



ISSN: 2467-9283

*INTERNATIONAL JOURNAL OF
GRADUATE RESEARCH AND
REVIEW*

website: www.ijgrr.org

INDEXING & ABSTRACTING



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ACADEMIC JOURNALS INDEX (OAJI), INFOBASE
INDEX, COSMOS, RESEARCHGATE,
CITEFACTOR, SCHOLAR STEAR, JOURINFO, ISRA:
JOURNAL-IMPACT-FACTOR (JIF), ROOT INDEXING
ETC.

Impact Factors*

IBI factor: 3

Impact factor (OAJI): 0.101





Research Article

Study of Heritability and Genetic Advancement of the Iron Content and Other Yield Attributing Trait in Barley

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Article Information

Received: 20 April 2020

Revised version received: 22 May 2020

Accepted: 25 May 2020

Published: 29 May 2020

Cite this article as:

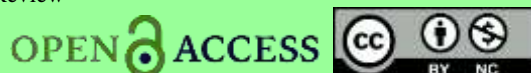
S. Rasaily et al. (2020) Int. J. Grad. Res. Rev. Vol 6(2): 43-46.

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Peer reviewed under authority of IJGRR

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Abstract

An experiment was conducted with a set of twenty barley genotypes in alpha lattice design with objective to screen out high iron content genotype with high yield. From the study of genetic parameters, days to booting, flag leaf area, spike length, and thousand grain weight had better genotypic variability, better broad sense heritability along with better genetic advance. Soluwa (309.395ppm), Bonus (235.035ppm) and 14-SB-NAK-MR#17 (154.065 ppm) had high iron content and the character of iron content was found to be 100% heritable with no environment effects. Similarly, SBYT2-13#1519 (3120 kg/ha), SBYT2-13# 108 (2780 kg/ha), 1STGSBYT#122 (2410 kg/ha) were found to be high yielding genotypes. As the genotype with high and high iron content were screened out and this may be further use in development yield of high yielding varieties along with high iron content which can address issues of both food scarcity and nutrition demand.

Keywords: heritability; genetic advance; barley; yield; iron content

Introduction

Barley (*Hordeum vulgare* L) is considered as fourth important cereal in the world, both in terms of quantity produced and in area of cultivation. Over the world, about 660 million tons of barley is produced annually on about 222 million hectares with productivity of 2.9 (FAO STAT, 2013). Barley (*Hordeum vulgare*) is the fifth important cereal crop in Nepal after rice, maize, wheat and finger millet in terms of acreage and production. Barley has also been used as animal fodder, as a source of fermentable material for beer and certain distilled beverages, and as a component of various health foods. In recent years, barley is becoming an important food grain for human consumption due to its nutritional and clinical values. Diets

containing barley are effective in lowering blood cholesterol in hypercholesterolemia; reduce the risk of cardiovascular diseases and colon cancer (Behall, Scholfield & Hallfrisch, 2004).

To ensure the food security, grain yield has been the major concern of the agriculture research study. Advancement of agriculture crops depends upon the selection of the suitable traits of plants. However, desirable selected traits should have high heritability which ensures the transfer of character from one generation to another. Heritability estimates of quantitative characters play an important role in expressing the reliability of variance value as a selection guideline to the plant breeder during the succeeding



generations. Heritability along with genetic advancement should be jointly considered to arrive at a more reliable conclusion (Johnso, Comstock & Robinson, 1955). Regarding the quality aspect, it is also indispensable for the study of quality aspect along with the yield. In accordance with the food security, a nutritive aspect of the crop should also be considered in the breeding program. Although the amount of Iron is relatively lower as compared to carbohydrate and protein, there is a great role of them in the human health. Generally, iron is about 12 to 15% of the total amount of mineral content in barley kernels. Screening of the genotypes helps to find out the presence of variability in the traits under study whereas the study of the heritability along with genetic advancement gives a reliable idea to select the suitable genotypes for particular traits.

Materials and Methods

The experiment was conducted at the research farm of AFU, Rampur from December 2014 to April 2015 in alpha lattice design with total plot size 12.5 m x13 m consisting 20 genotypes in 2 replications. There were 4 blocks within replication and 5 genotypes within block where each plot size was 2.5 m × 1 m with continuous sowing in 4 rows per plot. The row to row spacing was 25 cm, block to block spacing was 0.5 m and space between two replications was 1m. Eighteen genotypes were collected from ICARDA, Morocco and 2 of the genotypes i.e. Bonus and Soluwa were collected from HCRP, Kabre. Standard agronomic and plant protection practices were followed. Data for different traits viz. days to booting, days to heading, days to flowering, flag leaf area, flag-1 leaf area, spike length, plant height, peduncle length, thousand grain weight, harvest index, biological yield, grain length, grain diameter, yield per hectare and iron content were used for estimation of genetic parameters and cluster analysis.

Estimation of Genetic Parameters

Both genotypic and phenotypic coefficient of variation were computed according to Burton and Devane (1953) and expressed as percentage.

$$\text{Genotypic coefficient of variation (GCV)} = \left(\frac{\sigma_g}{X} \right) \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \left(\frac{\sigma_p}{X} \right) \times 100$$

where,

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

X = General mean of the trait

The broad sense heritability was estimated as the ratio of genotypic variance (V_g) to the phenotypic variance (V_p) and expressed in percentage (Hanson, Robinson, & Comstock, 1956).

$$\text{Broad sense heritability } (h_{bs}^2) = \left(\frac{V_g}{V_p} \right) \times 100$$

Likewise, the extent of genetic advance to be expected by selecting about five percent of the genotypes was calculated by using the following formula given by Robinson, Comstock and Harvey (1949).

$$GA = i \cdot \sigma_p \cdot h_{bs}^2$$

where,

i = Efficacy of selection which is 2.06 at 5% selection intensity

σ_p = Phenotypic standard deviation

h_{bs}^2 = Broad Sense Heritability

Result and Discussion

There were high significant differences among the genotypes for all characters except the plant height, peduncle length in the research material which imply that there is possibilities of selecting the superior and desired genotypes by the plant breeder for further improvement.

Means Performance and Analysis of Variance

The mean number of days to booting was found to be 68.68 days. Genotype SBYT2-13#1519 booted earliest in 53 days whereas genotype AM POP#11 booted at the last in 91 days. The mean number of days to heading was found to be 77.97 days. Genotype SBYT2-13#1519 headed earliest in 70 days whereas genotype AM POP#11 headed at the last in 97 days. The mean number of days to heading was found to be 83.6 days. Genotype 14-SB-NAK-MR#17 flowered earliest in 74 days whereas genotype AM POP#11 flowered at the last in 107 days. The mean leaf area was found to be 5.702 cm². Genotype SBYT2-13#2214 had lowest flag leaf area of 1.867 cm² and genotype SBYT2-13#1519 had highest flag leaf area of 13.75 cm². The mean length of flag leaf-1 area was found to be 13.28 cm². Genotype SBYT2-13#2204 had lowest flag leaf-1 area of 4.89 cm² and genotype SBYT3-13#1011 had highest flag leaf-1 area of 25.52 cm². The mean length of peduncle was found to be 24.3 cm. There was no significant difference among genotypes for peduncle length. The mean length of spike length was found to be 7.032 cm. Genotype 1ST GSBYT#121 had lowest spike length of 4.5 cm and genotype SBYT2-13#1519 had highest spike length of 8.65 cm. The mean length of plant height was found to be 80.79 cm. There was no significant difference among genotypes for plant height. The mean weight of thousand grain weight was found to be 42.172 gm. Genotype 1ST GSBYT #121 had lowest thousand grain weight of 28.83 gm and genotype SBYT2-13#1519 had highest thousand grain weight of 57.3 gm. The mean weight of biological yield was found to be 1.59 kg. Genotype SBYT3-13#1308 had lowest biological yield of 0.8893 kg and genotype SBYT3-13#1011 had highest biological yield of 2.415 kg. The mean harvest index was found to be

0.1855. Genotype 1ST GSBYT#121 had harvest index of 0.028 and genotype 1ST GSBYT#122 had highest harvest index of 0.38. The mean length of grain was found to be 7.269 mm. Genotype 1ST GSBYT#122 had lowest grain length of 6.28 mm and genotype SBYT3-13#1510 had highest grain length of 8.07 mm. The mean length of grain was found to be 3 mm. Genotype Bonus had lowest grain length of 2.6 mm and genotype 1st GSBYT #102 had highest grain length of 3.92 mm. The mean iron content of grain was found 112.73 ppm. Genotype SBYT3-13#1501 had lowest iron content of 19.51 ppm and genotype Soluwa had highest iron content of 309.395 ppm. The mean weight of grain yield per hectare was found to be 1456 kg. Genotype 1ST GSBYT#121 had lowest grain yield per hectare of 151.5 kg and genotype SBYT2-13#1519 had highest grain yield per hectare of 3120kg (Table 1).

Phenotypic and Genotypic Coefficient of Variation

There was remarkable difference in PCV and GCV of the consider traits except iron content (Table 2). Among the studied traits like harvest index, flag leaf area, flag leaf-1 area and biological yield showed high PCV and GCV this is also supported by the finding of Singh et al. (2014) and Lodhi et al. (2015). High PCV with moderate GCV was found in peduncle length was observed. In the same way moderate PCV and GCV were found in thousand grain weight, spike length and days to booting. Other trait like iron content days to heading, days to flowering, grain diameter, grain length and plant height had low value of both GCV and PCV. The difference between GCV and PCV ranged from 0.00 to 14.24 which is shown in Table 2.

Heritability

This study presented that the trait iron content is totally heritable to another generation (100%). Similarly, high value of heritability was found in grain length, yield per hectare, days to heading, and days to booting, days to flowering, thousand grain weight, biological yield and harvest index. High value of heritability implied that the presence of the variation in the genotype is mainly under the genetic control and under the less influence of the environment. Similar finding was also demonstrated by the study of Akanksha et al. (2012), Borthkur & Poehlman (1970).

Genetic Advance as Percentage of Mean

The genetic advance as percentage of mean at 5% selection intensity revealed remarkable differences among the traits under study. Yield per hectare showed the highest genetic advances as percentage of mean (116.72%) among the entire trait. Similarly, harvest index (87.29%) exhibited high genetic advance as percentage of mean followed by flag leaf area (72.25%), biological yield (48.81%), flag leaf-

Table 1: Mean, SEM, F-test, LSD0.05 and CV of 15 character of 20 barley genotype

Genotype	DB	DH	DF	FLA	PED.L	SPL	PHT	TGW	BY	HI	GL	GD	IC	Yield
Mean	66.95	77.97	83.6	5.702	24.3	7.03	80.79	42.17	1.59	0.18	7.26	3.33	112.73	1456
EMS	8.53	5.36	8.06	2.94	18.90	0.38	123.67	9.88	0.05	0.00	0.02	0.01	0.20	67527.00
LSD 0.05	5.84	4.63	5.68	3.43	8.70	1.23	22.24	6.29	0.46	0.09	0.29	0.24	0.89	519.72
CV(%)	4.36	2.97	3.40	30.08	17.89	8.74	13.77	7.45	14.49	24.17	1.99	3.65	0.40	17.85
Z value	**	**	**	**	Ns	***	Ns	**	**	**	**	**	**	***

**Significant at the 0.01 level (2-tailed)

*Significant at the 0.05 level (2-tailed)

1 area (40.18%), thousand grain weight (33.62), spike length (28.61%) and days to booting (24.35%). Likewise, genetic advance as percentage of mean was found to be moderate for days to heading (17.90%), days to flowering (17.90%), Peduncle length (16.55%), grain diameter (15.78%) and grain length (14.59%). Genetic advance as percentage of mean was found to be lowest for iron content (9.71) followed by plant height (6.89%).



Table 4: Heritability of 20 Different genotypes

Variables	GCV	PCV	h_{bs}^2	GA	GAM
DB	12.52	13.26	0.89	16.30	24.35
DH	9.14	9.61	0.90	13.96	17.90
DA	8.97	9.59	0.87	14.45	17.29
FLA	42.85	52.36	0.67	4.12	72.25
FL1A	29.06	43.30	0.45	5.34	40.18
PedL	13.40	22.35	0.36	4.02	16.55
SpL	15.86	18.11	0.77	2.01	28.61
PHT	7.21	15.54	0.22	5.56	6.89
TgW	17.71	19.21	0.85	14.18	33.62
BW	26.91	30.56	0.78	0.78	48.81
HI	47.54	53.33	0.79	0.16	87.29
GL	7.34	7.60	0.93	1.06	14.59
GD	8.36	9.12	0.84	0.53	15.78
IC	4.71	4.71	1	141.38	9.71
YH	59.18	61.81	0.92	1699.46	116.72

Conclusion

Genotype SBYT2-13#1519 was found to be high yielding with medium iron content. Similarly, local check Soluwa has high iron content with medium yield. From the study of genetic parameters, days to booting, flag leaf area, spike length and thousand grain weight had better genotypic variability, better broad sense heritability along with better genetic advance which considered the good estimates for effective selection of a trait.

Conflict of Interest

The authors declare that there is no conflict of interest with present publication.

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