Plant Archives Vol. 18, Special Issue (ICAAAS-2018), 2018 pp. 51-56 ***ISSN 0972-5210***

VARIABILITY HERITABILITY AND GENETIC ADVANCE FOR YIELD AND SOME QUALITY TRAITS IN SPRING WHEAT (*TRITICUM AESTIVUM* L.)

Mohammad Imran*, S. A. Kerkhi[1], Kausar Ali[1], Sukhdev Singh[1], Afsar Ahmad[2] and Sopal Singh[3]

[*,1]Department of Genetics and Plant Breeding, S. V. P. Univ. of Agricult. and Tech., Meerut - 250 110 (U.P.), India.
[2]Department of Genetics and Plant Breeding, Choudhary Charan Singh University, Meerut - 250 110 (U.P.), India.
[3]Department of Horticulture, S. V. P. Univ. of Agricult. and Tech., Meerut - 250 110 (U.P.), India.

Abstract

Fifty nine genotypes of spring wheat were studied for getting genetic information on nature and magnitude of genetic variability for designing suitable breeding programme. The parental lines were grown during *rabi*, 2012-13 and 44 cross combinations among lines and testers were made and the seeds of 15 parental lines and 44 crosses were procured. The parents and F_1s were evaluated in a Randomized Block Design in three replications at Crop Research Centre (Chirodi Block) of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, U.P. during *rabi*, 2013-14. The observations were recorded on fourteen yield components and four quality parameters. Analysis of variance revealed that a wide amount of variability among the genotypes were present for all the traits under study. Estimates of PCV were higher than the GCV for all the traits, but little differences were recorded between PCV and corresponding GCV values for all the traits, which indicated that there was not much influence of environment in the expression of the traits. High estimates (>30 %) of heritability in narrow sense were found for characters namely, biological yield per plant, peduncle length, plant height and days to 50 % flowering indicated that these traits may be relied upon while selecting the genotypes for improvement in wheat.

Key words : Spring wheat, phenol colour reaction, GCV, PCV, heritability.

Introduction

Wheat (*Triticum aestivum* L.) is a member of family Gramineae and the most important cereal crop for the world's populations. It is very popular among the farmers because of it is easy cultivate, ecologically suitable and wider adaptable in agro-climatic conditions. Wheat provides more nutrition's to the humans as compare to the other food crops; hence, it is considered as staple food for about 40% of the world's population. It is always a challenging job to the plant breeders to enhance the level of crop production as the emerging population of the developing country like India will require much more food as compare to the present day requirement. It is not possible to enhance the cultivated area under the production. Hence, there is need to enhance the productivity by developing high yielding disease resistant varieties and better management of crop by modern agricultural practices to build up the increasing food demands. The development of an effective breeding is depend upon the existence of genetic variability. The efficiency of selection largely depends upon magnitude of genetic variability present in the plant population. Therefore, analysis of genetic variation among the genotypes is play the key role before designing the breeding programme while selecting the elite genotypes on the basis of their performance. The success of genetic improvement in any character depends on the nature of variability present in the characters. Hence an insight into the magnitude of variability present in the gene pool of a crop species is of utmost importance to a plant breeder for starting a judicious plant breeding programme. In earlier years, the visual observations used to be the measure of variability in plant population.

In crop improvement programme, only genetic component of variation is important since only this component is transmitted to the next generation.

However, when we are dealing with segregating generations, the genetic variance consists of additive and dominance components (assuming there is no epistasis). Since in self-pollinated crops we develop homozygous lines, the dominance component will not contribute to the phenotype of homozygous lines derived from a population. Consequently, in such cases, only the additive component of the genetic variance is relevant. Therefore, for the segregating generation, the ratio of additive component of variance to the total phenotypic variance is a more appropriate estimate of heritability. Estimates of genetic advance help in understanding the type of gene action involved in the expression of various quantitative characters. High values of genetic advance are indicative of additive gene action and low values are indicative of non-additive gene action. Selection of the parents on the basis of phenotypic performance alone is not a sound procedure since phenotypically superior lines may yield poor recombinants in the segregating generations. It is, therefore, essential that parents should be chosen on the basis their genetic value. Keeping above in view, an effort has been made in the present investigation to evaluate a set offifty nine genotypes of spring wheat. The aim of this study is to analyse the genetic variability, heritability, genetic advance and to asses the component of variances for yield and quality traits.

Materials and Methods

The present investigation was carried out with 15 parents and 44 F's developed from line x tester mating design. The parental lines (11 lines and 4 testers) were grown during *rabi,* 2012-2013 and 44 cross combinations among lines and testers were made and the seeds of parental lines and 44 crosses were procured. The experiment was conducted at Crop Research Center (Chirodi Block) of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.), India under timely sown conditions during *rabi*, 2013-14. To avoid the border effects, the plots falling on the border were surrounded by non-experimental rows of varieties/strains. Recommended agronomic practices were adopted to raise a good crop. Observations on the basis of various quantitative characters were recorded on five randomly selected plants in each three replication. The data on days to ear emergence, days to 50% flowering and maturity were taken on the plot basis.The experimental data were compiled by taking the mean over selected plants of each treatment for each replication and mean data were subjected to the statistical and bio-metrical analysis for all the seventeen characters except for phenol colour reaction. Analysis of variance for the design of experiment was computed as suggested by Panse and Sukhatme (1985) while heritability in broad sense by Hanson (1963) and in narrow sense by Kempthorne and Curnow (1961) and expected genetic advance by Johnson *et al.* (1955).

Results and Discussion

Analysis of variance revealed high significant differences among the set of material used in the present investigation for all yield and quality characters showed wide spectrum of genetic variability. The mean squares for yield and quality components are presented in table 1. It is worthful to mention here that the parent K1006 took minimum days to ear emergence and days to 50% flowering and also found mean value for productive tillers per plant; RW346 was good for early maturity and also for maximum peduncle length; UP2565 found to be good for plant height; grains per spike and grain yield per plant; HD2824 found maximum mean value for spike length; MP3336 and GW433 found maximum average value for spike lets per spike; HD3076 had highest mean value for flag leaf area; HD3095 showed highest average value for biological yield per plant; HD2967 found maximum mean value for harvest index and for protein content; HD2733 had highest mean value for 1000 grain weight and for gluten content; PBW533 found maximum mean value for ash content. Among the 44 F_1s, HD2824 x HD2967 was observed good for days to ear emergence; HD2824 x HD2967 showed highest mean value and was good for early flowering; NW5038 x HD2967 was found early maturity type; K1006 x HD2733 showed dwarf stature; HD3076 x UP2565 had highest peduncle length; HD3095 x HD2967 was observed as having maximum spike length; HD3076 x UP2565 had maximum number of spikelets per spike; PBW533 x DBW17 was observed as highest productive tillers per plant; GW433 x HD2967 was having maximum number of grains per spike; HD2824 x UP2565 showed highest mean value for flag leaf area; MP3336 x HD2733 had highest mean value for biological yield per plant; HD2824 x DBW17 was observed as highest grain yielder; HD2824 x DBW17 showed highest mean value for harvest index; DBW90 x HD2733 had maximum 1000 grain weight; HD2824 x HD2967 showed highest average value for gluten content; HD2824 x HD2967 had maximum mean value for protein content and cross PBW533 x HD2733 for ash content. Such types of findings were also reported by Maan and Yadav (2010), Gollen *et al* (2011), Kumar *et al* (2013), Singh *et al* (2013). The results indicated that useful variability in progenies and parents was developed through hybridization, which could be properly utilized for selection of suitable genotypes on the basis of different genetic parameters to obtain suitable genotypes for further genetic improvement in spring wheat.

The estimates of coefficient of variation (i) Genotypic Coefficient of Variation (GCV) and (ii) Phenotypic Coefficient of Variation (PCV) along with grand mean and range for all the 17 traits are presented in table 2. A wide range of variability present in any crop always provides the better chances of selecting desired type (Vavilov, 1951). The success of plant improvement depends on careful management of variability and techniques to be employed in each case will depend upon clear understanding of extent and nature of variability. A thorough screening of the materials studied under present investigation revealed sufficient variability for all the 17 characters. Similar findings on variability has been reported by Maan and Yadav (2010), Tripathi *et al* (2011), Kumar *et al.* (2013), Kumar *et al.* (2014), Yadawad *et al.* (2015) for various yield and quality components in wheat. With regards to GCV & PCV, the present results revealed that the estimates of phenotypic coefficient of variation were in general slightly higher than their corresponding genotypic coefficient of variation for all the 17 characters studies which indicated that the variabilities for these traits in the genotypes was not much affected by the environments for the expression of these characters. Similar finding has been reported by Gollen *et al.* (2011), Dhananjay *et al.* (2012), Singh *et al.* (2013), Kumar *et al.* (2014) for days to flowering, days to maturity, plant height, productive tillers per plant, spike length, grains per spike, 1000 grain weight, biological yield per plant, gain yield per plant, harvest index, protein content, flag leaf area, biological yield per plant, grain yield per plant and ash content in wheat. In the present investigation, high estimates of heritability (>30%) in narrow sense were observed for biological yield per plant (45.25), peduncle length (45.17), plant height (31.23) and days to 50% flowering (30.40), while moderate heritability estimates were recorded for 11 characters *viz*; ash content (28.54), spike length (28.03), grain yield per plant (26.16), 1000 grain weight (25.34), flag leaf area (23.15), days to ear emergence (22.32), spikelets per spike (21.20), protein content (21.03), gluten content (20.86), harvest content (19.65) and grains per spike (13.45). Similar findings were reported by Singh *et al.* (2013), Kumar *et al.* (2014), Yadawad *et al.* (2015) for yield and its component traits in wheat. High heritability estimates for these characters indicated might be due to the presence of additive and additive x additive type of gene effects. This indicates that, if these traits may be subjected to mass or progeny or family selection or any selection

Table 1 : Analysis of variance for seventeen characters in spring wheat.

Source of variation	DF	DTEE	DTF	DTM	PH	PL	SL	SS	PTP	GS	FLA	BYP	GYP	HI	1000 GW	GC	PC	AC
Replication	2	6.1242	4.9209	4.6836	1.7279	0.1953	0.0329	0.4097	0.1232	3.3214	0.0127	1.6338	3.2710	4.1465	2.3042	0.1764	0.0766	0.0048
Treatments	58	23.5836**	27.2961**	27.2538**	45.6522**	10.4966**	0.9063**	1.6647**	0.5372**	7.5418**	24.4820**	44.0597**	29.3426**	92.3550**	5.7841**	0.5592**	0.4713**	0.1764**
Error	116	2.7449	2.3174	3.5054	1.1725	1.6919	0.2346	0.4976	0.2611	1.9518	1.9147	4.1098	2.1404	4.3635	2.7037	0.05386	0.1213	0.0252
Total	176	9.6506	10.5786	11.3450	15.8369	4.5765	0.4536	0.8812	0.3505	3.8095	9.3300	17.2470	11.1176	33.3583	3.7143	0.2218	0.2361	0.0748

*, ** Significant at 5% and 1% probability level respectively.

DF- Degree of Freedom, DTEE- Days to ear emergence, DTF- Days to 50 % flowering, DTM- Days to maturity, PH- Plant height (cm), PL- Peduncle length (cm), SL- Spike length (cm), SS- Spikelet's/spike, PTP- Productive tillers/plant, GS- Grains/spike, FLA- Flag leaf area (cm^2), BYP- Biological yield/plant (g), GYP- Grain yield/plant (g), HI- Harvest index (%), 1000 GW- 1000 grain weight (g), GC- Gluten content (%), PC- Protein content (%), AC- Ash content (%).

Table 2 : Grand mean, range, PCV, GCV, heritability and genetic advance for seventeen characters in spring wheat.

Characters	Grand Mean	Range	PCV (%)	GCV (%)	Heritability (%)		GA (5%)	Gen. Adv. as % of mean (5%)
					Broad sense	Narrow sense		
Days to ear emergence	81.59	74.66-87.33	3.81	3.22	71.68	22.32	5.89	7.21
Days to 50 % flowering	90.21	82.00-97.00	3.61	3.19	78.23	30.40	6.73	7.46
Days to maturity	140.70	130.66-145.66	2.40	1.99	69.31	4.24	6.18	4.39
Plant height (cm)	82.87	73.85-95.59	4.82	4.64	92.67	31.23	9.78	11.80
Peduncle length (cm)	33.57	30.25-38.09	6.40	5.10	63.43	45.17	3.60	10.72
Spike length (cm)	10.29	9.27-11.67	6.57	4.59	48.83	28.03	0.87	8.48
Spikelet's /spike	18.54	16.60-19.80	5.07	3.36	43.88	21.20	1.09	5.88
Productive tillers/plant	10.51	9.73-11.73	5.65	2.88	26.06	9.60	0.40	3.88
Grains/spike	55.19	52.33-63.33	3.53	2.47	48.84	13.45	2.51	4.56
Flag leaf area (cm^2)	28.91	23.59-35.69	10.62	9.48	79.71	23.15	6.46	22.35
Biological yield/plant (g)	50.03	42.19-58.48	8.34	7.29	76.42	45.25	8.42	16.83
Grain yield/plant (g)	26.63	21.58-35.49	12.56	11.30	80.90	26.16	7.15	26.84
Harvest index (%)	53.38	40.97-69.94	10.87	10.14	87.05	19.65	13.33	24.98
1000 grain weight (g)	42.64	38.58-45.30	4.52	2.37	27.52	25.34	1.40	3.29
Gluten content (%)	8.95	7.68-9.55	5.26	4.58	75.77	20.86	0.94	10.53
Protein content (%)	13.33	12.52-14.07	3.65	2.56	49.02	21.03	0.63	4.73
Ash content (%)	1.73	1.16-2.18	15.88	12.96	66.65	28.54	0.48	27.95

scheme, aimed at exploiting additive (fixable) genetic variance, a widely adapted genotype could be developed possessing good productivity and with better quality in wheat.

Johnson *et al.* (1955) stated that without genetic advance, the estimates of heritability would not be of practical importance based on phenotypic and emphasized the concurrent use of genetic advance along with heritability. High estimate of expected genetic advance expressed as percentage of mean (> 20%) was observed high for ash content (27.95), grain yield per plant (26.84), harvest index (24.98) and flag leaf area (22.35). Moderate (10-20%) estimate of genetic advance was recorded for biological yield per plant (16.83), plant height (11.80), peduncle length (10.72) and gluten content (10.53). Similar findings were also reported by Ali and Falahy (2011), Dhananjay *et al.* (2012), Kumar *et al.* (2013), Kumar *et al.* (2014), Yadawad *et al.* (2015) for yield and its contributing characters in wheat. The heritability estimates along with genetic advance is more reliable because heritability alone does not provide ample evidence regarding amount of genetic advance. Therefore, much reliance cannot be laid on the numerical values of heritability as a rational generalization. High heritability (narrow sense) coupled with moderate genetic advance in percent of mean were observed for biological yield per plant, peduncle length, plant height, indicated that there is least influence of environment in expression of these traits and selection of desirable plants could be easily made on the basis of these characters. Moderate heritability coupled with high genetic advance in percent of mean were observed for ash content, grain yield per plant, harvest index, flag leaf area which indicated that based on this trait the selection could also be made for desirable plants. Moderate heritability with moderate genetic advance were observed for gluten content, which indicating that there are chances of improvement with this character through simple selection procedure. High heritability along with low genetic advance in percent of mean was observed for days to 50% flowering. Similar findings were also reported by earlier researchers namely (Tripathi *et al.*, 2011; Dhananjay *et al.*, 2012; Kumar *et al.*, 2013; Kumar *et al.*, 2014; Yadawad *et al.*, 2015) for grain yield and its contributing traits in spring wheat.

Data recorded on phenol colour reaction was not statistically analyzed. Parents and their F$_1$s were categorized on the bases of colour intensity observed on grains after phenol colour reaction; it is summarized in table 3. The colour on the grains after phenol colour reaction were categorized in five groups *viz*; black, dark brown, light brown, light colour on the edge and no colour. On the bases of different grades, the parents and crosses were grouped in different category. Out of 59 genotypes (15 parental lines and 44 F$_1$s), 4 parents and 4 crosses

Table 3 : Parental lines/crosses appeared in different category with the help of phenol colour reaction at 1% phenol solution.

S.no.	Category		Parental lines/ testers/crosses
1	**Black**	**Parents**	PBW533 (L), HD2824 (L), HD2967 (T), HD2733 (T)
		Crosses	K1006 x HD2733, HD2824 x HD2967, DBW90 x UP2565, RW346 x DBW17
2	**Dark brown**	**Parents**	HD3076 (L), RAJ4246 (L), DBW90 (L), RW346 (L), DBW17 (T)
		Crosses	K1006 x HD2967, K1006 x DWB17, K1006 x UP2565, MP3336 x HD2967, MP3336 x UP2565, MP3336 x HD2733, HD3076 x DBW17, PBW533 x UP2565, NW5038 x DBW17, RAJ4246 x UP2565, RAJ4246 x HD2733, HD3095 x UP2565, HD2824 x UP2565, DBW90 x HD2967, DBW90 x DBW17, DBW 90 x HD2733, RW 346 x HD2967, RW346 x HD2733
3	**Light brown**	**Parents**	K1006 (L), MP3336 (L), NW5038 (L), GW433 (L), HD3095 (L), UP2565 (T)
		Crosses	MP3336 x DBW17, HD3076 x HD2967, HD3076 x UP2565, HD3076 x HD2733, PBW533 x HD2967, PBW533 x DBW17, PBW533 x HD2733, NW5038 x UP2565, NW5038 x HD2733, RAJ4246 x HD2967, RAJ4246 x DBW17, GW433 x HD2967, GW433 x DBW17, HD3095 x HD2967, HD3095 x HD2733, HD2824 x DBW17, HD2824 x HD2733, RW346 x UP2565
4	**Light colour**	**Crosses**	NW5038 x HD2967, GW433 x UP2565, GW433 x HD2733
5	**Negative (No colour)**	**Crosses**	HD3095 x DBW17

were in black categories; 5 parents and 18 crosses in brown to dark brown category; 6 parents and 18 crosses in light brown category; 3 crosses were in light colour category; in negative (no colour) category only 1 cross namely HD3095 x DBW17. In light brown category, there were six parents (line x tester) and eighteen Crosses *viz*; K1006 (L), MP3336 (L), NW5038 (L), GW433 (L), HD3095 (L), UP2565 (T); Crosses- MP3336 x DBW17, HD3076 x HD2967, HD3076 x UP2565, HD3076 x HD2733, PBW533 x HD2967, PBW533 x DBW17, PBW533 x HD2733, NW5038 x UP2565, NW5038 x HD2733, RAJ4246 x HD2967, RAJ4246 x DBW17, GW433 x HD2967, GW433 x DBW17, HD3095 x HD2967, HD3095 x HD2733, HD2824 x DBW17, HD2824 x HD2733, RW346 x UP2565 which indicated that these 6 parental lines and 22 crosses might be suitable for chapati making quality. Similar findings were reported by Abrol *et al*. (1970). Phenol colour reaction may be used in screening of genotypes and isolating for its suitability for chapati making.

Conclusion

Estimates of phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits, but little difference were recorded between PCV and corresponding GCV for all the traits. This little difference indicated that variability in the genotypes for the expression of different traitswas notmuch influenced by the environment. High estimates of heritability in narrow sense were observed for biological yield per plant, peduncle length, plant height and days to 50% flowering indicated that there is least influence of environment in expression of these traits and selection of desirable plants could be easily made on the basis of these characters. Twenty two cross combinations showed low phenol reaction (negative and light colour/light brown) indicated for better chapati making quality hybrids. Cross combinations, HD3095 x DBW17, HD3095 x HD2733 and RAJ4246 x DBW17 were common for yield and for low phenol reaction (negative & light brown colour), which may be exploited through heterosis breeding programme for increasing yield and chapati quality in wheat.The results indicated that useful variability in parents and progenies was developed through hybridization which can be properly utilized for selection of suitable genotypes on the basis of genetic parameters to obtained high yield potential in spring wheat.

References

Abrol (1970). Classified maxican and indigenous of wheat varieties with the help of phenol coloration.

Ali, I. H. and M. A. H. Falahy (2011). Analysis of partial diallel cross for yield and its components in durum wheat. Bulletin of Faculty of Agril. *Cairo-Uni*., **62** : 145-152.

Dhananjay, B. N., S. Singhraj, B. Bhushan and V. P. Rahul (2012). Genetic Variability in wheat (*Triticum aestivum*) under Normal and Timely Sown Condition. *Environment & Ecology*, **30** : 1085-1087.

Gollen, B., R. K. Yadav and P. Kumar (2011). Assessment of genetic parameters for spike traits and yield attributes in bread wheat genotypes following Line x Tester mating system. *Environment and Ecology*, **29** : 752-756.

Hanson, W. D. (1963). Heritability in Statistical Genetics and Plant Breeding. *Natl. Acad. Sci. Natl. Res*. Council No. **982** : 125-140.

Johnson, H. W., H. F. Robinson and R. E. Comstock (1955). Estimates of genetic and environmental variability in soybean. *Agron. J*., **47** : 314-318.

Kempthorne, O. and R. M. Curnow (1961). The partial diallel cross. *Biometrics*, **17** : 229-250.

Kumar, A., V. Kumar, S. A. Kerkhi, S. Chand Kumar, P. Kumar, N. Kumar and M. Kumar (2014). Evaluation of Heterosis for yield and yield related traits in bread wheat (*Triticum aestivum* L.). *Prog. Agric*., **14** : 151-159.

Kumar, G. Singh, S. K. Chand, P. B. Singh and D. K. Singh (2013). Genetic variability in wheat (*Triticum aestivum* L.). *Prog. Agric*., **13** : 239-242.

Maan, R. K. and A. K. Yadav (2010). Variability, heritability and genetic advance for quantitative characters in hexaploid wheat (*Triticum aestivum L.*). *Prog. Agric*., **10** : 355-357.

Panse, V. G. and P. V. Sukhatme (1985). *Statistical method for agricultural workers*. III^{ed} Ed. ICAR, New Delhi, pp. **547**.

Sidharthan, B. and S. K. Malik (2006). Association analysis in wheat. *International Journal of Agricultural Sciences*, **2** : 427-428.

Singh, M. K., P. K. Sharma, B. S. Tyagi and G. Singh (2013). Genetic analysis for morphological traits and protein content in bread wheat (*Triticum aestivum* L.) under normal and heat stress environments. *Indian J. Genet*., **73** : 320-324.

Tripathi, S. N., M. Shailesh, P. Pandey, K. K. Jaiswal and D. K. Tiwari (2011). Relationship between some morphological and physiological traits with grain yield in bread wheat (*Triticum aestivum* L.em.Thell.). *Trends in Applied Sci. Res*., **6** : 1037-1045.

Vavilov, N. I. (1951). Phyto-geographic basis of plant breeding. The origin, variation, immunity and breeding of cultivated plants. *Chronica Bot.*, **13** : 1-366.

Yadawad, A., R. R. Hanchinal, H. L. Nadaf, S. A. Desai, S. Biradar and V. Naik Rudra (2015). Genetic variability for yield parameters and rust resistance in F_2 population of wheat (*Triticum aestivum* L.). *The Bioscan-an International Quarterly Journal of Life Sciences*, **10** : 707-710.