

Research Article

Correlation and heritability estimates of seedling traits under salt stress conditions of bread wheat genotypes

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Citation

Naila Gandahi, Abdul Wahid Baloch, Muhammad Jurial Baloch and Muhammad Ubaidullah Shirazi. Correlation and heritability estimates of seedling traits under salt stress conditions of bread wheat genotypes. Pure and Applied Biology. <http://dx.doi.org/10.19045/bspab.2018.700170>

Received: 30/07/2018

Revised: 24/09/2018

Accepted: 12/10/2018

Online First: 15/10/2018

Abstract

The current study was aimed to estimate correlation and heritability of different seedling and physiological attributes of *Triticum aestivum* L. genotypes under normal and salinity stress conditions. In this context, a set of 22 bread wheat genotypes were grown in CRD with three replications having two treatments (control and 12dSm⁻¹). Mean squares from analysis of variance demonstrated significant ($P \leq 0.01$) with respect to treatment effect, genotype differences and treatment x genotype interaction on all studied parameters, revealing that evaluated bread wheat genotypes possessed valuable genetic resources, which may further be exploited in future breeding programs. With regard to correlation results obtained from normal and salinity stress conditions, the traits root length and shoot length associated positively and significantly with other seedling and physiological traits, suggesting that rise in any seedling/physiological trait congruently improve the other traits. Considering the heritability estimates, all traits showed high heritability under normal and stress conditions. The occurrence of high broad sense heritability in the present investigation demonstrated the suitability of genotypes for breeding programs for stress environments.

Keywords: Bread wheat; Correlation; Heritability; Salinity; Seedling traits

Introduction

To obtain superior yield with potential resistance against biotic and abiotic stresses in Pakistani bread wheat cultivars, many breeding efforts had been done in the recent past; consequently, due to its bidirectional breeding approaches a number of promising cultivars with better adaptability have also been released. Wheat has a unique position among cereal crops, mostly attributable to the

reason that grains retain protein with exceptionally good chemical and physical properties [1]. Correlation is a statistical technique that can show whether and how strongly pairs of variables are related. Among useful breeding characteristics, genotypic and phenotypic correlations are applied to determine extent of correlation of certain yield contributing traits with yield [2]. The correlation coefficients commonly are the

associations among different independent variables and the extent of linear relations. These variables could not describe association adequately in case apparent cause-result relationship is found among variables [3]. Heritability tends to have a great role in breeding, communicating the consistency of phenotype value as a guide to its breeding value. It is assumed that breeding value can only be derived from appropriate analyses when there is phenotypic value are being measured, while breeding value can suggest that what extent of phenotype would be conceded to the coming generation [4]. Not a huge achievement has been obtained in plant breeding with respect to improve the adaptation of crops against salinity. The limited genetic resources with regard to salinity stress in elite bread wheat genotypes advocate that selection due to domestication has turned against the ability for salt tolerance. The presence of negative associations between genetic recombination of high yielding and salt tolerance may be a key cause towards the reduction of desirable genes for salinity stress [5]. The breeding programs with successful results depend on a collection of various genetic resources [6]. After evaluation, genetic materials indicate the estimation of progeny performance on the basis of heritable and non-heritable variation, and therefore satisfactory selections can be made on the basis of heritability [7]. The study was designed to estimate correlation and heritability for various seedling and physiological traits of bread wheat genotypes under normal and salt stress conditions.

Materials and methods

This study was aimed to estimate correlation and heritability under control and salinity stress conditions. In this regard, twenty two wheat genotypes of diverse origin were used such as NIA-Sundar, NIA-Sarang, NIA-AS-14, NIA-AS-9, NIA-AS-10, NIA-2B, Hamal, NIA-5B, Salt-6, SRN-87, SRN-11, CT-49, NRC-1236, Bathoor-08, Tatar, TJ-83, TD-1,

Benazir, AS-2002, Sehar-2006, Kiran-95 and LU-26s for seedling and physiological traits under salinity stress conditions. The experiment was laid out in complete randomized design with three replications having two treatments (control and 12 dSm⁻¹). The experiment was conducted in water culture using 1/4th strength of Hoagland nutrient solution as growing media in plastic bowls (Size: 8.4 x 4.5cm). Seeds were planted on molded plastic sieves placed in plastic bowls, containing sufficient nutrient solution. The bowls were placed in programmed controlled growth cabinets maintain at 25/20°C day/night temperatures and 12 hours photoperiod. The experiment was terminated after 10 days (240 hours). The analysis of variances and correlation of coefficient was calculated with the help of computer package (Statistix Ver. 8.1), while heritability in broad sense was estimated as suggested by Allard [8].

Results and discussion

Mean squares from analysis of variance displayed significant treatment effect ($P \leq 0.01$) on all studied parameters (Table 1). Mean squares from analysis of variance demonstrated significant ($P \leq 0.01$) with respect to treatment effect, genotype differences and treatment x genotype interaction on all studied parameters, revealing that evaluated bread wheat genotypes possessed valuable genetic resources, exhibiting that used 22 bread wheat genotypes tend to possess valuable genetic resources, which may further be utilized in breeding programs. Similar to these results, Naggat *et al.* [9] reported that genotypes, treatments and their interaction were significant for all evaluated parameters. Akbarpour *et al.* [7] also evaluated a set of different wheat landraces in both conditions (normal and salt stress) and observed that mean squares of all traits indicated significant differences among used genotypes.

Correlations are very important in crop sciences because of its useful in disclosing the magnitude and direction of the relationship between various yield contributing traits and yield. Correlation studies give a clear picture of characters association which is generally due to linkage, pleiotropy, physiological association in developmental and biochemical pathway. The characters which are correlated are of much interest since change in one character influenced the other one [10]. In the present study, the obtained correlations results under normal conditions (Table 2) showed that root length made positive and significant associations with root fresh weight ($r = 0.39^{**}$) and shoot fresh weight ($r = 0.28^*$); shoot length correlated significantly and positively with Na^+/K^+ ratio ($r = 0.55^{**}$), while also showed significant and negative correlations with root fresh weight ($r = -0.39^{**}$) and Na^+ ($r = -0.37^{**}$); root fresh weight depicted positive and significant correlation with shoot fresh weight ($r = 0.28^*$) but negatively and significantly associated with Na^+/K^+ ratio ($r = -0.24^*$); whereas Na^+ showed negative and significant associated ($r = -0.34^{**}$) and K^+ associated positively and significant with Na^+/K^+ ratio ($r = 0.60^{**}$). Regarding the correlations under salt stress conditions (Table 3), root length made positive and significant associations with shoot length ($r = 0.43^{**}$), root fresh weight ($r = 0.37^{**}$), shoot fresh weight ($r = 0.49^{**}$), K^+ ($r = 0.53^{**}$) and Na^+/K^+ ratio ($r = 0.62^{**}$), while also showed significant but negative correlation with Na^+ ($r = -0.55^{**}$). Shoot length associated positively and significantly with shoot fresh weight ($r = 0.35^{**}$), K^+ ($r = 0.52^{**}$) and Na^+/K^+ ratio ($r = 0.69^{**}$), while also demonstrated significant but negative association with Na^+ ($r = -0.67^{**}$). Root fresh weight exhibited positive and significant associations with shoot fresh weight ($r = 0.58^{**}$) and Na^+/K^+ ratio ($r = 0.25^*$), however, also showed significant but negative

association with Na^+ ($r = -0.38^{**}$). Furthermore, the Na^+ showed negative and significant correlations with shoot fresh weight ($r = -0.51^{**}$), K^+ ($r = -0.35^{**}$) and Na^+/K^+ ratio ($r = -0.77^{**}$). While shoot fresh weight ($r = 0.48^{**}$) and K^+ ($r = 0.82^{**}$) developed positive and significant correlations with Na^+/K^+ ratio. The results obtained from normal and salinity stress conditions, the traits root length and shoot length associated positively and significantly with other seedling and physiological traits, signifying that rise in any seedling/physiological trait congruently improve the other traits. This unveils that if single trustworthy trait is picked in salinity stress and that may be used as a selection criterion that will certainly lead to improve other seedling traits for salt stress conditions and improved genotypes could be selected to get along with stress environments. Dashti *et al.* [11] observed a significantly negative associations between K^+/Na^+ and Na^+ concentration, while K^+/Na^+ was significantly and positively interrelated with K^+ . Moreover, these results are also in agreement with those of Dehdari *et al.* [12] and Dashti *et al.* [13]. Information on heritability is necessary for plant breeders. It has been predicted that increase of stress levels cause changes in heritability [14]; and such variations in heritability were also observed by Hoffmann and Parsons [15]. The decrease or increase in genetic variation would appear possibly due to increased stress, since diverse genes may contribute to similar character under varied environments [16]. With respect to heritability results (Table 4), high heritability were estimated for majority of characters under stress environments, such as root length ($h^2 = 99.02\%$), shoot length ($h^2 = 81.28\%$), root fresh weight ($h^2 = 98.33\%$), shoot fresh weight ($h^2 = 99.52\%$), K^+ ($h^2 = 93.27\%$) and Na^+/K^+ ratio ($h^2 = 99.37\%$); however, low but desirable heritability

estimated for Na^+ ($h^2 = 2.20\%$). Similarly, high heritability was also estimated for all the studied traits under salt stress conditions, such as root length ($h^2 = 84.17\%$), shoot length ($h^2 = 84.05\%$), root fresh weight ($h^2 = 93.96\%$), shoot fresh weight ($h^2 = 94.83\%$), Na^+ ($h^2 = 96.74\%$), K^+ ($h^2 = 92.60\%$) and Na^+/K^+ ratio ($h^2 = 99.55\%$). The presence of high heritabilities in the current research

exhibited that genotypes were suitable for breeding programs while considering stress environments. Most of the research studies suggest that improvement in crop salt tolerance is not at rapid pace since a limited knowledge is existed for numerous complex tolerance mechanisms and absence of variation for salt affected traits [5].

Table 1. Mean squares of different seedling traits of bread wheat genotypes

Sources of variances	Degree of freedom	Root length	Shoot length	Root fresh weight	Shoot fresh weight	Na^+	K^+	Na^+/K^+ ratio
Replication	2	1.51	5.17	0.01	0.02	357.90	15.56	0.01
Genotypes (G)	21	7.90**	75.09**	0.23**	0.93**	233.90**	192.09**	0.25**
Treatments (T)	1	175.76**	545.38**	1.96**	22.72**	11232.50**	3186.00**	8.28**
G x T	21	2.57**	5.95**	0.07**	0.05**	45.30**	51.68**	0.01**
Error	86	0.70	1.85	0.01	0.01	13.40	13.46	0.001

** shows significant differences at 1% of probability level

Table 2. Correlations of coefficient between different seedling traits of bread wheat genotypes under normal conditions

Traits	Root length	Shoot length	Root fresh weight	Shoot fresh weight	Na^+	K^+
Shoot length	0.11					
Root fresh weight	0.39**	-0.39**				
Shoot fresh weight	0.28*	0.09	0.28*			
Na^+	-0.09	-0.37**	0.18	-0.13		
K^+	0.06	0.12	0.02	0.08	0.10	
K^+/Na^+ ratio	0.20	0.55**	-0.24*	0.21	-0.34**	0.60**

** , * show significant differences at 1 and 5% of probability level

Table 3. Correlations of coefficient between different seedling traits of bread wheat genotypes under salt stress conditions

Traits	Root length	Shoot length	Root fresh weight	Shoot fresh weight	Na^+	K^+
Shoot length	0.43**					
Root fresh weight	0.37**	0.10				
Shoot fresh weight	0.49**	0.35**	0.58**			
Na^+	-0.55**	-0.67**	-0.38**	-0.51**		
K^+	0.53**	0.52**	0.13	0.23	-0.35**	
K^+/Na^+ ratio	0.62**	0.69**	0.25*	0.48**	-0.77**	0.82**

** , * show significant differences at 1 and 5% of probability level

Table 4. Heritability estimates (broad sense) of different seedling traits of bread wheat genotypes under salt stress conditions

Traits	Normal conditions			Salinity stress conditions		
	Genotypic variance (δ^2g)	Phenotypic variance (δ^2p)	Heritability % (Broad sense)	Genotypic variance (δ^2g)	Phenotypic variance (δ^2p)	Heritability % (Broad sense)
Root length	22.64	22.86	99.02	9.10	10.81	84.17
Shoot length	4.70	5.78	81.28	18.42	21.92	84.05
Root fresh weight	59.00	60.00	98.33	23.34	24.84	93.96
Shoot fresh weight	209.00	210.00	99.52	36.71	38.71	94.83
Na ⁺	0.18	8.16	2.20	31.39	32.45	96.74
K ⁺	6.02	6.45	93.27	11.43	12.35	92.60
K ⁺ /Na ⁺ ratio	15.84	15.94	99.37	55.62	55.87	99.55

Conclusion

It was concluded from results that root length and shoot length correlated positively and significantly with other seedling and physiological traits, signifying that increase in any seedling/physiological trait correspondingly improve the other traits. Moreover, all traits showed high heritability under normal and stress conditions. The occurrence of high broad sense heritability in the present study established the suitability of genotypes for breeding programs for stress environments.

Authors' contributions

Conceived and designed the experiments: MU Shirazi & N Gandahi. Performed the experiments: N Gandahi, Analyzed the data: N Gandahi & MJ Baloch, Contributed reagents/ materials/ analysis tools: MU Shirazi, Wrote the paper: AW Baloch & N Gandahi.

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Online first accepted article