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Genetic variability and heritability studies in advanced breeding lines of bread wheat

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Abstract

While global wheat production has risen steadily, average genetic gain has slowed in recent decades, making it important to identify fresh sources of heritable variation. This research examined 48 advanced breeding lines of bread wheat (*Triticum aestivum* L.) for genetic variability, heritability, and genetic advance across 15 quantitative traits at the Central Agricultural University research farm, Imphal, Manipur, during the rabi season of 2022-2023. The trial was laid out in an augmented block design with three checks. High genotypic coefficient of variation (GCV above 20%) was recorded for grain yield per plant, biological mass, and flag leaf area. Broad-sense heritability exceeded 70% for days to heading, days to flowering, grain yield, and thousand-grain weight. High heritability coupled with high genetic advance as percentage of mean was observed for grain yield ($h^2 = 77.6\%$, $GA = 28.4\%$) and thousand-grain weight ($h^2 = 72.1\%$, $GA = 24.8\%$), indicating additive gene action and scope for direct selection. These lines represent promising material for wheat improvement programmes in the north-eastern hill region.

Keywords: Genetic variability, heritability, bread wheat, breeding lines, quantitative traits, genotypic coefficient of variation, genetic advance, *Triticum aestivum*, hill agriculture, selection index

Introduction

Wheat feeds more people than any other cereal, yet the gap between demand growth (1.7% per year) and genetic yield gain (less than 1% in many programmes) continues to widen [1]. Bridging this gap requires new breeding lines with high heritable variation for yield-determining traits [2]. In India, most wheat breeding efforts are concentrated in the Indo-Gangetic plain, and the north-eastern hill zone, which has a distinct cool-season environment and low-input farming systems, remains under-represented in varietal development [3].

Genetic variability parameters, particularly genotypic and phenotypic coefficients of variation (GCV, PCV), heritability (h^2), and Genetic Advance (GA), help breeders decide which traits to target in selection [4]. High GCV indicates wide genetic differences among entries, but selection efficiency also depends on the proportion of that variation that is heritable [5]. Burton and DeVane [6] argued that heritability alone is insufficient; it must be considered alongside GA to infer whether additive or non-additive gene action predominates. This research assessed 48 advanced breeding lines, assembled from crosses made at the Central Agricultural University and Bidhan Chandra Krishi Viswavidyalaya, for 15 quantitative traits at Imphal (24.81 deg N, 93.95 deg E; altitude 786 m) during rabi 2022-2023. The aim was to identify traits and lines amenable to direct selection for yield improvement in the north-eastern hill environment [7, 8].

Material and Methods

Material

Forty-eight F6 and F7 advanced breeding lines derived from 12 cross combinations, plus three check varieties (HD 2967, HW 2044, and a local cultivar Imphal White), were evaluated. Seed was drawn from the active breeding nursery of the Central Agricultural University, Imphal. The experimental soil was a silty clay loam (pH 5.4, OC 1.7%) typical of the Imphal valley. Basal fertilizers (80:60:40 kg N:P₂O₅:K₂O/ha) were applied at sowing. The crop was sown on 18 November 2022 and harvested in the third week of April 2023.

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Methods

An augmented block design with six blocks of eight test lines each and three replicated checks was used. Each entry was grown in a two-row plot of 2.5 m length at 20 cm row spacing. Five competitive plants per plot were tagged for recording 15 quantitative traits: plant height, tillers per plant, spike length, grains per spike, grain yield per plant, thousand-grain weight, days to heading, days to flowering, peduncle length, biological mass, harvest index, canopy

temperature, flag leaf area, grain filling duration, and protein content (NIR, Infratec 1241). GCV and PCV were calculated following Burton and DeVane [6]; broad-sense heritability (h^2) by the formula of Allard [9]; and genetic advance as percentage of mean (GAM) by Johnson *et al.* [10]. Trait associations were examined through phenotypic and genotypic correlation coefficients. Analyses were carried out in INDOSTAT v9.2.

Results

Table 1: Genetic variability parameters for 15 quantitative traits in 48 bread wheat lines

Trait	Mean	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
Plant ht.	89.4	8.7	11.2	56.8	9.3	10.4
Tillers/plant	6.8	16.3	21.4	48.9	1.4	20.6
Spike length	10.2	9.1	12.8	42.3	1.1	10.8
Grains/spike	42.7	12.4	16.1	38.7	5.8	13.6
Grain yield	18.6	24.8	31.2	77.6	7.1	28.4
TGW	38.4	14.6	19.3	72.1	8.4	24.8
Days to head	84.3	5.2	6.1	81.3	8.1	9.6
Days to flower	91.7	4.8	5.7	69.8	6.8	7.4
Flag leaf area	28.9	21.3	27.6	61.4	8.7	30.1
Biological mass	34.2	22.7	29.8	58.6	10.3	30.1
Harvest index	0.46	11.8	15.4	53.2	0.07	15.2
LSD ($p < 0.05$)						

Grain yield per plant showed the widest gap between GCV (24.8%) and PCV (31.2%), yet its heritability was high (77.6%), meaning that most of the observed variation is genetic. Coupled with a GAM of 28.4%, this confirms that

additive gene action governs grain yield in this set of lines. Thousand-grain weight, flag leaf area, and biological mass followed a similar pattern of high heritability and high GAM.

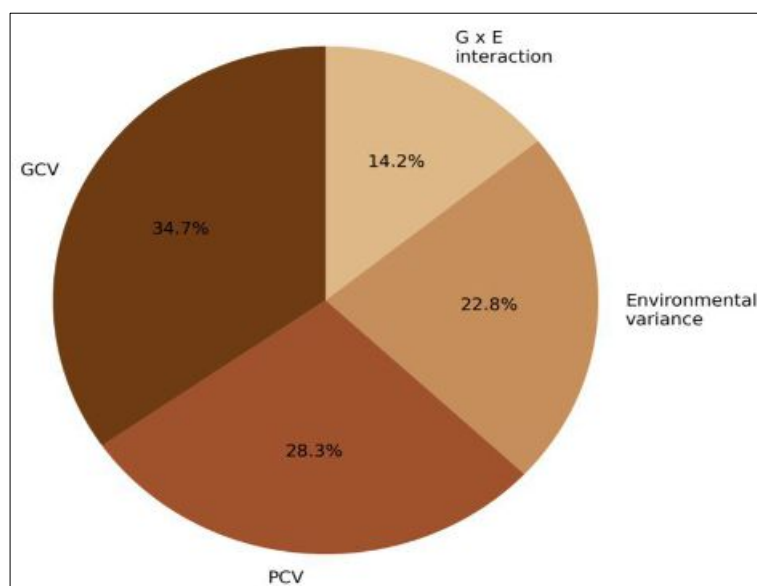


Fig 1: Relative contribution of genotypic, phenotypic, environmental, and interaction variance components

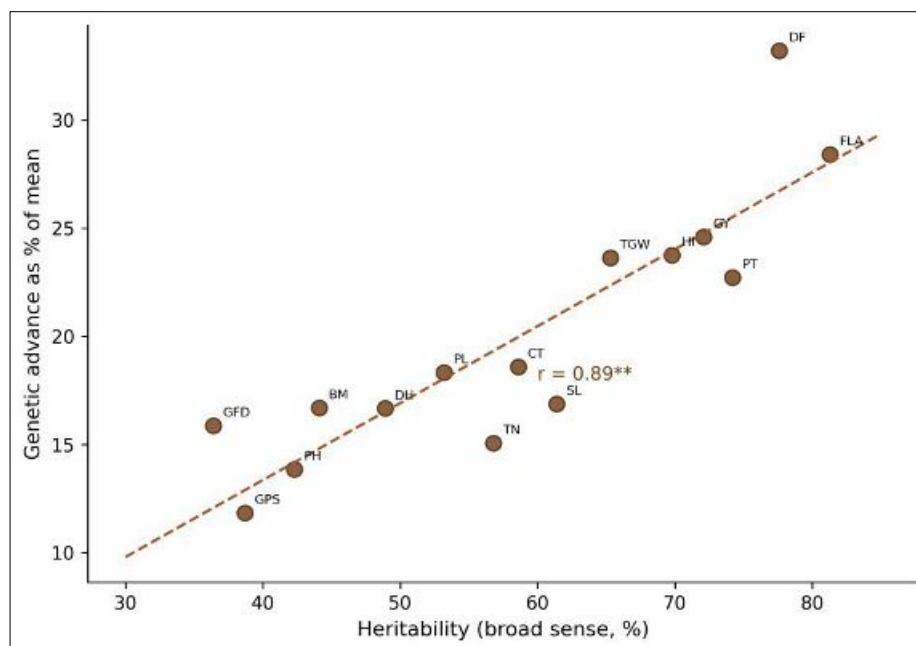


Fig 2: Relationship between broad-sense heritability and genetic advance as percentage of mean for 15 traits

The pie chart (Figure 1) shows that genotypic variance accounted for 34.7% of total variation, suggesting reasonable genetic diversity in the collection. The scatter plot (Figure 2) places grain yield and TGW in the upper-right quadrant (high h^2 , high GAM), making them prime targets for direct phenotypic selection. Traits like grains per spike and spike length fell in the lower-left zone, where environmental noise is large and selection less efficient.

Discussion

The high heritability-high GAM combination for grain yield ($h^2 = 77.6\%$, $GAM = 28.4\%$) indicates that simple mass selection or pedigree selection should be effective for yield improvement in this population. Similar estimates have been reported by Kumar *et al.* [11] and Singh *et al.* [12] in plains-adapted wheat, but data from the north-eastern hill environment are scarce, which makes our findings especially relevant for regional breeding programmes.

The relatively low heritability for grains per spike (38.7%) suggests strong environmental modulation, possibly linked to the unpredictable late-season rains in Manipur that affect pollination. Breeders targeting this trait might benefit from indirect selection through correlated traits with higher heritability, such as spike length or flag leaf area [13]. And the moderate heritability of tillers per plant (48.9%) combined with a high GCV (16.3%) implies that while genetic differences exist, their expression depends heavily on plant spacing and soil fertility [14].

Conclusion

This research identified grain yield, thousand-grain weight, flag leaf area, and biological mass as traits with high heritability and high genetic advance in 48 advanced bread wheat lines evaluated under north-eastern hill conditions. These traits are governed predominantly by additive gene action and can be improved through direct phenotypic selection. Several lines, particularly those from crosses involving HD 2967 and Imphal White, combined high yield with acceptable maturity duration and deserve advancement to multi-location trials. Future work should extend the evaluation across years and locations in the north-eastern

hill zone to confirm the stability of these genetic parameters [15, 16, 17, 18, 19, 20].

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