E1	2	WH 711, K 0307
	E2	5	Raj 4083, KRL 210, VL 907, HD 2985, VL 804
	E3	2	HS 490, UP 2338
	pooled	16	AKAW 4627, HD 2851, PBW 550, Raj 4083, VL 892, VL 829, HI 1544, GW 322, DBW 14, HD 2687, KRL 210, WH 711, VL 907, K 0307, HD 2985, VL 804
II	E1	2	HS 490, UP 2338
	E2	11	DBW 17, AKAW 4627, HD 2851, PBW 550, VL 892, KRL 213, VL 829, HI 1544, PBW 343, DBW 14, HD 2687
	E3	1	WH 1021
	pooled	5	GW 273, HS 490, UP 2338, NIAW 34, WR 544
III	E1	2	MP 4010, HI 1531
	E2	8	HD 2967, GW 322, CBW 38, WH 1021, DPW 621-50, WH 711, K 0307, Raj 1482
	E3	8	Raj 4083, HI 1544, GW 322, DBW 14, HD 2687, WH 711, VL 907, VL 804
	pooled	2	MP 4010, HI 1531
IV	E1	9	WR 544, PBW 550, UP 2425, Raj 4037, Raj 3765, HD 2987, GW 322, WH 1021, DPW 621-50
	E2	6	UP 2425, DBW 39, Raj 3777, Raj 3765, DBW 16, PBW 373
	E3	5	DBW 17, DBW 39, KRL 213, PBW 343, PBW 373
	pooled	16	DBW 17, UP 2425, DBW 39, Raj 4037, KRL 213, Raj 3777, HD 2967, Raj 3765, HD 2987, PBW 343, DBW 16, PBW 373, CBW 38, WH 1021, DPW 621-50, RAJ 1482
V	E1	7	AKAW 4627, Raj 4083, VL 892, VL 829, LOK 1, KRL 210, VL 804
	E2	1	LOK 1
	E3	7	AKAW 4627, HD 2851, PBW 550, VL 892, VL 829, LOK 1, HD 2985
	pooled	1	LOK 1
VI	E1	1	GW 273
	E2	4	GW 273, HS 490, UP 2338, NIAW 34
	E3	3	GW 273, NIAW 34, WR 544
VII	E1	6	DBW 17, HD 2851, NIAW 34, CBW 38, VL 907, HD 2985
	E2	2	MP 4010, HI 1531
	E3	2	MP 4010, HI 1531
VIII	E1	11	DBW 39, KRL 213, Raj 3777, HD 2967, HI 1544, PBW 343, DBW 14, HD 2687, DBW 16, PBW 373, Raj 1482
	E2	3	WR 544, Raj 4037, HD 2987
	E3	12	UP 2425, Raj 4037, Raj 3777, HD 2967, Raj 3765, HD 2987, DBW 16, KRL 210, CBW 38, DPW 621-50, K 0307, Raj 1482

In environment E1, the intra and inter cluster distances were ranged from 0 to 1.93 and 1.98 (clusters VII to VIII) to 9.10 (clusters III to VI), respectively. In environment E2, the highest inter cluster distances were exhibited between clusters VI to VII (6.81) followed by VII to VIII (6.51), etc. The higher genetic distance between the genotypes is desirable for high magnitude of the heterosis among the crosses [1, 11, 12, 16]. On pooled basis, the highest inter cluster distances were depicted between cluster II and III (7.20) followed by cluster III and IV (6.26), cluster II and V (5.59) etc., respectively.

The genotype GW 273 under severe water stress, WR 544 and Raj 4037 under medium water stress, whereas the genotypes HD2967 and DPW 621-50 were found promising under irrigated conditions. Initially selection of genetically diverse parents makes plant breeders enable to produce high heterotic cross combinations, which further yield desirable transgressive recombinants helping in saving land, resources and valuable efforts [4, 7, 9]. On pooled basis, the clusters II, III and IV contained the most divergent genotypes based on higher inter cluster distances. Therefore, the selection from these clusters of the genotypes viz. GW 273, HI 1531, HD 2967, Raj 3765 etc. would be promising either in bi-parental, diallel, three way or double crosses to set superior positive gene constellations under rainfed and as well under favourable environments.

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