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RESEARCH ARTICLE

Performance assessment of released quality protein maize hybrids in India based on correlation, regression and hybrid performance index

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Abstract

The present study evaluated the relationships among grain yield, protein, lysine, and tryptophan contents in released Quality Protein Maize (QPM) hybrids using regression analysis, scatter plots, and correlation heat mapping. The results revealed predominantly positive linear associations among the studied traits, while grain yield showed weak correlations with nutritional quality attributes, indicating the feasibility of improving productivity and nutritional quality independently. Notably, lysine and tryptophan exhibited the strongest positive correlation (r = 0.615), suggesting a coordinated improvement of these essential amino acids associated with the opaque2 gene and its modifier genes. Regression analysis further indicated that grain yield explained only a limited proportion of the variation in nutritional traits, supporting the possibility of simultaneous improvement of yield and protein quality through appropriate breeding strategies. The comprehensive Hybrid Performance Index (HPI) identified JHQPM-16, JHQPM-20, and Pusa hybrids among the superior performers, demonstrating a desirable balance between high grain yield and enhanced nutritional quality. These findings emphasize the potential of integrated breeding approaches, for developing high-yielding and nutritionally superior QPM hybrids, thereby contributing to both food security and nutritional security objectives. Such efforts can strengthen the role of biofortified maize in addressing protein malnutrition while maintaining agronomic productivity.

Keywords: Quality Protein Maize (QPM), grain yield, protein, lysine, tryptophan, regression analysis

Introduction

Maize (*Zea mays* L.) is one of the world's most important cereal crops and serves as a staple food, livestock feed, and industrial raw material owing to its high productivity, wide adaptability, and diverse end uses. Globally, maize contributes substantially to food and nutritional security, while in India it ranks third among cereal crops after rice and wheat in terms of area and production. Besides its economic importance, maize plays a critical role in supporting the poultry, dairy, starch, ethanol, and food processing industries (Shiferaw *et al.,* 2011). Although conventional maize grain contains approximately 8–12% protein, its nutritional quality is inherently poor because nearly 60–70% of the endosperm protein consists of zeins, which are deficient in the essential amino acids lysine and tryptophan (Mertz *et al.,* 1964; Prasanna *et al.,* 2001). Since these amino acids cannot be synthesised by humans and monogastric animals, populations that rely heavily on maize-based diets are vulnerable to protein-energy malnutrition and micronutrient deficiencies, particularly in developing countries (Vasal, 2000; Krivanek *et al.,* 2007). A major milestone in maize nutritional improvement was the discovery of the naturally occurring opaque2 (o2) mutation by Mertz *et al.,* (1964), which significantly enhanced the lysine and tryptophan content of maize endosperm by reducing the synthesis of zein storage proteins and increasing nutritionally superior non-zein proteins. However, the original opaque2 mutants possessed undesirable agronomic characteristics, including soft and chalky kernels, poor grain appearance, susceptibility to storage pests, and reduced yield, thereby limiting their commercial utilization (Bjarnason and Vasal, 1992). Through intensive breeding efforts at the International Maize and Wheat Improvement Center (CIMMYT), modifier genes were successfully incorporated into the opaque2 background, restoring kernel hardness while maintaining enhanced amino acid composition. This led to the development of Quality Protein Maize (QPM), which combines superior nutritional quality with desirable agronomic performance and competitive grain yield (Vasal, 2000; Pixley and Bjarnason, 2002). Quality Protein Maize has emerged as one of the most successful examples of nutritional biofortification in cereal crops. Compared with conventional maize, QPM contains nearly twice the concentration of lysine and tryptophan while maintaining kernel hardness, desirable grain characteristics, and yield potential comparable to normal maize (Prasanna *et al.,* 2001). Consequently, QPM has been widely recognized as an effective and sustainable strategy for alleviating protein malnutrition in populations where maize constitutes a major component of the diet (Krivanek *et al.,* 2007). Recent advances in conventional breeding, marker-assisted selection, and genomic-assisted breeding have further accelerated the development of improved QPM hybrids possessing enhanced nutritional quality, high grain yield, and broad adaptation (Gupta *et al.,* 2013; Hossain *et al.,* 2018; Muthusamy *et al.,* 2020). In India, the Indian Council of Agricultural Research (ICAR), through the Indian Institute of Maize Research (IIMR), the All India Coordinated Research Project (AICRP) on Maize, the Indian Agricultural Research Institute (IARI), and several State Agricultural Universities has developed and released numerous QPM hybrids adapted to diverse agro-climatic regions of India. Hybrids such as HQPM-1, HQPM-5, HQPM-7, Vivek QPM-9, Pusa HM and Pusa HQPM improved series, JHQPM hybrids, APQH hybrids, and the Shaktiman series, and many more recently released have substantially improved both grain yield and protein quality, contributing to food and nutritional security in India (Gupta *et al.,* 2013; Hossain et al., 2018; Muthusamy *et al.,* 2020; ICAR-IIMR, 2025). Grain yield, protein content, lysine concentration, and tryptophan

concentration are the principal traits used to evaluate the breeding success of QPM hybrids. While protein content reflects the total accumulation of grain protein, lysine and tryptophan serve as reliable indicators of protein quality and biological value. Simultaneous improvement of these nutritional traits together with grain yield remains a primary objective of modern maize breeding programmes because these traits collectively determine the agronomic performance and nutritional superiority of QPM hybrids (Prasanna *et al.,* 2001; Vivek *et al.,* 2008; Prasanna *et al.,* 2020). Despite the release of numerous QPM hybrids in India over the past two decades, comparative information on their grain yield, protein, lysine, and tryptophan contents remains scattered across peer-reviewed journal articles, institutional reports, AICRP on Maize annual reports, technical bulletins, and other scientific publications. Consequently, breeders, researchers, and policy makers lack a comprehensive assessment of the relative performance of released hybrids, the relationships among agronomic and nutritional traits, and the identification of consistently superior genotypes across studies. Furthermore, no comprehensive quantitative synthesis has integrated these dispersed datasets to evaluate the overall performance of released Indian QPM hybrids. The period from 2000 to 2026 represents the major phase of QPM hybrid development and commercialization in India and provides sufficient published information for a comprehensive meta-analysis. A quantitative meta-analysis offers a robust approach to synthesize results from independent studies, improve the precision of trait estimates, compare hybrid performance across diverse environments, and identify superior genetic resources. In addition, descriptive statistics, correlation and regression analyses facilitate understanding of the relationships among grain yield, protein, lysine, and tryptophan, while a multi-trait Hybrid Performance Index (HPI) provides an integrated measure of agronomic and nutritional superiority. Such an approach enables objective ranking of released hybrids and supports evidence-based decisions for parent selection, cultivar recommendation, and future QPM breeding programmes aimed at simultaneously improving productivity and nutritional quality. Therefore, the present study was undertaken to: (i) compile and standardize published information on grain yield, protein, lysine, and tryptophan contents of released Indian QPM hybrids; (ii) quantify variation in agronomic and nutritional traits using descriptive statistics; (iii) examine the relationships among grain yield and nutritional quality traits through correlation and regression analyses; (iv) rank released hybrids using a multi-trait Hybrid Performance Index (HPI); and (v) identify high-yielding and nutritionally superior QPM hybrids that can serve as valuable genetic resources for future breeding programmes, commercial cultivation, and nutritional security initiatives.

Materials and methods

Literature search and data compilation

Published information on released Quality Protein Maize (QPM) hybrids in India was compiled through a comprehensive literature survey covering the period from 2000 to 2026. Data were collected from peer-reviewed research articles, ICAR–Indian Institute of Maize Research (IIMR) publications, All India Coordinated Research Project (AICRP) on Maize annual reports, biofortified crop release documents, technical bulletins, and other authentic scientific publications. Only released QPM hybrids for which information on one or more of the target traits was available were included in the analysis. For each hybrid, information was extracted on grain yield (q ha^{-1}), protein content (%), lysine (%), tryptophan (%), year of release /publication,

testing location or state, source of information, and check variety whenever reported. The compiled dataset comprised 28 released QPM hybrids representing diverse agro-climatic regions of India (Table 1).

Data standardization and statistical analysis

Published reports frequently expressed grain yield, protein, lysine, and tryptophan as single values or value ranges. To obtain a single representative observation for each hybrid, range values were converted to their arithmetic midpoint using the following equation:

$$\text{Midpoint}=\frac{\text{Minimum value}+\text{Maximum value}}{2}$$

The midpoint values were considered representative estimates of hybrid performance and were subsequently used for all statistical analyses (Table 2). Traits reported as single values were used without modification. This standardization minimized inconsistencies among studies and enabled uniform comparison across hybrids. Descriptive statistics, including minimum, maximum, mean, range, and standard deviation, were computed separately for grain yield, protein, lysine, and tryptophan to summarize the variability among released QPM hybrids. Pearson's correlation coefficients were calculated to determine the relationships among grain yield, protein, lysine, and tryptophan contents. Scatter plots with fitted simple linear regression lines were generated for all pairwise combinations of the evaluated traits. Regression equations, Pearson's correlation coefficients (r), and coefficients of determination (R^2) were displayed on each graph to facilitate interpretation of the strength and direction of the relationships. A Pearson correlation heat map was constructed to visualize the overall association among the four traits. Correlation coefficients ranged from −1 to +1, where positive values indicated positive associations and negative values indicated inverse relationships.

Hybrid Performance Index (HPI)

An integrated Hybrid Performance Index (HPI) was developed to evaluate the overall performance of released QPM hybrids by simultaneously considering grain yield, protein, lysine, and tryptophan. Hazel LN. 1943 and Smith HF. 1936 starting was used and following formula used:

$$X_i=\frac{x_i-x_{\min}}{x_{\max}-x_{\min}}$$

where x_i is the observed value of a hybrid, and $x_{\min}$ and $x_{\max}$ represent the minimum and maximum values of the respective trait across all hybrids.

The HPI for each hybrid was calculated as the arithmetic mean of the normalized values of the four traits:

$$\mathrm{HPI}=\frac{Y+P+L+T}{4}$$

where:

Y = normalized grain yield,

P = normalized protein content,

L = normalized lysine content,

T = normalized tryptophan content.

The HPI values ranged from 0 to 1, with higher values indicating superior overall performance based on both agronomic productivity and nutritional quality. Based on HPI values, hybrids were classified into five performance categories. Based on the calculated Hybrid Performance Index (HPI), hybrids were classified into five performance categories to facilitate interpretation of their overall agronomic and nutritional performance. Hybrids with an HPI of ≥ 0.60 were categorized as Excellent, those with 0.50–0.59 as Very Good, 0.40–0.49 as Good,

0.30–0.39 as Moderate, and those with < 0.30 as Low. This classification enabled objective ranking of the released QPM hybrids and facilitated the identification of elite genotypes for breeding and commercial cultivation. This classification facilitated the identification of elite hybrids possessing balanced performance across all evaluated traits. All descriptive statistical analyses, correlation analysis, simple linear regression, scatter plots, Pearson correlation heat map, and graphical visualizations were performed using R statistical software (R Foundation for Statistical Computing, Vienna, Austria). Data compilation and preliminary calculations were carried out using Microsoft Excel 2021.

Table 1 : Available information through literature search on hybrid, grain yield q/ha, protein content, tryptophan and few checks available for comparison

Author / Source	Year	State/ Region	Hybrid	Grain yield (q ha^{-1})	Protein (%)	Lysine (%)	Tryptophan (%)	Check variety
Gupta *et al.*,	2013	Uttarakhand	Vivek QPM-9	51–61†	**9.20†**	3.25	0.83	Vivek Hybrid-9
Snehlata *et al.*,	2016	Rajasthan	HQPM-1	42.6	**10.09–11.64†**	3.3-4	0.75-0.94	HQPM-5, Pratap QPM Hybrid-1
Hossain *et al.*,	2018	Delhi	Pusa HM-4 Improved	64.2†	**9–10†**	3.61	0.89	Pusa HM-4
Hossain *et al.*,	2018	Delhi	Pusa HM-8 Improved	62.6	**9–10†**	4.18	1.06	Pusa HM-8
Hossain *et al.*,	2018	Delhi	Pusa HM-9 Improved	52.0	**9–10†**	2.97	0.68	Pusa HM-9
AICRP-IIMR Report	2018–19	Punjab and Delhi	IMHQPM 1530	45–60†	8.96	3.53	0.79	Vivek QPM-9, HQPM-1
AICRP-IIMR Report	2018–19	Punjab & Delhi	QPMMH27	55–60†	9.33	3.51	0.77	Vivek HQPM-1
AICRP-IIMR Report	2018–19	Punjab & Delhi	IIMRQPMH1601	50–80†	8.90	3.04	0.66	Vivek QPM-9, HQPM-1
AICRP-IIMR Report	2018–19	Punjab & Delhi	APQH5	68–75†	8.89	4.25	0.94	HQPM-5
AICRP-IIMR Report	2018–19	Punjab & Delhi	APQH7	65–75†	8.34	4.19	0.93	HQPM-7
Kumar *et al.*,	2020	Multi-location	HQPM-1	42.6†	11.64	2.7-4.5	0.70	HQPM-7
Kumar *et al.*,	2020	Multi-location	HQPM-7	70–85†	10.54	3.3-4	0.84	Commercial QPM check

Author/ Source	Year	State/ Region	Hybrid	Grain yield (q ha^{-1})	Protein (%)	Lysine (%)	Tryptophan (%)	Check variety
Muthusamy *et al.*,	2020	Punjab	JHQPM-16	137.6–148.2	12.50	2.7-4.5	0.97	Buland
Muthusamy *et al.*,	2020	Punjab	JHQPM-20	50–70†	12.42	3.3-4	0.96	Buland
Muthusamy *et al.*,	2020	Punjab	JHQPM-34	50–70†	11.85	2.7-4.5	0.95	PMH-1
Muthusamy *et al.*,	2020	Punjab	JHQPM-35	63.7–64.7	11.69	2.7-4.5	1.01	HQPM-1, HQPM-7
ICAR Biofortified Varieties	2020	Multi-location	Pusa HQPM-7 Improved	74.5	10–11†	4.19	0.93	HQPM-7
ICAR Biofortified varieties	2021	National	Pusa HQPM-1 Improved	50.9–81.9	10–11†	4.59	0.85	HQPM-1
ICAR	2024	NHZ and PZ	Pusa Vivek QPM-9 Improved	55.9–59.2	9–10†	2.67	0.74	Vivek Hybrid-9
IIMR Bulletin	2025	India	HQPM-1	42.6†	10.09	2.7-3.5	0.79	NR
IIMR Bulletin	2025	India	HQPM-4	43–58†	10.30	2.7-4	0.67	NR
IIMR Bulletin	2025	India	HQPM-5	43–58†	10.15	2.7-4.5	0.69	NR
IIMR Bulletin	2025	India	HQPM-7	70–85†	9.80	2.7-4.5	0.72	NR
IIMR Bulletin	2025	India	Vivek QPM-9	51–61†	9.20	3.25	0.70	NR
IIMR Bulletin	2025	India	Shaktiman-1	60–80†	10.62	2.7-3	0.70	NR
IIMR Bulletin	2025	India	Shaktiman-2	65–90†	10.29	2.7-3	0.72	NR
IIMR Bulletin	2025	India	Shaktiman-3	70–75†	9.27	2.7-4	0.70	NR
IIMR Bulletin	2025	India	Shaktiman-4	70–75†	8.86	2.7-4.5	0.67	NR

Note: Values marked with † are approximate literature-based ranges compiled from published reports or related release information because the original source did not report exact grain yield or protein values.

Table 2: Numerical dataset for correlation analysis (midpoint values)

Hybrid	Grain yield (q ha^{-1})	Protein (%)	Lysine (%)	Tryptophan (%)
Vivek QPM-9	56.0	9.20	3.25	0.83
HQPM-1 (2016)	42.6	10.87	3.65	0.85
Pusa HM-4 Improved	64.2	9.50	3.61	0.89
Pusa HM-8 Improved	62.6	9.50	4.18	1.06
Pusa HM-9 Improved	52.0	9.50	2.97	0.68
IMHQPM1530	52.5	8.96	3.53	0.79
QPMMH27	57.5	9.33	3.51	0.77
IIMRQPMH1601	65.0	8.90	3.04	0.66
APQH5	71.5	8.89	4.25	0.94
APQH7	70.0	8.34	4.19	0.93
HQPM-1 (2020)	42.6	11.64	3.60	0.70
HQPM-7	77.5	10.54	3.65	0.84
JHQPM-16	142.9	12.50	3.60	0.97
JHQPM-20	60.0	12.42	3.65	0.96
JHQPM-34	60.0	11.85	3.60	0.95
JHQPM-35	64.2	11.69	3.60	1.01
Pusa HQPM-7 Improved	74.5	10.50	4.19	0.93
Pusa HQPM-1 Improved	66.4	10.50	4.59	0.85
Pusa Vivek QPM-9 Improved	57.6	9.50	2.67	0.74
HQPM-1 (2025)	42.6	10.09	3.10	0.79
HQPM-4	50.5	10.30	3.35	0.67
HQPM-5	50.5	10.15	3.60	0.69
HQPM-7 (2025)	77.5	9.80	3.60	0.72
Vivek QPM-9 (2025)	56.0	9.20	3.25	0.70
Shaktiman-1	70.0	10.62	2.85	0.70
Shaktiman-2	77.5	10.29	2.85	0.72
Shaktiman-3	72.5	9.27	3.35	0.70
Shaktiman-4	72.5	8.86	3.60	0.67

Results and discussion

Regression analysis and scatter plot interpretation among grain yield and nutritional quality traits

Simple linear regression analysis was performed to evaluate the relationships among grain yield, protein, lysine, and tryptophan contents of released Quality Protein Maize (QPM) hybrids. Scatter plots with fitted linear regression lines are presented in Fig. 1–6 and 1a-6a, with the corresponding regression equations, Pearson's correlation coefficients (r), and coefficients of determination (R^2) displayed on each graph. The regression analyses revealed predominantly positive linear relationships among the evaluated traits, although the strength of association varied considerably. The regression analyses involving grain yield showed positive regression slopes for protein, lysine, and tryptophan. However, the comparatively low R^2 values indicate that grain yield explained only a small proportion of the variation in these nutritional traits. These result suggest that grain productivity is largely independent of protein and essential amino acid contents, indicating that improvements in grain nutritional quality can be achieved without substantial reductions in yield. positive regression slopes for protein, lysine, and tryptophan.

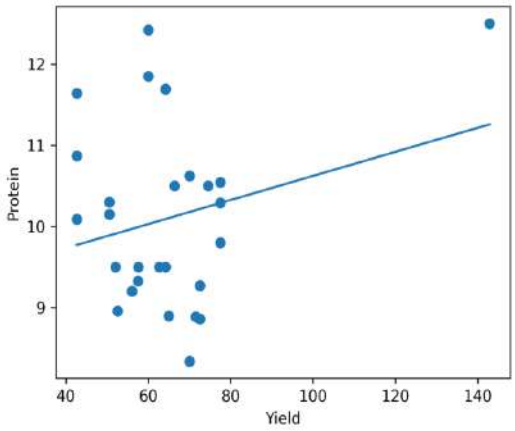
Correlation analysis among grain yield and nutritional quality traits

However, the comparatively low R^2 values indicate that grain yield explained only a small proportion of the variation in these nutritional traits. These results suggest that grain productivity is largely independent of protein and essential amino acid contents, indicating that improvements in grain nutritional quality can be achieved without substantial reductions in yield. Similar observations have been reported in QPM breeding programmes, where improvement in lysine and tryptophan has been achieved while maintaining competitive grain yield through conventional and marker-assisted breeding approaches (Maqbool *et al.*, 2021; Tufchi *et al.*, 2021). The regression between protein and lysine exhibited an almost flat trend with a very low R^2 value, indicating little or no linear relationship between these traits. This finding suggests that total protein concentration alone is not a reliable predictor of lysine content and highlights the importance of direct selection for lysine in Quality Protein Maize breeding programmes. The nutritional superiority of QPM is primarily attributed to alterations in protein composition caused by the opaque2 gene rather than to increases in total protein content (Maqbool *et al.*, 2021; Singh *et al.*, 2020). In contrast, the regression between protein and tryptophan (Figure 5) showed a moderate positive trend, indicating that hybrids with relatively higher protein content generally tended to possess higher tryptophan concentrations. Although the association was moderate, the positive regression trend suggests that simultaneous improvement of these nutritional attributes is achievable through appropriate breeding strategies, particularly when combined with marker-assisted selection (Maqbool *et al.*, 2021). The strongest linear relationship was observed between lysine and tryptophan, which exhibited the highest R^2 value among all trait combinations. This result demonstrates that improvement in lysine content is generally accompanied by a corresponding increase in tryptophan concentration, reflecting the coordinated enhancement of these essential amino acids in QPM germplasm. This coordinated improvement is a characteristic feature of Quality Protein Maize and is primarily governed by the opaque2 gene together with endosperm modifier genes that enhance protein quality while maintaining desirable kernel characteristics (Maqbool *et al.*, 2021; Tufchi *et al.*, 2021). Overall, the regression analyses indicate that grain yield is only weakly associated with protein and essential amino acid contents, whereas lysine and tryptophan exhibit a comparatively stronger linear relationship. These findings support the feasibility of simultaneously improving grain yield and nutritional quality, thereby facilitating the development of high-yielding QPM hybrids with enhanced protein quality, which remains a major objective of contemporary QPM breeding programmes (Maqbool *et al.*, 2021).

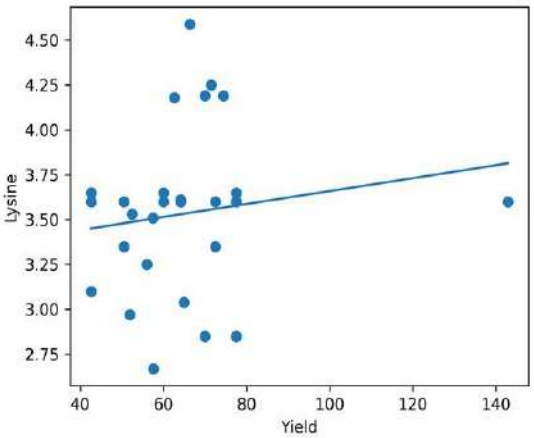
Figure 7 presents the Pearson correlation heat map illustrating the relationships among grain yield, protein, lysine, and tryptophan contents of released Quality Protein Maize (QPM) hybrids. Overall, the heat map revealed predominantly positive associations among the evaluated agronomic and nutritional traits, indicating that improvement of nutritional quality can be achieved without substantially compromising grain productivity. Pearson's correlation analysis showed that grain yield exhibited weak positive correlations with protein ($r = 0.247$), lysine ($r = 0.148$), and tryptophan ($r = 0.297$), suggesting that yield achieved without compromising grain yield through conventional and marker-assisted breeding approaches (Maqbool *et al.*, 2021). Protein content showed a negligible correlation with lysine ($r = 0.046$), indicating that total protein concentration alone is not a reliable indicator of lysine accumulation.

Fig1-6: Scatter plot interpretation among grain yield and nutritional quality traits

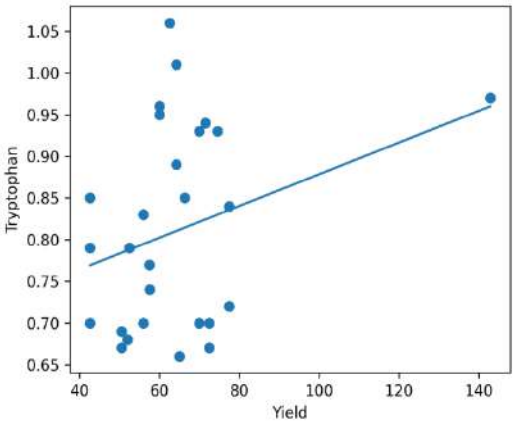
1 Grain yield vs Protein



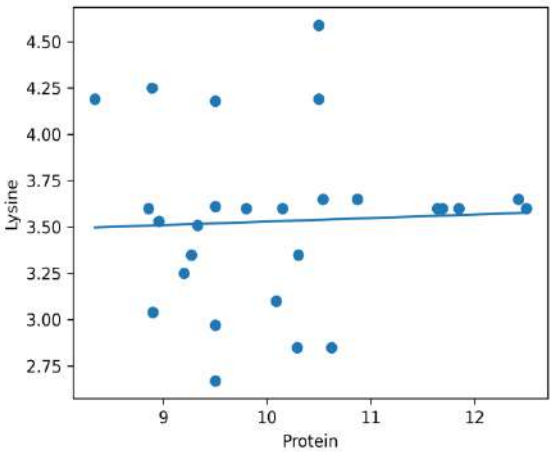
2 Grain yield vs Lysine



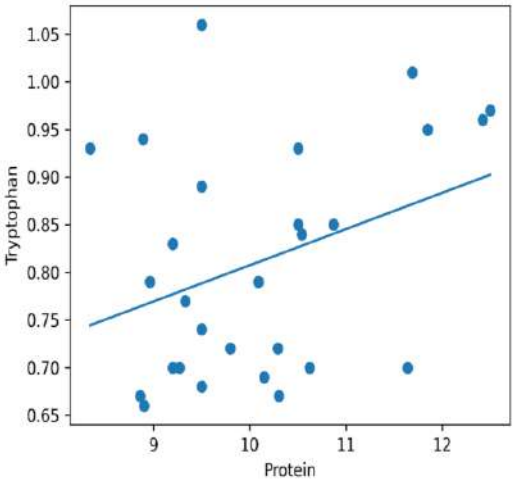
3 Grain yield vs Tryptophan



4 Protein vs Lysine



5 Protein vs Tryptophan



6 Lysine vs Tryptophan

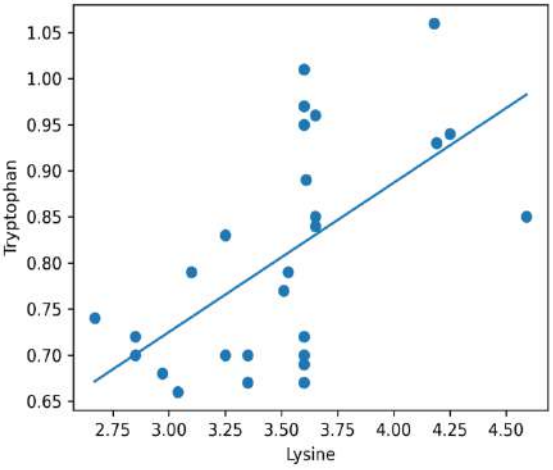
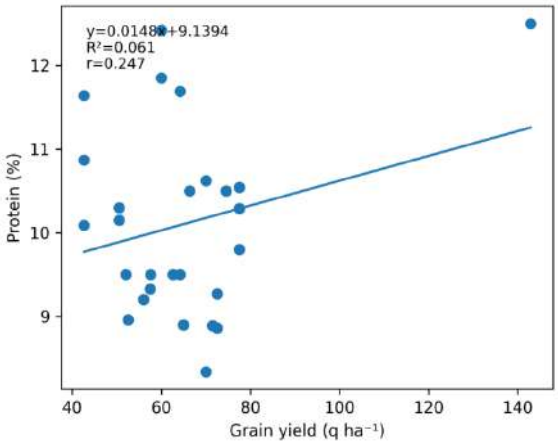
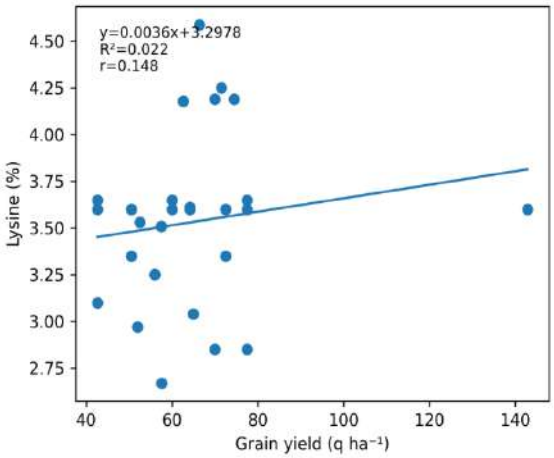


Fig. 1a-6a representing linear regression equation, Pearson's correlation coefficient (r), and coefficient of determination (R^2) displayed directly on each graph

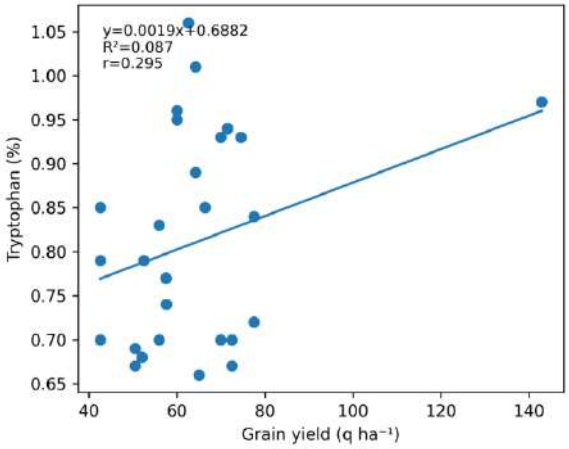
1a Grain yield vs Protein



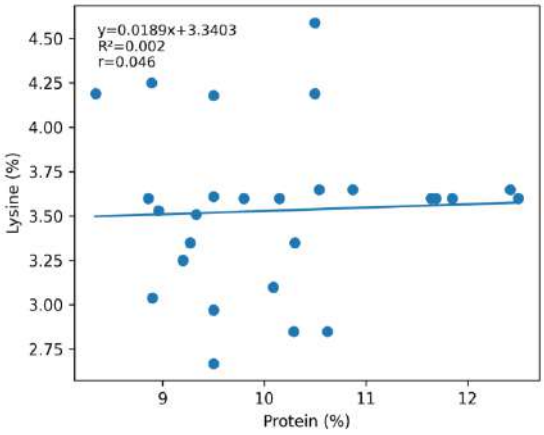
2 Grain yield vs Lysine



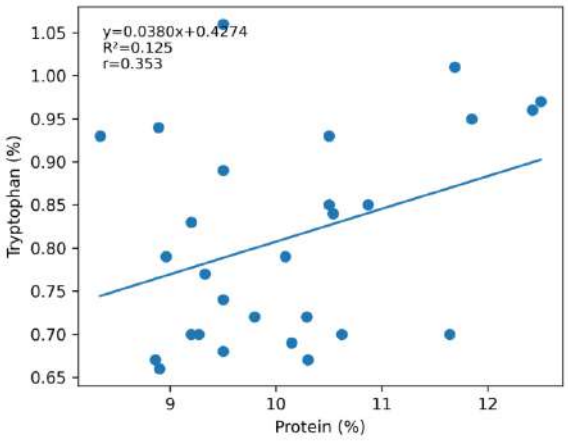
3a Grain yield vs Tryptophan



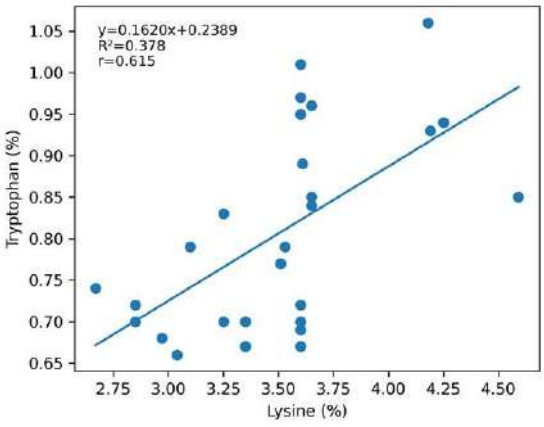
4a Protein vs Lysine



5aProtein vs Tryptophan

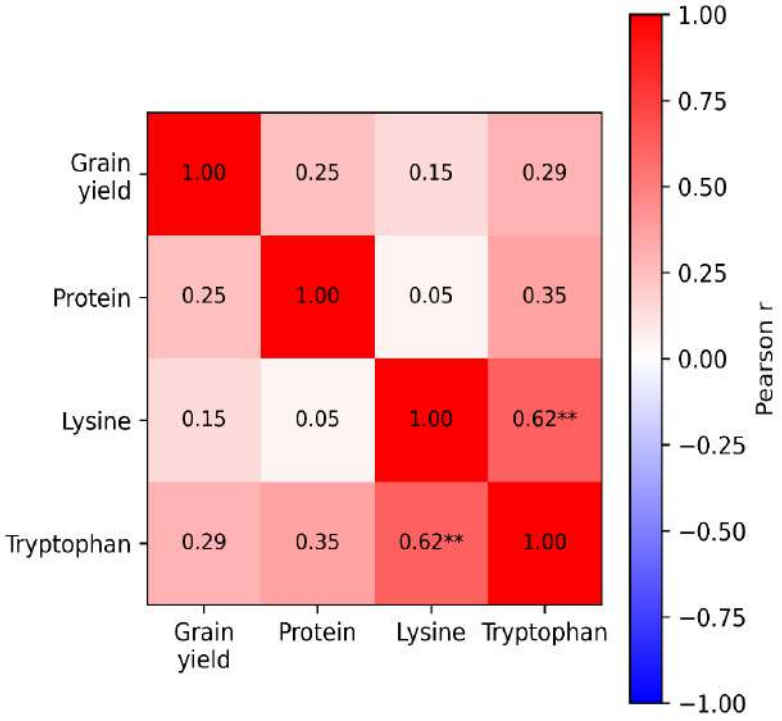


6aLysine vs Tryptophan



This finding is consistent with the genetic basis of QPM, in which improved protein quality results primarily from changes in the composition of storage proteins mediated by the opaque2 gene and associated endosperm modifier genes, rather than from increases in total protein content (Maqbool *et al.*, 2021).

Figure 7: Pearson correlation heat map showing the relationships among grain yield, protein, lysine, and tryptophan contents of released Quality Protein Maize (QPM) hybrids.. The color scale represents Pearson's correlation coefficient (r), ranging from −1 (strong negative correlation) to +1 (strong positive correlation). Numerical values within each cell indicate the corresponding correlation coefficients



In contrast, protein exhibited a moderate positive association with tryptophan (r = 0.352), suggesting that hybrids with higher protein content generally tended to possess higher tryptophan concentrations. This positive relationship indicates that improvement of protein concentration may be accompanied by enhanced tryptophan content in selected QPM germplasm, although the association remains moderate. The strongest positive relationship was observed between lysine and tryptophan (r = 0.615), demonstrating the coordinated enhancement of these essential amino acids, a characteristic feature of QPM germplasm. This strong association reflects the pleiotropic effects of the opaque2 gene and its modifier genes, which simultaneously increase the concentrations of lysine and tryptophan while maintaining acceptable kernel characteristics (Maqbool *et al.*, 2021). Overall, the positive correlation pattern observed among grain yield and nutritional traits suggests that concurrent improvement of grain yield, protein quality, and essential amino acid composition is feasible in QPM breeding programmes. These findings support the continued use of integrated breeding strategies to develop high

yielding QPM hybrids with superior nutritional quality for enhanced food and nutritional security (Maqbool *et al.,* 2021).

Hybrid performance index (HPI) of released quality protein maize hybrids

The Hybrid Performance Index (HPI) integrated grain yield, protein, lysine, and tryptophan into a single selection criterion, providing a comprehensive assessment of the overall performance of released Quality Protein Maize (QPM) hybrids. The HPI values ranged from 0.243 to 0.815, indicating considerable variation among the evaluated hybrids for combined agronomic and nutritional performance (Table 3). Integrating multiple agronomic and nutritional traits into a single selection index enables more effective identification of superior genotypes than selection based on individual traits alone (Smith, 1936; Hazel, 1943). Among the 28 hybrids, JHQPM-16 achieved the highest HPI (0.815), indicating outstanding overall performance resulting from its exceptionally high grain yield (142.9 q ha^{-1}), highest protein content (12.50%), and superior tryptophan concentration (0.97%). JHQPM-20 (0.604) and JHQPM-35 (0.595) ranked second and third, respectively, demonstrating balanced performance for grain yield and nutritional quality. Improved hybrids developed through marker-assisted breeding, including Pusa HQPM-7 Improved (0.576), Pusa HM-8 Improved (0.566), and Pusa HQPM-1 Improved (0.558), also ranked among the top-performing entries because of their superior lysine and tryptophan contents combined with competitive grain yields. The superior performance of these improved hybrids reflects the successful application of marker-assisted breeding for introgression of the opaque2 gene while maintaining high yield potential and desirable agronomic characteristics (Maqbool *et al.,* 2021; Muthusamy *et al.,* 2020). Among the released commercial hybrids, APQH5, HQPM-7, and APQH7 recorded moderate to high HPI values, suggesting that they possess favourable combinations of productivity and nutritional quality. In contrast, Shaktiman-4, Pusa Vivek QPM-9 Improved, and Vivek QPM-9 (2025) exhibited comparatively lower HPI values, primarily because of lower protein and essential amino acid contents despite acceptable grain yield. These results indicate that high grain yield alone is insufficient to achieve superior overall performance when nutritional quality traits are simultaneously considered. The HPI analysis demonstrated that superior hybrids were characterized by balanced performance across all four traits rather than by excellence in a single characteristic. Although some hybrids recorded high grain yield, their overall ranking declined because of lower nutritional quality, whereas hybrids combining moderate-to-high yield with enhanced protein, lysine, and tryptophan consistently achieved higher HPI values. This finding emphasizes the importance of simultaneous selection for agronomic performance and nutritional quality, which is a major objective of modern QPM breeding programmes aimed at developing nutritionally superior maize cultivars without sacrificing yield (Prasanna *et al.,* 2001; Maqbool et al., 2021). Overall, the HPI identified JHQPM-16, JHQPM-20, JHQPM-35, Pusa HQPM-7 Improved, Pusa HM-8 Improved, and Pusa HQPM-1 Improved as the most promising hybrids for future breeding and commercial cultivation. These hybrids represent valuable genetic resources for developing next-generation biofortified maize cultivars with enhanced productivity and improved protein quality, thereby contributing to nutritional security and sustainable maize improvement programmes, which remain the primary goals of Quality Protein Maize improvement worldwide (Prasanna *et al.*, 2001; Maqbool *et al.*, 2021).

Table3: Hybrid Performance Index (HPI) and performance category of released QPM hybrids

Rank	Hybrid	HPI	Performance Category
1	JHQPM-16	0.81	Excellent
2	JHQPM-20	0.60	Excellent
3	JHQPM-35	0.59	Very Good
4	Pusa HQPM-7 Improved	0.57	Very Good
5	Pusa HM-8 Improved	0.56	Very Good
6	Pusa HQPM-1 Improved	0.55	Very Good
7	JHQPM-34	0.55	Very Good
8	APQH5	0.48	Good
9	HQPM-7	0.45	Good
10	APQH7	0.43	Good
11	Pusa HM-4 Improved	0.42	Good
12	Shaktiman-2	0.42	Good
13	Shaktiman-1	0.40	Good
14	Pusa HM-9 Improved	0.37	Moderate
15	HQPM-1 (2016)	0.36	Moderate
16	QPMMH27	0.36	Moderate
17	HQPM-1 (2020)	0.35	Moderate
18	Vivek QPM-9	0.35	Moderate
19	Shaktiman-3	0.34	Moderate
20	IIMRQPMH1601	0.33	Moderate
21	HQPM-7 (2025)	0.32	Moderate
22	IMHQPM1530	0.32	Moderate
23	HQPM-5	0.32	Moderate
24	HQPM-4	0.30	Moderate
25	HQPM-1 (2025)	0.29	Low
26	Vivek QPM-9 (2025)	0.26	Low
27	Pusa Vivek QPM-9 Improved	0.25	Low
28	Shaktiman-4	0.24	Low

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