

RESEARCH ARTICLE

Exploring Maize (*Zea mays* L.) Landraces: Characterization for Yield and Quality Traits to Foster Genetic Improvement

Heena Sharma¹, Surinder Sandhu^{1*}, Gagandeep Kaur¹ and RK Bhavyasree²

Abstract

Maize (*Zea mays* L.) landraces, meticulously selected and preserved by farmers over generations, represent invaluable reservoirs of genetic diversity, providing enhanced adaptability, superior quality traits, and resilience against various stresses. This study harnessed the genetic potential of these traditional resources by collecting and evaluating 27 landraces, farmers' varieties, and cultivars from diverse agro-climatic regions. Key nutritional parameters, including protein, starch, and micronutrient content, as well as critical yield-related traits, were evaluated. The analysis revealed significant variation in grain colour, size, and nutritional composition, particularly for methionine, tryptophan, protein, starch, and β -carotene. Notable lines included HP Selection Kangra, Yellow op2 Composite, White op2 Composite, Kailer Solan, and Local 3, which exhibited superior levels of methionine (0.17%), tryptophan (0.052%), protein (11.95%), starch (69.62%), and β -carotene (6.24 ppm), respectively. Grain yield variability ranged from 0.42 to 4.78 t/ha, with significant differences observed in kernels per row (20–36) and thousand-kernel weight (139.80–359.83 g). Outstanding performers included JC 1455-1 for the highest grain yield (4.78 t/ha), Nadaun Selection for thousand-kernel weight (359.83 g), and JC 4 for kernels per row (36). These findings highlight the critical role of maize landraces as unique genetic resources for enhancing genetic diversity and trait improvement. The promising lines identified in this study offer a foundation for future genetic enhancement efforts, focusing on broadening the genetic base of maize and developing nutritionally enriched, high-yielding cultivars suited to diverse agro-ecologies.

Keywords: Farmers' varieties, Maize landraces, Nutritional traits, Yield traits

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Introduction

Maize (*Zea mays* L., $2n=20$) is the world's most widely distributed crop and one of the major and popular cereals grown worldwide as food, feed and biofuel (Tahir *et al.*, 2023). Maize has coevolved with human culture and exceeds all other cereals in its ability to adapt to varied agro-ecological conditions and is hence designated as the queen of cereals. Being inherently gluten-free, maize also presents an attractive option for developing alternative food sources. With its higher content of carbohydrates, fats, proteins and some of the important vitamins and minerals, the crop has acquired a well-deserved status as a poor man's 'nutricereal'. Moreover, maize is extensively used as poultry and animal feed because of its high energy value, nutrition and palatability. It is considered a major supplement and energy source of an animal's diet, contributing up to 30% protein, 90% starch and 60% of the energy requirements (Dado *et al.*, 1999). Approximately 13.8% of maize produced is utilized for food purposes, while around 61.2% is allocated for livestock and poultry feed, 4.7% is utilized for processing, 0.7% is dedicated to seed purposes, and 19.6% share is worldwide (Erenstein *et al.*, 2022).

Generally, maize endosperm is mainly composed of 70% starch, 8–10% protein (Lawton and Wilson, 1987; Prasanna *et al.*, 2020; Sharma *et al.*, 2024), providing 365 kcal of energy per 100 g (Nuss and Tanunihardjo, 2010). The protein in its endosperm is of two types *i.e.*, zeins and non-zeins. Zein (prolamin, prolamin-like protein), is the major seed storage protein of maize kernel that constitutes approximately 50–70% of kernel endosperm, whereas non-zein protein consists of globulins (3%), glutelins (34%), and albumins (3%). Maize grain protein is nutritionally imbalanced due to a deficiency of the essential amino acids such as methionine (Met), lysine (Lys), tryptophan (Try) and threonine (Thr) in the zein fraction (Holding, 2014). The average levels of three essential amino acids in grain maize *viz.*, Met (0.15%), Lys (0.019%), and Try (0.043%) are notably low (Fontaine *et al.*, 2002). The concentrations of these amino acids are more crucial than the total protein content in animal feed formulations. Therefore, nutritionally balanced maize is vital, as the majority of the maize produced is utilized for food and feed.

Maize was domesticated in Mesoamerica approximately 9,000 years ago from wild teosinte. As maize cultivation spread globally, diverse landraces, traditional, locally adapted varieties emerged through adaptation to varied environmental conditions and human preferences. Over time, breeders began selecting and stabilizing specific landraces or breeding lines to create open-pollinated varieties (OPVs). The development of OPVs involved further selection for desired characteristics such as yield, disease resistance, and regional adaptation. This process often involved selecting from a subset of available landrace diversity, thereby reducing overall genetic variation.

The transition from OPVs to hybrid maize varieties, particularly in the mid-20th century, marked a significant shift in maize breeding. While hybrids exhibit superior yield potential and other desirable traits, they are typically derived from a limited number of elite inbred lines selected for specific traits. This reliance on a narrow genetic base can lead to reduced diversity within commercial maize crops. Collectively, the processes of domestication, landrace formation, development of OPVs, and adoption of hybrids have contributed to a reduction in genetic diversity within cultivated maize populations.

The narrowing of genetic diversity in cultivated maize underscores the importance of conserving and utilizing diverse genetic resources, including landraces, wild relatives, and heirloom varieties, to broaden the genetic base of modern maize cultivars. The

characterization of maize landrace for both nutritional quality and yield-related traits is essential for understanding the genetic diversity and agricultural potential of these traditional varieties. Maize landraces, cultivated over generations by local farmers, represent a rich reservoir of genetic variability that offers unique advantages in terms of nutritional value, resilience to environmental stresses, and overall crop productivity. These landraces often exhibit a wide range of nutritional profiles, including variations in protein content, amino acid composition, essential fatty acids, vitamins, and minerals. This diversity can address specific dietary needs and combat malnutrition in various regions. Yield-related traits are crucial for determining the overall productivity and economic viability of the crop. The genetic diversity present in maize landraces for yield-related traits and nutritional parameters makes them a valuable resource for plant breeders and researchers. This diversity provides a pool of genes that can be used to develop new maize varieties with improved traits. By studying and preserving this genetic variability, scientists can identify lines with desirable characteristics and use them in breeding programs.

The study involves the exploration on collection of maize germplasm, 17 traditional varieties/landraces were collected from Bharmor, Chobiya, Tunda Valley, and Salooni in Chamba, and Chameti and Kandaghat in Solan district. Additionally, 20 landraces were obtained from the Kangra and Una districts of Himachal Pradesh. Two composites (White op2 composite and Yellow op2 composite) were obtained from Eternal University, Baru Sahib, Himachal Pradesh.

Himachal Pradesh is known for cultivating traditional maize landraces. Maize has been grown here for centuries, with farming practices passed down through generations. The Northwestern Himalayan regions and the foothills of Himachal Pradesh are home to a rich diversity of maize landraces due to suitable agro-climatic conditions. Two OPVs, More110 and Braz 1844, were acquired from CIMMYT, Mexico, the centre of origin for maize, known for its diverse landraces. These two landraces were modified in our local conditions using mass selection. Fifteen lines were collected from the rainfed area, designated as *Kandi* belt of Ropar, Hoshiarpur, and SBS Nagar districts of Punjab.

The *Kandi* belt, a sub-mountainous area near the Shivalik foothills, possesses diverse maize landraces, spanning a 6–8 kilometre belt along the Himachal Pradesh border. Most parts of Hoshiarpur and Pathankot districts and some parts of Ropar,

Nawanshahr, and Mohali districts lie in the *Kandi* belt of Punjab. The primary objective of our research was to collect diverse traditional varieties, cultivars and landraces from the hilly and rainfed regions, to meticulously characterize them, and to comprehensively profile them for their nutritional attributes and yield and their contributing related traits. This involved detailed phenotypic and biochemical-nutritional analyses to evaluate their potential for enhancing the genetic diversity and resilience of maize cultivars, ultimately aiming to improve both the quality and productivity of maize in varied agro-climatic conditions.

Materials and methods

Plant material and field experimentation

A total of 54 landrace/farmers' varieties were collected from different locations of Himachal Pradesh, *Kandi* area of Punjab and CIMMYT during 2020-21. For two to three cycles, these populations were subjected to mass selection at Punjab Agricultural University (PAU), Ludhiana and the seed was multiplied. Twenty seven landrace and farmers' varieties that exhibited complete purity were utilized as experimental material in our study (Fig. 1).

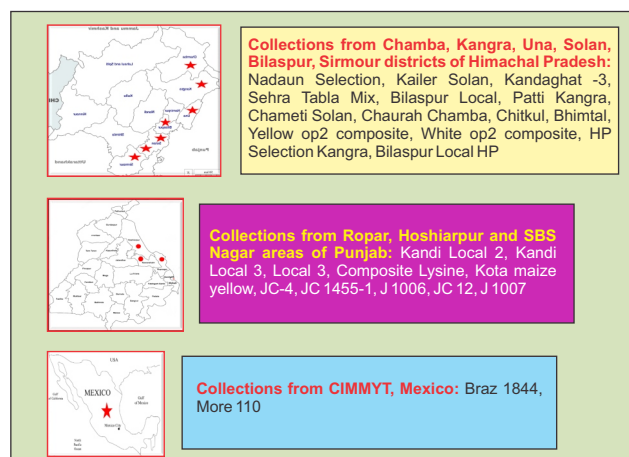


Fig. 1: The test material used for the study and its collection sites.

The test material was evaluated during rainy (*khariif*) season 2022 in alpha lattice design at two locations *i.e.*, Maize Experimental Area, PAU, Ludhiana (30° 54' 14.886"N, 75° 49' 0.4836 "E) representing the central plain zone of Punjab and PAU Regional Research Station, Gurdaspur (32° 2' 30.9948" N and 75° 24' 19.2024" E) representing the Sub-Mountain undulating zone of Punjab. The material was sown manually through the dibbling method, adhering to standard

agronomic practices at row to row and plant to plant spacing of 60 cm and 20 cm, respectively. For biochemical analysis, each entry was grown in a two-row plot, separately planted adjacent to the main plot and was self-pollinated to raise pure seed. The test material was maintained by pollinating them with their bulk pollen from at least 500 plants.

Evaluation of yield and contributing traits

For evaluation of yield and its contributing traits, the crop was harvested at physiological maturity (>70% of husk cover dried). Observations were recorded for grain yield (GY), thousand kernel weight (TKW) and number of kernels per row (K/R). For calculating the GY, the cobs/plot were harvested manually, sun-dried and shelled manually. Grain weight in kg/plot was converted to yield tons per hectare (t/ha) at 15% moisture. TKW was obtained by manually counting 1000 kernels from the shelled sample of the line and was weighted in grams (g) on an electronic weighing balance with 0.01g accuracy. K/R was calculated by counting the number of kernels in each row of 10 cobs/plot, and then the average was recorded as the number of kernels per row.

Evaluation of quality traits

The test material was evaluated for quality traits, Met, Typ, starch, protein, and β -carotene content. Met estimation followed the method outlined by Horn *et al.*, (1946), while Typ was determined using the method by Hernandez and Bates (1969). The micro-Kjeldahl method, a well-established analytical technique documented in AOAC (1975), was employed to estimate the protein content of the landraces. Total starch content was calculated according to the procedure described by Clegg (1956), and β -carotene was determined using the Rodriguez-Amaya *et al.*, (2004) method.

Statistical analysis

All biochemical estimations were performed in triplicate. The mean, range, and least-squares mean values for test traits of each genotype were derived using SAS software version 9.4 (SAS Institute, 2013). ANOVA (significance level = 0.05) for each trait was conducted using R Studio version 4.2.3 with the *agricolae* package. Graphical representations of clustering and correlation were also created using R software version 4.2.3. Clustering was performed using the Euclidean distance metric and the unweighted pair group method with arithmetic mean (UPGMA)

clustering procedure via the *hclust* package, while correlation analysis was carried out using the *metan* package.

Results

Analysis of variation in test material for yield and its component traits

The significant mean sum of squares due to genotype, based on pooled ANOVA, revealed ample genetic diversity for yield and its contributing traits in test material (Supplementary Table 1a). Grain yield (GY) is a crucial parameter in profiling landraces as it directly impacts overall food production and agricultural sustainability. Among the 27 genotypes studied, grain yield ranged from 0.42 to 4.78 t/ha, with an average yield of 2.56 t/ha and a coefficient of variation (CV) of 5.99%. The highest GY was observed in JC 1455-1, followed by JC 12 (4.59 t/ha), JC 4 (4.58 t/ha), J 1006 (4.26 t/ha), J 1007 (3.28 t/ha), and Chaurah Chamba (3.04 t/ha). Thousand kernel weight (TKW), an important yield-contributing trait, ranged from 139.80 to 359.83 g, with a mean of 250.00 g and a CV of 1.38%. The highest TKW was observed in the Nadaun selection, followed by

Chameti Solan (359.83 g), More 110 (303.94 g), Chaurah Chamba (302.95 g), and Patti Kangra HP (293.05 g) (Table 1). This diversity is illustrated in a radar plot. Another major yield-related trait is kernels per row (K/R), which varied from 20 to 36, with an average of 28 K/R and a CV of 3.99% (Fig. 2).

Genotypes JC 4 recorded the highest K/R (36), followed by JC 1455-1 and HP Selection Kangra (35 K/R), Yellow OP2OP2 Composite (34 K/R), and Braz 1844 (33 K/R). Grain colour exhibited a spectrum ranging from white to red/purple among the 27 landraces/farmer's varieties, representing each class: white (6), yellow (8), orange (7), and dark orange (3) (Fig. 3).

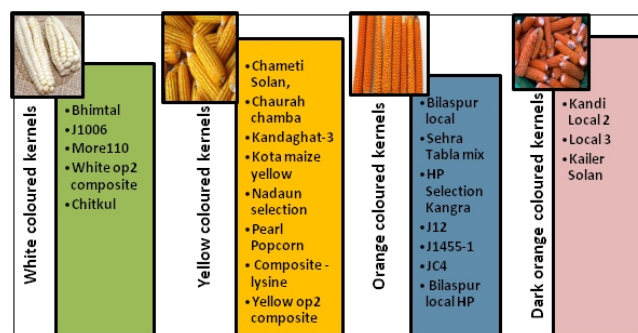


Fig. 3: Classification of landraces/farmers' varieties based on grain colour.

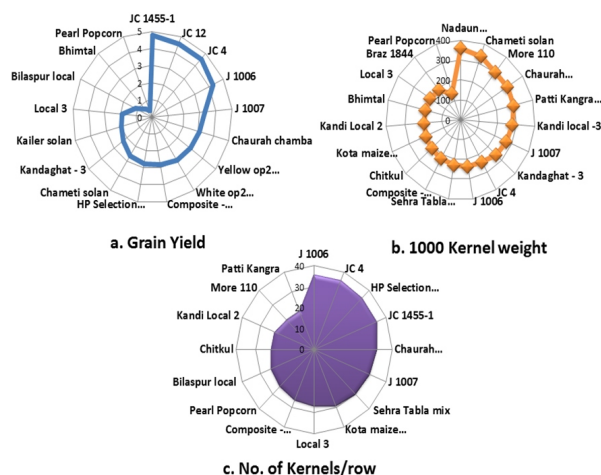


Fig. 2: Variation for grain yield and its contributing traits in test material.

Table 1: Promising genotypes for quality and yield traits

Trait	Promising genotypes for particular traits
Methionine ($\geq 0.134\%$)	HP Selection Kangra, JC 1455-1, Chameti Solan, Kota maize yellow, Local 3
Tryptophan ($\geq 0.043\%$)	Yellow op2OP2 composite, White op2OP2 composite, Braz 1844, JC 1455-1, Patti Kangra HP
Protein ($\geq 11.75\%$)	White op2OP2 composite, Patti Kangra HP, Chitkul, Kandaghat-3, HP Selection Kangra
Starch ($\geq 66.64\%$)	Kailer Solan, More110, Nadaun selection, Chitkul, Kota maize yellow
β -carotene (≥ 4.98 ppm)	Local 3, Patti Kangra HP, JC 12, Kandi Local 2, Bilaspur local
Yield (≥ 3.28 t/ha)	JC 1455-1, J 12, JC 4, J 1006, J 1007
1000 kernel weight (≥ 293.05 g)	Nadaun selection, Chameti Solan, More110, Chaurah Chamba, Patti Kangra HP
Kernels per row (≥ 34)	JC4, J1006, JC 1455-1, HP Selection Kangra, Yellow op2OP2 composite

Analysis of variance for nutritional traits

Pooled ANOVA for nutritional quality traits revealed that the mean sum of squares due to genotype was significant ($p < 0.01$) for these traits in the 27 landraces/farmers' varieties (Supplementary Table 1b), indicating genetic diversity. The mean sum of squares due to environment was non-significant for all quality traits under study.

Profiling of landraces/varieties for quality traits

The comprehensive evaluation of nutritional quality traits is presented in Supplementary Table 2. Met content varied from 0.03% to 0.17%, with an average of 0.095% (Fig. 4a). HP Selection Kangra (0.17%) had the highest Met content, followed by JC 1455-1 (0.164%),

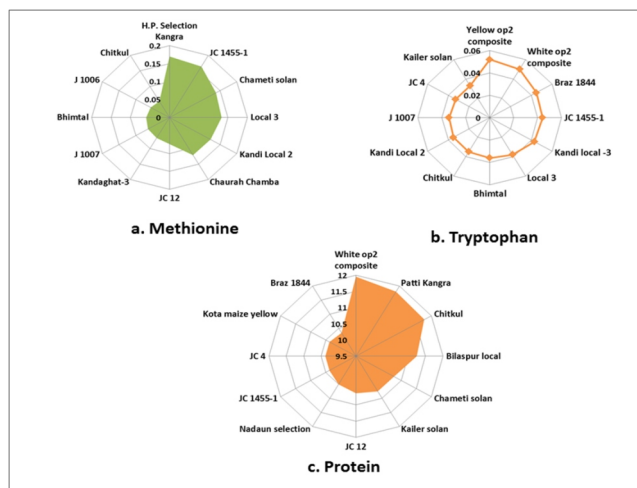


Fig. 4: Variation for various nutritional and biochemical traits like Methionine, Tryptophan and Protein in the test material.

Chameti Solan (0.138%), and Local 3 (0.134%). Typ content ranged from 0.033% to 0.052%, with an average of 0.038% (Fig. 4b). Yellow op2 composite (0.052%) was the most promising for Typ, followed by White op2 composite (0.05%), Braz 1844 (0.045%), JC1455-1 (0.044%), and Kandi Local-3 (0.043%). Protein content varied from 10.33% to 11.95%, with an average of 11.03% (Fig. 4c). White op2 composite (11.95%) had the highest grain protein content, followed by Patti Kangra HP (11.80%), Chitkul (11.77%), Kandaghat-3 (11.75%), Kailer Solan (11.75%), and HP Selection Kangra (11.75%). Starch content varied from 55.48 to 69.62%, with an average of 62.48% (Fig. 5a). Kailer Solan (69.62%) had the highest starch content, followed by More 110 (68.29%), Nadaun Selection (67.62%), Chitkul (67.60%), and Kota Maize Yellow (66.64%). β -Carotene content ranged from 0.78 ppm to 6.24 ppm, with an average of 3.56 ppm and a CV of 1.22%. Local-3 had the highest β -carotene content, followed by Patti Kangra (5.66 ppm), JC12 (5.64 ppm), Kandi Local 2 (5.55 ppm), and Bilaspur Local HP (4.98 ppm) (Fig. 5b).

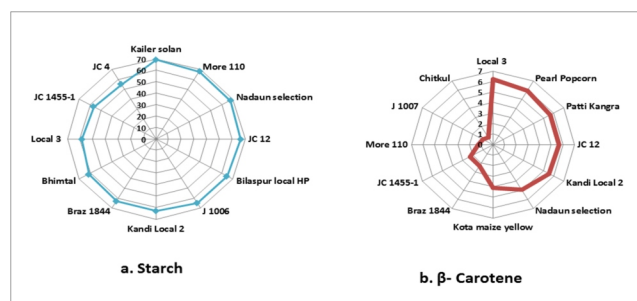


Fig. 5: Variation for various nutritional and biochemical traits like Starch and β -Carotene in the test material.

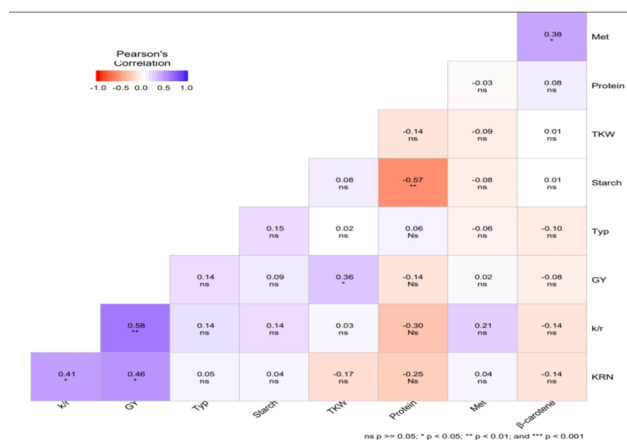


Fig. 6: Correlation among the quality and yield & its contributing traits.

Interrelationship among biochemical and yield traits

Pearson's correlation coefficients among the test traits are presented in Fig. 6. Met did not exhibit a significant correlation with other nutritional quality traits, yield, or its contributing factors, indicating that it is possible to improve Met content without compromising other quality parameters or yield. The correlation between Met and Typ was also non-significant. Protein showed a negative association with starch ($r = -0.57$), consistent with the general inverse relationship between these two components. Additionally, GY displayed a positive correlation with TKW ($r = 0.36$) and K/R ($r = 0.58$).

Clustering of landraces/farmers' varieties for test traits

The test material was grouped into five clusters based on the performance of each genotype for biochemical traits. Clustering was performed using the complete linkage method and Euclidean distances, resulting in two major groups, labelled 'A' and 'B' (Fig. 7). Group B was further subdivided into subgroups B1 and B2.

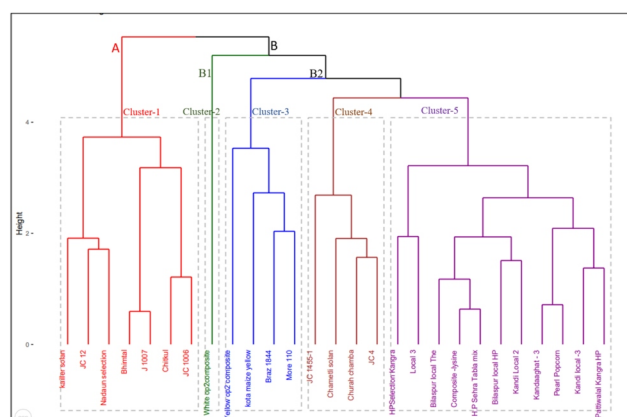


Fig. 7: Clustering of germplasm based on Euclidean distance.

Group A consisted of two branches: Cluster-1, which included seven landraces/farmers' varieties with high starch content, and Cluster-2, a separate lineage consisting of the farmer's variety "White op2 composite," known for its exceptionally high Typ content and above-average protein content. Cluster-3 included four individuals with above-average starch content, while Cluster-4 contained four individuals with high Met content. Cluster-5, the largest, comprised 11 individuals with above-average protein and β -carotene content. The Euclidean distance among the five clusters is given in Supplementary Table 3, with Clusters 3 and 4 being the most distant, separated by a Euclidean distance of 3.33. Lines exhibiting excellent quality traits and good seed potential from different clusters can be used for hybrid breeding programs.

Discussion

In recent years, there has been a growing trend towards developing speciality maize varieties for both food and industrial purposes. Local maize populations have become vital breeding sources in these programs, aimed at creating maize genotypes with improved grain quality characteristics. Consequently, significant efforts have been made to screen maize landraces and farmers' varieties for their quality components and yield-related traits.

Starch is the major component of maize grains, typically constituting about 70-75% of the grain's dry weight. This high starch content makes maize an essential crop for various applications in food, feed, and industrial products. The genetic material used in this study displayed significant variation in starch content, ranging from 55.48 to 69.62%. Similar studies, such as those by Nanker *et al.*, (2016) and Cömertpay *et al.*, (2016), have reported starch content variations between 59.7% to 61.9% and 73.3% to 80%, respectively, in different maize landraces. Kahrman *et al.*, (2020) also found a broad range of starch content (56.38-79.63%) in Turkish germplasm, with landraces showing more variability than standard varieties. Generally, starch content in normal maize grains varies between 61% and 78%, with structural and non-structural carbohydrates (simple sugars and other components) being the major contributors (Watson, 2019).

The second most important component in maize kernels is protein quality and content. Protein content in maize genotypes typically ranges between 8 and 11%. In our study, the protein content ranged from 10.33 to 11.95%, with an average of 11.03%. Previous

studies on Turkish landraces reported similar ranges of 6.6-11.6% (Cömertpay *et al.*, 2016), with Kahrman *et al.*, (2020) noting a broader range of 6.25-15.65%. The two deficient amino acids, Typ and Lys, are targeted in breeding programs to enhance protein quality (Shewry, 2007). Our study found Typ content ranging from 0.033 to 0.052%, averaging 0.038%. While Kahrman *et al.*, (2020) found a range of 0.03-0.09% in Turkish landraces and Goyanka *et al.*, (2021) reported a Typ content range of 0.3-0.6% in landraces from the NWH region. Met is another crucial amino acid in maize kernels. In our study, Met content varied from 0.03 to 0.17%, with an average of 0.095%. Studies by Scott and Blanco (2009) and Nanker *et al.*, (2016) reported Met content ranges of 0.09-0.19% and 0.2-0.34%, respectively. Similar ranges (0.06-0.18%) were found by Abou-Deif *et al.*, (2012) and Erdal *et al.*, (2019) in their hybrids.

In recent decades, maize has garnered increasing attention due to its significant natural variation in provitamin A carotenoids, essential nutrients that the human body converts into vitamin A. This variation is crucial because vitamin A deficiency remains a major public health issue, particularly in developing countries, leading to severe health problems such as blindness and increased mortality rates, especially among children and pregnant women. The focus on maize for provitamin A biofortification is driven by the crop's potential to address these deficiencies through dietary means. By enhancing the levels of provitamin A carotenoids in maize, researchers aim to develop biofortified maize varieties that can provide better nutrition without requiring major changes in dietary habits. Maize has the highest amount of β -carotene, the precursor of vitamin A, among all other cereals (Welch, 2002). Andjelkovic *et al.*, (2016) reported β -carotene content varying from 0 to 7.95 $\mu\text{g/g}$. Our study found β -carotene content ranging from 0.78 ppm to 6.24 ppm, averaging 3.56%. Other studies, like those by Selvi *et al.*, (2014) and Thakur *et al.*, (2016) have also found significant diversity in β -carotene content among maize landraces.

Maize yield and yield-related traits are complex but highly valuable attributes that significantly contribute to higher productivity, a crucial requirement for meeting food and feed demand and ensuring agricultural sustainability. Maize landraces exhibited significant diversity across a wide range of yield-related traits, including grain yield (GY), kernels per row (K/R), and thousand kernel weight (TKW). Typically, landraces exhibit poor agronomic traits (Miti, 2007), including

thin stalks, fewer leaves, lodging prone, manifested in poor grain yield. Identification of high-yielding landraces not only offers the scope of direct utilization but also widens the scope of deriving high-yielding potential parent lines for commercial hybrid breeding. In the research conducted by Twumasi *et al.*, (2017), 77 landraces collected from southern Ghana showed a mean GY of 2.7 t/ha, ranging from 1.3 to 4.5 t/ha. Nanker *et al.*, (2016) reported a hundred kernel weight variation from 21.7 to 31.8 g in six landrace accessions, while Rebourg *et al.*, (2001) found TKW ranging from 105-425.4 g in 130 European traditional maize populations. Kumari *et al.*, (2017) observed K/R ranging from 7.9 to 41.95 in various landraces from the NEH region. Our study's results for GY (0.42 to 4.78 t/ha), K/R (20 to 36), and TKW (139.80 to 359.83 g) showed significant differences among the test materials. The landraces harbouring useful variation for both nutritional and yield-related traits constitute a useful genetic reservoir for genetic enhancement in maize.

Interrelationship among biochemical and yield traits

The correlation between Met and Typ was found to be non-significant, consistent with findings by Scott *et al.*, (2009), indicating that there is no strong biological connection between Met concentration and the examined traits. This suggests potential for improving grain yield-related traits and grain quality without compromising Met concentration and vice versa. Protein was negatively associated with starch ($r=-0.57$), aligning with the general inverse relationship observed in earlier studies (Clark *et al.*, 2004; Zhang *et al.*, 2008; Langyan *et al.*, 2021). Moreover, grain yield displayed a positive correlation with TKW ($r=0.36$) and K/R ($r=0.58$), consistent with the findings of Beulah *et al.*, (2018). The understanding of association studies can assist in simultaneous breedings for traits of economic importance.

Identification of potential landraces/farmers' varieties for target traits

We identified promising varieties for important yield and biochemical traits, which can be utilized in population improvement programs or for line development through selfing. Certain lines showed potential for multiple traits, such as Kangra selection HP (elite for Met, protein, and K/R) and Patti Kangra (promising for protein, Typ, β -carotene, and TKW). The QPM lines with high Typ content, like PAU-developed composite JC 1455-1 (promising for Typ, yield, and K/R), are particularly valuable for farmers using maize as a

staple diet. High-yielding composites like J1006 and J1007 are promising for fodder purposes. Lines like Braz 1844 (promising for Typ) and More 110 (promising for starch) have shown improved adaptability in Punjab after several selection cycles. These identified lines hold significant potential and represent valuable genetic resources for further quality improvement programs. Utilizing these landraces and farmers' varieties can play a pivotal role in developing nutritionally enriched varieties of maize for food and feed.

Conclusion

Maize landraces exhibit vast genetic diversity. However, it is important to highlight that the genetic resources currently employed in maize breeding programs worldwide encompass less than 10% of these resources, indicating substantial untapped potential for genetic diversity. Prioritizing the collection and detailed study of diverse germplasm will play a pivotal role in preserving and enhancing maize landraces, ultimately ensuring sustainable access to superior genetic resources. The characterization of our landrace collection has revealed its diverse nature and substantial potential for key nutritional and yield traits. The selected elite lines hold potential for enhancing nutritional and yield characteristics and can effectively contribute to germplasm enhancement. This germplasm is also poised to contribute significantly to the development of high-performing maize lines for traits of substantial economic value.

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Supplementary Table 1a: Analysis of variance for yield and its contributing traits

Source of variation	Degree of freedom	Grain yield	Thousand kernel weight	Number of kernels per Row
Genotypes	26	4.877**	9252.1**	109.272**
Location	1	0.003	0.23	2.68
Replication	2	0.024	7.1	3.713
Block	8	0.0322	4.6	1.342
Genotype × Location	26	0.0217	6	0.541
Error	44	0.0235	12	1.235

** Significant at 1%, *Significant at 5%.

Supplementary Table 1b: Analysis of variance for nutritional quality traits

Source of variation	Degree of freedom	Methionine (%)	Tryptophan (%)	Protein (%)	Starch (%)	β-carotene (ppm)
Genotype	26	0.0047**	0.000103**	1.117**	50.63**	11.9**
Location	1	0.000008	0.00000020	0.0417	0.01	0.0016
Replication	2	0.0000016	0.00000045	0.0249	0.015	0.0025
Block	8	0.0000073	0.00000087	0.0117	0.045	0.0013
Genotype×Location	26	0.0000036	0.0000008	0.0124	0.08	0.0023
Error	44	0.000003	0.000000902	0.01885	0.103	0.0019

** Significant at 1%, *Significant at 5%.

Supplementary Table 2: Mean values observed in test material for nutritional quality traits

S.No.	Genotype	Methionine (%)	Tryptophan (%)	Protein (%)	Starch (%)	β-carotene (%)
1	Bhimtal	0.060	0.036	10.57	60.95	1.03
2	Bilaspur local HP	0.096	0.033	11.28	64.40	3.67
3	Bilaspur local	0.086	0.034	11.25	59.55	4.98
4	Braz 1844	0.113	0.045	10.33	62.47	2.35
5	Chameti Solan	0.138	0.034	10.76	60.75	2.32
6	Chitkul	0.052	0.035	11.77	67.60	0.79
7	Chaurah Chamba	0.121	0.036	10.60	59.03	4.73
8	Composite –lysine	0.091	0.037	10.94	60.98	3.83
9	H.P SehraTabla mix	0.076	0.037	10.94	59.80	4.32
10	H.P. Selection Kangra	0.170	0.034	11.75	61.50	4.48
11	J 1007	0.064	0.034	10.54	59.86	1.03
12	J 1006	0.056	0.038	11.58	64.33	1.13
13	JC 12	0.074	0.039	10.64	66.46	5.64
14	JC 1455-1	0.164	0.044	10.38	56.97	2.30
15	JC 4	0.111	0.033	10.38	55.48	3.13
16	Kandaghat-3	0.066	0.038	11.75	63.45	3.46
17	Kandi Local 2	0.122	0.035	11.33	62.60	5.55
18	Kandi Local 3	0.099	0.043	11.39	60.57	4.03
19	Kota maize yellow	0.134	0.036	10.38	66.64	4.11
20	Local 3	0.134	0.038	11.53	58.53	6.24
21	More 110	0.083	0.043	10.55	68.29	1.28
22	Nadaun selection	0.031	0.034	10.50	67.62	4.91
23	Patti Kangra HP	0.110	0.043	11.80	62.28	5.66
24	Pearl Popcorn	0.076	0.037	11.50	62.52	5.91
25	Kailer Solan	0.077	0.033	10.75	69.63	3.42

S.No.	Genotype	Methionine (%)	Tryptophan (%)	Protein (%)	Starch (%)	β-carotene (%)
26	White op2 composite	0.065	0.050	11.95	60.38	0.96
27	Yellow op2 composite	0.086	0.052	10.58	64.32	4.80
	Mean	0.095	0.038	11.03	62.48	3.56
	LSD	0.003	0.001	0.196	0.457	0.062
	CV (%)	1.83	2.49	1.26	0.51	1.23
	Max	0.170	0.052	11.95	69.62	6.24
	Min	0.031	0.033	10.325	55.48	0.79

Supplementary Table 3: Inter- cluster distances among the different clusters of test material

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster1	0				
Cluster2	2.59	0			
Cluster3	2.84	1.63	0		
Cluster4	2.49	3.15	3.33	0	
Cluster5	2.46	2.06	2.41	2.657	0