Ajeet Jaiswal
Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur, Uttar Pradesh, India

Lokendra Singh
Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur, Uttar Pradesh, India

Mahak Singh
Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur, Uttar Pradesh, India

Som Veer Singh
Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur, Uttar Pradesh, India

Sarvendra Kumar
Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur, Uttar Pradesh, India

AL Jatav
Department of Seed Science and Technology, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur, Uttar Pradesh, India

RK Singh
Department of Agricultural Statistics and Economics, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur, Uttar Pradesh, India

Corresponding Author:
Ajeet Jaiswal
Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur, Uttar Pradesh, India

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

Ajeet Jaiswal, Lokendra Singh, Mahak Singh, Som Veer Singh, Sarvendra Kumar, AL Jatav and RK Singh

Abstract
The experiment was conducted at Crop Research Farm, Nawabganj of C.S. Azad University of Agriculture and Technology, Kanpur (U.P.), India. The experiment was carried out with 100 diverse treatments (10x10 diallel cross set) grown in Randomized Block Design with three replications. Observations were recorded on five randomly selected plants in parents and F_1s and 10 randomly taken plants in F_2s for all 15 characters from each replication. The estimates of heritability revealed high value for plant height, number of productive tillers per plant, seed hardness and protein content; moderate heritability for spike length, number of spikelets per spike, 1000-grain weight, biological yield per plant and grain yield per plant; low heritability was observed for number of grains per spike in both F_1 and F_2 generation. While high genetic advance in percentage over mean were estimated for number of productive tillers plant, flag leaf area, number of grains per spike, biological yield per plant, grain yield per plant, phenol color and seed hardness; Moderate values were observed for spike length, 1000-grain weight, harvest index and protein content; Low values of genetic advance were recorded for days to 50% flowering, days to maturity and number of spikelets per spike in both the generation.

Keywords: Heritability, Genetic advance, *Triticum aestivum* L.

Introduction
Wheat (*Triticum aestivum* L.) is the most important grain and is being used as a staple food for more than one third of the world. Developing the varieties with high yielding potential having desirable combination of characters is always the main objective of wheat breeding programme. The estimation of the genetic association and description of genetic variability between various genotypes are essential for breeders, because the artificial crosses between dissimilar parents permit a huge segregation and the grouping of various favorable alleles (Bered *et al.,* 2002) [3].
Heritability estimates have been utilized as a selection criterion in the plant improvement programme. It has been widely adopted to estimate the degree to which a character may be transmitted from parent to offspring. In the narrow sense, heritability is the ratio of additive genetic variance to the phenotypic variance. On the other hand, genetic advance, though not an independent entity, has added advantage over heritability where character improvement through a series of segregating generations might be possible. Heritability and genetic advance are important as direct selection parameters. General or broad sense heritability estimate is the ratio of genotypic variance to the phenotypic variance or total variance, expressed in percent. In the present study, direct and indirect selection may be judged by their expected genetic gain and correlated response, respectively. The heritability portion of phenotypic variance showed a good index of a transmission of characters from parents to their offspring (Falconer, 1981) [5]. The heritability estimates along with genetic advance become more helpful in predicting the gain under selection than heritability alone. There is no parallel association between heritability and genetic advance (Johnson *et al*, 1955) [7].

Material and Methods

The present experimental work was carried out at Crop Research Farm, Nawabganj, C.S. Azad University of Agriculture and Technology, Kanpur-208002 (U.P.) during *Rabi*, 2019-20. The experimental material consisted of 100 treatments (45 F_1 + 45 F_2 +10 parents) were sown in Randomized Block Design with three replications. The entries were sown in a 3 m length with inter and intra-row spacing of 22.5 cm and 10 cm, respectively. The individual plant data of the sample were recorded in each treatment of all replications for the traits *viz.*, days to 50 per cent flowering, plant height, days to maturity, number of productive tillers per plant, flag leaf area, spike length, number of spikelets per spike, number of grains per spike, biological yield per plant, grain yield per plant, 1000-grain weight, harvest index, protein content, phenol color and seed hardness.

Heritability (in narrow sense) in F_1 generation was calculated by the formula proposed by Crumpacker and Allard, (1962) [4] and in F_2 generation was calculated according to the methodology proposed by Verhalen and Murray (1969) [10]. The estimates of heritability were arbitrarily categorized into three classes by Robinson (1966) [8] as:

(i) High- above 30 percent
(ii) Moderate- below 30 and above 10 percent
(iii) Low- below10 percent.

The genetic advance was calculated by the formula given by Robinson *et al*. (1949) [9].
Genetic advance (GA) was expressed as a percentage of the mean. This was categorized by Johnson *et al*. (1955) [7] as:

(i) High when it was above 20%
(ii) Moderate 10-20% and
(iii) Low when it was less than 10%.

Result and Discussion

The direct and indirect selection responses correlated with their genetic gain and association response between different characters have been studied. Analysis of variance showed highly significant differences among the treatment for all the fifteen characters. The estimated heritability (h^2) in narrow sense values depicted in table for all fifteen characters of F_1 and F_2 populations. According to Hanson *et al.* (1963) [6], her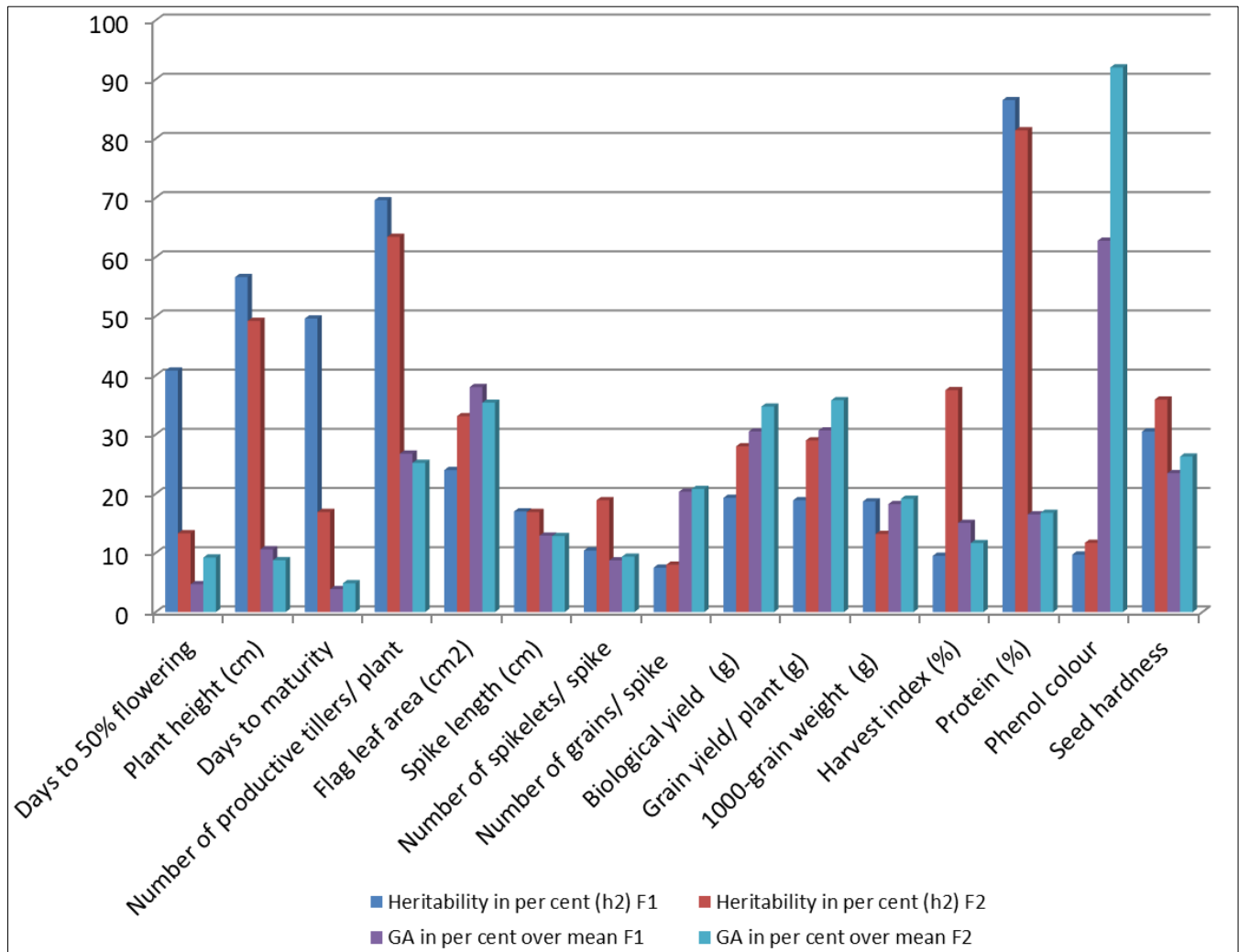itability and genetic advance are two complementary concepts. The perusal of heritability estimates showed high value for plant height, number of productive tillers per plant, seed hardness and protein content in both generations; for days to 50% flowering, days to maturity, in F_1 generation and for flag leaf area, harvest index in F_2 generation. The moderate magnitude of heritability was observed for the characters, spike length, number of spikelets per spike, 1000-grain weight, biological yield per plant, grain yield per plant in both generation, for flag leaf area in F_1 and days to 50 % flowering, phenol color in F_2 generation. The low magnitude of heritability observed in number of grains per spike in both generation; harvest index and phenol color in F_1 generation. It indicated that non additive gene action was more prevalent and thus, the heritability selection procedure expedited that these traits could be improved by selection in early generation. The related traits are greatly influenced by environment, which reduced the degree of correspondence due to its phenotypic and breeding values.

The estimated value of genetic advance (GA) for all the characters were shown in focused on direct selection in both the generation. High genetic advance in percentage over mean was estimated for number of productive tillers per plant, flag leaf area, number of grains per spike, biological yield per plant, grain yield per plant, phenol color and seed hardness in both the generation. Moderate values were also observed for spike length, 1000 grain weight, harvest index and protein content in both the generation and for plant height in F_1 generation exhibited the similar performance. It indicated that these traits were governed by additive genes, which could be fixable and the desired selection will be rewarding for improvement of such traits in early generations. Aycicek and Yildrim (2006) [1] reported the high heritability and high genetic advance for plant height, number of spikelets per spike. Balkan (2018) [2] observed high heritability and high genetic advance for plant height and number of grains per spike.

Thus, it is very much clear that high heritability accompanied with high genetic advance is governed by additive gene effects and selection may be effective but *vice versa* results are highly influenced by the environmental effect which will not be stable and selection would be ineffective.

Table 1: Direct selection parameters for 15 characters in 10 parent diallel cross set of F_1 and F_2 in wheat (*Triticum aestivum* L.).

Characters	Grand mean		Heritability in per cent (h^2)		GA		GA in per cent over mean	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Days to 50% flowering	87.64	85.72	40.8	13.3	4.10	7.89	4.70	9.21
Plant height (cm)	86.17	89.13	56.6	49.2	9.19	7.80	10.60	8.76
Days to maturity	119.68	117.94	49.6	16.9	4.63	5.75	3.87	4.87
Number of productive tillers/ plant	6.22	5.99	69.6	63.4	1.65	1.51	26.76	25.21
Flag leaf area (cm^2)	21.78	18.36	24.0	33.1	8.06	6.51	38.02	35.37
Spike length (cm)	9.89	9.07	17.0	16.9	1.26	1.17	12.91	12.84
Number of spikelets/ spike	20.22	19.05	10.4	18.9	1.76	1.79	8.74	9.36
Number of grains/ spike	53.67	48.75	7.5	8.0	10.79	10.20	20.34	20.80
Biological yield (g)	29.58	26.84	19.3	28.0	9.16	9.65	30.51	34.72
Grain yield/ plant (g)	13.53	11.28	18.9	29.0	4.13	4.16	30.69	35.80
1000-grain weight (g)	47.65	45.02	18.7	13.2	8.59	8.61	18.24	19.14
Harvest index (%)	45.79	42.10	9.5	37.5	6.77	4.88	15.06	11.65
Protein (%)	12.03	11.84	86.5	81.4	1.98	1.99	16.50	16.76
Phenol colour	2.14	2.04	9.7	11.7	1.41	2.00	62.75	92.03
Seed hardness	10.15	9.88	30.5	35.9	2.39	2.62	23.47	26.28

Fig 1: Graphical representation of heritability and genetic advance

References

1. Aycicek M and Yildirim T. Heritability of yield and yield component in bread wheat (*Triticum aestivum* L.) genotypes. Bangl. J. Bot. 2006;35(1):17-22.
2. Balkan A. Genetic variability, heritability and genetic advance for yield and quality traits in m_{2-4} generations of bread wheat (*Triticum aestivum* L.) genotypes. Turk J. Field Crop. 2018;23(2):173-179.
3. Bered F, Neto JFB, Rocha BMD and Carvalho FIFD. Genetic variability in wheat (*Triticum aestivum* L.) germplasm revealed by RAPD markers. Crop Breeding and Applied Biotechnology. 2002;2(4):499-506.
4. Crumpacker DW and Allard RW. A diallel cross analysis of heading date in wheat. Hilgradia. 1962;32:275-318.
5. Falconer DS. Introduction to Quantitative Genetics 2nd Longman, New York. 1981.
6. Hanson WD, Robinson HF and Hamblin, J Heritability. 'Statistical genetics and plant breeding') Washington, DC. National Academy of Sciences–National Research Council. 1963;982:125-140.
7. Johnson HW, Robinson HF and Comstock RE. Genotypic and phenotypic correlations in soybean and their implication in selection. Agron. J. 1955;47:477-483.
8. Robinson HF. Quantitative genetics in relation to breeding of the centennial of Mendalism. Indian J. Genet. 1966;26:171-187.
9. Robinson HF, Comstock RE and Harvey PH. Estimates of heritability and degree of dominance in corn. Agron. J. 1949;41:353-359.
10. Verhalen LM and Murray JC. A dillel analysis of several fibre property traits in upland cotton (*Gossypium hirsutum* L.). Crop Sci. 1969;9:311-315.