Original Research Article

Evaluation and selection of wheat (*Triticum aestivum* L.) advanced lines for salt tolerance in Bangladesh

Abstract: The present study was carried out to investigate the genetic variability in advanced wheat lines and to identify superior advanced lines under salinity stress based on yield and yield-related traits. The evaluated advanced lines were derived through accurate pedigree selection method. Fifty lines were evaluated in 2011-2012 wheat season at Regional Wheat Research Centre, Bangladesh Agricultural Research Institute Gazipur, Bangladesh under salinity stress condition. Various statistical tools were used in analyzing the data. Genetic variability was found among the evaluated wheat genotypes for all the traits studied. The evaluated lines were grouped into five clusters using cluster analysis ranging from high salt-tolerant to salt-sensitive genotypes. High to intermediate broad-sense heritability for measured traits showed their potential to be utilized under salinity stress for identifying salt-tolerant wheat lines. The traits under this study showed highly significant positive relationship with yield in terms of genotypic and phenotypic correlations. This indicated that all traits were important in influencing grain yield and could be exploited as selection criteria for improving grain yield of wheat under saline conditions. Eight wheat lines were selected as high salinity tolerant genotypes that would further be used in the breeding program to develop saline tolerant wheat varieties.

Key words: Genotypic, phenotypic, wheat, salinity, tolerance, genetic variability, yield

1. Introduction

Wheat (*Triticum aestivum* L.) is second high yielding cereal crop next to rice in Bangladesh as human food and it ranks third among the cereal crops in terms of production. In 2020-2021, Bangladesh produced about 1.085 million metric tonnes of wheat (BBS, 2022) against a demand of about 8.0 million metric tonnes which is very inadequate and import was 7.0 million metric tonnes (USDA, 2022). The demand for wheat is increasing day by day due to increased population and changing food habit towards wheat. Wheat is mostly grown in northern part of Bangladesh in rabi season (dry season) where now it is to compete with other high value rabi season crops. However, to increase production there is a possibility for expanding wheat cultivation in about 1.056 million hectares fallow cultivable land at rabi season in the southern part of Bangladesh affected by varying intensities of salinity (SRDI, 2010). "In these areas, most of the lands remain fallow in the dry season (January-May) because of soil salinity, lack of good quality irrigation water and late draining condition" (Karim et al., 1990; SRDI, 2001).

"Salinity adversely affects the growth and yield of crop plants by decreasing the availability of soil moisture, and increasing the toxicity effects of sodium and chloride ions at high concentrations" (Munns and Tester, 2008). "Salinity stress reduces Salinity stress accelerates all phenological phases of wheat (Grieve et al., 2001), the number of tillers (Abbas et al., 2013), decreases the number of spikelet number spike^{-1} (Frank et al., 1987), kernel weight (Abbas et al., 2013) and affects grain yield adversely" (Kalhoro et al., 2016). Rani et al. (2018) observed that "salt stress significantly decreases number of grains per spike, grain yield, test weight and biological yield irrespective of wheat varieties". "A severe reduction in wheat yield at moderate salinity levels has been documented" in a study of Sairam et al.

(2002). Kalhoro et al. (2016) reported that "69.6 percent yield reduced in wheat under 10 dS/m salinity condition".

"The destructive effects of salinity on wheat production can be mitigated by certain agronomic practices such as utilizing a large amount of gypsum or by leaching to reduce salt from the soil, but these processes are expensive. On the other hand, growing salt-tolerant genotypes provides a long-term inexpensive practical solution and can be utilized in a large area which is the most effective approach" (Al-Ashkar et al., 2019). "Thus, developing salt-tolerant and high yielding wheat genotypes has become more urgent, especially with increased population of Bangladesh as well as global and current climate changes" (Mansour et al., 2020). "However, developing salt-tolerant wheat genotypes are limited by factors such as lack of genetic diversity, limited selection effectiveness under salinity stress and inadequate knowledge of complex salt-tolerance mechanism" (Oyiga et al., 2016; El-Hendawy et al., 2017; Luo et al., 2017). "For these reasons, enhancing wheat breeding for salt-tolerance is a valuable global concern to cope with the constraints on agricultural production" (Mansour et al., 2020).

"Salt-tolerance can be described as the ability of the genotype to complete its growth cycle and produce appropriate grain yield under salinity stress compared to salt-sensitive genotypes" (Oyiga et al., 2016). "Wheat genotypes possess diverse efficiency in producing acceptable grain yield under salinity stress" (Mansour et al., 2020). "Grain yield is frequently used as the main criteria for salt tolerance in wheat" (Jafari-Shabestari *et al.*, 1995; Kafi *et al.*, 2001). "Crop salinity tolerance in field has to be evaluated as a function of yield" (Yamaguchi and Blumwald, 2005). "Therefore, it is essential to address wheat genotypes under salinity conditions to identify salt-tolerant and sensitive ones. Evaluation of wheat genotypes in soil with saline irrigation water under realistic and natural conditions such as soil heterogeneity, drought stress, and fluctuations of air temperature at the same time with salinity stress may be a complex approach" (Gavuzzi et al., 1997; Dadshani et al., 2019). Thus, genotypic evaluation under field conditions with saline irrigation water under controlled environmental conditions may be suitable in identifying suitable saline tolerant breeding lines that could be integrated into breeding programs for salt-tolerance (Mansour et al., 2020). It is well established fact that the progress in improvement of a crop depends on the degree of variability for the desired character in the existing material and the extent to which the desirable traits, are heritable. Little studies have been done systematically in Bangladesh on these to identify wheat genotypes which may act as supporting aspect for increasing wheat production in the country. The objectives of this study therefore were to: (i) investigate the genetic variability among advanced wheat lines under salinity stress; (ii) identify superior advanced lines under salinity stress that can be exploited in the breeding program to develop further adapted cultivars for salt-affected regions.

2. Materials and Methods

2.1. Plant Material and Experimental Design

Fifty wheat genotypes were evaluated presented in the Table 1. Of these, three were popular varieties and the rest were advanced lines (after F8) and these materials were collected from, Regional Wheat Research Centre (RWRC), Bangladesh Agricultural Research Institute (BARI), (Currently Regional Station, Bangladesh Wheat and Maize Research Institute) Gazipur, Bangladesh. Grain yield and its components were the main selection criteria in the wheat genotypes (advanced lines). The experiment was laid out in randomized complete block design (RCBD) with three replications. Seeds were sown in line on 25 November, 2011 2 @ 120 kg ha^{-1}. Each genotype was sown in one row of 50 cm.

2.2. Experimental Site and Agronomic Practices

The study was carried out on seed bed made of brick (Figure 1) at the research field of Regional Wheat Research Centre, BARI, Gazipur (Currently Regional Station, Bangladesh Wheat and Maize Research Institute (BWMRI)) during November 2011to March, 2012. The experimental site located at $23^0 46^/$ N latitude, $90^0 23^/$ E longitude at an elevation of 8.4 m above the sea level and it is under the sub-tropical region characterized by heavy rainfall during the months from July to September and scanty or no rainfall in the rest of the year. Each seed bed area was 2.8 m x 1.2 m. The seed beds were filled with sandy loam non saline soil. The beds were well prepared with spade followed by breaking the clods with hammer, levelling the bed with hands and collecting the stubbles. After sowing of seeds light irrigation was given to ensure uniform germination of seeds. At 15 (fifteen) days old seedling condition, irrigation were started with sodium chloride (NaCl) salt solution of 15 dSm^{-1} and continued up to physiological maturity and thus irrigation was done six times. Equal quantity of salt solution was applied for irrigation in each seed bed every time. To develop salinity in seed bed soil, four hundred and twenty liter (420) salt solution was applied in each bed at a time keeping as 0.25 18 m root zone and 50% pore space in soil. Fertilizers were applied @ 100-60-40-20-1 kg ha^{-1} N-P_2O_5-K_2O-S-B in the form of urea, triple super phosphate, muriate of potash, gypsum and boric acid respectively. Sixty seven (67) kg N/ha and total amount of other fertilizers were applied during final land preparation. The rest amount i.e. 33 kg N/ha urea was used as top dress at crown root initiation (CRI) stage. Intercultural operations were done uniformly in each bed to ensure normal growth of the crop. Weeding and mulching were done simultaneously for two times, firstly at 25 days after sowing (DAS) and secondly, at 35 DAS. Mulching were done to protect the excess evaporation from the soil.

3.3. Measured traits

The crop was harvested on 20 March, 2012 when the plants attained full maturity. Five plants were sampled randomly for data collection and their mean data were taken for statistical analysis. Data were recorded on spike per plant, spikelet number per spike, grain number per spike, 1000-grain weight (TGW), grain yield per plant, biological yield per plant and harvest index (HI). The grain yield was adjusted at 12% moisture content (MC) and HI was calculated using the following formulas:

$$\text{Adjusted grain yield } (\text{g plant}^{-1}) = \frac{100 - \text{Sample MC}}{100 - 12\%} \text{ x Fresh weight}$$

$$\text{HI} = \frac{\text{Grain yield}}{\text{Biological yield}}$$

2.4. Statistical Analysis

Analysis of variance (ANOVA), cluster analysis and principal component analysis for traits studied under salinity stress were performed using Statistical Tool for Agricultural Research (STAR) software version: 2.0.1 developed by IRRI, (2014). The D^2 analysis for intra-cluster distance was done according Mahalanobis (1936). Canonical variate analysis were done for inter cluster distance by GENSTAT 5.5 statistical software. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h_b), genetic advance

(GA), genetic advance in percentage of mean (GAM), genotypic correlation coefficient (r_p) and phenotypic correlation coefficient (r_p) among traits were computed by OPSTAT Statistical Software Package for Agricultural Research Workers developed by Sheoran et al. (1998). Genotypic variance (σ^2g) and phenotypic variance (δ^2p) were calculated from ANOVA by MS Excel program the presented table 2.

3. Results

3.1. Analysis of variance (ANOVA)

ANOVA results are shown in the Table 3. ANOVA for all the traits studied under salinity stress displayed highly significant differences among evaluated genotypes at 1% level of significance except spikelet spike^{-1} which was significant at 5% level indicated that there was ample scope for selection of promising genotypes for yield improvement under salinity stress.

3.2. Range and mean values

A wide range of variations were found in yield and yield attributes among the genotypes shown in Table 4. Box plots also showed variability under saline condition among wheat genotypes for measured traits (Figure 2). Spike number per plant ranged from 1.3 to 3.4 with an average of 2.35 in salt stressed plants. The spikelet number per spike varied significantly under saline condition. The maximum and minimum number of spike per spike were 11.6 and 19.9 respectively. Grain number per spike also showed a notable variation where maximum, minimum and mean number per spike were 24.4, 46.5 and 36.05 respectively. In the wheat genotypes studied, there was remarkable variation in TGW which ranged from 30.1 to 52.9 g with a mean of 39.30 g (Table 4). The grain yield ranged from 2.3 to 6.7 g/plant which was significantly different among the genotypes with its corresponding mean of 3.69 g per plant

(Table 4). The range of biological yield among the genotypes was 7.2 to 12.5 g with a mean 9.92 g per plant (Table 4). The range of harvest index was 0.297 to 0.445 and its mean was 0.372 (Table 4).

3.3. Genetic Variability

Genotypic and phenotypic variances (δ^2g and δ^2p), phenotypic and genotypic coefficients of variation (GCV and PCV) broad-sense heritability ($h^2{}_b$), genetic advance (GA) and genetic advance in percentage of mean for the wheat genotypes are presented in Table 5. It was found that the PCV was relatively higher than GCV for all characters (Table 5). PCV ranged from 9.86 to 18.70% with highest in spike per plant (18.70%) and lowest in TGW (9.86%). GCV ranged from 4.45 to 13.95% with minimum in spikelet per spike (4.45%) and maximum spike per plant (13.95%) followed by grain yield (12.71%) per plant. According to Deshmukh et al., (1986), phenotypic coefficient of variance (PCV) and Genotypic Coefficient of Variation (GCV) as well as GAM can be categorized as low as low (<10%), moderate (10-20%) and high (>20%). Accordingly moderate PCV were present in all the characters studied except 1000-grain weight and moderate GCV were recorded in spike per plant and grain yield per plant and others characters had low GCV. High GAM was obtained in spike per plant (21.43%) and yield per plant (22.84%). According to Singh (2001) high heritability was found in 1000-grain weight (96.22%; (>80%)) and all the rest traits had moderate heritability (40-80%) except spikelet per spike (15.36%; <40%). Banik et al. (2019) found almost similar trend regarding GCV, h_b and GAM in grain per spike, 1000-grain weight and yield per plant in wheat under salinity stress. Moustafa et al. (2021) obtained the low GCV in grain yield, grain number, 1000-grain weight with high h_b in 1000-grain weight, grain number and with moderate h_b in grain yield of F8 wheat generation under salinity stress.

Genotypic and phenotypic correlation coefficients for all pairs of seven characteristics are shown in Table 6. In both genotypic and phenotypic correlation grain yield showed highly significant positive relation with all the traits studied under salinity stress condition and genotypic correlation coefficients were greater than phenotypic correlation coefficients.

3.4. Principal Component Analysis (PCA)

Eigen vector the percent variations explained by each eigen roots and eigen values are presented in Table 7. The Eigen root of first principal component or eigen vector was accounted 57.94% of total variation followed by second to the seventh components as follows: 17.43, 8.77, 6.53, 6.17, 2.75 and 0.41% respectively. The first three PC axes with Eigen root>1 explained 84.14% of the total variation. The values of Eigen roots were interpreted as relative weight of the variables in each component.

.All the traits contributed in variation positively to PC1. The traits which contributed positively were spikelet per spike and harvest index and the rest of the traits contributed negatively in PC2 in variation. In PC3 spike per plant, spikelet per spike and biological yield contributed positively. Spikelet per spike and 1000-grain weight were the major contributor in PC4. The variation in the PC5 was mainly due to spike per plant, 1000-grain weight, harvest index, grain yield and biological yield. In PC6 the contributors were spike per plant, spikelet per spike and grain per spike. In PC7 all the traits contributed a little for genotypic variation (Table 7).

From the principal component analysis, PC1 and PC2 constructed PC-biplot (Figure 3). According to the PC-biplot, the different genotypes were scattered in the four quarters of the biplot and the trait vectors are represented by acute angles (Figure 3).

3.5. Cluster analysis

Cluster analysis is a more useful measure for estimating divergence. Cluster analysis using agglomerative-ward linkage method was used for grouping the genotypes for salt tolerance. Absolute values of seven agronomic traits were used in order to make comparison among the groups of genotypes and to rank the groups under saline condition.

The wheat genotypes were classified into five groups using cluster analysis shown in figure 4. Cluster I consisted of genotypes (G1(Shatabdi), G11(BAW 1153), G14(BAW 1158), G15 1 (BAW 1122), G16 (BAW 1130), G17(BAW 1051), G18(BAW 1111), G22 (BAW 1120), G23(BAW 1159), G28, G29, G34, G35, G36, G37, G40, G41, G42, G44, G46, G47, G48 and G49); Cluster II with 8 genotypes (G2(BARI Gom 25), G3(BARI Gom 26), G4(BAW1142), G7(BAW1147), G9(BAW 1150), G19(BAW 1135), G33 and G38); cluster III with 9 genotypes (G5(BAW 1143, G6(BAW 1146, G8(BAW 1148, G12(BAW 1154, G20(BAW1138), G25(BAW 1131, G27(BAW 1157, G30 and G39), cluster IV with 6 genotypes (G10(BAW 1151), G26(BAW 1141), G31, G32, G45 and G50) and cluster V with 4 genotypes (G13(BAW 1140), G21(BAW 1156), G24(BAW 1160) and G43. Cluster mean values of agronomic traits studied under salinity are presented in the Table 8. Among the five clusters, cluster II had the highest mean grain yield (4.21 g plant^{-1}) with highest mean spike number per plant (2.70), highest mean spikelet number per spike (16.35), highest mean TGW (45.16 g) and second highest mean biological yield (10.26 g plant^{-1}) and mean harvest index

(0.41) (Table 7); hence they could be considered as high salt-tolerant genotypes. The second highest mean grain yield (3.90 g plant^{-1}) was found in cluster III with highest mean harvest index (0.42) which was very close to mean grain yield of cluster V (3.89 g plant^{-1}) with highest mean biological yield (11.58 g plant^{-1}); consequently genotypes under cluster III & V could be considered as salt tolerant genotypes. Likewise Cluster 1 could be considered as medium or slightly salt tolerant because of its intermediate mean grain yield (3.62 g plant^{-1}). Cluster IV with lowest mean grain yield (2.68 g plant^{-1}) and all other traits could be considered as salt sensitive.

3.6. D^2 analysis and Canonical variate analysis (CVA)

D^2 analysis and CVA yielded intra (bold) and inter cluster distances are presented in Table 9. Genotypes grouped in the same cluster (intra cluster) are expected to be genetically related than genotypes grouped in different cluster (inter cluster). All the inter cluster distances were larger than the intra-cluster distances indicating that wider divergent was present among the genotypes of different clusters than those of the same cluster. The intra-cluster distances were low in all the clusters within the range of 1.6317 in cluster V to 2.5065 in cluster I which indicated homogeneous nature of the genotypes within the clusters.

Regarding inter cluster distance, the distance calculated by canonical variate analysis showed maximum distance (9.592) between cluster II & Cluster IV followed by the distance (9.279) between cluster IV & cluster V and the distance (8.617) between cluster III & cluster IV. The closer distance (2.877) was observed in between cluster II and cluster III. The maximum value of inter-cluster distance indicated that the genotypes belonging to cluster II were far diverged from those of other clusters. Genotype clusters were shown clearly in figure 5 with apparent inter and intra-cluster distances constructed from PC1 and PC2 scores.

4. Discussion

Genotypic variation is essential for developing salinity tolerant wheat genotypes (Gharib et al. 2020; Moustafa et al., 2021). "However, the genetic base of wheat breeding for salt tolerance is narrow" (Akbarpour et al., 2015; Genc et al., 2019). "The lack of genetic diversity limits the progress of improving salt-tolerance in wheat. Evaluation under field conditions is effective to exclude salt-sensitive genotypes, particularly in the yielding stage. Grain yield is frequently used in crops such as wheat as the main criteria for salt tolerance" (Jafari-Shabestari et al., 1995; Kafi et al., 2001). "Crop salinity tolerance in field has to be evaluated as a function of yield" (Yamaguchi and Blumwald, 2005). "Grain yield plant^{-1}, grains plant^{-1} and fertile tillers plant^{-1} are good screening criteria under field conditions" (El-Hendawy et al., 2009). The evaluated advanced lines displayed highly significant variations for all studied traits under salinity stress and indicated the presence of genotypic variations among the lines for these characters (Table 4, Figure 2) which offers scope of selection for different quantitative traits of wheat. Similar findings in wheat have also reported by Kaddem 18 et al. (2014), Banik et al., (2019) and Moustafa et al., (2021). In the present study it was found that PCV were greater than that of GCV for all the traits suggesting that the influence of environmental factors for the phenotype expression of genotypes was low and that are beneficial for utilization in breeding for salt tolerance. Among these traits, comparatively low magnitude between PCV and GCV were present in 1000-grain weight, biological yield, grain yield per plant and grain per spike (Table 5) than others implies that these traits were mostly genetically controlled than others. In addition, the lower environmental impact on these traits signified the improvement that can be achieved through selection based on phenotypic expression. Similar results were reported in wheat under salinity stress by Banik et al., (2019) and Moustafa et al., (2021). Additionally, intermediate to high broad-sense heritability except spikelet per spike obtained in this study confirmed the efficiency of these traits for direct phenotypic selection to identify salt-tolerant genotypes. The presumptions for most of the traits were supported by the pointed response of these traits to selection under salt stress (Banik et al., 2019; Moustafa et al., 2021).

Principal component analysis is a data reduction technique for investigating the interdependence attempts to simplify complex and diverse relationships existing among a set of observed variables, by revealing common dimensions or components that link seemingly unrelated variables. In the present study the first three PC showed the 84.14% of total variation suggesting considerable diversity among the genotypes variability under salinity condition (Table 7). From the PC values it showed that all the traits positively contributed for variation among the genotypes. Iqbal et al. (2008) reported that "quantitative traits that contributed positively in principal component analysis could be a considerable importance for the genetic materials under investigation". According to the PC-biplot (Figure 3), the different genotypes were scattered in the four quarters of the biplot, which indicated a high level of genotypic variation among the tested genotypes. The trait vectors are represented by acute angles, indicating positive associations (Figure 3) and these traits could help with grain yield to identify superior wheat genotypes.

Cluster analysis is a more useful measure for estimating divergence. The genotypes that are close to each other move into a group from a diverge genotypes through cluster analysis. In this study five groups were obtained using studied traits through cluster analysis (Figure 4). Many scientists have used cluster analysis to make group different wheat genotypes depending on the different traits and observed similarities of wheat genotypes within a group (Sarazafar et al., 2016; Moustafa et al., 2021). In this study, cluster II comprised of eight out of fifty genotypes, all genotypes performed significantly better than others for spike per plant, spikelet per spike grain per spike, TGW and grain yield and could be selected as salt tolerant lines for further breeding programmes for salt tolerance as reported by Moustafa et al., (2021) and Sarazafar et al., (2015.

In present study all the traits showed highly significant positive relationship with yield in terms of genotypic and phenotypic correlations and the genotypic correlation coefficients were greater than phenotypic correlation coefficients (Table 6) indicating that all traits were important in influencing grain yield and could be exploited as selection criteria for improving grain yield of wheat under salinity stress. The result is in agreement with several workers who described the importance of spike per plant, grain per spikelet, biological yield and harvest index in selection of wheat genotypes under salt stress condition by showing positive phenotypic and genotypic correlation with grain yield (Gholizadeh et al., 2014; Banik et al., 2019) and the higher genotypic correlation coefficients meant the association was due to genetic reason as indicated by Tripathi *et al*. (2015) and Banik et al. (2019). In PC-biplot all the traits displayed a strong positive association with grain yield, which indicated their importance as vital traits for indirect selection under salinity stress (Figure 3). A similar positive association between yield and yield attributes was proved by Moustafa et al. (2021). From the above discussions under different types of analysis it showed that grain yield and its attributed traits are valuable criteria for investigating genotypic responses to salinity stress and identifying salt-tolerant genotypes with high-yielding potential

Conclusion: It was concluded from this studies that there was high variability among the evaluated wheat lines based on yield and yield attributes under salinity conditions at maturity stage. The detected high to intermediate broad-sense heritability for studied traits demonstrated their efficiency in identifying salt-tolerant lines. The traits under this study showed highly significant positive relationship with yield in terms of genotypic and phenotypic correlations indicating that all traits used in this study were important as far as grain yield was concerned and that they could be used as basis for selecting salt tolerant wheat genotypes. Besides, the use of PC-biplot may be a helpful tool in studying the relationship of traits when evaluating wheat lines under saline conditions. Eight wheat lines namely BARI Gom 25, BARI Gom 26, BAW 1135, BAW1142, BAW1147, BAW 1150, G33 and 20 G38 were selected as salt tolerant genotypes in the present study. These genotypes could be exploited as a novel genetic material to enhance breeding for salt-tolerance in Bangladesh.

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Table 1. List of wheat genotypes.

	CROSS/PEDIGREE
G1(Shatabdi)	MRNG/BVC//BLO/PVN/3/PJB-81 CM98472-1 JO-0JO-0JO-1JO-0JO-0R2DI
G2 (BARI Gom 25)	ZSH 12/HLB 19/2*NL297
G3 (BARI Gom 26)	ICTAL 123/3/RAWAL 87/VEE/HD 2285 BD(JO)9585-0JO-3JE-0JE-0JE-HRDI-RC5DI
G4 (BAW 1142)	BCN//CEAT/AE.SQUA(895)/NL 745 NC 00B3273-2B-020B-020B-5B-0B
G5 (BAW 1143)	BAW 923/BAW 1004 BD(DI)1207S-0DI-4DI-010DI-010DI-0DI-DIRC7
G6 (BAW 1146)	KAN//IAS 63/ALDAN BD(DI) 961S-0DI-62DI-010DI-010DI-0DI-03DI-DIRC6
G7 (BAW 1147)	OASIS/3*ANGRA//708E BD01JA666S-3JA-010JA-010JA-010JO-HRJO-RC9JO
G8 (BAW 1148)	OASIS/3*ANGRA//708E BD01JA666S-15JA-010JA-010JA-010JO-HRJO-RC5JO
G9 (BAW 1150)	BL 1473/BL 1904 NC 001B3438-3B-020B-020M-1B-0B
G10 (BAW 1151)	UP2338*2/4/SNI/TRAP#1/3/ KAUZ*2/TRAP//KAUZ CGSS01Y00021T-099M-099Y-099M-099M-16Y-0B
G11 (BAW 1153)	BAW 968/SHATABDI BD(JO)358-0DI-1DI-010DI-010DI-DIRC5
G12 (BAW 1154)	KAN/GOURAB NCD99-01-0DI-1DI-0DI-0DI-0DI-0DI-18DI-0DI
G13 (BAW 1140)	SOURAV/GOURAB BD(JE)959S-0DI-5DI-010DI-010DI-010DI-1DI-DIRC8
G14 (BAW 1118)	BAW 969/SHATABDI BD(DI)1319S-0DI-6DI-1DI-DIRC7
G15 (BAW 1122)	GARUDA//BAW 970/NL 297 BD (JE) 1228T-0DI-9DI-1DI-DIRC3
G16 (BAW 1130)	GOURAB/PAVON 76 NCD99-04-0DI-1DI-0DI-0DI-0DI-0DI-22DI-DIRC4
G17 (BAW 1051)	KLAT/SOREN//PSN/3/BOW/4/VEE#5.10/5/CNO 67/MFD//MON/3/ SERI/6/NL297 NC2142-7B-020B-025B-3B-0B

G18 (BAW 1111)	AKR/3/URES/JUN//KAUZ BD(DI) 947S-0DI-5DI-010DI-010DI-1DI-HR2
G19 (BAW 1135)	BAW 969/SHATABDI BD(DI)1319S-0DI-6DI-1DI-DIRC6
G20 (BAW 1138)	CHEN/AE. SQ (TAUS)//BCN/3/2*PASTOR CMSS98Y00844S-040Y-0B0MXI-3DI-010DI-010DI-1DI-DIRC6
G21 (BAW 1156)	BL 3306 (SW89-3060/ACHYUT) NC 99B3173-3B-020B-020B-020M-3B-OB
G22 (BAW 1120)	WAXWING*2/VIVITSI CGSS01B00056T-099Y-099M-099Y-099M-14Y-0B
G23 (BAW 1159)	KAN//IAS 63/ALDAN BD(DI) 961S-0DI-62DI-010DI-010DI-0DI-03DI-DIRC5
G24 (BAW 1160)	BAW 1004/GARUDA BD(DI)1493-0DI-8DI-6DI-HR3R6DI
G25 (BAW 1161)	BAW 677/BIJOY BD(JA)1365S-0DI-15DI-3DI-HR12R3DI
G26 (BAW 1141)	CHIL/2*STAR/4/BOW/CROW//BUC/PVN/3/2*VEE#10 CMSS95Y00624S-0100Y-0200M-17Y-010M-5Y-0M
G27 (BAW 1157)	BAW 923/BAW 1004 BD(DI)1207S-0DI-4DI-010DI-010DI-0DI-DIRC6
G28	MINIVET/PRODIP BD(DI)1598S-0DI-15DI-R2DI
G29	SOURAV/PRODIP BD(DI)1377S-0DI-010DI-010DI-010DI-R4DI
G30	PRODIP/GOURAB BD(J)459S-0DI-8DI-010DI-010DI-R4DI
G31	PRODIP/GOURAB BD(J)459S-0DI-8DI-010DI-010DI-R5DI
G32	BIJOY/PRODIP BD(DI)1498S-43DI-010DI-010DI-3DI-R7DI
G33	BIJOY/PRODIP BD(DI)1498S-43DI-010DI-010DI-4DI-R5DI
G34	BIJOY/PRODIP BD(DI)1498S-43DI-010DI-010DI-8DI-R8DI
G35	KAL/BB/YD/3/PASTOR CMSS99M00981S-0P0M-040SY-040M-040SY-16M-0ZTY-0M
G36	A6/GLEN//NL 297*2/LR25 BD02JA884S-0JA-1JA-6JA-4JA-3JA-3JA-5JA
G37	NL297*2/LR25//CHIRYA 3 BD02JA874S-0JA-3JA-5JA-2JA-5JA-1JA-1JA
G38	BAW 966/3/BUC/BJY//BOW/PVN BD03JA122T-0JA-0JA-0JA-0JA-6JA-4JA
G39	PFAU/SERI.1B//AMAD/3/WAXWING CGSS02Y00153S-099M-099Y-099M-46Y-0B
G40	THELIN/WAXWING//ATTILA*2/PASTOR CGSS02Y00085T-099B-099B-099Y-099M-38Y-0B

G41	KANCHAN/BAW 1075 BD(DI)1563S-0DI-0DI-0JA-0JA-0JA
G42	CY 8801/GOURAB BD(DI)1650S-0DI-0DI-0JA-OJA-0JA
G43	SOURAV/3/ALTAR84/AE.SQ.(224)//2*YACO/4/JUNCO//YD/PCI BD04JA178T-0DI-0DI-0JA-0JA-OJA
G44	KANCHAN//INQALAB91*2/KUKUNA CMSS05Y00426S-0B-099Y-099ZTM-8WGY-0B
G45	WBLL1/KUKUNA//TACUPETO F2001/5/WAXWING/4/SNI/TRAP#1/3.. CMSS05B00053S-099Y-099M-099Y-099ZTM-25WGY-0B
G46	ATTILA/3*BCN//BAV92/3/TILHI/5/BAV93/3/PRL/SARA//TSI/.. CMSS05B00663S-099Y-099M-099Y-099ZTM-13WGY-0B
G47	WAXWING/PARUS//WAXWING/KIRITATI CGSS05B00224T-099TOPY-099M-099NJ-099NJ-8WGY-0B
G48	HUW234+LR34/PRINIA*2//YANAC CGSS0500242T-099TOPY-099M-099NJ-099NJ-18WGY-0B
G49	HUW234+LR34/PRINIA*2//YANAC CGSS0500242T-099TOPY-099M-099NJ-099NJ-28WGY-0B
G50	HUW234+LR34/PRINIA*2//YANAC CGSS0500242T-099TOPY-099M-099NJ-10WGY-0B

Table 2. List of formulas used in the calculation of genetic parameters.

Genetic parameter	Abbreviation	Formula	Author
Genotypic variance	$\delta^2 g$	$\delta^2 g = \frac{GMS-EMS}{r}$	Johnson et al (1955)
Phenotypic variance	$\delta^2 p$	$\delta^2 p = \delta^2 g + EMS$	Johnson et al (1955)

Note: GMS = Genotypic mean square, EMS = Error mean square, r = Number of replication

Table 3. Mean square (MS) of studied agronomic traits of evaluated genotypes under salinity stress

Traits	Replication	Genotype	Error	Total
Df	2	49	98	149
Spike plant^{-1} (no.)	0.872**	0.409**	0.086	30.21
Spikelet spike^{-1} (no.)	2.940	4.005*	2.593	456.24
Grain spike^{-1} (no)	75.873**	26.731**	7.678	2214.02
1000-grain weight (g)	0.017	43.898**	0.568	2206.67
Grain yield plant^{-1} (g)	0.090	0.730**	0.069	42.74
Biomass yield plant^{-1} (g)	0.564	2.743**	0.232	158.24
Harvest index	0.001	0.005**	0.001	0.335

df means degrees of freedom, $p^* < 0.05$, $p^{**} < 0.01$

Table 4. Descriptive statistics for studied agronomic traits of the evaluated advanced lines

Traits	Min	Max	Mean	SD	CV (%)
Spike plant^{-1} (no.)	1.3	3.4	2.35	0.45	12.45
Spikelet spike^{-1} (no.)	11.6	19.9	15.41	1.75	10.45
Grain spike^{-1} (no)	24.4	46.5	36.05	3.85	7.69
1000-grain weight (g)	30.1	52.9	39.30	3.85	1.92
Grain yield plant^{-1} (g)	2.3	6.7	3.69	0.54	7.12
Biomass yield plant^{-1} (g)	7.2	12.5	9.92	1.03	4.85
Harvest index	0.273	0.699	0.373	0. 05	8.70

Min: Minimum, Max: Maximum, SD: Standard deviation, CV: Coefficient of Variation

Table 5. Genetic variability variables for the studied traits in the evaluated bread wheat advanced lines

Traits	σ^2g	σ^2p	GCV (%)	PCV (%)	h_b (%)	GA	GAM
Spike per plant	0.11	0.19	13.95	18.70	55.66	0.505	21.43
Spikelet per spike	0.47	3.06	4.45	11.36	15.36	0.554	3.59
Grain per spike	6.35	14.03	6.99	10.39	45.27	3.493	9.69
1000-grain weight	14.44	15.01	9.67	9.86	96.22	7.679	19.54
Biological yield per plant	0.84	1.07	9.23	10.43	78.32	1.668	16.82
Harvest index	0.001	0.002	9.33	12.96	53.47	0.052	14.05
Grain yield per plant	0.22	0.29	12.71	14.57	76.11	0.844	22.84

σ^2g: Genotypic variance, σ^2p: Phenotypic variance, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, h_b: Heritability (broad-sense), GA: Genetic advance, GAM: Genetic advance in percentage of mean

Table 6. Genotypic (r_g) (upper diagonal) and phenotypic (r_p) (lower diagonal) correlation with yield.

Traits	SPP	SPS	GPS	TGW	BY	HI	GY
SPP		0.802^{**}	0.700^{**}	0.677^{**}	0.695^{**}	0.657^{**}	0.938^{**}
SPS	0.226^{**}		0.498^{**}	0.670^{**}	0.157^{NS}	0.990^{**}	0.973^{**}
GPS	0.335^{**}	0.256^{*}		0.672^{**}	0.452^{**}	0.710^{**}	0.827^{**}
TGW	0.504^{**}	0.232^{**}	0.444^{**}		0.433^{**}	0.474^{**}	0.653^{**}
BY	0.411^{**}	0.126^{NS}	0.322^{**}	0.371^{**}		0.028^{NS}	0.681^{**}
HI	0.371^{**}	0.267^{**}	0.258^{**}	0.349^{**}	-0.155^{NS}		0.748^{**}
GY	0.591^{**}	0.322^{**}	0.442^{**}	0.565^{**}	0.520^{**}	0.76^{**}	

$p^{*}<0.05$, $p^{**}<0.01$, NS= Non-significant, GY= Grain yield, SPP= spike per plant, SPS= spikelet per spike, GPS= grain per spike, TGW= 1000-grain weight, BY= biological yield (g plant^{-1}), HI= harvest index

Table 7. Eigen vector, Eigen root and associated variation for principal component in wheat genotypes based on traits studied under salinity stress

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Spike plant^{-1}	0.4261	-0.1356	0.1828	-0.2492	0.4970	0.6662	0.1174
Spikelet spike^{-1}	0.3120	0.4520	0.5839	0.3195	- 0.4645	0.1857	0.0716
Grain spike^{-1}	0.3766	-0.0359	-0.6372	-0.1755	-0.5791	0.2774	0.0882
TGW	0.3836	-0.0821	-0.3084	0.8020	0.3042	-0.1132	0.0499
Biological yield plant^{-1}	0.2912	-0.6668	0.3151	-0.0897	-0.1998	-0.3692	0.4325
Harvest index	0.3414	0.5646	-0.1231	-0.3421	0.2635	-0.4623	0.3864
Grain yield plant^{-1}	0.4803	-0.0766	0.1010	-0.1918	0.0058	-0.2862	-0.7965
EigenValues	4.0555	1.2202	0.6140	0.4572	0.4316	0.1927	0.0288
Proportion of variance (%)	57.94	17.43	8.77	6.53	6.17	2.75	0.41

Cumulative proportion (%)	57.94	75.37	84.14	90.67	96.84	99.59	100

Table 8. Mean values of four clusters on traits studied under salinity stress

Cluster no.	Spike plan^{-1} (±SD)	Spikelet spike^{-1} (±SD)	Grain spike^{-1} (±SD)	TGW (g) (±SD)	BY (g plant^{-1}) (±SD)	HI (±SD)	GY (g plant^{-1}) (±SD)
I	2.27±0.22	15.16±1.00	35.02±1.90	38.25±2.43	10.1 ±0.60	0.36±0.02	3.62±0.15
II	2.70±0.13	16.35±0.53	39.74±2.74	45.16±4.12	10.26±0.65	0.41±0.02	4.21±0.38
III	2.59±0.19	16.17±1.19	37.10±2.46	38.79±1.97	9.50±0.18	0.42±0.03	3.90±0.10
IV	1.65±0.18	14.07±1.03	32.63±1.46	35.27±2.17	8.23±0.57	0.33±0.02	2.68±0.29
V	2.68±0.05	15.30±0.42	37.42±2.87	40.81±1.09	11.58±0.40	0.34±0.01	3.89±0.03

Note, BY= Biological yield, TGW= 1000- grain weight, HI= Harvest index, GY= Grain yield

Table 9. Intra (bold) and inter group distances (D^2) among the four clusters of wheat genotypes under salinity stress

Clusters	1	2	3	4	5
1	**2.5065**	4.682	3.972	5.724	4.682
2	-	**2.2510**	2.877	9.592	4.344
3	-	-	**2.2366**	8.617	4.928
4	-	-	-	**2.2168**	9.279
5					**1.6317**

Figure 1. Experimental Site.

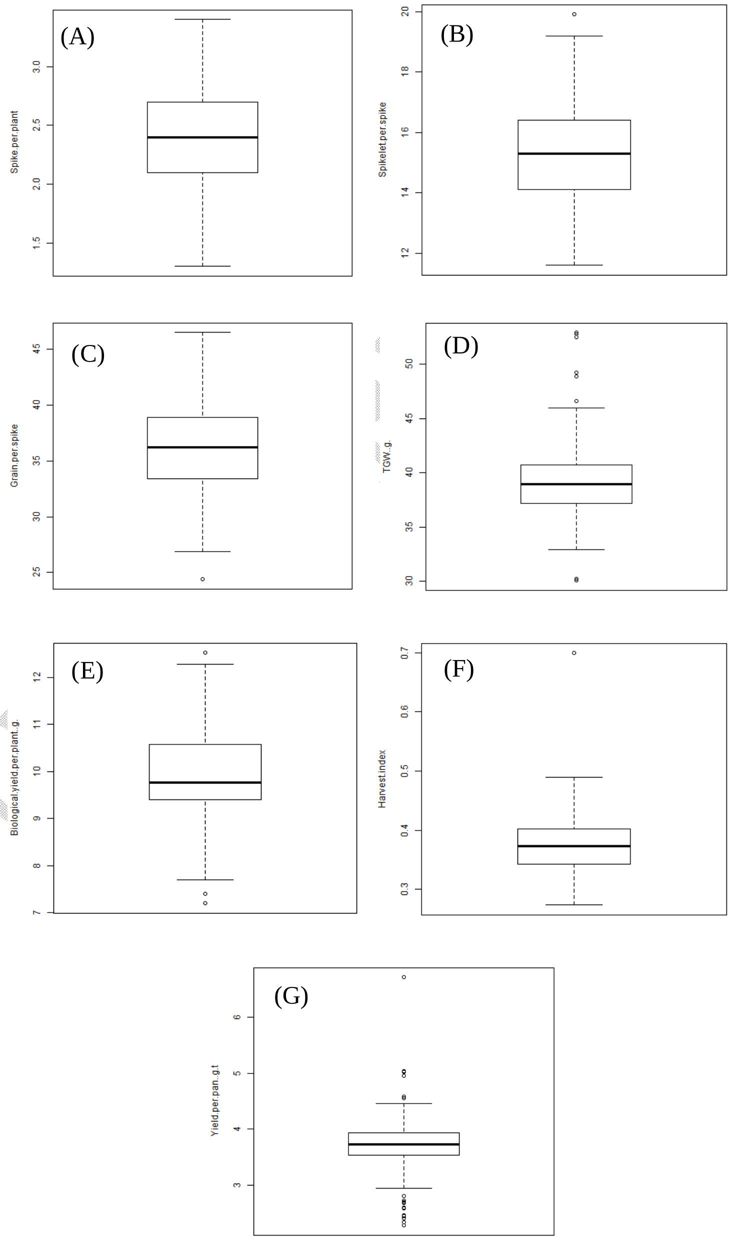

Figure. 2. Boxplots with minimum, maximum and mean values for (**A**) spike plant^{-1}, (**B**) spikelet spike^{-1}, (**C**) grain spike^{-1}, (**D**) TGW (g), (**E**) biological yield (g plant^{-1}), (**F**) harvest index and (G) grain yield (g plant^{-1})

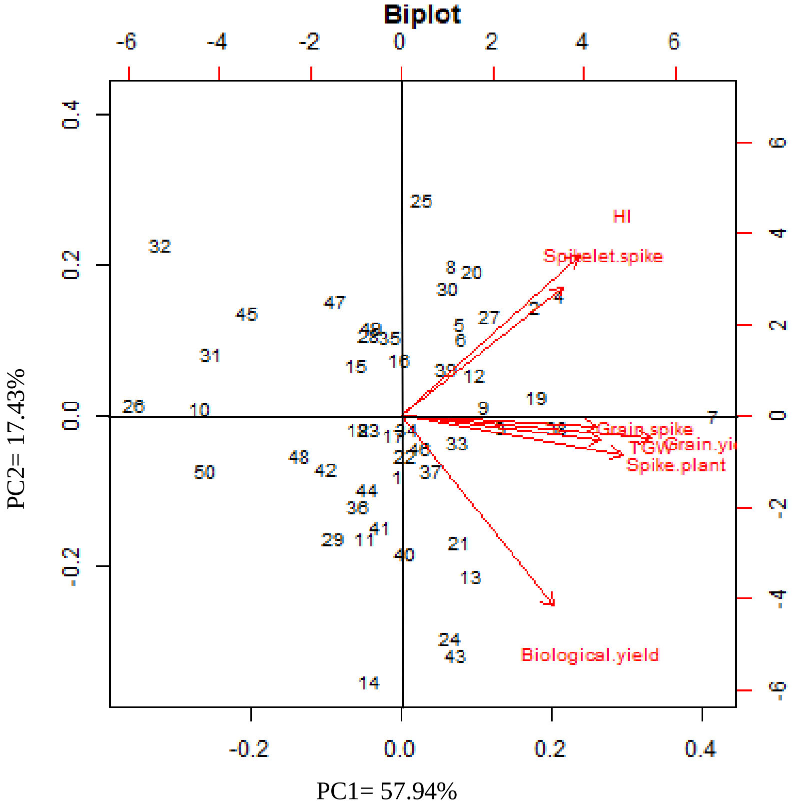

Figure 3. Biplot of the first two principal components for traits of 50 wheat genotypes studied under salinity stress.

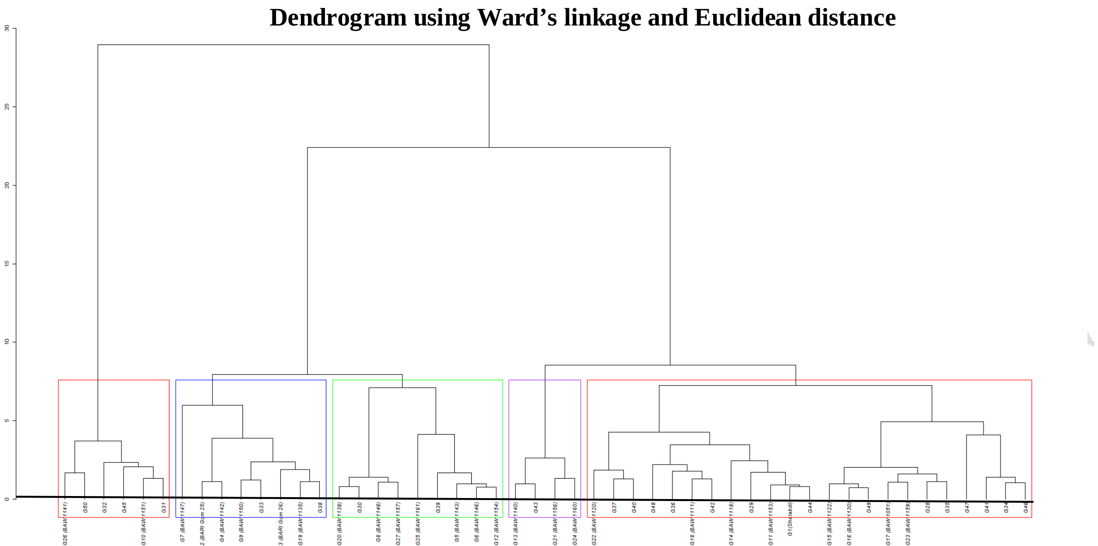

Figure 4. Dendrogram of 50 wheat genotypes using Agglomerative method with Ward's linkage and Euclidean distance based on traits under study

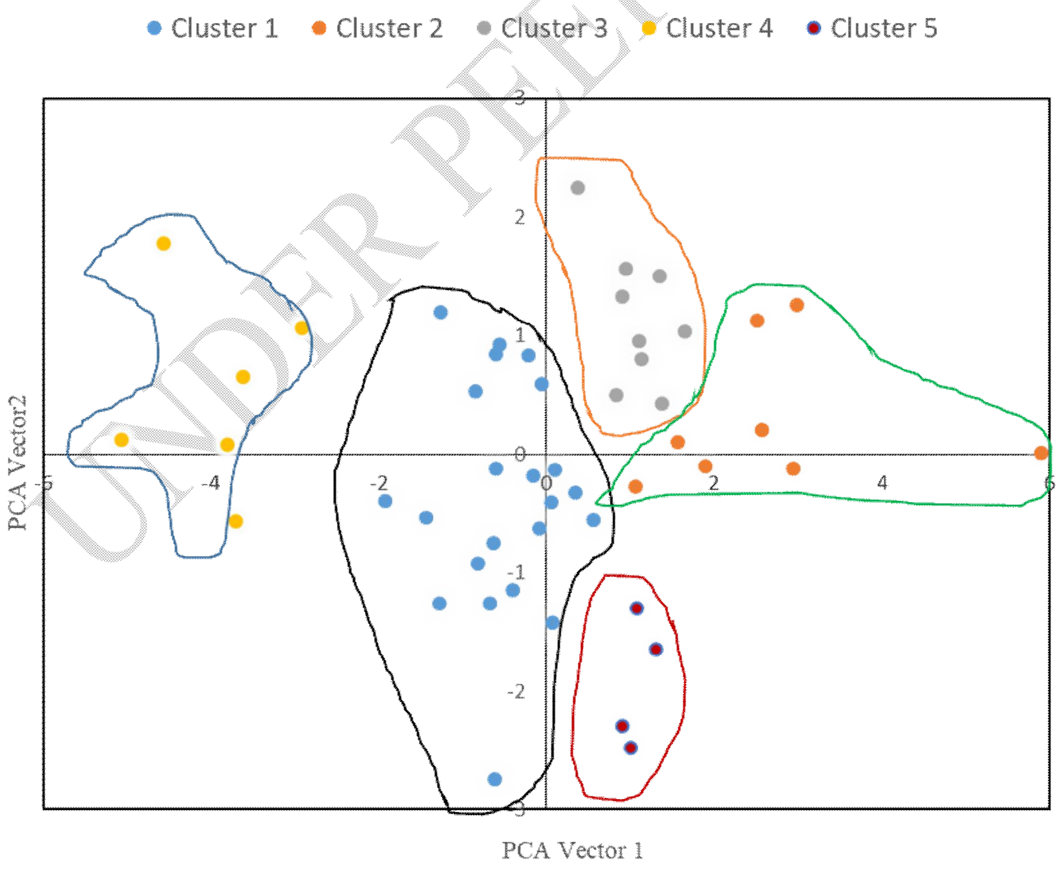

Figure 5. Two dimensional graph showing relative position of 5 cluster wheat genotypes based on PCA scores