

Research Article

Genetic Variability, Correlation, and Path Analysis of Thai Commercial Melon Varieties

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In the selection phase of melon breeding programs, genetic variability is a critical component for yield improvement. The goals of this study were to discover the variables that affect melon fruit weight and examine genetic variability, correlation, and path analysis of eight melon varieties. The experiment was arranged as a completely randomized block design with 4 blocks. It was conducted between July and September 2021 at the School of Agricultural Technology, Walailak University, Nakhon Si Thammarat, Thailand. The result found that stem diameter and length, leaf length, width, number, and chlorophyll, day to 50% male and female flowering, and fruit perimeter, height, and weight were highly significant across the varieties. The genotypic coefficients of variation (GCV) of observed variables were all lower than phenotypic coefficients of variation (PCV). Fruit weight (15.462 and 19.865%) had the highest GCV and PCV. High broad-sense heritability was linked to high (H) or moderate (M) genetic advance as a percentage of the mean from stem length (67.606%: H and 21.992%: H), fruit weight (60.586%: H and 24.793%: H), fruit perimeter (76.395%: H and 12.258%: M), and fruit height (69.828%: H and 12.122%: M). The maximum and significant genotypic correlation value was obtained between leaf length and leaf width ($r=1.000$). Fruit weight is positively correlated with fruit perimeter ($r=0.940$) and fruit height ($r=0.831$). According to correlation and path analyses, stem diameter and length, leaf chlorophyll, and fruit perimeter and height were considered variables for fruit weight improvement in the breeding programs. It suggests that the increase in traits with a favorable direct influence on fruit weight may directly contribute to fruit weight.

1. Introduction

Melon, also called muskmelon (*Cucumis melo* L.), is one of the world's most important commercial fruit crops [1]. It is well known for its flavor, taste, and phytonutrient content [2]. Melon fruit is high in phytonutrients, including potassium, vitamin C, and provitamin A, also known as beta-carotene [3]. Melon is regarded as one of the most expensive fruits in Thailand due to its difficulty in production. For excellent fruit quality and quantity, suitable conditions for melon production are considered, such as varieties, climatic considerations, soil kinds and qualities, irrigation, and illnesses [4]. Several melon genotypes are grown in different parts of Thailand. It had been imported from other countries

and was bred by Thai breeders. However, the research report on melon breeding and genetics, on the other hand, is inadequate.

Melon has a chromosomal number of $2n=24$ and is a cross-pollinated crop. In germplasm, there is a vast spectrum of genetic variability [5]. The success of a hybrid combination in the melon breeding program is determined by the selection of elite accessions for fruit attributes during the selection process. Fruit quality (such as color, shape, and rind pattern) and quantity (fruit number, fruit width, and fruit weight) are the most important factors for breeders to consider when developing a breeding strategy. In the selection process, genetic diversity is a critical component for increasing production [5]. In breeding efforts, determining the genotypic and phenotypic

correlation between melon features is critical and advantageous. The positively correlated characteristics can be promptly improved at the same time [6]. A correlation is a statistical measure of the relationship between two variables. Correlation coefficient values range from -1 to $+1$, where 0 indicates that there is no correlation [7]. Path analysis is a multivariate statistical tool for investigating postulated (causal) links between two or more variables [8]. It is extensively used in plant breeding programs to describe the direct or indirect effect of each variable's results and to compare the relative relevance of each variable. The broad-sense heritability is the proportion of phenotypic variance that is attributable to an effect for the whole genotype, comprising the sum of additive, dominance, and epistatic effects. It can be used to predict the feasibility of improving targeted traits [9].

The objectives of this study were to (1) discover the variables that affect melon fruit weight and (2) examine genetic variability, correlation, and path analysis of eight marketed melon varieties. Breeders, researchers, and farmers may find the conclusions of this study useful for further investigation.

2. Materials and Methods

2.1. Research Places and Plant Materials. This research was conducted between July and September 2021 at the School of Agricultural Technology and Food Industry's greenhouse ($8^{\circ} 38' 43.2''\text{N } 99^{\circ} 54' 04.2''\text{E}$), Walailak University, Nakhon Si Thammarat Province, Thailand. During the research, monthly rainfall ranges between 97.8 and 133.4 mm and the relative humidity ranges between 84 and 87 percent with the highest rainfall and humidity occurring in September. The temperature ranges between 22.3 and 35.8°C , with August is the hottest month. The weather data were obtained from the greenhouse's weather station. In a soilless cultivation method, eight Thai commercial melon varieties were gathered and planted. The varieties are Sandee, Baramee, Sanwan, Melon cat 697, Kissme, Snowgreen, Melon princess, and Kimoji. Plant media consisted of chopped coconut mesocarp mixed with coconut coir (1:1). Irrigation and fertigation were applied to each melon using a modified method of Asao et al. [10]. The melon varieties were divided into four blocks in a completely randomized block design (RCBD). The plot size is 400×50 cm, and the melon is spaced 50 cm. Four melons from each block were measured for agronomic and fruit characteristics at 5 weeks after pollination, including stem diameter (SD) (cm), stem length (SL) (cm), leaf length (LL) (cm), leaf width (LW) (cm), leaf chlorophyll (LC) (SPAD unit) (using a Chlorophyll Meter SPAD-502 Plus), leaf number (LN) (no.), day to 50% male flowering (DMF) (day), day to 50% female flowering (DFE) (day), fruit perimeter (FP) (cm), fruit height (FH) (cm), and fruit weight (FW) (cm).

2.2. Data Observation. The agronomic and fruit characteristics of melons were calculated in genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability (H_b^2), genetic advance (GA), genetic advance as

percentage of mean (GAM), genotypic and phenotypic correlation coefficients (r_g and r_p), and genotypic and phenotypic path coefficients.

GCV and PCV are calculated according to Al-Tabbal and Al-Fraihat [11] as follows:

$$\text{GCV} = \frac{\sigma_g^2}{\sqrt{\bar{x}}} \times 100, \quad (1)$$

$$\text{PCV} = \frac{\sigma_p^2}{\sqrt{\bar{x}}} \times 100, \quad (2)$$

where \bar{x} is the mean of the genotype or phenotype and σ_p^2 and σ_g^2 are the phenotypic and genotypic variances, respectively.

Heritability is calculated according to Covarrubias-Pazarán [12] as follows:

$$H_b^2 = \frac{\sigma_g^2}{\sigma_p^2}. \quad (3)$$

GA is calculated and categorized according to Teklu et al. [13] as follows:

$$\text{GA} = k \times \sigma_g \times \frac{H_b^2}{100}, \quad (4)$$

where k is the standardized selection differential at 5% (2.063).

GAM is calculated according to Teklu et al. [13] as follows:

$$\text{GAM}(\%) = \frac{\text{GA}}{X} \times 100. \quad (5)$$

Genotypic and phenotypic correlations are calculated according to Oladosu et al. [14] as follows:

$$r_g = \frac{\text{Cov}_{g1,2}}{\sqrt{\sigma_{g1}^2 \times \sigma_{g2}^2}}, \quad (6)$$

$$r_p = \frac{\text{Cov}_{p1,2}}{\sqrt{\sigma_{p1}^2 \times \sigma_{p2}^2}}, \quad (7)$$

where $\text{Cov}_{g1,2}$ and $\text{Cov}_{p1,2}$ are the genotypic and phenotypic covariance of 1st and 2nd traits.

Genotypic and phenotypic path analyses are calculated according to Kruelee et al. [15] as follows:

$$R^2 = b'_1 r_{1y} + b'_2 r_{2y} + b'_3 r_{3y} + \dots \quad (8)$$

Residual effect = $1 - R^2$.

b'_1, b'_2, b'_3, \dots are standardized partial regression of X_1, X_2, X_3, \dots

$r_{1y}, r_{2y}, r_{3y}, \dots$ are correlation coefficient between X_1, X_2, X_3, \dots and Y .

2.3. Statistical Analysis. The statistical analysis was calculated by using the R software (version 3.6.1) with Variability and TraitStats packages [16, 17].

3. Results and Discussion

3.1. Genetic Variability. Table 1 shows the analysis of variance for agronomic and fruit traits of melons. Among the melon varieties, all observed attributes were statistically significant ($p < 0.01$). The maximum coefficient of variation (CV) of observed variables was obtained in stem length (8.99), followed by stem diameter (8.76%), leaf chlorophyll (7.70%), and day to 50% female flowering (7.33%). The lowest CV was found in fruit perimeter (3.78).

Table 2 shows the results of the melon genetic variability. The genotypic coefficients of variation (GCVs) of observed variables were all lower than the phenotypic coefficients of variation (PCVs), indicating that the environment has a significant impact on the expression of melon characteristics [5]. According to Reddy et al. [18], only the GCV and PCV of fruit weight and stem length were categorized as moderate, and the others were categorized as low. Fruit weight (15.462 and 19.865%) had the highest GCV and PCV, followed by stem length (12.984 and 15.791%), and day to 50% female flowering (3.004 and 7.380%) had the lowest of both GCV and PCV. The findings of this study's GCV and PCV are similar to those of Kumbar et al. [5], who investigated the genetic variability and correlation of the Mangalore melon traits. In every attribute they looked at, the GCVs were lower than the PCVs. The high GCV and PCV were obtained from average fruit weight, fruit width, fruit yield per plant, flesh thickness, vine length, seed cavity length, and the number of branches.

The heritability (H_b^2) of observed characteristics ranged from 16.559 to 76.395%. According to Covarrubias-Pazarán [12], fruit perimeter (76.395%), fruit height (69.828), stem length (67.606), and fruit weight (60.586%) had high heritability, while the others had moderate (leaf width, length, and number) and low (leaf chlorophyll and day to 50% male and female flowering) heritability.

The genetic advance (GA) ranged from 0.036 to 50.250%. According to the classification by Schmidt et al. [19], stem length was categorized as "high," while the others were categorized as "low." The genetic advance as a percentage of the mean (GAM) ranged from 2.518 to 24.793%. According to Teklu et al. [13], fruit weight (24.793%) and stem length (21.992%) were high and fruit perimeter (12.258%) and fruit height (12.122%) were moderate.

Muthuselvi et al. [20] assessed the genetic variability of snap melon genotypes. The majority of observed traits were found to have high heritability. However, the traits including the number of primary branches (57.88%), the node of the first male (70.30%) and female (37.86%) flower appearance, internodal length (36.49%), stem thickness (40.06%), peduncle length (25.55%), flesh thickness (40.58%), the number of male (25.19%) and female (32.44%) flowers per vine, length of the fruit (56.33%), fruit weight (60.54%), fruit number per plant (61.10%), yield per plant (70.95%), and vine length (45.06%) showed substantial heritability related to high GAM. Ibrahim [21] evaluated the genetic variability of Egyptian sweet melon traits. Fruit weight, length, and width, fruit number and total yield per plant, and flesh fruit thickness have a high heritability (>90%). However, the traits which have high both heritability and high genetic

advance were fruit weight (99.36 and 90.19%) and total yield per plant (97.31 and 77.15%). As a result, the success of the selection process is determined by both broad-sense heritability and genetic advancement.

3.2. Genotypic and Phenotypic Correlation. Table 3 shows the genotypic and phenotypic correlations among melon characteristics. The maximum and significant genotypic correlation value was obtained between leaf length and leaf width ($r = 1.000$, $p < 0.01$). Fruit weight is positively correlated with fruit perimeter ($r = 0.940$, $p < 0.01$) and fruit height ($r = 0.831$, $p < 0.01$). For the phenotypic correlation, fruit weight is positively correlated with fruit perimeter ($r = 0.880$, $p < 0.01$), fruit height ($r = 0.758$, $p < 0.01$), stem length ($r = 0.350$, $p < 0.01$), leaf number ($r = 0.207$, $p < 0.05$), stem diameter ($r = 0.199$, $p < 0.05$), and leaf chlorophyll ($r = 0.197$, $p < 0.05$) but negatively correlated with day to 50% female flowering ($r = -0.244$, $p < 0.01$). According to the findings of Iathet and Piluek [22], the fruit length of Thai slicing melon had a positive correlation with fruit weight ($r = 0.79$, $p < 0.01$). It indicates that increasing the length of melon fruit resulted in a higher weight. Ibrahim and Ramadan [23] reported that the fruit weight of sweet melon was positively correlated with total yield per plant ($r = 0.973$, $p < 0.01$), fruit length ($r = 0.850$, $p < 0.01$), and flesh fruit thickness ($r = 0.847$, $p < 0.01$).

3.3. Path Analysis. Table 4 presents the genotypic path analysis among melon characteristics on fruit weight. Fruit perimeter (0.896), fruit height (0.288), stem diameter (0.258), day to 50% female flowering (0.135), and leaf chlorophyll (0.110) had a strongly positive direct effect on fruit weight, whereas stem length (-0.174) had a strongly negative direct effect. Furthermore, stem length had a strongly positive indirect effect through fruit perimeter (0.594) and height (0.243). Table 5 presents the phenotypic path analysis among melon characteristics on fruit weight. Fruit perimeter (0.833), stem diameter (0.167), leaf chlorophyll (0.117), and fruit height (0.109) had a strongly positive direct effect on fruit weight. However, stem length (-0.158) had a strongly negative direct effect. Furthermore, through fruit perimeter, fruit height had a strongly positive indirect effect (0.713). It suggests that the increase in traits with a favorable direct influence on fruit weight may directly contribute to fruit weight.

This finding is consistent with that of other investigations. Feyzian et al. [24] used a path model to examine certain yield-influent variables in Iranian melon under pruning and nonpruning conditions. They found that under both conditions, fruit number per plant (0.79 and 0.96) and the average weight of fruit per plant (1.14 and 1.042) had a positive direct effect on the total weight of fruit per plant. Ibrahim and Ramadan [23] evaluate the path analysis of morphological and physiological characteristics on sweet melon productivity under drought and watered settings. Fruit weight (1.263), fruit number per plant (0.198), and stem length (0.070) were found to have a considerable direct effect on total fruit yield per plant.

TABLE 1: Analysis of variance for agronomic and fruit characteristics of melon varieties.

Values	SD	SL	LW	LL	LN	LC	DMF	DFF	FW	FP	FH
No. of replications (rep)	4	4	4	4	4	4	4	4	4	4	4
No. of treatments (trt)	8	8	8	8	8	8	8	8	8	8	8
Trt mean sum of square	0.03**	14504.26**	26.83**	27.00**	73.23**	70.12**	9.85**	11.75**	0.74**	127.64**	13.54**
Rep mean sum of square	0.01*	2124.24**	13.54**	7.78**	13.23**	8.00 ^{ns}	0.75 ^{ns}	1.62 ^{ns}	0.07**	13.47**	1.66**
Error mean sum of square	0.01	421.74	2.40	2.18	3.12	10.77	1.37	2.81	0.03	2.42	0.36
Trait mean	0.94	228.49	24.71	22.09	35.61	42.59	15.95	24.88	1.36	41.09	12.89
Minimum	0.74	140.00	18.00	15.00	29.00	32.90	13.00	22.00	0.90	32.00	10.05
Maximum	1.21	330.00	30.00	27.50	44.00	53.20	17.00	29.00	2.20	50.00	15.44
CV	8.76	8.99	6.27	6.69	4.96	7.70	7.33	6.74	12.47	3.78	4.63
Standard error	0.02	5.13	0.39	0.37	0.44	0.82	0.29	0.42	0.04	0.39	0.15

ns, not significantly different; *Significant at $p < 0.05$; **Significant at $p < 0.01$. SD, stem diameter; SL, stem length; LL, leaf length; LW, leaf width; LC, leaf chlorophyll; LN, leaf number; DMF, day to 50% male flowering; DFF, day to 50% female flowering; FP, fruit perimeter; FH, fruit height; and FW, fruit weight.

TABLE 2: Genotypic and phenotypic coefficient of variations, broad-sense heritability, genetic advance, and genetic advance as percentage of mean among agronomic and fruit characteristics of melons.

Values	SD	SL	LW	LL	LN	LC	DMF	DFF	FW	FP	FH
GCV	4.227: L	12.984: M	4.999: L	5.638: L	5.879: L	4.522: L	4.565: L	3.004: L	15.462: M	6.808: L	7.042: L
PCV	9.724: L	15.791: M	8.022: L	8.751: L	7.691: L	8.934: L	8.634: L	7.38: L	19.865: M	7.789: L	8.427: L
h_b^2	18.896: L	67.606: H	38.830: M	41.520: M	58.425: M	25.624: L	27.953: L	16.559: L	60.586: H	76.395: H	69.828: H
GA	0.036: L	50.250: H	1.586: L	1.653: L	3.296: L	2.008: L	0.793: L	0.626: L	0.338: L	5.037: L	1.562: L
GAM	3.785: L	21.992: H	6.417: L	7.484: L	9.256: L	4.716: L	4.972: L	2.518: L	24.793: H	12.258: M	12.122: M

GCV, genotypic coefficient of variation; PCV, phenotypic coefficient of variation; h_b^2 , broad-sense heritability; GA, genetic advance; GAM, genetic advance as percentage of mean; L, low; M, medium; and H, high; SD, stem diameter; SL, stem length; LL, leaf length; LW, leaf width; LC, leaf chlorophyll; LN, leaf number; DMF, day to 50% male flowering; DFF, day to 50% female flowering; FP, fruit perimeter; FH, fruit height; FW, fruit weight.

TABLE 3: Genotypic (upper) and phenotypic (lower) correlations among agronomic and yield traits of melons.

Variables	SD	SL	LW	LL	LN	LC	DMF	DFF	FP	FH	FW
SD	1.000	-0.413	-0.323	-0.354	-0.306	-0.162	-0.067	0.562	-0.124	-0.151	0.231
SL	-0.101	1.000	0.244	0.354	0.448	0.672	-0.029	-0.600	0.663	0.846**	0.550
LW	-0.181*	0.325**	1.000	1.000**	-0.530	-0.232	0.306	-0.080	0.070	0.037	-0.132
LL	-0.219*	0.372**	0.805**	1.000	-0.550	-0.252	0.427	-0.208	0.236	0.170	0.013
LN	-0.027	0.467**	-0.126	-0.114	1.000	0.615	-0.681	-0.468	0.186	0.501	0.193
LC	0.048	0.269**	-0.108	-0.014	0.278**	1.000	-0.113	0.176	0.227	0.363	0.314
DMF	-0.062	-0.088	0.055	0.091	-0.357**	-0.034	1.000	0.104	0.487	0.017	0.420
DFF	0.041	-0.188*	-0.064	-0.098	-0.376**	0.085	0.293**	1.000	-0.738*	-0.880**	-0.511
FP	0.020	0.474**	0.103	0.202*	0.165	0.098	0.186*	-0.296**	1.000	0.893**	0.940**
FH	-0.029	0.598**	0.135	0.211*	0.382**	0.123	-0.065	-0.377**	0.856**	1.000	0.831*
FW	0.199*	0.350**	0.005	0.064	0.207*	0.197*	0.171	-0.244**	0.880**	0.758**	1.000

*Correlated at $p < 0.05$; **Correlated 0.01; SD, stem diameter; SL, stem length; LL, leaf length; LW, leaf width; LC, leaf chlorophyll; LN, leaf number; DMF, day to 50% male flowering; DFF, day to 50% female flowering; FP, fruit perimeter; FH, fruit height; FW, fruit weight.

TABLE 4: Genotypic path analysis among melon characteristics on fruit weight.

Variables	Direct (bold and diagonal values) and indirect effects										r_g
	SD	SL	LW	LL	LN	LC	DMF	DFF	FP	FH	
SD	0.258	0.072	-0.021	0.034	-0.013	-0.018	-0.003	0.076	-0.111	-0.043	0.231
SL	-0.107	-0.174	0.016	-0.034	0.020	0.074	-0.001	-0.081	0.594	0.243	0.550
LW	-0.084	-0.042	0.066	-0.098	-0.023	-0.026	0.013	-0.011	0.063	0.011	-0.132
LL	-0.091	-0.062	0.066	-0.097	-0.024	-0.028	0.018	-0.028	0.211	0.049	0.013
LN	-0.079	-0.078	-0.035	0.054	0.044	0.068	-0.028	-0.063	0.166	0.144	0.193
LC	-0.042	-0.117	-0.015	0.025	0.027	0.110	-0.005	0.024	0.203	0.104	0.314
DMF	-0.017	0.005	0.020	-0.042	-0.030	-0.012	0.041	0.014	0.436	0.005	0.420
DFF	0.145	0.104	-0.005	0.020	-0.021	0.019	0.004	0.135	-0.661	-0.253	-0.511
FP	-0.032	-0.115	0.005	-0.023	0.008	0.025	0.020	-0.100	0.896	0.257	0.940
FH	-0.039	-0.147	0.002	-0.017	0.022	0.040	0.001	-0.119	0.799	0.288	0.831

Residual effect = -0.026. SD, stem diameter; SL, stem length; LL, leaf length; LW, leaf width; LC, leaf chlorophyll; LN, leaf number; DMF, day to 50% male flowering; DFF, day to 50% female flowering; FP, fruit perimeter; FH, fruit height.

TABLE 5: Phenotypic path analysis among melon characteristics on fruit weight.

Variables	Direct (bold and diagonal values) and indirect effects										r_p
	SD	SL	LW	LL	LN	LC	DMF	DFE	FP	FH	
SD	0.167	0.016	-0.014	0.019	-0.003	0.006	-0.004	0.001	0.017	-0.003	0.199
SL	-0.016	-0.158	0.025	-0.032	0.046	0.031	-0.005	-0.002	0.395	0.065	0.350
LW	-0.028	-0.051	0.077	-0.070	-0.012	-0.013	0.003	-0.001	0.086	0.015	0.005
LL	-0.034	-0.059	0.062	-0.087	-0.011	-0.002	0.005	-0.001	0.168	0.023	0.064
LN	-0.004	-0.074	-0.010	0.010	0.099	0.032	-0.020	-0.005	0.138	0.042	0.207
LC	0.008	-0.042	-0.008	0.001	0.028	0.117	-0.002	0.001	0.082	0.013	0.197
DMF	-0.010	0.014	0.004	-0.008	-0.035	-0.004	0.056	0.004	0.155	-0.007	0.171
DFE	0.006	0.030	-0.005	0.009	-0.037	0.010	0.016	0.013	-0.247	-0.041	-0.244
FP	0.003	-0.075	0.008	-0.018	0.016	0.011	0.010	-0.004	0.833	0.093	0.880
FH	-0.005	-0.094	0.010	-0.018	0.038	0.014	-0.004	-0.005	0.713	0.109	0.758

Residual effect = 0.164. SD, stem diameter; SL, stem length; LL, leaf length; LW, leaf width; LC, leaf chlorophyll; LN, leaf number; DMF, day to 50% male flowering; DFE, day to 50% female flowering; FP, fruit perimeter; FH, fruit height.

4. Conclusions

According to the analysis of variance, all the observed characteristics among the melon varieties were highly statistically significant. The assessment of genetic variability revealed that fruit weight, perimeter, height, and stem length had a high broad-sense heritability related to the moderate or high genetic advance as a percentage of the mean. According to the correlation and path analyses, stem diameter and length, leaf chlorophyll, and fruit perimeter and height were considered characteristics in breeding programs for fruit weight improvement. It suggests that the increase in traits with a favorable direct influence on fruit weight may directly contribute to fruit weight.

Data Availability

All the data used to support the findings of this study are available from the corresponding author upon request.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

Authors' Contributions

TK conceptualized the experiment, conducted the work, analysed the data, and prepared the manuscript. WI supervised the study and suggested the study. AP conducted the study and reviewed statistical analysis. SS reviewed the manuscript and checked for writing.

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