Analysis of variance and estimation of genetic variability parameters for quality traits in bread wheat (*Triticum aestivum* L. em. Thell) genotypes

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Abstract
In the present investigation ten wheat genotypes were crossed in half diallel mating design to produce 45 F_1's, which along with ten parental lines were evaluated in randomized block design in 3 replications. Estimates of genetic variability parameters as range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), environmental coefficient of variation (ECV), genetic advance, genetic advance % mean and heritability were calculated for various quality traits viz. protein content (%), sedimentation value (ml), hectolitre weight (kg/hl) and phenol colour reaction. Analysis of variance showed significant differences amongst genotypes for all the traits studied except for hectolitre weight. Sedimentation value and phenol colour reaction showed moderate estimates of PCV and GCV while ECV for all the traits studied was low. High heritability estimates were observed for sedimentation value while phenol colour reaction exhibited moderate estimates of heritability. High heritability coupled with high genetic advance % mean for sedimentation value indicated that the quality trait was controlled by additive genes. This indicates that variation amongst genotypes for sedimentation value and phenol colour reaction was heritable and improvement by selection was possible for these traits.

Introduction
Wheat (*Triticum aestivum* L.) is one of the most important cereal food crop of the world. It originally belongs to the Levant region but presently is being grown across the world. Globally the area under wheat is 220.41 million hectares with a production of 729.01 million tonnes and productivity of 3307.4 kg/ha (FAO, 2014) [9]. The main wheat producing regions in world are China, India, United States, Russian Federation, France, Australia, Germany, Ukraine, Canada, Turkey, Pakistan, Argentina, Kazakhstan and United Kingdom (FAO, 2003) [10]. With an area of 30.23 million hectare, production of 93.50 million tonnes and 3093 kg/ha productivity, India ranks second in world after China in terms of production. Wheat is a source of 55% carbohydrate and 20% of the total food calories consumed in the world (Breiman and Graur, 1995) [5]. Wheat quality can be determined in terms of different parameters as test weight, kernel weight, vitreousness, kernel hardness, grain appearance score, moisture content, protein content, protein quality, amylase activity and fat acidity. Protein content is the most important trait from product making point of view (Blakeney *et al.*, 2009 [4]. As surplus production of wheat have already been achieved, the major thrust of modern plant breeding is to bring about improvement in quality of wheat genotypes. Identification of the basic components determining quality and explaining their modes of function and interrelationships has perplexed scientists for decades (Fowler and De La Roche, 1975) [10]. For the effective improvement of quality and yield, a plant breeder must have knowledge of the inheritance of quality traits and of the joint inheritance of quality and agronomic traits (Baker *et al.*, 1971) [3], (Tabassum *et al.*, 2017) [25]. Qualitative traits in wheat are controlled both by genetic and environmental factors. They are polygenic in nature and so the inheritance of the components of quality is complex. For the development of quality wheat varieties better suited to present processing and consumption needs, there is a need to estimate variability prominently of genetic nature which can be exploited by selection. Heritability in broad sense is the proportion of phenotypic variance that is due to genetic constitution of the plant. It is a measure of the phenotypic variance attributable to genetic causes, has predictive function of

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breeding crops (Songsri *et al*., 2008) [24] and is used to estimate the genetic advance which indicates the degree of gain in a character obtained under a particular selection pressure (Eid, 2009) [7]. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program (Shukla *et al*., 2004) [22]. For the accurate estimation of the type of genetic control of a particular trait heritability estimates along with genetic advance are used for selection. High heritability with high genetic advance indicates the predominance of additive gene action hence improvement in such trait can be brought about by direct selection (Harshwardhan *et al*., 2016) [11]. The present investigation was, therefore, conducted to estimate genetic variability, heritability, genetic advance and genetic advance % mean for quality traits in wheat.

Materials and Methods

The present investigation was carried out at Norman E. Borlaug Crop Research Centre, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, India. The F_1's were produced by crossing ten wheat genotypes viz. QLD 39, KAUZ/ALTAR84/3/MILAN/KAUZ/4/HUITES, UP 2762, KFA/2*KACHU, Raj 4419, PBW 729, WH 1187, HD 2967, DBW 50 and NIAW 1594 in half diallel fashion in Rabi 2015-16 and F_1's of progenies, their parents along with two checks viz. UP 2628 and WH 1105 were evaluated in Rabi 2016-17. Experiment was carried out in randomized block design and replicated thrice. Each genotype was planted in two rows of 1m each. Spacing between rows was 20 cm and that between plants was 10 cm. Observations on various quality traits as protein content, sedimentation value, hectolitre weight and phenol colour reaction were analysed. For determination of protein content samples were evaluated with NIT based Whole Grain Analyser (Infratech 1241 Grain Analyser). Sedimentation value was determined by SDS sedimentation test suggested by Zeleny, 1947 [26]. Hectolitre weight was determined by using hectolitre weight instrument. Phenol colour reaction value of seed samples was determined by phenol colour reaction test. Analysis of variance was conducted according to Panse and Sukhatme (1969) [21] and significance of differences between genotypes was determined for each of the four quality traits studied. Variability parameters as phenotypic, genotypic, environmental coefficient of variation, heritability, genetic advance and genetic advance % mean was calculated for different characters. Phenotypic, genotypic and environmental coefficient of variation was estimated according to formula suggested by Singh and Chaudhary (1985) [23] while formula given by Allard (1960) [2] was used in estimation of heritability in broad sense. Genetic advance was calculated as suggested by Allard (1960) [2] and estimation of genetic advance % mean was done according to Johnson, Robinson and Comstock (1955) [12].

Results and Discussion

The results for analysis of variance indicated highly significant differences among genotypes for sedimentation value and phenol colour reaction, significant differences were observed for protein content while for hectolitre weight the differences were insignificant (Table 1 and 2). This revealed that variability was present in the population for all the traits studied except for hectolitre weight and that these traits can be improved by selection. Mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), environmental coefficient of variation (ECV), heritability,

genetic advance and genetic advance % mean are shown in Table 3. Phenotypic, genotypic and environmental coefficient of variation were characterised as high (>20%), medium (10-20%) and low (<10%) as suggested by Deshmukh *et al*. (1986) [6]. Moderate estimates of GCV were exhibited by sedimentation value (17.673%) and phenol colour reaction (13.657%) while protein content (2.548%) and hectolitre weight (0.682%) exhibited low estimates of GCV. PCV values were higher than the GCV values for all the characters studied confirming environmental influence in the expression of all the traits. Moderate PCV and GCV was seen for Sedimentation value (18.350 and 17.673) and phenol colour reaction (16.367 and 13.657). Low ECV was observed for all four quality traits studied. Moderate PCV and GCV for sedimentation value and phenol colour reaction accompanied with low ECV (4.937 and 9.021) indicates that these traits have less environmental influence suggesting the reliability of selection of genotype on the basis of phenotype for improvement of these quality traits. Low PCV, GCV and ECV observed for protein content and hectolitre weight showed that although the environmental influence on these traits is low as evident by the ECV but improvement of these traits by direct selection is not possible as the heritable variation among genotypes is insufficient.

Heritability in broad sense (h^2_b) was evaluated for each trait. High h^2_b estimates (≥75%) was witnessed for sedimentation value (92.756%), moderate heritability estimates were observed for phenol colour reaction (69.621%). Similar results were also reported by Ali *et al*. (2008) [1], Kumar *et al*. (2014) [18], Kumar et al. (2015a) [17] and Kumar *et al*. (2015b) [13]. The estimates of heritability were low for protein content (15.083%) and hectolitre weight (3.966%). High and moderate estimates of heritability indicated that in the total phenotypic variance a larger amount of variation is attributed to the genotype of the individual. However, low estimates of heritability indicated that the variability cannot be passed on to the next generation as it was mainly due to environmental influence. This makes the utilisation of selection for crop improvement might be ineffective.

As per Deshmukh *et al*. (1986) [6] the genetic advance as % mean (GAM) is classified as high (>20%), moderate (10-20%) and low (<10%). High GAM was observed for sedimentation value (35.06%) and phenol colour reaction (23.474%). GAM estimates were low for protein content (2.038%) and hectolitre weight (0.279%). These results are in general agreement with findings of Kumar *et al*. (2014) [18], Kumar *et al*. (2015c) [14], Kumar *et al*. (2015d) [15] and Pandey *et al*. (2015) [20] in ricebean.

Genetic advance and heritability in broad sense are together used as an important parameter for selection of genotypes (Kumar *et al*., 2016) [16]. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Johnson *et al*., 1955) [12]. High heritability accompanied with high genetic advance specifies that the trait was mainly governed by additive gene effects and this association was seen for sedimentation value and so it could be improved by direct selection. Low heritability with low genetic advance was observed for protein content and hectolitre weight exhibited greater influence of environment in the expression of these traits made selection was ineffective in the improvement of these traits.

Conclusion

The main aim of present crop improvement programmes was to produce improved quality wheat varieties better suited to meet present processing and consumption demands. In the present study significant differences has been made among genotypes for protein content, sedimentation value and phenol colour reaction showing possibility of improvement of these traits by selection. Moderate PCV and GCV for sedimentation value and phenol colour reaction accompanied with low ECV indicated that improvement in these traits might be achieved by direct selection. Sedimentation value showed high broad sense heritability along with high genetic advance depicted that characters were driven by additive genes and, therefore, direct selection might be effective in its improvement.

Table 1: Analysis of variance (Mean squares) for different characters in bread wheat

S. No.	Characters	Replication (df=2)	Treatment (df =54)	Error (df=108)
1.	Protein content (%)	0.289	0.699*	0.455
2.	Sedimentation value (ml)	6.836	162.712**	4.126
3.	Hectolitre weight (Kg/hl)	18.681	6.668	5.932
4.	Phenol colour reaction	0.296	2.971**	0.377

*, ** significant at 5% and 1% levels, respectively.

Table 2: Analysis of genotypes for quality traits in wheat

S. No.	Characters	GM	CV	CD at 1%	CD at 5%	SEM±
1.	Protein content (%)	11.172	6.044	1.446	1.093	0.389
2.	Sedimentation value (ml)	41.139	4.937	4.349	3.287	1.172
3.	Hectolitre weight (Kg/hl)	72.576	3.355	5.214	3.941	1.406
4	Phenol reaction	6.806	9.024	1.315	0.994	0.354

GM: General mean, CV: Coefficient of variation, CD: Critical difference, SEM: Standard error mean

Table 3: Range, coefficient of variance, heritability and genetic advance for various characters in wheat

Sl. No.	Character	Range	PCV (%)	GCV (%)	ECV (%)	Heritability (%)	Genetic advance	Genetic value % mean
1.	Protein content	9.9-12.8	6.559	2.548	6.045	15.083	0.227	2.038
2.	Sedimentation value	24.3-57.0	18.350	17.673	4.937	92.756	14.424	35.06
3.	Hectolitre weight	66.26-78.93	3.424	0.682	3.356	3.966	0.203	0.279
4.	Phenol colour reaction	2-8	16.367	13.657	9.021	69.621	1.597	23.474

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