

Genetic diversity analysis for yield and other agronomic traits in bread wheat under water logged sodic soil condition

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Abstract

An experiment was conducted with 108 bread wheat accessions from India and Australia to assess the genetic diversity for yield and yield traits in waterlogged sodic soils. The genotypes were grouped into eleven clusters and distribution pattern indicated that maximum number of genotypes were grouped into the cluster IV (26) followed by cluster VI (22) and cluster II (12). The inter-cluster distance in most of the cases was higher than the intra-cluster distance, indicating wider genetic diversity among the accessions of different groups. The highest inter-cluster distance was observed between cluster VIII and IX (113.94) followed by VIII and X (97.72), showing wide diversity among the groups. The highest intra-cluster distance was observed for the cluster X (13.96) and the lowest for the cluster VII (00.00). Genotypes of cluster X had highest mean value for grain yield, harvest index and spike weight. The genotypes in these clusters *i.e.* Perenjori, KRL 261 and KRL 283 from cluster X, and Gutha from cluster IX may be used as potential donors for hybridization programme to develop genotypes with high grain yields in waterlogged sodic soils.

Keywords: Wheat, water logging, genetic diversity, sodic soil

1. Introduction

Wheat (*Triticum aestivum* L.) is the second most important cereal crop of India next to rice and plays a vital role in food and nutritional security. Nearly 55 per cent of the world population depends on wheat for intake of about 20 per cent of food calories; and wheat is the major food grain of the country particularly of the people of North India, where people have preference for chapatti. Grain yield in wheat is reduced due to various biotic and abiotic factors at different stages of crop growth. Among the important abiotic factors, salinity and water-logging stresses are the major yield limiting factors influencing wheat production in the hostile sodic soils (Anonymous, 2012; Setter *et al.*, 2011; Sharma and Kulshreshtha, 2011 and Singh *et al.*, 2013). According to one study, about 10 million ha of crops are exposed to waterlogged soil each year (Sayre *et al.*, 1994).

Water logging for about 30 days during any of the growth stages can cause 50-60 per cent grain yield losses or

more due to poor seed set and reduced effective tillers per unit area. The decrease in yield supports the finding of Setter *et al.* (2001). McDonald *et al.* (2006) screened wheat varieties under severe water logging condition where grain yield was reduced to 65 percent. It is now well recognized fact that wheat crop is very sensitive to water logging particularly during seedling, flowering and grain filling periods. The work being carried out on multifactorial importance of crop improvement, crop management and physiological intervention to address issues related to abiotic stresses particularly waterlogging and salinity in India and Australia is very relevant to enhancing wheat production under a changing climate (Setter *et al.*, 2011; Singh *et al.*, 2003 and Anonymous, 2012). Therefore, information on the genetic diversity for grain yield in waterlogged soil is important to meet the diversified goal of plant breeding such as breeding for increasing yield, wide adaptation and desirable quality

(Lal *et al.*, 2009). Information on genetic diversity in wheat under waterlogged environment is scanty; therefore this experiment was conducted to identify genetically divergent genotypes as donors with desirable traits for hybridization particularly for water logging in sodic soils coupled with high yield and its contributing traits.

2. Materials and methods

A study was conducted taking 108 diverse genotypes including four checks (DBW 14, DBW 17, HD 2009 and KRL 3-4) of wheat collected from Australia and India. The experiment was planted during *rabi* season in 2010-11 at the Main Experimental Station (MES) of Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, India. The experimental site of Kumarganj is situated at 26.47° N, 82.12° E and at an altitude of 113 meter. The experimental material was grown in waterlogged sodic (pH >8.8) soil conditions in an augmented block design having four blocks, where each block contains 26 test entries and 4 checks (randomly allocated). The water logging condition was initiated at 27 days after sowing and it was maintained continuously for 10 days with 8.5 centimeter water depth. Each genotype was grown in a 4-row plot of 2.5 meter with 23 centimeter distance between rows. The recommended cultural practices were adopted to raise a good crop. Data were recorded on ten randomly selected competitive plants from each plot on eleven quantitative characters namely, days to 50 per cent flowering, days to maturity, plant height (cm), productive tillers per plant (tillers/plant) spike length (cm), spike weight per plant(g), grains per spike, 1000-grain weight (g), biological yield per plant (g), harvest index (%) and grain yield plant (g). The estimates of genetic

parameters *viz*: mean, range, broad-sense heritability (h^2), genetic advance (GA % of mean), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were worked out. Also, data were subjected to non-hierarchical Euclidean cluster statistic (Beal, 1969; Spark, 1973) and statistical software (Window Version 8.6) was used for analyzing the diversity among the genotypes.

3. Results and discussion

The analysis of variance indicated significant differences for all the traits under waterlogged sodic soil conditions. The results revealed that genotypic variability was high as indicated by a large range in values, prompted further analysis. The observations on field performance of material under waterlogged conditions for eleven metric traits revealed that there was more than a 10-fold range in grain yield of wheat grown in waterlogged sodic soil and there were similar large ranges in other traits associated with yield or yield potential (Table1).

The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits. Higher PCV and GCV indicated that there was high variability existing among the genotypes. Higher values for genetic coefficient of variability (GCV) are shown for grain yield, biomass, grains per spike, productive tillers per plant and plant height under waterlogged environment indicating better opportunity for improvement in these traits through selection.

The heritability estimates ranged from 46 to 92 per cent for harvest index and spike weight, respectively in waterlogged conditions.

Table 1. Descriptive statistics of the 11 quantitative traits of 108 wheat lines under waterlogged sodic soil condition

Character	Parameter						
	Range	Mean	Heritability (h^2)	GA	GCV	PCV	SD
Days to flowering	74-94	83	78.85	5.56	3.05	3.44	3.10
Days to maturity	116-131	122	78.29	3.19	1.75	1.98	2.57
Plant height	52-96	72	86.67	20.42	10.65	11.43	9.07
Tillers/plant	2-7	4	72.37	39.83	22.72	26.71	1.22
Spike length	5-12	9	75.61	15.56	8.68	9.99	1.14
Spike weight /plant	1-14	6	92.33	65.31	32.99	34.33	2.45
Grains/spike	23-47	35	88.84	21.45	11.04	11.72	4.52
1000-grain weight	21-43	34	85.92	22.82	11.95	12.89	4.50
Biological yield	6-24	14	96.70	53.76	26.54	26.99	4.09
Harvest index	20-47	34	46.08	12.40	8.86	13.06	5.07
Grain yield	1-11	5	94.32	68.18	32.08	33.03	1.76

Where, GA=Genetic advance, GCV=Genotypic coefficient of variation, PCV=Phenotypic coefficient of variation, SD=Standard deviation

Table 2. Distribution pattern of 108 genotypes of wheat into eleven clusters based on non-hierarchical Euclidean cluster analysis

Cluster	Total genotype	Genotype
I	4	K 0807, K 0808, NW 4098, DBW 46
II	12	NW(S) 2-4, KRL 210, RAJ 3765, KRL 19, RAJ 4205, DBW 50, NW 2036, HI 1563, HD 3027, NW 1014, Krichauff, KRL 3-4©
III	8	Chara, KRL 213, BT-Schomburgk, KRL 227, NW 3069, NW 1076, HD 2997, HUW 636
IV	26	PBW 343, KRL 240, NW 1012, DBW 51, DBW 58, PBW 631, PBW 634, NW(S) 6-5, DBW 55, RSP 561, DBW 39, PBW 621, DBW 52, KRL 1-4, NWL 7-4, KRL 105, HUW 638, NWL 9-24, PBW 635, NW 4082, Tincurran, PBW 590, KRL 99, RAJ 4201, WH 1094, PBW 639
V	9	BH 1146, HD 2009©, DBW 60, UP 262, CBW 38, Cunderdin, RW 3684, NW 4092, KRL 35
VI	22	NW 4099, HD 3024, KRL 266, UP 2003, Westonia, Gamenya, PBW 550, KRL 238, NW 1067, KRL 236, Brookton, Amery, KRL 229, KRL 259, HUW 635, HD 3028, KRL 268, HD 2967, DBW 59, NW 3087, NW 4091, HD 2733
VII	4	NWL 9-22, PBW 642, PBW 636, Schomburgk
VIII	1	CAMM
IX	3	NWL 9-25, DBW 14©, GUTHA
X	10	NW 4081, KRL 249, Perenjori, NW 4035, K 9107, Spear, Kharchia 65, KRL 283, KRL 261, HD 2985
XI	9	Ducula 4, KRL 233, Chirya 7, Kalannie, DBW 17©, NW 4018, NWL 9-23, NW 4083, KRL 104

High estimates of heritability were obtained for all the traits except harvest index. This might be possible owing to low effect of environment on these traits. High heritability coupled with high genetic advance gives the most effective criteria for selection (Johnson *et al.*, 1955). In the present study, high heritability estimates coupled with high genetic advance were observed for biomass, grain yield, spike weight, 1000-grain weight, grains per spike, productive tillers per plant and plant height. Panse and Shukhatme (1978) have expressed that if a character is governed by additive gene action, heritability and genetic advance both would be high. High to moderate heritability along with low genetic advance were noticed for days to 50 per cent flowering, days to maturity, ear length, and harvest index, indicating that these characters might be controlled by non-additive gene action and improvement for these characters through selection would be rather limited. Singh *et al.* (2006) however reported high heritability under waterlogging for most of the traits except days to maturity and grains/ear. This might be due to different set of genotypes used in the study. High heritability along with high genetic advance for some metric traits was reported by Singh *et al.* (2011).

A clear understanding of the extent of variability that prevails for each trait in germplasm is essential for the improvement of characters through selection. Moreover, in hybridization programmes, selection of a genetically diverse parent is important to create a wide array of recombinants, and this means that the knowledge of

genetic diversity among the accessions is necessary. Based on the results of diversity analysis, 108 genotypes were grouped into eleven clusters by non-hierarchical Euclidean cluster statistic in such way that the genotypes within a cluster had a small or low D^2 values than those of in between the clusters. The composition of clusters presented (Table 2 & Figure 1) revealed that Cluster IV had the largest number of genotypes (26) followed by cluster VI (22) and cluster II (12), whereas cluster VIII had only one genotype. The clustering pattern showed that genotypes collected from the same geotropical region got distributed in several clusters; Indian genotypes occurred in all 11 clusters and the limited number of Australian genotypes occurred in 10 out of 11 clusters. The clustering which occurred might be due to selection differential and / or genetic drift under diverse environmental conditions within same geographical region. This pattern of clustering further indicated that there was no association between geographical distribution of genotypes and genetic divergence. Similar results were also reported in wheat under non waterlogged conditions by Yousaf *et al.* (2008).

The inter-cluster distance was higher than the intra-cluster, indicating wide genetic diversity among the genotypes (Table 3 & Fig.2). The inter-cluster distance varied from 113.94 (clusters VIII and IX) to 12.14 (clusters IV and VI). The other notable inter-cluster distances recorded were between clusters VIII and X (97.72) and clusters VII and X (68.97). The inter-cluster values that indicated close relationship were to be considered that hybridization

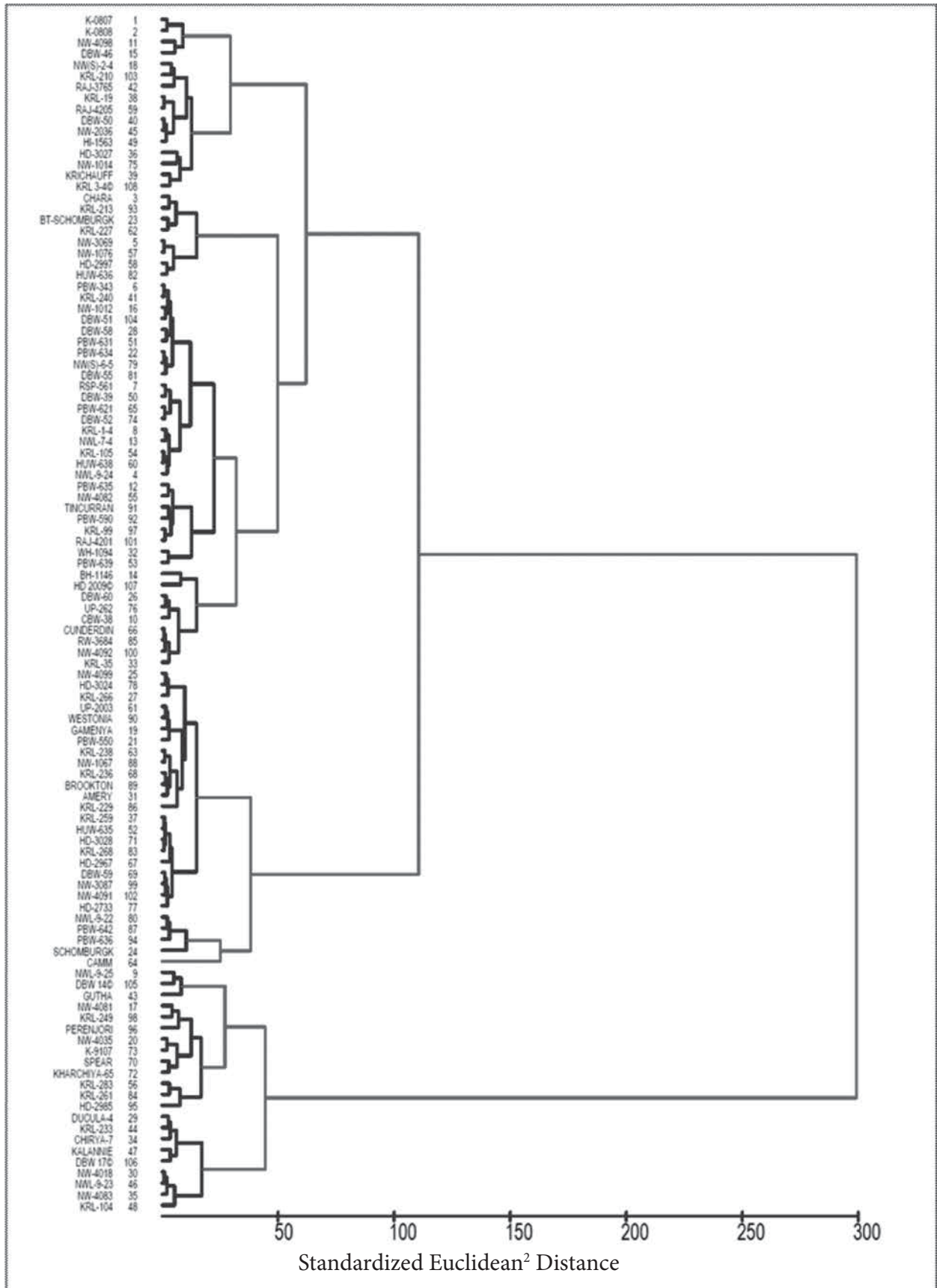


Fig 1. Clustering for 108 genotypes in wheat based on eleven characters in wheat

among the genotypes of these clusters would not provide good levels of segregation. It is well recognized that greater the distance between clusters, wider the genetic diversity would be between the genotypes. Therefore, highly divergent genotypes would produce a broad spectrum of segregation in the subsequent generations enabling further selection and improvement. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregants of high magnitude of heterosis. This would be useful in a wheat breeding programme particularly for targeting hostile conditions of water logging and sodicity. Redhu *et al.* (1995), Sharma *et al.* (1998), Singh *et al.* (2012) and Deshmukh *et al.* (1999) also found similar results of diversity in wheat for non-waterlogged conditions.

The maximum intra-cluster distance was observed for clusters X (13.96) followed by cluster IX (13.29) and cluster II (10.61). On the other hand, cluster VIII had minimum intra-cluster distance (00.00) (Table 3). It was reported that genotypes within the cluster with high degree of divergence

would produce more desirable breeding materials for achieving maximum genetic advance (Singh *et al.*, 2010). The eleven clusters showed considerable differences in mean values for different characters under study (Table 4). Four entries of cluster I, were responsible for highest cluster mean for plant height (87.19) and 1000-grain weight (38.44). Cluster II, comprising 12 genotypes, exhibited by highest cluster mean for harvest index (40.63). Cluster VII, consisting four genotypes, was characterized by lowest cluster mean performance for days to maturity (120.81). Cluster VIII, containing single, least number of entry, exhibited highest cluster mean value for days to 50 per cent flowering (94.44) and days to maturity (131.44). Cluster IX was represented by 3 entries which were responsible for highest mean performance for spike length (12.06) and grains per spike (43.13). The ten entries of cluster X produces moderately high grain yield (8.58 g/plant), productive tillers per plant (6.18), spike weight (11.41) and biological yield (22.49).

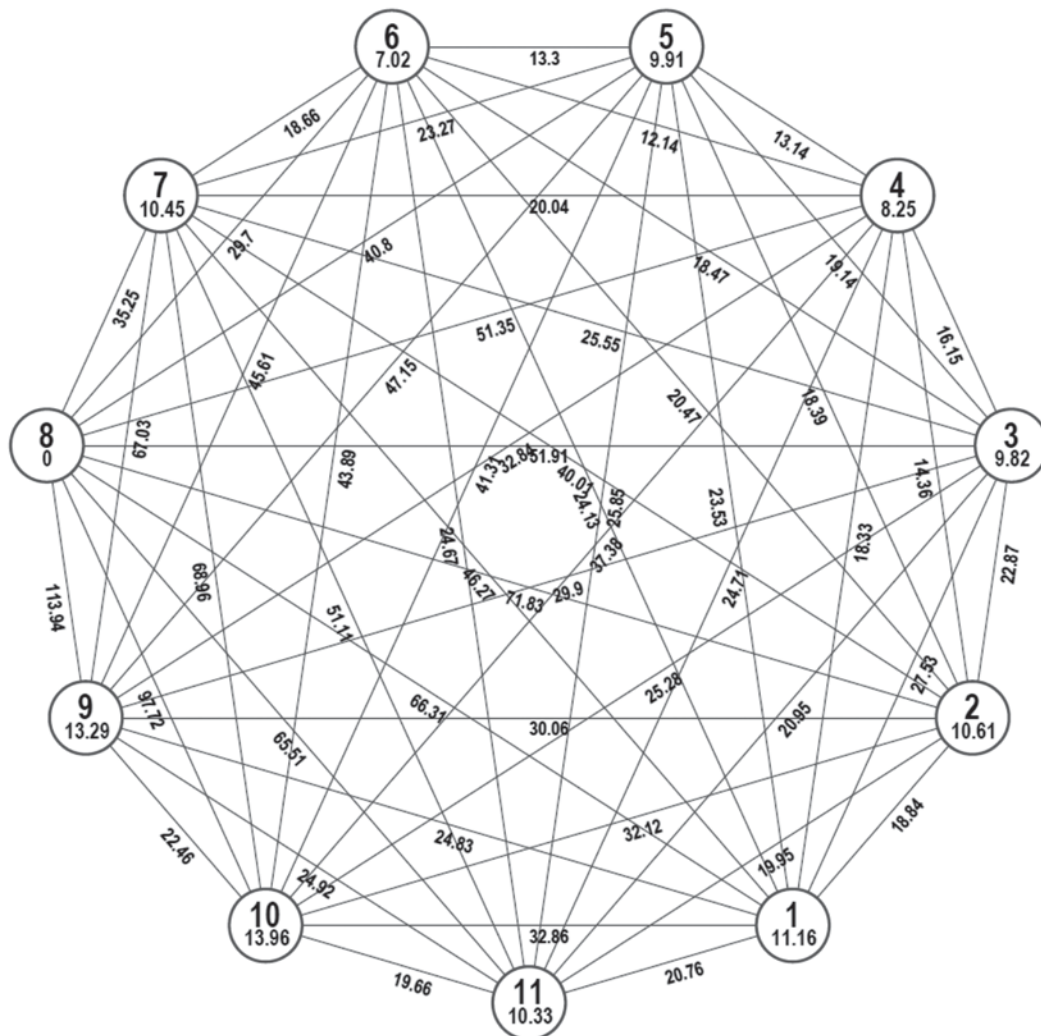


Fig 2. Intra and inter-cluster distance (D) for wheat genotypes grown in waterlogged sodic soil

The genotype ‘Perenjori’ in the cluster X showed good grain yield, harvest index and spike weight, whereas, K 9107, KRL 283 and KRL 261 of same cluster showed highest 1000-grain weight, number of grains and biological yield, respectively. The accession NW 4083 in cluster XI showed highest number of productive tillers whereas spike length was found maximum in genotype ‘Gutha’ of cluster IX. The minimum plant height was found in genotype ‘Schomburgk’ of cluster VII. Ramzi *et al.* (2011) also suggested that the number of fertile tillers and shoot dry weight might be useful for salinity tolerance improvement programs of the analyzed genotypes. A study on genetic diversity by Lal *et al.* (2009) has revealed that grain yield per plant, tillers per plant and plant height, spike length, grains per spike and early maturity contributed maximum to genetic diversity.

On the basis of divergence and cluster mean it may be concluded that maximum heterosis and good recombinants would be possible from crosses between genotypes of clusters VII, VIII, IX and X in varietal improvement programme; these crosses would capture the extremes in grain yield for wheat grown in waterlogged sodic soils. For bringing improvement in a specific trait, genotypes like ‘Perenjori’ from cluster X for grain yield/plant, harvest index and spike weight/plant; KRL 261 from cluster X for biological yield; K 9107 from cluster X for 1000-grain weight; KRL 283 from cluster X for grains per spike; ‘Gutha’ from cluster IX for spike length; NW 4083 from cluster XI for productive tillers per plant may be considered for hybridization in wheat improvement programme as shown by their performance (Table 5).

Table 3. Average intra and inter cluster values among eleven clusters for 108 wheat genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	11.16	18.84	27.53	18.33	23.53	24.13	46.27	66.31	24.83	32.87	20.76
II		10.61	22.87	14.36	18.39	20.47	40.01	71.83	30.06	32.12	19.95
III			9.82	16.15	19.14	18.47	25.55	51.91	29.90	25.28	20.95
IV				8.25	13.14	12.14	20.04	51.35	32.84	37.38	24.71
V					9.91	13.30	23.27	40.81	47.15	41.31	25.85
VI						7.02	18.66	29.70	45.61	43.89	24.67
VII							10.46	35.25	67.03	68.97	51.11
VIII								0.00	113.94	97.72	65.51
IX									13.29	22.46	24.92
X										13.96	19.66
XI											10.33

Table 4. Mean values of clusters and contribution of different characters towards genetic divergence in 108 wheat genotypes

Cluster/ Trait	Days to flowering	Days to maturity	Plant height	Tillers/ plant	Spike length	Spike weight	Grains/ spike	1000-grain weight	Biological yield	Harvest index	Grain yield
I	82.69	123.69	87.19	4.13	12.05	6.92	37.81	38.44	16.44	31.01	5.08
II	80.17	121.65	81.42	4.01	9.95	6.37	37.43	37.01	12.33	40.63	5.04
III	83.16	122.13	67.00	5.31	8.52	7.40	37.72	30.59	17.94	31.31	5.64
IV	82.28	120.97	71.54	3.64	10.04	5.46	35.49	33.82	12.78	32.42	4.12
V	84.61	123.47	77.22	3.50	8.42	5.59	32.69	36.94	12.45	32.06	3.97
VI	86.12	124.78	66.28	3.61	9.89	4.88	33.80	31.45	11.58	34.73	4.06
VII	84.31	120.81	57.56	3.44	8.72	4.33	29.25	26.25	10.63	24.98	2.72
VIII	94.44	131.44	70.94	3.88	8.66	3.03	27.56	21.69	10.13	25.73	2.65
IX	77.63	120.88	70.04	5.67	12.06	10.53	43.13	38.29	21.71	34.00	7.36
X	84.49	121.14	76.64	6.18	9.58	11.41	41.71	37.74	22.49	38.35	8.58
XI	83.42	125.33	77.89	5.92	10.32	9.35	34.72	36.50	17.55	40.08	6.99

Table 5. Promising wheat genotypes for different characters selected from diverse cluster under waterlogged sodic soil condition

Character	Genotype
Days to flowering	NWL 9-25 (74), HD 3027 (75), NW 1014 (78)
Days to maturity	NW 1014 (116), NWL 9-25 (116), NW 4082 (117)
Plant height	Schomburgk (52.43), KRL 229 (52.93), PBW 642 (54.93)
Tillers/plant	NW 4043 (7.62), NW 4081 (6.87), BT-Schomburgk (6.89)
Spike length	Gutha (12.83), K 0808 (12.29), NW 4098 (12.27)
Spike weight	Perenjori (14.14), K 9107 (12.84), KRL 261 (12.12)
Grains/spike	KRL 283 (47.56), RAJ 3765 (45.56), Perenjori, Spear (45.57)
1000-grain weight	K 9107 (43.68), KRL 249 (43.18), K 0808 (42.43)
Biological yield	KRL 261 (24.43), Spear (24.25), Gutha (24.07)
Harvest index	Perenjori (47.86), Krichauff (44.48), RAJ 4205 (44.19)
Grain yield	Perenjori (11.15), KRL 261 (9.07), KRL 283 (8.93)

Figures in parameters are values for each trait

The transgressive segregants coming out of such crossing programme would be better adapted to water logged and sodic soils provided proper breeding methodology and careful selection is followed for trait specific and condition suited approach is implemented to make yield improvement in wheat for such conditions.

Finally, the data presented are from one trial in one soil type in one season. These data need replication and validation in other soil types and seasons, especially where the timing, duration and severity of waterlogging may differ. Such results are also important to contrast to the non-waterlogged conditions. This will assist breeding programs to identify (1) what level of tolerance is required, *i.e.* performance under waterlogged relative to non-waterlogged conditions, versus (2) to what extent high “yield potential” may contribute to high grain yields in sodic soils, *i.e.* whether there is a correlation between yield in waterlogged sodic soil (as used here) and non-waterlogged sodic soil.

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