International Journal of Chemical Studies

P-ISSN: 2349–8528
E-ISSN: 2321–4902
www.chemijournal.com
IJCS 2021; 9(1): 2408-2411

Received: 02-10-2020
Accepted: 09-11-2020

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Studies on heritability and genetic advance for yield and yield attributing traits in barley (*Hordeum vulgare* L.)

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DOI: https://doi.org/10.22271/chemi.2021.v9.i1ah.11587

Abstract
In my study, a set of 20 genotypes of Barley (*Hordeum vulgare* L.) were evaluated over two years from 2016-17 to 2017-18 to evaluate the genetic analysis of these genotypes for yield and its contributing characters over years and environments. These were evaluated in randomized complete block with 3 replications and two dates of sowing i.e. 3rd week of November (timely sown) and 1st week of January (very late sown). Significant variability was found in all the environments for all the traits. Traits *viz*., biological yield plant^{-1}, yield plant^{-1}, ear head length (cm), peduncle length, harvest index (%), ear weight and number of grains plant^{-1} was recorded high heritability coupled with high genetic advance in all the environments. High heritability coupled with moderate genetic advance were reported by days to 50% flowering, 100 grain weight (g) and plant height. The medium estimates of heritability with high genetic advance was recorded by number of tillers plant^{-1}, number of effective tillers plant^{-1} and number of ears plant^{-1}, number of spikelets ear^{-1}, number of grains plant^{-1}, ear weight, ear head length, peduncle length, harvest index and number of dead tillers plant^{-1}. The medium estimate of heritability with moderate genetic advance was recorded by number of spikelets ear^{-1}, number of grains ear^{-1}, plant height and 100 grain weight. The high or moderate heritability is accompanied with high or moderate genetic advance that mean preponderance of additive gene action involved in the inheritance of concerned traits. Therefore, selection for grain yield plant^{-1} can be done through above traits will be beneficial.

Keywords: Genetic analysis, heritability, genetic advance, additive gene action

Introduction
Barley (*Hordeum vulgare* L.) is an important winter cereal crop grown in northern plains of India and belongs to the family Poaceae. It is a fourth most important cereal crop after wheat, rice and maize, cultivated successfully in a wide range of climate. This crop has potentials for growing under drought and saline conditions. Being an important food crop of India, it is cultivated over an area of 7.60 lakh ha with an annual production of 13.70 lakh tones grain and productivity of 19.40 q/ha (Raikwar *et al*., 2014) [8]. The low productivity of barley in India is due to wide seasonal variability, low amount of rainfall, poor soil moisture conservation, poor stand resulting from lack of weed control and low yield potential genotypes. Different methods could be used to increase cereal production, such as increasing area of production, effective cultural practices, and using improved cultivars (Cassman, observed among individuals arose as a result of differences in genetic make up or due to environmental forces. Genetic variability gives an idea of possible improvement of new population through selections, when compared to the original population. One of the main objectives of any breeding program is to produce high-yielding and better-quality lines for release as cultivars to farmers. The prerequisite to achieve this goal is to find sufficient amount of variability, in which desired lines are to be selected for further manipulation to achieve the target. Introduction of new populations can be made from one region to the other easily and may be used for further manipulation to develop new breeding lines (Ifftikhar *et al*., 2009) [4]. Analysis of variability among the traits and the association of a particular character in relation to other traits contributing to yield of a crop would be of great importance in planning a successful breeding program (Mary and Gopalan, 2006) [7]. Development of high-yielding cultivars requires a thorough knowledge of the existing genetic variation for yield and its components. The observed variability is a combined

estimate of genetic and environmental causes, of which only the former one is heritable. However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic variability, the change in mean value among successive generations (Shukla *et al*., 2006) [10]. These efforts have led to the development of a range of new cultivars for different purposes production conditions and production technologies. The major function of heritability estimates is to provide information on transmission of characters from the parents to the progeny. A survey of genetic variability with the help of suitable parameters such as genetic coefficient of variation, heritability estimates and genetic variability are absolutely necessary to start an efficient breeding program

(Atta *et al*., 2008) [2]. Assessment of the extent of genetic variability within barley, is fundamental for barley breeding programs and the conservation of genetic resources, and is particularly useful as a general guide in the choice of parents for breeding hybrids.

Only high heritability does not get any desirable achievement from selection, if not sufficient genetic advance found to present additive gene action. The estimates of heritability in broad sense include part from additive as well as non-additive gene effects thus they are of limited importance. Though, high heritability coupled with high genetic advances as percentage of mean are measured significant.

Materials and Methods

The experiment was carried out at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture Tikamgarh, Jawaharlal Nehru Krishi Vishwa Vidhyalaya, Jabalpur (M.P.) under irrigated timely and very late sown conditions. The trial area occupied was quite uniform and fertile. The experimental material comprised of 20 promising genotypes of Barley, procured from different Barley Improvement Projects, research centers of India. Experiment was grown in a Randomized Complete Block Design with three replications. Each plot consists of three rows of 2.5 m length and 22.5 cm apart under irrigated normal sown and very late sown conditions during both experimental years. These observations *viz*., Days to 50% flowering, Days to maturity, Plant height (cm), No. of tillers plant^{-1}, No. of effective tillers plant^{-1}, No. of dead tillers plant^{-1}, No. of spikelet's ear^{-1}, No. of ears plant^{-1}, No. of grains ear^{-1}, No. of grains plant^{-1}, Ear head length (cm), Ear weight (g), Peduncle length (cm), 100 grain weight (g), Biological yield plant^{-1} (g), Yield plant^{-1} (g), Harvest index (%) was recorded on 5 randomly selected plant from each plot. The genetic parameters heritability and genetic advance were computed according to the method suggested by Johnson *et al.,* 1955 [5]. Heritability in broad sense (h2b) may be defined as the proportion of genotypic variance to phenotypic variance. The heritability percentage in broad sense (h2b) was calculated as the ratio of the total genetic variance to the phenotype variance and the formulae as suggested by Johnson *et al*. (1955a, b) [5]. Where, h2b = Heritability estimates in broad sense VG = Genotypic variance

VP = Phenotypic variance

Heritability percentage in narrow sense (h2n) was estimated as suggested by Warner (1952) [12].

h2n = (1/2 D/VF2) x 100

Result and Discussion

Heritability (broad sense) is a calculation of proportion of phenotypic variation contributed to the genotypic variation for a given trait. This is the good index of transmission of characters from parent to their offspring.

Seeing as the heritability values are influenced by environment, consequently the utility of genetic material and also other factors will be restricted. Only high heritability does not get any desirable achievement from selection, if not sufficient genetic advance found to present additive gene action. The estimates of heritability in broad sense include part from additive as well as non-additive gene effects thus they are of limited importance. Though, high heritability coupled with high genetic advances as percentage of mean are measured significant.

Heritability and genetic advance are offered according to their sowing environments in both the years (2015 & 2016). E1 and E3 environments representing the timely sown condition for the first (2015) and second (2016) experimental year, whereas E2 and E4 representing the very late sown conditions of both the years (2015 & 2016, respectively) in the table 1, 2.

High heritability coupled with high genetic advance (as percentage of mean) was recorded under both timely sown condition (E1 & E3) for biological yield plant^{-1} and yield plant^{-1}. Whereas, high value of heritability with high genetic advance for ear head length (cm), peduncle length, harvest index (%) in E1 and ear weight in E3 only. Under both late sown condition (E2 & E4) high heritability coupled with high genetic advance was recorded for the traits *viz.,* biological yield plant^{-1} and yield plant^{-1} while number of grains plant^{-1} in E4 only. High heritability coupled with moderate genetic advance were exposed by days to 50% flowering and 100 grain weight (g) in both the timely environments (E1 & E3), whereas plant height in E1 only. While under vary late sown condition plant height and 100 grain weight recorded in E2 only.

The medium estimates of heritability with high genetic advance was recorded by number of tillers plant^{-1}, number of effective tillers plant^{-1} and number of ears plant^{-1} under E1 & E3, number of spikelets ear^{-1}, number of grains plant^{-1} and ear weight in E1, ear head length and peduncle length in E3 only, while traits *viz.,* number of tillers plant^{-1}, number of effective tillers plant^{-1}, number of ears plant^{-1} and harvest index in E2 & E4, number of grains plant^{-1}, ear head length in E2 & number of dead tillers plant^{-1} and peduncle length in E4 only.

The medium estimate of heritability with moderate genetic advance was recorded by number of spikelets ear^{-1} (E3), number of grains ear^{-1} (E3/E4), plant height (E4) and 100 grain weight (E4). High / moderate heritability coupled with high / moderate genetic advance was indicative of the presence of additive gene effects and the selection for such traits will be rewarding for further varietal improvement.

Similar result were recorded by Ullah *et al.,* (2011) [11] for plant height, days to 50% flowering and spikelets spike^{-1}, Kumar *et al.,* (2014) [6] for plant height, 1000 seed weight and harvest index, Avinashe (2015) [1] for number of ears per plant, biological yield per plant, grain yield per plant, harvest index, number of productive tillers per plant, ear weight, 1000-grain weight & high heritability with moderate genetic advance for days to 50% heading, number of spikelets ear^{-1}, number of grains ear^{-1}, 1000 grain weight, ear length, number of grains ear^{-1}.

The conclusion were found that the traits *viz*., biological yield plant^{-1}, yield plant^{-1}, ear head length (cm), peduncle length, harvest index (%), ear weight, number of grains plant^{-1}, days

to 50% flowering, 100 grain weight (g), plant height, number of tillers plant^{-1}, number of effective tillers plant^{-1}, number of ears plant^{-1}, number of spikelets ear^{-1}, number of dead tillers plant^{-1}, number of grains ear^{-1} was governed by additive gene action in different environments. Thus the above characters were given due importance.

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. 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: Pooled parameters of heritability and genetic advance for yield and its component traits in Barley genotypes for over both experimental year

S. No.	Traits	Mean	Range		h² (Broad Sense)%	Gen. Adv as % of Mean 1%
			Minimum	Maximum		
1	Days to 50% flowering	76.57	71.35	81.98	87.55	20.80
2	Days to maturity	117.89	111.87	124.71	67.83	7.38
3	Plant height (cm)	101.23	89.98	107.88	51.11	7.72
4	No's of Tillers plant^{-1}	9.30	8.49	22.32	61.13	33.88
5	No's of Effective tillers plant^{-1}	8.09	6.32	10.22	49.40	25.71
6	No's of dead tillers plant-^{1}	2.21	2.02	2.40	9.22	4.79
7	No's of Spikelets ear^{-1}	27.17	25.28	28.63	26.59	5.51
8	No's of Ears plant-^{1}	8.09	6.32	10.22	49.40	25.71
9	No's of Grains ear-^{1}	53.03	45.87	59.06	35.10	7.92
10	No's of Grains plant-^{1}	347.52	262.07	420.60	40.82	23.92
11	Ear head length (cm)	9.33	8.05	10.51	38.55	9.56
12	Ear weight (g)	3.44	3.12	3.83	23.47	5.92
13	Peduncle length(cm)	27.30	25.64	28.93	9.97	3.86
14	100 grain weight (g)	5.37	4.84	5.80	72.45	20.13
15	B. yield plant-^{1} (g)	42.82	38.62	48.89	57.55	22.91
16	Harvest index (%)	50.43	45.96	56.51	32.50	7.39
16	Yield plant-^{1} (g)	23.43	20.76	27.28	60.64	31.54

Table 2: Estimate of heritability and genetic advance under all the conditions

Traits	Timely Sown				Very Late Sown				Pooled	
	E1		E3		E2		E4			
	h²	GA	h²	GA	h²	GA	h2	GA	h²	GA
Days to 50% flowering	H	M	H	M	H	L	H	L	H	L
Days to maturity	H	L	H	L	H	L	H	L	M	L
Plant height (cm)	H	M	M	L	H	M	M	M	L	L
No. of tillers plant^{-1}	M	H	M	H	M	H	M	H	L	M
No. of effective tillers plant^{-1}	M	H	M	H	M	H	M	H	L	H
No. of dead tillers plant^{-1}	L	H	L	H	L	M	M	H	L	L
No. of spikelets ear^{-1}	M	H	M	M	L	L	M	L	L	L
No. of ears plant^{-1}	M	H	M	H	M	H	M	H	L	H
No. of grains ear^{-1}	L	M	L	M	M	M	M	M	L	L
No. of grains plant^{-1}	M	H	L	H	M	H	H	H	L	M
Ear head length (cm)	H	H	M	H	M	H	L	M	L	L
Ear weight (g)	M	H	H	H	L	M	L	M	L	L
Peduncle length(cm)	H	H	M	H	L	M	M	H	L	L
100 grain weight (g)	H	M	H	M	H	M	M	M	M	M
Biological yield plant^{-1} (g)	H	H	H	H	H	H	H	H	L	M
Harvest index (%)	H	H	L	L	M	H	M	H	L	L
Yield plant^{-1} (g)	H	H	H	H	H	H	H	H	M	H

H- High M- Medium L - Low

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