

Genetic Variability and Selection of Doubled Haploid Lines of Eggplant (*Solanum melongena* L.) Obtained from Anther Culture

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Genetic variability is essential for accelerating the selection of high-yield varieties. Therefore, this study aims to evaluate the genetic variability and agronomic performance of eggplant doubled haploid obtained through anther culture. A total of 18 genotypes (15 doubled haploid lines and 3 commercial varieties) were assessed using a randomised complete block design with 4 replications. Data were analysed for heritability, cluster analysis, phenotypic correlations, and a weighted selection index. Significant variation was observed among genotypes, with stem diameter, plant height, fruit number, fruit weight, and fruit length showing high heritability and extensive genetic diversity. In addition, cluster analysis grouped the genotypes into 3 clusters at a 20% similarity threshold. The results showed that fruit weight per plant exhibited strong positive correlations with fruit weight, diameter, length, stalk length, plant height, and stem diameter. The weighted selection index identified 11 promising doubled haploid lines, including derivatives of Hitavi F1 (AM8H, AM9H, AM10H, and AM11H), Mustang F1 (AM13M and AM14M), and Provita F1 (AM4P, AM6P, AM23P, AM28P, and AM29P). These results indicated the strong potential of the selected doubled haploid lines for eggplant variety development.

Key words: cluster analysis, doubled haploid, heritability, phenotypic correlation, weighted selection index

Eggplant (*Solanum melongena* L.) is a significant horticultural commodity in the Solanaceae family and ranks as the third most widely cultivated vegetable globally, after tomato and potato (Taher *et al.* 2017). High consumption of eggplant has been observed particularly in Asia and the Mediterranean (Chapman 2019). Recognised for its nutritional value, it is typically low in calories, as well as contains vitamins, minerals, and bioactive compounds that

are beneficial to human health (Docimo *et al.* 2016). The importance of eggplant as a food commodity has become increasingly significant due to the continued growth of the global population and increasing demand for nutritious vegetables.

According to the FAO (2023a), global eggplant production increased by 10.58%, from 53.5 million tonnes in 2019 to 59.3 million tonnes in 2022. This increase in production is inversely related to the ex-

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pansion of harvest area. The FAO (2023b) reported that the harvested area of eggplant fluctuated during the same period. Therefore, productivity improvements must increasingly depend on genetic enhancements rather than land expansion. This emphasises the urgent need to develop high-yielding and genetically stable varieties capable of maximising production efficiency under limited land resources.

Conventional plant breeding through crosses is expensive and usually requires 8 to 10 generations to produce pure lines (Wanga *et al.* 2021), making the process time-consuming and resource-intensive. The anther culture technique provides a more efficient option by generating doubled haploid plants in a considerably shorter period, compared to selfing or repeated selection methods in traditional breeding (Sendra *et al.* 2017; Mulyana *et al.* 2023a). This indicates that the technique enables the creation of pure lines in a generation (Niazian & Shariatpanahi 2020), speeding up breeding cycles and enhancing the accuracy of phenotypic evaluation. The resulting doubled haploid plants can be used directly as hybrid parents (Mulyana *et al.* 2023a), making doubled haploid technology a potent tool to accelerate genetic improvement in eggplant breeding programmes.

Despite these advantages, doubled haploid lines must be carefully analysed by assessing genetic variability to facilitate the effective selection of superior genotypes for variety development. Genetic variability is a vital prerequisite for plant breeding as it influences the efficiency of selection and the potential for genetic improvement. High genetic variability enhances the success of breeding programmes by providing a broader range of genetic diversity, thereby enabling the effective selection of superior genotypes based on specific criteria (Begna 2021).

Previous studies have produced doubled haploid lines from anther culture, which require assessment of genetic variability and performance (Mulyana *et al.* 2023a). However, comprehensive information on the genetic variability and agronomic performance of these lines is still lacking. This shows that their evaluation is crucial to identify promising genotypes and optimise the use of doubled haploid technology in eggplant breeding programmes. Therefore, this study aims to assess the genetic variability and agronomic traits of doubled haploid lines of eggplant

(*Solanum melongena* L.) produced through anther culture. The results are expected to help in identifying superior genotypes with high yield potential and to enhance the use of doubled haploid technology in eggplant breeding programmes.

MATERIAL AND METHODS

Study Design

This study was conducted from September 2023 to February 2024 in a greenhouse at the Indonesian Center for Standard Testing of Biotechnology and Agricultural Genetic Resources (BBPSI Biogen), Bogor, West Java, Indonesia (6.57°S, 106.7°E). The average daily temperature ranged from 26°C to 36°C. The experimental design used was a randomised complete block design (RCBD) with 4 replications. The genotype factors included 15 doubled haploid lines and 3 check varieties, namely Hitavi F1, Provita F1 and Mustang F1. In addition, the ploidy levels of the doubled haploid lines were previously validated using flow cytometry, as reported by Mulyana *et al.* (2023b). Each experimental unit consisted of a single plant, resulting in a total of 72 experimental units. The 18 eggplant genotypes used in this study are shown in Table 1.

Study Procedure

The growing medium consisted of soil, husk charcoal, and manure in a ratio of 7:1:1. Each genotype was sown with 10 seeds in seedling trays and grown for 4 weeks or until the plants developed 3 to 5 true leaves. The seedlings were then transferred to plastic buckets containing 10 kg of substrate. Maintenance activities included watering, replanting, fertilising, weeding, as well as pest and disease control. Basic fertilisation involved NPK 16-16-16 at a concentration of 10 g/L per plant, applied during sowing. Additional fertilisation was carried out at 1 to 3 weeks after planting (5 g/L) and at 4 to 6 weeks after planting (10 g/L) through watering. Each fertilisation dose was 250 mL per plant. Pest and disease control measures were implemented according to the recommended dose. Harvesting was conducted in stages, with up to 12 harvests occurring between December 2023 and February 2024. The observed agronomic characteristics followed the individual

observation guide (IOP) issued by the Center for Plant Variety Protection and the Agricultural Licensing Center (PPVTPP) of the Ministry of Agriculture of Indonesia (2007).

Data Analysis

Analysis of variance (ANOVA) was performed on agronomic traits, and Dunnett's t-test was carried out at the $\alpha=5\%$ level using SAS software (OnDemand for Academics; SAS Institute Inc.; Cary, NC, USA). Variability among genotypes was assessed through the range, mean, standard error, phenotypic variance, genotypic variance, and coefficient of variation (CV). The variance components were used to calculate phenotypic and genotypic variation. Genetic parameters and heritability were estimated following the methodology described by Magar *et al.* (2021):

$$\sigma^2_e = MSE$$

$$\sigma^2_g = \frac{MSG - MSE}{r}$$

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

Description: σ^2_e : error variance, σ^2_g : genotypic variance, σ^2_p : phenotypic variance, MSG : mean square of genotypes, MSE : mean square error, r : number of replications.

The standard deviation of genetic variability was calculated using the following formula:

$$\sigma_{\sigma^2_g} = \sqrt{\frac{2}{r^2} \left[\frac{[MSG^2]}{dfg+2} + \frac{[MSE^2]}{dfe+2} \right]}$$

Criteria: $\sigma^2_g > 2 \sigma_{\sigma^2_g}$: broad, $\sigma^2_g < 2 \sigma_{\sigma^2_g}$: narrow (Asghar & Mehdi 2010).

Description: dfg : degrees of freedom for genotypes, dfe : degrees of freedom for error.

The coefficient of variability for the genotypes and phenotypes was calculated using the formula described by Holland *et al.* (2010):

$$GCV (\%) = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100\%$$

$$PCV (\%) = \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100\%$$

Description: $\bar{x}$: means, σ^2_g : genotypic variance, σ^2_p : phenotypic variance, GCV : genotypic coefficient of variation, PCV : phenotypic coefficient of variation.

The GCV and PCV values were categorised into three classes: low ($<10\%$), medium ($10-20\%$), and high ($>20\%$).

Heritability in the broad sense is the ratio of the total genotypic variance (σ^2_g) to the phenotypic variance (σ^2_p), which is calculated as a percentage (%). Heritability was calculated for each trait using the following formula:

$$h^2_{bs} = \frac{\sigma^2_g}{\sigma^2_p} \times 100\%$$

Description: h^2_{bs} : heritability in the broad sense, σ^2_g : genotypic variance, σ^2_p : phenotypic variance.

Heritability in the broad sense was categorised into three classes (Yeshiwas & Negash 2017): low ($<30\%$), moderate ($30-60\%$), and high ($>60\%$).

Pearson's correlation test was performed using the matrix method of Singh and Chaudhary (1979) with RStudio software (version 2024.04.2+764; RStudio).

T a b l e 1

Genetic material of eighteen eggplant genotypes

No	Genotype	No	Genotype	No	Genotype
1.	AM3 [P]	7.	AM10 [H]	13.	AM28 [P]
2.	AM4 [P]	8.	AM11 [H]	14.	AM29 [P]
3.	AM5 [P]	9.	AM13 [M]	15.	AM34 [P]
4.	AM6 [P]	10.	AM14 [M]	16.	Hitavi F1
5.	AM8 [H]	11.	AM22 [P]	17.	Provita F1
6.	AM9 [H]	12.	AM23 [P]	18.	Mustang F1

Note: The letters in parentheses represent the codes indicating the parent's name: (P) – Provita F1, (H) – Hitavi F1, (M) – Mustang F1. No – Number.

dio, PBC; Boston, MA, USA). The strength of correlation was interpreted as negligible (0.00–0.10), weak (0.10–0.39), moderate (0.40–0.69), strong (0.70–0.89), and very strong (0.90–1.00) following (Schober *et al.* 2018). Selection was based on a weighted selection index constructed from 6 characteristics, namely fruit weight per plant (+5), weight per fruit (+5), fruit diameter (+5), fruit length (+5), dichotomous height (+2), and stem diameter (+2). These 6 characters were selected based on F-test results, high heritability values, and their correlations with yield. The weighted selection index was calculated using a linear combination of standardized trait values, following the general selection index approach described by Rathod *et al.* (2023):

$$I = \sum b_i Z_i$$

Description: I : selection index, b_i : weight of the i -th variable, Z_i : standardized value (Z-score) of the i -th variable.

$$Z_i = \frac{(x_i - \bar{x})}{\sigma}$$

Description: x_i : the observed value of the variable, $\bar{x}$: the mean value of the variable, σ : standard deviation.

RESULTS AND DISCUSSION

Agronomic Characters of Eighteen Eggplant Genotypes

ANOVA showed that genotype significantly influenced most traits, except for petiole length, leaf length, leaf width, and flowering time (Table 2). The coefficient of variation reflected the relative variability and precision of the experiment. A lower coefficient of variation suggested precise data collection (Ritonga *et al.* 2018).

The observation of growth characteristics (Table 3) showed that the average plant height ranged from 80.85 to 120.58 cm. Variation in plant height reflected differences in vegetative vigour among genotypes, which was a key determinant of canopy architecture, light interception efficiency, and assimilate production. The genotype with the tallest plant was AM11H (120.58 cm), and the shortest was

AM22P (80.85 cm). Dichotomous height exhibited a mean value ranging from 18.50 to 36.88 cm. The genotype with the greatest dichotomous height was AM29P (30.35 cm), while the one with the lowest was AM4P (18.50 cm). Both plant height and dichotomous height affected the position of the fruit on the ground. Shorter dichotomous heights could increase the risk of disease, as the fruit was in direct contact with mulch and was more exposed to water splashes. Based on this study, the average stem diameter ranged from 1.06 to 2.05 cm. Differences in stem diameter reflected variation in vascular tissue development and mechanical strength, which were essential for assimilate translocation and lodging resistance. The genotype with the thickest stem was AM14M (2.05 cm), and the thinnest was AM34P (1.21 cm). A greater stem diameter enhanced the number of vascular cells, which improved structural strength and resistance to lodging (Bisht *et al.* 2022). Therefore, plant height, dichotomous height, and stem diameter could be considered important selection criteria for improving plant architecture and yield stability.

Leaf length and width did not show significant differences among the tested genotypes, with mean values ranging from 19.83 to 29.95 cm and 12.93 to 14.68 cm, respectively (Table 3). The lack of significant variation showed limited genetic variability for these traits within the evaluated population. The genotypes AM8H (29.95 cm) and AM22P (15.03 cm) had the longest and widest leaves, respectively. A larger leaf area provided greater light-interception capacity and enhanced photosynthetic efficiency (Yang *et al.* 2022). However, the relatively uniform leaf size showed that these traits contributed less to yield differentiation under the present conditions and could not be priority targets for selection. Petiole length did not differ significantly among the tested genotypes, with mean values ranging from 5.93 to 9.28 cm. The genotype with the longest petiole was AM10H (9.28 cm) (Table 3).

Flowering time was influenced by genetic and environmental factors, including exposure duration, temperature, and stress (Cho *et al.* 2016), and early flowering was a desirable trait in plants. This study found that flowering time had a mean range from 30.5 to 33.0 days after planting (DAP), as shown in Table 3. The genotype with the earliest flowering

time was AM10H (30.5 DAP). The average harvest time ranged from 40.5 to 47.3 DAP (Table 3). The genotype with the shortest harvest time was Hitavi F1 (40.5 DAP). Harvest time was an important trait used to evaluate the superiority of varieties.

Yield components were essential traits for crop selection. Fruit weight per plant was one of the key traits for domestication and long-term improvement (Zhao *et al.* 2022). The fruit weight per plant depended on both the number of fruits and the weight of each fruit. This study observed that the average number of fruits per plant ranged from 6.3 to 43.0, with the genotype AM28P having the highest number of fruits (43.0). The average fruit weight per plant ranged from 345.16 to 1,292.20 g, while the weight per fruit varied from 24.15 to 137.69 g. The genotype with the highest weight per fruit and the greatest fruit weight per plant was Hitavi F1, with a weight per fruit of 137.69 g and a fruit weight per plant of 1,292.20 g (Table 4).

The observations on fruit diameter, fruit stalk length, and fruit length ranged from 3.57 to 5.11 cm,

2.96 to 7.77 cm, and 3.78 to 21.57 cm, respectively (Table 4). The genotype with the largest fruit diameter was AM11H (4.88 cm), the longest fruit stalk was AM10H (7.77 cm), and the longest fruit was Hitavi F1 (22.16 cm). The observed variation in fruit morphology further confirmed the presence of considerable genetic diversity among genotypes. Variability in fruit morphology was mainly caused by genetic factors and was slightly affected by environmental factors. Fruit morphological variability was also influenced by adaptability to salinity stress (Sobir *et al.* 2018) and temperature changes (Angio 2016). This variability was particularly important for breeding programmes, as it allowed the development of varieties tailored to specific market preferences and environmental conditions.

Cluster Analysis of 18 Eggplant Genotypes

Cluster analysis aimed to group genotypes with similar characteristics into distinct clusters. The Euclidean distance measured the similarity between the genotypes. Smaller Euclidean distances indica-

T a b l e 2

Mean square for 14 characters in 18 eggplant genotypes

Character	Means	S.E	Range	Mean square		CV [%]
				Replication	Genotype	
Plant height	107.92	14.80	80.85–120.58 cm	66.56	441.36 ⁺⁺	11.49
Dichotomous height	26.28	6.74	18.50–36.88 cm	55.00	131.11 ⁺⁺	15.40
Stem diameter	1.52	0.35	1.06–2.05 cm	0.01	0.36 ⁺⁺	14.68
Leaf length	24.91	4.29	19.83–29.95 cm	13.57	24.43 ^{ns}	16.41
Leaf width	13.17	0.78	12.93–15.03 cm	0.39	1.30 ^{ns}	9.75
Petiole length	7.23	1.81	5.93–9.28 cm	12.39	4.16 ^{ns}	21.65
Flowering time	31.30	1.23	30.50–33.00 days	7.94	2.46 ^{ns}	5.26
Harvesting time	44.00	3.63	40.50–47.30 days	16.48	22.21 ⁺	7.18
Fruit diameter	4.15	0.49	3.57–5.11 cm	0.04	0.68 ⁺⁺	7.82
Fruit length	10.39	7.98	3.63–22.16 cm	1.62	259.94 ⁺⁺	12.94
Fruit stalk length	4.47	1.90	2.96–7.77 cm	1.09	8.18 ⁺⁺	12.02 ^t
Number of fruits	17.61	11.64	6.30–43.00	0.61	6.12 ⁺⁺	16.49 ^t
Weight per fruit	68.01	49.17	24.15–137.69 g	727.70	8,820.66 ⁺⁺	14.51 ^t
Fruit weight per plant	843.99	353.52	249.63–1,292.20 g	23,676.99	315,879.88 ⁺⁺	15.36 ^t

Note: CV – coefficient of variation; t – transformed data $\sqrt{(x+0.25)}$, ns ($p > 0.05$), ⁺($p < 0.05$), ⁺⁺($p < 0.01$), ⁺⁺⁺($p < 0.001$). S.E – standard error.

T a b l e 3

Growth characters of eighteen eggplant genotypes

Genotype	PH [cm]	DH [cm]	SD [cm]	PL [cm]	LL [cm]	LW [cm]	FT [DAP]	HT [DAP]
AM3 [P]	111.50	27.00	1.25 ^b	5.93	19.83	13.38	33.0	42.0
AM4 [P]	92.35	18.50 ^b	1.26 ^b	5.98	23.48	12.93	30.8	47.3 ^a
AM5 [P]	105.53	20.28 ^b	1.27 ^{ab}	6.50	26.45	13.15	32.8	45.5
AM6 [P]	102.15	22.65	1.30 ^b	8.25	25.25	14.28	32.0	45.5
AM8 [H]	115.85	28.15	1.90 ^c	9.05	29.95	14.48	31.0	47.3 ^a
AM9 [H]	112.15	24.18	1.55 ^b	7.55	27.25	13.20	31.3	47.3 ^a
AM10 [H]	113.50	35.30 ^{ac}	1.54 ^b	9.28	27.13	14.20	30.5	42.0
AM11 [H]	120.58	33.05	1.64	7.40	22.95	14.10	32.3	40.5
AM13 [M]	119.05	32.93	1.82 ^c	6.78	22.08	13.40	31.5	45.5
AM14 [M]	118.58	36.88 ^{abc}	2.05 ^c	7.30	25.85	14.08	31.0	41.0
AM22 [P]	80.85 ^{abc}	18.83 ^b	1.06 ^{ab}	7.63	24.78	15.03	32.5	45.5
AM23 [P]	113.20	25.48	1.29 ^b	6.03	23.30	14.43	32.8	42.0
AM28 [P]	91.73	20.03	1.49 ^b	5.93	23.58	13.98	31.3	45.5
AM29 [P]	106.23	30.35	1.70	7.38	27.98	14.50	33.0	43.3
AM34 [P]	107.88	21.23	1.21 ^{ab}	7.73	26.93	13.45	31.5	45.5
Hitavi F1	112.38	25.53	1.70	8.08	26.78	14.43	32.5	40.5
Mustang F1	112.13	27.95	2.03	6.68	24.38	13.73	32.5	42.3
Provita F1	108.40	25.88	1.29	6.30	22.60	14.68	31.5	43.8

Note: PH – plant height; DH – dichotomous height; SD – stem diameter; PL – petiole length; LL – leaf length; LW – leaf width; FT – flowering time; HT – harvesting time; DAP – days after planting; a – significantly different from hitavi F1 at the 5% level of *t*-Dunnnett test; b – significantly different from Mustang F1 at the 5% level of *t*-Dunnnett test; c – significantly different from Provita F1 in the *t*-Dunnnett test at the 5% level.

ted greater similarity between genotypes (Tan *et al.* 2022). A heatmap was a commonly used statistical visualisation tool for revealing patterns between columns and rows (Zuguang 2022). Cluster analysis based on quantitative traits grouped the 15 lines and 3 check varieties into 3 main clusters (similarity levels of 22.02–80.07), as shown in Figure 1. This wide range of similarity values indicated the presence of substantial phenotypic divergence among the evaluated genotypes.

The key distinguishing features included fruit weight per plant, weight per fruit, fruit length, petiole length, and fruit diameter. Cluster 1a comprised 10 genotypes with short fruits, a high number of fruits, low fruit weight per plant, and small fruit diameters. Cluster 1b consisted of 1 genotype with short fruits, many fruits, high fruit weight per plant,

and a large fruit diameter. Cluster 2 included 4 genotypes with long fruits, fewer fruits, high fruit weight per plant, and large diameters. Cluster 3 contained 3 genotypes with long, purple fruits, few fruits, high fruit weight per plant, and large fruit diameters. Photographs of representative plants and fruits from all 18 genotypes are shown in Figure 3 to further illustrate the clustering results. These images confirmed the phenotypic uniformity of the doubled haploid lines and showed the morphological differences among the clusters.

The colour intensity in the cluster analysis indicated the strength or level of each genotype's value for a specific trait (Lee *et al.* 2016). This visual representation facilitated the identification of key traits contributing to genotype differentiation and emphasised the relative importance of yield-rela-

T a b l e 4

Yield characters of eighteen eggplant genotypes

Genotype	FD [cm]	FSL [cm]	FL [cm]	NFP	WPF [g]	FWP [g]
AM3 [P]	3.97	3.35 ^a	3.91 ^{ab}	23.0 ^b	27.61 ^{ab}	652.45 ^a
AM4 [P]	3.93	3.14 ^a	4.24 ^{ab}	26.0 ^{ab}	32.97 ^{ab}	782.68
AM5 [P]	4.02	3.75 ^a	3.94 ^{ab}	11.3 ^c	28.39 ^{ab}	345.16 ^{abc}
AM6 [P]	3.91	4.17 ^a	3.99 ^{ab}	31.0 ^{ab}	29.34 ^{ab}	722.62
AM8 [H]	4.57 ^c	5.70	19.50 ^c	7.5 ^c	131.52 ^c	996.05
AM9 [H]	4.00	3.69 ^a	4.20 ^{ab}	23.0 ^b	33.99 ^{ab}	666.03 ^a
AM10 [H]	3.57 ^{ab}	7.77 ^c	18.27 ^c	8.8 ^c	112.73 ^c	952.48
AM11 [H]	4.88 ^c	5.74	20.45 ^c	7.0 ^c	106.72 ^c	1,049.18
AM13 [M]	4.28	4.71	21.57 ^c	6.3 ^c	130.61 ^c	785.82
AM14 [M]	4.28	4.50 ^a	18.48 ^c	10.8 ^c	114.32 ^c	1,030.67
AM22 [P]	4.02	3.76 ^a	3.91 ^{ab}	8.5 ^c	33.88 ^{ab}	249.63 ^{abc}
AM23 [P]	4.04	3.63 ^a	4.67 ^{ab}	22.3	32.02 ^{ab}	764.36
AM28 [P]	3.63 ^{ab}	2.96 ^a	3.78 ^{ab}	43.0 ^{abc}	24.15 ^{ab}	1,091.94
AM29 [P]	5.11 ^{ac}	3.62 ^a	5.59 ^{ab}	18.5	59.08 ^{ab}	1,116.23
AM34 [P]	3.77 ^b	3.36 ^a	3.63 ^{ab}	23.8 ^{ab}	24.52 ^{ab}	580.05 ^a
Hitavi F1	4.33	7.62	22.16	9.8	137.69	1,292.20
Mustang F1	4.52	5.24	20.58	9.0	133.28	1,130.90
Provita F1	3.82	3.61	3.83	27.8	30.29	1,001.66

Note: FD – fruit diameter; FSL – fruit stalk length; FL – fruit length; NFP – number of fruits per plant; WPF – weight per fruit; FWP – fruit weight per plant. a – significantly different from hitavi F1 at the 5% level of *t*-Dunnnett test; b – significantly different from Mustang F1 at the 5% level of *t*-Dunnnett test; c – significantly different from Provita F1 in the *t*-Dunnnett test at the 5% level.

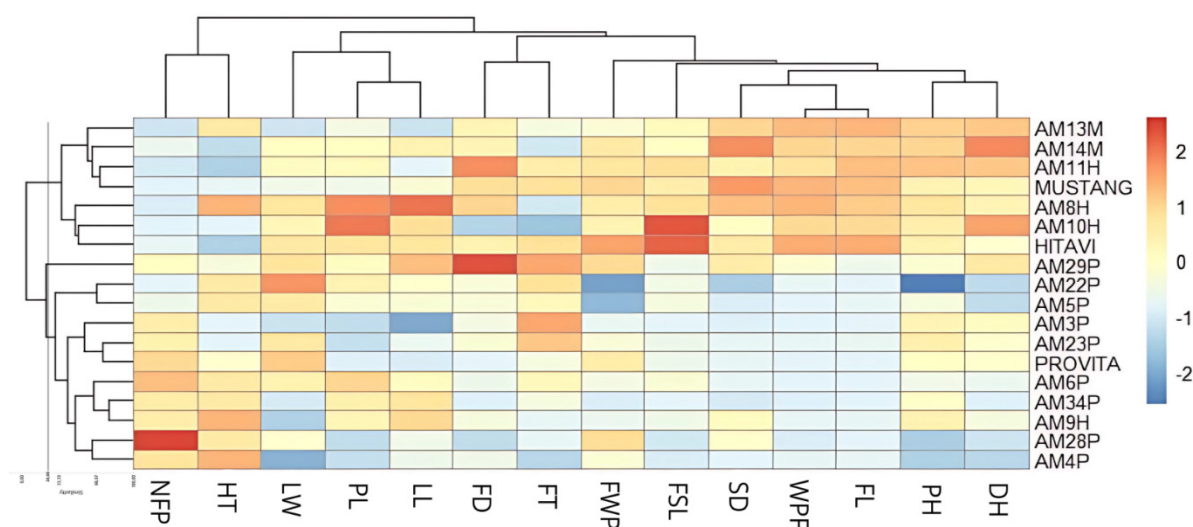


Figure 1. Cluster analysis between 15 doubled haploid lines and 3 comparison varieties based on quantitative characters. Note: PH – plant height; DH – dichotomous height; SD – stem diameter; PL – petiole length; LL – leaf length; LW – leaf width; FT – flowering time; HT – harvesting time; FD – fruit diameter; FSL – fruit stalk length; FL – fruit length; NFP – number of fruits per plant; WPF – weight per fruit; FWP – fruit weight per plant.

ted characters in cluster formation. Darker colours signified a higher value for that trait. This made it easy to interpret genotype group characteristics by observing the colour contrasts between groups. The 3 commercial check varieties (Mustang F1, Hitavi F1 and Provita F1) were grouped with their respective doubled haploid derivatives (suffixes M, H and P), confirming that the doubled haploid lines originated from anther culture. This grouping pattern suggested similarity between several doubled haploid lines and their respective source cultivars.

However, several doubled-haploid lines were distinctly separated from their parental checks, reflecting relatively high phenotypic variability. This differentiation suggested variation in trait expression among the doubled haploid lines, which was associated with underlying genetic differences. This variability offered an important advantage for breeding, as it allowed the identification of both doubled haploid lines similar to their parents and divergent

lines that contributed to novel trait combinations. Greater phenotypic differences among genotypes increased the potential for selecting contrasting parental lines in breeding programmes. Genetic variability among genotypes enhanced breeding potential, as crosses between genetically distant genotypes tended to produce better results (Pahadi *et al.* 2017). High yields were mainly attributed to the high productivity of the selected parent genotypes (Khan *et al.* 2022).

Genetic Parameters of Eighteen Eggplant Genotypes

Broad genetic variability was crucial for plant breeding, especially in selecting improved traits (Andini *et al.* 2021). This study identified significant variability in stem diameter, dichotomous height, number of fruits, fruit length, fruit weight, fruit diameter, fruit stalk length, and fruit weight per plant (Table 5). The presence of broad variability in these

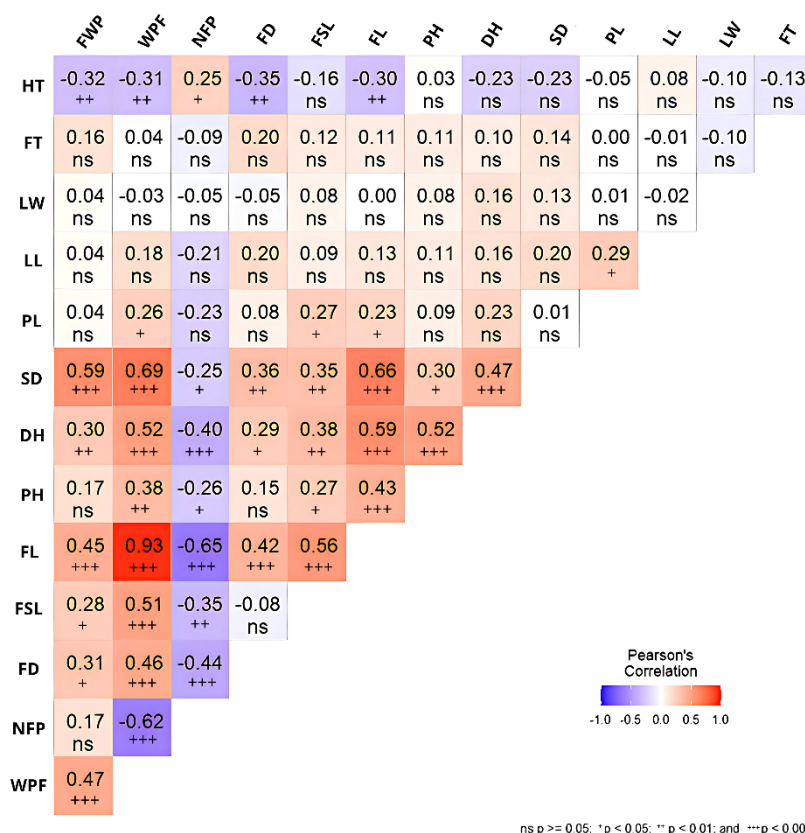


Figure 2. Pearson's correlation coefficients among agronomic traits of 18 eggplant genotypes (15 doubled haploid lines and 3 commercial checks). Red indicates positive correlations, blue indicates negative correlations, and the significance levels are shown as ns (not significant), + $p < 0.05$, ++ $p < 0.01$, and +++ $p < 0.001$. Note: PH – plant height; DH – dichotomous height; SD – stem diameter; PL – petiole length; LL – leaf length; LW – leaf width; FT – flowering time; HT – harvesting time; FD – fruit diameter; FSL – fruit stalk length; FL – fruit length; NFP – number of fruits per plant; WPF – weight per fruit; FWP – fruit weight per plant.

traits indicated a wide genetic base within the evaluated population, which was essential for achieving effective selection gains. The success of selection relied on variability influenced by genetic factors (Usman *et al.* 2017). A high GCV value signified substantial genetic variability in a trait, while a low GCV value indicated limited genetic variability (Sudika *et al.* 2021). In this study, traits with high GCV values, such as the number of fruits, weight per fruit, and fruit length, demonstrated a high potential for improvement through selection.

The broad genetic variability and high heritability estimate for stem diameter, dichotomous height, number of fruits, weight per fruit, and fruit length (Table 5) showed that genotype exerted a greater influence on these traits than the environment. Heritability estimation was used to evaluate the contribution of genetic factors to phenotypes (Ketthaisong *et al.* 2014). In addition, it was commonly used to predict the response to selection in plant breeding programmes (Schmidt *et al.* 2019). Heritability in

the broad sense was classified as high when $h^2_{bs} > 60\%$, medium when $30 \leq h^2_{bs} \leq 60\%$, and low when $h^2_{bs} < 30\%$ (Yeshiwas & Negash 2017).

Traits exhibiting both high heritability and broad genetic variability were particularly important, as most were likely to respond effectively to selection and could be improved in early generations. A high heritability value suggested that genetic factors played a more significant role than environmental factors. High heritability values implied that parental traits were more likely to be inherited by offspring, thereby increasing the likelihood of successful selection (Magar *et al.* 2021). Meanwhile, traits with low heritability and narrow variability, such as leaf-related traits and flowering time, were more influenced by environmental factors and could require more advanced selection strategies or multi-environment testing.

Correlation Analysis of 18 Eggplant Genotypes

Correlation analysis revealed several significant associations between agronomic traits. This

T a b l e 5

Genetic parameters of eighteen eggplant genotypes

Character	σ^2_e	σ^2_g	$2\sigma\sigma^2_g$	Criteria	GCV	PCV	h^2_{bs} [%]	Criteria
SD	0.05	0.08	0.06	Broad	18.36	23.55	60.78	High
DH	16.37	28.69	21.74	Broad	20.38	25.54	63.67	High
PH	153.7	71.92	83.12	Narrow	7.86	13.92	31.88	moderate
LL	16.71	1.93	6.06	Narrow	5.58	17.33	10.35	Low
LW	0.54	0.06	0.26	Narrow	1.78	5.86	9.24	Low
PL	2.45	0.43	0.95	Narrow	9.04	23.45	14.86	Low
FT	1.36	0.03	0.55	Narrow	0.51	3.76	1.81	Low
HT	9.98	3.06	4.53	Narrow	3.97	8.21	23.45	Low
NFP	43.02	97.72	11.86	Broad	56.13	67.36	69.43	High
WPF	382.15	2,109.63	1,434.75	Broad	67.54	73.40	84.66	High
FD	0.11	0.14	0.11	Broad	9.10	12.12	56.44	Moderate
FL	1.81	64.53	42.17	Broad	77.28	78.36	97.27	High
FSL	2.25	1.48	1.46	Broad	27.22	43.19	39.72	Moderate
FWP	67,303.11	62,144.19	54,476.20	Broad	29.54	42.63	48.01	Moderate

Note: σ^2_e – error variance; σ^2_g – genotypic variance; $\sigma\sigma^2_g$ – standard deviation of genetic variability; h^2_{bs} – broad sense heritability; GCV – genotypic coefficient variance; PCV – phenotypic coefficient variance; PH – plant height; DH – dichotomous height; SD – stem diameter; PL – petiole length; LL – leaf length; LW – leaf width; FT – flowering time; HT – harvesting time; FD – fruit diameter; FSL – fruit stalk length; FL – fruit length; NFP – number of fruits per plant; WPF – weight per fruit; FWP – fruit weight per plant.

T a b l e 6

Selection index of eighteen eggplant genotypes

Genotype	FWP	WPF	FD	FL	DH	SD	WINDEX
Hitavi F1	0.11	0.21	0.01	0.23	-0.01	0.02	2.82
AM8 [H]	0.04	0.19	0.02	0.18	0.01	0.05	2.27
AM11 [H]	0.05	0.12	0.04	0.20	0.05	0.02	2.14
AM10 [H]	0.03	0.13	-0.03	0.15	0.07	0.00	1.58
AM9 [H]	-0.04	-0.10	-0.01	-0.12	-0.02	0.00	-1.39
Mustang F1	0.07	0.20	0.02	0.20	0.01	0.07	2.58
AM13 [M]	-0.01	0.19	0.01	0.22	0.05	0.04	2.18
AM14 [M]	0.05	0.14	0.01	0.16	0.08	0.07	2.06
AM29 [P]	0.07	-0.03	0.05	-0.09	0.03	0.02	0.07
Provita F1	0.04	-0.11	-0.02	-0.13	0.00	-0.03	-1.17
AM28 [P]	0.06	-0.13	-0.03	-0.13	-0.05	0.00	-1.24
AM23 [P]	-0.02	-0.11	-0.01	-0.11	-0.01	-0.03	-1.30
AM4 [P]	-0.01	-0.11	-0.01	-0.12	-0.06	-0.03	-1.45
AM6 [P]	-0.03	-0.12	-0.01	-0.13	-0.03	-0.03	-1.53
AM3 [P]	-0.05	-0.12	-0.01	-0.13	0.01	-0.04	-1.58
AM34 [P]	-0.06	-0.13	-0.02	-0.13	-0.04	-0.04	-1.89
AM5 [P]	-0.13	-0.12	-0.01	-0.12	-0.06	-0.04	-2.02
AM22 [P]	-0.14	-0.10	-0.01	-0.13	-0.06	-0.06	-2.14

Note: FWP – fruit weight per plant; WPF – weight per fruit; FD – fruit diameter; FL – fruit length; DH – dichotomous height; SD – stem diameter; WINDEX – weighted selection index.

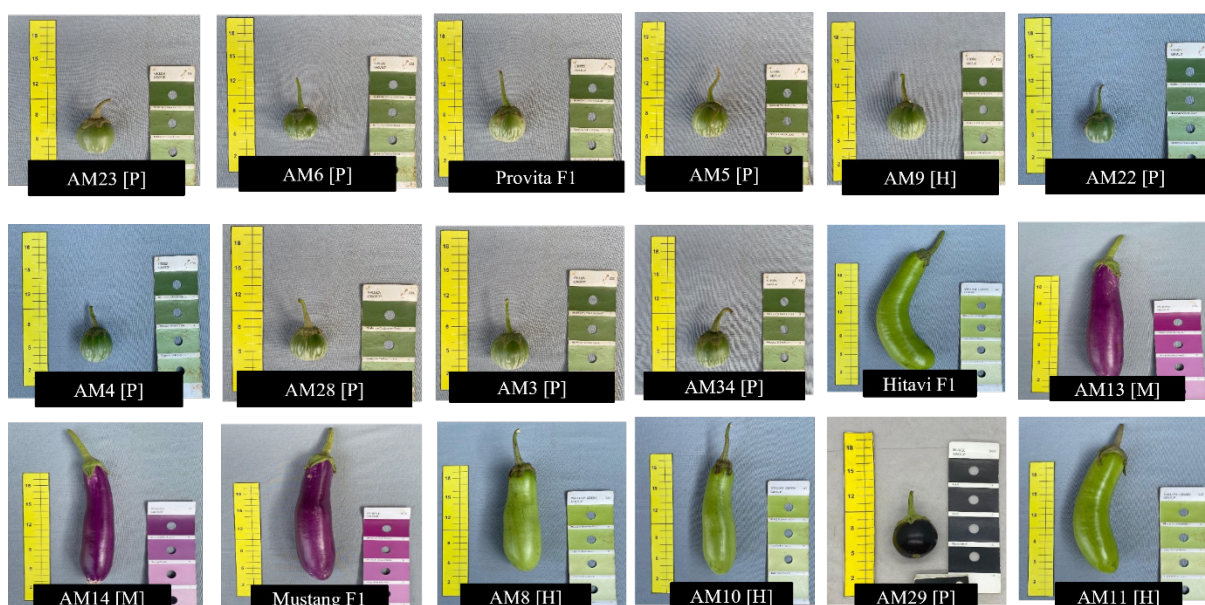


Figure 3. Fruit morphology of 15 doubled haploid eggplant lines obtained from anther culture and 3 commercial check varieties (Mustang F1, Hitavi F1, and Provita F1).

was also a useful measure for predicting yield responses based on changes in specific traits (Shekar *et al.* 2013). The results of the correlation analysis for eggplant are shown in Figure 2. Fruit weight per plant (FWP) exhibited a significant positive correlation with weight per fruit ($r=0.47^{+++}$), fruit length ($r=0.45^{+++}$), stem diameter ($r=0.59^{+++}$), fruit stalk length ($r=0.26^{+}$), dichotomous height ($r=0.30^{+}$), and fruit diameter ($r=0.31^{++}$). These relationships, ranging from weak to moderate, showed that both fruit size and vegetative vigour contribute to yield formation. In particular, the relatively stronger correlation between FWP and stem diameter ($r=0.59^{+++}$) suggested that vegetative strength played a significant role in supporting assimilate transport and fruit development. Based on the correlation coefficients, these relationships ranged from weak to moderate, showing that both fruit size and vegetative vigour were vital in determining yield potential. Notably, the fruit weight per plant increased with larger fruit size and stronger vegetative growth, emphasising the importance of these traits in influencing yield. This result implied that improving both source capacity (vegetative growth) and sink strength (fruit size) was essential for enhancing yield performance.

Weight per fruit (WPF) showed a very strong positive correlation with fruit length ($r=0.93^{+++}$) and a moderate positive correlation with fruit diameter ($r=0.46^{+++}$), confirming that fruit morphology was a major determinant of individual fruit weight. Meanwhile, the number of fruits per plant (NFP) showed moderate negative correlations with fruit length ($r=-0.65^{+++}$) and weight per fruit ($r=-0.62^{+++}$), reflecting a trade-off between fruit number and size. This showed that some genotypes allocate assimilates towards producing fewer but larger fruits, while others favour producing a greater number of smaller fruits.

Significant positive correlations demonstrated a linear relationship between the observed variables, while negative correlation coefficients indicated the opposite. Generally, the strength of the correlation between characters significantly influenced plant development (Yeshitilla *et al.* 2023).

Weighted Selection Index of Eighteen Eggplant Genotypes

Index selection was used to identify genotypes

based on the best agronomic traits. The calculation of the index selection relied on the heritability and economic value of the traits (Gazal *et al.* 2017). The weighted index selection used 6 traits as criteria, such as fruit weight per plant (+5), weight per fruit (+5), fruit diameter (+5), fruit length (+5), dichotomous height (+2), and stem diameter (+2). The selection criteria were determined based on the F-test results, heritability values, correlation with yield traits, and parental traits. The results of the selection index are presented in Table 6.

The weighted selection index model was represented as $I = \sum b_i Z_i$. In this study, the index was calculated as $I = 5Z(\text{FWP}) + 5Z(\text{WPF}) + 5Z(\text{FD}) + 5Z(\text{FL}) + 2Z(\text{DH}) + 2Z(\text{SD})$. The weighted index technique ranked the genotypes from highest to lowest. A total of 11 doubled haploid (DH) lines were subsequently selected according to their index ranking, while maintaining proportional representation across parental genetic backgrounds. These included 4 lines derived from Hitavi F1 (AM8H, AM9H, AM10H, and AM11H), 2 lines from Mustang F1 (AM13M and AM14M), and 4 lines from Provita F1 (AM4P, AM6P, AM23P, AM28P, and AM29P).

CONCLUSIONS

In conclusion, the doubled haploid eggplant lines exhibit high heritability and considerable genetic diversity in traits such as stem diameter, dichotomous height, fruit number, fruit weight, and fruit length, indicating ample variation to enable effective selection. Fruit weight per plant is significantly and positively correlated with fruit weight, fruit diameter, fruit length, fruit stalk length, dichotomous height, and stem diameter. Cluster analysis divides the 18 genotypes into 3 distinct groups, showing phenotypic divergence among the lines. A total of 11 genotypes (AM13M, AM14M, AM4P, AM6P, AM23P, AM28P, AM29P, AM8H, AM9H, AM10H, and AM11H) demonstrate promising agronomic performance and can be considered as potential candidates for further evaluation in eggplant breeding programmes. However, further evaluation across multiple environments and growing seasons is required to validate their stability, adaptability, and breeding value.

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