Print ISSN : 0972-8813
e-ISSN : 2582-2780

[Vol. 22(2) May-August 2024]

Pantnagar Journal of Research

(Formerly International Journal of Basic and Applied Agricultural Research ISSN : 2349-8765)

G.B. Pant University of Agriculture & Technology, Pantnagar

PANTNAGAR JOURNAL OF RESEARCH

Vol. 22(2) May-August 2024

CONTENTS

Impact of *Zea nicaraguensis* introgression on Kernel Trait Variability in maize lines

SENTHILKUMAR V., PRIYA GARKOTI., THOTLA NARESH, MAYANK TIWARI, ANIRUDH T. V. and NARENDRA KUMAR SINGH*

Department of Genetics and Plant Breeding, College of Agriculture, G. B. Pant University of Agriculture and Technology, Pantnagar-263145 (U.S. Nagar, Uttarakhand)
**Corresponding author's email id: narendraksingh2@gmail.com*

ABSTRACT: Maize (*Zea mays* L.) is a crucial global cereal crop for food, feed, and industrial use. This study explored the introgression of *Zea nicaraguensis* into maize lines LM13 and LM14 to enhance kernel traits. The BC_1F_2 individuals, were compared with diverse maize varieties, including hybrids, popcorn, inbreds, sweet corn, and composites. Kernel traits were assessed through qualitative and quantitative analyses. Results showed significant genetic diversity, with LM13 lines exhibiting greater kernel length variability and LM14 lines displaying diverse kernel colours. Flint kernels predominated, indicating resilience and suitability for breeding. Heritability analysis revealed moderate heritability for endosperm colour, while genetic advance values indicated substantial potential for improving kernel dimensions and hundred-seed weight. Principal Component Analysis (PCA) identified kernel dimension traits, colour of top of the grain and hundred-seed weight, and endosperm colour as key differentiators, highlighting the genetic diversity within BC_1F_2 lines. This study underscored the importance of wild relatives in maize breeding, providing insights for developing resilient, high-performing maize varieties to support sustainable agriculture and food security.

Key words: Kernel Traits and Genetic Enhancement, maize, *Zea nicaraguensis*, wild introgression

Maize (*Zea mays* L.) is one of the most important cereal crops globally, serving as a staple food, animal feed, and a key industrial raw material (Murdia *et al.,*2016). Enhancing the genetic diversity and adaptability of maize is crucial for meeting the growing demand, particularly to combat climate change and evolving agricultural challenges (Ahmad *et al.,*2024). Conventional breeding methods have significantly contributed to maize improvement; however, the introgression of genetic material from wild relatives offers a promising approach to further enhance desirable traits (Adhikari *et al.,*2021). *Zea nicaraguensis*, a wild relative of maize, has been identified as a valuable genetic resource for its potential to introduce beneficial traits such as enhanced waterlogging tolerance, improved kernel quality, and increased yield traits (Sahoo *et al.,* 2021). This study focused on the introgression of *Zea nicaraguensis* into cultivated maize lines LM13 and LM14, resulting in BC_1F_2 individuals. The primary objective is to evaluate the impact of this introgression on kernel traits through comprehensive qualitative and quantitative analyses. By comparing these introgressed lines with a diverse set of maize lines, including hybrids, popcorn inbreds, sweet corn, and composite varieties, the study aims to identify key traits contributing to genetic diversity and adaptability. Understanding the genetic and phenotypic variations introduced by *Zea nicaraguensis* will provide valuable insights for targeted breeding programs aimed at developing high-performing, resilient maize varieties (Senthilkumar *et al.,* 2024). The mean performance studies are integral to this evaluation, as they provide a detailed assessment of the kernel traits in BC_1F_2 individuals compared to their parental lines and other maize varieties. This analysis focuses on key attributes such as Kernel Length (KL), Length-To-Breadth Ratio (LBR), Kernel Width (KW), and Hundred-Seed Weight (HSW). By examining these traits, the study aims to identify superior lines that exhibit desirable characteristics for further breeding efforts. The mean performance data will help to determine the extent of trait improvement achieved through the introgression process and guide the selection of promising lines for future breeding programs (Allier *et al.,* 2020). In addition to mean performance, genetic variability analysis plays a crucial role in understanding the consistency and range of trait expression within the BC_1F_2 population. This analysis involves estimating heritability and genetic advance (GA) values for key traits, which indicate the potential for genetic improvement through selective breeding. Traits with high heritability and substantial GA are prioritized for breeding efforts, as they are more likely to respond favourably to selection and contribute to the development of superior maize varieties (Derera, 2005). Principal Component Analysis (PCA) serves as a pivotal tool in this study, offering a detailed comparative analysis of kernel traits and encapsulating the complexity and variability within the dataset. The PCA biplot reveals the distribution and clustering of samples, highlighting distinct genetic backgrounds and the influence of specific traits on variability (Mahmood *et al.,*2022). This research paper underscores the significance of utilizing wild relatives in maize breeding programs and emphasizes the potential of *Zea nicaraguensis* to enhance kernel quality and adaptability. The findings will direct future breeding strategies, aiming to develop maize varieties with superior traits, thereby contributing to sustainable agricultural practices and food security.

MATERIALS AND METHODS

Plant Material and Development of BC_1F_2 Individuals

This experimental study was conducted at the N.E.B. Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, and focused on the development of BC_1F_2 individuals through the introgression of *Zea nicaraguensis* into cultivated maize lines. The parental lines used for this introgression included two inbred maize lines, LM13 and LM14, along with *Zea nicaraguensis*. During the first season (*Kharif* 2020), F_1 hybrids were produced by crossing LM13 and LM14 with *Zea nicaraguensis*. In the subsequent season (*Kharif* 2021), backcrosses were made using LM13 and LM14 as the recurrent parents to produce BC_1F_1 kernels, which were then self-pollinated to generate the BC_1F_2 generation during the *Rabi* 2021-2022 season.

Sampling and Comparative Analysis

A sample of 50 randomly selected LM13 BC_1F_2 and LM14 BC_1F_2 individual's kernels were taken for detailed analysis of the kernel characteristics at the Plant Molecular Biology and Molecular Breeding Laboratory to compare traits and assess the genetic influence of *Z. nicaraguensis* on kernel development. Additionally, a set of 50 diverse maize lines are represented in the Table 1, including hybrids, popcorn, inbreds, sweet corn, and composite varieties, was selected for comparative purposes to provide a benchmark for evaluating the introgressed individuals. The development process and steps are clearly represented in Figure 1.

Qualitative and Quantitative Trait Assessment

Qualitative traits such as kernel type, shape, and color were categorized based on standard key descriptors for maize genetic resources (CIMMYT, 2009). Quantitative traits included measurements of kernel width, length, width-to-length ratio, and 100-seed weight. Kernel width and length were measured using a graph sheet for precision, and the width-to-length ratio was calculated by dividing the width by the length of each kernel. The 100-seed

Table 1: List of Diverse Maize Lines

Types of Corn	Genotypes
Inbreds	CAL 159, LM 13, LM 14, BML 7, CAL 144, CAL 147, CML 563, BML 6, CAL 155
Hybrids	CAL 159 X TEO 1, CAL 147 X CML 451, CAL 1427 X LM 13, BAIJM 209 X CML 451, BAJIM 20-3 X LM 13, 473 X TEO 1, DOP 339 X TEO 1, LM 16 X CML 451, LM 13 X CML 451, LM 13 X LM 14 X TEO 1, LM 14 X CML 451 X TEO 1, BML 6 X BML 7 X TEO 1
Composites	DOP 339, CHIK-244, CHIK-245, CHIK-248, CHIK-249, CHIK-250, CHIK-252
Sweet Corn	TSC 82, TSC 44, TSC 55, TSC 78, TSC 48, TSC 47, TSC 37, TSC 40, TSC 66, TSC 45, TSC 56
Pop Corn	PANT POP CORN 1, POP-546, POP-547, POP-548, POP-549, POP-555, POP-556, POP-557, POP-565, POP-569, POP-558

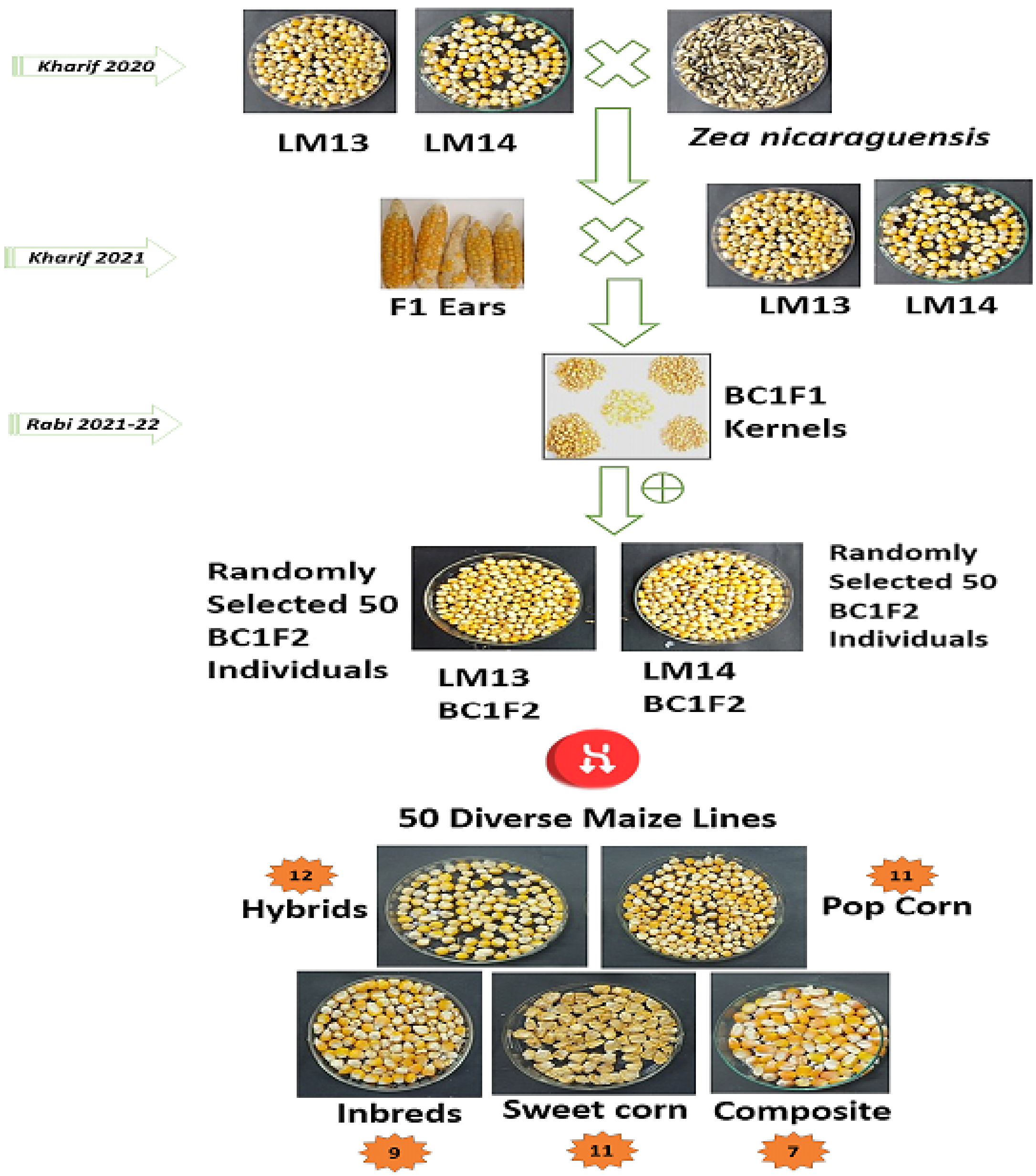

Fig. 1: Pictorial flowchart representation of BC_1F_2 development and comparative trait evaluation with diverse lines

weight was assessed by weighing balance on sample of 100 kernels.

Statistical Analysis

Mean performance provided initial insights into the distribution of traits across both BC_1F_2 introgressed individuals and diverse maize lines. Genetic variability analysis examined the consistency and range of trait expression, which is crucial for selecting traits with desirable genetic stability. Principal Component Analysis (PCA) offered a comprehensive assessment of the impact of *Zea nicaraguensis* introgression on maize kernel traits. All data analyses were performed using the R software version 4.1.2 of Agricolae package.

RESULTS AND DISCUSSION

Kernel Trait Performance Overview

The comprehensive investigation had focused on the kernel characteristics within BC_1F_2 introgressed maize lines, originating from *Zea nicaraguensis*, and a range of diverse maize lines. The study had initially embarked on qualitative evaluations which had catalogued a multitude of kernel types, shapes, and colours. These qualitative observations had been meticulously recorded, setting the stage for the subsequent quantitative analyses that had detailed the kernel dimensions and the 100-seed weight across the different lines, as illustrated in the series of figures provided.

Qualitative Analysis of Kernel Traits

Visual Insights: Kernel Type and Colour

Specifically, Figure 2 had offered a vivid pictorial representation of the kernel type and colour variations. The observed dominance of Flint kernels in the 29 LM13 BC_1F_2 and 33 LM14 BC_1F_2 lines highlights their hardness of kernels are resilience and storage capabilities, making them ideal for breeding robust maize used for cornmeal, livestock feed and biofuels (Shiferaw *et al.,* 2011). Also, including variation in the presence of popcorn and absence of dent and sweet corn, highlights key areas for targeted genetic enhancement to meet specific market demands and consumer preferences (Veljkovi *et al.,* 2018). For analysis of kernel colour (Top of the grain), yellow emerged as the predominant hue particularly within the 38 LM14 BC_1F_2 lines, highlighting its prevalence in this genotype. Following yellow, 24 LM14 BC_1F_2 lines exhibited substantial quantities of orange kernels, suggesting a diverse phenotypic expression within these lines. In contrast, white and red kernels were observed less frequently, with red kernels exclusively present in LM13 BC_1F_2, and no instances of whitecap were recorded. This distribution underscores a rich tapestry of phenotypic variability, reflecting the complex genetic architecture of these introgressed lines. These colour variations not only influence consumer preference and nutritional aspects but also offer potential markers for breeding programs aimed at enhancing specific traits (Murdia *et al.,*2016).

Morphological Diversity: Shape of upper surface of kernel and Endosperm Colour

Figure 3 had highlighted the diversity in the shape of upper surface of kernel and the endosperm colour.

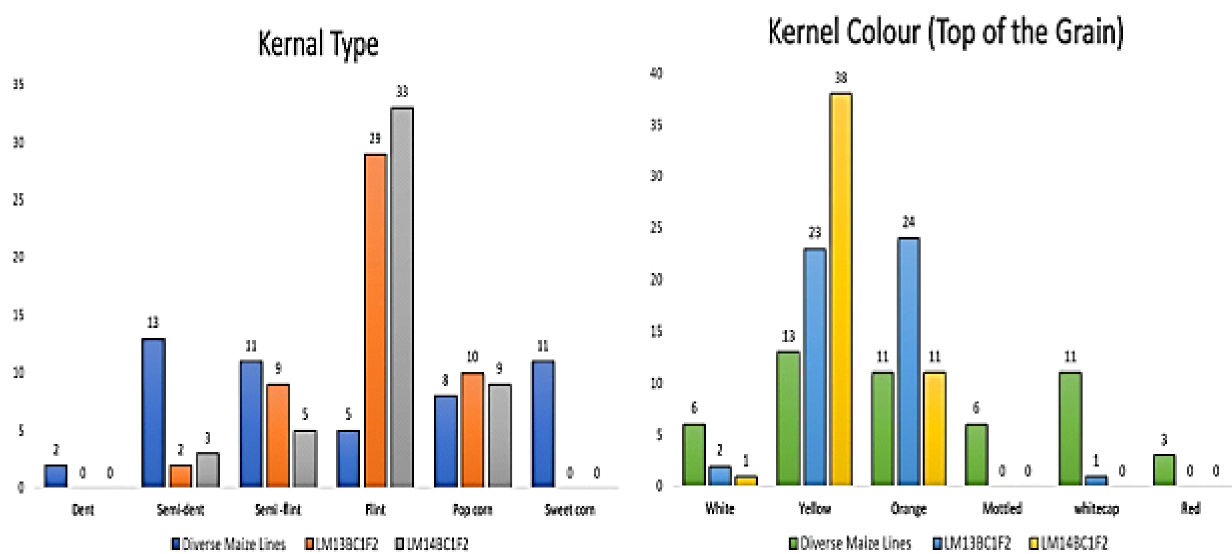

Fig. 2: Pictorial Representation of Kernel type and Colour

It had been recorded that the LM14 BC_1F_2 and LM13 BC_1F_2 lines predominantly featured 25-rounded and 63-pointed kernel shapes, respectively. The 'Strongly Pointed kernels ' attribute had been a distinctive feature of 5 - LM13 BC_1F_2 and 3 - LM14 BC_1F_2 lines. Some previous results obtained when another perennial teosinte introgressed population of maize was studied, pointed out that perennial teosinte germplasm produced a significant increase in the protein content and that this trait was not significantly associated with other plant, ear, or kernel traits. This fact showed the certain possibility of increasing the protein content by using those wild genetic resources (Varalakshmi *et al.,*2023). On the spectrum of endosperm colours, 'Orange' had been evenly distributed between the lines, 'Pale Yellow' had taken precedence in 26 LM13 BC_1F_2, and 29 LM14 BC_1F_2 lines. Such variation had reflected the genetic richness that the introgression of *Zea nicaraguensis* brought to cultivated maize. The distinct kernel shapes and colour traits that had been documented in this study could have served as critical markers in breeding programs aimed at enhancing desirable agronomic and consumer traits (Senthilkumar *et al.,* 2024). Such diversity had been essential for the development of maize varieties that were adaptable to varying climatic conditions and changing consumer preferences, thereby supporting the sustainability and resilience of maize cultivation (Cairns *et al.,* 2012).

Quantitative Analysis of Kernel Traits

Dimensional Characteristics: Kernel Size and Shape

In Figure 4, the depiction of kernel dimension characteristics through boxplots and scatter plots had elucidated the significant variability in kernel width and length. The figure highlights kernel dimension characteristics, emphasizing significant variability in kernel width, length, and length-to-breadth (LB) ratio among diverse maize lines, LM13BC_1F_2, and LM14 BC_1F_2 lines.

The diverse maize lines exhibit the broadest range for both width and length but have lower median values compared to the introgressed lines. LM13 BC_1F_2 lines show a narrower range but higher median values for both traits, indicating more

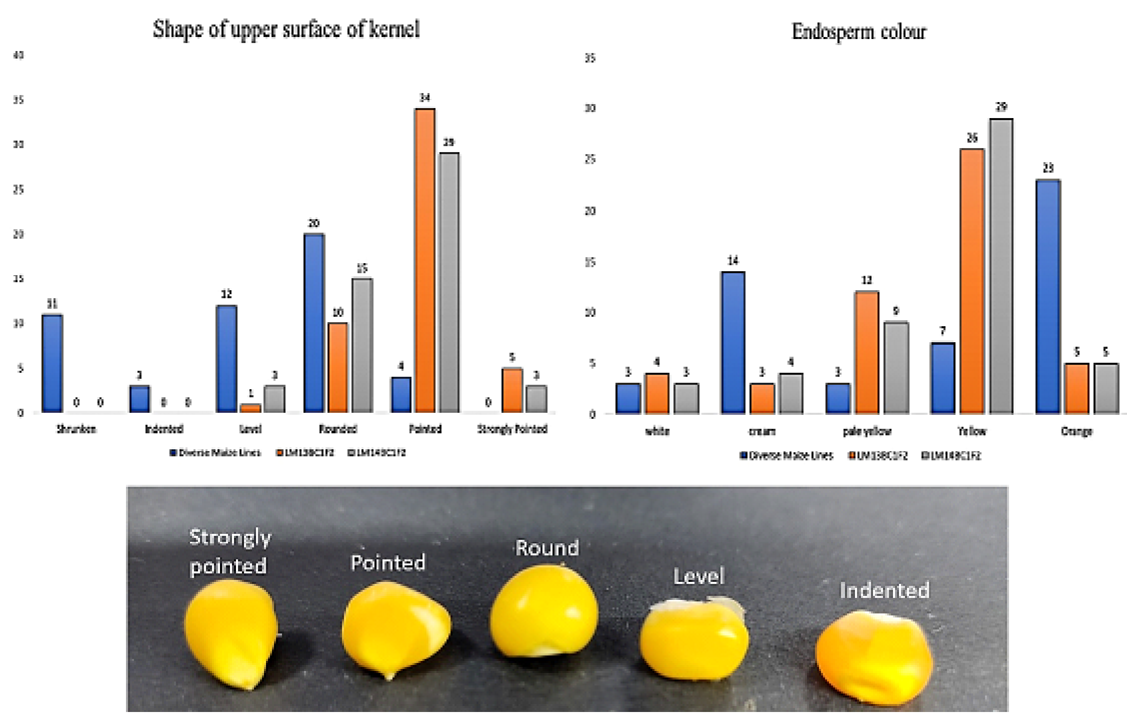

Fig. 3: Pictorial Representation of Shape of Upper Surface of Kernel and Endosperm Colour

consistent and generally larger kernels. LM14 BC_1F_2 lines display intermediate variability and median values, suggesting moderate potential for improvement. The LB ratio scatter plot reveals considerable overlap among all lines, with LM13 BC_1F_2 showing a slight clustering towards higher ratios, indicating longer kernels relative to their width, while LM14 BC_1F_2 leans towards broader kernels. These findings underscore the genetic diversity within the introgressed lines, with LM13 BC_1F_2 lines being suitable for breeding programs focused on larger kernel dimensions, and LM14 BC_1F_2 lines offering variability for selective enhancement. The variability in L:B ratio reflects a complex genetic influence on kernel shape, providing insights for optimizing kernel form in breeding strategies. Overall, the introgressed lines present valuable genetic resources for improving kernel traits in maize (Senthilkumar *et al.,* 2024).

Weight Variability: 100-Seed Weight Analysis

The investigation of 100-seed weight variability among LM13 BC_1F_2, LM14 BC_1F_2 maize lines, and a collection of diverse maize lines, as depicted in Figure 5. It provides a wealth of data critical to genetic analysis and maize breeding programs. The substantial fluctuations in seed weight within the LM14 BC_1F_2 line uncover a rich genetic diversity range of 13.34 to 26.08 g, indicating a potential for these lines to contribute valuable alleles to breeding programs focused on enhancing grain yield and size. In contrast, the relative genetic stability observed range 11.80 to 44.00 g in the LM13 BC_1F_2 line suggests that these genotypes may offer a reliable foundation for developing new varieties with consistent grain qualities, a desirable trait for commercial maize production.

The significant disparity in seed weight variability between these lines and the diverse maize lines underlines the potential of the latter in adaptive breeding strategies. Furthermore, the extensive range of phenotypic expression in these introgressed lines are indicative of ample opportunity for phenotypic selection, where breeders can capitalize on the observable traits to cultivate maize varieties that harmonize high seed weight with other beneficial agronomic characteristics (Shiferaw *et al.,* 2011). Importantly, the data suggests that the introgressed lines could serve as a rich source for the development of genetic markers associated with seed weight, paving the way for the integration of marker-assisted selection in maize breeding to expedite the improvement of this trait (Karn *et al.,* 2017).

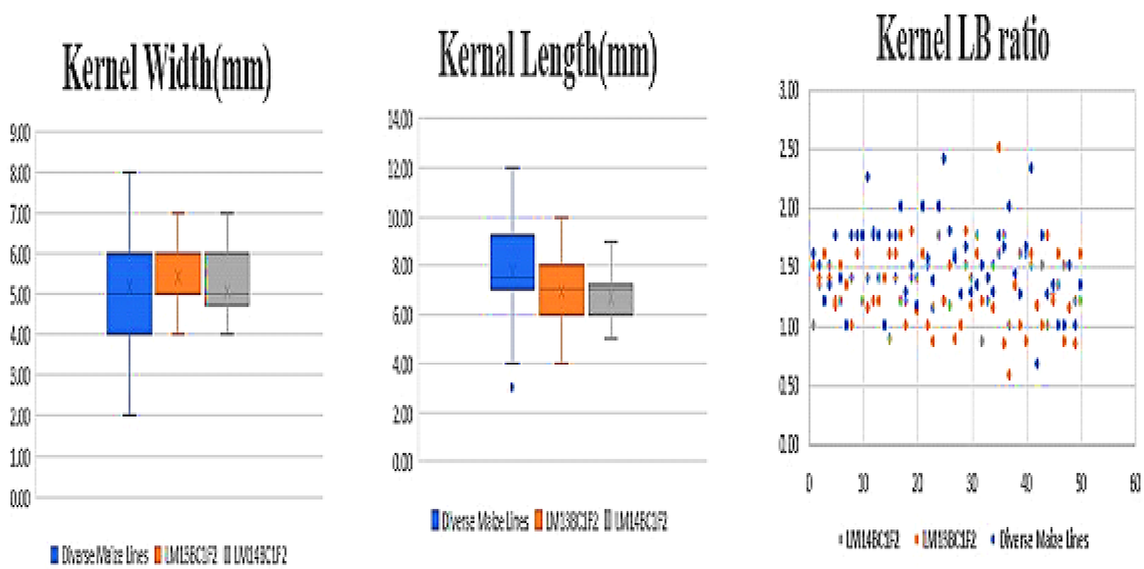

Fig. 4: Pictorial Representation of Kernel Dimension of Diverse Maize Lines, LM13BC_1F_2, and LM14 BC_1F_2 lines

Additionally, the variability highlighted in the study facilitates the estimation of crop yields, where the 100-seed weight serves as an integral parameter in predicting overall productivity, especially when considering the potential impact of various genetic backgrounds and cultivation environments on yield (Ibirinde *et al.,*2021). Such comprehensive data on 100 seed weight variability is invaluable for the ongoing efforts to increase maize yield, improve grain quality, and bloster the crop's resilience to environmental stress, thereby contributing to sustainable agricultural practices and food security (Wimalasekera , 2015).

Genetic Parameters of Kernel Traits

Heritability Insights

The figure 6 illustrates the heritability of kernel traits in BC_1F_2 populations for LM13 BC_1F_2 and LM14BC_1F_2 lines. Endosperm Colour (EC) exhibits the highest heritability in both lines, with LM14 BC_1F_2 slightly surpassing LM13 BC_1F_2, indicating a strong genetic influence and significant potential for selective breeding. Shape of the Upper Surface of Grain (SUSG) also shows notable heritability, suggesting moderate genetic control. Kernel Width (KW), Kernel Length (KL), Length-to-Breadth Ratio (LBR), and Hundred Seed Weight (HSW) display lower heritability, indicating a more substantial environmental influence or polygenic control. Kernel Type (KT) and Colour of the Top of the Grain (CTG) exhibit the lowest heritability, suggesting limited genetic contribution. Overall, the high heritability of EC and SUSG highlights these traits as prime targets for genetic improvement in breeding programs, while the lower heritability traits may require more complex strategies for enhancement (Cobb *et al.,* 2013).

Genetic Advance Results

The genetic advance (GA) of various kernel traits was measured for two backcross populations, LM13BC_1F_2 and LM14BC_1F_2, derived from the introgression of *Zea nicaraguensis* into maize. Genetic advance indicates the expected improvement in a trait under selection and is an important parameter for evaluating the potential of breeding programs (Eid, 2009). The analysis of genetic advance (GA) values in kernel traits for the LM13BC_1F_2 and LM14BC_1F_2 backcross populations reveals significant potential for genetic improvement through selection, particularly for kernel type, colour of the top of the grain, kernel width, kernel length, and hundred-seed weight (HSW). These traits exhibit high GA values, indicating substantial expected gains from selective breeding. Specifically, kernel length and HSW show the highest potential,

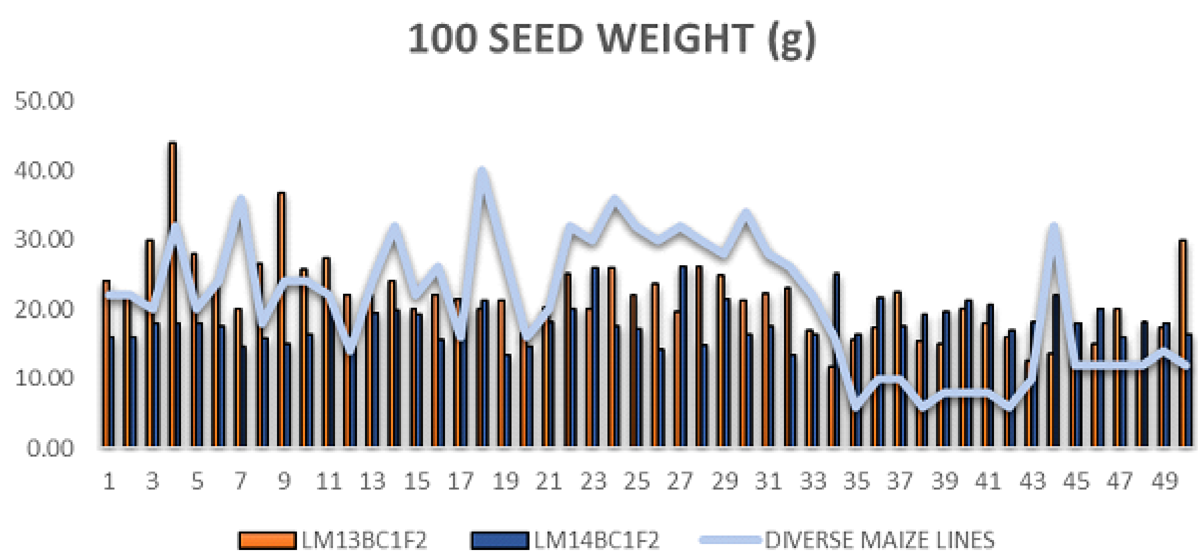

Fig. 5: Pictorial Representation of 100 seed weight (grams)

suggesting strong responsiveness to selection and significant improvements in yield and commercial value. Moderate GA values for endosperm colour and the shape of the upper surface indicate achievable genetic improvements, with LM13BC$_1$F$_2$ showing a slightly higher potential for endosperm colour. Conversely, low GA values for LBR suggest limited potential for improvement through selection, highlighting the need to prioritize other traits or alternative approaches. Overall, the GA values provide a strategic roadmap for breeding programs, emphasizing traits with the highest potential for genetic enhancement to optimize kernel quality and yield in maize (Bello *et al.,* 2012).

Principal Component Analysis (PCA): Kernel Trait Differentiation and Clustering

The Principal Component Analysis (PCA) biplot provides a comprehensive comparative analysis of kernel traits in introgressed Maize x *Zea nicaraguensis* BC$_1$F$_2$ individuals, encapsulating the complexity and variability of the studied traits.

LM13 BC$_1$F$_2$ Results

The first two principal components of the LM 13 BC$_1$F$_2$ line score (Figure 8), PC1 and PC2, explain 33.2% and 19.1% of the total variation, respectively, and account for 52.3% of the variance. Results are presented in Table 2. Key traits influencing PC1 include kernel breadth, colour of top grain, and kernel type, with kernel length and KLB ratio positively correlated with PC1. PC2 is influenced by endosperm colour, HSW, and the shape of the upper surface of the kernel. Lines such as 1, 15, 16, and 31 cluster together, showing higher values in kernel length and KLB ratio, indicating longer and denser kernels, which could be beneficial for breeding programs focused on these traits. Lines 48,

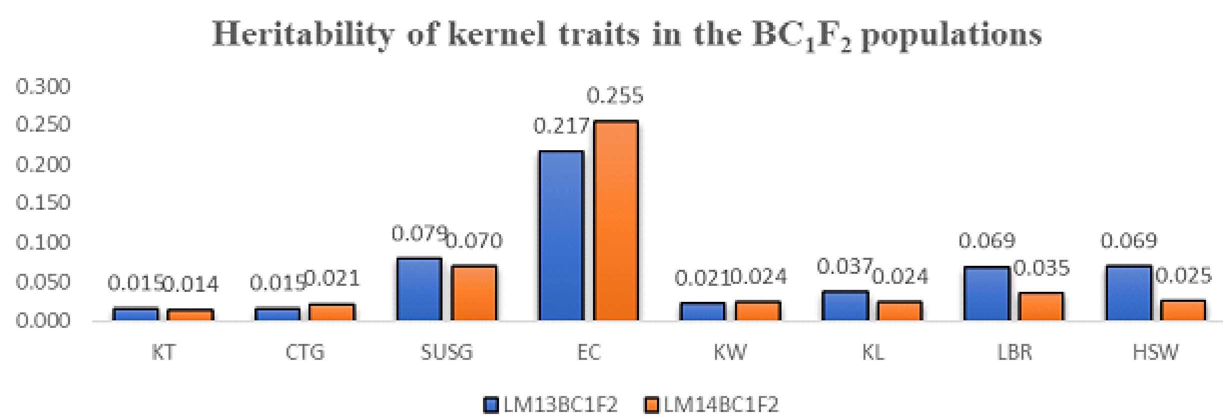

Fig. 6. Heritability of kernel traits in the BC$_1$F$_2$ populations

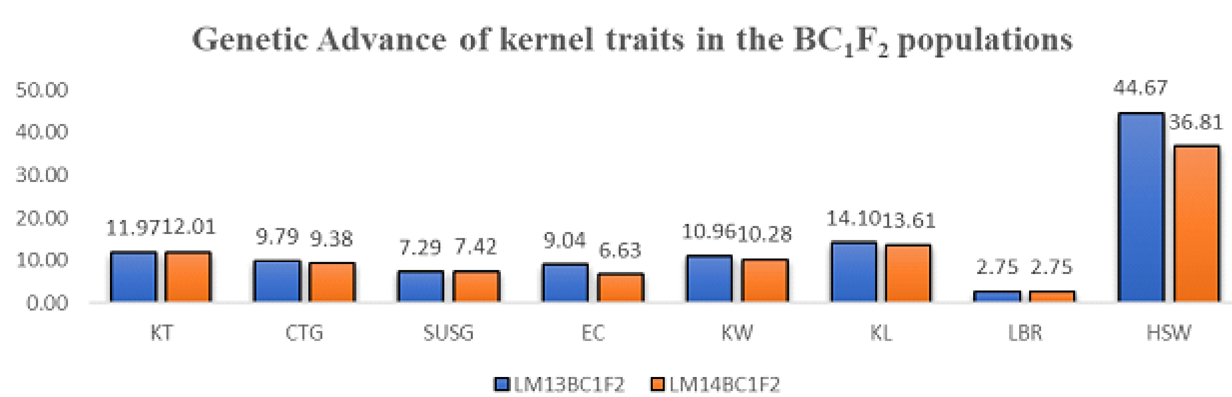

Fig. 7. Genetic Advance of kernel traits in the BC1F2 populations

39, 42, and 34 form another cluster characterized by kernel type and colour of top grain, suggesting a focus on market-preferred aesthetic traits (Senthilkumar *et al.,* 2024).

LM14 BC_1F_2 Results

The LM14 results of first two principal components (PC1 and PC2) explaining 24.5% and 16.3% of the total variation, respectively, cumulatively accounting for 40.8% of the variance. The results are given in Table 2 and shown graphically in Figure 9. Key traits influencing PC1 include kernel length, colour of top grain, and KLB ratio, while kernel type and kernel breadth have significant loadings on the negative

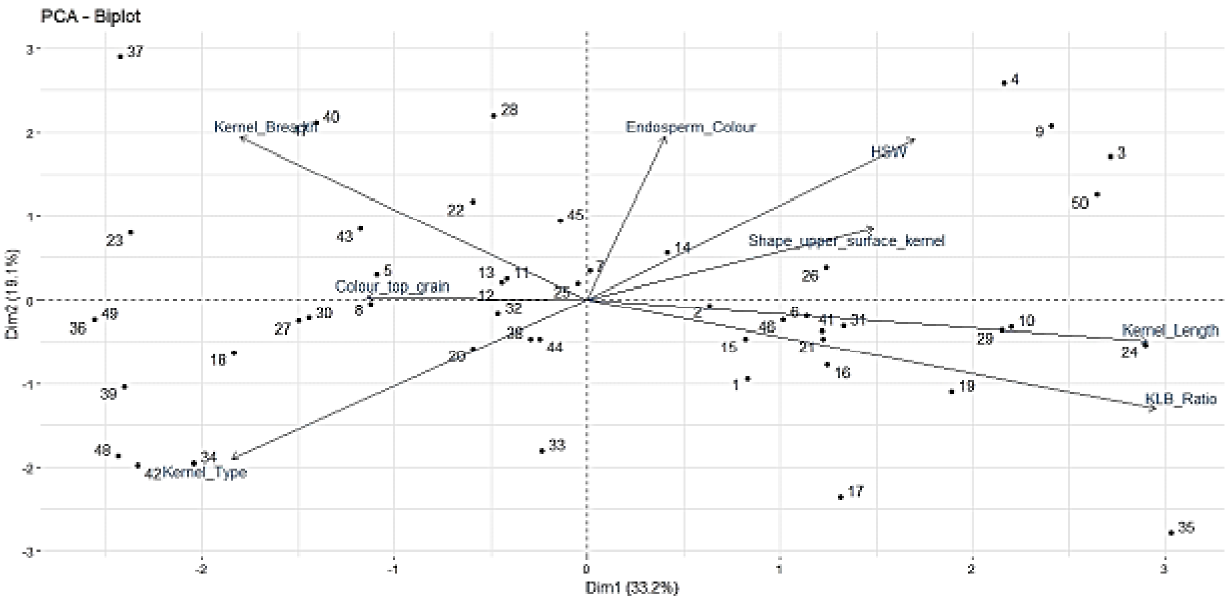

Fig. 8: PCA Biplot of Kernel Traits in Maize LM 13 BC_1F_2 Lines (PCA1 an PCA2)

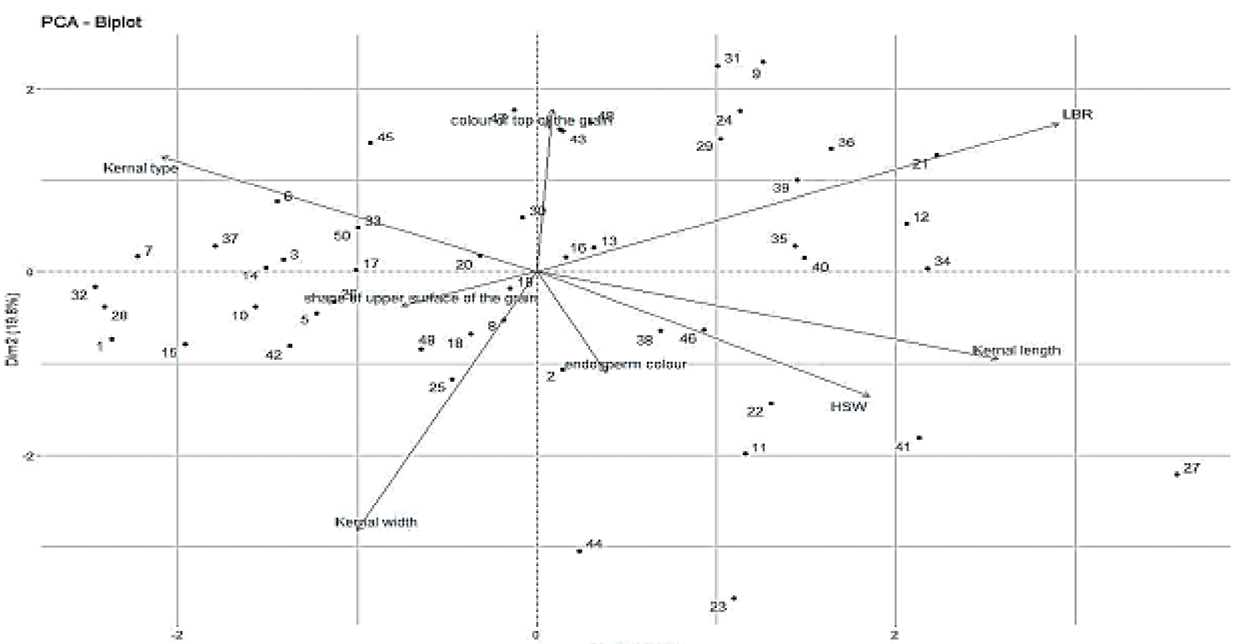

Fig. 9: PCA Biplot of Kernel Traits in Maize LM 13 BC_1F_2 Lines

Table 2: Principal Component Analysis Results of LM13 BC_1F_2 and LM14 BC_1F_2

Component	LM13 BC_1F_2		LM14 BC_1F_2	
	Eigenvalue	Percentage of Variance	Eigenvalue	Percentage of Variance
Comp 1	2.65	33.18	1.96	24.53
Comp 2	1.53	19.13	1.31	16.35
Comp 3	1.17	14.63	1.23	15.42
Comp 4	0.91	11.33	1.02	12.74
Comp 5	0.71	8.90	0.79	9.83
Comp 6	0.56	6.97	0.65	8.15
Comp 7	0.40	5.01	0.58	7.27
Comp 8	0.07	0.86	0.46	5.72

side of PC1. PC2 is mainly influenced by endosperm colour, HSW and shape of upper surface of the kernel. The biplot illustrates clear groupings of maize lines, with Cluster 1 (Lines 1, 10, 29, and 6) exhibited higher values in kernel type and kernel breadth, indicating a broader and different kernel morphology, and Cluster 2 (Lines 16, 12, 28, and 9) characterized by traits related to kernel length and KLB ratio.

Key Findings and Implications of PCA results

These key findings underscore the importance of kernel dimension traits and colour of top of the grain in distinguishing the samples. As well as the significant roles of endosperm colour and HSW in explaining additional variability. The analysis highlights the significant influence of introgression from *Zea nicaraguensis* on the kernel traits of BC_1F_2 individuals. The close association of these individuals with specific trait vectors implies the successful incorporation of desirable attributes, such as increased kernel dimensions. These insights are particularly valuable for breeding programs focused on enhancing kernel quality and adaptability (Yang *et al.,* 2019). By leveraging the identified key traits contributing to variability, breeders can make informed selections of parent lines that exhibit optimal characteristics, thereby improving the overall performance and resilience of maize crops. (Reynolds *et al.,* 2020). In summary, the PCA biplot serves as a powerful tool for visualizing and interpreting the genetic diversity and trait distribution among maize lines, providing actionable insights for targeted breeding strategies (Naggar *et al.,* 2020). This detailed analysis not only highlights the critical kernel traits influenced by the introgression of *Zea nicaraguensis* but also paves the way for developing superior maize varieties with enhanced kernel quality and adaptability, ultimately contributing to more resilient and productive agricultural systems (Badu-Apraku *et al.,* 2012).

CONCLUSION

In conclusion, the introgression of *Zea nicaraguensis* into cultivated maize lines, specifically LM13 and LM14, has resulted in BC_1F_2 individuals exhibiting notable genetic diversity and significant variability in kernel traits. This comprehensive study meticulously analysed kernel traits through both qualitative and quantitative measures, providing a robust comparison between BC_1F_2 individuals and diverse maize lines. The mean performance of kernel traits highlighted the superior performance of BC_1F_2 lines in terms of the dominance of Flint kernels in LM13 and LM14 BC_1F_2 lines underscored their resilience and storage capabilities, making them ideal for breeding robust maize varieties. The colour analysis revealed the prevalence of yellow and orange kernels, particularly in LM14 lines, reflecting diverse phenotypic expressions and potential for targeted breeding programs. Quantitative analyses indicated significant variability in kernel dimensions and 100-seed weight across the studied lines. The LM13 BC_1F_2 lines demonstrated a wider range and higher median kernel length compared to LM14 BC_1F_2, while the substantial fluctuations in 100-seed weight among LM14 BC_1F_2 lines indicated rich genetic diversity. The relative genetic stability observed in LM13 BC_1F_2 lines suggested their potential as a reliable foundation for developing consistent grain qualities. Heritability analysis identified endosperm colour as having moderate heritability, indicating its potential for genetic improvement through selective breeding. Traits such as KL, LBR, and hundred-seed weight (HSW), despite lower heritability, still offered valuable genetic contributions that can be targeted with precise breeding efforts. The genetic advance (GA) values for kernel traits revealed significant potential for improvement, particularly for KL, HSW, and kernel type, suggesting substantial gains from selective breeding. PCA provided a comprehensive analysis of kernel traits, highlighting variability and complexity. In LM13, the first principal component (Dim1) accounted for 33.8% of the variance, influenced by Kernel Length (KL) and Length-to-Breadth Ratio (LBR), while the second component (Dim2), explaining 19.6%, was affected by Hundred Seed Weight (HSW), upper surface shape, and grain colour. In LM14, Dim1 accounted for 25.2% of the variance, influenced by KL and LBR, with Dim2 explaining 19.8%, mainly affected by HSW, upper surface shape, and Kernel Width (KW). The PCA biplot revealed distinct genetic backgrounds within the dataset, indicating successful incorporation of desirable traits from *Zea nicaraguensis*. These findings highlight the significant influence of *Zea nicaraguensis* introgression on maize kernel traits, offering valuable insights for breeding programs aimed at enhancing kernel quality and adaptability (Karn *et al.,* 2017). Key traits, such as Length-to-Breadth Ratio (LBR) and Hundred Seed Weight (HSW), should be prioritized to develop high-performing, resilient maize varieties. The genetic diversity in the introgressed lines presents ample opportunities for improvement through marker-assisted selection and targeted breeding efforts (Senthilkumar *et al.,*2024).

Future research should focus on the nutritional implications of kernel trait diversity, aiming to enhance protein content and other nutritional attributes. Exploring the biochemical pathways and genetic markers associated with these traits could lead to the development of maize varieties with improved nutritional profiles, benefiting both human and animal consumption. Additionally, breeding programs should prioritize developing maize varieties with improved tolerance to environmental stresses, leveraging the observed genetic variability and phenotypic diversity. Advancements in genomic tools and technologies, such as CRISPR/Cas9 for precise genome editing, should be integrated into breeding strategies to accelerate the development of superior maize varieties. Investigating the epigenetic factors influencing kernel traits and their heritability could further refine selection criteria and improve breeding efficiency. By integrating advanced genetic insights with practical breeding approaches, future efforts can significantly enhance maize production, quality, and resilience, addressing both current and future agricultural challenges.

REFERENCES

Adhikari, S., Joshi, A., Kumar, A., and Singh, N. K. (2021). Diversification of maize (*Zea mays* L.) through teosinte (*Zea mays* subsp. *parviglumis* Iltis & Doebley) allelic. *Genetic Resources and Crop Evolution, 68*(7): 2983-2995.

Ahmad, U., Hussain, M. A., Ahmad, W., Javed, J., Arshad, Z., and Akram, Z. (2024). Impact of global climate change on maize (*Zea mays*): physiological responses and modern breeding techniques. *Trends in Biotechnology and Plant Sciences,* 2(1): 62-77.

Allier, A., Teyssèdre, S., Lehermeier, C., Moreau, L., and Charcosset, A. (2020). Optimized breeding strategies to harness genetic resources with different performance levels. *BMC Genomics,* 21: 1-16.

Badu-Apraku, B., Oyekunle, M., Obeng-Antwi, K., Osuman, A. S., Ado, S. G., Coulibay, N., Yallou, C. G., Abdulai, M., Boakyewaa, G. A., and Didjeira, A. (2012). Performance of extra-early maize cultivars based on GGE biplot and AMMI analysis. *The Journal of Agricultural Science,* 150(4): 473-483.

Bello, O. B., Ige, S. A., Azeez, M. A., Afolabi, M. S., Abdulmaliq, S. Y., and Mahamood, J. (2012). Heritability and genetic advance for grain yield and its component characters in maize (*Zea mays* L.). *International Journal of Plant Research,* 2(5): 138-145.

Cairns, J. E., Sonder, K., Zaidi, P. H., Verhulst, N., Mahuku, G., Babu, R., Nair, S. K., *et al.* (2012). Maize production in a changing climate: impacts, adaptation, and mitigation strategies. *Advances in Agronomy,* 114: 1-58.

Cobb, J. N., DeClerck, G., Greenberg, A., Clark, R., and McCouch, S. (2013). Next-generation phenotyping: requirements and strategies for enhancing our understanding of genotype–phenotype relationships and its relevance to crop improvement. *Theoretical and Applied Genetics,* 126: 867-887.

Derera, J. (2005). Genetic effects and associations between grain yield potential, stress tolerance and yield stability in southern African maize (*Zea mays* L.) base germplasm, Doctoral Thesis, University of KwaZulu-Natal, South Africa, 189p

Eid, M. H. (2009). Estimation of heritability and genetic advance of yield traits in wheat (*Triticum aestivum* L.) under drought condition. *International Journal of Genetics and Molecular Biology*, 1(7): 115-120.

Ibirinde, D. O., Iliya, N. M., and Bitrus, S. (2021). Assessment of Maize (*Zea mays*) Genotypes for Seed Metrics, Agronomic Performance, Yield and Nutritional Content in the Southern Savanna Agro-ecological Zone of Nigeria (Wukari as Case Study), *Asian Journal of Agricultural and Horticultural Research* 9 (4):220-27.

International Maize and Wheat Improvement Center (CIMMYT). (2009). Key access and utilization descriptors for maize genetic resources, Published by CIMMYT, Mexico, 6 p.

Karn, A., Gillman, J. D., and Flint-Garcia, S. A. (2017). Genetic Analysis of Teosinte Alleles for Kernel Composition Traits in Maize. *G3: Genes, Genomes, Genetics*, 7(4), 1157-1164.

Mahmood, T., Ghafoor, S., Shahid, M., Ahmad, B., Tahir, N., Abdullah, M., and Aslam, M. (2022). Morphological standard based genetic diversity among maize (*Zea mays* L.) accessions indigenous to Pakistan, *International Journal of Agriculture and Bioscience*, 11(4):212-221.

Murdia, L. K., Wadhwani, R., Wadhawan, N., Bajpai, P., and Shekhawat, S. (2016). Maize utilization in India: an overview. *American Journal of Food and Nutrition*, 4(6): 169-176.

Naggar, A.A., Shafik, M.M., Musa, R.Y., Younis, A.S.M. and Anany, A.H., (2020). Genetic variability of maize hybrids and populations and interrelationships among grain yield and its related traits under drought and low n using multivariate analysis. *Asian Journal of Biochemistry, Genetics and Molecular Biology*, 4(2):26-44.

Prasanna, B. M., Cairns, J. E., Zaidi, P. H., Beyene, Y., Makumbi, D., Gowda, M., and Zhang, X. (2021). Beat the stress: breeding for climate resilience in maize for the tropical rainfed environments. *Theoretical and Applied Genetics*, 134(6): 1729-1752.

Reynolds, M., Chapman, S., Crespo-Herrera, L., Molero, G., Mondal, S., Pequeno, D. N., and Sukumaran, S. (2020). Breeder friendly phenotyping. *Plant Science*, 295: 110396.

Sahoo, S., Adhikari, S., Joshi, A., and Singh, N. K. (2021). Use of wild progenitor teosinte in maize (*Zea mays* subsp. *mays*) improvement: present status and future prospects. *Tropical Plant Biology*, 14(2): 156-179.

Senthilkumar, V., Garkoti, P., Varalakshmi, S., Naresh, T., and Singh, N.K., (2024). Kernel trait and genetic variability analysis in BC_2F_1 maize lines derived from *Zea nicaraguensis* crosses. *Journal of Advance in Biology and Biotechnology*, 27(8): 268-279.

Shiferaw, B., Prasanna, B. M., Hellin, J., and Bänziger, M. (2011). Crops that feed the world 6. Past successes and future challenges to the role played by maize in global food security. *Food Security*, 3: 307-327.

Varalakshmi, S., Singh, N.K., Senthilkumar, V., Sahoo, S., Singh, P. and Garkoti, P. (2022). Morphological characterization for leaf architecture in teosinte (*Zea mays* subsp. *parviglumis*) derived BC_1F_2 population of maize. *Pantnagar Journal of Research*, 20: 3.

Veljković, V.B., Biberdžić, M.O., Banković-Ilić, I.B., Djalović, I.G., Tasić, M.B., Nježić, Z.B. and Stamenković, O. S. (2018). Biodiesel production from corn oil: A review. *Renewable and Sustainable Energy Reviews*, 91 :531-548.

Wimalasekera, R. (2015). Role of Seed Quality in Improving Crop Yields. In: Hakeem, K. (eds) Crop Production and Global Environmental Issues. Springer, Cham.: 153-168.

Yang, N., Liu, J., Gao, Q., Gui, S., Chen, L. U., Yang, L., and Yan, J. (2019). Genome assembly of a tropical maize inbred line provides insights into structural variation and crop improvement. *Nature genetics*, 51(6): 1052-1059.

Received: June 11, 2024
Accepted: July 16, 2024