



Genetic Variation for Grain Quality and Yield Attributing Traits in Upland Rice (*Oryzasativa* L.) Landraces of Nagaland

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Abstract

Rice holds a central place in the cultural heritage of the ethnic tribes of Nagaland, symbolizing a deeply rooted, traditional crop. Enhancing rice strains to create elite varieties that combine both qualitative and complex traits, such as increased yield, is feasible by harnessing the genetic diversity within the population. This study focused on evaluating genetic variability and the relationships between grain quality and yield traits in 50 rice landraces. Data were collected on eleven traits contributing to yield and eleven parameters related to grain quality. The analysis of variance revealed significant variability across all measured traits. Yield-related traits, particularly the number of tillers per plant, total grains per plant, number of panicles per plant, number of filled grains per plant, grain yield per plant, and test weight, exhibited substantial genotypic and phenotypic variation. Similarly, grain quality traits such as amylose content, gelatinization temperature, and gel consistency also displayed notable variation. Most traits, except the number of tillers and panicles per plant, demonstrated high heritability. Furthermore, grain yield per plant showed a strong positive correlation with the number of tillers and panicles per plant at both genotypic and phenotypic levels.



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Introduction


Rice (*Oryza sativa* L.) is one of the most important staple cereal crops globally, cultivated across diverse environmental conditions in more than 114 countries.¹ It constitutes a critical food source for over 3.5 billion people worldwide, contributing more

than 20% of their daily caloric intake. Asia accounts for approximately 90% of global rice production and consumption, underscoring its significance in the region.² In India, rice is cultivated on 43.79 million hectares, with a production of 116.42 million tonnes recorded during the 2022-23 season.³

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Grain yield is a highly complex and pivotal trait in rice, playing a crucial role in addressing the increasing global demand fueled by population growth and industrialization.⁴ It is governed by quantitative trait loci (QTL) and is profoundly influenced by external environmental factors. Critical agronomic traits such as plant height, panicle length, number of grains per panicle, number of panicles per plant, and test weight serve as key determinants of grain yield in rice.⁵

Grain quality is a critical trait in rice breeding, as it addresses the diverse preferences and expectations of producers, processors, retailers, and consumers across production, processing, marketing, and consumption stages.⁶ It encompasses both physical attributes, which influence the grain's appearance, and chemical properties, which affect its cooking and eating qualities (ECQs). Key aspects of grain quality include grain appearance, milling properties, ECQs, and nutritional composition.⁷ Grain appearance is defined by traits such as whiteness, translucency, and the uniformity of grain shape and size. Milling properties, including milled rice yield and head rice yield, are essential indicators of processing efficiency. Cooking quality, a major determinant of consumer satisfaction, is primarily governed by starch composition. Starch, composed of amylose and amylopectin, plays a pivotal role, with amylose content significantly influencing cooking behavior. ECQs are further determined by amylose content, gel consistency, and gelatinization temperature,

collectively shaping the overall culinary and sensory experience of rice.⁸

In Nagaland, tribal farmers preserve a diverse range of local rice varieties and landraces with substantial genetic variability, offering significant potential for improvement through selective breeding, despite their often-low yields. Enhancing these local cultivars in terms of yield and quality traits while ensuring they remain well-suited to local conditions—could boost production and productivity per unit area, reducing pressure to expand land for rice cultivation. Identifying genetic variability associated with yield related traits enables the development of new rice cultivars with desirable characteristics. Quantitative assessment of each trait forms the foundation for analyzing variance, aiding in targeted improvement efforts.

Materials and Methods

Experiment Materials and location

The experimental material for this study comprised pure seeds of 50 upland rice landraces, sourced from the ICAR Research Centre for the North Eastern Hill (NEH) region. These landraces were evaluated for grain quality and yield-contributing traits during the kharif season of 2020 at the research farm of the ICAR Nagaland Centre. Bhalum-1 and Bhalum-3 served as the check varieties for the experiment. The detailed list of upland rice landraces included in the study is provided in Table 1.

Table 1: List of upland races of rice under investigation

S. No	Accessions	Location	S. No	Accessions	Location
1	Mapok	Longjang village (Mokokchung)	26	TeiYoh	Hukpang, Longleng Dist.
2	Mepongchuket Masu	Khensa village, (Mokokchung)	27	Nukjan Shola	Tangha, Longleng Dist.
3	Angja	Tangha village, (Longleng)	28	MapokTsuk	Longkhum, Mokokchung Dist.
4	ChaliYoh	Tangha village, (Longleng)	29	Khemaru	Longkhum, Mokokchung Dist.
5	MotsoTsuk	Wokha town, (Wokha)	30	Arunachal	Kilomi, Zunheboto Dist.
6	YimsoTsuk	Mopongchuket, Mokokchung Dist.	31	Dulong	Hukpang, Longleng Dist.
7	Doiha	Tangha, Longleng Dist.	32	Lamjet	Hukpang, Longleng Dist.

8	Tsuksembla	Dibuia, Mokokchung Dist.	33	Yamchinga	Hukpang, Longleng Dist.
9	Amiisu	Kiding, Tuensang Dist	34	Vam	Tangha, Longleng Dist.
10	Samaro	Sanis, Wokha Dist.	35	Yamuk	Hukpang, Longleng Dist.
11	Aor Chang	Ungma, Mokokchung Dist.	36	MasoTsuk	Dibuia, Mokokchung Dist.
12	Aphagi	Sumisetsu, Zunheboto Dist.	37	ManenTsuk	Longjang, Mokokchung Dist.
13	ChamnyaYoh	Dungkhao, Longleng Dist.	38	Bhalum-1	Check Variety
14	HyungYoh	Hukpang, Longleng Dist.	39	Neikedoulhatsia	Kohima, Kohima Dist.
15	Toiya	Hukpang, Longleng Dist.	40	Moya Tsuk	Longkhum, Mokokchung Dist.
16	Hahnyak	Nyang, Longleng Dist.	41	Maibo	Tangha, Longleng Dist.
17	Shuphok	Nyang, Longleng Dist.	42	China Tsone	Noklak, Noklak Dist.
18	Yunghah	Tangha, Longleng Dist.	43	Laza	Longjang, Mokokchung Dist.
19	SamroYoh	Tangha, Longleng Dist.	44	KD 5-2-8	Longkhum, Mokokchung Dist.
20	NangzaTsuk	Wokha, Wokha Dist.	45	Malanken	Wokha, Wokha Dist.
21	VepsuTsuk	Wokha, Wokha Dist.	46	MaroEtyo	Wokha, Wokha Dist.
22	EngchaYoh	Dungkhao, Longleng Dist.	47	Meitak	Kohima, Kohima Dist.
23	Nukneyi	Nyang, Longleng Dist.	48	Eshie	New Chungliyimti, Mokokchung Dist.
24	Pfutsero Ru	Pfutsero, Phek Dist.	49	Sopa	Wokha, Wokha Dist.
25	MatiPasi	Kohima, Kohima Dist.	50	Bhalum 3	High yielding check variety

Data Collection

Genetic variation for eleven yield attributing parameters and eleven quality parameters were assessed among the rice genotypes. These characteristics were chosen based on descriptions and guidelines provided by PPV&FR in 2001 (DUS). Observations were recorded on DF50% = Days to 50% flowering, 80%DM = Days to 80% maturity, GYPP = Grain yield per plant (g), NOFG = Number of filled grains per plant, NOP = Number of panicles per plant, NOT = Number of tillers per plant, NOUG = Number of unfilled grains per plant, TNGPP = Total number of grains per plant, PH = Plant height (cm), PL = Panicle length (cm), TW = Test weight (g), AC = Amylose content (%), DGL = Decorticated grain length (cm), DGL:B = Decorticated grain length-

to-breadth ratio, DGW = Decorticated grain width (cm), GC = Gel consistency, GL = Grain length (cm), GL:B = Grain length-to-breadth ratio, GLAC = Grain length after cooking (cm), GT = Gelatinization temperature, GW = Grain width (cm) GWAC = Grain width after cooking (cm) and ASV = Alkali spreading value. Amylose content (AC) was determined by the method as described⁹. Gelatinization temperature (GT) was assessed indirectly as the alkali spreading value (ASV) of hulled kernels as per the modified procedure¹⁰. Gel consistency (GC) was measured by the procedure of.¹¹ Physical grain quality parameters were measured using a vernier caliper. The analysis of variance was carried out according to 12 by using the mean performance of the genotypes.

Statistical Analysis

The analysis of variance (ANOVA) was performed using the OPSTAT open-source software to evaluate the experimental data. The phenotypic, genotypic, and environmental coefficients of variation were calculated following the method described by.¹³ Heritability estimates were computed as outlined by,¹⁴ and the genetic advance through selection was determined using the approach detailed by.¹⁵ Phenotypic and genotypic correlation coefficients were calculated following the methodology proposed by.¹⁶ Additionally, the partitioning of genotypic

correlation coefficients into direct and indirect effects was conducted using the procedure described by.¹⁷

Analysis of Variance

The combined analysis of variance (ANOVA) for grain yield and quality traits is summarized in Tables 2a and 2b. The analysis revealed significant differences ($p < 0.05$) among the rice landraces for both yield and quality traits. These significant effects indicate the presence of substantial genetic variation among the evaluated landraces, highlighting their potential for further breeding and selection efforts.

Table 2a: Analysis of variance for yield attributing traits

Source of variation	Df	50% F	80% M	PH	NOT	NOP	PL	TNG PP	NOFG	NOUG	GYPP	TW
Genotypes	49	90.5 2**	95.6 2**	666. 62**	4.32**	3.88**	18.8 9**	231 4.05**	2704. 79**	507. 34**	15.15**	6340 .94**
Replication	1	84. 64	2.25	84. 07	6.76	2.89	6.93	72.25	29.16	0.01	1.59	324
Error	49	6.88	3.7	63.4 7	2.58	1.91	4.54	439. 98	500. 91	74.52	2.93	131 .02

** = Significant at 1 % and * = Significant at 5 % level of significance.

Table 2b: Analysis of variance for grain quality traits

Source of variation	Df	GL	GW	GL:B	DGL	DGW	DGL:B	GLAC	GWAC	AC	GT	GC
Genotypes	49	2.12**	0.29**	0.28**	1.20**	0.20**	0.20**	1.90**	0.40**	76.37**	3.30**	1939.7**
Replication	1	0.41	0.1	0.01	0.19	0.09	0.01	0.11	0.07	34.49	0.25	32.49
Error	49	0.05	0.01	0.01	0.02	0.01	0.01	0.07	0.02	2.53	0.35	11.92

** = Significant at 1 % and * = Significant at 5 % level of significance.

Genetic Variability Analysis

The success of crop breeding is contingent upon the availability of genetic variability within the population and the heritability of the traits under selection. Table 3 summarizes the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), mean range, broad-sense heritability (H^2), and genetic advance as a percentage of the mean (GAM) for the studied traits.

The findings revealed that PCV consistently exceeded GCV, indicating that environmental

factors influenced the expression of the traits. High GCV and PCV (>20%) were observed for several traits, such as NOT (GCV: 18.25%, PCV: 42.51%), TNGPP (GCV: 21.70%, PCV: 28.33%), NOP (GCV: 22.99%, PCV: 45.40%), NOFG (GCV: 34.11%, PCV: 44.24%), GYPP (GCV: 47.88%, PCV: 62.78%), and TW (GCV: 21.88%, PCV: 22.56%). Among quality traits, AC (GCV: 42.02%, PCV: 44.13%), GT (GCV: 46.56%, PCV: 54.25%), and GC (GCV: 38.34%, PCV: 38.70%) exhibited similarly high values, signifying substantial genetic variability and their potential suitability for direct selection.

Table 3: Genetic variability of grain yield and quality parameters

SI. No	Parameters	GV	PV	H ² (%)	GA (%)	GCV	PCV	Min	Max	Mean
1	Days to 50% flowering	27.88	34.76	80.00	11.06	5.99	6.69	76.00	111.50	88.08
2	Days to 80% maturity	30.64	34.34	89.00	9.66	4.97	5.26	102.00	136.00	111.45
3	Plant height	200.69	264.17	76.00	25.05	13.95	16.00	69.15	144.35	101.52
4	Number of tillers per plant	0.58	3.16	1.00	16.13	18.25	42.51	2.00	7.00	4.18
5	Number of panicles per plant	0.66	2.57	26.00	23.97	22.99	45.40	1.50	6.50	3.53
6	Panicle length	4.78	9.32	51.00	12.47	8.45	11.79	20.30	35.15	25.89
7	Total number of grains per plant	624.69	1064.67	59.00	34.24	21.70	28.33	39.00	229.00	115.17
8	Number of filled grains per plant	734.62	1235.54	59.00	54.18	34.11	44.24	25.50	189.50	79.46
9	Number of unfilled grains per plant	2.27	2.27	100.00	8.62	4.18	4.18	8.50	82.00	36.01
10	Grain yield per plant	4.07	7.00	58.00	75.23	47.88	62.78	1.10	10.50	4.22
11	Test weight	2069.97	2200.99	94.00	43.71	21.88	22.56	107.00	329.00	207.96
12	Grain length	0.69	0.74	93.00	21.44	10.77	11.15	5.65	9.75	7.71
13	Grain width	0.09	0.10	85.00	19.10	10.50	11.36	2.12	3.98	2.86
14	Grain length to breadth ratio	0.09	0.10	87.00	21.12	11.01	11.83	1.93	3.57	2.72
15	Decorticated grain length	0.39	0.41	96.00	22.73	11.28	11.54	3.97	7.12	5.56
16	Decorticated grain width	0.06	0.07	90.00	20.34	10.38	10.91	1.80	3.10	2.47
17	Decorticated grain length to breadth ratio	0.06	0.07	91.00	22.22	11.29	11.82	1.57	2.77	2.27
18	Grain length after cooking	0.61	0.68	90.00	22.79	11.66	12.29	4.71	8.83	6.70
19	Grain width after cooking	0.13	0.15	88.00	21.95	11.38	12.16	2.19	4.01	3.15
20	Amylose content	24.61	27.14	91.00	82.43	42.02	44.13	1.43	28.43	11.80
21	Gelatinization temperature	0.98	1.33	74.00	82.30	46.56	54.25	1.00	6.50	2.13
22	Gel consistency	642.59	654.51	98.00	78.27	38.34	38.70	24.00	122.50	66.11

GV= Genotypic variance, PV= Phenotypic variance, H²(Heritability Broad sense), GA= Genetic advance, GCV= Genotypic coefficient of variation (GCV), PCV= Phenotypic coefficient of variation.

Moderate GCV and PCV (10–20%) were observed for other traits, with duration-related traits showing heightened environmental sensitivity. Heritability estimates were high (>60%) for most traits, excluding NOT and NOP. Traits such as PH, NOP, TNGPP,

NOFG, GYPP, and TW demonstrated high genetic advance, highlighting their genetic potential for selection. Traits exhibiting high heritability coupled with high GAM included all quality traits and yield components like PH, NOP, TNGPP, NOFG, GYPP and

TW. These traits are primarily governed by additive gene action, making them suitable for improvement through simple selection methods. Conversely, traits with high heritability but moderate GAM suggest the involvement of both additive and non-additive gene actions, with environmental factors exerting a considerable influence on their expression.

Correlation Studies

Correlation studies are fundamental in understanding the magnitude and direction of associations between yield and its contributing factors, which are pivotal for designing efficient breeding strategies. The genotypic and phenotypic correlation coefficients for the evaluated traits are presented in Tables 4a and 4b.

In this study, GYPP exhibited positive and significant correlations with NOT ($r_g = 0.320^*$, $r_p = 0.373^{**}$) and NOP ($r_g = 0.357^*$, $r_p = 0.383^{**}$) at both the genotypic and phenotypic levels. Additionally, TNGPP ($r_p = 0.349^{**}$) and NOFG ($r_p = 0.398^{**}$) displayed positive

and significant correlations at the phenotypic level. Among quality parameters, correlation analysis identified 27 significant positive associations and 4 significant negative associations, with varying levels of significance ($p < 0.05$). High genotypic and phenotypic correlations ($r > 0.66$) were observed between GL and GL:B ($r_g = 0.609^{**}$, $r_p = 0.595^{**}$), DGL ($r_g = 0.988^{**}$, $r_p = 0.976^{**}$), DGL:B ($r_g = 0.600^{**}$, $r_p = 0.577^{**}$), and GLAC ($r_g = 0.835^{**}$, $r_p = 0.825^{**}$). Similarly, strong correlations were recorded between GW and DGW ($r_g = 0.982^{**}$, $r_p = 0.933^{**}$) and GWAC ($r_g = 0.713^{**}$, $r_p = 0.662^{**}$). A high magnitude of association was observed between GL:B and DGL:B ($r_g = 0.986^{**}$, $r_p = 0.944^{**}$) at both the genotypic and phenotypic levels. DGL was strongly correlated with DGL:B ($r = 0.608^{**}$, $r_p = 0.592^{**}$) and GLAC ($r_g = 0.853$, $r_p = 0.837^{**}$). Furthermore, DGW exhibited strong correlations with GLAC ($r_g = 0.523^{**}$, $r_p = 0.521^{**}$) and GWAC ($r_g = 0.736^{**}$, $r_p = 0.706^{**}$). GLAC was also highly correlated with G AC ($r_g = 0.777$, $r_p = 0.736^{**}$).

Table 4 a: Genotypic (G) and Phenotypic (P) correlation co-efficient of grain yield per plant and 10 yield attributing traits in 50 upland races of rice grown in Nagaland.

Characters	DF	DF	PH	NOT	NOP	PL	TNGPP	NOFG	NOUG	TW	GYPP	
	50%	80%										
DF 50 %	G	1										
	P	1										
DM 80 %	G	0.658 ^{**}	1									
	P	0.622 ^{**}	1									
PH	G	-0.152	0.231	1								
	P	-0.204	0.17	1								
NOT	G	-0.082	0.307 [*]	0.105	1							
	P	0.022	0.135	-0.046	1							
NOP	G	-0.12	0.199	0.017	0.987 ^{**}	1						
	P	-0.01	0.108	-0.079	0.961 ^{**}	1						
PL	G	-0.106	-0.012	0.253	-0.149	-0.158	1					
	P	-0.118	-0.031	0.303 ^{**}	-0.029	-0.069	1					
TNGPP	G	-0.312 [*]	-0.1	0.654 ^{**}	-0.269	-0.236	0.331 [*]	1				
	P	-0.167	-0.059	0.462 ^{**}	0.117	0.093	0.227 [*]	1				
NOFG	G	-0.205	0.052	0.754 ^{**}	-0.002	-0.008	0.427 ^{**}	0.902 ^{**}	1			
	P	-0.101	0.052	0.578 ^{**}	0.2 ^{**}	0.179	0.316 ^{**}	0.908 ^{**}	1			
NOUG	G	-0.182	-0.346 [*]	-0.350 [*]	-0.544 ^{**}	-0.484 ^{**}	-0.262	0.045	-0.390 ^{**}	1		
	P	-0.111	-0.253 [*]	-0.369 ^{**}	-0.234 [*]	-0.241 [*]	-0.251 [*]	0.032	-0.386 ^{**}	1		
TW	G	0.243	0.087	-0.441 ^{**}	0.281 [*]	0.204	-0.013	-0.497 ^{**}	-0.374 ^{**}	-0.187	1	
	P	0.214	0.075	-0.396 ^{**}	0.148	0.136	-0.014	-0.405 ^{**}	-0.301 ^{**}	-0.171	1	
GYPP	G	0.04	0.036	-0.106	0.320 [*]	0.357 [*]	-0.04	0.259	0.249	-0.035	0.151	1
	P	0.048	0.02	-0.05	0.373 ^{**}	0.383 ^{**}	0.037	0.349 ^{**}	0.398 ^{**}	-0.191	0.129	1

G= Genotypic, P=Phenotypic correlation. *, ** Significant at 5% and 1% respectively.

Table 4 b: Genotypic (G) and Phenotypic (P) correlation co-efficient between 11 grain quality parameters in 50 upland races of rice grown in Nagaland.

Character		GL	GW	GLBR	DGL	DGW	DGL:B	GLAC	GWAC	AC	GT	GC
GL	G	1										
	P	1										
GW	G	0.380**	1									
	P	0.361**	1									
GLBR	G	0.609**	-0.498**	1								
	P	0.595**	-0.523**	1								
DGL	G	0.988**	0.357*	0.611**	1							
	P	0.976**	0.345**	0.583**	1							
DGW	G	0.386**	0.982**	-0.482**	0.386**	1						
	P	0.381**	0.933**	-0.465**	0.387**	1						
DGL:B	G	0.600**	-0.492**	0.986**	0.608**	-0.493**	1					
	P	0.577**	-0.475**	0.944**	0.592**	-0.507**	1					
GLAC	G	0.835**	0.492**	0.363**	0.853**	0.523**	0.348*	1				
	P	0.825**	0.474**	0.323**	0.837**	0.521**	0.318**	1				
GWAC	G	0.470**	0.713**	-0.193	0.468**	0.736**	-0.198	0.777**	1			
	P	0.432**	0.662**	-0.198*	0.439**	0.706**	-0.213*	0.736**	1			
AC	G	0.23	-0.141	0.327*	0.247	-0.075	0.278	0.167	0.07	1		
	P	0.213*	-0.117	0.293**	0.230*	-0.063	0.246*	0.156	0.096	1		
GT	G	0.326*	-0.018	0.306*	0.281*	-0.013	0.271	0.16	0.069	0.272	1	
	P	0.279**	0.009	0.232*	0.245*	0.005	0.227*	0.176	0.077	0.261**	1	
GC	G	0.338*	0.222	0.159	0.326*	0.203	0.15	0.193	0.012	0.084	0.271	1
	P	0.327**	0.201	0.155	0.319**	0.192	0.148	0.186	0.011	0.078	0.25	1

G= Genotypic, P=Phenotypic correlation. *, ** Significant at 5% and 1% respectively.

These results underscore the potential utility of strongly correlated traits for simultaneous improvement of yield and grain quality in breeding programs. By leveraging these associations, breeders can effectively select genotypes with enhanced performance in both domains.

Discussion

Rice is a staple food crop grown globally and holds high nutritional value in the human diet. Many breeders have contributed to enhancing the genetic variability in rice cultivars.¹⁸ Grain yield is a primary objective for many plant breeders in developing new rice varieties, but grain quality traits are also prioritized in certain regions for the acceptance of cultivars on a large scale.¹⁹ The best strategy for improving rice cultivars is to focus on a combination of traits preferred by farmers.²⁰ Considering these points, the present experiment evaluated local rice landraces to assess the magnitude of genetic variation and genetic relationships between these local landraces for grain yield and quality traits.

To identify desirable traits for trait modeling, it is essential for plant breeders to analyze the genetic variation within existing populations. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are typically categorized as high (>20%), medium (10–20%), or low (<10%). In this study, both yield and grain quality traits exhibited higher PCV values compared to GCV, highlighting the significant influence of environmental factors on trait expression.^{21,22}

High genotypic and phenotypic variability was evident in traits such as NOT, TNGPP, NOP, NOFG, GYPP, and TW. Similarly, grain quality traits, including AC, GT, and GC, also demonstrated notable genetic and environmental variation. Traits with high to moderate GCV and PCV values indicate substantial genetic variability, making them ideal candidates for improvement through direct selection methods. Conversely, traits with low variability may not respond effectively to selection. Findings consistent with this study have been reported in prior research.²³⁻²⁵

The analysis of heritability in this study provides valuable insights for identifying genotypes from a broad genetic pool. High heritability (>60%) was observed for all yield and grain quality traits, except for certain traits related to NOT and NOP. This indicates a strong correlation between phenotypic and genotypic values, with minimal environmental influence on the expression of these traits. Thus, selection for these traits is likely to be effective, as polygenic control governs the high heritability traits.²⁶ This information can aid plant breeders in making more informed decisions. The low heritability observed for certain traits may be attributed to factors such as geographical location, plant materials, and test design, as reported in previous studies.²⁷⁻²⁹

High heritability, coupled with a high genetic advance percentage, was observed for all grain quality traits, while among yield-related traits, significant findings were noted for PH, NOP, TNGPP, NOFG, GYPP, and TW. These traits are predominantly governed by additive gene action, suggesting that simple selection methods may effectively improve these traits.^{30,31} Correlation analysis revealed a significant positive association between GYPP and both NOT and NOP at both the genotypic and phenotypic levels. Among the grain quality parameters, 27 significant positive correlations and 4 significant negative correlations were observed. These findings align with similar studies in the field.³²⁻³⁵ This study underscores the potential for selection of high heritability traits to drive improvements in GYPP and grain quality, providing a framework for further breeding efforts.

Conclusions

The present study revealed substantial variability across all observed characteristics, highlighting considerable genetic diversity among the genotypes. High heritability, coupled with significant genetic advance, was observed for grain quality traits. Similarly, among yield-related traits, PH, NOP, TNGPP, NOFG, GYPP, and TW demonstrated both high heritability and genetic advance. These findings indicate that these traits are primarily governed by additive gene action, suggesting that simple and effective selection methods could be employed to

enhance them. Furthermore, correlation analysis revealed a strong positive association between GYPP and both NOT and NOP, observed consistently at genotypic and phenotypic levels. This study underscores the potential for leveraging high heritability and additive gene action in breeding programs to achieve genetic improvements in yield and grain quality.

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Conflict of Interest

The authors do not have any conflict of interest.

Data Availability Statement

The data presented in this study are available on request from the corresponding author.

Ethics Statement

This research did not involve human participants, animal subjects, or any material that requires ethical approval.

Author Contributions

- **H. Lalrindiki:** Data Collection, Analysis, Writing – Review & Editing.
- **Kigwe Seyie:** Conceptualization, Methodology, Writing – Original Draft.
- **Harendra Verma:** Visualization, Supervision, Project Administration.
- **D. Purushotama Rao:** Data Collection and Analysis.
- **H. P. Chaturvedi:** Conceptualization, Methodology, Writing – Original Draft

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