Study Of Variability In Wheat (Triticum aestivum L.) Under Saline Condition

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ABSTRACT

A pot experiment was conducted at the Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur, Bangladesh during the period from November 2012 to April 2013 in order to study the genetic variability of 10 wheat genotypes in saline condition. The experiment was laid out in a Completely Randomized Design (CRD) with three replications. In this experiment, the seeds of the 10 wheat genotypes were used viz. Aghrani, Sawrav, Shatabdi, BARI-25, BARI-27, PYT-12, PYT-13, PYT-15, PYT-20 and BAW – 1135. Mean performance, mean separation, variance, heritability, genetic advance and genetic advance of percent of mean were done on yield and yield contributing characters namely days to heading, number of tillers, days to maturity, plant height (cm), spike length (cm), spikelet per spike, grain per spike, root length (cm), root volume (cm^3), root weight (gm), root dry weight (gm) and grain yield per plant. The highest grain yield per plant (3.297 gm) was recorded from BAW – 1135 again the lowest (1.637 gm) was found from Aghrani. Analysis of variance reveals that, plant height (23.03) is significant at 5% level of probability. On the other hand days to heading (21.328), spike length (0.703) and grain per spike (67.470) are significant at 1 % level of probability. Phenotypic variance (0.2433) was higher than genotypic (0.138) variance which was supported by low difference between phenotypic (21.455%) coefficient of variation and genotypic (16.158) coefficient of variation. Heritability estimates revealed that characters like days to heading exhibited highest heritability followed by spike length and grain per spike. Genetic Advance revealed that it was low in all the characters. Genetic Advance as percent of

mean revealed that it was high for grain per spike, yield per plant, root volume and root weight and moderate estimates were exhibited by root dry weight and number of tillers per plant and low genetic advance as percent of mean was observed for days to heading, days to maturity, plant height, spike length, spikelet per spike and root length. Moderate heritability (56.72%) was supported by high genetic advance over mean (25.068). Characters like grain per spike showed high heritability coupled with high genetic advance as percent of mean therefore, this character should be given top priority during selection breeding in wheat in saline condition

Keywords: genetic variation; heritability; genetic diversity, wheat (*Triticum aestivum* L.)

1. INTRODUCTION

Wheat (*Triticum aestivum*) belonging to the family gramineae is a leading cereal throughout the world. It is one of the most important cereal crops of the world ranking first both in acreage and production among the puffed rice crops. In Bangladesh, Wheat is the second largest grain cereal crop next to rice. Wheat offers a great wealth of material for genetical studies due to its wide ecological distribution and enormous variation encountered for various morphological and physiological characters (Rangare *et al.* 2013). Increasing population together with food shortage and land insufficiency is enforcing the nation to grow food crops on the land that has been unutilized because of soil problems. In 1998–99, wheat area and production was 883,000 ha and 1,908,000 t, which represented the highest wheat area and production in the history of Bangladesh (BBS, 2002). But gradually wheat cultivation land and production decrease in course of time due to intrusion of salinity and strong competition with other high yielding cereals.

There are a number of environmental issues and problems that are hindering development of Bangladesh. Salinity is a current problem, which is expected to exacerbate by climate change and sea level rise. Salinity intrusion due to reduction of freshwater flow from upstream, salinization of ground water and fluctuation of soil salinity are major concern of Bangladesh. Cyclones and tidal surge is adding to the problem. Tidal surge brings in saline water inside the polders in the coastal area. Due to drainage congestion, the area remains waterlogged, increasing the salinity (Abedin, 2010). Salinity is one of the most important environmental stresses which severely limit plant growth and productivity worldwide (Tester and

Davenport, 2003). The problem is ever increasing because of irrational human acts causing secondary salinization and climate change with consequent rise in sea level (Haque, 2006). However, some research on varietals performance was also obtained in various coastal region of the world with some scientist to find out the most suitable variety. Due to salinity problems the yield of wheat is not satisfactory in our country. While the other country enjoy a better average yield of wheat ours is still a poor average yield. Yield of improved cultivars in Bangladesh is about 3 tons per hectare in farmer's field whereas in some developed countries it is 10 tons per hectare (FAO, 2012). This fact emphasizes the necessity of increasing yield potentiality through breeding programme An effective breeding programme depends upon the availability of genetic variation of the breeding materials. If the variability in the population is largely due to genetic cause with least environmental cause, the probability of selecting superior genotypes is high. But it is often difficult to judge as to what proportion of the observed variability is heritable (genotype) and what proportion is non-heritable (environment), particularly in case of characters controlled by a polygenic system. The progress of breeding in such a population is primarily conditioned by the magnitude, nature and interaction of genotype and environmental variation for yield and yield contributing characters. It then becomes necessary to partition the observed variability into its heritable and non-heritable components with the help of suitable genetic parameters such as genotypic and phenotypic coefficient of variation, heritability, genetic advance under selection etc. Moreover, the interaction of variance indicate as the variability in the relative performance of genotypes under different environments and their magnitude in comparison to genetic variances for various characters and different populations determine the need for replication in location, years and individual tests in the accurate estimation of the means upon which selection is based.

Therefore the present investigation was carried out to study the variability, heritability and genetic advance, evaluate the performance of the wheat genotypes in saline condition and to identify the suitable wheat variety in saline soil

2. MATERIALS AND METHODS

The experiment was set up at the central research farm and laboratory of Genetics and Plant Breeding Department, Hajee Mohammad Danesh Science and Technology University (HSTU), Dinajpur during October 2013 to June 2014. The experimental site is situated under the Dinajpur Sadar Upazila and located at 25º39′ N latitude and 88º41′ E longitude with an

elevation of 37.58 meter above the sea level. For conducting the present study, the base materials were collected from the Wheat Research Center (WRC), Dinajpur. The experiment was laid out in Completely Randomized Design (CRD) with three (3) replications. The layout of the experiment was prepared for distributing the genotypes into the every pot of each block. The 10 genotypes of the experiment were assigned at each replication maintaining equal pot to pot distance. In this experiment two different treatment of salinity were used. One of those was controlled condition i.e 0 ds/m and another was 10 ds/m. Both dose of salinity was applied in equal amount in the pots at same time and same methodThe seed germination and stand establishment in saline conditions were evaluated in pot experiment filled with soil collected from the field experiment site of Genetics and Plant Breeding Departments Research field. The soil of pot prepared by mixing 50% cow dung, 50% soil and with inorganic fertilizer (Urea, Mop). Soils were prepared 10 days prior to seed sowing. On 15 November wheat seeds were sown on the pots. All the characters were observed at appropriate growth and development stages of wheat plants. Observations were recorded both in the field and in the laboratory in chronological order following the guidelines of the UPOV (1981) and NIAB (1986). The characters included in the study were heading days, productive tillers per plant, maturity days, plant height, spike length, number of spikelet's per spike, number of grains per spike, root length, root volume, root mass/weight, root dry weight, yield per plant. The data for different parameters were compiled and tabulated in proper form. The obtained data on different parameters under the experiment were statistically analyzed to obtain the level of significance using MS Excel MSTAT-C computer program developed by Russell (1986).

Table 1: List of 10 Genotypes of wheat with their entry

SL. No.	Salinity	Entry	Genotypes
1.	10 ds	E-1	Aghrani
2.	10 ds	E-3	Sawrav
3.	10 ds	E-5	Shatabdi
4.	10 ds	E-9	BARI-25
5.	10 ds	E-11	BARI-27
6.	10 ds	E-15	PYT-12

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7.	10 ds	E-16	PYT-13
8.	10 ds	E-18	PYT-15
9.	10 ds	E-22	PYT-20
10.	10 ds	E-24	BAW-1135

3. RESULTS AND DISCUSSION

3.1 Analysis of variance of yield and yield contributing characters of 10 wheat genotypes

In the present experiment the yield and yield contributing characters showed significant differences for different wheat genotypes. Analysis of variance (ANOVA) of the data of different parameters is presented in Table 2. The range of mean values could present a rough estimate about the variation in magnitude of variability present among genotypes. The characters showing high range of variation have more scope for improvement. As range for most of the all genotypes was less there was scope for improvement of their traits.

3.2 Mean performance and mean separation of 12 important characters of 10 wheat genotypes

The range and mean performance of the genotypes are presented in Table 3Among the different wheat genotypes that were used in present experiment the maximum days to heading (71.65) was recorded from Sawrav and the minimum days (63.47) was recorded from PYT – 13. The maximum number of tiller 3.00 was observed from Sawrav while the minimum number of tiller was found (1.900   ) from PYT – 13. Akram *et al.* (2002) reported that salinity causes a significant reduction in development of spike, tillering ability, spikelets and grain per spike. Wheat yield starts decline at $6 – 8$ m^{-1} (Maas and Hoffman, 1977). The maximum days to maturity (104.566) was observed from PYT – 20 and the minimum was found (99.700) from BAW – 1135. In case of different wheat genotypes the tallest plant (65.17) was recorded from PYT – 15 and again the shortest plant (55.67) was observed from BAW - 1135. The highest spike length (10.57) was found from PYT – 13 and the lowest (9.003) was observed from BARI – 27. The maximum spikelet per

spike (14.48) was found from Aghrani and the minimum was observed from PYT – 12. The maximum number of grains per spike (41.60) was observed from Aghrani and the minimum was observed from PYT – 15. The highest root length (21.40) was found from BAW – 1135 and the lowest (16.64) was observed from BARI – 25. The maximum root volume (2.853) was observed from BARI – 25 and the minimum was (1.310) observed from BARI – 25.The highest root weight (1.503) was found from Shatabdi and the lowest (0.5467) was observed from BARI – 25. The highest dry root weight (1.357) was observed from Sawrav and the lowest (0.5900) was observed from PYT – 15. The highest grain yield per plant (3.297) was recorded from BAW – 1135 and the lowest (1.637) was recorded from Aghrani.

Table 2: Analysis of variance of yield and yield contributing characters of 10 wheat genotypes

Source of Variation	Replication	Treatment	Error	Coefficient of Variance (%)
df	2	9	18	
Days to heading	3.383	21.328 **	2.568	2.40
Tiller number	4.464	0.387	0.245	21.594
Days to maturity	87.403	9.138	7.359	2.687
Plant height(cm)	103.463	23.031 *	8.964	4.927
Spike length (cm)	1.399	0.703 **	0.148	3.803
Spikelet / spike	35.559	1.502	0.658	6.14
Grain/ Spike	109.075	67.470 **	13.490	12.284
Root length	3.661	6.732	2.901	9.15
Root volume	0.145	0.483	0.227	24.906
Root weight	0.131	0.283	0.185	42.74
Root dry weight	1.533	0.166	0.115	36.01
Yield/ plant	5.379	0.730	0.316	24.46

*Significant at 5 % level of probability; ** significant at 1 % level of probability

Table 3: Mean performance and mean separation of 12 important characters of 10 wheat genotypes

Genotypes	Days to heading	No. of tillers	Days to maturity	Plant height	Spike length	Spikelet/ Spike
Aghrani	66.23 b	2.000 b	100.933 a	59.82 abc	10.42 ab	14.48 a
Sawrav	71.65 a	3.000 a	104.000 a	60.28 abc	9.458 de	14.19 ab
Shatabdi	70.32 a	2.567 ab	99.866 a	61.83 ab	9.488 cde	12.84 bc
BARI-25	64.67 b	2.233 ab	101.200 a	63.18 a	10.20 abc	12.92 abc
BARI-27	65.60 b	2.767 ab	99.933 a	57.08 bc	9.003 e	13.26 abc
PYT-12	66.21 b	2.100 ab	101.266 a	61.27 abc	10.10 abcd	11.96 c
PYT-13	63.47 b	1.900 b	100.50 a	61.78 ab	10.57 a	13.04 abc
PYT-15	66.20 b	2.133 ab	99.766 a	65.17 a	10.05 abcd	12.98 abc
PYT-20	69.40 a	2.200 ab	104.566 a	61.65 ab	9.640 cde	13.39 abc
BAW-1135	65.00 b	2.100 ab	99.700 a	55.67 c	9.791 bcd	13.09 abc
Range	63.47-71.65	1.900-3.000	99.70-104.566	55.67-65.17	9.003-10.57	11.96-14.48
Mean	66.875	2.3	101.173	60.773	9.87	13.215
LSD value	2.749	0.8525	4.652	5.137	0.6418	1.391
CV%	2.40	21.594	2.687	4.93	3.803	6.14

Within columns means followed by the same letter are not significantly different at the 0.05 level according to Duncan's multiple range test.

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Table 3: Contd…..

Genotypes	Grains/Spike	Root length	Root volume	Root weight	Root dry weight	Yield/ Plant
Aghrani	41.60 a	18.84 ab	1.699 b	1.387 ab	1.183 ab	1.637 b
Sawrav	33.67 b	18.06 ab	2.050 ab	1.210 ab	1.357 a	2.727 ab
Shatabdi	28.32 bc	19.92 ab	1.953 b	1.503 a	1.090 ab	2.523 ab
BARI-25	29.58 bc	16.64 b	1.310 b	0.5467 b	0.6733 b	2.413 ab
BARI-27	28.40 bc	17.22 ab	1.641 b	1.017 ab	0.9200 ab	2.323 ab
PYT-12	27.02 bc	17.22 ab	1.781 b	0.9600 ab	1.030 ab	2.260 ab
PYT-13	26.35 c	17.83 ab	1.930 b	0.9900 ab	0.9267 ab	1.740 b
PYT-15	25.75 c	19.98 ab	1.805 b	0.7433 ab	0.5900 b	1.870 b
PYT-20	27.30 bc	18.94 ab	2.093 ab	1.057 ab	0.8967 ab	2.197 b
BAW-1135	31.12 bc	21.40 ab	2.853 a	0.6433 b	0.7400 ab	3.297 ab
Range	25.75-41.6	17.22-21.40	1.31-2.853	0.5467-1.503	0.590-1.357	1.637-3.297
Mean	29.91	18.605	1.911	1.006	0.941	2.299
LSD value	6.303	2.922	0.7805	0.7378	0.5817	0.9643
CV%	12.285	9.15	24.906	42.74	36.01	24.46

Table 4: Estimation of genetic parameters for yield and yield contributing characters of 10 wheat genotypes

Characters	Vg	Vp	GCV (%)	PCV (%)	h^2 (%)	GA	GA (%)
Days to heading	6.253	7.109	3.739	3.987	87.959	4.83	7.224
No. of tiller	0.04733	0.12899	9.459	15.616	36.69	0.2715	11.803
Days to maturity	0.593	3.046	0.761	1.725	19.468	0.6999	0.692
Plant height	4.689	7.677	3.563	4.56	61.079	3.486	5.736
Spike length	0.185	0.23433	4.3574	4.904	78.96	0.787	7.9763
Spikelet/spike	0.28133	0.43766	4.014	5.006	64.28	0.876	6.6288
Grain/spike	17.993	22.49	14.18	15.86	79.987	7.814	26.126
Root length	1.277	2.244	6.074	8.052	56.91	1.756	9.4398
Root volume	0.0853	0.16097	15.283	20.995	52.992	0.438	22.918
Root weight	0.03267	0.0943	17.967	30.525	34.645	0.219	21.789
Root dry weight	0.017	0.05533	13.86	24.997	30.725	0.1489	15.822
Yield/ plant	0.138	0.2433	16.158	21.455	56.72	0.5763	25.068

Vg = genotypic variance, Vp = phenotypic variance, GCV (%) = genotypic coefficient variation, PCV (%) = phenotypic coefficient of variation, h^2 (%) = heritability, GA = genetic advance, GA (%) = genetic advance as percent of mean

3.3 Genetic parameters for yield and yield contributing characters of 10 wheat genotypes

The expected genetic parameters for twelve characters of the genotypes evaluated is presented in Table 4.Days to heading in terms of phenotypic variation (7.109) were higher than genotypic variance (6.253) which was supported by narrow difference between phenotypic (3.987%) and genotypic (3.739%) coefficient of variation. High heritability

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(87.959%) for days to heading coupled with low genetic advance in percentage of mean (7.224%). Due to consideration of phenotypic variation (0.128997) was higher than genotypic variation (0.04733) which was supported by narrow difference between phenotypic (15.616%) and genotypic (9.459%) coefficient of variation. Moderate heritability (36.69%) for numbers of tillers attached with moderate genetic advance over mean (11.803%).

Considering days to maturity for phenotypic variation (3.046) was higher than the genotypic variance (0.593) which was supported by narrow difference between phenotypic (1.725%) and genotypic (0.761%) coefficient of variation. Low heritability (19.468%) for days to maturity with low genetic advance (0.6999) and low genetic advance in percentage of mean (0.692%).In context of phenotypic variation (7.677) was higher than genotypic variance (4.689) and supported by low difference between phenotypic (4.56%) and genotypic (3.563%) coefficient of variation. High heritability (61.079%) for plant height along with low genetic advance in percent of means (5.736%) for this trait. Phenotypic variation (0.23433) was higher than the genotype variance (0.185) which was supported by narrow difference between phenotypic (4.904%) and genotypic (4.3574%) coefficient of variation considering spike length. High heritability (78.96%) for spike length along with low genetic advance in percentage of mean (7.9763%) for this trait.

Considering the parameter spikelet per spike the phenotypic variance was higher (0.43766) than genotypic variance (0.28133) supported by narrow difference between phenotypic (5.006%) and genotypic (4.014%) coefficient of variation. High heritability (64.28%) for spikelet per spike along with narrow genetic advance over means (6.6288%). Due to the consideration of number of grain per spike in respect of phenotypic variation (22.49) was higher than genotypic variation (17.993) and was supported by narrow difference between phenotypic (15.86%) and genotypic (14.18%) coefficient of variation. High heritability (79.987%) for grain per spike coupled with high genetic advance in percentage of mean (26.126%). Kumar *et al.*(2003) reported high heritability coupled with high genetic advance for plant height, number of spikelet's/ear, 1000-grain weight and number of days to 50% heading in wheat.

In context of root length in terms of phenotypic variation (2.244) was higher than the genotypic variance (1.277) which was supported by narrow divergence between phenotypic (8.052%) and genotypic (6.074%) coefficient of variation. Moderate heritability (56.91%) for root length coupled with low genetic advance in percentage of mean (9.4398%). Due to the

consideration of root volume phenotypic variation (0.16097) was higher than the genotypic variance (0.0853) which was supported by narrow divergence between phenotypic (20.995%) and genotypic coefficient of variation. Moderate heritability (52.992%) for root volume coupled with high genetic advantage in percentage of mean (22.918%). Azhar *et al.* (1989) estimates broad sense heritability of salt tolerance root growth data of four-week-old seedlings of 98 wheat accessions grown in 0, 10 and 15 dSm-1 NaCl solutions. Estimates of broad sense heritability for absolute and relative root length were moderate in size (0.44 to 0.62) suggesting the scope for enhancing salt tolerance in wheat through selection and breeding.

Due to consideration of root weight phenotypic variation (0.0943) was higher than the genotypic variance (0.03267) which was supported by moderate divergence between phenotypic (30.525%) and genotypic (17.967%) coefficient of variation. Moderate heritability (34.645%) for root weight coupled with high genetic advantage in percentage of mean (21.789%). Khaliq *et al.* (2009) conducted an experiment on board sense heritability and genetic advance values for some yield contributing traits like plant height, spike length, spikelets per spike, spike density, grains per spike, and 1000-grain weight and grain yield per plant in wheat. In this experiment the Broad sense heritability estimates for F_2 population were generally low to moderate and moderate to high with genetic advance potential and quantitative pattern of inheritance was observed. They also observed genetic improvement in material can be done by proper selection method.

Considering the parameter root dry weight the phenotypic variance was higher (0.05533) than genotypic variance (0.017) supported by moderate difference between phenotypic (24.997%) and genotypic (13.86%) coefficient of variation. Moderate heritability (30.725%) for root dry weight along with moderate genetic advance over means (15.822%). Due to consideration of yield per plant phenotypic variance (0.2433) was higher than genotypic variance (0.138) which was supported by narrow difference between phenotypic (21.455%) and genotypic (16.158%) coefficient of variation. Moderate heritability (56.72%) was supported by high genetic advance over mean (25.068%).

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Grain yield per plant of wheat showed positive and significant association with days to heading (21.328), plant height (23.031), spike length (0.703) and grain per spike (67.470) in wheat genotypes. Whereas insignificant positive association was recorded from days to tiller number (0.387), days to maturity (9.138), spikelet per spike (1.502), root length (6.732), root volume (0.483), root weight (0.283) and root dry weight (0.166).

4. Conclusion

From the above calculated data it is found that there is enough difference in coefficient of variation among the traits and from DMRT study it is clear that spike length obtained maximum lettering followed by plant height and spikelet's per spike which indicates more variability among the genotypes i.e. less environmental influence and greater scope for improvement for the characters viz., spike length, spikelet per spike, plant height, grain per spike and yield per plant. As most of the traits are different in heritability and genetic advance it indicates variability on the genotypes. So finally it can be concluded that there is enough variability on spike length, plant height spikelets per spike and grain per spike.

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