Genetics for salinity tolerance traits in wheat (*Triticum aestivum* L)

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ABSTRACT

Combining ability and genetic architecture for salinity tolerance traits in wheat to determine the nature and extent of gene action on salinity tolerant characters. Combining ability analysis revealed that significant general combining ability (GCA) and specific combining ability (SCA) for all the characters viz. shoot length, reduction of shoot length (RSL), total shoot dry matter (TDM), reduction of shoot dry matter (RSDM), relative total dry matter (RTDM), scoring based on RTDM and visual scoring indication involvement of both additive and non-additive gene actions in the inheritance of these salinity traits. GCA: SCA exhibited less than one suggesting preponderance non-additive gene action for controlling these characters. No single parent contained all the desirable traits. P45 and P33 were appeared to be the best general combiner for salt tolerance traits. The cross P1 X P15, P11 X P15 and P15 X P22 were found the best specific combiner for the traits. The best cross involved poor x poor general combiner indicating over dominance and transgressive segregation gene action on resistance of salt. Vr-Wr analysis also showed over dominant type of gene action in the inheritance of salt tolerance trait.

INTRODUCTION

Wheat is one of the important cereal crops produced widely and intensively all over the world. It is grown in a wide range of latitudes (67^0N to 45^0S). Major world production comes from the south temperate zones. It ranks second in position among the cereals in Bangladesh next to rice. The winter season of Bangladesh is favorable for wheat cultivation. The varieties grown in Bangladesh belong to spring wheat wheat (*Triticum aestivum*). Wheat is gaining popularity as a staple crop of our country day by day. It plays a vital role in the national economy to reduce the deficit between the food production and food import. Bangladesh has made considerable progress in producing wheat and it produces about 1.38 million tons from about 0.44 million hectare with an average yield of 3.1 t/ha (Anonymous, 2016). However, these production levels are still not sufficient to feed the country's rapidly growing population and are met by import from the international market.

Bangladesh has almost three million hectares of land affected by salinity, mainly in the coastral and south-eastern districts, with EC values ranging between 4 and 16 dS/m (Rahman *et al.* 2012, Zaman, and Bakri. 2003.). This salinity is caused primarily by seawater intrusion in both surface and ground water. More areas are under threat of salinisation due to the effect of sea level rise, coastral subsidence, increased tidal effect and continuous reduction of river flow, particularly during dry period (Rahman *et al.* 2012, Anonymous, 1998). Due to low upland flow in the rivers, it is estimated that salinity level moves up to 160 Km inland and the salinity level of the shallow aquifers in the coastal area reaches up to 60m (Anonymous, 1990 and Islam, 1990). Aman rice is the major crop cultivated in salt affected areas (saline/coastal belt) of the country. After harvesting Aman rice, a vast area of land in the coastal belt remains either fallow or covered by some minor crops at marginal level of production. Wheat cultivation in those areas is limited mostly due to non-availability of suitable varieties. Therefore, it would be highly useful if wheat

variety(s) tolerant to salinity could be developed to alleviate food deficiency in the country.

Several authors Ray and Islam (2007), Paramasivan (1979); Moeljopawiro and Ikehashi, (1981); Gregoria and Senadhura (1993) reported that most of the hybrids between tolerant and susceptible varieties enhanced tolerance to adverse soil conditions. So it is possible to incorporate salt tolerance through hybridization between tolerant and susceptible parents. Combining ability analysis is a useful tool that helps the breeders in understanding the gene action of various parameters to design effective breeding plan. Information on combing ability for salinity tolerance characters in wheat are very scanty. Therefore, the present study was done to know the genetic behaviour of salt tolerant gene(s) and to find out the nature of combing ability of the parents.

MATERIALS AND METHODS

The experiment was conducted at the Experimental Farm of the Regional Agricultural Research Station, Rahmatpur, Barisal which lies at the 22^0 42″ North latitude and 90^0 23″ East longitude at an elevation of 4 meter above the sea level. It belongs to the Non-calcareous Grey Floodplain Soils (Non saline, Ganges Tidal Alluvium) under AEZ 13 (Anonymous. 2015). The parental materials (Table 1) those were screened previously were sown in crossing block during 2008-2009. At flowering stage eight parents were crossed in all possible combinations excluding reciprocals. Eight parents and 28F1 hybrids were grown in pot culture under semi-controlled environment (inside plastic green house) and natural light during the season of 2009-2010. The materials were evaluated under control (non-saline) and 16 dS/m salinity level following a randomized complete block. Salt solution was prepared artificially by dissolving calculated amount of commercially available NaCl with tap water to make 160 mM NaCl solution. The salt solution was applied with an increment of 40 mM at every alternate day till the respective concentrations were attained. Plants in control were irrigated with tap water. Treatment solution was applied in excess so that extra solution

dripped out from the bottoms of the pots. Treatments began 12 days after sowing and were continued for 10 days, after which the pots were flushed with tap water to leach out the accumulated salt and the plants were irrigated with tap water until maturity (Ashraf and McNeilly. 1988 and Aziz et. al., 2006.). Data on different salinity parameters were recorded as follows:

Shoot length (cm): Shoot length was measured from the root base to the tip of the shoot. This was measured at 30 days after sowing.

Reduction of shoot length (%)
$$= \frac{\text{Shoot length at nonsaline} - \text{shoot length at saline}}{\text{Shoot length at nonsaline}} X\ 100$$

Reduction of shoot dry matter (RSDM)=
$$\frac{\text{Shoot dry wt. at non-saline} - \text{Shoot dry wt. at saline}}{\text{Shoot dry wt. at nonsaline}} X\ 100$$

Relative total dry matter (RTDM %)=
$$\frac{\text{Shoot dry wt. at saline} - \text{Shoot dry wt. at non-saline}}{\text{Shoot dry wt. at nonsaline}} X\ 100$$

Salinity scoring was done with 0-9 scale based on RTDM% (Ashraf et. al., 1990) and 1-9 scale based on visually using the modified standard evaluation system (SES) of IRRI (Ray and Islam, 2007). Combining ability using half diallel crosses were analysed following Method 2, Model 1 (Griffing, 1956). The Vr-Wr analysis was done according to Hayman (1954).

RESULTS AND DICUSSION

Analysis of variance for combining ability test showed highly significant different for all the characters related to salinity studied (Table 2). It suggested that the role of additive and non-additive genotypes effects in controlling these characters. Variance due to SCA was higher in magnitude than GCA for all characters, which revealed preponderance of non-additive gene effects in controlling these traits. All the characters exhibited less than one GCA: SCA ratio. It also indicated non-additive gene action for controlling these characters. The presence of non-additive genetic variance offers scope for exploitation of hybrid vigor of wheat in salinity (Ray et. al., 1995). Moeljopawiro and Ikehashi (1981) reported

the significance of GCA and SCA in diallel cross of rice, showing the importance of additive and non-additive types of gene effects in controlling the salinity traits.

General combining ability effect

The GCA effects for different characters under study are presented in Table 3. Two parents exhibited desirable GCA effects for shoot length. It indicates P11 and P15 were the best combiners for shoot length. P22 was the poor general combiner for shoot length. Negative GCA effect in desirable for reduction of shoot length (RSL). P45 was good combiner followed by P11, P24 and P40 for RSL. The estimate of GCA effects for total dry matter (TDM) showed that P33 and P45 exhibited desirable general combining performance. P22 was poor general combiner followed by P1 for TDM. Negative GCA effect is preferable for reduction of shoot dry matter (RSDM) because of their tolerance to salinity. P33 recorded as the best general combiner followed by P45 for RSDM. P1 was recorded as poor general combiner for this trait. Positive GCA effects are desirable for relative total dry matter (RTDM). Estimates of GCA effects revealed that P33 was the best one for GCA effect followed by P45 for RTDM. P22 showed significant negative effect for GCA and was classified as poor general combiner followed by P1 for RTDM. Negative GCA effect is desirable for the both scoring method. Two parents (P45 and P33) exhibited the best general combiner for these traits. P1 showed poor general combiner for both traits. Singh and Gupta (1969) and Akhter *et al.,* (2004) reported that parents with high mean performance and significant GCA effect might be selected in crossing for wheat yield improvement. The overall study of GCA effects of the parents suggested that P45 and P33 were the best general combiner for salt tolerance characters. Therefore, these parents could be used for salinity improvement programmed in wheat.

Specific combining ability effect

The SCA effects of the crosses for different characters in wheat are shown in Table 4. For shoot length positive and significant SCA effects are desirable. In this study 12 crosses showed positive and significant SCA effect. The crosses

P1 X P15, P1 X P22, P1 X P24, P1 X P33, P1 X P45, P11 X P15, P11 X P40, P15 X P22, P15 X P45, P22 X P24, P22 X P33 and P22 X P45, were best specific combiner for shoot length. For reduction of shoot length (RSL), negative and significant SCA effects indicates tolerant in salinity and were observed in P1 X P11, P1 X P15, P1 X P33, P1 X P45, P11 X P15, P11 X P40, P15 X P22, P15 X P40, P15 X P45, and P40 X P45, were the best specific combiner for RSL. Positive and significant SCA effects are preferable for total dry matter (TDM). The SCA effect indicates that P1 X P15, P1 X P24, P11 X P33, P15 X P22, P22 X P45 and P40 X P45 appeared as good specific combiner for TDM. The crosses P1 X P11, P1 X P24, P11 X P15, P11 X P33, P15 X P22, P22 X P40, P22 X P45, P24 X P45, P33 X P40 and P40 X P45 showed negative significant SCA effects, indicating best specific combiner for RSDM. The estimate of SCA effect indicated that the crosses P1 X P15, P1 X P24, P11 X P15, P11 X P33, P15 X P22, P22 X P45, P33 X P40 and P40 X P45 appeared positive significant SCA effect and exhibited as good specific combiner for RTDM. Negative significant SCA effects are desirable for the both scoring method. For scoring based on RTDM, the crosses P1 X P15, P1 X P24, P11 X P15, P11 X P33, P15 X P22, P22 X P45, P24 X P45 and P40 X P45 were the best specific combiner. While the crosses P1 X P15, P1 X P22, P1 X P45, P11 X P15, P22 X P24, P24 X P40, P24 X P45 and P33 X P45 were the best specific combiner for visual scoring trait.

The above study revealed that P1 X P15, P11 X P15 and P15 X P22 crosses were the best specific combiners and had significant SCA effects for salinity related traits. The cross P1 X P15 involved both the poor combining parents for RSDM, RTDM and score based on RTDM and on visual. The parents of the crosses P11 X P15 and P15 X P22 were not also good combiners for salinity traits. This superiorly of poor x poor general combiners might be due to over dominance. Similar results were also obtained by Singh and Singh (1985), Sardana and Borthakur (1987) and Akhter et al, (2004) for different traits. Such crosses are excepted to throw transgressive segregation, be exploited in the further breeding programmer to developed lines with optimum homozygous balance. Moeljopawiro and Ikehashi

(1981) obtained over dominance and transgressive segregation for resistance in a cross between two tolerant cultivars when evaluated the genetic behaviors of salt tolerance in terms of shoot dry weight and the number of leaves at 15.2m mhos/cm salinity.

Variance–covariance (Vr-Wr) analysis

Variance-covariance (Vr-Wr) analysis shows that salinity tolerance score based on RTDM followed the simple additive–dominance genetic model. The regression line for salinity tolerance score (RTDM) intercepted the Wr axis below the origin (Figure 1). The results indicated the over dominant type of gene action involved in the inheritance of the trait which confirmed the previous study. Placement of array points displayed that P22 had the maximum dominant genes for the trait being nearest to the origin, whereas P11 had the most recessive genes as the array point for P11 took the position farthest away from the origin. The parents P15 and P33 possessed equal proportion of dominant and recessive genes with some modifying effect. $(Wr_+Vr)/Yr$ graph (Figure 2) shows dominant gene control for salinity tolerance score based on RTDM. Therefore, diallel and recurrent matting system is useful for the salinity trait inheritance that allows for greater recombination and gene accumulation and selection would be effective in later generation (Inamullah et al. 2005).
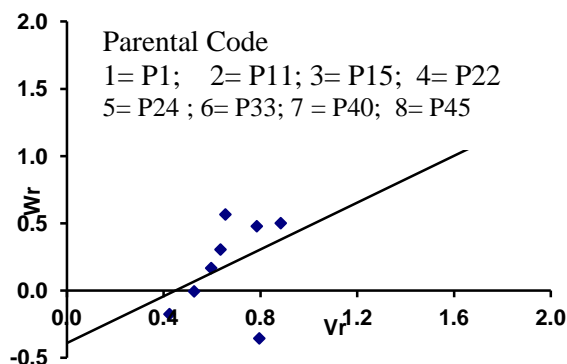

Figure 1
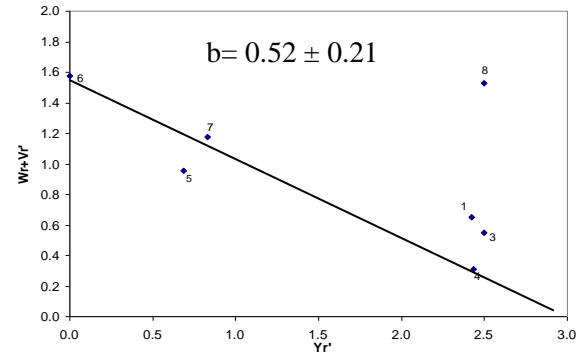Wr/ Vr graph for salinity tolerance score based on RTDM.

Figure 2
Wr+ Vr/Yr graph for salinity tolerance score based on RTDM.

CONCLUSIONS

The study suggested that the role of both additive and non-additive gene actions in the inheritance of salinity characters viz. reduction of shoot length (RSL), total shoot dry matter (TDM), reduction of shoot dry matter (RSDM), relative total dry matter (RTDM), scoring based on RTDM and visual scoring. P45 and P33 were appeared to be the best general combiner for salt tolerance traits. The cross P1 X P15, P11 X P15 and P15 X P22 were found the best specific combiner for the traits. The best cross involved poor x poor general combiner indicating over dominance and transgressive segregation gene action on resistance of salt.

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