Shivom
Student, Genetics and Plant Breeding, C S A University of Agriculture & Technology Kanpur, Uttar Pradesh, India

Dr. Som Veer Singh
Section of Rabi Cereals, Assistant Professor/ Wheat Breeder. C S A University of Agriculture & Technology Kanpur, Uttar Pradesh, India

Pawan Kumar Saini
Student, Genetics and Plant Breeding C S A University of Agriculture & Technology Kanpur, Uttar Pradesh, India

Harshit Tripathi
Student, Genetics and Plant Breeding, C S A University of Agriculture & Technology Kanpur, Uttar Pradesh, India

Jai Saxena
Student, Genetics and Plant Breeding, C S A University of Agriculture & Technology Kanpur, Uttar Pradesh, India

Study of heritability and genetic advance for yield and its contributing traits in bread wheat (*Triticum aestivum* L.)

Shivom, Dr. Som Veer Singh, Pawan Kumar Saini, Harshit Tripathi and Jai Saxena

DOI: https://doi.org/10.22271/chemi.2020.v8.i3n.9342

Abstract
Wheat (*Triticum aestivum* L.) is number one cereal of the world and is grown on the largest area. Field experiment conducted at Crop Research Farm, Nawabganj of CSAUA&T in Kanpur. In this study the high heritability and high genetics advance for the twelve characters were observed in normal conditions. In different genotypes, high heritability (narrow sense) were recorded for days to maturity, one thousand grains weight, grain weight per spike, number of grains per spike, number of tillers per plant and while moderate heritability were found for plant height, harvest index, grain yield per plant, biological yield, spike length (cm) and days to 50% heading whereas number of spikelets per spike showed low heritability. The estimate of genetic advance in percentage over mean ranged from 5.56 (days to maturity) to 43.04 (number of productive tillers per plant) in F_1 generation. The high value of genetic advance was recorded for number of tillers per plant. Moderate genetic advance were recorded for days to 50% heading, plant height (cm), spike length (cm), 1000 grain weight (g), grain weight per spike (g), biological yield per plant (g), grain yield per plant and harvest index. Low values of genetic advance were recorded for days to maturity, number of spikelets per spike and number of grain per spike in F_1 generation.

Keywords: Wheat, genotypes, heritability and genetics advance

Introduction

Wheat is the world's most widely cultivated food crop. It is stable food of millions of people. Wheat (*Triticum aestivum* L.) is number one cereal of the world and is grown on the largest area. The major wheat growing countries in the world are China, India, U.S.A., Russia and France. Globally, wheat is being grown more than in 122 countries and occupies an area of 214.29 million hectares producing nearly 734.04 million tonnes and productivity is 3425 kilogram per hectare (FAO 2018). India stands second rank both in area and production next to China in the world. At national level area under wheat is 29.58 million ha with the production of 99.70 million tonnes with a productivity of 3371 kilogram per hectare (DACFW 2018). Diallel mating system studied the parental material by all means particularly in terms of genetic component of variance for different characters, general and specific combining ability, gene effects, heterosis, heritability, genetic advance and other useful genetic parameters. In addition study will also be helpful in evolution of high yielding varieties with better quality. In crop improvement only the genetic component variation is important since only this component is transmitted to the next generation. Heritability is the ratio of genotypic variance to the phenotypic variance. Heritability is a key parameter in quantitative genetics because it determines the response to selection. Heritability is often used by plant breeders to quantify the precision of single field trials or of series of field trials. Results suggest that heritability on an entry-difference basis is a well-suited alternative for obtaining an overall heritability estimate, and in addition provides heritability per genotype as well as one per difference between genotypes. Estimates of heritability with genetic advance are more reliable and meaningful than individual consideration of the parameters. Therefore, the present study was to assess the extent of genetic heritability and genetic advance among eight wheat genotypes for yield and related traits with the objectives of estimating heritability and genetic advance for yield and yield related traits.

Corresponding Author:
Shivom
Student, Genetics and Plant Breeding, C S A University of Agriculture & Technology Kanpur, Uttar Pradesh, India

Material and Method
Field experiments of wheat crop were conducted in two cropping season as first Rabi season 2017-18 and second Rabi season 2018-19 at locations, namely Crop Research Farm, Nawabganj of C. S. A. University of Agriculture and Technology, Kanpur-208002 UP India. The experimental material for present investigation comprised of 28 F_1s developed by crossing 8 lines *viz.*, HD 2967, WH 1105, K 307, K 1601, DBW 187, WH 1218, K 9107, and DBW 14, following half diallel mating design. A total of 36 treatments (28 F_1s and 8 parents) were used for the "Genetic study on grain yield and its contributing characters in bread wheat (*Triticum aestivum* L.)". The salient features of these parental lines are given in Table-1

Table 1: Details of genotypes

S. No.	Genotype	Species	Pedigree	Place of origin
1.	HD 2967	*T. aestivum*	ALD/CUC//URES/HD2160M/HD2278	IARI, New Delhi
2.	WH 1105	*T. aestivum*	MILAN/S87230/BABAX.	CCS, Hisar
3.	K 307	*T. aestivum*	K 9321/UP 2003	CSA, Kanpur
4.	K 1601	*T. aestivum*	K 9107/DBW 14	CSA, Kanpur
5.	DBW 187	*T. aestivum*	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KACHU/6/KACHU	IIWBR, Karnal
6.	WH 1218	*T. aestivum*	KA/NAC//TRCH/3/VORB	CCS, Hisar
7.	K 9107	*T. aestivum*	K 8101/K68	CSA, Kanpur
8.	DBW 14	*T. aestivum*	RAJ 3765/DBW 345	IIWBR, Karnal

The genotypes under study were planted in a randomized complete block design (RCBD) with three replications per entry and one row (3m) per replication. The entries were sown in a single row plot of three meter length with inter and intra-row spacing of 25cm and 10cm, respectively. Recommended agronomic practices were adopted to raise a good crop. The observation was recorded from the five randomly selected plants in parents and their F_1 for all the following traits *viz.* (1) Days to 50% heading (2) Plant height(cm) (3) Days to maturity (4)Number of productive tillers/plant (5) Number of spikelets per spike (6) Spike length(cm) (7) Number of grains per spike (8) One thousand grain weight(g) (9) Grain Weight per spike(g) (10) Biological yield per plant (g) (11) Grain yield per plant (g) (12) Harvest index (%).
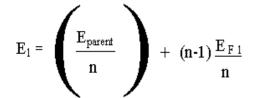
Estimation of selection parameters
(a) Heritability: Heritability in narrow sense (h^2_{ns}) and broad sense (h^2_{bs}) was calculated as suggested by Crumpacker and Allard, (1962) [2].

$$\text{Heritability } (\hat{h}^2) = \frac{\frac{1}{4}\hat{D}}{\frac{1}{4}\hat{D} + \frac{1}{4}\hat{H}_1 + E_1 - \frac{1}{4}F}$$

$$H\,(bs) = \frac{\frac{1}{4}\hat{D} + \frac{1}{4}\hat{H}_1 - \frac{1}{4}F}{\frac{1}{4}\hat{D} + \frac{1}{4}\hat{H}_1 + E_1 - \frac{1}{4}F}$$

$$E_1 = \left(\frac{E_{parent}}{n}\right) + (n-1)\frac{E_{F1}}{n}$$

Where,
$\hat{D}$ = Component of variation due to additive effects of genes

$\hat{H}_1$ = Component of variation due to dominance effects of gene

$\hat{F}$ = The mean of F_r over arrays, where F_r is the covariance of additive and dominance effects in a single array.

$\hat{E}_1$ = the expected environmental component of variation

(b) Genetic advance: The genetic advance was calculated as per formula given by Robinson *et al.* (1949).
Genetic Advance = $(\sigma_{ph}) \times (K) \times (h^2_{bs})$
Genetic advance in per cent of mean of the character

$$\text{G.A. (\%)} = \frac{\sigma_{ph} \times K \times h^2}{\overline{X}} \times 100$$

Where,

G.A. = Estimate of genetic advance
K = Selection differential at 5% selection intensity (K = 2.06)
h^2 = Heritability coefficient in broad sense.
σ_{Ph} = Phenotypic standard deviation.
$\overline{X}$ = Mean value of the character concerned

Result and Discussion
Among the selection parameters the heritability and genetic advance are the most important direct selection parameters. Amount of total variability exists which has been transmitted from the parent to the progenies. In view of this, the heritability (in narrow sense) and genetic advance in % for the twenty eight crosses have been furnished in Table-3.

(1) Heritability: Generally the estimates of heritability and genetic advance were arbitrarily categorized in three by Robinson (1966) as under.
1. High (above 30%),
2. Moderate (above 10% & below 30%)
3. Low (below 10%)

Heritability (in narrow sense) in F_1 generation was calculated by the method proposed by Crumpacker and Allard, (1962) [2]. Accordingly, high estimates of heritability were observed for days to maturity, 1000 grain weight (g), grain weight per spike (g), No of grain per spike and number of tiller per plant

in F₁ generation. The moderate estimates were found for plant height, harvest index, grain yield per plant (g), biological yield per plant (g), spike length (cm) and days to heading. The low heritability estimate was found only for number of spikelets per spike.

2 Genetic advance
Genetic advance, though not an independent identity, has an added advantage over heritability as a guiding factor to the breeders in selection Programme. Stated that without genetic advance, estimates of the heritability would not be of practical importance based on phenotypic expression and emphasized the concurrent use of genetic advance along with heritability.In order to ascertain relative merit of different

attributes, genetic advance in per cent of mean was worked out for all the twelve characters in F₁ generation. The estimate of genetic advance in percentage over mean ranged from 5.56 (days to maturity) to 43.04(No. of tiller per plant) in F₁ generation. The high value of genetic advance was recorded for number of tillers per plant. Moderate genetic advance was recorded for days to heading, plant height(cm), spike length (cm), grain weight per spike (g), 1000 grain weight(g), biological yield(g), grain yield and harvest index. Low values of genetic advance were recorded for number of spikelets per spike, days to maturity and number of grain per spike in F₁generation. Same thing was observed by Kumar *et al.* (2013) [9], Navin Kumar *et al.* (2014) [11].

Table 2: Analysis of variance of parents, F₁s and P vs F₁s for twelve traits in 8 parents diallel cross of bread wheat

Source of variance	d.f.	Days to Heading	No. of tiller/ plant	Plant height (cm)	Days to maturity	Spike length (cm)	No. of spkelets /spike	No. of grains /spike	Grain weight /spike (g)	Biological yield /plant(g)	Grain yield/ plant (g)	1000 grain weight (g)	Harvest index %
Replications	2	1.56	1.82	0.21	1.28	0.46	0.77	7.69**	0.02	2.02	0.38	0.57	0.484
Treatments	35	52.22**	38.86**	94.63**	36.19**	2.13**	2.51**	14.97**	0.34**	138.10**	11.15**	69.73**	65.22**
Parents	7	29.81**	38.25**	67.62**	46.32**	2.55**	2.32**	24.18**	0.58**	21.24**	24.26**	80.99**	73.90**
F₁s	27	59.89**	35.15**	104.3**	31.17**	1.87**	2.63**	12.30**	0.28**	169.26**	7.66**	67.63**	65.33**
P vs F₁s	1	2.22	143.31**	20.25**	101.11**	6.47**	0.74	22.47**	0.14	114.73**	13.50**	47.46**	1.43
Error	70	0.95	0.662	2.54	0.98	0.21	0.41	1.43	0.06	2.24	0.70	0.46	0.86

*Significant at 5% level; **Significant at 1% level

Table 3: Grand mean heritability (narrow scence), genetic advance & genetic advance % over mean in twelve traits of bread wheat

Characters	Grand mean	Narrow sense heritability [(h²) %]	Genetic advance	Genetic advance over % mean
Days to heading	80.27	11.8	8.29	10.33
Plant height (cm)	95.49	29.2	10.97	11.49
Days to maturity	121.81	51.1	6.78	5.56
No. of tillers/plant	16.65	30.3	7.16	43.04
No. of spikelets /spike	19.98	7.1	1.37	6.86
Spike length(cm)	10.74	15.0	1.43	13.31
No. of grains / spike	47.10	35.3	3.81	8.09
1000 grain weight(g)	47.24	43.2	9.80	20.74
Grain weight/spike (g)	1.79	42.8	0.48	26.89
Biological yield/plant(g)	52.92	18.7	13.53	25.57
Grain yield / plant(g)	20.01	20.7	3.51	17.54
Harvest index (%)	38.12	27.2	9.35	25.54

Conclusion
In this study the high heritability and high genetics advance for the characters were observed for number of tiller per plant indicated that the trait will be responsible for selection and selection will be profitable for high yield in wheat. studies related that the grain yield per plant with high heritability and genetics advance with the traits as days to maturity, number of tiller per plant, number of grain per spike, 1000 grain weight, grain weight per spike were the major yield attributing traits coupled with moderate and low genetics advance, so due to consideration should be given for these characters at the time of selection further evaluate of germplasm.

Acknowledgement

Reference
1. Burton GW, DeVane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953; 45(10):478-481.
2. Crumpacker DW, Allard RW. A diallel cross analysis of heading date in wheat. Hilgardia. 1962; 32(6):275-318.
3. Dhakar MR, Jat BL, Bairwa LN, Gupta JK. Genetic Variability, Heritability Genetic advance and genetics divergence in bread Wheat (*Triticum* species). Environment & Ecology. 2012; 30(4A):1474-1480.
4. Erkul A, Unay A, Konak C. Inheritance of yield and yield components in a bread wheat (*Triticum aestivum* L.) cross. Turkish J of Field Crops. 2010; 15(2):137-140.
5. Fray KJ, Horner T. Heritability in standard units. Agronomy Journal. 1957; 49(2):59-62.
6. Freeman GF. Hereidity of quantitative characters in wheat. Genetics. 1919; 4(1):1-93.
7. Griffing B. A generalized treatment of the use of diallel crosses in quantitative inheritance. Heredity. 1956b; 10:31-50.
8. Hanson WD. Heritability Statistical Genetics and Plant Breeding NAS-NRC, Washington, Publication. 1963; 982:125-140.

9. Kumar P, Yadav A, Singh L. Estimation of heritability and genetic advance in 10x10 diallel crosses in bread wheat (*Triticum aestivum* L.em. Thell.).Pantnagar Journal of Research. 2013; 11(3):354-356.

10. Kumar P, Singh G, Kumar S, Kumar A, Ojha A. Genetic analysis of grain yield and its contributing traits for their implications in improvement of bread wheat cultivars. Journal of Applied and Natural Science. 2016; 8(1):350-357.

11. Kumar N, Markar S, Kumar V. Studies on heritability and genetic advance estimates in timely sown bread wheat (*Triticum aestivum* L.). Bioscience Discovery. 2014; 5(1):64-69.

12. Laghari KA, Sial MA, Arain MA *et al*. Heritability studies of yield and yield associated traits in bread wheat. Pak. J of Botany. 2010; 42(1):111-115.

13. Nagireddy AV, Jyothula DPB. Heritability and interrelationship of yield and certain agronomic traits in wheat. Res. on Crops. 2009; 10(1):124-127.

14. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and degree of dominance in corn. Agron. J. 1949; 41(8):353-359.

15. Saini M, Shweta. Genetic variability, heritability, correlation co-efficient and of yield and yield contributing traits in bread wheat (*Triticum aestivum* L.). International Journal of Plant Sciences (Muzaffarnagar). 2017; 12(2):173-180.

16. Saini PK, Kumar S, Singh SV. Heritability and genetic advance for yield and its contributing traits in bread wheat (*Triticum aestivum* L.).International Journal of Chemical Studies. 2019; 7(3):3078-3081.

17. Yadav AK, Maan RK, kumar S, Kumar P. Variability, heritability and genetic advance for quantitative characters in hexaploid wheat (*Triticum aestivum* L.). Electronic Journal of Plant Breeding. 2011; 2(3):405-408.