The Pharma Innovation

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Assessment of genetic parameters for yield and yield attributes of triticale and wheat genotype under salt affected condition

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Abstract
Thirty genotypes comprising of wheat (*T. aestivum* and *T. durum*) and hexaploid triticale was studied in Randomized Block Design with three replications under saline condition during 2016-17 to assess the variability, heritability and genetic advance of these genotypes for yield and its contributing traits. The treatment, i.e. mean sum of squares due to genotypes revealed significant differences for all characters studied revealing the presence of high genetic variability among the genotypes. The estimates of GCV were lower than the respective PCV; it means that the apparent variation is not only due to genotypes but also due to the influence of environmental factors on the expression of the traits studied. Characters like seed yield/plant, spike length, number of grains per spike, number of effective tillers and test weight showed high GCV, PCV, heritability coupled with high genetic advance as percent of mean, suggesting that selection for the improvement of these characters may be rewarding. High heritability estimates with expected moderate genetic advance were observed for the traits like biological yield and harvest index depicting the greater role of additive gene action in their inheritance.

Keywords: Hexaploid triticale, wheat, variability, heritability, genetic advance

Introduction
Wheat is a cereal crop belongs to family *Graminae* (*Poaceae*). It is the world's largest cereal crop. It has been described as the "King of cereals" because of the acreage it occupies, high productivity and prominent position it holds in the international food grain trade. Wheat is a crop of global significance grown in diversified environments. It is an important cereal crop of cool climate, and plays an important role in food and nutritional security of world. It provides food for 36% of the global population and contributes 20% of the food calories (Singh and Choudhary, 2006) [20, 21]. Wheat is widely grown all over the world and stands first among the cereals both in area and production. Triticale is quite different from other cereals in that it shows wider adaptability and high nutritional quality (Oettler, 2005) [17] as well as high yield potential, and it is generally more competitive against weeds than wheat is (Beres *et al.,* 2010) [2]. It also shows greater tolerance toward drought and pests than its progenitors (Darvey *et al.,* 2000; Erekul and Kohn, 2006) [4, 7]. Since the growing period of the crop becomes restricted due to sudden increase in the temperature after winter; the sowing time has an important bearing on production potential of a genotype. Temperature stress, drought and salinity is the major problems limiting wheat production. Therefore, as an alternative to more sensitive crops such as wheat and barley, triticale varieties are being developed with the aim of improving grain yields. Crop breeders have been improving to develop genotypes with superior grain yield, quality and other desirable traits over a wide range of different environmental conditions. The presence of genetic variation within a plant population is very important in achieving an effective breeding program (*i.e.,* in terms of yield and other agronomic traits). Knowledge of the nature and magnitude of genotypic and phenotypic variability present in any crop species plays an important role in evolving superior cultivars. Importance of estimation of genotypic and phenotypic variability is formulating efficient breeding procedures in cotton have been emphasized by Hutchinson (1940) [10]; Miller *et al*. (1958) [16]. Many researchers studied the phenotypic and genotypic coefficients of variation were estimated using genotypic and phenotypic variances respectively (Do Thi *et al*., 2008; Kulkarni *et al*., 2011; Erande *et al*., 2014; Ranjan *et al*., 2014) [5, 6, 14, 18]. The coefficient of variation indicated only the extent of existing variability for various traits, but does not give any information about the heritable portion of it. Therefore, heritability accompanied by estimates of genetic advance and genetic

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advance as per cent mean were also estimated. Heritability and genetic advance are other important selection parameters. Hanson *et al*. (1956) [9] defined heritability in broad sense as the ratio of genotypic variance to the phenotypic variance in the non-segregating populations. Thus, heritability is the heritable portion of phenotypic variance. It is a good index of transmission of characters from parents to their offspring (Falconer, 1981) [8]. The estimates of heritability help the plant breeder in determining the character for which selection would be rewarding of elite genotypes from diverse genetic populations. The breeders are interested in selection of superior genotypes based on their phenotypic expression in stress and stress free environments. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone.

Material and Methods
The material comprising of 11 triticale, 10 bread wheat and 9 durum wheat genotypes was planted in Randomized Block Design with three replications under saline environment (six irrigation 4 Ec) during *rabi* 2016-17. The observation were recorded on the randomly selected plants of each genotypes from each replication and environment for eleven character *viz*., days to 50% flowering, days to maturity, plant height, number of effective tillers per plant, number of grain per spike, spike length, 1000-seed weight, biological yield per plant, harvest index, protein content, seed yield per plant. The data recorded on the above eleven characters were subjected to the following statistical analysis: Analysis of variance (ANOVA), variance and co-efficient of variance, heritability (broad sense) and genetic advance. Statistical analysis was carried out by using replicated data over sample plants through INDO STAT package.

Results and Discussion
The mean sum of squares due to genotypes showed significant differences for all the ten characters studied among 30 genotypes (Table 1), indicating the presence of high genetic variability among the genotypes. The significant differences among the genotypes studied suggest that variability can be further utilized in crop improvement programme. The estimates of genetic parameters including genotypic variance, phenotypic variance, genotypic co-efficient of variation, phenotypic co-efficient of variation, heritability (broad sense), genetic advance and genetic advance as percent of mean (Table 2) deserve attention in deciding selection criteria for improvement in the concerned characters. High magnitude of variation in the experimental material was reflected by high values of mean and range for almost all the characters. The observation recorded for seed cotton yield and related traits indicating the present of wide range of variation. Seed yield per plant and its contributing traits exhibited wide variation. High amount of PCV and GCV has been reported by Khiziri *et al.* (2010) and Kumar *et al.* (2014) [15, 21] for seed yield per plant. A perusal of heritability estimates indicated that seed yield and its

contributing traits showed high heritability estimates. The genetic advance as well as genetic advance percentage of mean (GAM) was found to be the high for this trait.
In present investigation, the highest estimates of genotypic coefficient of variation were observed for 1000 seed weight (19.27%) followed by spike length (19.02%) and number of effective tillers per plant (18.61%). Moderate genotypic coefficient of variation observed for number of grains per spike (14.27%) followed by seed yield per plant (13.39%) where as other remaining characters depicted low genotypic coefficient of variation. Similar results were also observed by Kalimulla *et al.* (2012), for flag leaf area, grains/plant, number of tillers/plant.
Most of the characters recorded highest broad sense heritability *viz*. days to 50% flowering, days to maturity, plant height, number of effective tillers per plant, number of grain per spike, spike length, 1000- seed weight, biological yield per plant, harvest index and seed yield per plant except protein content which showed moderate broad sense heritability. Similar results were observed by Ahmad *et al*. (2007), Cheema *et al.* (2006) [3], Khan *et al.* (2007) [12, 13] and Kumar *et al.* (2014) [15, 21]. The high heritability indicates that selection on the basis of phenotype may prove effective for these characters.
Estimates of genetic advance percentage of mean was highest for seed yield per plant (24.07%) and its contributing traits *viz*. 1000- seed weight (39.68%), spike length (38.96%), number of effective tillers per plant (36.80%) and number of grains per spike (28.57%). Similar results were observed by Kumar *et al.* (2014) [15, 21], Singh *et al.* (2005) [20, 21]; Ahmad *et al*. (2007) and Sharma and Garg (2002) [20, 21].
The estimates of GCV were lower than the respective PCV; it means that the apparent variation is not only due to genotypes but also due to the influence of environmental factors on the expression of the traits studied. Characters like seed yield/plant, spike length, number of grains per spike, number of effective tillers and test weight showed high GCV, PCV, heritability coupled with high genetic advance as percent of mean, suggesting that selection for the improvement of these characters may be rewarding. High heritability estimates with expected moderate genetic advance were observed for the traits like biological yield and harvest index depicting the greater role of additive gene action in their inheritance.

Table 1: Mean squares for ten characters under study

Source of variation	Replication	Treatment	Error
Days To 50% Flowering	4.04	62.26**	0.17
Days To Maturity	3.51	44.52**	0.22
Plant Height	6.83	135.78**	1.47
Spike Length	1.24	4.87**	0.05
Number Of Grain Per Spike	60.03	124.81**	6.89
Number Of Effective Tillers Per Plant	1.06	2.29**	0.18
1000-Seed Weight	0.17	205.34**	0.10
Biological Yield Per Plant	3.95	51.11**	11.21
Harvest Index	3.74	24.06**	3.91
Seed Yield Per Plant	1.63	9.60**	2.29
**Significant at (*p*=0.01) levels			

Table 2: Variability parameters for different quantitative characters

Traits	Variance			GCV (%)	PCV (%)	ECV (%)	H2bs (%)	GA	GAM (%)
	GV	PV	EV						
Days To 50% Flowering	20.69	20.75	0.05	5.96	5.97	0.54	99.70	9.35	12.27
Days To Maturity	14.76	14.84	0.07	3.25	3.26	0.40	99.50	7.89	6.68
Plant Height	44.77	45.26	0.49	9.24	9.29	1.67	98.90	13.70	18.94

Spike Length	1.60	1.62	0.01	19.02	19.13	3.49	98.90	2.59	38.96
Number Of Grain Per Spike	39.30	41.60	2.29	14.27	14.68	5.97	94.50	12.55	28.57
Number Of Effective Tillers Per Plant	0.70	0.76	0.06	18.60	19.38	9.40	92.20	1.66	36.80
1000- Seed Weight	68.41	68.44	0.03	19.27	19.28	0.76	99.9	17.03	39.68
Biological Yield Per Plant	13.30	17.03	3.73	9.96	11.27	9.15	78.10	6.63	18.13
Harvest Index	6.71	8.02	1.30	8.16	8.92	6.22	83.8	4.88	15.39
Seed Yield Per Plant	2.43	3.20	0.76	13.39	15.35	12.99	76.10	2.80	24.07

GV: Genotypic variance; PV: Phenotypic variance; EV: Environmental variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; ECV: Environmental coefficient of variation; H2bs: Heritability broad sense; GA: Genetic advance and GAM (%): Genetic advance as % of mean

Conclusion
Characters having high GCV, PCV, heritability, coupled with high genetic advance as percent of mean that indicating presence of additive gene effects in its inheritance and such characters could be improved by selection. Whereas low heritability and low genetic advance also indicates greater role of non-additive gene action in their inheritance suggesting heterosis breeding could be useful for improving these traits.

Acknowledgement

References
1. Ahmed N, Chowdhry MA, Khaliq I, Maekawa M. The inheritance of yield and yield components of five wheat hybrid population under drought conditions. Indonesian J Agric. Sci 2007, P53-59.
2. Beres BL, Harker KN, Clayto GW, Bremer E, Blacksha RE, Graf RJ. Weed competitive ability of spring and winter cereals in the Northern Great Plains. Weed Technol 2010;24:108-116.
3. Cheema NM, Mian MA, Ihsan M, Rabbani G, Mahmood A. Studies on variability and some genetic parameters in spring wheat. Pak. J Agric. Sci 2006;43(1-2).
4. Darvey NL, Naeem H, Gustafson JP. Triticale production and utilization in K. Kulp and J Ponte. Handbook of cereal science and technology, Marcel Dekker, New York 2000, P257- 274.
5. Do Thi ha an, Ravikesavan, Iyanar R. Genetic advance and heritability as a selection index for improvement of yield and quality cotton. Journal of Cotton Research and Development 2008;22(1):14-18.
6. Erande CS, Kalpande HV, Deosarkar DB, Chavan SK, Patil VS, Desmukh JD *et al*. Genetic variability, correlation and path analysis amomg different traits in desi cotton (*G. arboreum* L.). African Journal of Agricultural Research 2014;9(29):2278-2286.
7. Erekul O, Kohn W. Effect of weather and soil conditions on yield components and bread making quality of winter wheat (*Triticum aestivum* L.) and winter triticale (*Triticosecale* wittm.) varieties in north-east Germany. J Agron. Crop Sci 2006;192:452-464.
8. Falconer DS. Introduction of Quantitative Genetics, Longman Inc. Ltd., New York 1981.
9. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield and segregating populations of Korean lespedza. Agronomy Journal 1956;47:313-318.
10. Hutchinson JB. The application of genetics to plant breeding. I. The genetic interpretation of plant breeding problems. Journal of Genetics 1940;40:271-282.
11. Kahrizi D, Maniee M, Mohammadi R, Cheghamirza K. Estimation of genetic parameters related to morpho-agronomic traits of Durum wheat (*Triticum turgidum* var. durum). Biharean Biol 2010;4(2):93-97.
12. Kallimullah, Khan SJ, Irfaq M, Rahman HU. Genetic variability, correlation and diversity studies in bread wheat (*Triticum aestivum* L.) germplasm. J Animal and Plant Sci 2012;22(2):330-333.
13. Khan I, Khalil IH, Nisir-ud-Din. Genetic parameters for yield traits in wheat under irrigated and rainfed environments. Sarhad. J Agric No. 4 2007.
14. Kulkarni AA, Nanda HC, Patil SG. Studies on genetic divergence in upland cotton (*Gossypium hirsutum* L.). Journal of Cotton Research and Development 2011;25(1):9-13.
15. Kumar Navin, Markar Shailesh, Kumar Vijay. Studies on heritability and genetic advance estimates in timely sown bread wheat (*Triticum aestivum* L.). Bioscience Discovery 2014;5(1):64-69.
16. Miller PA, Williams JC, Robinson HF, Comstock RR. Estimates of genotypic and environmental variance and covariance in upland and their implications in selection. Agronomy Journal 1958;50:126-131.
17. Oettler G. The fortune of a botanical curiosity – triticale: past, present and future. J Agric. Sci 2005;143:329-346.
18. Ranjan R, Sangwan RS, Siwach SS, Sangwan O, Sah MK. Studies of genetic parameters for seed cotton yield and its contributing characters in *Gossypium arboreum* L. Journal of Cotton Research and Development 2014;28(2):227-229.
19. Sharma AK, Garg DK. Genetic variability in wheat (*Triticum aestivum* L.) crosses under different normal and saline environments. Annals Agric. Res 2002;23(3):497-499.
20. Singh G, Chaudhary H. Selection parameters and yield enhancement of wheat (*Triticum aestivum* L.) under different moisture stress condition. Asian J Plant Sci 2006;5:894-898.
21. Singh V, Singh D, Singh N, Kumar S. Genetic analysis of wheat varieties for yield and its components. Agric. Sci. Digest 2005;25(2):145-146.