SABRAO Journal of Breeding and Genetics 57 (5) 1809-1817, 2025 http://doi.org/10.54910/sabrao2025.57.5.3 http://sabraojournal.org/pISSN 1029-7073; eISSN 2224-8978





CHARACTERIZATION OF MAIZE GERMPLASM AND PROMISING GENOTYPES SELECTION BASED ON MORPHOLOGICAL TRAITS, HERITABILITY, AND MULTIVARIATE ANALYSIS

N. FADHLI¹, Y. MUSA², T. DARIATI², N.E. DUNGGA², M. FARID^{2*}, M. AZRAI², A. NUR³, R. EFENDI⁴, M.F. ANSHORI², and F. NOVIANTI⁵

¹Postgraduate Program, Hasanuddin University, Indonesia

²Department of Agronomy, Faculty of Agriculture, Hasanuddin University, Indonesia

³Indonesian Cereal Testing Instrument Standard Institute, Indonesia

⁴National Research and Innovation Agency, Indonesia

⁵Department of Agriculture and Food Security, Indonesia

*Corresponding author's email: farid_deni@yahoo.co.id

Email addresses of co-authors: nur.fadhli016@gmail.com, yunusmusa@yahoo.com, tigindariati@unhas.ac.id, ndungga@agri.unhas.ac.id, azrai@agri.unhas.ac.id, Iceriamin76@gmail.com, roysereal@yahoo.com, fuad.anshori@unhas.ac.id, fira1204462@gmail.com

SUMMARY

The success in hybrid seed assembly depends upon the availability of strains with high receptivity and compatibility with their parental genotypes. The presented study aimed to characterize the maize germplasm and select high-yielding genotypes by studying them through morphological parameters, heritability, correlation, and multivariate analysis. The study had a randomized complete block design comprising 27 genotypes with three repetitions. These genotypes are those with wider adaptability obtained as procured from the Cereal Crops Instrument Standard Testing Centre, Maros, South Sulawesi, Indonesia. The results showed the cob length and grain yield percentage were the best traits besides the harvest cob weight. Based on the path analysis, the cob length gave the highest direct effect (0.46), followed by yield percentage (0.45). An increasing cob length and yield percentage is relevant to increasing productivity, meaning this character can be beneficial as the most effective secondary quality in selecting maize genotypes. Direct effect is a trait influence that has an impact on the main character. Principal component analysis (PCA) through multivariate analysis can reduce numerous interrelated variables. Based on the PCA, the maize genotypes JHD 14 and JHD 15 were notably promising strains with the highest productivity.

Communicating Editor: Dr. Gwen Iris Descalsota-Empleo

Manuscript received: December 04, 2024; Accepted: April 22, 2025. © Society for the Advancement of Breeding Research in Asia and Oceania (SABRAO) 2025

Citation: Fadhli N, Musa Y, Dariati T, Dungga NE, Farid M, Azrai M, Nur A, Efendi R, Anshori MF, Novianti F (2025). Characterization of maize germplasm and promising genotypes selection based on morphological traits, heritability, and multivariate analysis. *SABRAO J. Breed. Genet.* 57(5): 1809-1817. http://doi.org/10.54910/sabrao2025.57.5.3.

Keywords: Maize (*Z. mays* L.), characterization, heritability, correlation, multivariate analysis, morphological parameters

Key findings: Knowledge of genetic variation is indispensable in predicting the performance of maize (*Z. mays* L.) hybrids to be developed, and that can considerably assist the breeders in selecting promising genotypes through breeding programs. Based on selection, JHD14 and JHD15 emerged as the best strains with the highest productivity potential.

INTRODUCTION

Maize (*Zea mays* L.) is one of the most important food crops for daily calorie intake worldwide. Corn uses can be as a raw material in feed, food, and pharmaceutical industries, and as a source of vitamins and minerals in maintaining energy in the human body (Jiao *et al.*, 2022). With increasing world population, meeting the needs of a global market, which includes an innovative design, is a top priority for these industries (Gari *et al.*, 2024).

Maize cultivars with improved seeds play an effective role in increased productivity and food security (Kalsa et al., 2024; Menkir et al., 2024). However, conventional hybrid breeding strategies have proven to be very challenging and constrained by the difficulty of large-scale seed production determined by crossability, growth and morphological structures, and yield component traits with a major impact on the overall production (Paril et al., 2024).

The hybrid assembly's success mainly depends upon available desirable strains with high receptivity and compatibility with their parents to obtain the highest rate of natural cross-pollination (Bai et al., 2022). Phenological characters, such synchronization of flowering time of both parents, yield component characteristics, and other growth and morphological characters that significantly affect the production, proved to play a pivotal role in selecting genotypes with the highest productivity (Rajandran et al., 2022).

Developing better hybrids than existing cultivars is one of the urgent goals of plant breeding. Genetic dispersal is an effective tool in selecting the parental genotypes for hybridization programs. Knowledge of genetic variation is indispensable in predicting the

performance of hybrids to be developed, which can considerably assist the breeders in selecting suitable parents in breeding programs. The values of genetic potential can have successful determination by investigating the genetic diversity, heritability, and genetic progress in the germplasm (Korsa et al., 2024). However, the genetic progress in the genotypes' potential is an important indicator in the selection process (Begna, 2021). Heritability can measure the relative portion of heritable variation, while genetic gain can measure the extent of effectiveness that could result through selection (Norman et al., 2024). In addition to genetic diversity, the relationship yield characters between and other components is also indispensable in increasing productivity (Fadhli et al., 2023).

The correlation coefficient provides an overview of simple relationships between the characters, while path analysis is generally applicable in determining the nature of relationships among the characters (Leite et al., 2022). Path analysis can evaluate the magnitude of causal association among the growth and yield characters (Guo et al., 2023). Determining the effectiveness characterization and selection in maize can succeed by selection criteria that require appropriate statistical approaches. Knowing the correlation and relationship between the traits is essential in breeding to identify superior genotypes through indirect selection. Multivariate analysis be helpful to can categorize and select the pure strains of potential maize hybrids in breeding (Duc et al., 2024). Therefore, it is crucial to identify the relationship among various characters of strains under development through conventional approaches. Based on the above discussion, the latest study investigate the morphological parameters,

heritability, correlation, and multivariate analysis in characterizing the germplasm and selection of high-yielding maize genotypes. Expectedly, at the end of the research, an outcome will be a corn strain that is the best candidate with high productivity.

MATERIALS AND METHODS

Breeding material

This research commenced from April until July 2024 at the Bajeng Agricultural Technology Instrument Standard Testing and Application Installation (IP2SITP) Farm, Cereal Crops Instrument Standard Testing Centre, District Bajeng, Gowa Regency, South Sulawesi, Indonesia. The study area location has coordinates at 5°18'29" S - 119°30'28" E at 92 masl, and the type of rainfall was D4, as defined by the Oldeman climatic classification. Rainfall in the field throughout the research period ranged from 0 to 160 mm each month (BMKG, 2024). The genetic material used comprised 27 maize genotypes (Table 1). These genotypes had features with wider adaptability obtained from the Cereal Crops Instrument Standard Testing Centre, Maros, South Sulawesi, Indonesia.

Procedure

The experimental layout used a randomized complete block design (RCBD) with three repetitions, consisting of 27 maize genotypes and resulting in 81 experimental units. Maize genotypes' seeds bore planting on $5 \text{ m} \times 3 \text{ m}$

plots, with a spacing of 75 cm × 20 cm. Each seed, as placed in a planting hole, corresponded to the genotype Maintenance in this study included watering, weeding, and hilling. Fertilization occurred twice, with the urea fertilizer applied at 150 kg N ha^{-1} and NPK (15:15:15) at 300 kg ha^{-1} after 10 days of planting, and later, after 30 days of planting with urea (200 kg ha⁻¹). For weed management, the spraying of herbicides Atrazine (600 g L^{-1}) and Mesotrione (60 g L^{-1}) controlled the weeds. For controlling the plant's pests and diseases, applying the insecticide emamectin benzoate (30 g L^{-1}) ensued. Harvesting continued at the physiological age marked by yellow corn husks, hardened seeds, and the appearance of a black layer at the growing point.

Traits measurement and analysis

The observations proceeded on 10 randomly selected maize plants in each genotype and replication. The variables included plant height, height of cob, male flowering days, female flowering days, cob length, cob diameter, rows per cob, grains per cob row, harvested cob weight, moisture content, yield percentage, and productivity.

All the recorded data's analysis used the analysis of variance (ANOVA) with a standard error of 5%. The data analysis results served to determine the heritability values for each character. Broad-sense heritability (h²) has the formula as follows (Jain and Allard, 1960):

Heritability (h²) = $\sigma^2 g/\sigma^2 p$

Tabl	le 1	. The	genotypes	used	in	this	stud	у.
------	------	-------	-----------	------	----	------	------	----

Rank	Lines	Rank	Lines	Rank	Lines
1	862	10	HDMT 29-1-1-1-2	19	MDKL
2	AVLN 118	11	HDMT 30	20	Mgold
3	BCY	12	HDMT 52-L5	21	Mpop 24-13
4	BLI 6-1	13	HDMT 8-3-2-1-1	22	Mpop 27
5	Clyn 231	14	HR-5	23	MSM 53
6	ERC 24	15	HR-6	24	P2
7	GLT 22-8	16	JHD14	25	P6
8	HDMT 16	17	JHD15	26	Pop 23
9	HDMT 28-1-1-1-1	18	MCL88	27	T3-11-3-1

Determination of selection criteria took place using the Pearson correlation and path analysis to identify characters with high correlations and the highest direct effect on Furthermore, grain yield. the analysis continued using the principal component analysis (PCA) to reduce the number of interrelated variables while maintaining existing variations. Analysis also ensued with the selection of the best genotype using the LSD test at the 5% level based on selected traits in the path analysis and PCA. Analyses succeeded using the STAR 2.0.1 application for correlation coefficients, ANOVA, principal component analysis biplot, and Tukey tests. Meanwhile, using Excel helped perform path analysis.

RESULTS AND DISCUSSION

Analysis of variance showed significant ($P \le 0.01$) differences among the maize genotypes for almost all the traits, except moisture content (Table 2). The coefficient of variance (CV) values ranged from 1.87% to 16.12%. According to Fadhli *et al.* (2023), the greater the ratio between genotype variance and error variance, the more diversity in the character. This indicated that the observed maize genotypes were highly variable and a scope of

genetic improvement through selection exists. Genetic progress plays an important role in the efficiency of a selection, and the genotype by environment interaction is of major concern for maize breeders (Chaves et al., 2023). Higher genetic variability gives an idea of the desired recombinants in the next generation (Kovačević et al., 2024). Reports on the of variance analysis also stated effectiveness in being used in assessing the spatiotemporal variability of maize grain yield (De-Villiers et al., 2024) and in the genetic improvement of the hybrid maize (Tarekegne et al., 2023).

In genetic parameters of the maize genotypes, the phenotypic variance (PV) was higher than the genotypic variance (GV). Heritability values ranged from 0.11 (moisture content) to 0.98 (weight of harvested cob, yield percentage, and productivity), and the observed heritability values were almost high (Table 2). The low heritability value shown by the trait of moisture content can be a choice in advanced generations by using the pedigree method. High heritability values were notably considerably helpful in deciding the direction of selection to be used (Norman et al., 2024). Knowing the heritability estimates can give an idea that genetic parameters significantly affect the productivity (Sahito et al., 2024).

Table 2. Analysis of variance of maize genotypes for various traits.

Traits	Mean squares			Genetic p	arameters	
ITails	Replications	Genotypes	CV	Gv	Pv	H ²
PH	29.84ns	1465.08**	3.44	477.68	509.73	0.94
HC	25.62ns	668.23**	6.90	211.80	244.62	0.87
MFD	2.78ns	17.67**	1.87	5.46	6.75	0.81
FFD	2.75ns	19.93**	2.12	6.08	7.78	0.78
LC	5.35**	30.98**	6.66	10.13	10.74	0.94
DC	12.35ns	100.93**	7.15	31.69	37.55	0.84
NRC	7.28**	4.82**	6.63	1.34	2.13	0.63
NGR	42.74**	129.23**	16.12	40.65	47.92	0.85
WHC	0.09ns	6.51**	6.92	2.16	2.20	0.98
MC	2.94ns	1.87ns	10.19	0.17	1.54	0.11
Υ	0.00ns	0.06**	3.01	0.02	0.00	0.98
Р	0.10ns	10.21**	8.80	3.38	3.45	0.98

Notes: **significant effect at 1%; ns=not significant; PH=plant height; HC=height of cob; MFD=male flowering days; FFD=female flowering days; LC=length of cob; DC=diameter of cob; NRC=number of rows per cob; NGR=number of grains per cob row; WHC=weight of harvested cob; MC=moisture content; Y=yield percentage; P=productivity; G=genotype; E=environment; CV=coefficient of variance; Gv=genotypic variance; Pv=phenotypic variance; and h^2 =heritability.

Table 3. Pearson correlation analysis of various maize traits.

Characters	PH	HC	MFD	FFD	LC	DC	NRC	NGR	WHC	Υ
PH	1.00									
HC	0.89**	1.00								
MFD	-0.41*	-0.28	1.00							
FFD	-0.24	-0.15	0.86**	1.00						
LC	0.50**	0.49*	-0.41*	-0.13	1.00					
DC	0.35	0.46*	-0.39*	-0.24	0.42*	1.00				
NRC	0.15	0.30	-0.27	-0.01	0.34	0.63**	1.00			
NGR	0.30	0.31	-0.40*	-0.25	0.59**	0.69**	0.35	1.00		
WHC	0.52**	0.56**	-0.60**	-0.36	0.80**	0.75**	0.54**	0.81**	1.00	
Υ	0.01	0.17	-0.13	-0.15	0.09	0.68**	0.28	0.68**	0.54**	1.00
Р	0.46*	0.51**	-0.57**	-0.35	0.74**	0.76**	0.54**	0.84**	0.99**	0.62**

Notes: **significant effect at 1%; *significant effect at 5%; PH=plant height; HC=height of cob; MFD=male flowering days; FFD=female flowering days; LC=length of cob; DC=diameter of cob; NRC=number of rows per cob; NGR=number of grains per cob row; WHC=weight of harvested cob; Y=yield percentage; and P=productivity.

Table 4. Path analysis of the various maize traits.

Traits	DE	PH	HC	MFD	LC	DC	NRC	NGR	Υ	Residuals
PH	0.10		0.00	0.08	0.23	-0.01	0.02	0.04	0.01	0.06
HC	0.00	0.09		0.06	0.22	-0.02	0.05	0.04	0.08	0.06
MFD	-0.21	-0.04	0.00		-0.19	0.02	-0.04	-0.05	-0.06	0.06
LC	0.46	0.05	0.00	0.09		-0.02	0.06	0.07	0.04	0.06
DC	-0.04	0.04	0.00	0.08	0.19		0.10	0.08	0.31	0.06
NRC	0.16	0.02	0.00	0.06	0.16	-0.02		0.04	0.13	0.06
NGR	0.12	0.03	0.00	0.08	0.27	-0.03	0.06		0.31	0.06
Υ	0.45	0.00	0.00	0.03	0.04	-0.03	0.05	0.08		0.06

Notes: DE=direct effect; PH=plant height; HC=height of cob; MFD=male flowering days; LC=length of cob; DC=diameter of cob; NRC=number of rows per cob; NGR=number of grains per cob row; and Y=yield percentage.

Genotypic differences affecting the have production received considerable attention. Based on the correlation coefficient analysis, the harvested cob weight and grains per cob row revealed significant correlations (0.99)and 0.84, respectively), authenticated that these characters have the highest relationship with productivity (Table 3). Results regarding the correlation coefficient also appeared in the evaluation of high-yielding hybrid maize (Farid et al., 2024) and in the morphological and physiological response of maize (Yasin et al., 2024). The independent relationship of the harvested cob weight and grains per cob row with productivity is generally useful in the selection of these characteristics in the early generations and to obtain the maize strains with the superior productivity. Therefore, characters showing a significant correlation to productivity

underwent further evaluation using the path analysis.

Path analysis continued without including the trait of harvest cob weight. This is because the said character was indicating a high level of multicollinearity on productivity. Based on the path analysis, the cob length expressed the highest direct effect (0.46), followed by yield percentage (0.45) (Table 4). The traits of plant height (0.10), height of cob (0.00), grain rows per cob (0.16), and grains per cob row (0.12) also expressed positive direct effects on productivity. The traits of male flowering days (-0.21) and cob diameter (-0.04) revealed the negative direct effects on the production. Direct effect is an indicator that shows the trait's influence on the main character. The outcomes further disclosed that the cob length and yield percentage were the best characteristics besides the harvest cob

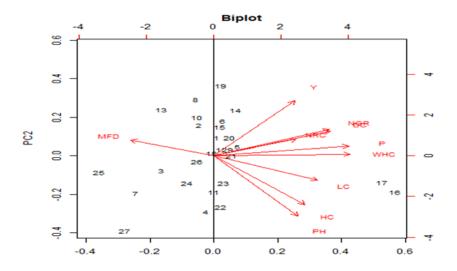


Figure 1. Principal components-based biplot analysis in maize. PH=plant height; HC=height of cob; MFD=male flowering days; LC=length of cob; DC=diameter of cob; NRC=number of rows per cob; NGR=number of grains per cob row; WHC=weight of harvested cob; Y=yield percentage; and P=productivity.

Table 5. Principal component analysis of maize characters.

Variable	PC1	PC2	
Proportion of variance	0.56	0.16	
Cumulative proportion	0.56	0.72	
Eigenvalue	5.63	1.61	

Notes: PC=principal component.

Path analysis weiaht. can provide understanding of the causal relationship among the different attributes, thus increasing the efficiency of the selection process (Tolera et al., 2024). An increasing cob length and yield percentage signified a relationship with increased productivity, meaning this character can be beneficial as the most effective secondary feature in selecting maize genotypes.

Multivariate analysis was applicable to those traits that affect productivity. Principal component analysis (PCA) can interrelated variables while numerous maintaining the variation that exists in the data set (Zewdu et al., 2024). Based on the PCA biplot analysis, almost all characters have the same grouping as productivity, except for the trait of male flowering days (Figure 1). This explains that these qualities can be favorable as effective criteria in the selection. The result of principal component analysis also showed the eigenvalue greater than 1, with eigenvalues of 5.63 (PC1) and 1.61 (PC2), as the proportion for Principal Component 1 (PC1) is 0.56 and for Principal Component 2 (PC2) is 0.16 (Table 5), based on the principle that their eigenvalues less than 1, respectively, can explain the cumulative factor and diversity between characters. An eigenvalue of 1 is the effective limit of dimensionality and enhances the representation of the data's inherent structure (Kaviriri et al., 2023; Li, 2024).

Multivariate analysis can serve to analyze and integrate the large variable data into simpler ones (Afzal *et al.*, 2024). Principal component biplot analysis has been widely reported in previous studies, such as the in evaluation of maize cultivars via multivariate analysis (Khan *et al.*, 2024) and to assess the effects of complex foliar fertilizers regarding *Z. mays* L. productivity (Crista *et al.*, 2024).

Table 6. Selected characters based on path analysis and PCA.

Genotype	LC (cm)	Y (%)	P (t ha ⁻¹)
862	12.94e	0.75h	3.39ef
AVLN 118	9.35lm	0.78f	2.63jk
BCY	6.97n	0.75gh	1.80m
BLI 6-1	12.90e	0.66k	2.39kl
Clyn 231	9.22lm	0.83cd	3.54de
ERC 24	9.73kl	0.81de	3.54de
GLT 22-8	8.88m	0.48m	0.96n
HDMT 16	9.13lm	0.92a	3.18fg
HDMT 28-1-1-1-1	13.88d	0.84bc	4.32c
HDMT 29-1-1-1-2	10.36ijk	0.82de	3.46de
HDMT 30	11.18h	0.631	2.281
HDMT 52-L5	15.61c	0.69j	3.07gh
HDMT 8-3-2-1-1	10.79hij	0.83cd	2.301
HR-5	12.25ef	0.82de	3.60de
HR-6	12.08fg	0.78f	3.15fg
JHD 14	21.30a	0.86b	9.04a
JHD 15	20.14b	0.82de	8.01b
MCL88	7.65n	0.80e	2.72j
MDKL	10.29jk	0.85bc	3.72d
Mgold	9.18lm	0.82de	3.35ef
Mpop 24-13	11.48gh	0.74h	2.98ghi
Mpop 27	11.97fg	0.75gh	2.87hij
MSM 53	11.15h	0.77fg	2.81ij
P2	12.52ef	0.64kl	1.55m
P6	11.08hi	0.44n	0.390
Pop 23	11.50gh	0.71i	2.34l
T3-11-3-1	11.40gh	0.240	0.370

Notes: Numbers followed by the same letter in a column indicate no significant difference from LSD tests level of 5%. LC=length of cob; Y=yield percentage; and P=productivity.

Selection of the best genotypes through PCA showed 14 maize genotypes with the promising values for the selected characters (Figure 1). Based recapitulation of selected characters, the maize genotypes JHD14 (16) and JHD15 (17) emerged as the best strains having the potential for highest productivity, with a value of 9.04 t ha⁻¹ and 8.01 t ha⁻¹, providing a value of 21.30 and 20.14 cm for cob length, and providing a value of 0.86% and 0.82% for yield percentage, respectively (Table 6). Additionally, maize genotypes MDKL (19), HR-5 (14), ERC (6), HR-6 (15), 862 (1), Mgold (20), HDMT 52-LS (12), HDMT 28-1-1-1-1 (9), Clyn 231 (5), Mpop 24-13 (21), MSM 53 (23), and Mpop 27 (22) can be recommendations as lines with the potential to be the best candidate genotypes with high productivity.

CONCLUSIONS

In conclusion, the morphological parameters, heritability, correlation, and multivariate analysis proved useful in characterizing the maize germplasm for high productivity. An increasing cob length and yield percentage occurred relevant to increased productivity, meaning this character can be beneficial as the most effective secondary character in selecting maize genotypes. Selection based on promising traits resulted in 14 maize lines (JHD 14, JHD 15, MDKL, HR-5, ERC, HR-6, 862, Mgold, HDMT 52-LS, HDMT 28-1-1-1, Clyn 231, Mpop 24-13, MSM 53, and Mpop 27) with ratings as the best candidate genotypes with maximum productivity.

ACKNOWLEDGMENTS

Authors are grateful to the Directorate of Research, Technology, and Community Service, and the Directorate General of Higher Education, Research, and Technology for the financial support and facilities provided for this research, with the cooperation agreement number 050/E5/PG.02.00.PL/2024.

REFERENCES

- Afzal S, Hayat A, Amin M, Afzal A, Gardezi S (2024). Exploring spatial variability and yield-determining factors in cotton production: A multivariate analysis. *Commun. Soil Sci. Plant Anal.* 55(20): 3117-3132. doi: 10.1080/00103624.2024.2381595
- Bai Z, Ding X, Zhang R, Yang Y, Wei B, Yang S, Gai J (2022). Transcriptome analysis reveals the genes related to pollen abortion in a cytoplasmic male-sterile soybean (*Glycine max* [L.] Merr.). *Int. J. Mol. Sci.* 23: 12227. doi: 10.3390/ijms232012227.
- Begna T (2021). Role and economic importance of crop genetic diversity in food security. *J Agric. Sci. Food Technol.* 7(1): 164-169. doi: https://dx.doi.org/10.17352/2455-815X.000104.
- BMKG (2024). Badan Meteorologi Klimatologi Dan Geofisika (BMKG). Monthly rainfall data. Meteorology, Climatology and Geophysics Agency, Climatology Station Class I, Maros, South Sulawesi. (In Indonesian).
- Chaves SFS, Evangelista JSPC, Trindade RS, Dias LAS, Guimarães PE, Guimarães LJM, Alves RS, Bhering LL, Dias KOG (2023). Employing factor analytic tools for selecting high-performance and stable tropical maize hybrids. *Crop Sci.* 63(3): 1114-1125. doi: 10.1002/csc2.20911.
- Crista L, Radulov I, Crista F, Imbrea F, Manea DN, Boldea M, Gergen I, Ienciu AA, Laţo A (2024). Utilizing principal component analysis to assess the effects of complex foliar fertilizers regarding maize (*Zea mays* L.) productivity. *Agriculture* 14: 1428. doi: 10.3390/agriculture14081428.
- De-Villiers C, Mashaba-Munghemezulu Z, Munghemezulu C, Chirima GJ, Tesfamichael SG (2024). Assessing maize yield spatiotemporal variability using unmanned aerial vehicles and machine learning. *Geomatics* 4(3): 213-236. doi: 10.3390/geomatics4030012.
- Duc NT, Tuan PQ, Anh NTN, Liet VV (2024).

 Phenotypic diversity and selection of

- superior tropical sweetcorn inbred lines by multivariate method and combining ability analysis. *Ecol. Genet. Genom.* 30: 100215. doi: 10.1016/j.egg.2023.100215.
- Fadhli N, Farid M, Azrai M, Nur A, Efendi R, Priyanto SB, Nasruddin AD, Novianti F (2023). Morphological parameters, heritability, yield component correlation, and multivariate analysis to determine secondary characters in selecting hybrid maize. *Biodiversitas* 24(7): 3750-3757. doi: 10.13057/biodiv/d240712.
- Farid M, Azrai M, Nur A, Anshori MF, Fadhli N, Efendi R, Salengke, Musa Y, Baharuddin, Kuswinanti T, Thamrin S, Suwarno WB, Andayani NN, Bunyamin Z, Mirsam H, Priyanto SB, Suriani (2024). Evaluation of high yielding hybrid lines of unhas corn based on a systematic approach and genetic analysis. *Asian J. Plant Sci.* 23(1): 81-87. doi: 10.3923/ajps.2024.81.87.
- Gari MT, Asfaw BT, Abo LD, Jayakumar M, Kefalew G (2024). Effective utilization of agricultural cereal grains in value-added products: A global perspective. In: E. Cherian E and B. Gurunathan (eds.) Value Added Products from Food Waste. Springer Nat. Switz. doi: 10.1007/978-3-031-48143-7_3.
- Guo Y, Huang G, Guo Q, Peng C, Liu Y, Zhang M, Li Z, Zhou Y, Duan L (2023). Increase in root density induced by coronatine improves maize drought resistance in North China. *Crop J.* 11(1): 278-290. doi: 10.1016/j.cj.2022.05.005.
- Jain SK, Allard RW (1960). Population studies in predominantly self-pollinated species, I. evidence for heterozygote advantage in a closed population of barley. *Proc. Natl. Acad. Sci. USA* 46 (10): 1371-1377. doi: 10.1073/pnas.46.10.1371.
- Jiao Y, Chen H, Han H, Chang Y (2022).

 Development and utilization of corn processing by-products: A review. Foods 11: 3709. doi: 10.3390/foods11223709.
- Kalsa KK, Kolech S, Worku M, Abate T, Teklewold A (2024). The formal seed system of maize in Ethiopia: Implications for reducing the yield gap. *Int. J. Agron.* 2024: 10-12. doi: 10.1155/2024/2135433.
- Kaviriri DK, Yang L, Zhao C, Pei X, Fan Z, Wang J, Xu L, Tigabu M, You X, Li Y, Liu HZ, Zhao X (2023). Morphological growth performance and genetic parameters on Korean pine in Northeastern China. *Silvae Genet.* 72(1): 34-48. doi: 10.2478/sq-2023-0004.
- Khan R, Gao F, Khan K, Shah MA, Ahmad H, Fan ZP, Zhou XB (2024). Evaluation of maize varieties via multivariate analysis: Roles of

- ionome, antioxidants, and autophagy in salt tolerance. *Plant Physiol.* 196(1): 195-209. doi: 10.1093/plphys/kiae335.
- Korsa F, Dessalegn O, Zeleke H, Petros Y (2024). Genetic variability for the yield and yield-related traits in some maize (*Zea mays* L.) inbred lines in the central highland of Ethiopia. *Int. J. Agron.* 2024. doi: 10.1155/2024/9721304.
- Kovačević A, Pavlov J, Stevanović M, Delić N, Mutavdžić D, Živanović T (2024). Direct selection parameter estimates and path coefficient analysis for grain yield and quantitative traits in maize (*Zea mays* L.). *Rom. Agric. Res.* 41. doi: 10.59665/rar4101.
- Leite JT, Junior ATdA, Kamphorst SH, Lima VJd, Junior DRdS, Alves UO, Azeredo VC, Pereira JL, Bispo RB, Schmidt KFM, Viana FN, Viana AP, Vieira HD, Ramos HCC, Ribeiro RM, Campostrini E (2022). All are in a drought, but some stand out: Multivariate analysis in the selection of agronomic efficient popcorn genotypes. *Plants* 11: 2275. doi: 10.3390/plants11172275.
- Li K (2024). Research on the factors influencing the spatial quality of high-density urban streets:

 A framework using deep learning, street scene images, and principal component analysis. Land 13: 1161. doi: 10.3390/land13081161.
- Menkir A, Dieng I, Gedil M, Mengesha W, Oyekunle M, Riberio PF, Adu GB, Yacoubou AM, Coulibaly M, Bankole FA, Derera J, Bossey B, Unachukwu N, Ilesanmi Y, Meseka S (2024). Approaches and progress in breeding drought-tolerant maize hybrids for tropical lowlands in West and Central Africa. *Plant Genome* 17: e20437. doi: 10.1002/tpg2.20437.
- Norman PE, Kamara L, Beah A, Gborie KS, Saquee FS, Kanu SA, Kassoh FA, Norman YSGE, Kargbo AS (2024). Genetic and agronomic parameter estimates of growth, yield and related traits of maize (*Zea mays* L.) under different rates of nitrogen fertilization. *Am. J. Plant Sci.* 15: 274-291. doi: 10.4236/ajps.2024.154020.

- Paril J, Reif J, Fournier-Level A, Pourkheirandish M (2024). Heterosis in crop improvement. Plant J. 117(1): 23-32. doi: 10.1111/tpj.16488.
- Rajandran V, Ortega R, Schoor JKV, Butler JB, Freeman JS, Hecht VFG, Erskine W, Murfet IC, Bett KE, Weller JL (2022). Genetic analysis of early phenology in lentil identifies distinct loci controlling component traits. *J. Exp. Bot.* 73(12): 3963-3977. doi: 10.1093/jxb/erac107.
- Sahito JH, Zhang H, Gishkori ZGN, Ma C, Wang Z,
 Ding D, Zhang X, Tang J (2024).

 Advancements and prospects of genomewide association studies (GWAS) in maize.

 Int. J. Mol. Sci. 25: 1918. doi:
 10.3390/ijms25031918.
- Tarekegne A, Wegary D, Cairns JE, Zaman-Allah M, Beyene Y, Negera D, Teklewold A, Tesfaye K, Jumbo MB, Das B, Nhamucho EJ, Simpasa K, Kaonga KKE, Mashingaidze K, Thokozile N, Mhike X, Prasanna BM (2023). Genetic gains in early maturing maize hybrids developed by the International Maize and Wheat Improvement Center in Southern Africa during 2000–2018. Front. Plant Sci. 14: 1321308. doi: 10.3389/fpls.2023.1321308.
- Tolera B, Gedebo A, Tena E (2024). Genetic variability, character association and path analysis in sugarcane genotypes. *Arch. Agron. Soil Sci.* 70(1): 1-15. doi: 10.1080/03650340.2024.2331036.
- Yasin S, Zavala-García F, Niño-Medina G, Rodríguez-Salinas PA, Gutiérrez-Diez A, Sinagawa-García SR, Lugo-Cruz E (2024). Morphological and physiological response of maize (*Zea mays* L.) to drought stress during reproductive stage. *Agronomy* 14: 1718. doi: 10.3390/agronomy14081718.
- Zewdu D, Mekonnen F, Geleta N (2024). Cluster and principal component analysis for yield and yield-related traits of bread wheat (*Triticum aestivum* L.) genotypes. *Agric. Biol. Res.* 40(2). doi: 10.35248/0970-1907.24.40.962-967.