International Journal of Agriculture System
Vol. 11 Issue 2, December 2023
Nationally Accredited Journal Decree No. 48a/E/KPT/2017
P-ISSN: 2337-9782, E-ISSN: 2580-6815. **DOI: 10.20956/ijas.v11i2.4994**

Identification of Lines Inducing Male Sterility in Hybrid Maize

Muh Farid[1]*, Muhammad Azrai[1], Amin Nur[2], Nur Fadhli[1], Roy Efendi[3], Salengke[1], Yunus Musa[1], Baharuddin[1], Tutik Kuswinanti[1], Sulaeha Thamrin[1], Willy Bayuardi Suwarno[4], Muhammad Fuad Anshori[1], Nining Nurini Andayani[3], Bunyamin Z[3], Hishar Mirsam[3], Slamet Bambang Priyanto[3], Suriani[3], Fira Novianti[5]

[1] *Faculty of Agriculture, Universitas Hasanuddin. Jl. Perintis Kemerdekaan Km 10, Makassar 90245, South Sulawesi, Indonesia.*
[2] *Indonesian Cereal Testing Instrument Standard Institute. Jl. Dr. Ratulangi No. 274, Maros 90514, South Sulawesi, Indonesia.*
[3] *Research Center for Food Crops, Research Organization for Agriculture and Food, National Research and Innovation Agency. Cibinong Science Center, Jl. Raya Jakarta-Bogor Km. 46, Cibinong, Bogor 16911, West Java, Indonesia.*
[4] *Department of Agronomy and Horticulture, Faculty of Agriculture, IPB University, Bogor 11680, Indonesia.*
[5] *Department of Agriculture and Food Security. Jl. Dr. Ratulangi No. 57, Maros 90516, South Sulawesi, Indonesia.*

* *Corresponding author's e-mail: farid_deni@yahoo.co.id*

How to Cite: Farid, M., M. Azrai, A. Nur, N. Fadhli, R. Efendi, Salengke, Y. Musa, Baharuddin, T. Kuswinanti, S. Thamrin, W.B. Suwarno, M.F. Anshori, N.N. Andayani, B. Z, H. Mirsam, S.B. Priyanto, Suriani, F. Novianti. (2023). Identification of Lines Inducing Male Sterility in Hybrid Maize. *Int. J. Agr. Syst.* 11(2): 65-73.

ABSTRACT

Efficiency and effectiveness in controlling crossbreeding are pivotal in yielding superior hybrid varieties with desired traits such as genetic purity and high productivity. Cytoplasmic Male Sterile (CMS) is a crucial component in hybrid variety assembly. This study aims to identify the genotypes that can induce male sterile lines based on genetic diversity and the level of pollen sterility in the prospective male sterile genotypes tested, consisting of seventeen genotypes. The research findings revealed that the genetic diversity among the seventeen observed male-sterile candidate genotypes tends to vary in quantitative traits. Among the quantitative traits, JHD14 exhibited indications of being a male sterility inducer compared to the other genotypes observed, demonstrating a value of 0.00 g in terms of pollen weight. This is further substantiated by the microscopic examination of JHD14 pollen grains, which displayed 100% sterility.

Keywords:
Genotype; heritability; maize; male sterility; variance.

1. Introduction

The world's population continues to increase every day and is projected to reach 9 billion people by 2050 (Bahar et al., 2020). Experts estimate that agricultural consumption will also rise during this period. Food production needs to increase by

70%, excluding feedstock for biofuels. The agricultural sector is both the most promising and the most challenging, given its susceptibility to the impacts of global climate change. The demand for food, particularly maize, is set to surge in line with the rapidly growing population (Akdemir et al., 2023).

Maize is considered one of the most essential cereal crops globally due to its utilization in human consumption, animal feed, and food industry production (Donmez, 2022; Erenstein et al., 2022). Maize production can be enhanced through the use of high-quality hybrid seeds (Bahtiar et al., 2023). Hybrid varieties represent superior cultivars derived from plant breeding that have demonstrated increased yields compared to composite varieties. Hybrid breeding has emerged as the most effective breeding system for enhancing plant genetics, increasing yields, and improving product quality (ter Steeg et al., 2022). However, in recent years, the average national production of hybrid maize seeds has remained relatively low when compared to multinational hybrid maize varieties. Accordingly, efforts are needed to increase the yield of hybrid maize seeds to achieve high-quality hybrid maize seed production.

Achieving maximum maize production in sufficient quantities necessitates the support of appropriately designated, high-quality seeds (Donovan et al., 2022). The availability of quality seeds derived from superior hybrid varieties holds appeal for private seed companies to propagate and distribute seeds across diverse regions in adequate quantities (Bahtiar et al., 2022). Flower characteristics determine hybrid seed production, the synchronization of flowering times between parental lines, and other morphological traits influencing pollen transfer from male to female parents (Chakrabarty et al., 2023).

Morphology and floral structure wield significant influence on maize kernel yields. The development of hybrid maize is impeded by the challenging large-scale seed production, which is determined by crossbreeding capabilities (Tiwari et al., 2023). The exploitation of the male sterility phenomenon is intended to obviate the need for emasculation, which can otherwise diminish yield potential (Xu et al., 2023). Efficient and effective crossbreeding control is imperative in attaining desirable traits such as genetic purity and high productivity for the creation of superior hybrid varieties. As such, improvements in parental lines, particularly male-sterile lines, are essential for the commercialization of hybrid maize.

Male-sterile lines can be obtained spontaneously among breeding lines resulting from crosses between distantly related (interspecific) relatives or through mutagenesis. In the process of hybrid maize production, male sterile lines must possess not only perfect and stable sterility but also exhibit favorable flowering characteristics and effective cross-pollination capabilities. The success of hybrid assembly depends on the availability of lines with high receptivity and compatibility with their female counterparts, thereby ensuring a high rate of natural cross-pollination (Bai et al., 2022). The development of these male-sterile lines requires the assembly of donor and restorer lines, enabling the sustainable production of cytoplasmic male-sterile source seeds (Qin et al., 2020; Santayana et al., 2022). Increasing the efficiency of breeding programs can be done by considering genetic, phenotypic and heritability diversity (Kuswantoro, 2017). Genetic diversity is an important factor in plant breeding (Fadhli et al., 2023). This study aims to identify the genotypes that induce male sterile lines by examining genetic diversity and the level of pollen sterility in 17 candidate genotypes of male sterile lines.

2. Materials and Methods

The genetic materials used in this study were sourced from the Center for Standard Testing of Cereal Plant Instruments, Maros, South Sulawesi, Indonesia. The study was conducted in the Bajeng District, Gowa Regency, South Sulawesi, Indonesia. The collection of materials occurred between March and July 2023, at an elevation of 90 meters above sea level, with geographical coordinates of 5°18′30″ S - 119°30′22″ E. The precipitation pattern falls within the E2 classification of the Oldeman climate system, with monthly rainfall ranging from 35 - 280 mm (BMKG, 2023).

2.1 Research Design and Procedures

The study was organized following a randomized complete block design (RCBD), with each treatment unit replicated three times. The treatments consisted of 17 genotypes, resulting in a total of 51 experimental plots. Each experimental plot was planted in 5 x 1.5 m plots with a planting spacing of 75 x 20 cm. As reported by Li et al. (2022) in the effect of plant density. One seed was placed in each planting hole of adjusted to the genotype label. Each treatment unit comprised 10 plant samples, yielding a total of 510 observational samples. Maintenance activities included fertilization, pest and disease control, irrigation, and weeding. Fertilization was carried out twice according to Munir et al. (2023) with modification on the effective application of fertilizer on maize. First at 10 days after planting with 150 kg ha^{-1} of urea and 300 kg ha^{-1} of NPK (15:15:15), and later at 30 days after planting with 200 kg ha^{-1} of urea.

The observed parameters included plant height, cob height, cob length, cob diameter, row count, tassel length, pollen weight, and the identification of male sterility through the staining of pollen grains using Potassium Iodide Iodine (I_2KI), which was examined under a microscope at a magnification of 100 X. The observation technique adhered to the technical guidelines for maize adaptation experiment observation (CIMMYT, 1994)

2.2 Data Analysis

The data analysis was conducted using the STAR 2.0.1 application (IRRI, 2014). The data underwent several stages of analysis. Initially, the data were subjected to variance analysis using the analysis of variance (ANOVA) method, with a standard error of 5%. The results of this analysis were then used as the basis for determining the heritability values for each character. Subsequently, post hoc analysis least significant differences (LSD) tests were performed at a 5% significance level.

3. Results and Discussion

The analysis of variance results revealed significant differences in all observed parameter characteristics (Table 1). This indicates that each genotype exhibits distinct growth patterns and displays notable variations in various observed traits. Genotypic diversity with a significant influence of 1% (**) was evident in plant height, cob height, stem diameter, leaf length, cob length, row count, seeds per row, tassel length, and pollen weight. Meanwhile, cob diameter exhibited a significant influence of 5% (*).

The utilization of these genotypes in plant breeding programs can broaden the available germplasm diversity (Ali et al., 2023). The coefficient of variance (CV) for the observed traits ranged from 1.04% to 8.81%, signifying that it can offer a robust insight into predicting plant populations. The variability within each population caused by genotype and phenotype shows the share that is inherited in character-based phenotypic expression (Alam et al., 2022).

Table 1. Analysis of variance and morphological parameters of observed characters

Characters	MS genotype	MS error	CV (%)
Plant Height	436.34 **	29.46	2.55
Cob Height	277.76 **	16.30	3.70
Cob Length	3.88 **	0.58	3.75
Cob Diameter	18.17 *	7.12	5.76
Row Count	2.05 **	0.54	4.91
Tassel Length	20.19 **	0.60	1.93
Pollen Weight	3.95 **	0.03	8.81

Remark: **significant effect on 1%, *significant effect on 5%, MS: mean square, CV: coefficient of variance

The heritability values range from 0.34 (CD) to 0.98 (PW), indicating variations across all traits (Table 2). Almost all traits exhibit high heritability values, except for stem diameter (CD) and row count (RC), with values of 0.34 and 0.48, respectively. Meanwhile, traits demonstrating high heritability values are represented by Pollen Weight (PW) with a value of 0.98, followed by Tassel Length (TL) with a value of 0.92. Plant breeding programs can be based on the diversity of heritability values, which assist breeders in making selection decisions (Bartaula et al., 2019; Maulana et al., 2023). This implies that traits with high heritability values have a better chance of being inherited by the next generation. Heritability measures the extent to which a trait can be passed on to subsequent generations (Demeke et al., 2022).

Table 2. Estimates of genetic variance, phenotypic variance, environmental variance, and heritability

Characters	Genetic variance	Phenotypic variance	Environmental variance	Heritability
PH	135.63	165.08	29.46	0.82 (H)
CH	87.15	103.45	16.30	0.84 (H)
CL	1.10	1.68	0.58	0.66 (H)
CD	3.68	10.81	7.12	0.34 (M)
RC	0.50	1.04	0.54	0.48 (M)
TL	6.53	7.13	0.60	0.92 (H)
PW	1.31	1.34	0.03	0.98 (H)

Remark: PH: plant height, CH: cob height, CL: cob length, CD: cob diameter, RC: row count, TL: tassel length, PW: pollen weight, H: high, M: moderate.

The success of improving a particular trait through selection depends on the congruence between phenotype and genotype. Hence, the estimation of heritability values is considered highly valuable in comprehending the patterns of trait inheritance (Thakur et al., 2023). Several researchers have extensively documented heritability analysis in the selection process. As reported by Anshori et al. (2022) in the selection of salt-tolerant rice plants and Fadhli et al. (2023) in the selection of hybrid maize plants.

Based on the characterization of quantitative traits, there is one hybrid from each genotype that shows an indication as a male-sterile inducer (Table 3). JHD14 demonstrates a clear indication as a male-sterile inducer when compared to the other observed genotypes, as it exhibits a value of 0.00g for the pollen weight trait. JHD14 also displays high yield potential, with values of 21.30cm for cob length, 41.81mm for cob diameter, and 14.87 rows for row count. Therefore, it can be recommended as a candidate male-sterile inducer genotype. Genotype response to its environment also significantly determines the superiority of a hybrid in testing (Jackson et al., 2022).

Table 3. Characteristics of quantitative traits in 17 candidate male-sterile genotypes

Genotype	PH (cm)	CH (cm)	CL (cm)	CD(mm)	RC (row)	TL (cm)	PW(g)
JHD01	218.87^{bcd}	117.53^{c}	19.77^{efg}	46.08^{abcd}	14.07^{cde}	42.84^{ab}	2.69^{b}
JHD02	219.37^{bc}	117.90^{c}	22.45^{a}	40.46^{e}	14.87^{abcd}	43.79^{a}	1.24^{fg}
JHD03	191.47^{g}	95.53^{hi}	19.23^{fg}	47.08^{abc}	15.07^{abcd}	41.01^{cd}	2.59^{bcd}
JHD04	226.83^{ab}	119.23^{bc}	20.53^{bcde}	47.09^{abc}	15.33^{ab}	40.91^{cd}	5.47^{a}
JHD05	204.57^{ef}	99.53^{ghi}	20.29^{cdef}	44.64^{cde}	13.93^{de}	41.28^{cd}	2.10^{cde}
JHD06	232.80^{a}	125.40^{ab}	21.50^{abc}	45.85^{abcd}	13.40^{e}	40.20^{de}	2.69^{bc}
JHD07	209.63^{e}	109.57^{de}	19.85^{efg}	49.82^{a}	15.93^{a}	41.04^{cd}	2.00^{de}
JHD08	211.83^{cde}	109.67^{de}	20.32^{cdef}	48.44^{abc}	13.60^{e}	36.52^{hi}	1.77^{ef}
JHD09	209.80^{e}	101.27^{fghi}	19.74^{efg}	47.45^{abc}	15.60^{a}	37.42^{gh}	1.75^{ef}
JHD10	207.63^{e}	105.37^{efg}	19.90^{efg}	47.93^{abc}	15.27^{abc}	38.24^{fg}	2.42^{bcd}
JHD11	234.57^{a}	126.67^{a}	21.78^{ab}	45.29^{bcd}	14.27^{bcde}	43.48^{a}	2.65^{bc}
JHD12	204.03^{ef}	105.67^{efg}	18.88^{gh}	46.93^{abc}	15.73^{a}	39.00^{ef}	1.38^{fg}
JHD13	196.23^{fg}	101.83^{fgh}	17.67^{h}	49.40^{ab}	16.07^{a}	36.28^{hi}	1.26^{fg}
JHD14	210.03^{de}	113.40^{cd}	21.30^{abcd}	41.81^{de}	14.87^{abcd}	42.70^{ab}	0.00^{h}
JHD15	208.43^{e}	107.13^{def}	20.14^{defg}	45.66^{abcd}	15.20^{abc}	41.57^{bc}	0.96^{g}
P36	227.20^{ab}	94.63^{i}	20.88^{bcde}	44.83^{cde}	15.40^{ab}	41.30^{cd}	1.54^{efg}
BISI-18	208.07^{e}	106.20^{efg}	20.12^{defg}	48.26^{abc}	15.73^{a}	35.43^{i}	1.52^{efg}

Remark: Values followed by the same letters in one column indicate no significant difference at the 5% LSD level. PH: plant height, CH: cob height, CL: cob length, CD: cob diameter, RC: row count, TL: tassel length, PW: pollen weight.

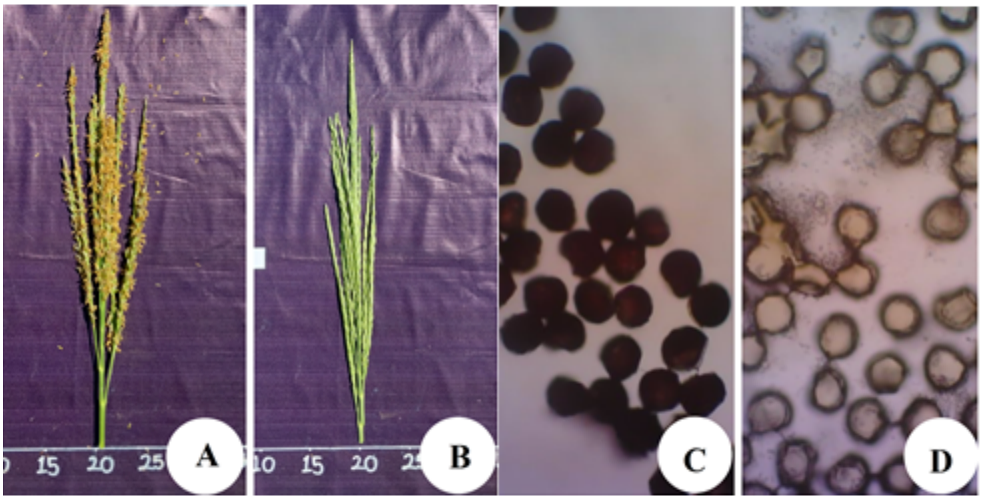

Figure 1. Visual and microscopic appearance of pollen grains. A: visual appearance of fertile pollen grains, B: visual appearance of sterile pollen grains, C: microscopic appearance of fertile pollen grains, D: microscopic appearance of sterile pollen grains.

From the above image (Figure 1), it is evident that there exists a non-functional male reproductive organ in the plant. This signifies a form of male sterility and is widely employed in plant breeding programs for hybrid variety development. This trait is typically caused by mutations in the mitochondrial genome, resulting in the production of aberrant proteins. Male sterility can be utilized to produce high genetic purity in hybrid plant varieties (Yoosefzadeh et al., 2023).

Male sterility in plants is defined as the failure of pollen to develop due to the incapacity to produce or release functional pollen. Morphological structure and flowering have a significant impact on seed yield and seed purity (Wang et al., 2022).

The utilization of male sterility allows plant breeders to develop hybrids with higher commercial potential (Dadlani, 2023). The utilization of male sterility has been extensively reported in plant breeding, as observed in studies such as Cheng et al. (2023) on cotton plants and Xiao et al. (2023) on maize plants.

4. Conclusion

Based on the research findings, it is evident that there is significant genetic diversity among the quantitative traits of the seventeen observed candidate male-sterile genotypes. In quantitative traits, JHD14 exhibits indications of being a male-sterile inducer when compared to the other observed genotypes, as it registers a value of 0.00 g for the pollen weight trait. This is further confirmed by the microscopic analysis of JHD14's pollen grains, which show a sterility rate of 100%.

Acknowledgments

We express our gratitude to the National Research and Innovation Agency (Badan Riset dan Inovasi Nasional/BRIN) and the Education Fund Management Institute (Lembaga Pengelola Dana Pendidikan/LPDP) for their financial support and the facilities provided for this research, with the cooperation agreement number 96/IV/KS/11/2022 and 4538/UN4.22/PT.01.03/2022.

References

Akdemir, S., Y.E. Miassi, I.S. Ismailla, K.F. Dossa, K.F. Oussou & O. Zannou. (2023). Corn production and processing into ethanol in Turkey: An analysis of the performance of irrigation systems at different altitudes on energy use and production costs. *Journal of Agriculture and Food Research*, 14: 1-10. https://doi.org/10.1016/j.jafr.2023.100740.

Alam, M.A., M. Rahman, S. Ahmed, N. Jahan, M.A.A. Khan, M.R. Islam, A.M. Alsuhaibani, A. Gaber & A. Hossain. (2022). Genetic variation and genotype by environment interaction for agronomic traits in maize (*Zea mays* L.) hybrids. *Plants*, 11(11): 1-16. https://doi.org/10.3390/plants11111522.

Ali, N., A. Qayyum, A. Sher, F. Nadeem, S. Fiaz, S. Kumar, B. Alharthi & S. Ercisli. (2023). Analyzing phenotypic diversity in Brassica rapa genotypes based on morpho-physiological characteristics using multivariate analyses. *Genetic Resources and Crop Evolution*, 1-12. https://doi.org/10.1007/s10722-023-01757-8.

Anshori, M.F., B.S. Purwoko, I.S. Dewi, W.B. Suwarno & S.W. Ardie. (2022). Salinity tolerance selection of doubled-haploid rice lines based on selection index and factor analysis. *AIMS Agriculture & Food*, 7(3): 520-535.

Bahar, N.H.A., M. Lo, M. Sanjaya, J.V. Vianen, P. Alexander, A. Ickowitz & T. Sunderland. (2020). Meeting the food security challenge for nine billion people in 2050: What impact on forests. *Glob. Environ. Chang*, *62*, 102056: 1-21. https://doi.org/10.1016/j.gloenvcha.2020.102056.

Bahtiar, M. Arsyad, D. Salman, M. Azrai, A. Tenrirawe, M. Yasin, A. Gaffar, A. Sebayang & P.J. Ochieng. (2023). Promoting the new superior variety of national hybrid maize: Improve farmer satisfaction to enhance production. *Agriculture*, 13(1): 174. *https://doi.org/10.3390/agriculture13010174.*

Bahtiar, D. Salman, M. Arsyad & M. Azrai. (2022). Synergy of Innovation between Hybrid Corn Seed Production and Seed Companies: A Review. *AGRIVITA, Journal of Agricultural Science*, 44(3): 604-615. http://doi. org/10.17503/agrivita. v44i3.3907.

Bai, Z., X. Ding, R. Zhang, Y. Yang, B. Wei, S. Yang and J. Gai. (2022). Transcriptome analysis reveals the genes related to pollen abortion in a cytoplasmic male-sterile soybean (*Glycine max* (L.) Merr.). *International Journal of Molecular Sciences*, 23(20): 12227. https://doi.org/10.3390/ijms232012227.

Bartaula, S., U. Panthi, K. Timilsena, S.S. Acharya & J. Hrestha. (2019). Variability, heritability and genetic advance of maize (*Zea mays* L.) genotypes. *Research in Agriculture Livestock and Fisheries*, 6(2): 163-169.

BMKG [Badan Meteorologi Klimatologi dan Geofisika]. 2023. Monthly Rainfall Data. Meteorology, Climatology and Geophysics Agency, Climatology Station Class I, Maros, South Sulawesi.

Chakrabarty, S.K., S. Basu & W. Schipprach. (2023). Hybrid seed production technology. *In: Seed Science and Technology: Biology, Production, Quality* (Ed. Dadlani, M., & Yadava, D. K.), Springer, Singapore, 173-212.

Cheng, C., H. Nie, H. Li, D. Adjibolosoo, B. Li, K. Jiang, Y. Cui, M. Zhu, B. Zhou, A. Guo & J. Hua. 2023. Identification of fertility restoration candidate genes from a restorer line R186 for Gossypium harknessii cytoplasmic male sterile cotton. *BMC Plant Biology*, *23*(1): 1-15. https://doi.org/10.1186/s12870-023-04185-z.

CIMMYT [International Maize and Wheat Improvement Center]. 1994. Managing trials and reporting data for CIMMYT's international maize testing program. CIMMYT, Mexico.

Dadlani, M. (2023). Emerging trends and promosing technologies. In: Dadlani, M., Yadava, D. K. (eds) Seed Science and Technology. Springer, Singapura.

Demeke, B., T. Dejene & D. Abebe. (2022). Genetic variability, heritability, and genetic advance of morphological, yield related and quality traits in upland rice (*Oryza sativa* L.) genotype at pawe, northwestern Ethiopia. *Cogent Food & Agriculture*, 9(1): 2157099. https://doi.org/10.1080/23311932.2022.2157099.

Dönmez, E. (2022). Enhancing classification capacity of CNN models with deep feature selection and fusion: A case study on maize seed classification. *Data & Knowledge Engineering*, 141: 102075. https://doi.org/10.1016/j.datak.2022.102075.

Donovan, J., P. Rutsaert, C. Dominguez & M. Peña. (2022). Capacities of local maize seed enterprises in Mexico: Implications for seed systems development. *Food Security*, 1-21. https://doi.org/10.1007/s12571-021-01247-8.

Erenstein, O., M. Jaleta, K. Sonder, K., Mottaleb & B.M. Prasanna. (2022). Global maize production, consumption and trade: trends and R&D implications. *Food Security,* 14: 1295-1319. https://doi.org/10.1007/s12571-022-01288-7.

Fadhli, N., M. Farid, M. Azrai, A. Nur, R. Efendi, S.B. Priyanto, A.D. Nasruddin & F. Novianti. (2023). Morphological parameters, heritability, yield component correlation, and multivariate analysis to determine secondary characters in selecting hybrid maize. *Biodiversitas,* 24(7): 3750-3757. https://doi.org/10.13057/biodiv/d240712

IRRI [International Rice Research Institute]. (2014). Statistical tool for agricultural research version 2.0.1. Biometrics and Breeding Informatics. Plant Breeding, Genetics, and Biotechnology Division. International Rice Research Institute, Los Banos, Laguna.

Jackson, D., F. Tian & Z. Zhang, (2022). Maize genetics, genomics, and sustainable improvement. *Molecular Breeding*, 42(1), 2. https://doi.org/10.1007/s11032-021-01266-5.

Kuswantoro, H. (2017). Genetic variability and heritability of acid-adaptive soybean promising lines. *Biodiversitas,* 18 (1): 378-382. https://doi.org/10.13057/biodiv/d180148.

Li, Y.C., H.Y. Dai & H. Cgen. (2022). Effects of plant density on the aboveground dry matter and radiation-use efficiency of field corn. *Plos One*, 17(11): e0277547. https://doi.org/10.1371/journal.pone.0277547.

Maulana, H., Y. Maxiselly, Y. Yuwariah & D. Ruswandi. (2023). Heritability and Selection Using GGE Biplots and the Sustainability Index (SI) of Maize Mutants under Different Cropping Systems in Upland. *Sustainability,* 15(8): 6824. https://doi.org/10.3390/su15086824.

Munir, J., S. Syahrial, Y. Rahmawati, L. Hasmi & W. Relmayeni. (2023). Effectiveness application of fertilizer on maize: The case study of maize farmers in West Pasaman Regency. *E3S Web. Conferences,* 373: 03011. DOI:10.1051/e3sconf/202337303011.

Qin, X., W. Zhang, X. Dong, S. Tian, P. Zhang, Y. Zhao, Y. Wang, J. Yan and B. Yue. (2020). Identification of fertility-related genes for maize CMS-S via bulked segregant RNA-seq. *PeerJ.* 8: e10015. https://doi.org/10.7717/peerj.10015.

Santayana, M., M. Aponte M. Kante, R. Eyzaguirre, M. Gastelo & H. Lindqvist-Kreuze. (2022). Cytoplasmic Male Sterility Incidence in Potato Breeding Populations with Late Blight Resistance and Identification of Breeding Lines with a Potential Fertility Restorer Mechanism. *Plants*, 11(22): 3093. https://doi.org/10.3390/plants11223093.

ter Steeg, E.M.S., P.C. Struik, R.G.F. Visser & P. Lindhout. (2022). Crucial factors for the feasibility of commercial hybrid breeding in food crops. *Nature Plants*, 8(5): 463-473. https://doi.org/10.1038/s41477-022-01142-w.

Thakur, D.K., S.K. Sinha, N.M. Mehta & N. Prabha. (2023). Studies of genetic variability, heritability and genetic advance for grain yield and its contributing traits in maize (*Zea mays* L.) hybrids. *Pharma Innov. J.,* 12(7): 754-757.

Tiwari, A., S.K. Tikoo, S.P. Angadi, S.B. Kadaru, S.R. Ajanahalli & M.J.V. Rao. (2023). Inbred Line Development and Hybrid Breeding. In: *Market-Driven Plant Breeding for Practicing Breeders.* Springer, Singapore, 101-106. https://doi.org/10.1007/978-981-19-5434-4_4.

Wang, Y., J. Bao, X. Wei, S. Wu, C. Fang, Z. Li, Y. Qi, Y. Gao, Z. Dong & X. Wan. (2022). Genetic structure and molecular mechanisms underlying the formation of tassel, anther, and pollen in the male inflorescence of maize (*Zea mays* L.). *Cells*, 11: 1753. https://doi.org/10.3390/cells11111753.

Xiao, S., W. Song, J. Xing, A. Su, Y. Zhao, C. Li, Z. Shi, Z. Li, S. Wang, R. Zhang, Y. Pei, H. Chen & J. Zhao. (2023). ORF355 confers enhanced salinity stress adaptability to S-type cytoplasmic male sterility maize by modulating the mitochondrial metabolic homeostasis. *J. Integr. Plant Biol,* 65(3): 656-673. https://doi.org/10.1111/jipb.13382.

Xu, C., Y. Xu, Z. Wang, X. Zhang, Y. Wu, X. Lu, H. Sun, L. Wang, Q. Zhang, Q. Zhang, X. Li, J. Xiao, X. Li, M. Zhao, Y. Ouyang, X. Huang & Q. Zhang. (2023). Spontaneous movement of a retrotransposon generated genic dominant male sterility providing a useful tool for rice breeding. *National Science Review*, 10(9): nwad210. https://doi.org/10.1093/nsr/nwad210.

Yoosefzadeh N.M., M. Hesami & I. Rajcan. (2023). Unveiling the Mysteries of Non-Mendelian Heredity in Plant Breeding. *Plants*, 12(10), 1956: 1-20 https://doi.org/10.3390/plants12101956.