BIODIVERSITAS
Volume 26, Number 4, April 2025
Pages: 1870-1880

ISSN: 1412-033X
E-ISSN: 2085-4722
DOI: 10.13057/biodiv/d260436

Analysis of similarity and dissimilarity of combining ability and heterosis for melon (*Cucumis melo*) fruit characters using multi-environments

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Manuscript received: 28 January 2025. Revision accepted: 15 April 2025.

Abstract. *Saputra HE, Syukur M, Suwarno WB, Sobir. 2025. Analysis of similarity and dissimilarity of combining ability and heterosis for melon (*Cucumis melo*) fruit characters using multi-environments. Biodiversitas 26: 1870-1880.* Evaluating combining ability and heterosis simultaneously across different environments facilitates the identification of hybrids with comparative advantages for melon breeding. Therefore, this study aimed to evaluate the consistency of General Combining Ability (GCA), Specific Combining Ability (SCA), heterosis, and heterobeltiosis on the characteristics of melon fruit in three environments, namely Bengkulu, Cilegon, and Argamakmur. The method used a completely randomized block design with one factor for each environment. The full diallel population (30 F1+6 parents) was repeated thrice, leading to 108 experimental units in each environment. The results showed that the best combined GCA value was followed by the optimal GCA value in each environment, despite genetic × environment and GCA × environment interaction. The consistency of GCA was due to the additive effect role that was not influenced by the environment. The best combined SCA value was not followed by the optimal SCA value in each environment, showing inconsistency due to non-additive effect roles (dominance and epistasis), which were easily influenced by the environment. The results also showed that genetic distance affected the values of heterosis and heterobeltiosis. Furthermore, crossbreeding between melon groups produced better heterosis and heterobeltiosis values than crossbreeding within the same group. Combining ability (GCA and SCA), mid-parent value, heterosis, and heterobeltiosis across multiple environments helped identify hybrids with comparative advantages for melon breeding.

Keywords: Combining ability**,** genetic distance, genetic parameters, genetic studies, heterobeltiosis

INTRODUCTION

Melon (*Cucumis melo* L.) plants are among the most diverse horticultural commodities globally. In Indonesia, the most commonly grown melon belongs to the reticulatus and inodorus groups, although the makuwa group has begun to be cultivated. Genetic studies have been extensively conducted, particularly on melon breeding (Merheb et al. 2020; Chikh-Rouhou et al. 2021; Pandey et al. 2021; Shafiin et al. 2021; Yusuf and Daryono 2021; Can and Türkmen 2022; Khomphet et al. 2022; Soltani et al. 2022; Naznin et al. 2024; Liu et al. 2025). Several methods have been developed to study the genetic control of traits in plants. This information is obtained through quantitative genetic analysis, such as diallel analysis. Diallel crosses are the most popular mating design used in plant breeding research to estimate the combining ability of each cross (Badami et al. 2020; Esmaeili et al. 2022; Handayani et al. 2022). Selecting the correct genotypes is essential to produce excellent hybrid melon cultivars. To create the optimal appearance, crossings from different parents need to be analyzed for their genetic roles and combining ability, identifying the potential genotypes to have a good combined character performance. Combining ability analysis is classified into two types, namely General Combining Ability (GCA-additive role) and Specific Combining Ability (SCA-non-additive role). In crossbreeding, a good GCA value is used to select genotypes as parents for crossing, while a high SCA value suggests good genotype combinations for best hybrid performance. Heterosis and heterobeltiosis are also measured together in the evaluation of combining ability because of their involvement in determining the best cross-combination. Additionally, the level of genetic dissimilarity between the parental genotypes must be considered.

Melon plants comprising reticulatus, inodorus, and makuwa, show various dissimilar genetic distances. Saputra et al. (2022, 2024) found a narrow genetic difference between reticulatus and inodorus melon but a considerable genetic difference between reticulatus, inodorus, and makuwa group. Based on dissimilar genetic distances, evaluating combining ability and heterosis in various melon groups is required to understand how genetic diversity influences heterosis and optimize hybrid performance. A method to assess combining ability and heterosis is through diallel populations to achieve hybrids for broad or specific areas that allow the expression of maximum agronomic potential (Amzeri et al. 2024). This type of experiment allowed the

detection of possible combining ability × environment interaction (Nardino et al. 2020).

While genetic factors play a crucial role in hybrid performance, environmental conditions also significantly impact combining ability and heterosis. The significant influence of the environment on a character poses considerable difficulty in assessing the genetic role under different environmental conditions. The testing environment heavily influences the combining ability and heterosis. Consequently, variations in testing conditions can impact a character's performance in terms of heterosis and combining ability. Different combining abilities are caused by testing with other genotypes, according to several studies (Napolitano et al. 2020; Shajari et al. 2021; Esmaeili et al. 2022; Kaur et al. 2022; Patel et al. 2024). Previous investigations reported that melon plants showed high heterosis in some fruit characteristics, namely fruit weight 6.71-95.63% (Badami et al. 2020; Handayani et al. 2022; Saha et al. 2022), fruit length 13.04-49.68% (Badami et al. 2020; Saha et al. 2022), flesh thickness 40-100% (Badami et al. 2020; Handayani et al. 2022), and total soluble solid 16.62-40.43% (Badami et al. 2020; Handayani et al. 2022). These results suggested the importance of assessing combining ability and heterosis across many contexts with the same genotype. Next, to improve the accuracy and reliability of selecting hybrids, it is essential to evaluate combining ability in numerous environments. GCA and heterosis must be consistently observed across several test locations to ensure the hybrids function better. This process benefits plant breeding by analyzing combining ability and heterosis across different conditions, providing more accurate information about a character's performance. Previous studies have never used the same crossbred population for genetic parameter analysis in multiple locations. Hence, the information on the consistency of genetic parameter values is a novelty in this research. Therefore, this study aimed to evaluate the consistency of General Combining Ability (GCA), Specific Combining Ability (SCA), heterosis, and heterobeltiosis on melon fruit characteristics in three environments.

MATERIALS AND METHODS

Study area and genetic material

This study was conducted from January to April 2024 in three environments, namely Bengkulu, Cilegon, and Argamakmur. The characteristics of the environment are presented in Table 1. The method used a completely randomized block design with three replications. The genetic material used 6 parents' genotypes for the formation of the full diallel population, including the reticulatus (2 genotypes), inodorus (2 genotypes), and makuwa (2 genotypes), resulting in 36 genotypes (30 F1 and 6 parents). The characteristics of the 6 parents are presented in Table 2.

Procedures

Each genotype was cultivated with 10 plants per replication in every environment, and data were collected from five plants per replication. Fundamental fertilizer was applied in the field seven days before planting, containing 10 tons ha^{-1} of chicken manure and 300 kg ha^{-1} of NPK. Melon planting was carried out in beds measuring 5 m × 1 m covered with black-silver plastic mulch at a hole distance of 50 cm × 50 cm. Each hole was planted with one seed melon and given 5-10 grains of Carbofuran. Pruning of melon plant shoots is carried out on every lateral shoot that appears from the 1st to the 8th nodes. Meanwhile, the shoots appearing from the 9th to the 15th nodes were maintained to produce one fruit per plant (Ye et al. 2020; Saputra et al. 2022, 2024).

Pollination is carried out after the hermaphrodite flowers bloom on nodes 9th to 15th. After two weeks of pollination, fruit selection is carried out. After selecting one fruit, only the fruit branches were maintained, and other lateral shoots were pruned. Supplementary NPK fertilizer was applied in solution (concentration of 20 g L^{-1} water) and given at the base of the plant stem 7, 14, 21, 28, 35, 42, and 49 Days After Planting (DAP). This step was followed by applying KNO3 fertilizer in solution (concentration of 5 g L^{-1} water) at 200 ml per plant at 45 DAP. Every week, fungicide: mancozeb 70% with a concentration of 5 g L^{-1} water, bactericide: copper oxide (concentration of 5 g L^{-1} water), and pesticide: Profenofos 500 g L^{-1} (concentration of 1.5 mL L^{-1} water) were sprayed. Ripe melon fruits were picked 6 to 7 weeks after pollination, as shown by the abscission layer on the fruit stem, the wilt leaves near the fruit, or the bottom of the fruit feels mushy when it is pushed and emits a fragrant aroma (Handajaningsih et al. 2019; Khomphet et al. 2023; Salamah et al. 2023). Further specific characteristics were observed, including fruit weight, length, flesh thickness, and total soluble solids.

Table 1. The environmental characteristics were used for the evaluation of 36 melon genotypes

Environment	Location	Period	Altitude (masl)	Average rainfall (mm $month^{-1}$)	Average temperature (°C $month^{-1}$)	Average relative humidity (% $month^{-1}$)
Bengkulu	-3.752851 latitude; 102.28341 longitude	January-April 2024	14	182.25	26.37	86.24
Cilegon	-5.9681282 latitude; 106.052894 longitude	January-March 2024	57	264.20	27.98	83.67
Argamakmur	-3.431783 latitude; 102.21232 longitude	January-April 2024	204	193.5	28.07	84.65

Table 2. The characteristics of melon parent genotypes

Parent genotype	Botanical group	Characteristic	
IPB283	Reticulatus	The fruit's flesh is greenish-white, with thin netting; the skin color is white, and the fruit shape is round	
UME90	Reticulatus	Orange fruit flesh, medium netting, ocher skin color, round fruit shape	
IPBM21	Inodorus	White fruit flesh, yellow fruit skin, round fruit shape	
IPBM23	Inodorus	Orange fruit flesh, yellow skin, slightly elongated shape	
UME99	Makuwa	White fruit flesh, white fruit skin, oval-shaped fruit, and thin fruit flesh	
UME101	Makuwa	White fruit flesh, yellow striped fruit skin, and elongated fruit shape	

Data analysis

All data were collected in each environment and analyzed using a combined Analysis of Variance (ANOVA) with a 5% level test. GCA effects from parents and SCA from F1 crosses are analyzed using a 6 × 6 diallel analysis Method 1, Model 1 (Griffing 1956). The fixed effects model is assumed for the parents and F1 crosses, while this study considers the model environment to be random. The linear model for the evaluation of GCA and SCA combined across three environments is as follows (Nardino et al. 2020; Nasser et al. 2020):

$$Y_{ijkl} = \mu + g_i + g_j + s_{ij} + r_{ij} + l_k + bl(k) + g_{lik} + g_{ljk} + s_{lijk} + r_{lijk} + \varepsilon_{ijkl}$$

Where:

Y_{ijkl} : Observation value from each unit
μ : Overall mean value
g_i : Effect of GCA of parent i
g_j : Effect of GCA of parent j
s_{ij} : Effect of SCA F1 between parents ij
r_{ij} : Effect of reciprocal SCA F1 between parents ij
l_k : Effect of environments k
$bl(k)$: Effect of repetition l in environments k
g_{lik} : Effect of interaction GCA × Env F1 between of the i parent in the environments k
g_{ljk} : Effect of interaction GCA × Env F1 between of the j parent in the environments
s_{lijk} : Effect of interaction SCA × Env F1 between parents ij in environment k
r_{lijk} : Effect of reciprocal interaction SCA × Env F1 between parents ij in environment k
ε_{ijkl} : Effect of the error

Heterosis and heterobeltiosis are calculated for each environment based on the average value of the parents and the best parent (Badami et al. 2020; Handayani et al. 2022; Saha et al. 2022). All data were analyzed by using R, ADGR, and Microsoft Excel software.

$$\text{Heterosis (\%)} = \frac{F_1 - MP}{MP} \; x \; 100\ \% \text{ , Heterobeltiosis (\%)} = \frac{F_1 - BP}{BP} \; x \; 100\ \%$$

Where:

F_1 : Mean of the crosses
MP : Mean of the two parents
BP : Better Parents

RESULTS AND DISCUSSION

General and specific combining ability

Combining ability analysis helps breeders identify and select the best parental genotypes to obtain new hybrid combinations with better genetic potential. In this study, the test significantly affected 4 characteristics, namely fruit weight, fruit length, fruit flesh thickness, and total soluble solids. There was a highly significant interaction effect of GCA, SCA, reciprocal, genetic × environment, GCA × environment, and SCA × environment for all characteristics, as shown in Table 3. Several previous studies have shown similar results in melons, namely significant GCA, SCA, and reciprocal (Shajari et al. 2021; Handayani et al. 2022; Kaur et al. 2022). The highly significant GCA effect implies that certain parent genotypes have higher GCA than other genotypes, and the highly significant SCA effect shows that the resulting hybrids have distinct appearances. GCA and SCA are significant indicators that help breeders choose the finest parents and hybrids, respectively. The extremely large reciprocal influence also reveals that F1's appearance differs from F1R's, emphasizing the importance of identifying the best hybrids. The GCA and SCA values are presented in Table 4, Figures 1 and 2.

The considerable GCA for all analyzed features indicates the possibility of establishing a new melon variety by selecting desirable attributes. However, given the strong positive SCA in many of the hybrids, the utilized lines may also be helpful for hybrid production (Shajari et al. 2021). Multi-environment testing has many advantages, including determining which hybrids operate best in all conditions. The highly significant interaction effect between genetic parameters and the environment demonstrates that the estimated values of genetic parameters differ across environments (Table 4, Figures 1 and 2). Several studies show the same thing about the significant interaction of genetic parameters with the environment, such as in melons (Handayani et al. 2022), corn (Badu-Apraku et al. 2020; Bhusal and Lal 2020; Nardino et al. 2020; Arulselvi et al. 2024), sorghum (Fonseca et al. 2021), kenaf (Al-Mamun et al. 2022), and wheat (Dudhat et al. 2025).

The combined GCA and GCA in each environment for all characteristics are presented in Table 4. The genotype IPBM23 has the best combined GCA and GCA in each environment for the fruit weight character, while the genotype UME99 has the worst. The genotypes with the best combined GCA and GCA in each environment for the fruit length character are IPBM23 and UME101, while IPB283 has the worst. The best combined GCA and GCA in each environment for the fruit flesh thickness is possessed by the genotype UME90, and UME99 shows the worst performance. For the total soluble solids, the genotypes with the best and worst combined GCA and GCA in each environment are UME99 and IPB283, respectively. Based on all observed characteristics, there is a consistent value of combined GCA with GCA for each environment. The consistency of combined GCA with GCA in each environment indicates that genotypes with the best or worst GCA in a particular environment will be followed in other environments. However, it differs for genotypes with medium GCA, not the best or the worst. Genotypes with medium GCA have different rankings in each environment. This is supported by the very significant GCA × environment interaction data in Table 3, resulting in differences in the rankings of genotypes with medium GCA in each environment. Although the ranking order of the GCA genotypes varies in each environment, it does not mean that the GCA genotype in a specific environment will be the best in other environments. Thus, the consistent GCA remains in all environments.

Compared to GCA, each cross-combination with the best SCA is not followed by the same cross-combination in every environment. The combined SCA values and SCA for each environment for the fruit weight as well as fruit length are presented in Figure 1. Meanwhile, the fruit flesh thickness and total soluble solids are shown in Figure 2. SCA does not refer to a single individual genotype but measures the potential of each parent combination to produce the best performance.

Table 3. Analysis of variance full diallel population for melon fruit characters in three environments

Source of variation	df	FW		FL		FFT		TSS	
		MS		MS		MS		MS	
Env	2	50859.122	ns	1.917	ns	11.578	**	52.704	**
Rep (Env)	6	73546.486	**	2.204	ns	0.156	**	11.472	**
Cross	35	266823.371	**	34.961	**	0.886	ns	7.712	ns
GCA	5	473933.923	**	73.484	**	2.439	**	31.469	**
SCA	15	273214.027	**	47.858	**	0.720	**	5.289	**
Reciprocal	15	191395.865	**	9.224	**	0.534	**	2.216	**
Maternal	5	237521.575	**	7.905	**	0.489	**	3.606	**
No Maternal	10	168333.011	**	9.883	**	0.557	**	1.521	ns
Env × Cross	70	132069.783	**	10.225	**	0.593	**	5.523	**
Env × GCA	10	116505.135	**	5.570	**	0.625	**	16.922	**
Env × SCA	30	151567.647	**	14.438	**	0.636	**	3.900	**
Env × Reciprocal	30	117760.136	**	7.565	**	0.540	**	3.347	**
Env × Maternal	10	102183.538	**	5.348	**	0.635	**	3.810	**
Env × No Maternal	20	125548.435	**	8.673	**	0.492	**	3.115	**
Residual	210	16850.297		1.162		0.063		0.919	

Notes: **: Significant at 1 % level; ns: Not significant at 5 % level; FW: Fruit Weight; FL: Fruit Length; FFT: Fruit Flesh Thickness; TSS: Total Soluble Solids; df: Degree of freedom; MS: Means of Square

Table 4. Combined and each environment GCA values for all characters

Characters	Environment	Genotype					
		IPB283	IPBM21	IPBM23	UME101	UME90	UME99
FW	Combined	-0.687 (4)	4.249 (3)	**95.254 (1)**	-6.512 (5)	19.220 (2)	**-111.524 (6)**
	Bengkulu	29.159 (2)	14.616 (4)	**129.639 (1)**	-78.940 (5)	25.306 (3)	**-119.782 (6)**
	Cilegon	-50.481 (5)	-50.468 (4)	**104.129 (1)**	97.108 (2)	39.912 (3)	**-140.201 (6)**
	Argamakmur	19.260 (3)	48.599 (2)	**51.992 (1)**	-37.705 (5)	-7.557 (4)	**-74.589 (6)**
FL	Combined	**-0.890 (6)**	0.180 (3)	**1.022 (1)**	**0.893 (2)**	-0.551 (4)	-0.654 (5)
	Bengkulu	**-1.004 (5)**	0.215 (3)	**1.599 (1)**	**1.020 (2)**	-1.047 (6)	-0.782 (4)
	Cilegon	**-0.829 (6)**	-0.244 (4)	**0.687 (2)**	**0.772 (1)**	-0.090 (3)	-0.296 (5)
	Argamakmur	**-0.838 (5)**	0.571 (3)	**0.779 (2)**	**0.888 (1)**	-0.516 (4)	-0.884 (6)
FFT	Combined	0.066 (3)	0.001 (4)	0.092 (2)	-0.160 (5)	**0.192 (1)**	**-0.192 (6)**
	Bengkulu	0.138 (2)	0.090 (4)	0.160 (1)	-0.231 (5)	**0.122 (3)**	**-0.281 (6)**
	Cilegon	-0.026 (4)	-0.093 (6)	0.046 (2)	0.022 (3)	**0.086 (1)**	**-0.035 (5)**
	Argamakmur	0.088 (2)	0.006 (4)	0.071 (3)	-0.272c (6)	**0.367 (1)**	**-0.260 (5)**
TSS	Combined	**-0.690 (6)**	-0.28 (4)	-0.338 (5)	0.151 (3)	0.371 (2)	**0.790 (1)**
	Bengkulu	**-0.654 (6)**	0.249 (2)	0.196 (3)	-0.232 (5)	0.437 (1)	**0.003 (4)**
	Cilegon	**-0.308 (4)**	-0.897 (6)	0.116 (3)	-0.379 (5)	0.400 (2)	**1.069 (1)**
	Argamakmur	**-1.109 (5)**	-0.200 (4)	-1.329 (6)	1.067 (2)	0.275 (3)	**1.297 (1)**

Notes: FW: Fruit Weight; FL: Fruit Length; FFT: Fruit Flesh Thickness; TSS: Total Soluble Solid. The numbers in parentheses indicate the ranking of genotype scores

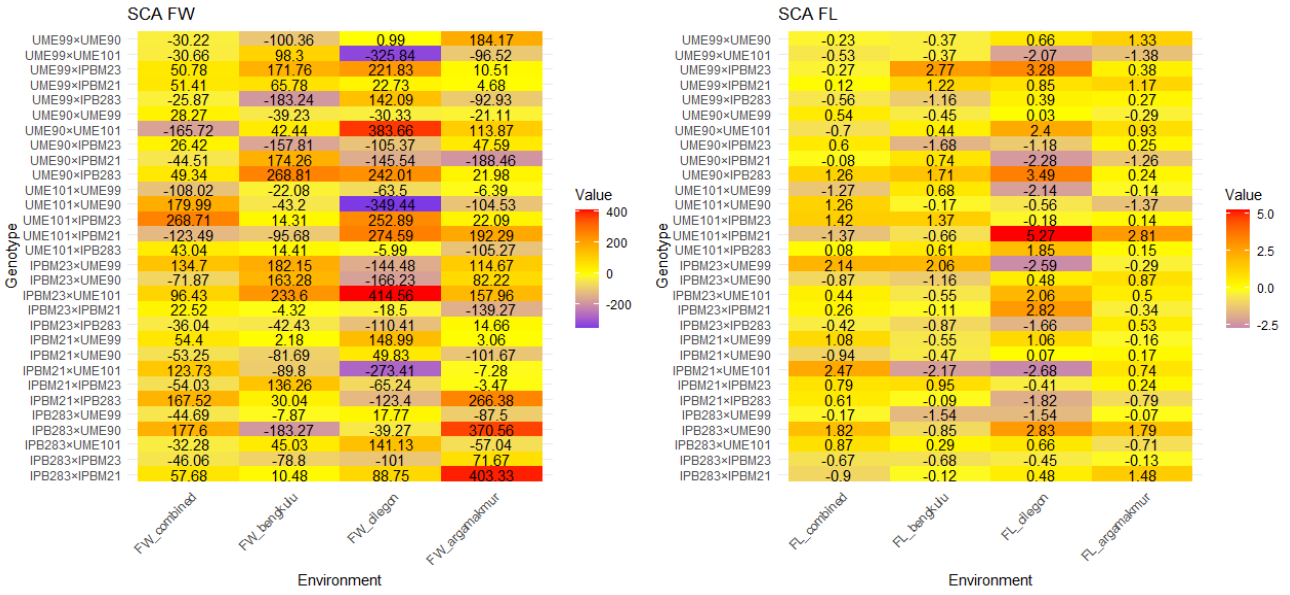

Figure 1. The combined SCA values and SCA for each environment for: FW: Fruit Weight; and FL: Fruit Length

The genotype IPBM23 × UME90 produced a combined fruit weight GCA of -71.87, while the cross combination with the best GCA was UME101 × IPBM23 for fruit length. This showed that parents with good GCA values x good GCA values do not always produce cross-combination with high SCA. The cross of low GCA × low GCA produces cross-combinations with low SCA, such as UME101 × UME99, and their reciprocals for fruit weight and fruit length characters. The cross-combination with the best combined SCA value for the fruit length is IPBM21 × UME101 (GCA medium × GCA good). The genotype IPB283 × UME90 and its reciprocal have high SCA, while IPB283 × UME99 and its reciprocal show low SCA. Furthermore, IPB283, UME90, and UME99 have low GCA for the fruit length character, which facilitates crossing among low GCA to produce combinations with high and low SCA.

The genotype UME90 has the best combined GCA and GCA in each environment for the fruit flesh thickness, compared to UME101 and UME99 (Table 4). UME90 × IPBM23 produces the best combined SCA value fruit flesh thickness, and its reciprocal has optimal SCA value fruit flesh thickness for Bengkulu environment (Figure 2). IPB283 × UME90 produces the highest SCA value for fruit

flesh thickness in Argamakmur, while UME101 × IPBM21 has the optimal value for Cilegon. Genotypes UME101 × UME99 and their reciprocals produce a low combined SCA, followed by all environments except Bengkulu. Furthermore, UME90 × UME99 has the best combined SCA for the total soluble solids. IPBM23 × UME90, UME101 × IPBM21, and IPB283 × UME90 have the best SCA for Bengkulu, Cilegon, and Argamakmur, respectively.

Heterosis and heterobeltiosis

From the crossbreeding, 30 F1 genotypes in the inodorus, reticulatus, and makuwa groups showed varying values of heterosis and heterobeltiosis for fruit weight, length, flesh thickness, and total soluble solids. The heterosis and heterobeltiosis values for fruit weight characteristics in the environments of Bengkulu, Cilegon, and Argamakmur are -27.57%-113.22% and -46.99%-95%, -26.99%-358.26% and -36.31%-304.85%, -35.49%-131.98% and -41.87%-124.42%, respectively (Figure 3). Genotypes with the best heterosis and heterobeltiosis for fruit weight characteristics in Cilegon, Bengkulu, and Argamakmur are UME90 x UME101, UME101 x IPBM21, and IPB283 x IPBM21, respectively.

The fruit length character has heterosis and heterobeltiosis values in Bengkulu, Cilegon, and Argamakmur environments of -5.76%-44.92% and -18.66%-37.75%, 5.74%-204.88% and -5.52%-196.21%, -11.54%-48.36% and -17.60%-45.73%, respectively (Figure 4). Heterosis and heterobeltiosis showed the best performance in UME101 × IPM21 for Bengkulu and Cilegon environments, while IPBM21 x UME101 has optimal value in Argamakmur.

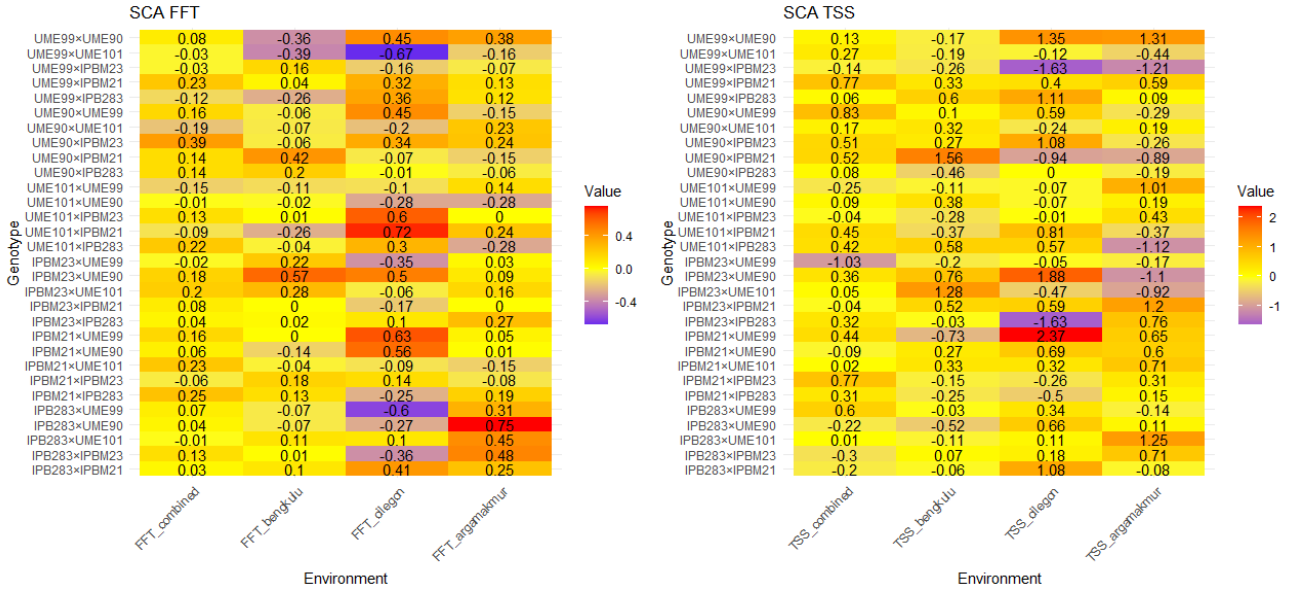

Figure 2. Combined SCA values and the SCA for each environment for: FFT: Fruit Flesh Thickness; and TSS: Total Soluble Solids

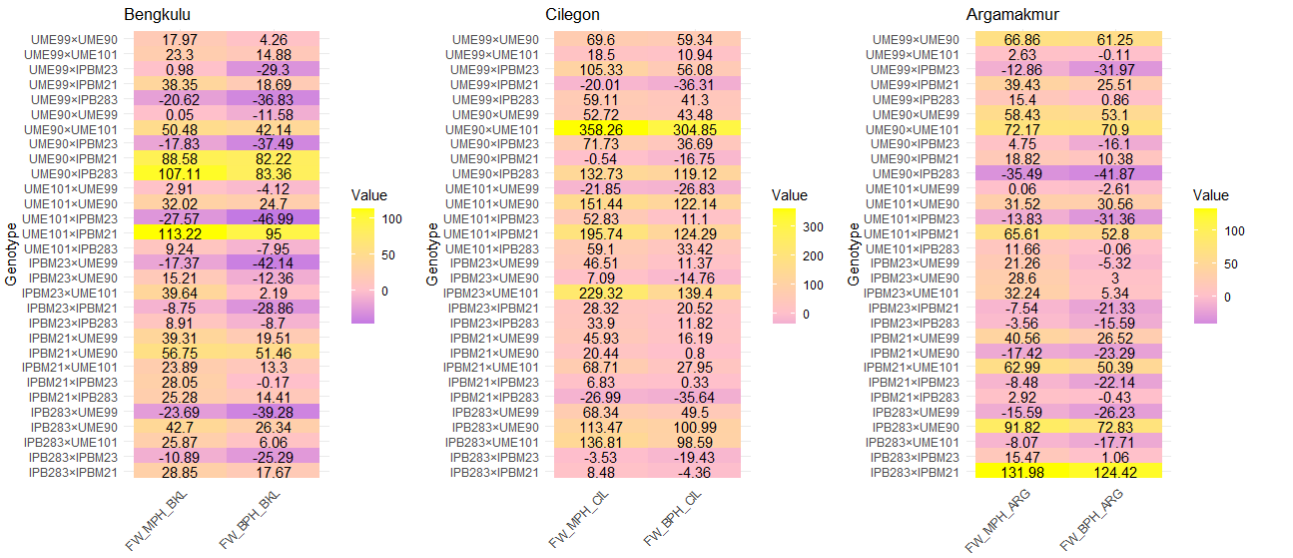

Figure 3. Heterosis Fruit Weight (FW MPH); and heterobeltiosis Fruit Weight (FW BPH) in each environment

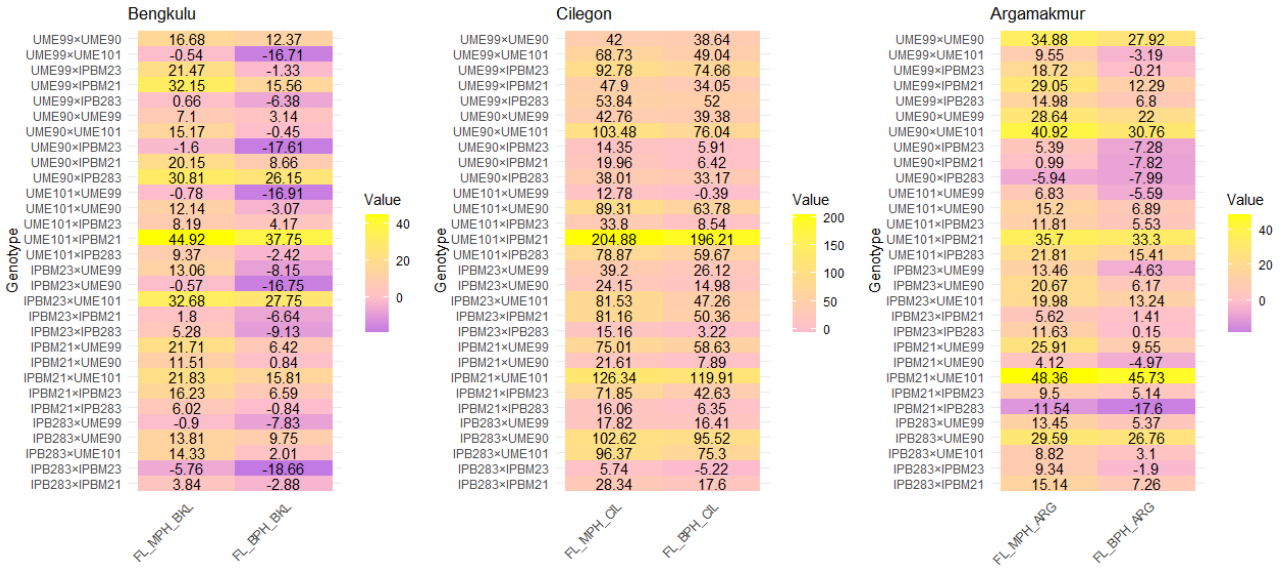

Figure 4. Heterosis Fruit Length (FL_MPH); and heterobeltiosis Fruit Length (FL_BPH) in each environment

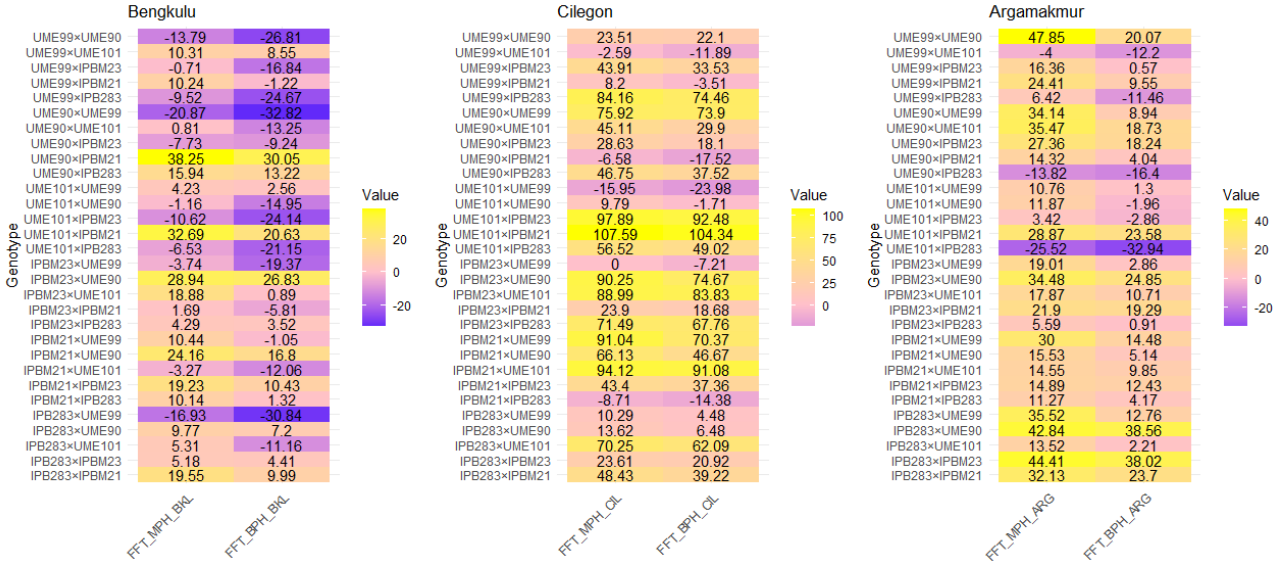

Figure 5. Heterosis Fruit Flesh Thickness (FFT_MPH); and heterobeltiosis Fruit Flesh Thickness (FFT_BPH) in each environment

The range of heterosis and heterobeltiosis for fruit flesh thickness in Bengkulu (-20.87%-38.25% and -32.82%-30.05%), Cilegon (-15.95%-107.59% and -23.98%-104.34%), and Argamakmur (-25.52%-47.85% and -32.94%-38.56%). Heterosis and heterobeltiosis for fruit flesh thickness in Bengkulu are best in UME90 × IPBM21 (Figure 5). For Cilegon, genotype with the best heterosis and heterobeltiosis is UME101 × IPBM21. For Argamakmur environment, the best heterosis is not followed by the optimal heterobeltiosis. Regarding Argamakmur, the genotype with the best heterosis for fruit flesh thickness is UME99 x UME90, while heterobeltiosis is found in the genotype IPB283 x UME90. The genotype with the best heterosis does not have the optimal heterobeltiosis due to the range of parental values. This suggests that a wider range of parental values correlates with better heterosis, without ensuring the highest heterobeltiosis.

As shown in Figure 6, the heterosis and heterobeltiosis of the total soluble solids in Bengkulu were -13.88%-37.08% and -16.69%-32.48%. The heterosis and heterobeltiosis values for total soluble solids in Cilegon and Argamakmur were -28.89%-41.80% and -35.47%-23.97%, as well as -30.25%-31.06% and -44.42%-12.15%. IPBM21 × UME90 and IPBM21 × IPBM23 are the genotypes with the best heterosis and heterobeltiosis for total soluble solids in Bengkulu and Argamakmur environments, respectively. In Cilegon environment, the genotype with the best heterosis for total soluble solids differs from heterobeltiosis. The genotype IPBM21 × UME99 has the best heterosis, while UME90 × UME99 shows the highest heterobeltiosis.

Figure 7 presents the average values of fruit weight and length, followed by fruit flesh thickness and total soluble solids in Figure 8. Based on the results, crosses between parents in the same melon group have lower heterosis and heterobeltiosis values. This shows that genetic distance determines the values of heterosis and heterobeltiosis. This study's findings are also congruent with those reported by Yu et al. (2020), which found that heterosis between groups is better than within the same groups.

Discussion

In this study, the interaction between genetic parameters and the environment shows substantial variation. The interaction of genetic parameters with the environment indicates that there are differences in the value of genetic parameters in each environment. The effects of GCA show that the contribution of inbred lines varies according to the crosses. However, variability among SCA effects shows that hybrid combinations are performing differently (Nardino et al. 2020; Fonseca et al. 2021; Arulselvi et al. 2024). GCA is the average genotype potential for hybrid production when crossed with a series of other genotypes. Meanwhile, SCA is defined as the characteristics of specific crosses, such as measuring the potential of each parent combination for hybrid production. The utilization of genotypes from three groups of melons with different genetic backgrounds is expected to provide both positive and negative information on GCA and SCA values. Generally, combined GCA value can serve as a basis for the consistency of GCA values. This suggests that genotypes with the best combined GCA will also have the optimal GCA in each environment for all characters.

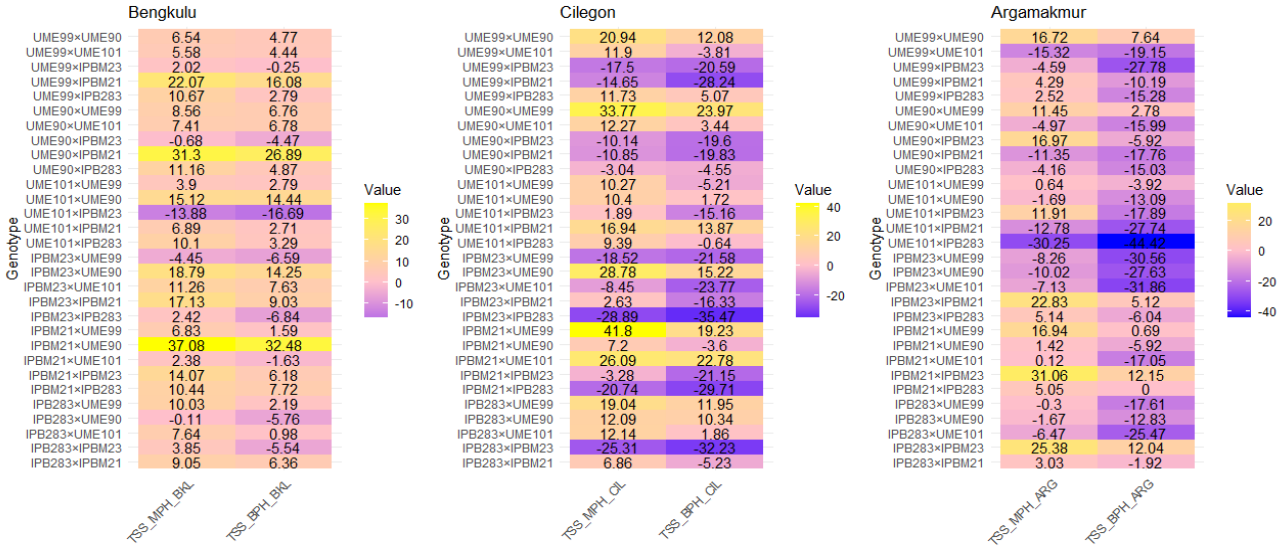

Figure 6. Heterosis Total Soluble Solid (TSS_MPH) and heterobeltiosis Total Soluble Solid (TSS_BPH) in each environment

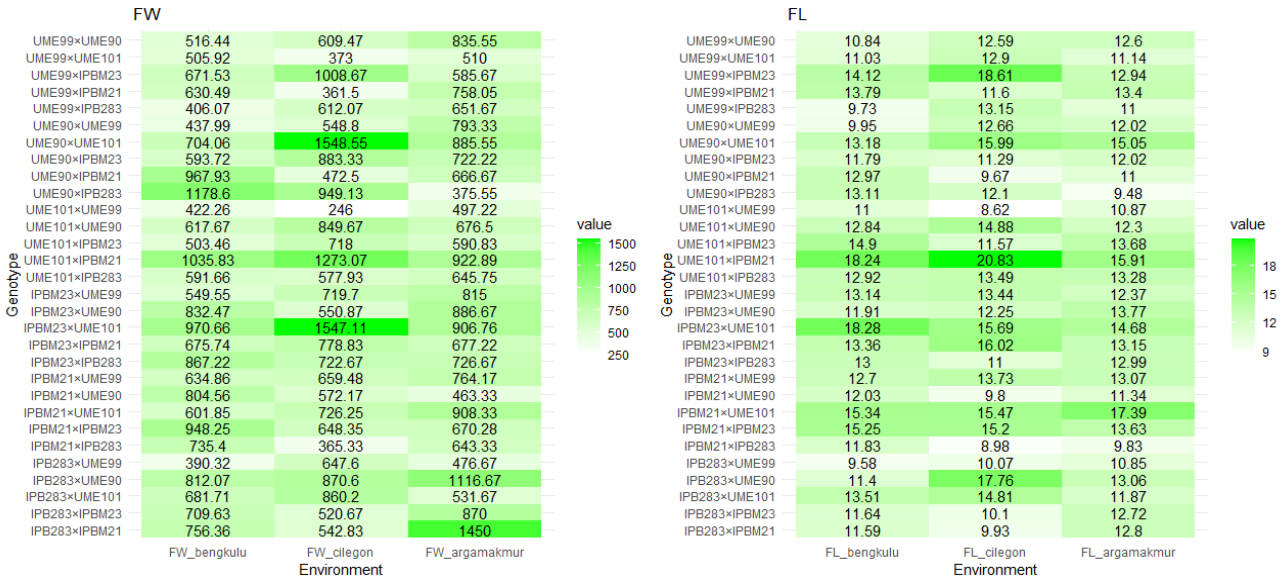

Figure 7. The average values of: FW: Fruit Weight; and FL: Fruit Length

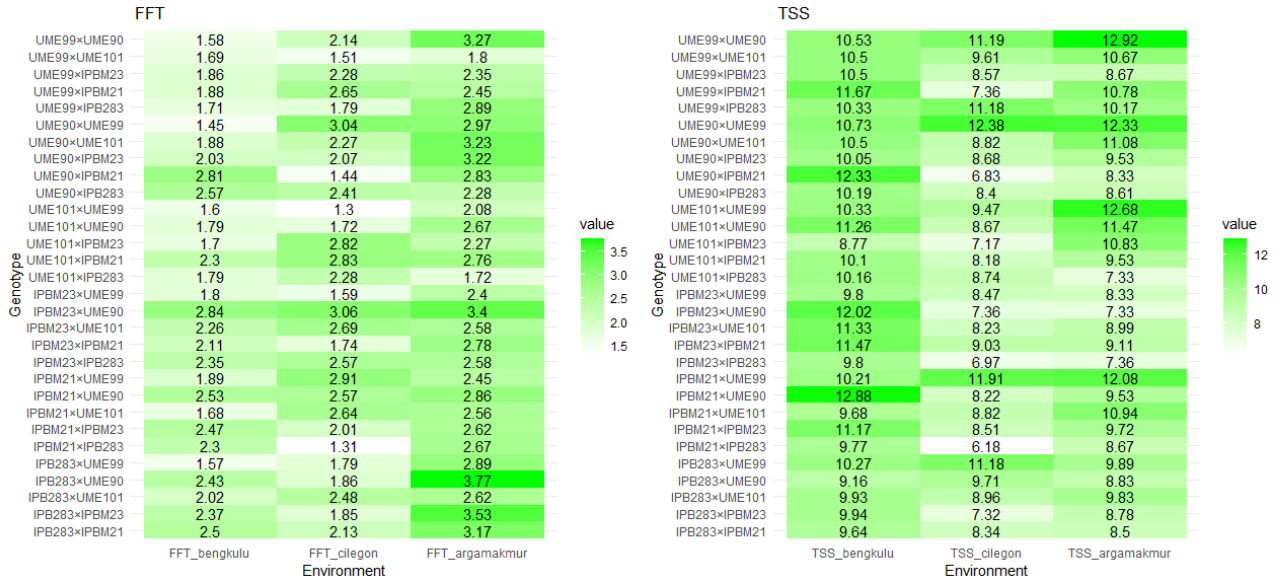

Figure 8. Average values of: TSS: Total Soluble Solids; and FFT: Fruit Flesh Thickness (FFT)

The optimal GCA follows the genotype with the best combined GCA value in each environment. According to (Giri et al. 2020; Esmaeili et al. 2022), GCA is the additive gene role and is not influenced by the environment, which causes consistent values. Furthermore, GCA represents the average potential of a genotype for hybrid production when crossed with a series of other genotypes. The results suggest that genotypes with high GCA will produce good hybrids. A low GCA value, whether positive or negative, indicates that the average of one parent with another in the cross does not vary significantly from the overall value (Bhusal and Lal 2020). In contrast, a high GCA value indicates that the parent average is superior or inferior to the overall values. This shows strong evidence of the desired gene inheritance from parents to offspring with high intensity and a more excellent representation of information regarding the additive gene playing a more significant role.

Based on the observation results of all characteristics, the consistency of combined SCA and SCA in each environment is difficult to achieve. This is shown by low GCA × low GCA parents, which can produce combinations of low and high SCA. Parents in the same melon group can create combinations with low SCA, such as UME101 × UME99 and their reciprocals for fruit weight and flesh thickness, if they have low GCA. However, it differs for the fruit length and total soluble solids, where genotypes in the same melon group produce high SCA combinations despite having low GCA. The inconsistency in SCA values is suspected to be due to the non-additive gene roles (dominance and epistasis), suggesting that the environment greatly influences the genotype's appearance. These results are similar to previous investigations, where the high SCA effects from GCA good × GCA good can be attributed to cumulative influence of additive and additive × additive interactions (Al-Mamun et al. 2022; Gaballah et al. 2022; Sharma et al. 2024; Yadav et al. 2024). The high SCA effects from crosses, including parents with GCA good × GCA low, are attributed to the favorable additive influence of parents and the epistatic impact of the low GCA (Gaballah et al. 2022; Rout et al. 2025). The high SCA effect manifested by GCA low × GCA low crosses (Chiuta and Mutengwa 2020; Engida et al. 2024) is due to the interaction of non-allelic genes of the dominance × dominance type, leading to overdominance that cannot be improved.

Heterosis in fruit varies similarly to previous studies reported by Badami et al. (2020), Handayani et al. (2022), and Saha et al. (2022). The values of heterosis and heterobeltiosis are needed for hybrid assembly. The superiority of hybrids is observed from the values of heterosis and heterobeltiosis. However, not all observed traits in horticultural plants must show the highest heterosis and heterobeltiosis. Since fruit weight is not the primary consumer option (Tores et al. 2020), investigating its heterosis and heterobeltiosis is not essential. In melon plants, consumer preferences regarding fruit quality become important in exploring heterosis and heterobeltiosis. For example, consumers always desire sweet fruit with thick flesh, showing the need to examine heterosis and heterobeltiosis for total soluble solids and thick flesh. Regarding shape, there is a high preference for elongated and round fruits. Heterosis and heterobeltiosis studies tested in multiple environments show consistency based on genetic distance. The consistency is demonstrated by the same pattern that crossing between melon groups produces hybrids with the highest heterosis and heterobeltiosis.

The results showed that no cross-combination genotype had consistently superior heterosis and heterobeltiosis across the three test environments. The genotype × environment interaction is very evident, showing the appearance of different cross-combination genotypes in each environment. The difference in genotype appearance affects the heterosis and heterobeltiosis values in each environment, making them inconsistent. Díaz et al. (2017) also reported that the consistency of heterosis did not occur in melon plants

tested in three environments. The diverse heterosis and heterobeltiosis in various environments occurred because hybrids and parental lines respond to environmental stimuli differently (Yu et al. 2020).

One of the most essential aspects of heterosis is the assignment of plant genotypes to heterotic groups, which serve as the foundation for effective hybrid programs. A heterotic group consists of plant genotypes that are linked or not related. The genotypes may come from the same or distinct populations (Fasahat et al. 2016). The finding of unique heterotic groups should help to generate remarkable hybrids and improve the efficiency of hybrid development programs. Genetic distance estimates are important because they aid in assigning genotypes to heterotic groups in hybrid formation caused by various inter-group crossings. Information on genetic diversity and heterotic groups is especially beneficial to both inbred line creation and plant breeders in terms of exploiting their germplasm more efficiently and consistently by using complementing lines that maximize the outcome of hybrid breeding operations. Therefore, the use of three groups of melons is the basis for the formation of the heterotic group.

Crossbreeding between parents from different melon groups produced better heterosis and heterobeltiosis than the same group. Similarly, Yu et al. (2020) reported that heterosis between groups was better than in the same group. Based on the results, parents with a significant difference in average values will produce high heterosis, but do not necessarily have the best mean values. Crosses with the highest heterobeltiosis also have the best average values, making heterobeltiosis an important indicator in evaluating crossing combinations compared to heterosis. By using three groups of melons (reticulatus, inodorus, and makuwa) in this study, the greater genetic distance shows better heterosis and heterobeltiosis values. However, the mid-value, the target for improvement, needs to be considered. As the genetic distance increases, the significant difference improves in the mid-parent value, leading to a smaller chance of obtaining heterobeltiosis. The best mid-parent value for individual characteristics is marked by the highest heterobeltiosis (Figures 3-6). This indicates that crosses with the best heterobeltiosis will produce the optimal appearance. The expression of heterosis and combining ability can vary significantly across different environments. Previous studies stated that the environment played an important role in the performance of melon hybrids (Napolitano et al. 2020). Therefore, breeding programs should consider genetic and environmental interactions to optimize hybrid performance.

In conclusion, the optimal GCA value in each environment followed the best combined GCA value. However, there were genetic × environment and GCA × environment interactions. The consistency of GCA was due to the additive role that was not influenced by the environment. Among all genotypes, IPBM23 had the best GCA for fruit weight and fruit length, UME101 showed optimal performance for fruit length, and UME90 possessed the best flesh thickness. UME99 and IPB283 were the parents with the best GCA for total soluble solids. The optimal SCA value did not follow each environment's best combined SCA value. The inconsistency of SCA was due to the non-additive roles (dominance and epistasis) that were easily influenced by the environment. Genetic distance affected the values of heterosis and heterobeltiosis. Compared to intra-group, inter-group crossings of melon plants produced better heterosis and heterobeltiosis values. The results showed that breeding programs should focus on selecting parents with high GCA and consider environmental interactions to maximize the benefits of heterosis and heterobeltiosis. Therefore, the evaluation of GCA and SCA, mid-parent value, and heterobeltiosis in several environments helped identify hybrids with comparative advantages for melon breeding.

ACKNOWLEDGEMENTS

The authors are grateful to (i) *Beasiswa Pendidikan Indonesia* (The Indonesian Education Scholarship), (ii) *Pusat Pelayanan Pembiayaan dan Asesmen Pendidikan Tinggi* (Center for Higher Education Funding and Assessment), Ministry of Higher Education, Science, and Technology, Republic of Indonesia, (iii) *Lembaga Pengelola Dana Pendidikan* (Endowment Fund for Education Agency), Ministry of Finance, Republic of Indonesia, for granting a scholarship and supporting the publication of this study.

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