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Evaluation of agronomic traits, correlation, and genetic diversity in S4 inbred Adlay (*Coix lacryma-jobi* L.) lines in Vinh Phuc province, Vietnam

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Abstract:

Adlay is recognised as both a food source and a medicinal plant in various Asian countries. This study evaluated 18 S4 inbred Adlay lines for agro-biological traits and genetic diversity in Tam Dao district, Vinh Phuc province, Vietnam. The field experiment was arranged in a randomised complete block design (RCBD) with two replications. The results revealed that the S4 inbred Adlay lines exhibited significant variation in agro-biological traits. Individual yield was positively correlated with the weight of 100 fruits and the number of branches, and negatively correlated with leaf claw length and the number of leaves. Additionally, the number of branches and fruits per branch were shown to be influenced by environmental conditions. Individual yield traits were determined to be controlled by additive genes. At a coefficient of 0.08, the inbred lines were categorised into 13 groups, while at a coefficient of 0.15, 17 distinct groups were observed. These findings provide valuable information on inbred line traits for Adlay breeding programmes, particularly in relation to crossbreeding.

Keywords: ***Coix lacryma-jobi*** **L., correlation, genetic diversity, genetic variation, inbred lines.**

Classification numbers: **3.1, 3.3, 3.5**

1. Introduction

Adlay (*Coix lacryma-jobi* L.) is widely recognised as both a cereal and a traditional medicinal plant. Adlay seeds are rich in polysaccharides, lipids, flavonoids, phenols, proteins, vitamins, and other bioactive compounds [1-3], earning it the title of "king of the Gramineae" [4]. Every part of the plant is used medicinally [5-7], with the seeds being particularly valued in medicine, food, and cosmetics across Asia [4, 8-10]. *Coix lacryma-jobi* exhibits a range of therapeutic properties, including anti-tumour, antibacterial, antiviral, lipid-regulating, and anti-inflammatory effects. It also has antioxidant properties [11] and can help with digestion, diarrhoea, enteritis, dysentery, and acts as a diuretic, particularly in cases of oedema, reduced urination, and arthritis. Furthermore, it promotes bodily nourishment, enhances lactation, and is noted for its potential anti-cancer properties [12]. The seed oil, which is predominantly composed of triglycerides and other fatty acid esters, has demonstrated strong anti-tumour activity [13-15].

The growing demand for Adlay seeds has significantly increased the pressure to cultivate them [4], prompting a surge in research efforts, particularly in breeding programmes aimed at the selection of elite genetic resources. Sexual hybridisation-induced mutagenesis is widely employed in *Coix lacryma-jobi* breeding across countries such as Japan, Taiwan (China), and the Philippines [16-19]. To develop pure lines for crossbreeding purposes, this study aims to evaluate the agro-biological traits and genetic diversity of S4 inbred Adlay lines using morphological markers.

2. Materials and methods

2.1. Materials

The research materials consisted of S4 generation inbred Adlay lines, developed and selected from an Adlay collection at the Tam Dao Medicinal Material Research Station from 2019 to 2022. These are presented in the following Table 1.

Table 1. Origin and basic traits of the lines used in this research.

No.	Symbols of lines in generations				Origin (province/city)	Traits
	First generation (S1)	*Second generation (S2)*	*Third generation (S3)*	*Fourth generation (S4)*		
1	YD1	YD1.1	YD1.1.1	YD1.1.1.1	Son La	Soft pods
2	YD3	YD3.1	YD3.1.1	YD3.1.1.1	Lao Cai	Soft pods
3	YD4	YD4.1	YD4.1.1	YD4.1.1.1	Ha Giang	Soft pods
4	YD5	YD5.1	YD5.1.1	YD5.1.1.1	Yen Bai	Soft pods
5	YD5	YD5.1	YD5.1.2	YD5.1.2.1	Yen Bai	Soft pods
6	YD6	YD6.1	YD6.1.1	YD6.1.1.1	Kon Tum	Soft pods
7	YD6	YD6.2	YD6.2.1	YD6.2.1.1	Kon Tum	Soft pods
8	YD7	YD7.1	YD7.1.1	YD7.1.1.1	Thanh Hoa	Soft pods
9	YD7	YD7.2	YD7.2.1	YD7.2.1.1	Thanh Hoa	Soft pods
10	YD7	YD7.3	YD7.3.1	YD7.3.1.1	Thanh Hoa	Soft pods
11	YD8	YD8.1	YD8.1.1	YD8.1.1.1	Thai Binh	Soft pods
12	YD8	YD8.1	YD8.1.2	YD8.1.2.1	Thai Binh	Soft pods
13	YD9	YD9.1	YD9.1.1	YD9.1.1.1	Hanoi	Soft pods
14	YD9	YD9.2	YD9.2.2	YD9.2.2.1	Hanoi	Soft pods
15	YD10	YD10.1	YD10.1.1	YD10.1.1.1	Hanoi	Soft pods
16	YD10	YD10.1	YD10.1.2	YD10.1.2.1	Hanoi	Soft pods
17	YD10	YD10.2	YD10.2.1	YD10.2.1.1	Hanoi	Soft pods
18	YD11	YD11.1	YD11.1.1	YD11.1.1.1	Son La	Soft pods

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2.2. Research methods

The experiment was conducted during the Spring-Summer 2022 crop at the Tam Dao Medicinal Material Research Station, Vinh Phuc province. It was arranged in a RCBD with two replications, using a 10 m² experimental plot [20]. Planting and care techniques were applied according to T.V. Vuong, et al. (2021) [19].

The monitored indicators included: germination rate (%), the duration from sowing to germination, tillering, flowering, and harvesting (days), leaf height (cm), number of leaves (leaves), stem diameter (cm), number of branches (branches), effective number of branches (branches), weight of 100 fruits (g), number of fruits per branch (fruits/branch), individual yield (g/plant), theoretical yield (quintal/ha), and actual yield (quintal/ha). Fifteen individual plants from each replication were randomly selected to measure these criteria.

Genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated according to G.N. Burton, et al. (1953) [21]:

$$\mathrm{PCV} = \frac{\sqrt{\sigma^2 p}}{\bar{x}} \text{ x } 100 \qquad (1)$$

$$\mathrm{GCV} = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \text{ x } 100 \qquad (2)$$

The heritability was calculated according to H.W. Johnson, et al. (1955) [11]:

$$H^2b = \frac{\sigma^2 g}{\sigma^2 p} \text{ x } 100 \qquad (3)$$

where the environmental variance σ^2e=Mse/r, genotype variance $\sigma^2g=\frac{\mathrm{MSg-Mse}}{r}$, phenotypic variance $\sigma^2p=\sigma^2g+\sigma^2e$, MSg is the mean square of genotypic, Mse is the mean square of error, $\bar{x}$ is mean, and r is repetition.

Genetic progress was calculated according to H.W. Johnson, et al. (1955) [11]:

$$\mathrm{GA}\ (\%) = \mathrm{K}.\mathrm{H}^2\mathrm{b} \text{ x } \mathrm{p} \qquad (4)$$

where H^2b is the heritability coefficient in the broad sense, p is the phenotypic error, K is the coefficient of selection, and K=2.06 at 5% selection pressure.

The average percent genetic progress is given as:

$$\mathrm{GAM} = \frac{GA}{\bar{x}} \text{ x } 100 \qquad (5)$$

A genetic relationship diagram, based on morphological markers, was constructed using data from nine traits: harvest time, leaf claw height, number of leaves, stem diameter, number of branches, number of effective branches, weight of 100 fruits, number of fruits per branch, and individual yield. Clustering was performed using the UPGMA (unweighted pair group method with arithmetic mean) algorithm in the SHAN sub-program. Statistical analysis was conducted using NTSYS 2.1e software. Data processing was carried out using IRRISTAT 5.0 and Microsoft Office Excel 2016.

3. Results and discussion

3.1. Agro-biological traits of the S4 generation inbred lines

The S4 generation inbred lines in this experiment exhibited varying germination rates and growth durations (Table 2). Germination rates ranged from 45.25 to 80.38%, with lines YD3.1.1.1, YD4.1.1.1, YD5.1.1.1, YD6.1.1.1, YD7.3.1.1, YD8.1.1.1, YD10.1.2.1, and YD10.2.1.1 having germination rates above 70%. Conversely, the YD8.1.2.1 line had a germination rate of less than 50%. In general, the germination rates of the S4 generation were slightly lower than those observed in the S1-S3 inbred lines reported by T.V. Vuong, et al. (2021) [19]. This decrease in germination rates is likely due to the effects of inbreeding over several generations, which causes the population's mean value to shift towards recessive genes, thereby reducing the expression of certain traits and overall plant vitality [22].

Table 2. Germination rate and growth duration of S4 generation inbred lines.

Accession	Germination rate (%)	Duration from sowing to ... (days)			
		Germination	*Tillering*	*Flowering*	*Harvesting*
YD1.1.1.1	66.25	9	32	112	174
YD3.1.1.1	72.50	9	33	85	138
YD4.1.1.1	71.92	12	33	115	179
YD5.1.1.1	79.09	13	34	126	191
YD5.1.2.1	60.00	11	35	118	190
YD6.1.1.1	80.38	12	34	130	172
YD6.2.1.1	69.50	9	31	81	138
YD7.1.1.1	61.25	12	33	121	188
YD7.2.1.1	60.73	13	34	86	139
YD7.3.1.1	76.50	10	39	86	137
YD8.1.1.1	73.75	11	32	110	173
YD8.1.2.1	45.25	12	32	88	145
YD9.1.1.1	69.99	13	36	113	183
YD9.2.2.1	67.50	11	32	91	144
YD10.1.1.1	65.63	9	32	81	139
YD10.1.2.1	71.25	9	32	82	141
YD10.2.1.1	75.25	9	35	83	139
YD11.1.1.1	50.00	12	33	89	136
$LSD_{0.05}$	9.92	-	-	-	-
CV(%)	7.0	-	-	-	-

The increasing rate of homozygous recessive individuals also influenced the growth duration of the inbred lines. In this experiment, the duration from sowing to germination varied between 9 and 13 days. Similarly, the duration from sowing to tillering for the S4 inbred lines ranged from 31 to 39 days, which was somewhat longer than the values recorded by T.V. Vuong, et al. (2021) [19]. The time from sowing to flowering and harvesting ranged from 81 to 130 days and 136 to 191 days, respectively, and these values were lower than those reported in previous studies [19].

The inbred Adlay lines exhibit different agronomic traits. Plant height varied from 121.30 to 211.85 cm (Table 3). Based on plant height, the lines can be divided into three groups with an interval of 38 cm (step size) between the shortest and tallest plants. The first group, with plant heights ranging from 121.3 to 159.3 cm, includes nine lines: YD3.1.1.1, YD6.2.1.1, YD7.2.1.1, YD7.3.1.1, YD8.1.2.1, YD10.1.1.1, YD10.1.2.1, YD10.2.1.1, and YD11.1.1.1. The second group, with heights between 159.3 and 197.3 cm, consists of six lines: YD1.1.1.1, YD4.1.1.1, YD5.1.2.1, YD8.1.1.1, YD9.1.1.1, and YD9.2.2.1. The third group, with heights ranging from 197.32 to 235.3 cm, includes three lines: YD5.1.1.1, YD6.1.1.1, and YD7.1.1.1 (Fig. 1). However, the taller plants pose a challenge for farmers during harvesting. Ease of mechanisation, or the ability to harvest with machinery, is a key criterion in Adlay breeding. One solution is to select varieties with shorter plant heights, such as Taichung No. 5 [18].

Table 3. Morphological traits of S4 generation inbred lines at harvest time.

Accession	Plant height (cm)	Number of leaves (leaves/branch)	Stem diameter (cm)	Number of branches (branches/clump)
YD1.1.1.1	192.40	21.95	0.88	8.50
YD3.1.1.1	150.10	16.65	1.05	9.15
YD4.1.1.1	175.20	20.30	0.96	14.75
YD5.1.1.1	203.05	21.45	0.94	12.15
YD5.1.2.1	181.85	20.90	0.91	11.85
YD6.1.1.1	211.85	22.75	1.25	8.25
YD6.2.1.1	139.40	16.90	1.21	8.55
YD7.1.1.1	209.90	22.60	1.04	10.85
YD7.2.1.1	141.80	16.50	1.04	8.65
YD7.3.1.1	131.20	16.50	0.98	7.70
YD8.1.1.1	179.25	20.30	1.18	12.00
YD8.1.2.1	149.80	18.00	1.16	11.70
YD9.1.1.1	167.25	21.40	1.30	8.25
YD9.2.2.1	172.15	18.70	1.30	7.90
YD10.1.1.1	134.70	16.50	1.14	6.25
YD10.1.2.1	135.00	17.30	1.12	8.55
YD10.2.1.1	121.30	15.95	1.15	8.05
YD11.1.1.1	144.80	17.10	1.25	8.90
$LSD_{0.05}$	14.94	0.76	0.04	3.16
CV (%)	4.3	4.2	4.6	9.7

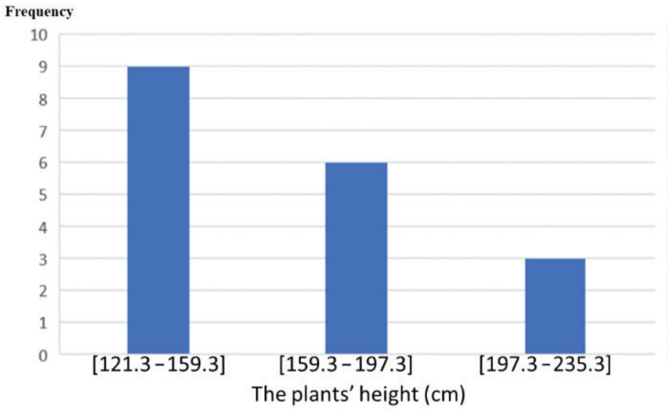

Fig. 1. Plant height classification of S4 inbred Adlay lines.

The number of leaves per branch in the inbred Adlay lines ranged from 15.95 to 22.75. Lines with more than 20 leaves per branch include YD1.1.1.1, YD4.1.1.1, YD5.1.1.1, YD5.1.2.1, YD6.1.1.1, YD7.1.1.1, YD8.1.1.1, and YD9.1.1.1. Lines with fewer than 17 leaves per branch include YD3.1.1.1, YD6.2.1.1, YD7.2.1.1, YD7.3.1.1, YD10.1.1.1, and YD10.2.1.1. Stem diameters ranged from 0.88 to 1.30 cm, with lines YD1.1.1.1, YD4.1.1.1, YD5.1.1.1, YD5.1.2.1, and YD7.3.1.1 exhibiting smaller diameters (less than 1 cm).

The number of branches per clump varied significantly among the lines, ranging from 6.25 to 14.75 branches per clump. Lines with a higher number of branches include YD4.1.1.1, YD5.1.1.1, YD5.1.2.1, YD7.1.1.1, YD8.1.1.1, and YD8.1.2.1, with branch counts of 14.75, 12.15, 11.85, 10.85, 12.00, and 11.70, respectively. In contrast, lines YD7.3.1.1, YD9.2.2.1, and YD10.1.1.1 had fewer branches, with counts of 7.70, 7.90, and 6.25 branches per clump, respectively (Table 3). These results are consistent with those observed in S3 inbred Adlay lines in a study by T.V. Vuong, et al. (2021) [19]. However, the variation in the traits of the S4 lines, ranging from 4.3 to 9.7%, was lower than the variation observed in S3 lines. This suggests that the traits in the S4 lines were relatively uniform, which may indicate potential for further evaluation of combining ability in the next generation. These results differ from those reported by X.Y. Lu, et al. (2023) [23], where plants were taller and had fewer leaves.

The inbred Adlay lines also showed differences in yield components. The number of effective branches per clump ranged from 4.75 to 9.75. Lines YD4.1.1.1, YD7.1.1.1, YD8.1.1.1, and YD8.1.2.1 had the highest number of effective branches, with values of 8.35, 8.45, 8.60, and 9.75 branches per clump, respectively. Conversely, lines YD6.2.1.1, YD9.2.2.1, and YD10.1.1.1 had the fewest effective branches, with values of 5.80, 5.65, and 4.75, respectively. Effective branches accounted for approximately 56.61 to 90.68% of the total number of branches. High ratios of effective branches were observed in lines YD3.1.1.1, YD7.2.1.1, YD7.3.1.1, YD8.1.2.1, YD9.1.1.1, YD10.2.1.1, and YD11.1.1.1, with ratios of 82.51, 89.02, 88.96, 83.33, 89.70, 90.68, and 83.15%, respectively (Table 4). The number of effective branches in the S4 lines was generally lower than in the S3 lines, as reported by T.V. Vuong, et al. (2021) [19]. This difference may be attributed to variations in the genes regulating branch number between the S3 and S4 generations.

Table 4. Yield components and productivity of S4 inbred Adlay lines.

Accession	Number of effective branches (branches)	Weight of 100 fruits (g)	Number of fruits per branch (fruits)	Individual yield (g/plant)	Theoretical yield (quintals/ha)	Actual yield (quintals/ha)
YD1.1.1.1	6.60	10.83	56.57	24.48	8.57	4.40
YD3.1.1.1	7.55	10.38	44.58	36.71	12.85	6.59
YD4.1.1.1	8.35	10.50	29.59	34.11	11.94	6.12
YD5.1.1.1	7.95	8.10	39.45	18.13	6.35	3.26
YD5.1.2.1	7.85	6.94	29.62	17.39	6.09	3.12
YD6.1.1.1	6.40	9.05	46.28	18.55	6.49	3.33
YD6.2.1.1	5.80	9.60	54.72	37.16	13.01	6.68
YD7.1.1.1	8.45	9.95	39.96	21.55	7.54	3.87
YD7.2.1.1	7.70	9.84	59.93	41.20	14.42	7.39
YD7.3.1.1	6.85	8.45	68.60	31.88	11.16	5.74
YD8.1.1.1	8.60	9.03	35.73	14.67	5.14	2.63
YD8.1.2.1	9.75	9.36	53.61	42.07	14.73	7.54
YD9.1.1.1	7.40	9.61	61.72	15.17	5.31	2.72
YD9.2.2.1	5.65	10.51	59.58	40.13	14.04	7.20
YD10.1.1.1	4.75	10.80	65.79	22.42	7.85	4.02
YD10.1.2.1	6.65	9.47	66.06	32.55	11.39	5.84
YD10.2.1.1	7.30	9.62	48.38	22.89	8.01	4.11
YD11.1.1.1	7.40	13.89	63.95	63.88	22.36	11.46
$LSD_{0.05}$	1.31	5.90	18.53	1.78	0.62	0.33
CV (%)	8.6	9.9	9.8	5.6	5.4	5.9

The weight of 100 fruits varied from 6.94 to 13.89 g. Lines YD1.1.1.1, YD3.1.1.1, YD4.1.1.1, YD9.2.2.1, YD10.1.1.1, and YD11.1.1.1 were noted for having higher fruit weights (>10 g/100 fruits), with values of 10.83, 10.38, 10.50, 10.51, 10.80, and 13.89 g, respectively. In contrast, lines YD5.1.1.1, YD5.1.2.1, and YD7.3.1.1 had lower fruit weights, at 8.10, 6.94, and 8.45 g, respectively. The fruit weights of the S4 inbred lines were not significantly different from those of the S3 lines in the study by T.V. Vuong, et al. (2021) [19], indicating minimal variation between the two generations.

The number of fruits per branch ranged from 29.59 to 68.60. Lines YD7.3.1.1, YD9.1.1.1, YD10.1.1.1, YD10.1.2.1, and YD11.1.1.1 had higher numbers of fruits per branch, with values of 68.60, 61.72, 65.79, 66.06, and 63.95, respectively. Lines YD4.1.1.1, YD5.1.1.1, YD5.1.2.1, YD7.1.1.1, and YD8.1.1.1 had fewer fruits per branch, with values of 29.59, 39.45, 29.62, 39.96, and 35.73 fruits, respectively (Table 4). The number of fruits per branch in the S4 lines was lower than that observed in the S3 lines reported by T.V. Vuong, et al. (2021) [19], likely due to genetic differences between the generations.

Individual yields of the Adlay lines ranged from 14.67 to 63.88 g per clump. Lines YD7.2.1.1, YD8.1.2.1, YD9.2.2.1, and YD11.1.1.1 had high individual yields (>40 g/clump), with values of 41.20, 42.07, 40.13, and 63.88 g/clump, respectively. In contrast, lines YD5.1.1.1, YD5.1.2.1, YD6.1.1.1, YD8.1.1.1, and YD9.1.1.1 had lower individual yields, ranging from 14.67 to 18.55 g/clump (Table 4). Similarly, the theoretical yield of the lines ranged from 5.14 to 22.36 quintals/ha. The actual yield varied between 2.63 and 11.46 quintals/ha, with higher yields observed in lines YD7.2.1.1, YD8.1.2.1, YD9.2.2.1, and YD11.1.1.1 (7.39, 7.54, 7.20, and 11.46 quintals/ha, respectively), compared to lower yields in lines YD5.1.1.1, YD5.1.2.1, YD6.1.1.1, YD7.1.1.1, YD8.1.1.1, and YD9.1.1.1 (3.26, 3.12, 3.33, 3.87, 2.63, and 2.72 quintals/ha, respectively). These yields are lower than those reported by T.V. Vuong, et al. (2021) [19], which may be due to reduced productivity over successive generations of inbreeding [22].

3.2. Genetic variation of quantitative traits of the S4 generation inbred Adlay lines

In this experiment, the phenotypic coefficient of variation (PCV%) was consistently higher than the genotypic coefficient of variation (GCV%) for all studied traits (Table 5), indicating that environmental factors significantly impacted the traits under investigation. The traits relating to the number of branches and number of fruits per branch showed particularly large differences between PCV and GCV, with values of 22.50 and 24.62% compared to 19.58 and 21.44%, respectively. The disparity between PCV and GCV highlights the influence of environmental factors on these traits [24]. This suggests that the number of branches and the number of fruits per branch can be enhanced through optimised environmental conditions.

Heritability estimates for the studied traits were high, ranging from 75.75 to 99.78%. Particularly high heritability was observed for traits such as plant height, number of leaves, stem diameter, and individual yield (96.94, 98.90, 99.08, and 99.78%, respectively, Table 5). These findings suggest that all traits of interest can be improved through selection methods.

Table 5. Genetic composition of quantitative traits in the S4 generation inbred Adlay lines.

	PCV (%)	GCV (%)	H^2b (%)	GAM$_{(5\%)}$
Plant height	17.52	17.25	96.94	34.99
Number of leaves	12.78	12.71	98.90	26.03
Stem diameter	12.16	12.11	99.08	24.83
Number of branches	22.50	19.58	75.75	35.11
Number of effective branches	16.49	15.34	86.52	29.38
Number of fruits per branch	24.62	21.44	75.85	38.46
Individual yield	42.71	42.67	99.78	87.80

PCV: Phenotypic coefficients of variation, GCV: Genotypic coefficients of variation, H^2b: Heritability, GAM: Average percent genetic progress.

In the experiment, traits such as plant height, number of leaves, stem diameter, number of branches, number of effective branches, and number of fruits per branch were controlled by non-additive genes. These traits exhibited high heritability but low genetic progress, with heritability values of 96.94, 98.90, 99.08, 75.75, 86.52%, and genetic advance as a percentage of mean values (GAM) of 34.99, 26.03, 24.83, 35.11, and 29.38%, respectively. Conversely, the individual yield trait was regulated by additive genes, showing both high heritability (99.78%) and high genetic progress (87.80%) (Table 5). Traits controlled by non-additive genes typically have high heritability but low genetic progress, while those regulated by additive genes exhibit high heritability and high genetic progress [25]. These results indicate that the number of branches and fruits per branch can be improved through environmental conditions, while individual yield is primarily governed by additive genetics.

3.3. Phenotypic correlation between the traits of the S4 generation inbred Adlay lines

Several traits exhibited phenotypic correlations among the inbred Adlay lines studied. Plant height had a very strong positive correlation with the number of leaves (0.95) and a moderate positive correlation with the number of branches (0.45). However, plant height was moderately negatively correlated with the number of fruits per branch (-0.58) and individual yield (-0.47). The number of leaves was also moderately negatively correlated with the number of fruits (-0.53) and individual yield (-0.57), while showing a moderate positive correlation with the number of branches (0.43). Stem diameter was moderately negatively correlated with the number of branches (-0.41).

The number of branches displayed a strong positive correlation with the number of effective branches (0.77) and a very strong negative correlation with the number of fruits per branch (-0.81). The number of effective branches was moderately negatively correlated with the number of fruits per branch (-0.54). The weight of 100 fruits showed a moderate positive correlation with individual yield (0.68) and the number of fruits per branch (0.40). The number of fruits per branch was also moderately positively correlated with individual yield (0.41). Other traits exhibited lower correlations (Table 6).

Table 6. Phenotypic correlation coefficients between traits of S4 generation inbred Adlay lines.

Codes	CC	SL	DKT	SN	SNHH	M100Q	SQ/N	NSCT
CC	1							
SL	0.95	1						
DKT	-0.21	-0.18	1					
SN	0.45	0.43	-0.41	1				
SNHH	0.24	0.26	-0.26	0.77	1			
M100Q	-0.23	-0.27	0.35	-0.27	-0.20	1		
SQ/N	-0.58	-0.53	0.39	-0.81	-0.54	0.40	1	
NSCT	-0.47	-0.57	0.22	-0.11	0.00	0.68	0.41	1

CC: Plant height; SL: Number of leaves/branches; DKT: Stem diameter; SN: Number of branches; SNHH: Number of effective branches (number of branches flowering, setting seeds); M100Q: Weight of 100 fruits; SQ/N: Number of fruits/branches; NSCT: Individual yield.

These results suggest that increasing individual yield in inbred Adlay lines can be achieved by selecting plants with high fruit weight, more branches, greater plant height, and fewer leaves. Yield component selection focused on fruit weight and the number of fruits per branch will contribute to improved individual yield. Additionally, selecting plants with lower heights and fewer leaves can reduce stem breakage caused by rain and strong winds.

3.4. Phenotype-based genetic diversity of S4 generation inbred Adlay lines studied

Using nine traits that varied among the experimental lines, a genetic relationship diagram was constructed based on morphological markers (Fig. 2). At a coefficient of 0.08 (8%), the 18 lines were divided into 13 groups. Lines YD1.1.1.1, YD10.1.1.2.1, YD7.1.1.1, YD7.3.1.1, YD8.1.2.1, YD9.2.2.1, YD11.1.1.1, YD5.1.1.1, and YD5.1.2.1 each formed their own group. Group 10, consisting of lines YD3.1.1.1 and YD6.2.1.1, shared growth periods of approximately 138 days, with plant heights of 139.4-150.1 cm, leaf counts of 16.65-16.90 per branch, stem diameters of 1.05-1.21 cm, and branch counts of 8.55-9.15 branches per clump. The weight of 100 fruits in this group ranged from 9.60 to 10.38 g, the number of fruits per branch from 44.58 to 54.72, and individual yield from 36.71 to 37.16 g/plant. YD4.1.1.1 and YD8.1.1.1 lines of the 11th group have a growth period of 173-179 days, the height of the claws is about 175.2-179.3 cm, the number of leaves is about 2.3 leaves/branch, the number of effective branches is about 8.35-8.6 branches/clump, the number of fruits/branch is about 28.59-35.73 fruits. The 12th group includes YD7.2.1.1, YD10.1.1.1, and 10.2.1.1 lines has the growth period of about 139 days, the height of the claws is about 121.3-141.8 cm, the number of leaves is about 15.95-16.5 leaves/branch, the diameter of the stem is about 1.04-1.15 cm, and the weight of 100 fruits is about 9.62-10.84 g. The 13th group includes the YD6.1.1.1 and YD9.1.1.1 lines. This group has a growth period of about 172-183 days, the number of leaves is about 21.4-22.75 leaves/branch, the diameter of the trunk ranges between 1.25-1.30 cm, the number of branches is about 8-25 branches, the weight of 100 fruits is about 9.04-9.61 g, and the yield is about 15.17-18.5 g/plant (Fig. 2).

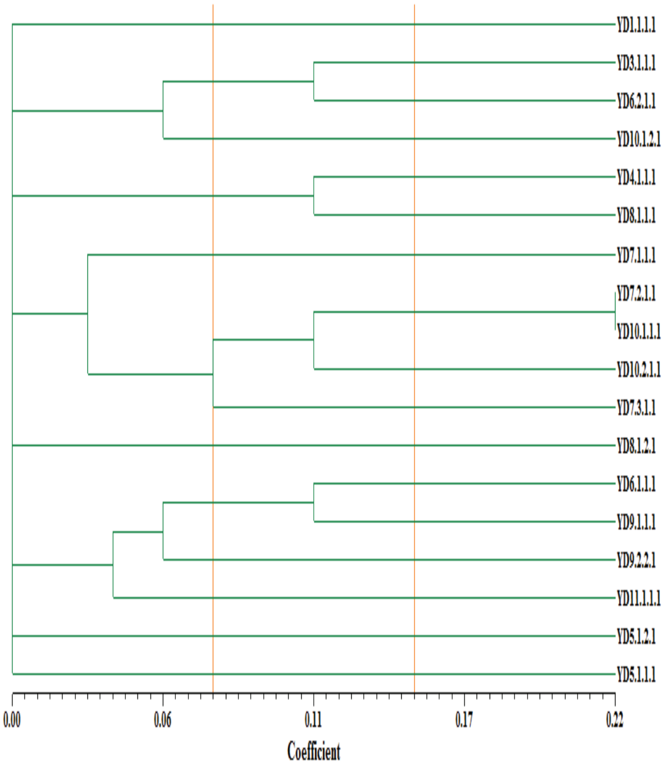

Fig. 2. Diagram of genetic relationships in a tree constructed by morphological markers of S4 generation inbred lines.

At a coefficient of 0.15 (15%), the 18 lines involved in the experiment were divided into 17 groups, with almost each group containing one line, except for one group consisting of two lines: 7.2.1.1 and YD10.1.1.1 (Fig. 2). This group had a leaf height of approximately 134.7-141.8 cm, with about 16.50 leaves per branch, stem diameters of 1.04-1.14 cm, a weight of 100 fruits ranging from 9.62 to 10.80 g, and a fruit count per branch of 60.00-65.79. These results indicate that the Adlay lines in the experiment possess significant potential for crossbreeding to achieve hybrid vigour. Most of the lines, according to their coefficients, were found in distinct groups. Lines with larger genetic distances were positioned in separate groups in the genetic tree diagram with higher coefficients. Genetic distance was positively correlated with hybrid yield, as well as with the heterosis of the hybrids [26]. In other studies, the relationship between genetic distance, based on molecular markers, and agronomic performance with hybrid vigour and specific combining ability (SCA) of hybrids has also been evaluated, with similar results. The response depends on the cultivar, the conditions, the markers used, and the traits examined [27-30].

4. Conclusions

The agro-biological traits of the Adlay lines have been extensively studied. The number of branches and fruits per branch could be modified and enhanced by environmental factors, while yield was primarily controlled by additive genes. High values for yield components such as fruit weight and the number of fruits per branch were regarded as positive criteria for selecting individual yields. All of these traits can be improved through selection. A total of 18 lines were divided into 13 groups at a coefficient of 0.05 (8%) and into 17 groups at a coefficient of 0.15 (15%). This provides the foundation for evaluating the combining ability of Adlay lines from different groups to achieve the desired heterosis for the development of soft-pod Adlay hybrids.

CRediT author statement

Van Tam Nguyen: Methodology, Formal analysis, Data curation; Original draft preparation, Visualisation; Thi Huong Nguyen: Visualisation; Xuan Khanh Nguyen, Thi Ngan To: Investigation; Van Vuong Trinh: Methodology, Conceptualisation, Visualisation, Formal analysis.

COMPETING INTERESTS

The authors declare that there is no conflict of interest regarding the publication of this article.

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