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Genetic Variability & Path Analysis studies in Barley (*Hordeum Vulgare* L.)

Vivek Vats[1], R.K. Gupta[2]
[1]P.G. Student, Department of Genetics and Plant Breeding, J.V. College, Baraut (Baghpat).
[2]Associate Professor, Department of Genetics and Plant Breeding, J.V. College, Baraut (Baghpat)

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Abstract

The current study was carried out during the Rabi season of 2023 at the Research Farm of the Department of Genetics and Plant Breeding at J. V. College, Baraut, Baghpat. It aimed to evaluate 22 diverse barley genotypes using a randomised block design with three replications. The findings showed that the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were notably high for traits such as grain yield per plant, biological yield per plant, harvest index, 1000 grain weight, and productive tillers per plant. Additionally, high heritability along with a significant genetic advance as a percentage of the mean was observed for grain yield per plant, biological yield per plant, 1000-grain weight, plant height, harvest index, and days to maturity. Based on the average performance of the genotypes, BH946, Lakhan, JB-1, RD-907, and DWRB-28 stood out as superior not only in terms of seed yield per plant but also for various other yield-related traits.

Keywords- Phenotypic coefficient of variation (PCV), heritability, genetic advance, grain yield per plant, plant height etc.

Introduction

Barley (*Hordeum Vulgare* L.) holds the distinction of being the cereal crop cultivated across the most extensive geographically areas globally. Among cereals, Barley ranks fourth in terms of worldwide production, trailing behind maize (*Zea mays L.),* wheat (*Triticum aestivum L.),* and rice (*Oryza sativa L.)* (Horsley *et.al*, 2009). It serves as a versatile crop, used for animal feed, malting, brewing, and even food in many parts of the world (Svobodova, *et al*., 2024). Given the current climatic challenges, the need for improving barley's yield potential and adaptability to different environments has gained paramount importance (Safhi, *et al*., 2024). Genetic variability forms the foundation of breeding programs, allowing the selection of superior genotypes that can enhance crop productivity under diverse environmental conditions (Allard, 1999).

Barley is a winter- friendly cereal originating from the Middle East, belonging to the Poaceae family. With a diploid genome size of 2n=2x=14 and a genome size of approximately 25.3 x 109 bp, it has played a pivotal role in human history since the Stone Age (El- Hashash *et al.,*2019). Barley is one of the oldest domesticated plants in history, having been grown since the Stone Age. In ancient civilizations, such as Mesopotamia and Egypt, barley was a staple food crop. It was used to make bread, porridge and even fermented into beer. Barley was highly valued for its ability to grow in diverse climates and its nutritional value. It plays a significant role in the diets and economies of many ancient cultures (Riehl, S., 2019).

Understanding genetic components such as combining ability and heritability is crucial for developing high-yielding barley varieties tailored to diverse agro- climatic conditions, Nevo, E., & Shewry, P.R., 1992 Schulze, 1998). Outbreeding in plants is usually marked by heterozygosity, while inbreeding is marked by homozygosity. Barley's floral morphology causes inbreeding, and homozygosity is usually an intrinsic trait. Despite numerous generations of selfing, some Heterozygosity exists in its genetic system.

The assessment of genetic variability is essential for identifying traits that contribute to yield improvements and stress tolerance (Pour-Aboughadareh *et al*., 2021). Several studies have documented that barley exhibits considerable genetic variation for key agronomic traits such as grain yield, plant height, and days to maturity, making it a promising candidate for breeding efforts (Sreenivasulu *et al*., 2008).

In addition to genetic variability, understanding the interrelationships among yield-contributing traits is crucial for designing effective breeding strategies (Dewey & Lu, 1959). Path analysis is an important statistical tool that provides insight into the direct and indirect effects of various traits on grain yield, thereby helping breeders to make informed selections (Wright, 1921). Studies applying path analysis in barley have shown significant correlations between yield and components such as grain number per spike and plant height, underscoring the relevance of such approaches in barley breeding (Manhas *et al*., 2023).

This study aims to evaluate the extent of genetic variability in barley and to assess the direct and indirect contributions of yield-contributing traits through path analysis. By identifying key traits influencing yield, the findings of this research will provide valuable insights for improving barley productivity under both optimal and stressed conditions.

Materials and Methods-The study was carried out in Rabi 2023-24 at the Genetics and Plant Breeding Research Farm of J.V. College in Baraut, Baghpat, and Uttar Pradesh. Baghpat district has a semi-arid climate characterized by hot summers and cold winters. Recommended cultural norms were followed to elevate successful crop. The observation was recorded on five randomly selected plants per plot for ten characters *viz.*, plant height (cm), spike length, 1000-seed weight (g),biological yield per plant (g), harvest index (%), and grain yield per plant (g). Whereas, the observations for days to 50 % flowering and days to maturity was recorded on plot basis. Analysis of variance was carried out as per standard procedure (Fisher, 1938). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) (Burton, 1952), heritability (Burton and Devane, 1953), genetic advance (Johnson *et al*., 1955), were estimated.

Result & Discussion -

Analysis of Variance- The study titled "Genetic Variability and Path Analysis Studies in Barley (*Hordeum vulgare* L.)" involved 22 different genotypes of barley grown during the Rabi season of 2023-24. The data collected on seed yield and its component traits were analyzed using various statistical methods. Variance analysis for all the characters revealed significant variation among the genotypes studied (Table1). The analysis of variance results indicated significant variations among the genotypes for various traits like days to 50% flowering (heading), plant height (cm), tillers per plant, flag leaf area (cm²), spike length (cm), 1000 grain weight (g), and biological yield per plant (g), harvest index (%), and grain yield per plant (g). Differences were also observed among the varieties for several traits. High amount of genetic variability for most of these traits has also been reported earlier by Singh *et al.* (2014), and (2021), Kobir *et al.* (2023)

Variability Parameters and per se Performance- Mean values of 22 genotypes for ten characters were recorded carefully and presented in (table 2).

Source of variation	**DF**	**D50% F**	**DM**	**PH (cm)**	**GPSL (cm)**	**1000GW (g)**	**BYPP (g)**	**HI (%)**	**GYPP (g)**	**TPP**	**FLA (cm²)**
Replications	2	3.65	5.05	0.83	1.28	10.52	0.96	10.58	12.69	1.20	7.24

Treatment	21	68.93**	58.33**	200.83**	3.17**	150.90**	3529.09**	159.57**	649.61**	4.77**	1.34**
Error	42	2.41	1.81	1.79	0.36	0.62	2.89	1.08	0.57	1.59	0.44

Table 1. Analysis of variance of Random block design for 10 characters in Barley (Hordeum vulgare L.)

*** &** Significant at 5% & 1% respectively**

Table No. 2 Mean performance for 10 characters in 22 genotypes in Barley.

Genotypes	**D50%F**	**DM**	**PH(cm)**	**GPSL(cm)**	**1000GW(cm)**	**BYPP(g)**	**HI%**	**GYPP(g)**	**TPP**	**FLA(cm^2)**
DWRB – 64	82.67	121.33	86.50	8.37	37.51	24.38	41.44	10.21	7.33	5.47
DWRB -137	77.33	111.67	85.57	8.04	57.68	29.30	37.27	10.47	7.00	4.98
HUB – 113	77.33	120.67	95.77	6.80	43.85	55.54	38.72	10.57	6.00	5.75
BH – 946	89.67	121.33	95.63	6.60	39.30	28.12	33.16	8.02	8.67	4.78
PL – 891	77.00	113.67	76.53	6.72	37.43	24.93	53.91	12.57	8.33	4.51
RD – 2786	76.33	124.67	78.73	6.78	52.94	37.13	37.69	8.13	7.00	5.47
RD – 2794	75.33	122.33	84.83	7.46	38.33	19.41	56.04	11.46	8.00	5.61
RD – 2907	75.67	128.00	83.57	9.67	58.30	87.28	30.50	9.41	6.33	6.74
DWRB – 28	89.33	117.67	77.87	7.73	62.23	55.90	44.59	11.52	10.00	4.86
EB – 921	73.33	121.67	86.47	8.78	41.80	67.54	35.92	10.50	8.67	4.66
JYOTI	79.00	124.00	95.90	7.16	40.20	20.18	38.49	7.95	9.00	5.43
K – 12	78.67	116.67	96.50	6.79	42.78	52.12	52.25	11.72	8.00	4.41
DWRB – 192	80.00	116.00	77.47	7.98	48.69	77.81	27.33	8.70	9.33	5.46
RD – 2552	77.67	113.67	85.07	5.76	37.89	23.26	34.04	8.54	8.00	4.51
RD – 2899	77.67	112.00	96.53	8.08	39.88	22.08	50.31	10.36	7.33	4.48
DL – 88	80.67	124.00	90.93	8.60	42.87	99.16	42.44	41.99	10.00	5.37
JB – 1	82.00	120.00	89.63	9.20	44.04	113.03	36.77	43.33	11.00	5.53
AZAD	77.67	122.00	89.87	8.26	42.27	98.93	40.55	40.99	9.00	6.48
LAKHAN	82.33	123.67	110.37	9.17	42.56	108.90	38.18	40.10	7.67	4.53
NB-1	72.67	121.33	91.13	8.68	41.47	107.27	39.18	42.50	9.33	6.14
NB -2	72.00	121.33	97.30	8.75	42.58	93.23	39.11	38.44	8.67	5.58
NB – 3	71.00	123.33	93.30	8.67	41.90	90.07	41.71	37.38	9.67	5.93
Mean	78.42	120.05	89.34	7.91	44.39	60.71	40.44	19.77	8.38	5.30
C.V.	1.98	1.12	1.50	7.59	1.77	2.80	2.58	3.84	15.07	12.49
S.E.	0.90	0.78	0.77	0.35	0.45	0.98	0.60	0.44	0.73	0.38
C.D. 5%	2.56	2.22	2.20	0.99	1.30	2.80	1.72	1.25	2.08	1.09
C.D. 1%	3.42	2.96	2.94	1.32	1.73	3.75	2.29	1.66	2.78	1.46
MIN	71.00	111.67	76.53	5.76	37.43	19.41	27.33	7.95	6.00	4.41
MAX	89.67	128.00	110.37	9.67	62.23	113.03	56.04	43.33	11.00	6.74

Table 3: - Mean Coefficient of variations for 10 characters of Barley genotypes.

	D50%F	**DM**	**PH (cm)**	**GPSL (cm)**	**1000GW (g)**	**BYPP (g)**	**HI%**	**GYPP (g)**	**TPP**	**FLA (cm^2)**
Var Environmental	0.80	0.60	0.60	0.12	0.21	0.97	0.36	0.19	0.53	0.15
ECV	1.98	1.12	1.50	7.59	1.77	2.80	2.58	3.84	15.07	12.49
Var Genotypical	22.17	18.84	66.35	0.94	50.10	1175.40	52.83	216.35	1.06	0.30
GCV	6.00	3.62	9.12	12.22	15.95	56.47	17.98	74.42	12.28	10.33
Var Phenotypical	22.98	19.44	66.94	1.06	50.30	1176.36	53.19	216.54	1.59	0.45

PCV	6.11	3.67	9.16	12.99	15.98	56.50	18.04	74.45	15.05	12.7
h2 (Broad sense)	0.97	0.97	0.99	0.89	1.00	1.00	0.99	1.00	0.67	0.67
Genetic Advancement 5%	9.53	8.80	16.71	1.88	14.55	70.60	14.92	30.29	1.73	0.93
Genetic Advancement 1%	12.21	11.28	21.41	2.40	18.65	90.47	19.12	38.81	2.22	1.19
Gen. Adv as % of Mean 5%	12.15	7.33	18.70	23.70	32.78	116.29	36.90	153.23	20.65	17.45
Gen. Adv as %Mean 1%	15.57	9.40	23.96	30.37	42.01	149.03	47.29	196.37	26.46	22.36

The assessment of the average performance of barley genotypes across various traits provides important insights into the variability within the germplasm, which is a crucial step in the selection of superior parents for breeding programs. In Table No. 2, the considerable variation observed in traits such as days to 50% flowering, plant height, and tillers per plant highlights the diversity in the genetic materials studied. Early flowering is often considered desirable in barley breeding, especially in regions with shorter growing seasons, as it allows plants to escape late-season drought or high temperatures. In this study, 13 genotypes flowered significantly earlier than the general mean, which is consistent with findings from Abebe *et al*. (2023), who also reported wide variability for days to 50% flowering in barley.

The variability in plant height, where genotypes ranged from 76.53 cm to 110.37 cm, also presents opportunities for selection depending on breeding goals. Shorter plants are typically preferred for lodging resistance, while taller plants may contribute to higher biomass (Manhas *et al*., 2023). In this study, 10 genotypes were significantly shorter than the average, indicating their potential utility in breeding for reduced height and increased lodging resistance.

The number of tillers per plant, an important yield-contributing trait, varied widely among genotypes. Eleven genotypes had significantly more tillers than the average, demonstrating the genetic potential for selecting plants with higher tiller numbers, which could lead to increased grain yield (Singh *et al*., 1978). Similar variability was observed for days to maturity, flag leaf area, spike length, 1000-seed weight, and biological yield, all of which are key traits influencing final yield outcomes. For example, larger flag leaf area and longer spikes are positively associated with higher photosynthetic capacity and grain yield (Richards *et al*., 2002).

The variation in 1000-seed weight, ranging from 37.43 to 62.23 grams, is particularly significant, as seed size is an important component of yield and quality in barley. Five genotypes exhibited a higher 1000-seed weight than the average, indicating their potential for breeding programs aimed at improving grain weight (Malik *et al*., 2018).

For biological yield per plant and grain yield per plant, the highest values were observed in JB-1, a genotype that showed superior performance across several traits. This genotype had not only the highest biological yield but also the highest grain yield per plant, demonstrating its potential as a candidate for high-yielding varieties. A high harvest index, as observed in seven genotypes, is an indicator of efficient partitioning of assimilates to the grain, a key trait for improving grain yield in breeding programs (Bennett *et al*., 2012).

The differences between the genotypic (GCV) and phenotypic (PCV) coefficients of variation provide insights into the influence of environmental factors on trait expression. In this study, the PCV was higher than the GCV for all traits, which is a common observation in plant breeding as environmental factors typically increase the phenotypic variation (Burton & DeVane, 1953). However, the relatively small differences between GCV and PCV for traits like 1000-grain weight, biological yield per plant, and grain yield per plant suggest that these traits are under strong genetic control and can be reliably selected for improvement in breeding programs (Saade *et al*., 2016).

Overall, the high GCV and PCV values for traits such as 1000-grain weight, biological yield per plant, and grain yield per plant indicate that these traits have high potential for selection and improvement (Johnson *et al*., 1955). The observed variability in other traits such as plant height, spike length, and days to maturity further reinforces the potential for improving these traits through selection, providing breeders with a diverse set of genetic resources to enhance barley productivity.

Genotypic and Phenotypic Coefficient of Variation- Variation is essential for selecting and improving crops through genetic means. Variation is the cornerstone of any successful breeding program, as it provides the raw material for selection (Allard, 1999). To make selection more effective, it's important to understand the nature and extent of variability in genotypes. The higher phenotypic coefficient of variation (PCV) compared to the genotypic coefficient of variation (GCV) observed in this study is typical of many crops, where environmental factors influence trait expression (Johnson *et al*., 1955). We measured both genotypic and phenotypic coefficients of variation to compare the levels of variability in different traits (see Table 3). Generally, phenotypic coefficients of variation (PCV) were found to be higher than genotypic coefficients of variation (GCV). However, in some cases, the differences between PCV and GCV were minimal, indicating that environmental impact on these traits was relatively low. Assessing both genotypic and phenotypic coefficients of variation is crucial for understanding how environmental factors influence different traits. The disparity between GCV and PCV highlights the extent to which environmental variations contribute to trait expression. Moderate magnitude of GCV and PCV was recorded for biological yield per plant and tillers per plant. It also showed a positive correlation with spike length, plant height, flag leaf area, days to maturity, but a non-significant negative correlation with days to 50% flowering, 1000 grain weight, harvest index indicating a good deal of genetic variability for the characters under study to allow further improvementby selection of the individual traits.

However, in cases where the difference between PCV and GCV is minimal, such as for biological yield per plant and tillers per plant, the environmental influence is relatively low, indicating that these traits are primarily governed by genetic factors (Burton & DeVane, 1953).

This limited environmental impact is crucial for breeding programs, as it suggests that these traits will exhibit consistent performance across diverse environments, making them ideal targets for selection (Hill *et al*., 2004). The moderate magnitude of both GCV and PCV for traits such as biological yield per plant and tillers per plant points to the existence of adequate genetic variability, which can be harnessed for further improvement (Pour-Aboughadareh *et al*., 2021).

Moreover, the positive correlation of biological yield with spike length, plant height, flag leaf area, and days to maturity supports the role of these traits as important yield components. Previous studies in barley and other cereals have highlighted similar associations, where traits like spike length and plant height are directly linked to improved grain yield (Manhas *et al*., 2023; Richards *et al*., 2002). Conversely, the non-significant negative correlations with days to 50% flowering, 1000-grain weight, and harvest index suggest that selecting for early flowering or larger grain size may not always result in higher overall yield (Kobir *et al*., 2023). These results reinforce the importance of balanced selection for multiple traits to optimize yield potential.

Heritability and genetic advance in percentage of mean- Heritability plays a pivotal role in determining the effectiveness of selection in crop improvement. It provides insights into the proportion of observed variation in a trait that can be attributed to genetic factors rather than environmental influences (Falconer & Mackay, 1996). In the current study, heritability estimates for key traits in barley were generally high, with several traits—such as 1000-grain weight, biological yield per plant, and grain yield per plant—recording heritability values of 100%. High heritability for these traits indicates that the observed phenotypic variation is primarily driven by genetic factors, suggesting that significant progress can be made through selection (Johnson *et al*., 1955).

High heritability alone, however, does not guarantee that a trait will respond effectively to selection. To accurately predict the genetic improvement achievable through selection, it is essential to consider heritability in conjunction with genetic advance, as it provides a more comprehensive understanding of the trait's potential for improvement (Singh *et al*., 1978). In this study, genetic advance as a percent of the mean was highest for grain yield per plant, biological yield per plant, and harvest index. This suggests that selecting for these traits will likely lead to considerable gains in overall yield and productivity, as both additive genetic effects and high heritability contribute to the traits' improvement (Burton & DeVane, 1953). Interestingly, the traits with the highest genetic advance, such as grain yield and biological yield per plant, also showed high heritability, indicating the predominance of additive gene action. This is advantageous for breeders since additive gene action facilitates more predictable and consistent responses to selection, making these traits ideal targets for breeding programs aimed at enhancing yield (Pour-Aboughadareh *et al*., 2021). On the other hand, traits such as plant height, 1000-grain weight, and spike length exhibited moderate genetic advance despite high heritability, suggesting that these traits might also be governed by both additive and non-additive gene actions, and while genetic progress is possible, it may be less straightforward compared to traits dominated by additive genetic variance. Conversely, traits like days to 50% flowering and days to maturity exhibited low heritability and low genetic advance. This indicates that these traits are influenced more by environmental factors and non-additive gene actions, making them less amenable to improvement through selection alone (Choudhary et al., 2019). The low genetic progress observed in these traits suggests that other breeding strategies, such as hybridization or marker-assisted selection, may be necessary to enhance these traits effectively (Bennett et al., 2012). The dominance of non-additive gene action in these traits, as indicated by low heritability and genetic advance, also suggests that heterosis or hybrid vigor might be exploited to improve early flowering or maturity traits in future breeding efforts (Singh *et al*., 1978). Moderate heritability combined with moderate genetic advance was recorded for traits such as plant height, flag leaf area, and tillers per plant, suggesting that both additive and non-additive genetic components contribute to their expression. For these traits, selection can still be effective, but improvement may require a combination of strategies, including recurrent selection or the development of hybrid varieties (Johnson *et al*., 1955). These traits can be valuable in breeding programs aiming to improve barley's adaptability and yield stability under varying environmental conditions, as they influence overall plant architecture and yield potential (Richards *et al*., 2002). In conclusion, heritability and genetic advance are interrelated and should be considered together when predicting the response to selection. Traits with high heritability and genetic advance, such as grain yield and biological yield, present the greatest potential for genetic improvement through simple selection methods. For traits with moderate heritability and genetic advance, more sophisticated breeding approaches may be required. For traits with low heritability and genetic advance, breeding efforts should focus on hybridization and other advanced techniques to enhance the effectiveness of selection. These findings provide valuable insights for designing effective breeding strategies for improving barley productivity.

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