The Pharma Innovation

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Assessment of genetic variability parameters in bread wheat (*Triticum aestivum* L.) genotypes under southern Chhattisgarh conditions

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Abstract
A field study was conducted at Research cum Instructional Farm, S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur, IGKV, Raipur (C.G.), in *Rabi* -2020, in a Randomized Block Design with 2 replications to evaluate 21 accessions of wheat (*Triticum aestivum* L.). The observations of 8 qualitative and 13 quantitative characters were recorded at different stages of plant growth from flowering stage to harvest, according to the Guidelines for the test of DUS on wheat by PPV& FRA, Government of India. The genotypes exhibited wide range of variation for all the traits except. Genetic coefficient of variation ranged from 4.39 for days to 50% flowering to 32.81 for seed yield per plot. All the traits exhibited high heritability, however very high values of heritability were observed for seed yield per plot (90.88%), harvest index (88.33%) and flag leaf length (87.09%). The traits grain yield per plot and fodder yield per plot showed high heritability and genetic coefficient of variation along with high genetic advance. Therefore, these traits could be considered as suitable selection criteria to develop high yielding genotypes with high sedimentation value. Thus, these characters may be effective as selection indices during breeding programme for improving grain yield and quality.

Keywords: *Triticum aestivum*, PCV, GCV, genetic advance, grain yield, quality

Introduction
Wheat (*Triticum aestivum* L.) is an important cereal and main food crop for people over the entire world, occupying commanding position in Indian Agriculture, which occupies 28 percent area under cereals and contributing 33 percent of the total food grain production in the country (Rangare *et al*. 2010) [11]. Materialization of wheat yield fluctuates widely as a result of its interaction with environment because grain yield in wheat is a polygenic inherited trait and is the product of several contributing factors affecting yield directly or indirectly (Akram *et al*. 2008) [2]. Use of varieties with better yield potential and wide range of adaptability is of prime importance for increasing wheat production. Today, the most challenging task for wheat breeders is not only to increase grain yield but also to improve the grain quality for end products to meet the food requirement of ever increasing population. Wheat quality becomes a major target in wheat breeding program for the world wheat trade. Thus, development of high yielding wheat cultivars with better and acceptable quality has always been a major objective of wheat breeding programs throughout the world (Bhutta 2006) [7]. Generating information about the genetic variability, relationships and mechanisms of inheritance of the genetic traits involved is the key task in genetic improvement of any crop plant. The knowledge of heritability helps the plant breeder in predicting the behavior of the succeeding generation and making desirable selections. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program. Genetic advance is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi *et al*. 1992) [8]. The present research with 78 wheat genotypes was conducted to estimate the level of genetic coefficient of variation, heritability and genetic advance for the purpose to ascertain and develop appropriate selection indices for the increased grain production with better quality.

Materials and Methods
The present investigation was planned to assess genetic diversity for yield, yield contributing traits and quality traits in seventy eight germplasm of bread wheat evaluated in RBD with two replications at Research cum Instructional Farm, S.G. College of Agriculture and Research

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Station, Kumhrawand, Jagdalpur, IGKV, Raipur (C.G.) during rabi 2020. The lines were sown in a double row of two meter length spaced at 20 cm with an approximate plant to plant spacing of 4 cm under late sown conditions. The recommended agronomic practices were followed. Five plants were selected randomly from each genotype per replication for agronomic data and observations on days to heading and days to maturity were recorded on plot basis. The data obtained were subjected to the biometrical analysis that included analysis of variance, heritability, and genetic advance. Genotypic variance ($\sigma^2 g$), phenotypic variance ($\sigma^2 p$), genotypic coefficient of variation (GCV %), phenotypic coefficient of variation (PCV %), broad sense heritability (h^2 (bs) %) and genetic advance in percent mean (GAPM) were estimated by the formula suggested by Singh and Chaudhary (1985) [13]. The estimate of GCV and PCV were classified as low, medium and high (Sivasubramanian and Madhavamenon 1973) [14]. The heritability was categorized as suggested by Robinson et al. (1949). Again, genetic advance was classified by adopting the method of Johnson et al. (1955) [9].

Results and Discussion
Highly significant mean squares due to genotypes for all the characters in 16 wheat genotypes revealed the presence of enough genetic variability in the material under study (Table 1). This result implied that this population of wheat genotypes would respond positively to selection. The results pertaining to mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h2) and expected genetic advance as percent of mean (GAM) for all the characters studied are furnished in (Table 2). Variability is essential for wide adaptability and resistance to biotic and abiotic factors and hence, an insight into the magnitude of genetic variability present in a population is of paramount importance to a plant breeder for starting a judicious breeding programme. The magnitude of genetic variability for days to maturity was ranged from 78.39 to 104.29 days with the mean value of 98.10 days and for plant height 48.70 to 70.60cm with the mean value of 62.30 cm. Variability of days to 50% flowering ranged from 51.00 to 61.00 with the mean value of 55.69 percent and for harvest index varied from 16.88 to 54.62 with the mean value of 35.87. Thus, these results indicate the presence of wide range of genetic variability in the material. The genotypic coefficient of variation (GCV) ranged from 4.39 percent to 32.81 percent and phenotypic coefficient of variation (PCV) from 4.88 percent to 34.41 percent (Table 2). The result of genotypic and phenotypic coefficient of variation revealed that seed yield per plot and harvest index exhibited highest genotypic coefficient of variation of 32.81 percent and 21.09 percent and highest phenotypic coefficient of variation of 34.41 percent and 22.44 percent, respectively. The high PCV and GCV observed are evident from their high variability that in turn offers good scope for selection (Table 2). In their study, Ali et al. (2008) [3] reported high GCV and PCV

estimates for grain yield per plant. The lowest GCV and PCV were recorded for days to 50% flowering (4.39% and 5.63%) respectively, and days to maturity (4.51% and 4.88%) respectively, indicating difficulty of improvement for these traits through selection (Table 2). The GCV values were higher than PCV values for all the traits which reflect the less influence of environment in expression of traits.

Heritability is a useful quantitative parameter, which considers the role of heredity and environment determining the expression of a trait (Allard 1960) [4]. Effective selection can be achieved only when additive effects are substantial and environmental effects are small. Heritability estimates ranged from 45.70 (for grain filling period) to 90.88 percent (for seed yield). High heritability estimates for plant height (Tripathi et al. 2011) [15], days to heading (Baranwal et al. 2012) [6], thousand kernel Naik et al. 2015 Research Journal of Agricultural Sciences 6(1) 124 weight (Ashraf et al. 2002), and spike length (Ali et al. 2008) [3], were also reported. Expected genetic advance indicates the expected genetic progress for particular trait under selection cycle and measures the extent of its stability under selection pressure. The highest value was recorded for harvest index (14.64), days to maturity (8.43) and seeds per spike (7.32) and flag leaf width (0.17) and seed yield (0.68) tillers per plant (0.78). Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone in selecting best individuals (Johnson et al. 1955) [9]. High heritability along with moderate genetic advance was noticed for harvest index and days to maturity suggesting predominance of additive and non-additive gene action in the expression of this trait. Therefore, these traits can be improved by mass selection. High heritability accompanied by low genetic advance for seed yield and flag leaf length, indicates predominance of non-additive gene action which could be exploited through heterosis breeding. Akanda et al. (1997) [1] reported that high genotypic coefficient of variation along with high heritability and genetic advance provide better information than other parameters alone. These traits are the most important quantitative traits to be taken into consideration for effective selection in wheat. Similar results have been reported by Ali et al. (2008) [3], Sharma and Garg (2002) [12]. From the present study, it is evident that genotypes studied may provide good source of material for further breeding program. Therefore, information on the genetic parameters such as genetic correlation coefficient, coefficient of variation, heritability and genetic advance can help the breeder to evolve suitable cultivars within a short time. The knowledge on heritability of traits is helpful to decide the selection procedure to be followed to improve the trait in a situation. On the basis of results as summarized above, it is concluded that traits like plant height, thousand kernel weight, sedimentation value and grain yield per plot can be considered as suitable selection criteria for the development of high yielding bread wheat varieties with better quality.

Table 1: Analysis of variance for quantitative characters wheat

Characters	Mean sum of Errors			Total
	Replication	Treatment	Error	
Degree of freedom (D.F)	1	15	15	31
Flag leaf length (cm)	2.54	16.43	0.77	19.74
Flag leaf width (cm)	0.004	0.037	0.006	0.047
Awn length	0.05	1.67	0.20	1.92
Grain filling period	15.26	14.52	4.12	33.90
Ear length	0.82	3.08	0.59	4.49
Plant height	1.07	54.77	11.57	67.41
Tillers per plant	0.018	0.678	0.079	0.775
Seeds per spike	0.38	48.36	2.98	51.72
Days to 50%flowring	0.84	21.78	3.87	26.49
Days to maturity	0.50	62.08	3.32	65.90
1000 grain weight	2.78	57.57	13.23	73.58
Harvest index	205.55	179.14	7.56	392.25
Seed yield	0.003	0.367	0.012	0.382

Table 2: Genetic parameters for yield attributing characters in wheat

Sl. No.	Characters	Range		Mean	h^2 [b] (%)	GA	GA % Mean	GCV %	PCV %
		Min	Max						
1.	Flag leaf length (cm)	8.95	21.35	13.53	87.09	4.39	32.46	16.89	18.09
2.	Flag leaf width (cm)	1.00	1.55	1.36	63.64	0.17	12.22	7.43	9.32
3.	Awn length (cm)	6.21	9.33	7.31	70.63	1.21	16.57	9.57	11.39
4.	Grain filling period	24.50	35.00	27.06	45.70	2.59	9.58	6.88	10.18
5.	Ear length (cm)	12.63	16.17	14.47	58.36	1.43	9.91	6.29	8.24
6.	Plant height	48.70	70.60	62.30	55.46	5.82	9.34	6.09	8.18
7.	Tillers per plant	2.30	4.65	3.24	71.58	0.78	24.04	13.80	16.31
8.	Seeds per spike	16.85	33.00	22.91	83.53	7.32	31.96	16.98	18.57
9.	Days to 50% flowering	51.00	61.00	55.69	60.69	3.92	7.04	4.39	5.63
10.	Days to maturity	78.39	104.29	98.10	85.52	8.43	8.59	4.51	4.88
11.	1000 Grain weight (g)	20.87	42.04	34.63	52.77	5.75	16.61	11.10	15.28
12.	Harvest index	16.88	54.62	35.87	88.33	14.64	40.82	21.09	22.44
13.	seed yield	0.37	1.91	1.05	90.88	0.68	64.43	32.81	34.41
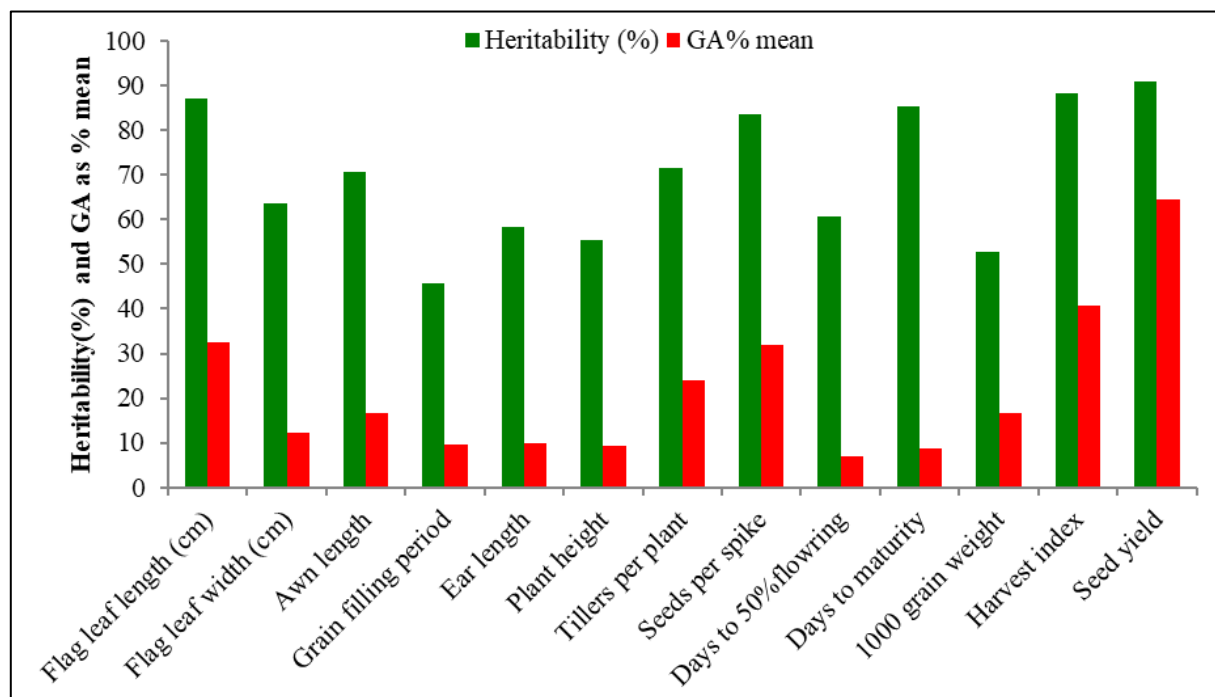
Fig 1: Heritability (%) and GA as % mean
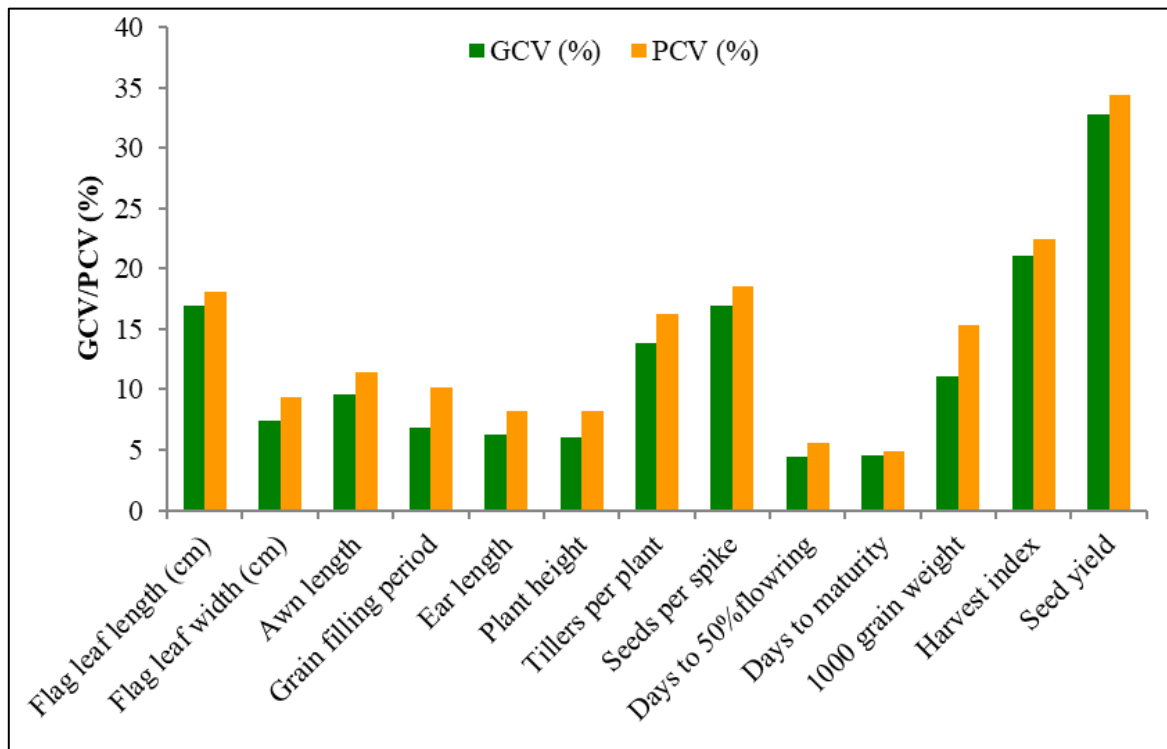
Fig 2: Illustration of GCV/PCV

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