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Estimation of heritability and genetic advance for yield components under timely and late sown condition in wheat (*Triticum aestivum* L.)

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Abstract

Analysis of variance revealed significant difference between genotypes for all the characters studied. Sufficient variability was present in the genotypes under study for all the characters indicating sufficient genetic variability among the genotypes. Estimates of genetic variability, heritability and genetic advance for fifteen characters including yield and quality have been investigated by studying six generations in wheat crosses. Genetic advance predicts the quantum gain expected by imposing a particular intensity of selection. Under timely and late sown, heritability in broad sense and narrow sense varied cross to cross. High heritability (>75%) coupled with high genetic advance (>40%) were recorded for weight of grains per main spike (cross I and II), number of grains per spike (cross V), grain yield per plant (cross I, II and III) in timely sown. The traits, number of effective tiller per plant (cross I), weight of grains per spike (cross IV), grain yield per plant (cross II, III and IV) and lysine content (cross III) had high heritability with high genetic advance in late sown condition. High magnitude of the parameters is expected due to presence of additive gene action. Basic information on heritability and expected genetic advance is a prerequisite for effective improvement through selection. Though range varied from 5.19 (plant height, h^2_n) to 99.50 (Amylose content h^2_b).

Keywords: *Triticum aestivum*, broad sense heritability, genetic advance, metric traits, wheat

Introduction

Wheat (*Triticum aestivum* L.; $2n = 6x = 42$), belongs to the family Poaceae, is one of the most important staple food amongst major cereals of the world, occupying 17% of crop acreage worldwide, feeding about 40% of the world population and provide 20% of the total food calories and protein in human nutrition. Wheat originated from South West Asia. It is a self-pollinated crop and an annual plant having height about 60 to 150 cm long. Inflorescence of wheat is erect terminal spike of spikelet's called as ear or head of grains, flower grouped into 15-20 spikelet's arranged alternatively on rachis, each spikelet's with 2-6 flowers out of which only 2-3 flowers are fertile and produce grains. Wheat grain contains 2-3% germ, 13-17% bran (outer layers of wheat grain) and 80-85% mealy endosperm on dry matter basis (Belderok *et al.*, 2000) [2]. Bran is rich in vitamin B and minerals. The endosperm mainly contains food reserves which are needed for growth of the seedling. Endosperm contains fats (1.5%) and proteins (13%), albumins, globulins and the major proteins of the gluten complex glutenins and gliadins-proteins that will form the gluten at dough stage. Globally, wheat (*Triticum spp.*) is grown in about 220.83 million hectares holding the position of highest acreage among all crops with annual production hovering around 769.31 million tones (USDA, 2019) [22]. In India, it is grown in area of 30.55 million hectares with a production of 107.18 million tones and productivity of 3508 kg/ha. (Anonymous, 2019) [1]. Grain yield in wheat is a complex character and is depend on its component traits. For genetic manipulation of grain yield, quality and other characters in wheat, there is a need to examine the nature of genetic variability for the yield related attributes and quality traits. The major function of heritability estimates is to provide information on transmission of characters from the parents to the progeny. Such estimates facilitate evaluation of hereditary and environmental effects in phenotypic variation and thus aid in selection. Heritability estimates can be used to predict genetic advance under selection so that breeder can anticipate improvement from different kinds and intensities of selection. Information on estimates of heritability and genetic advance in early segregating generations on seed yield and its components in barley is very limited, thus present investigation was planned to get precise information.

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Materials and Methods

Ten homogygous and genetically divers varieties of wheat namely, MP 3211, JWS-922, JWS-948, JWS-952, JWS-957, JWS-1027, JWS-1117, JWS-1119, MP-3288, JWS-1013 were selected for building up the experimental materials. The F₁s were obtained by crossing 10 diverse parents, Cross-I (MP 3211 x JWS-922), Cross-II (JWS-948 x JWS-952), Cross-III (JWS-957 x JWS-1027), Cross-IV (JWS-1117 x JWS-1119) and Cross-V (MP-3288 x JWS-1013) during 2017-18. In the next season, a part of F₁ seed of these crosses and 10 parents were sown in a crossing block to obtain F₂, BC₁ and BC₂ generations in each cross. A final comparative studies with P₁, P₂, F₁, F₂, BC₁ and BC₂ were made in Randomized Block Design with three replications in two environments, one set was timely sown and other late sown during 2020-21 at Regional Agricultural Research Station Sagar, Jawaharlal Nehru Krishi Vishwa Vidyalaya Jabalpur (MP). Planting were done in rows of 3 m long. Row to row distance was kept 25 cm apart. The parent (P₁ and P₂) and F₁s were sown in 2 rows, while back cross generations and F₂ generations were sown in 5 and 6 rows, respectively, of 3 m length. Fifteen random plants in parent and F₁ generation, 60 plants in F₂ generation and 45 plants in back cross generations were used for recording observations in each replication.

The heritability in narrow sense and broad sense were computed as per Warner's method (1952) [23] and genetic advance was worked out as proposed by Robinson *et al.* (1949) [18] and Interpretation and use of estimates of heritability and genetic variance by Dudley, *et al.* (1969) [6].

Results and Discussion

It is evident from Table 2 that estimates of narrow sense heritability was found negative for all the traits in most of crosses except for days to maturity (cross V), number of effective tillers (cross II, IV and V), length of main spike (cross IV and V), grain yield per plant (cross I), flour recovery (cross III), husk content (cross I and II), protein content (cross II and V) and pelshenke value (cross V) in timely sown condition. These results were also supported by findings of several scientists, Kumar, N. *et al.* (2014) [13] reported similar finding.

Likewise under late sown condition also, most of the crosses showed negative estimates of narrow sense heritability except days to ear emergence (cross IV), plant height (cross I), number of effective tillers per plant (cross V), length of main spike (cross I), days to maturity (cross III) weight of grains per main spike (cross IV), number of grains per spike (cross V), 1000-grain weight (cross II and IV), grain yield per plant (cross I), flour recovery (cross I), husk content (cross IV and V), protein content (cross I), lysine content (cross II) and pelshenke value (cross I, III and V) which had positive estimates respectively. These results were also supported by findings of several scientists, Kahrizi D *et al.* (2010) [12], Yadav, S.K. *et al.* (2014) [26] Yu *et al.* (1988) [27], Zao *et al.* (1991) [28]. EI-Scidy (1997) [7] reported similar finding and noticed that inheritance of positive estimates of related components were controlled by additive and dominance effects. Thus, heritability in broad sense and genetic advance in per cent of mean in combination provide clear picture regarding the effectiveness of selection in improving the plant characters.

On the other hand, the high magnitude of broad sense heritability (more than 75%) was estimated for most of the

crosses for plant height, weight of grains per main spike, grain yield per plant, number of grains per spike, husk content, protein content, lysine content and amylose content in both the environments, except grain yield per plant in cross V. Similar finding were noted except protein content, lysine content amylose content and pelshenke value by several research workers.

High heritability (h²b) coupled with high genetic advance were recorded for weight of grains per main spike in cross I and II, number of grains per spike in cross V, grain yield per plant in cross I, II and III in timely sown condition.

Under late sown condition, number of effective tillers per plant in cross I, weight of grains per main spike in cross IV, grain yield per plant in cross II, III and IV and lysine content in cross III had high heritability with high genetic advance. Most likely, the high heritability is due to additive gene effects. These results were also supported by Panse (1957) [16]. Under late sown condition, high heritability coupled with moderate genetic advance were observed for most of the traits. It denotes that non-additive gene action may provide good response to selection due to its high heritability and moderate genetic advance. This high heritability is being exhibited due to favorable influence of environment. More or less these findings were supported by Wolde, T. *et al.* 2016 [24], Martinez and Foster (1998) [14]. This implies that high value of heritability is not always an indication of high genetic gain Johnson *et al.* (1955) [11].

Low heritability (<50%) coupled with low genetic advance (<20%) denoted that such characters were highly influenced by environmental effects. These findings were also supported by Yadav, A. K. *et al.* 2011 and EI-Scidy (1997) [25, 7]. This indicated that much improvement is not possible through selection in this characters due to low value of heritability. Genetic analysis had also shown that these characters are mainly governed by dominance components. High heritability with low genetic advance indicated the presence of non-additive gene action, therefore, selection in early generation for above cited traits may not be effective due to linkage. Wolde, T. *et al.* 2016, Thomas and Topsell (1983) [24, 20] viewed that high magnitude of heritability in segregating generation would be more helpful to the breeder in selection practices.

The overall review of gene effects for metric traits under study revealed that, simple selection procedure may not bring the expectacular gains. This has also been indicated by low genetic advance for exploitation for part of total genetic variation i.e. additive gene effects and additive type of epistatic effects.

Under a situation, where dominance gene effect plays major role, one can go for heterosis breeding otherwise use of intermating followed by selection in early generations to exploit both types of gene effects. These were advocated by several scientists (Ukani, J. D *et al.* 2015, Zecevic, V. *et al.* 2010, Gill *et al.*, 1972; 1974, Ranadhawa and Gill, 1978) [21, 29, 9, 10, 17]. Zao *et al.* (1991) [28] reported that grain yield per plant, ear number per plant and ear length were mainly controlled by dominant genes. However, straw weight, grain number per ear and plant height were mainly controlled by additive genes. Similar results were noticed by several workers such as Yadav, A. K. *et al.* 2011, Yu *et al.*, 1988 and Sethi, 1989 [25, 27, 19]. Similar trend of results were also reported by Yadav, A. K. *et al.* 2011 [25] and Esparza *et al.* (1998) [8]. They suggested that value of heritabilities obtained for grain yield were more

consistent among broad sense than narrow sense estimates. Genetic advance estimates were low due to lack of additive variance. Nevertheless, the moderate narrow sense heritabilities ranged from 18 to 62% and the considerable proportion of additive variance found under nutrient shortage suggest that on improvement of rooting ability under less favourable nutrition through conventional selection is an important objective in barley breeding.

The heritability estimates in broad sense were quite high for most of the characters indicated that strong genetic nature for all the traits. The higher heritability implied that selection for most of the traits might be effective in this set of genotypes.

High estimates of heritability coupled with high genetic advance were observed for number of grains per spike, biological yield per plant, days to 50% heading and plant height which indicated that above characters was governed by additive gene action and as such expected to exhibit improvement by direct selection. Similar findings were also reported by Bhushan *et al.* (2013) and Nukasani *et al.* (2013) [3, 15].

However, the degree of improvement attained through selection is not only dependent on heritability but also on the amount of genetic variation present in the breeding population and the extent of selection pressure applied by the breeder

Table 1: Heritability in broad sense ($h^2 b$ %) for 15 metric traits in cross I-V in timely and late sown condition

Characters	Heritability (%)									
	Timely Sown Condition					Late Sown Condition				
	Cross I	Cross II	Cross III	Cross IV	Cross V	Cross I	Cross II	Cross III	Cross IV	Cross V
Days to ear emergence	70.55	96.35	90.85	98.15	96.57	96.75	81.26	90.08	91.87	99.69
Plant height (cm)	85.35	98.03	99.45	96.81	96.61	88.62	90.13	98.49	98.85	94.73
No. of effective tillers/plant	92.18	74.61	91.00	75.04	57.65	98.11	68.68	97.67	87.64	79.64
Length of main spike (cm)	44.40	97.28	93.50	95.30	67.60	34.12	66.43	90.96	88.39	26.02
Days to maturity	66.25	76.75	95.35	41.95	93.90	94.05	84.16	85.08	85.77	95.19
Weight of grains/main spike (g)	94.03	88.85	97.44	82.06	81.11	61.76	91.96	96.29	94.89	51.69
No. of grains/spike	99.74	99.07	98.87	99.71	99.75	98.45	97.26	96.06	97.76	99.19
1000-grain weight (g)	98.22	99.53	91.12	88.82	93.75	94.63	75.44	99.12	86.12	96.39
Grain yield/plant (g)	99.95	100.49	99.92	99.01	60.76	96.59	99.48	99.38	94.84	92.72
Flour recovery (g)	78.44	78.52	45.92	56.87	60.25	78.40	73.71	52.87	91.08	93.14
Husk content (g)	91.49	96.23	94.21	82.17	92.23	93.40	83.32	95.95	90.18	94.86
Protein content (%)	98.72	97.89	100.48	95.16	99.49	96.36	98.1	98.14	91.54	99.30
Lysine content (mg/g)	81.90	97.14	97.97	94.34	95.94	95.85	98.87	75.28	95.69	95.41
Amylose content (%)	99.14	88.33	100.55	99.06	99.73	96.83	97.58	99.46	99.42	97.78
Pelshenke value (min)	91.10	89.53	98.89	71.49	91.83	79.36	96.30	94.36	63.36	40.64

Table 2: Heritability in narrow sense ($h^2 n$ %) for 15 metric traits in cross I-V in timely and late sown condition

Characters	Heritability (%)									
	Timely Sown Condition					Late Sown Condition				
	Cross I	Cross II	Cross III	Cross IV	Cross V	Cross I	Cross II	Cross III	Cross IV	Cross V
Days to ear emergence	-	-	-	-	17.29	-	-	-	48.21	-
Plant height (cm)	-	-	-	-	-	9.14	-	-	-	-
No. of effective tillers/plant	-	65.13	-	56.82	62.07	-	-	-	-	24.51
Length of main spike (cm)	-	-	-	61.75	14.19	21.12	-	-	-	-
Days to maturity	-	-	-	-	-	-	-	45.61	-	-
Weight of grains/main spike (g)	-	-	-	-	-	-	-	-	43.39	-
No. of grains/spike	-	-	-	-	-	-	-	-	-	82.97
1000-grain weight (g)	-	-	-	-	-	-	62.98	-	28.25	-
Grain yield/plant (g)	12.17	-	-	-	-	37.56	-	-	-	-
Flour recovery (g)	-	-	24.47	-	-	25.49	-	-	-	-
Husk content (g)	38.18	83.87	-	-	-	-	-	-	19.15	51.08
Protein content (%)	-	79.74	-	-	29.55	82.14	-	-	-	-
Lysine content (mg/g)	-	-	-	-	-	-	43.38	-	-	-
Amylose content (%)	-	-	-	-	-	-	-	-	-	-
Pelshenke value (min)	-	-	-	-	18.49	54.29	-	64.07	-	34.68

- indicates negative estimates

Table 3: Genetic advance in per cent of mean (G_a %) for 15 metric traits in cross I-V in timely and late sown condition

Characters	Timely Sown Condition					Late Sown Condition				
	Cross I	Cross II	Cross III	Cross IV	Cross V	Cross I	Cross II	Cross III	Cross IV	Cross V
Days to ear emergence	4.94	16.60	8.41	18.21	16.00	16.13	7.42	11.33	11.56	7.59
Plant height (cm)	10.94	15.01	20.87	22.05	23.45	6.22	14.12	25.65	22.14	17.50
No. of effective tillers/plant	22.71	12.27	27.60	20.47	20.03	46.70	16.68	57.73	25.18	13.82
Length of main spike (cm)	5.97	32.06	18.73	30.75	9.58	4.34	5.08	25.06	13.03	2.87
Days to maturity	4.25	3.02	10.53	2.46	4.20	4.37	1.16	3.09	4.14	9.77
Weight of grains/main spike (g)	51.14	22.58	55.68	15.63	15.34	10.78	36.44	9.34	50.29	7.88
No. of grains/spike	25.01	22.20	35.5	27.34	55.05	20.62	20.39	14.46	30.66	29.86
1000-grain weight (g)	34.53	38.21	15.85	12.08	22.09	23.37	12.59	35.32	20.26	20.83

Grain yield/plant (g)	46.01	63.73	48.36	33.88	7.61	33.00	72.21	56.07	51.73	22.02
Flour recovery (g)	3.01	3.64	2.56	1.70	3.11	3.97	4.22	2.17	4.95	6.84
Husk content (g)	10.66	20.90	11.47	11.52	10.97	16.63	20.51	19.29	25.48	35.24
Protein content (%)	15.48	26.30	27.08	11.42	28.08	18.13	27.88	32.57	12.64	22.24
Lysine content (mg/g)	13.29	34.89	35.74	1.37	36.22	35.82	37.94	44.21	2.6	32.90
Amylose content (%)	27.53	25.63	33.60	32.6	26.48	26.85	29.3	33.31	31.28	23.78
Pelshenke value (min)	11.12	13.77	28.25	4.32	5.64	8.85	14.77	25.86	7.47	2.66

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