HERITABILITY AND GENETIC VARIABILITY FOR YIELD COMPONENTS UNDER TWO REGIMES OF SOIL IN BARLEY (*HORDEUM VULGARE L.*)

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ABSTRACT

The present investigation was undertaken to evaluate the variability of heritability and genetic variability for 15 morphological traits including yield and quality of six generations in barley crosses under two soil conditions with ten genetically divers varieties of barley in randomized block design with three replications during winter season 2012-2013. The results indicated that the heritability percentage in narrow sense to broad sense ranged varied from 5.19 h^2n (plant height) to 99.75 h^2b (number of grains/spike). High heritability percentage (>75 h^2b) coupled with high genetic variability percentage (>40 Ga) were recorded for weight of grains/main spike in cross I (92.98 h^2b and 50.10 Ga) and cross III (96.39 h^2b and 54.75 Ga), number of grains/spike in cross V (92.90 h^2b and 54.20 Ga), grain yield/plant in cross I (98.90 h^2b and 44.97 Ga), cross II (99.24 h^2b and 62.71 Ga) and cross III (98.87 h^2b and 47.43 Ga), respectively under normal soil. The traits, number of effective tiller/plant in cross I (97.06 h^2b and 45.67 Ga) and cross III (97.39 h^2b and 57.48 Ga), weight of grains/spike in cross IV (94.60 h^2b and 50.05 Ga)), grain yield per plant in cross II (99.22 h^2b and 71.23 Ga), cross III (99.10 h^2b and 55.80 Ga) and cross IV (94.54 h^2b and 51.49 Ga), respectively and lysine content in cross III (75.06 h^2b and 43.96 Ga) had high heritability with high genetic variability under saline sodic soil. It was concluded that 12 cases showed high heritability (h^2b) percentage coupled with high genetic variability particularly grain yield/plant in cross I (DL 88 x K 560) and cross II (K 603 x Azad) under normal situation and emerged as ideal traits for improvement through simple selection in succeeding generations.

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). 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, 1999). The concept of heritability explains whether differences 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). 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). 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). 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). 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. The adequate information on extent of variability parameters may be helpful to improve the yield by selecting the yield component traits because yield is a complex trait, whose manifestation depends on the component traits. Generally, the estimates of heritability (h^2) of traits are environment specific (Shimelis and Rhandzu, 2010). These estimates should be incorporated and specifically applied only to the population and environment sampled (Dudley and Moll, 1969). Thus, selection of traits based on h^2 and genetic variability as percent of mean is of great importance to the breeder for making criteria for improvement in a complex character. Information on estimates of heritability and genetic variability in early segregating generations on seed yield and its components in barley is very limited, thus present investigation was conducted to assess and estimate the extent of heritability and expected genetic variability of barley varieties to provide necessary information that could be useful in barley improvement programmes aimed at improving agro-morphological and quality traits.

MATERIALS AND METHODS

The proposed study was carried out at J.N.K.V.V., KVK Research Farm, Chhatarpur, Madhya Pradesh. The experimental material used in this study included ten homozygous and genetically divers varieties of barley namely; DL-88, K 560, K 603, Azad, RD 2552, NDB 1020, RD 2618, PL 708, NDB 1173 and Lakhan were selected for building up the experimental materials. The F_1s were obtained by crossing 10 diverse parents during 2011-12. In the next season, a part of F_1 seed of these crosses and 10 parents were sown in a crossing block to obtain F_2, BC_1 and BC_2 generations in each cross. Final comparative studies with P_1, P_2, F_1, F_2, BC_1 and BC_2 were evaluated in Randomized Block Design with three replications in two environments (normal soil and saline sodic soil) during rabi season 2012-13. Each genotype was grown in 5 rows of 3 m long bed with spacing of 25 cm between the rows. An approximate distance of 10 cm was maintained between plant to plant by hand thinning. The parent (P_1 and P_2) and F_1s were sown in 2 rows, while back cross generations and F_2 generations were sown in 5 and 6 rows, respectively, of 3 m long bed. Fifteen competitive random plants from middle row of the experimental plot in parent and F_1 generation, 60 plants in F_2 generation and 45 plants in back cross generations were taken for recording the observations in each replication on days to ear emergence, plant height (cm), number of effective tillers per plant, Length of the main spike (cm), days to maturity, weight of grains per main spike (g), number of grains/spike, 1000-grain weight (g), grain yield/plant (g), flour recovery (g), husk content (%), protein content (%), lysine content (mg/g), amylose content (%) and pelshenke value (min.). For quality analysis, the total nitrogen was estimated by the micro-Kjeldahl method according to AOAC (1995). Total nitrogen was then used for estimation of protein by multiplying with a factor of 6.25. Lysine content was estimated by the method of Felker *et al.* (1978) and amylose content was determined by Juliano (1979). Heritability in broad sense (h^2b) may be defined as the proportion of genotypic variance to phenotypic variance. The heritability percentage in broad sense (h^2b) 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).

$$h^2b = \frac{VG}{VP}$$

Where, h^2b = Heritability estimates in broad sense

VG = Genotypic variance

VP = Phenotypic variance

Heritability percentage in narrow sense (h^2n) was estimated as suggested by Warner (1952)

$h^2n = (1/2\ D/VF_2) \times 100$

or

$= [(2VF_2 - (VB_1 + VB_2/VF_2)] \times 100$

Expected genetic variability (Ga) was estimated by using the method suggested by Johnson *et al.* (1955a)

$Ga = \sigma^2g\ \sigma^2p\ X\ K\ x\ \sigma p$

$= \sigma^2g\ \sigma p\ X\ K$

Where,

σ^2g = Genotype variance

σ^2p = Phenotypic variance

σp = Phenotypic standard deviation

K = Selection differential at 5% selection intensity, *i.e.* 2.06

RESULTS AND DISCUSSION

The results obtained from the present investigations as well as related discussions are given in followings heads:

Narrow sense heritability (h^2n)

Result revealed that estimates of narrow sense heritability ($h^2n\%$) was found negative for all the traits in most of crosses (Table 1) except for number of effective tillers in cross II (62.13), cross IV (53.58) and cross V (60.27), length of main spike in cross IV (59.75) and crossV (11.11), grain yield/plant in cross I (11.27), flour recovery in cross III (21.47), husk content in cross I (36.38) and cross II (80.87), protein content in cross II (76.74) and cross V (28.50) and pelshenke value in cross V (14.28) under normal soil condition. Likewise under saline sodic soil also, most of the crosses showed negative estimates of narrow sense heritability except days to ear emergence in cross IV (44.23), plant height in cross I (5.19), number of effective tillers/plant in cross V (16.54), length of main spike in cross I (11.11), days to maturity in cross III (35.71), weight of grains/main spike in cross IV (33.33), number of grains/spike in cross V (92.77), 1000-grain weight in cross II (72.18) and IV (25.20), grain yield/plant in cross I (39.66), flour recovery in cross I (23.40), husk content in cross IV (13.07) and cross V (41.03), protein content in cross I (87.09), lysine content in cross II (33.33) and pelshenke value in cross I (56.25), cross III (54.27) and cross V (24.66), respectively which had positive estimates. These results were also supported by findings of several scientists, Yu *et al.* (1988), Zao *et al.* (1991) and El-Scidy (1997) noticed that inheritance of positive estimates of related components were controlled by additive and dominance effects. Thus, heritability in broad sense and genetic variability in per cent of mean in combination provide

clear picture regarding the effectiveness of selection in improving the plant characters.

Broad sense heritability (h²b)

The high magnitude of broad sense heritability percentage (>75 h²b%) was estimated for most of the crosses for plant height, weight of grains/main spike, grain yield/plant, number of grains/spike, husk content, protein content, lysine content and amylose content in both the soil conditions, except grain yield/plant in cross V (59.91) under normal soil (Table 2). Similar finding were noted except protein content, lysine content amylose content and pelshenke value by several research workers and also the finding in tomato with respect to plant height by Meena and Bahadur (2014).

Genetic variability (Ga)

Data in Table 3 reveals that genetic variability percentage (>40 Ga%) was estimated under normal soil. Weight of grains/main spike were found in cross I (50.10) and cross III (54.75) and, grains yield/plant in cross I (44.97), cross II (62.71) and cross III (47.43), respectively under normal soil condition. Number of effective tillers/plant in cross I (45.67) and cross III (57.48),

weight of grains/main spike in cross IV (50.05), grain yield/plant in cross II (71.23), cross III (55.82) and cross IV (51.49) and lysine content in cross III (43.96) under saline sodic soil.

High heritability percentage (>75 h²b%) coupled with high genetic variability percentage (>40 Ga) were recorded for weight of grains/main spike in cross I (92.98 h²b and 50.10 Ga) and cross III (96.39 h²b and 54.75 Ga), number of grains/spike in cross V (92.90 h²b and 54.20 Ga), grain yield/plant in cross I (98.90 h²b and 44.97 Ga), cross II (99.24 h²b and 62.71 Ga) and cross III (98.87 h²b and 47.43 Ga), respectively under normal soil. The traits, number of effective tiller/plant in cross I (97.06 h²b and 45.67 Ga) and cross III (97.39 h²b and 57.48 Ga), weight of grains/spike in cross IV (94.60 h²b and 50.05 Ga)), grain yield/plant in cross II (99.22 h²b and 71.23 Ga), cross III (99.10 h²b and 55.80 Ga) and cross IV (94.54 h²b and 51.49 Ga), respectively and lysine content in cross III (75.06 h²b and 43.96 Ga) had high heritability with high genetic variability under saline sodic soil. These results were also supported by several scientists (Kumar, 2013; Singh *et al.,* 2013 and Bhujbal *et al.,* 2013).

Under saline sodic soil, high heritability coupled with moderate

Table 1: Heritability in narrow sense (h²n%) for 15 metric traits in cross I-V in Normal and Saline sodic soil

| Characters | Heritability (%) | | | | | | | | | |
| | Normal soil | | | | | Saline sodic soil | | | | |
	Cross I	Cross II	Cross III	Cross IV	Cross V	Cross I	Cross II	Cross III	Cross IV	Cross V
Days to ear emergence	-	-	-	-	14.29	-	-	-	44.23	-
Plant height (cm)	-	-	-	-	-	5.19	-	-	-	-
No. of effective tillers/plant	-	62.13	-	53.82	60.27	-	-	-	-	16.54
Length of main spike (cm)	-	-	-	59.75	11.11	11.11	-	-	-	-
Days to maturity	-	-	-	-	-	-	-	35.71	-	-
Weight of grains/main spike (g)	-	-	-	-	-	-	-	-	33.33	-
No. of grains/spike	-	-	-	-	-	-	-	-	-	92.77
1000-grain weight (g)	-	-	-	-	-	-	72.18	-	25.20	-
Grain yield/plant (g)	11.27	-	-	-	-	39.66	-	-	-	-
Flour recovery (g)	-	-	21.47	-	-	23.40	-	-	-	-
Husk content (g)	36.38	80.87	-	-	-	-	-	-	13.07	41.03
Protein content (%)	-	76.74	-	-	28.5	87.09	-	-	-	-
Lysine content (mg/g)	-	-	-	-	-	-	33.33	-	-	-
Amylose content (%)	-	-	-	-	-	-	-	-	-	-
Pelshenke value (min)	-	-	-	-	14.29	56.25	-	54.27	-	24.66

- indicates negative

Table 2: Heritability in broad sense (h²b%) for 15 metric traits in cross I-V in Normal and Saline sodic soil

| Characters | Heritability (%) | | | | | | | | | |
| | Normal soil | | | | | Saline sodic soil | | | | |
	Cross I	Cross II	Cross III	Cross IV	Cross V	Cross I	Cross II	Cross III	Cross IV	Cross V
Days to ear emergence	69.50	95.10	89.80	97.10	95.72	95.70	81.00	89.80	91.60	98.80
Plant height (cm)	84.30	96.78	98.40	95.76	95.76	87.57	89.87	98.21	98.58	93.84
No. of effective tillers/plant	91.13	73.36	89.95	73.99	56.80	97.06	68.42	97.39	87.37	78.75
Length of main spike (cm)	43.35	96.03	92.45	94.25	66.75	33.07	66.17	90.68	88.12	25.13
Days to maturity	65.20	75.50	94.30	40.90	93.05	93.00	83.90	84.80	85.50	94.30
Weight of grains/main spike (g)	92.98	87.60	96.39	81.01	80.26	60.71	91.70	96.01	94.62	50.80
No. of grains/spike	98.69	97.82	97.82	99.71	99.75	97.40	97.00	95.78	97.49	98.30
1000-grain weight (g)	97.17	98.28	90.07	87.77	92.90	93.58	75.18	98.84	85.85	95.50
Grain yield/plant (g)	98.90	99.24	98.87	99.01	59.91	95.54	99.22	99.10	94.57	91.83
Flour recovery (g)	77.39	77.27	44.87	55.82	59.40	77.35	73.45	52.59	90.81	92.25
Husk content (g)	90.44	94.98	93.16	81.12	91.38	92.35	83.06	95.67	89.91	93.97
Protein content (%)	97.67	96.64	99.43	94.11	99.49	95.31	97.84	97.86	91.27	98.41
Lysine content (mg/g)	80.85	95.89	96.92	93.29	95.09	94.80	98.61	75.06	95.42	94.52
Amylose content (%)	98.09	87.08	99.50	99.60	98.88	95.78	97.32	99.18	99.15	96.89
Pelshenke value (min)	90.05	88.28	97.84	70.44	90.98	78.31	96.04	94.08	63.09	39.75

Table 3: Genetic variability in per cent of mean (Ga%) for 15 metric traits in cross I-V in Normal and Saline sodic soil

Characters	Normal soil					Saline sodic soil				
	Cross I	Cross II	Cross III	Cross IV	Cross V	Cross I	Cross II	Cross III	Cross IV	Cross V
Days to ear emergence	3.90	15.58	7.48	17.65	15.15	15.10	6.44	11.08	11.32	7.47
Plant height (cm)	9.90	13.99	19.94	21.49	22.60	5.19	13.14	25.40	21.90	17.38
No. of effective tillers/plant	21.67	11.25	26.67	19.91	19.18	45.67	15.70	57.48	24.94	13.70
Length of main spike (cm)	4.93	31.04	17.80	30.19	8.73	3.31	4.10	24.81	12.79	2.75
Days to maturity	3.21	2.00	9.60	1.90	3.35	3.34	0.18	2.84	3.90	9.65
Weight of grains/main spike (g)	50.10	21.56	54.75	15.07	14.49	9.75	35.46	9.09	50.05	7.76
No. of grains/spike	23.97	21.18	34.57	26.78	54.20	19.59	19.41	14.21	30.42	29.74
1000-grain weight (g)	33.49	37.19	14.92	11.52	21.24	22.34	11.61	35.07	20.02	20.71
Grain yield/plant (g)	44.97	62.71	47.43	33.32	6.76	31.97	71.23	55.82	51.49	21.90
Flour recovery (g)	1.97	2.62	1.63	1.14	2.26	2.94	3.24	1.92	4.71	6.72
Husk content (g)	9.62	19.88	10.54	10.96	10.12	15.60	19.53	19.04	25.24	35.12
Protein content (%)	14.44	25.28	26.15	10.86	27.23	17.10	26.90	32.32	12.40	22.12
Lysine content (mg/g)	12.25	33.87	34.81	0.81	35.37	34.79	36.96	43.96	2.36	32.78
Amylose content (%)	26.49	24.61	32.67	32.04	25.63	25.82	28.32	33.06	31.04	23.66
Pelshenke value (min)	10.08	12.75	27.32	3.76	4.79	7.82	13.79	25.61	7.23	2.54

genetic variability was 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 variability. This high heritability is being exhibited due to favorable influence of environment. More or less these findings were supported by Martinez and Foster (1998). This implies that high value of heritability is not always an indication of high genetic gain Johnson *et al.* (1955). Mehandi *et. al.* (2013) observed that plant height, number of clusters per plant and number of pods per plant in mungbean exhibited high heritability (>60) coupled with high to moderate genetic variability as percent of mean (>20), which may be improved through simple plant selection methods. Low heritability (<50%) coupled with low genetic variability (<20%) denoted that such characters were highly influenced by environmental effects. These findings were also supported by El-Seidy (1997). This indicated that much improvement is not possible through selection in these 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 variability indicated the presence of non-additive gene action, therefore, selection in early generation for above cited traits may not be effective due to linkage. Thomas and Topsell (1983) 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 variability 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 (Gill *et al.*, 1972; 1974, Ranadhawa and Gill, 1978). Zao *et al.* (1991) reported that grain yield per plant, ear number per plant and ear length were mainly controlled by dominant genes. However, straw weight, grain number/ear and plant height were mainly controlled by additive genes. Similar results were noticed by several workers such as Yu *et al.*, 1988 and

Sethi *et al.* 1989. Similar trend of results were also reported by Esparza *et al.* (1998). They suggested that value of heritabilities obtained for grain yield were more consistent among broad sense than narrow sense estimates. Genetic variability 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. 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.

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Only original research papers are considered for publication. The authors may be asked to declare that the manuscript has not been submitted to any other journal for consideration at the same time. Two hard copies of manuscript and one soft copy, complete in all respects should be submitted. The soft copy can also be sent by e-mail as an attachment file for quick processing of the paper.

FORMAT OF MANUSCRIPT

All manuscripts must be written in English and should be typed double-spaced with wide margins on all sides of good quality A4 paper.

First page of the paper should be headed with the title page, (in capital, font size 16), the names of the authors (in capitals, font size 12) and full address of the institution where the work was carried out including e-mail address. A short running title should be given at the end of the title page and 3-5 key words or phrases for indexing.

The main portion of the paper should be divided into Abstract, Introduction, Materials and Methods, Results, Discussion (or result and discussion together), Acknowledgements (if any) References and legends.

Abstract should be limited to 200 words and convey the main points of the paper-outline, results and conclusion or the significance of the results.

Introduction should give the reasons for doing the work. Detailed review of the literature is not necessary. The introduction should preferably conclude with a final paragraph stating concisely and clearly the aims and objectives of your investigation.

Materials and Methods should include a brief technical description of the methodology adopted while a detailed description is required if the methods are new.

Results should contain observations on experiment done illustrated by tables and figures. Use well known statistical tests in preference to obscure ones.

Discussion must not recapitulate results but should relate the author's experiments to other work on the subject and give their conclusions.

All tables and figures must be cited sequentially in the text. Figures should be abbreviated to Fig., except in the beginning of a sentence when the word Figure should be written out in full.

The figures should be drawn on a good quality tracing/ white paper with black ink with the legends provided on a separate sheet. Photographs should be black and white on a glossy sheet with sufficient contrast.

References should be kept to a minimum and listed in alphabetical order. Personal communication and unpublished data should not be included in the reference list. Unpublished papers accepted for publication may be included in the list by designating the journal followed by "in press" in parentheses in the reference list. The list of reference at the end of the text should be in the following format.

1. **Witkamp, M. and Olson, J. S. 1963.** Breakdown of confined and non-confined Oak Litter.*Oikos.* **14**:138-147.

2. **Odum, E.P. 1971.** *Fundamentals of Ecology.* W. B. Sauder Co. Publ. Philadelphia.p.28.

3. **Macfadyen, A.1963.** The contribution of microfauna to total soil metabolism. In:*Soil organism*, J. Doeksen and J. Van Der Drift (Eds). North Holland Publ. Comp., pp 3-16.

References in the text should be quoted by the **author's name and year** in parenthesis and presented in year order. When there are more than two authors the reference should be quoted as: first author followed by *et al.,* throughout the text. Where more than one paper with the same senior author has appeared in on year the references should