Original Research Article

Evaluation and selection of wheat advanced lines for salt tolerance using yield and yield attributes as screening tool

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. Huge genetic variability was found among the evaluated wheat genotypes using different analyses for all the traits studied. The evaluated lines had been grouped into five clusters using cluster analysis ranging from high salt-tolerant to salt-sensitive genotypes. The detected 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 indicated that all traits were the important variables influencing grain yield and could be exploited as selection criteria for improving grain yield of wheat under saline conditions. Eight wheat lines i.e BARI Gom 25, BARI Gom 26, BAW 1135, BAW1142, BAW1147, BAW 1150, G33 and G38 under cluster number II were selected as high salinity tolerant that would be used in the breeding program develop further adapted varieties for salt-affected regions.

Key words: Evaluation, selection, wheat, salinity, tolerance, genetic variability, yield and yield attributes

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 about1.085 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 of 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) and most of the land remains 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 due to the toxicity effects of sodium and chloride ions at high concentrations to the plant (Munns and Tester, 2008). Salinity stress accelerates all phenological phases of wheat (Grieve et al., 2001), reduces 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 (Ahmed 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).

The destructive effects of salinity on wheat production can be mitigated by certain agronomic practices 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). So, 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, improving salt-tolerant genotypes faces inhibiting factors as a 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 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 characterized 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 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). 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 is a crucial assessment approach, since 18 the plants are screened under realistic and natural conditions such as soil heterogeneity, drought stress, and fluctuations of air temperature at the same time with salinity stress (Gavuzzi et al., 1997; Dadshani et al., 2019). Thus, genotypic evaluation under field conditions with saline water irrigation assists in identifying suitable genotypes that could be grown under salinity conditions, as well as potential parents that could be integrated into breeding programs for salt-tolerance (Mansour et al., 2020). The objectives of this study were to: (i) investigate the genetic variability of among the advanced wheat lines using the variables yield and yield attributes 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 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. Two third of urea and total amount of other fertilizers were applied during final land preparation. The rest amount of urea was top dressed at crown root initiation (CRI) stage followed by first irrigation. 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.

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. 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, phenotypic coefficient of variation, heritability, genotypic and phenotypic correlation coefficients among traits were computed by OPSTAT Statistical Software Package for Agricultural Research Workers developed by Sheoran et al. (1998). Genotypic variance and phenotypic variance were calculated from ANOVA by MS Excel program the presented table 2.

3. Results

3.1. Analysis of variance (ANOVA)

ANOVA results were 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 salt stress.

3.2. Range and mean values

A wide range of variations were found in yield and yield attributes among the genotypes shown in the table (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 wheat genotypes, 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 which was significantly different among the genotypes with its corresponding mean of 3.67 g per plant (Table 4). The range of biological yield among the genotypes treated with salinity 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). The wide range of variation observed in all the characters offers scope of selection for different quantitative traits of wheat. Similar findings in wheat have also reported by Kaddem 18 et al. (2014)

3.3. Genetic Variability

Genotypic and phenotypic variances (δ^2g and δ^2p), phenotypic and genotypic coefficients of variation (GCV and PCV) and broad-sense heritability (h^2_b) for the wheat genotypes are presented in table 5. It was found that the PCV was higher than GCV for all characters (Table 5) indicating that all interacted with the environment to some extent. PCV ranged from 9.86 to 18.70 with highest in spike per plant and lowest in TGW. GCV ranged from 4.45 to 13.95 with minimum in spikelet per spike and maximum spike per plant followed by grain per plant. High GCV in spike per plant, TGW, biological yield per plant, harvest index and grain yield per plant indicated the scope for effective selection. Low magnitude of GCV and PCV was observed in TGW, biological yield per plant and grain yield per plant indicated also suggested that the variability present among the genotypes grown under salinity stress were mainly due to genetic reason with minimum influence of environment and hence heritable. In the present study heritability values in broad sense ranged from 15.36% to 96.22% with lowest in spikelet per spike and highest in TGW (96.22%) followed by biological yield per plant (78.32%) and grain yield (76.11%). High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection under salinity stress condition.

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 revealed that genotypic correlation was higher than phenotypic correlation.

3.4. Principal Component Analysis (PCA)

The percent variations explained by each Eigen roots are presented in table 6. The Eigen root of first principal component was accounted 57.94% of total variation followed by second to 20 seventh components which accounted 17.43, 8.77, 6.53, 6.17, 2.75 and 0.41% of total variation presented among the genotypes, respectively. The first three PC axes with Eigen root>1 explained 84.14% of the total variation suggesting considerable diversity among the genotypes for all the traits studied under salinity stress and, the rest of the components not considered. The values of Eigen roots were interpreted as relative weight of the variables in each component.

The principal component score based on the correlation of 7 traits of 50 wheat genotypes explained by each Eigen roots are also presented in table 7. Negative values for traits in any of the vectors indicated lower contribution of the trait in variability while positive values indicated higher contribution (Table 7). The first principal component had high positive scores for all the traits which indicated selection of wheat genotypes based the traits studied under salinity stress were justified (Table7). Iqbal et al. (2008) reported that quantitative traits that contributed positively in principal component analysis could be considerable importance for the genetic materials under investigation. The traits contributed maximum to the variability are used to give greater emphasis for further selection of genotypes (Jagadeb and Samal, 1991). Principal component analysis reflects the importance of the largest contributor to the total variation (Sharma, 1998).

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, which indicate a high level of genotypic variation among the tested genotypes. The trait vectors are represented by acute angles, indicating positive associations (Figure 3). Thus, the traits spike per plant, spikelet number per spike, grain number per spike, TGW were strongly correlated with yield and these traits could help with grain yield to identify superior wheat genotypes.

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 showed 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 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 indicated the presence of genetic variations among the lines for these characters (Table 4, Figure 2). The results of current studied showed the similarity of research works of some researcher (Banik et al., 2019; Moustafa et al., 2021). Furthermore, the genotypic variance (σ^2g) and genotypic coefficient of variation (GCV) demonstrated the presence of inherent genetic differences among the evaluated lines in respect of measured agronomic traits (Table 5). The results of Banik et al. (2019) and Moustafa et al. (2021 supported the results of the present study. These genetic differences of measured agronomic traits reflected the potential of these lines in enhancing the genetic diversity through favorable alleles that could be exploited through breeding for improving salt-tolerance. On the other hand, the values of phenotypic variance (σ^2p) and phenotypic coefficient of variation (PCV) were slightly higher than those of genotypic variance (σ^2g) and genotypic coefficients of variation (GCV) for evaluated traits. These findings demonstrate the inherent variations among the evaluated lines that remain unaltered by environmental conditions that are beneficial for utilization in breeding for salt-tolerance. In addition, the lower environmental impact on these traits signified the improvement that can be achieved through selection based on phenotypic expression. Additionally, finding intermediate to high broad-sense heritability for evaluated traits studied confirmed the efficiency of these traits for direct phenotypic selection to identify salt-tolerant genotypes. The presumptions were supported by the pointed response of these traits to selection under salt stress (Banik 14 et al., 2019; Moustafa et al., 2021).

Principal component analysis being 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). The first principal component had high positive scores for all the traits which indicated selection of wheat genotypes based the traits studied under salinity stress were justified (7). Iqbal et al. (2008) reported that quantitative traits that contributed positively in principal component analysis could be 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 indicate a high level of genotypic variation among the tested genotypes. The trait vectors are represented by acute angles, indicating positive associations (Figure 3). Thus, the traits spike per plant, spikelet number per spike, grain number per spike, TGW were strongly correlated with yield 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 had been made 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. Literature emphasizes on the use of cluster analysis to screen the wheat genotype for salt tolerance (Moustafa et al., 2021; Sarazafar et al., 2015).

The traits under this study showed highly significant positive relationship with yield in terms of genotypic and phenotypic correlations (Table 6) indicated that all traits were the important variables influencing grain yield and could be exploited as selection criteria for improving grain yield of wheat under saline conditions. Some researcher 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). The results under this study demonstrated the genotypic correlation coefficients were higher than phenotypic correlation coefficients (Table 6) represented the association was due to genetic reason which was 8 similar with the results of research Tripathi *et al.* (2015) and Banik et al. (2019). 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. All the traits displayed a strong positive association with grain yield, which indicates 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)

Conclusion: From the above discussion it could be concluded huge variability was identified among the evaluated wheat lines based on yield and yield attributes under salinity conditions at yielding 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 indicated that all traits were the important variables influencing grain yield and could be exploited as selection criteria for improving grain yield of wheat under saline conditions. Besides, the PC-biplot displayed the strong relationship of traits studied with grain yield that could help to identify superior wheat genotypes. Thus, eight wheat lines i.e BARI Gom 25, BARI Gom 26, BAW 1135, BAW1142, BAW1147, BAW 1150, G33 and

20 G38 under cluster II had been selected as salt tolerant wheat lines under salinity which could be exploited as a novel genetic material to enhance breeding for salt-tolerance.

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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

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 (%)
Spike per plant	0.11	0.19	13.95	18.70	55.66
Spikelet per spike	0.47	3.06	4.45	11.36	15.36
Grain per spike	6.35	14.03	6.99	10.39	45.27

1000-grain weight	14.44	15.01	9.67	9.86	96.22
Biological yield per plant	0.84	1.07	9.23	10.43	78.32
Harvest index	0.001	0.002	9.33	12.96	53.47
Grain yield per plant	0.22	0.29	12.71	14.57	76.11

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.

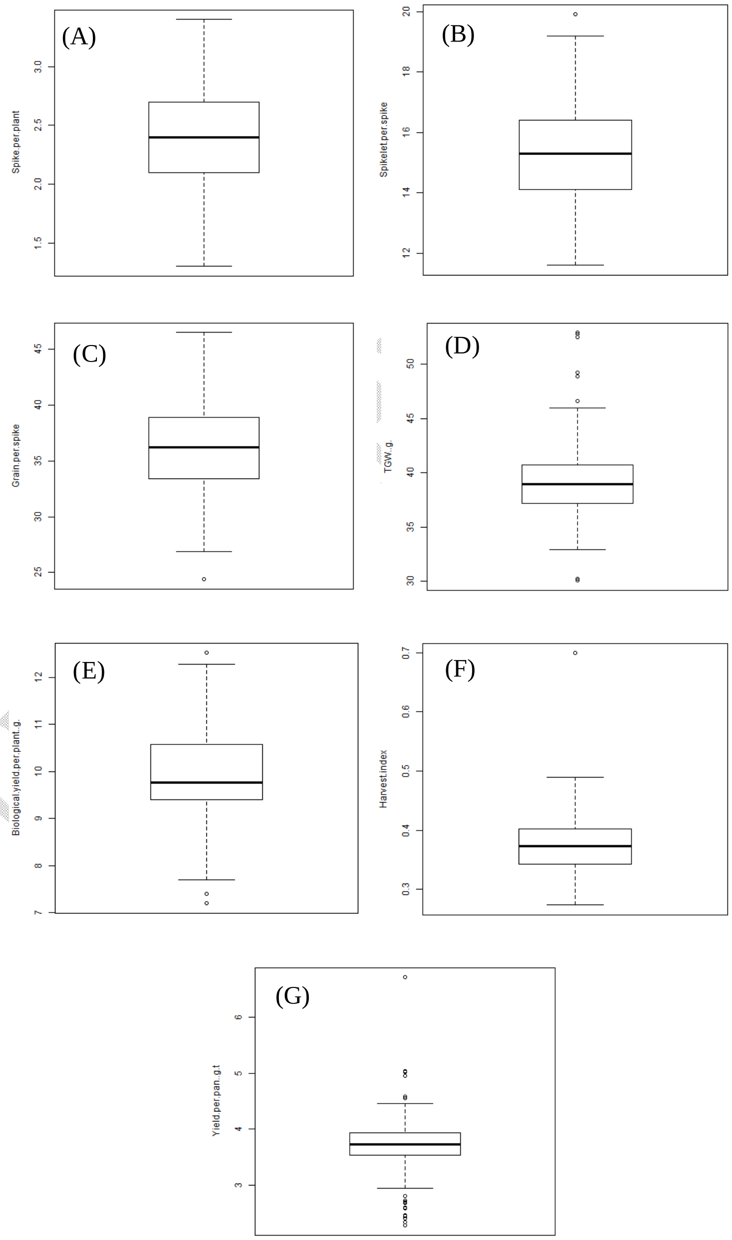

Figure. 2. Boxplots with minimum, maximum and mean values for (**A**) spike plant^{-1}, (**B**) spikelet spike^{-1}, (**C**) grain spike^{-1}, (**D**) TGW (g), (**E**) biological yield (g plant^{-1}), (**F**) harvest index and (G) grain yield (g plant^{-1})

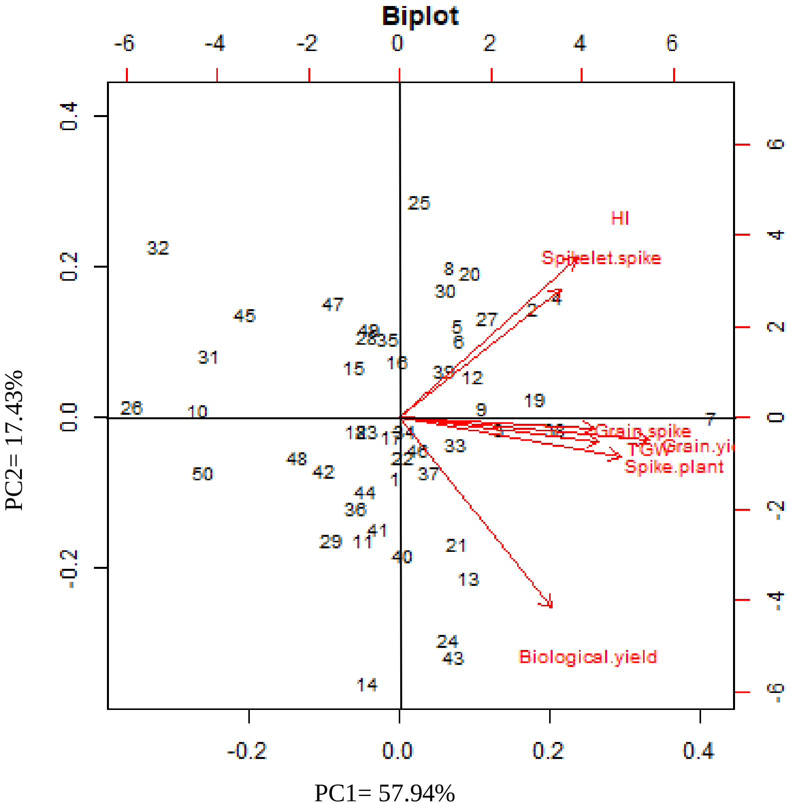

Figure 3. Biplot of the first two principal components for traits of 50 wheat genotypes studied under salinity stress.

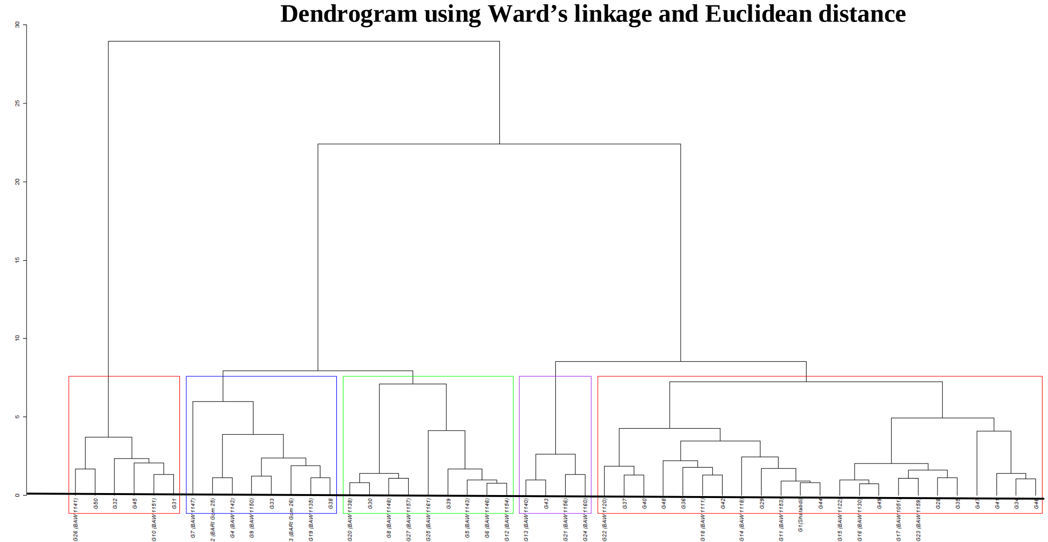

Figure 4. Dendrogram of 50 wheat genotypes using Agglomerative method with Ward's linkage and Euclidean distance based on traits under study

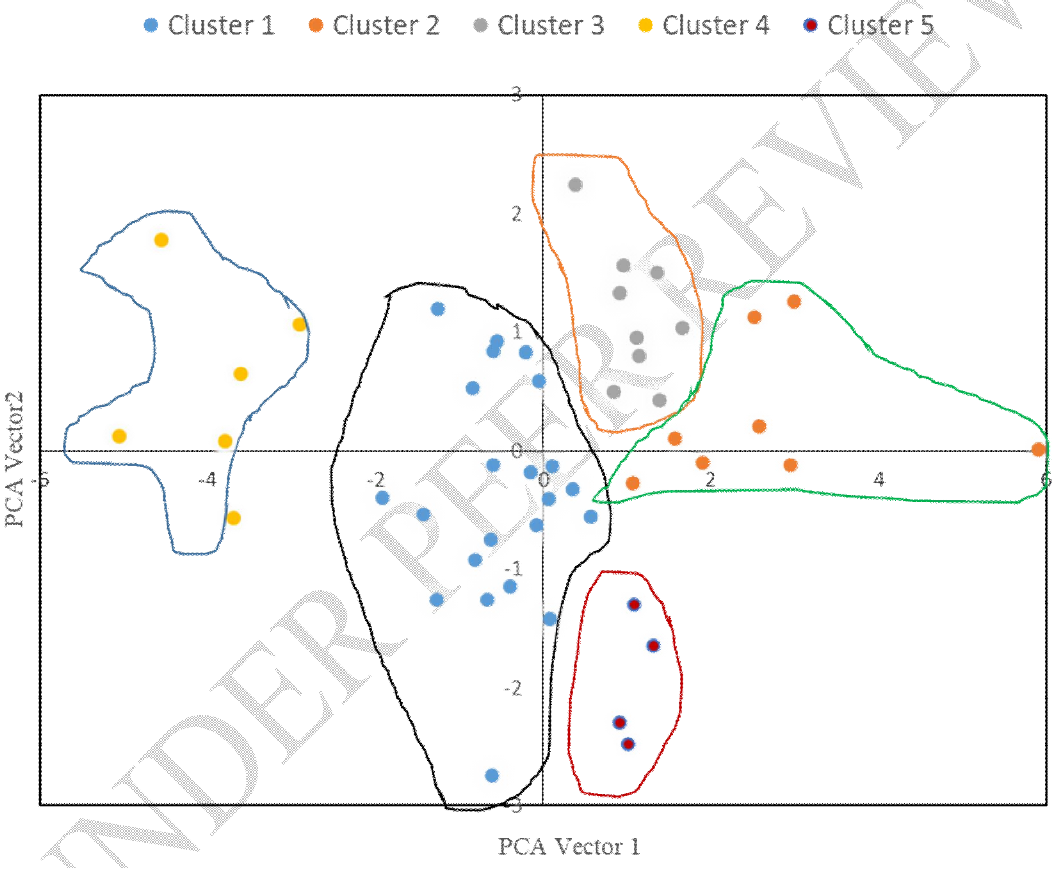

Figure 5. Two dimensional graph showing relative position of 5 cluster wheat genotypes based on PCA scores