



## Article

# Combining Ability and Hybrid Breeding in Tunisian Melon (*Cucumis melo* L.) for Fruit Traits

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**Abstract:** A half-diallel cross study of seven melon inbred lines was carried out. The seven parents and their 21 F<sub>1</sub> hybrids were evaluated for precocity of maturity, average weight per fruit, and fruit quality (fruit size, rind thickness, and soluble solids). The Diallel analysis was investigated for breeding values of these melon genotypes via general and specific combining ability, relationships between general and specific combining ability, and heterosis for the evaluated traits. The analysis of variance of the traits evaluated indicated highly significant differences among genotypes, suggesting the presence of adequate genetic variation for breeding. Additive genetic effects were most important with respect to fruit weight, while genetic dominance and epistasis effects mainly controlled fruit quality traits (fruit size, rind thickness, and TSS). Parent 1 (P1) and parent 3 (P3) had significant positive general combining ability effects for fruit weight. Also, P3 had positive general combining ability effects for fruit length and diameter, and cavity diameter. P3 was found to show maximum significant GCA in the desirable direction for all the traits except for TSS. Evaluation of heterosis (%) revealed that hybrid P1 × P3 can be considered as the best-performing hybrid for average fruit weight, TSS, and precocity, which also exhibited the highest positive and significant SCA effect for these traits. These results suggested that, among the melon genotypes studied, there is the potential to generate superior new varieties in hybrid production.

**Keywords:** diversity; combining ability; diallel analysis; gene action; heterosis; heritability



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## 1. Introduction

Melon (*Cucumis melo* L.,  $2n = 2x = 24$ ), belonging to the Cucurbitaceae family, is a cross-pollinating crop with a small diploid genome size of 450 Mb [1]. It is a commercially important horticultural crop worldwide and exhibits high levels of diversity in morphological, physiological, and biochemical properties [2]. With its diverse cultivars and growing adaptation to various climates, melon has become a staple in the global fruit market, serving as a delectable addition to a wide array of culinary delights and a vital source of nutrition [3,4]. The increasing demand for melon, both locally and internationally, necessitates a concerted effort to enhance its productivity, ensuring a consistent supply of high-quality fruits year-round.

Melon improvement strategies aim to create melon cultivars that exhibit not only improved fruit yield but also other desirable traits such as resistance to diseases, adaptability to changing environmental conditions, and post-harvest fruit quality [5]. A critical

component of these breeding programs is the evaluation of genetic variability and the identification of promising parental combinations.

The concept of combining ability has revolutionized the field of plant breeding. It serves as a key tool for assessing the genetic potential of different cultivars and identifying which combinations result in superior progeny. Understanding the combining ability of parental lines for fruit yield is instrumental in achieving the ultimate goal of producing high-yielding melon hybrids [6,7].

In parallel, the concept of heterosis, also called hybrid vigor, has garnered significant attention in plant breeding [8–10]. Heterosis describes the phenomenon in which hybrid offspring of two genetically distinct parental lines exhibit superior performance compared to their parents, especially in terms of yield, growth, and adaptability. The exploitation of heterosis in melon breeding programs holds the promise of unlocking new levels of productivity and crop resilience [11–13].

The selection of superior parents for hybridization is very important for melon improvement programs because the performance of a hybrid is related to the general (GCA) and specific (SCA) combining abilities of the inbred lines involved in the cross. According to Feyzian et al. [12], the most promising hybrids are those originating from the crossing of divergent parents, where at least one of them presented high GCA.

Melon breeding includes the development of breeding lines, cultivars, and hybrids using different crossing methods. To increase the efficiency of breeding, it is necessary to know the genetic basis of the traits that are being improved in the available material selection. As stated by several authors [10,12,14,15], the diallel crossing method is most frequently used in genetic research and breeding because it provides maximum information about gene effects and the number, combining ability (GCA and SCA), heterosis, heritability, and possible gene interactions [16].

Combining ability analysis helps to identify superior parents to be used in breeding programs or to identify promising cross combinations for cultivar development [11,17]. General combining ability is directly related to the breeding value of a parent and is associated with additive genetic effects and is theoretically fixable, while SCA is the relative performance of a cross, which is associated with non-additive gene action, predominantly contributed by dominance, epistasis, or both, and is non-fixable [14,18]. Therefore, both GCA and SCA effects are important in the selection or development of breeding populations [11,14].

In Tunisia, numerous studies have explored the significance of *Cucumis melo* as a valuable genetic resource [19–21]. These melons harbor genes that have been selected by researchers, farmers, or even nature itself due to their adaptability, productivity, and resistance to various stresses [22–25]. Notably, there is a lack of prior research on hybridizing melons, a crucial aspect that warrants further exploration for hybrid creation. Consequently, this study was designed to address the following objectives: (1) unravel the genetic mechanisms by determining gene action; (2) quantify the extent of hybrid vigor in comparison to both the average and superior parent; (3) evaluate the components of variance and the combining ability effects; and (4) estimate the heritability, both in a broad and narrow sense, for fruit traits in melon.

## 2. Materials and Methods

### 2.1. Plant Material

Seven local inbred lines (Table 1) were crossed in  $7 \times 7$  half diallel crosses to produce 21  $F_1$  hybrids, without reciprocals. Six plants were used for each cross. The parents were selected for their resistance to aphids [24], Fusarium wilt [23,25], or Powdery mildew [22,26] and also for their agronomical traits and fruit characteristics [21].

Individual plants from each of the seven cultivars were selfed for four successive generations to obtain uniform inbred lines for crossing. The seven inbred lines were then crossed during the spring season of 2019 to produce a non-reciprocal diallel set of F<sub>1</sub> hybrids, i.e., 21 single crosses. For the crossing, male and female flower buds that were expected to open in the next morning were covered by small paper bags the day before, where the crossing was usually made 6.00–8.00 o'clock in the morning. The pollinated flowers were covered with small paper bags and tagged. In February 2021, seeds of each parental genotype and their 21 single crosses were planted in the experimental station.

**Table 1.** Melon parents, their fruit characteristics, and resistance to the main biotic stress.

Parents	Descriptive Features	Biotic Stress and Resistant Genes	Reference
P1	Ovate shape, light-orange skin, white flesh, big fruit size.	Resistant to powdery mildew and carrying both the <i>Vat</i> gene and <i>Fom-1</i> gene in homozygosis.	[23,24]
P2	Elliptical shape, yellow skin.	Resistant to powdery mildew	[22]
P3	Oblate shape, greenish-orange skin.	-	[25]
P4	Elliptical shape, orange skin.	Resistant to powdery mildew	[26]
P5	Oblate shape, greenish skin.	Carrying <i>Fom-1</i> gene in homozygosis	[23]
P6	Elliptical shape, greenish skin.	Resistant to powdery mildew and carrying the <i>Fom-1</i> gene in homozygosis.	[22,23]
P7	Flattened shape, greenish skin.	Carrying the <i>Fom-1</i> gene in homozygosis.	[23]

Parents and their F<sub>1</sub> hybrids (Figure 1) were evaluated. The experiment was carried out from February to July during two successive seasons, 2021 and 2022, at the experimental station of Sahline located in the Central East Region of Tunisia (35°45'02" N, 10°42'44" E). The 28 genotypes (7 inbred lines' parents and their 21 F<sub>1</sub> hybrids) were initially sown in compost, and seedlings at the three-leaf stage were transplanted into a greenhouse. Three replications were conducted, with each replication consisting of 10 plants per genotype. The experimental layout was arranged in a randomized complete block design with a row spacing of 80 cm and a within-row spacing of 40 cm. During the cultivation period, agronomic practices such as irrigation, weeding, and fertilization were uniformly conducted in all plots as required.

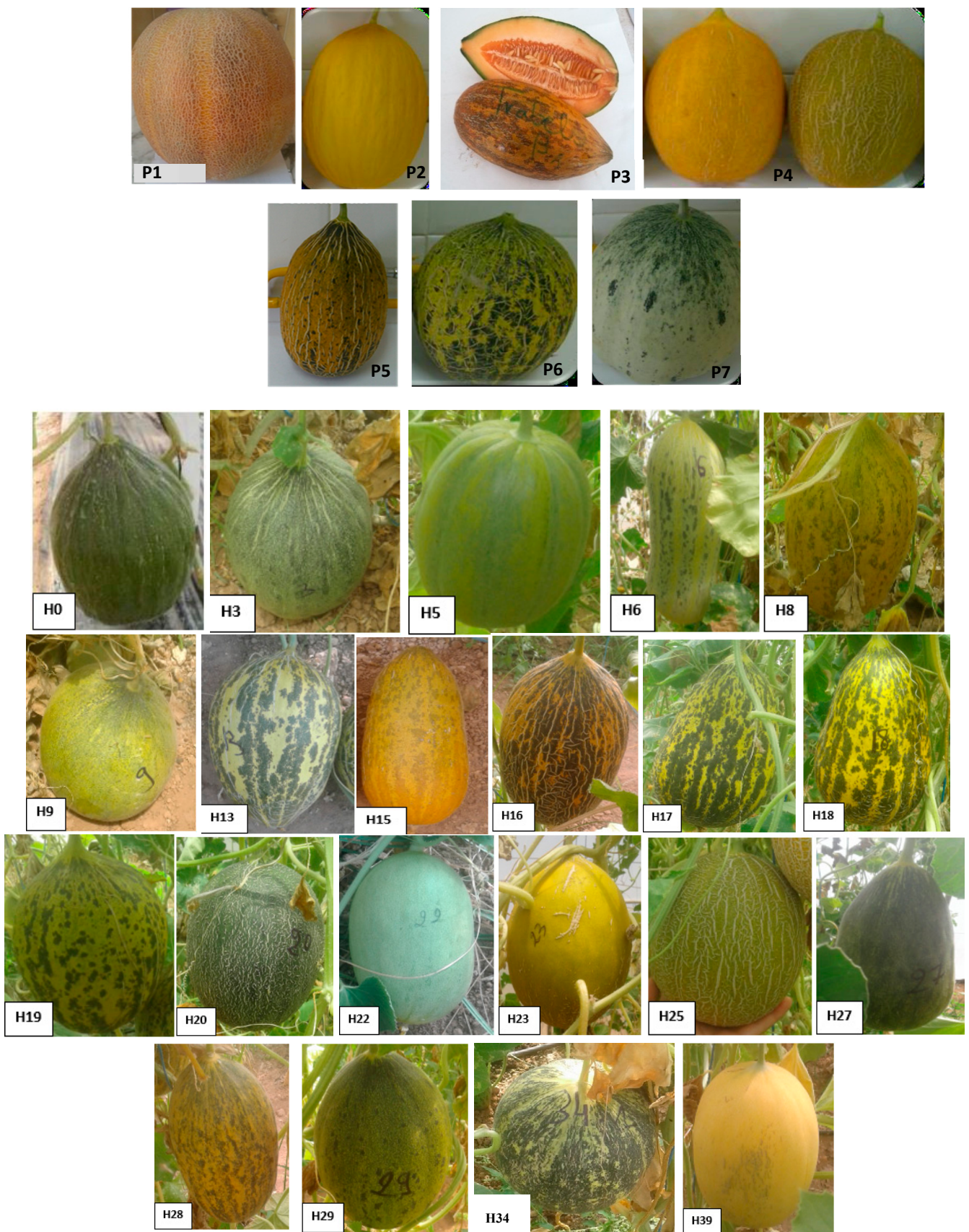


Figure 1. The evaluated parent inbred lines and their F<sub>1</sub> hybrids.

## 2.2. Fruit Traits and Yield Related Parameters

At harvest, the studied melon genotypes were evaluated for 8 quantitative traits related to fruit characters and yield components. Five central plants of each genotype in each replication were selected for sampling. Quantitative data were recorded on (1) precocity determined as days to maturity, from sowing to harvest, (2) number of fruits per vine, (3) fruit weight, (4) fruit length, (5) fruit diameter, (6) rind thickness, (7) cavity diameter, and (8) total soluble solids.

The fruit traits (length, width, and diameter) were measured with a ruler or caliper, fruit weight was measured with an electronic balance, and total soluble sugars (TSS), expressed as degree Brix ( $^{\circ}$ Brix) in fruit juice, were determined using a digital refractometer (Atago, Tokyo, Japan).

## 2.3. Data Analysis

The breeding value of the plant material was evaluated by analyzing the data on heterosis and combining ability in the  $F_1$  generation. The following analyses were performed: (i) analysis of variance, (ii) estimation of GCA and SCA effects, (iii) estimation of heritability, (iv) evaluation of heterosis, (v) least squares means analysis of hybrid offspring and parents, and (vi) correlation analysis and visualization.

(i) Analysis of variance: The significance of differences among genotypes for the studied traits was tested using Tukey's test ( $p < 0.05$ ) with the Statistical Package (SPSS) 18.0 Software for Windows. All other analysis results were obtained using Rversion 4.3.2 (R Core Team 2021).

(ii) Combining ability estimates: GCA and SCA effects were calculated to identify superior parent lines and crosses. This was carried out according to diallel cross analysis using Griffing's [27] model 1, method 2, a fixed effect model, which involves parents and one set of  $F_1$  hybrids. Estimates of GCA, SCA and their variances;  $\sigma^2_{gca}$  (general combining ability variance), and  $\sigma^2_{sca}$  (specific combining ability variance) were computed using the 'mme' function of the sommer package in R [28]. From the variance components,  $\sigma^2_A$  (additive variance) and  $\sigma^2_D$  (dominance variance; the non-additive effects) were calculated as  $\sigma^2_A = 2 \sigma^2_{gca}$  and  $\sigma^2_D = \sigma^2_{sca}$  [27].

The relative importance of GCA and SCA effects for each trait was determined following the general predicted ratio (GPR):  $GCA/SCA = 2 MS_{GCA} / (2MS_{GCA} + MS_{SCA}) = 2 \sigma^2_{gca} / (2 \sigma^2_{gca} + \sigma^2_{sca})$  [29]. In this index ratio, a higher value indicates that the additive genetic effects are given a higher weight than SCA.

(iii) Heritability estimates: Heritability values were calculated using the following formulas:

$$\text{Broad-sense heritability } (H^2) = V_G / V_P = \sigma^2_G / (\sigma^2_G + \sigma^2_E),$$

$$\text{Narrow-sense heritability } (h^2) = V_A / V_P = \sigma^2_A / (\sigma^2_G + \sigma^2_E),$$

where:

$V_P$  (phenotypic variance) is the total variance observed in the trait,

$V_G$  (genetic variance) is the portion of the phenotypic variance attributed to genetic differences among individuals, calculated as  $V_G = V_A + V_D + V_I$  (Additive + dominance + interaction or epistatic variances),

$V_E$  (environmental variance) is the portion of the phenotypic variance attributed to environmental factors.

(iv) Heterosis estimates: Heterosis was determined to evaluate the performance advantage of hybrids over their parents. We calculated the mid-parent heterosis (MPH) and better-parent heterosis (BPH) by using the formulas as follows:

$$\begin{aligned} \text{MPH} &= (\text{value of } F_1 - \text{mean of parents} / \text{mean of parents}) \text{ in percent} \\ &= [F_1 - (P_1 + P_2)/2] / [(P_1 + P_2)/2] \times 100, \end{aligned}$$

where  $F_1$  is the value of  $F_1$  hybrids and  $P_1$  and  $P_2$  are the phenotypic value of parents.

$$\begin{aligned} \text{BPH} &= (\text{value of } F_1 \text{ value of better parent} / \text{value of better parent}) \text{ in percent.} \\ &= [(F_1 - P_B) / P_B] \times 100, \end{aligned}$$

where  $P_B$  is the phenotypic value of higher value parents, the better parent.

These heterosis measures provide insights into the extent to which hybrid offspring outperform their parents in terms of the specific traits being evaluated. Theoretically, if a heterozygous dominance effect is greater than the mean parental homozygous effects for a cross, a positive mid-parent (MP) heterosis would be expected; otherwise, a negative MP heterosis would be expected [30].

(v) Orthogonal comparisons between hybrids and parents for the evaluated parameters were carried out with the 'emmeans' R package [31]. This analysis displayed hybrid performance by the parents in a matrix format, providing a clear and comprehensive comparison of the evaluated traits through least squares means.

(vi) Correlation analysis and visualization: A correlation matrix illustrating Pearson correlations among phenotypic traits was generated using the 'ggpairs' function within the ggally package [32]. This analysis included the complete raw dataset encompassing all parental lines, offspring, and replications. Visualization of mean phenotypic values (MPH) and best parental hybrids (BPH) among the  $F_1$  hybrids, along with the correlation analysis between parental lines and  $F_1$  hybrid performance in MPH and BPH, was performed utilizing the ggplot2 package [33]. Correlation coefficients were determined via Pearson product-moment correlation, with corresponding  $p$ -values provided.

### 3. Results

#### 3.1. Hybrid Performance by Parent

The performances of the  $F_1$  hybrids varied according to the studied traits and their parents (Supplementary Table S1). ANOVA showed highly significant differences between the genotypes (parents and hybrids) for all the evaluated traits (Supplementary Table S2). The significant differences observed among the studied melon genotypes for most traits suggest the presence of adequate genetic variation for breeding.

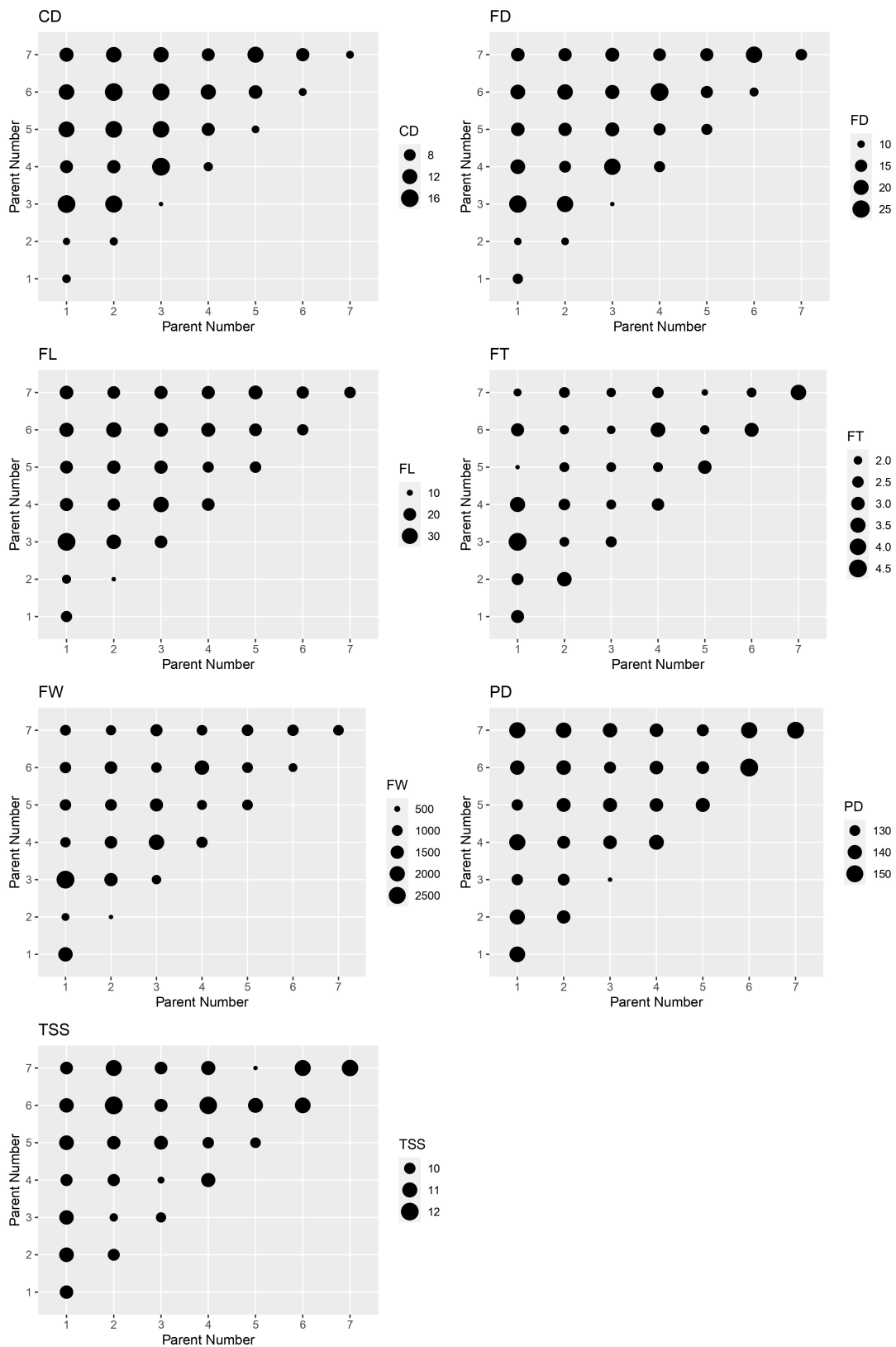
For precocity, the mean performance of this trait varied between 123 days for the parental line P3 (the earliest line to mature) to 154 days for P6 (Figure 2). A tendency can be seen that the offspring of the earliest parent P3 also showed rather early maturity.

For fruit weight, the parental line P2 exhibited the significantly smallest mean value of 468 g, whereas P1 combined with P3 had the significantly highest fruit weights of 2803 g, which seems to be a non-additive effect.

In fruit length, P2 showed the significantly shortest fruits at 9.6 cm, whereas P1 combined with P3 produced not only the significantly heaviest but also the longest fruits at 37 cm in length. P3 showed the smallest fruit diameter of 9.1 cm, varying to the significantly highest with 26.3 cm in  $P4 \times P6$ .

In cavity diameter, the parental lines performed low, and then the hybrids all showed some kind of heterosis in the 21 crosses. In rind thickness, there was again a superior effect of the hybrid combination  $P1 \times P3$ , whereas the parents performed rather low.

In TSS, P6 and its offspring showed a rather high value, with the hybrid combination  $P2 \times P6$  exhibiting the significantly highest value of 12.05 °Brix (Figure 2).



**Figure 2.** Matrix display of means of the F<sub>1</sub> hybrids by parent for the evaluated fruit traits. PD: precocity in days, FW: fruit weight (g), FL: fruit length (cm), FD: fruit diameter (cm), CD: cavity diameter (cm), FT: fruit rind thickness (mm), and TSS: total soluble solids (°Brix). Larger bubbles indicate higher trait values.

### 3.2. Combining Ability

The analysis of variance for the evaluated traits indicated significant GCA and SCA, with the exception of a non-significant GCA for fruit length. GCA variance and thereby additive gene effects were most important with respect to fruit weight, while SCA variance was much higher in precocity, fruit length, fruit diameter, cavity diameter, rind thickness, and TSS, indicating a higher influence of dominance and epistasis effects.

The GPR ratio underlines these findings by displaying the highest ratio for fruit weight, followed by precocity. The ratios of GCA/SCA effect were  $>0.5$  for only FW suggesting the predominance of additive over non-additive genetic effects. This ratio was  $<0.5$  for precocity, FL, FD, CD, RT, and TSS, implying a significant role of non-additive genetic effect on these traits (Table 2).

In general, broad-sense heritabilities were very high, ranging from 0.890 to 1 with the exception of fruit weight was high (0.615), indicating minimal environmental influences on GCA and SCA and consistent results across replicates (Table 2). These high  $H^2$  values suggest that a significant proportion of the phenotypic variance is attributable to genetic factors.

Narrow-sense heritabilities ( $h^2$ ) were generally low, ranging from 0.011 to 0.270, except for FW ( $h^2 = 0.500$ ). This indicates that, for most traits, additive genetic factors contribute to a relatively small portion of the phenotypic variance. Consequently, non-additive genetic effects (dominance and epistasis) play a substantial role in the expression of these traits. However, the narrow-sense heritability for the FW trait is comparatively higher, suggesting that additive genetic factors play a more significant role in determining the variation observed in this trait.

**Table 2.** ANOVA analysis of combining ability, variance components, GPR ratio, and heritability estimates for the evaluated quantitative traits in melon.

	DF	PD <sup>a</sup>	FW	FL	FD	CD	RT	TSS
GCA	6	641.732 **	726,120.616 **	49.149 ns	118.379 **	19.505 **	0.797 *	3.522 *
SCA	21	773.208 **	542,237.899 **	75.228 **	660.073 **	58.176 **	1.392 *	0.951 *
Error	54	32.649	116,607.226	31.527	15.885	3.331	0.015	0.016
$\sigma^2_{GCA}$		9.045	32,620.055	1.675	0.279	0.342	0.004	0.079
$\sigma^2_{SCA}$		24.429	32,620.055	18.751	17.931	12.765	0.383	0.326
$\sigma^2_{Residual}$		0.266	40,681.210	0.033	0.131	0.023	0.020	0.051
GPR		0.425	0.667	0.152	0.030	0.051	0.020	0.326
$H^2$		0.992	0.615	0.998	0.993	1.000	0.951	0.890
$h^2$		0.270	0.500	0.082	0.015	0.026	0.011	0.173

\*\* and \*: significant at 1% and 5%, respectively; ns: denote not significant. <sup>a</sup> PD: precocity in days, FW: fruit weight (g), FL: fruit length (cm), FD: fruit diameter (cm), CD: cavity diameter (cm), RT: rind thickness (mm), TSS: total soluble solids ( $^{\circ}$ Brix),  $\sigma^2_{GCA}$ : variance of general combining ability;  $\sigma^2_{SCA}$ : variance of specific combining ability;  $H^2$ : Broad-sense heritability;  $h^2$ : Narrow-sense heritability; GPR: General predicted ratio is the GCA/SCA ratio (Baker [29]).

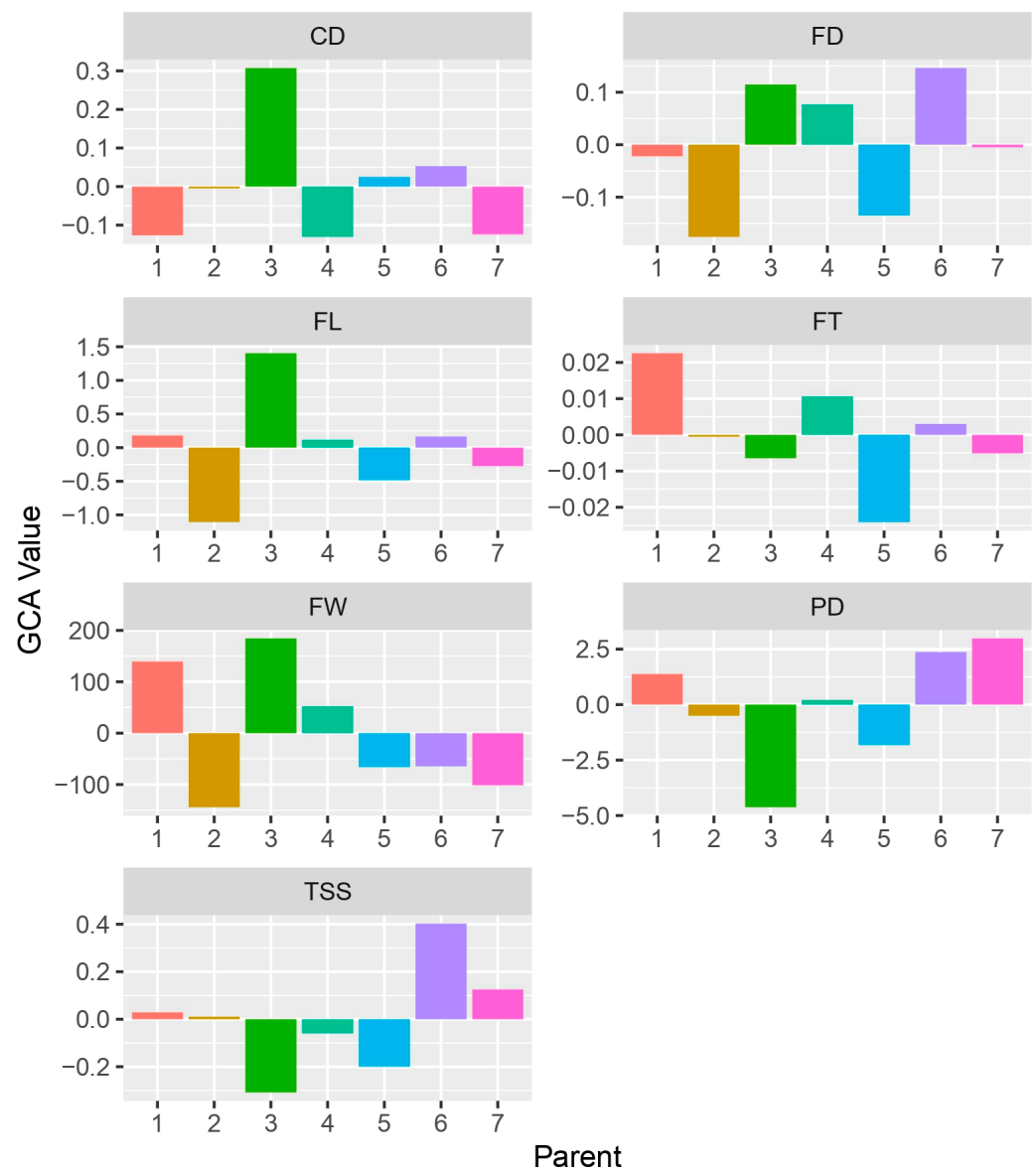
### 3.3. General and Specific Combining Ability Effects

In general, genotypes yielded very heterogeneous GCA and SCA effects among traits (Supplementary Table S3, Figure 3, Table 3).

Negative GCA effects were estimated for the following parents: P2 (−0.503), P3 (−4.624), and P5 (−1.815) for precocity (PD), which is in a desirable direction for selection (Figure 3). The highest GCA effects for fruit weight (FW) were 139.48, 184.41, and 52.16 for the parental genotypes, P1, P3, and P4, respectively (Figure 3).

The parental genotypes that revealed the highest GCA effects for fruit length (FL) and fruit diameter (FD) were P3 (1.404 and 0.115 respectively), P6 (0.165 and 0.146), and P4 (0.116 and 0.077). The highest GCA effects of 0.403 and 0.125 for TSS were observed in the parent's P6 and P7, respectively (Figure 3).

It was notable that P3 had positive general combining ability effects for fruit weight, fruit length and diameter, and cavity diameter.



**Figure 3.** Estimation of general combining ability (GCA) effects of parental lines in the F<sub>1</sub> generation for the evaluated traits. PD: precocity in days, FW: fruit weight (g), FL: fruit length (cm), FD: fruit diameter (cm), CD: cavity diameter (cm), FT: fruit rind thickness (mm), TSS: total soluble solids (°Brix).

Regarding precocity (PD), parental line P3 had negative GCA effects resulting in earlier maturity than the mean of the population, whereas P6 and P7 contributed to later maturity, exhibiting positive GCA effects (Figure 3). A significant negative SCA effect was observed in 12 crosses out of 21, for PD trait, resulting in early maturity such as the P1 and P3 in combination (Table 3).

For fruit weight (FW), P1 and P3 showed positive GCA effects (Figure 3). A significant positive SCA effect was observed in 10 crosses out of 21 for this trait (Table 3). In combination, P1 and P3 exhibited a high positive SCA, resulting in higher fruit weight compared to the additive effects of the individual parents (Table 3). This suggests a dominance effect contributing to the superior performance of the hybrid.

For fruit length (FL), P3 contributes to higher fruit length (Figure 3), whereas P2 acts in the opposite way with reducing effect on fruit length. A significant positive SCA effect for FL was observed in 8 crosses out of 21 and a clear SCA effect can be seen in the combination of P1 and P3 (Table 3).

In fruit diameter (FD), P6 revealed the highest GCA effect whereas P2 reduced the fruit diameter notably (Figure 3). A significant positive SCA effect was observed in several crosses such as the combination of P1 and P3. The combination of P4 and P6 resulted in the highest positive value of SCA for fruit diameter (Table 3).

Regarding cavity diameter (CD), some parent combinations showed significant SCA effects in reducing cavity diameters, such as P1 and P2 in combination (Table 3). Additionally, there was a significant positive SCA effect observed in several crosses such as the combination of P1 and P3 (Table 3).

For TSS, P6 exhibited a positive GCA effect, suggesting its potential contribution to higher TSS levels. Conversely, P3 seems to have a reducing effect on TSS (Figure 3). Furthermore, the combination of parents P2 and P6 showed the highest SCA effects, indicating their significant influence on TSS levels when crossed together (Table 3).

**Table 3.** Estimation of specific combining ability (SCA) in the F<sub>1</sub> generation for the evaluated traits.

Cross	PD	FW	FL	FD	CD	RT	TSS
1 × 2	2.946 *	−209.241 *	−7.190	−6.577 *	−5.432 *	0.000 *	0.263 **
1 × 3	−4.606 *	486.220 **	14.400 *	8.230 **	5.526 **	1.884 **	0.493 **
1 × 4	6.157 *	−166.897 *	−0.037	2.372 **	−1.029 *	0.874 **	−0.368 *
1 × 5	−7.305 *	−56.662 *	−0.383	0.465 **	2.824 **	−0.829 *	0.485 **
1 × 6	−2.737 *	−58.822 *	2.936	2.469 **	2.319 **	0.278 *	−0.174 *
1 × 7	3.158 *	−82.547 *	1.709	0.269 *	0.431 *	−0.658 *	−0.379 *
2 × 3	−1.413 *	103.458 **	3.987 *	5.843 **	4.325 **	−0.398 *	−0.757
2 × 4	−3.656 *	89.175 **	−0.606	−2.286 *	−0.684 *	−0.054 *	−0.306 *
2 × 5	1.614 *	71.326 **	2.305	0.286 *	4.001 **	−0.347 *	0.112 *
2 × 6	−0.222 *	135.166 **	7.120 *	4.202 **	5.649 **	−0.472 *	1.017 **
2 × 7	2.346 *	−13.934 *	0.375	−0.110 *	2.241 **	−0.209 *	0.593 *
3 × 4	2.675 *	239.089 **	5.747 *	5.824 **	5.747 **	−0.394 *	−0.830 *
3 × 5	6.105 *	60.241 **	−0.393	1.127 **	3.413 **	−0.365 *	0.529 *
3 × 6	−4.240 *	−129.044 *	0.768	1.213 **	4.235 **	−0.565 *	−0.243 *
3 × 7	2.775 *	−9.644 *	−0.968	0.920 *	1.660 **	−0.455 *	−0.084 *
4 × 5	−0.147 *	−114.417 *	−4.181	−1.905 *	−1.027 *	−0.378 *	−0.296 *
4 × 6	−4.242 *	224.298 **	2.331 *	9.298 **	1.757 **	0.762 **	0.947 **
4 × 7	−5.017 *	−64.302 *	0.352	−1.237 *	−1.065 *	−0.082 *	0.079 *
5 × 6	−4.733 *	−19.551 *	−0.521	−1.854 *	−0.457 *	−0.449 *	0.183 *
5 × 7	−7.341 *	43.099 **	3.371 *	−0.383 *	3.044 **	−0.736 *	−1.204
6 × 7	2.441 *	32.939 **	−1.695	5.921 **	−0.748 *	−0.399 *	0.220 *

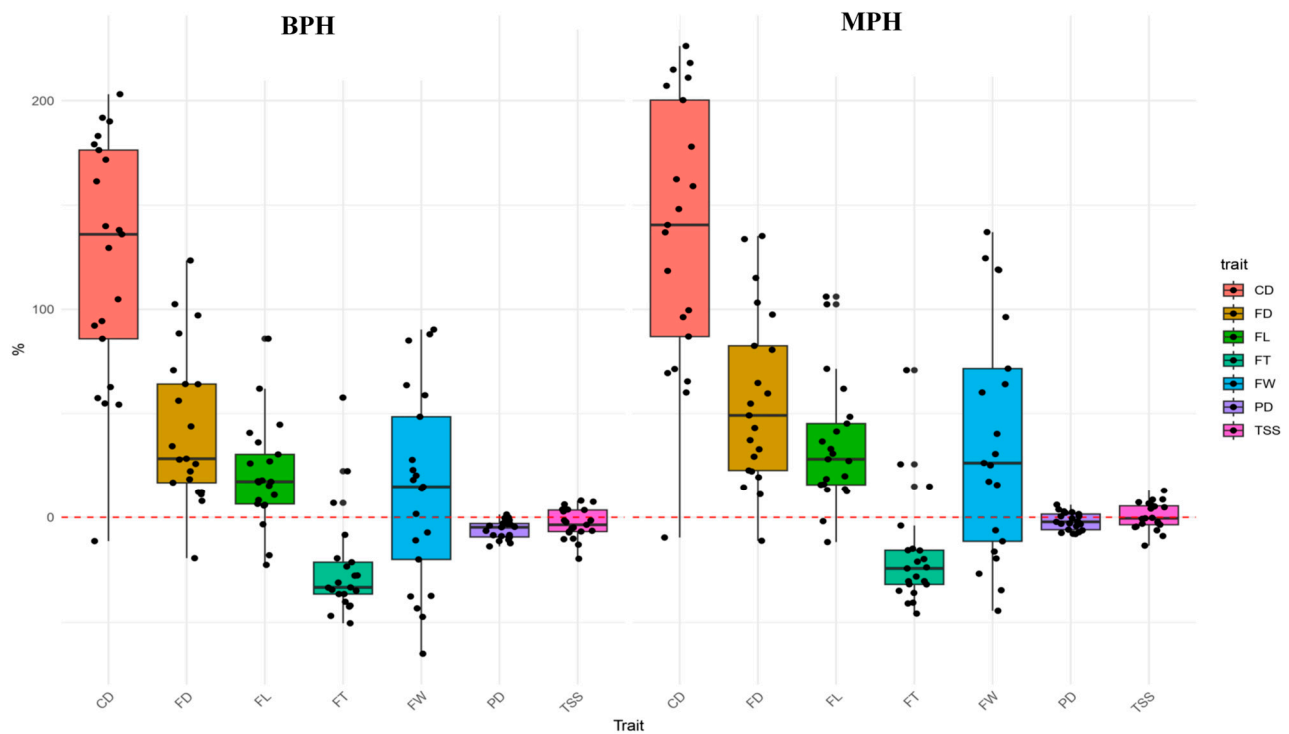
PD: precocity (days), FW: fruit weight (g), FL: fruit length (cm), FD: fruit diameter (cm), CD: cavity diameter (cm), RT: rind thickness (mm), TSS: total soluble solids (°Brix). \*\* and \* denote significant differences at 0.01 and 0.05 probability levels respectively.

### 3.4. Heterosis Performance

In general, we found low heterosis for soluble solid content (TSS), from negative to positive heterosis for fruit weight (FW), and rind thickness. Negative heterosis was observed for precocity and general positive heterosis for cavity diameter (CD), fruit diameter (FD), and fruit length (FL) (Figure 4).

Favorable heterosis over the better parent was found for fruit length, fruit diameter, cavity diameter, days to maturity, and fruit weight (Figure 4, Supplementary Table S4). The better parent heterosis (BPH) for fruit weight was positive in 13 hybrids out of 21 (Supplementary Table S4). In particular, the maximum BPH value (90.32) was recorded by the hybrid P1 × P3, thus confirming its highest SCA value.

Comparing mid-parent heterosis (MPH) and better-parent heterosis (BPH) showed very similar trends (Figure 4), with some exceptions of a higher MPH in cavity diameter and fruit diameter. The MPH values ranged from  $-45$  to  $226$ . The fruit-related traits (cavity diameter, fruit diameter) showed the highest heterosis, whereas rind thickness and TSS ranged last in heterosis, with rind thickness even displaying negative heterosis.



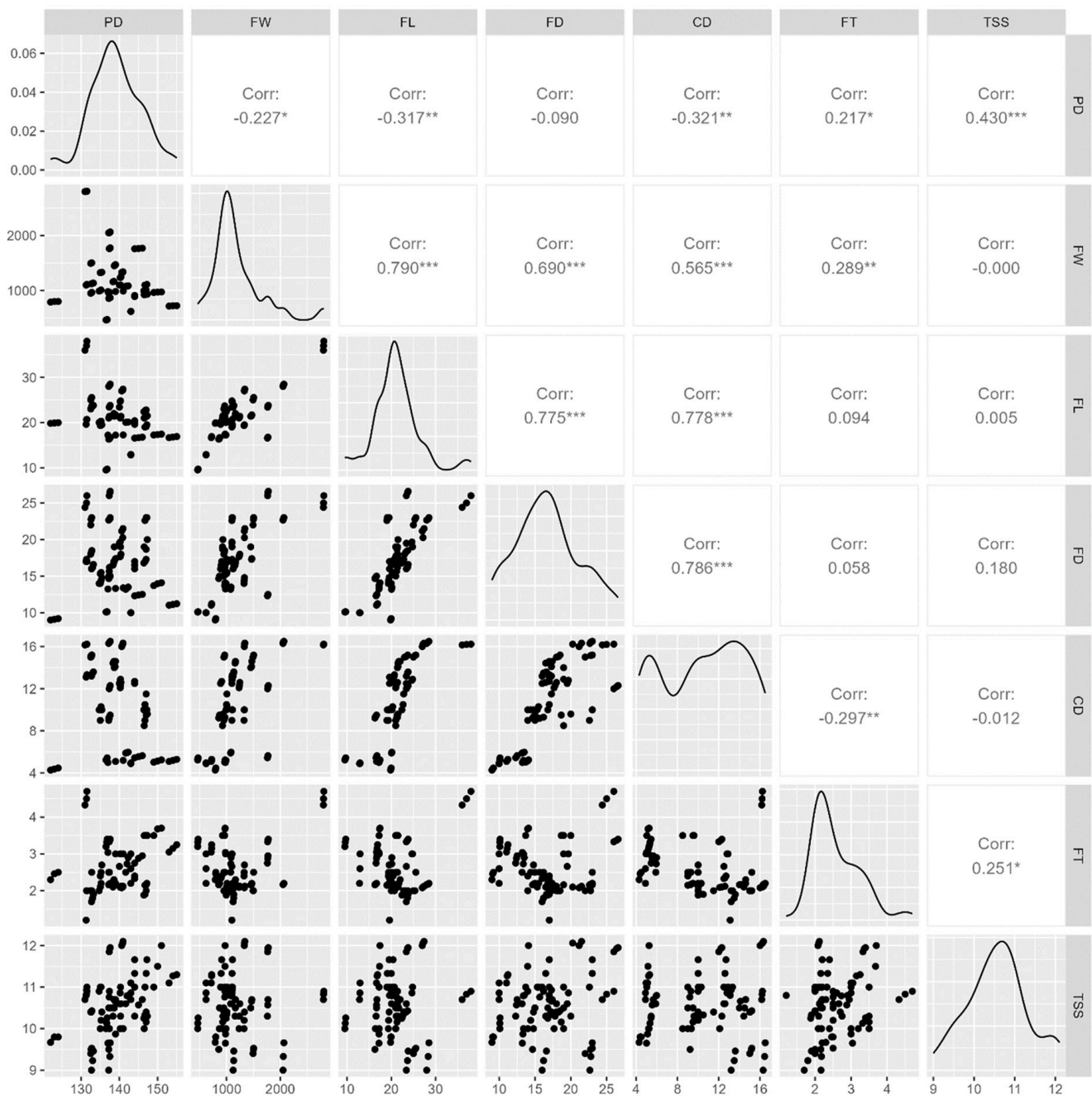
**Figure 4.** Heterosis performance of  $F_1$  hybrids. Boxplots of mid-parent (MPH) and better-parent (BPH) heterosis (%) for all the analyzed traits. The traits are ordered in descending order by heterosis value. The black points in the figure correspond to the mean of the hybrid replicates per cross. PD: precocity in days, FW: fruit weight (g), FL: fruit length (cm), FD: fruit diameter (cm), CD: cavity diameter (cm), FT: fruit rind thickness (mm), TSS: total soluble solids ( $^{\circ}$ Brix).

### 3.5. Correlation Analysis of Phenotypic Traits

When selecting superior parents for future crosses in breeding programs, taking correlations between traits into consideration is important to make use of indirect selection. In the trial conducted, precocity highly correlated most with the TSS content ( $r = 0.430$ ,  $p < 0.001$ ), meaning that genotypes ripening later show higher TSS (Figure 5).

In addition, there is a negative correlation between precocity and fruit weight ( $r = -0.227$ ,  $p < 0.05$ ), fruit length ( $-0.317$ ,  $p < 0.001$ ), and cavity diameter ( $-0.321$ ,  $p < 0.001$ ), indicating lower these measured values when the genotype is ripening earlier (Figure 5).

Fruit length, fruit weight, and fruit diameter are highly correlated to each other, indicating common genetic factors. These findings provide valuable insights into the relationship between precocity and fruit traits, highlighting the importance of balancing early ripening with desirable fruit characteristics in breeding programs. Understanding the genetic basis of fruit traits and their interaction with environmental factors is crucial for developing cultivars that meet market demands while maximizing yield and resilience.



**Figure 5.** Correlation between phenotypic traits including parents and  $F_1$  hybrids. PD: precocity in days, FW: fruit weight (g), FL: fruit length (cm), FD: fruit diameter (cm), CD: cavity diameter (cm), FT: fruit rind thickness (mm), TSS: total soluble solids ( $^{\circ}$ Brix). \*\*\* highly significant at  $p < 0.001$ ; \*\* significant at  $p < 0.01$ , \* significant at  $p < 0.05$ .

### 3.6. Correlation between Parent Performance, $F_1$ Performance and Heterosis

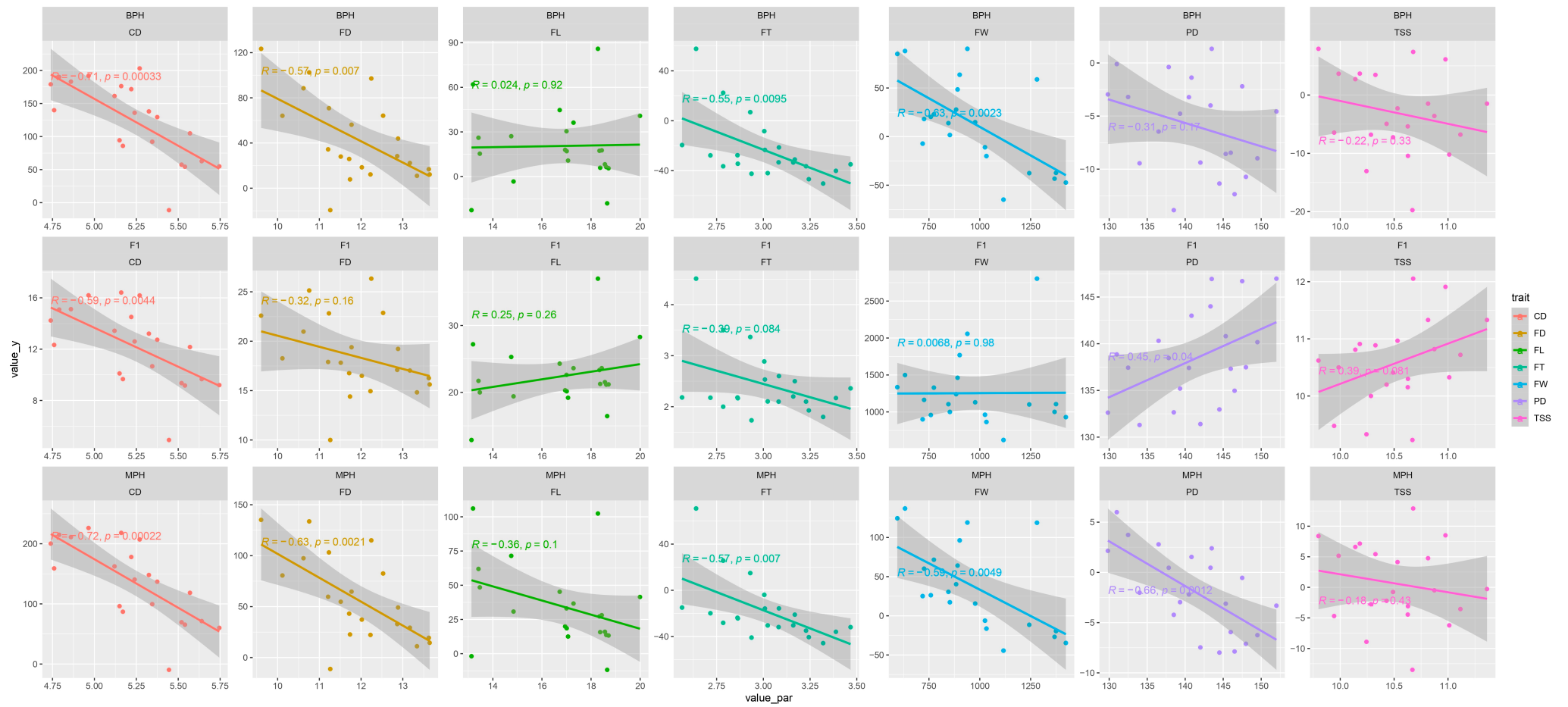
The correlation analysis between the performance of parents and the hybrid performance was studied to investigate the effect of the parents on the performance of the hybrids (Figure 6).

The result showed that the correlation between parents and  $F_1$  performance was non-significant (ranged from  $-0.59$  to  $0.45$ ) in the studied traits except for precocity, showing a significant positive correlation of  $0.45$  ( $p < 0.05$ ) and cavity diameter, which showed a significantly negative correlation of  $-0.59$  ( $p < 0.01$ ). Therefore, this result suggested that the performance of parents cannot be used to predict the hybrid performance of these traits

(Figure 6). The observed non-significant correlations between the performance of parents and F<sub>1</sub> progeny across most studied traits suggest that the transmission of these traits from the parental generation to the F<sub>1</sub> generation may not follow a straightforward pattern of direct inheritance. This indicates that the phenotypic expression of these traits in the F<sub>1</sub> generation is not strongly influenced by the performance of the parental lines. However, the significant positive correlation between parental precocity and F<sub>1</sub> performance suggests a degree of heritability for early ripening tendencies. This suggests that while certain traits may exhibit direct inheritance and be influenced by parental performance, others may be subject to dominance, epigenetic influences, or environmental effects that obscure direct inheritance patterns.

The performance of parents showed a negative correlation with MPH of all the studied traits (ranging from  $-0.72$  to  $-0.18$ ). For cavity diameter, fruit diameter, fruit weight, precocity, and fruit thickness, the correlation between parent performance and MPH values showed a significant negative association, indicating that lower-performing parents tend to produce hybrids with higher levels of heterosis for these traits. For fruit length and TSS, there was no significant correlation observed between parent performance and MPH. The lack of significant correlation between parent performance and MPH/BPH for fruit length and TSS suggests that parental performance may not be a reliable predictor of hybrid vigor for these traits.

The correlation statistics between parent performance and BPH showed that the correlations were significantly negative for all the traits (ranging from  $-0.71$  to  $0.024$ ) except for fruit length and TSS, where the negative correlation was not significant (Figure 6). This negative correlation implies that for these traits, selecting parents with lower performance may lead to the development of hybrids with improved performance, suggesting potential targets for breeding programs aimed at enhancing these traits.



**Figure 6.** Correlation matrix of parental performance, F<sub>1</sub> performance, and heterosis. PD: precocity in days, FW: fruit weight (g), FL: fruit length (cm), FD: fruit diameter (cm), CD: cavity diameter (cm), FT: fruit rind thickness (mm), and TSS: total soluble solids (°Brix).

#### 4. Discussion

Choosing proper parents and crosses is a challenge for breeders. The hybrid combining abilities of parental lines of melon can be an efficient tool to improve their production. Combining ability analysis is one of the most practical approaches to estimating its effects on the selection of desired parents and crosses [34].

Identifying promising lines for hybridization, capable of outperforming established varieties, marks a critical phase in melon breeding programs. To achieve this, the adoption of diallel cross designs proves invaluable. Such designs allow for the estimation of both the general combining ability (GCA) of parental lines and the specific combining ability (SCA) of resulting hybrids, as elaborated by Griffing [27].

Through diallel analysis, parental lines belonging to different heterotic groups can be selected to create hybrids with optimal combining ability, leading to the development of superior varieties. This approach is commonly employed in plant breeding programs to maximize genetic gain and achieve desired breeding objectives.

In Griffing's framework, GCA arises from additive and additive  $\times$  additive (*aa*) interactions, while SCA is influenced by dominance effects as well as additive  $\times$  dominant (*ad*) and dominant  $\times$  dominant (*dd*) interactions [8]. Christie and Shattuck [35] provided an extensive review of the applications of diallel crosses, further elucidating their significance in melon breeding endeavors.

We presented herein the combining ability analysis of melon fruit traits and their relevance in melon breeding programs. Indeed, additive gene effects were shown to be the most important genetic component for fruit weight, as a result, the narrow sense heritability was found rather high (0.50), indicating the possibility of achieving good selection gains for this trait. Moreover, our data indicated a central role of dominance and epistasis for most of the examined traits (PD, FD, FL, CD, RT, TSS). In fact, significant heterosis was recorded for most of the traits, especially fruit weight, and this can be explained entirely by *aa* epistatic effects included in GCA [8]. Additionally, since SCA was significant, dominant and *ad* and *dd* epistatic gene effects are likely to influence heterosis for the remaining traits.

The GCA/SCA ratio ranged from 0.020 to 0.667, very low in comparison to those reported by Napolitano et al. [8] (2.23 to 7.52) but similar to those reported by Feyzian et al. [12]. This ratio  $>0.5$  for FW suggesting the predominance of additive over non-additive genetic effects. For PD, FW, RT, and TSS, this ratio was  $<0.5$ , clearly indicating that SCA effects surpass GCA, and suggesting the importance of non-additive gene actions. Indeed, narrow sense heritability ranged from 0.011 to 0.500, lower than those reported by Napolitano et al. [8], but consistent with those reported by Feyzian et al. [12] and confirming the results of the GCA/SCA ratio. The high  $H^2$  values in our study indicate that a significant proportion of the phenotypic variance is attributable to genetic factors. However, the low  $h^2$  values suggest that the additive genetic variance is a smaller component of the total genetic variance. This implies that non-additive genetic effects, such as dominance and epistasis, play a substantial role in the expression of these traits with low  $h^2$ , except for FW.

For the FL trait, the SCA source is not significant and in such case, Baker [29] suggested that the value of the hybrids could be predicted by the GCAs of the parents. Despite the absence of dominance effects, MPH and BPH were still relevant, probably due to *aa* epistatic effects. A priori knowledge of the genetic background of the possible parents could be useful to create pools to maximize the fruit weight and sugar content of the hybrids [8].

Barros et al. [10], mentioned that total melon fruit number, yield, flesh firmness, and total soluble solids content were controlled by additive and non-additive effects, while average fruit weight, longitudinal diameter, flesh thickness, and internal cavity size were controlled by additive effects. El-Sayed et al. [6] found that the GCA effects of the melon parents were reflected in the SCA effects of the crosses for the main stem length, number of leaves, fruit quality, and yield. Melgoza et al. [36] found that GCA effects participated in most of the outstanding melon crosses in yield, average fruit weight, fruit length, fruit width, flesh thickness, seed cavity, and soluble solids.

Heterosis in melon was investigated, but the results were strictly dependent on the parents and traits considered [8,37,38]. In our study, heterosis was found for fruit traits (diameter, length, and weight) and no heterosis for rind thickness or TSS content. As reported previously, Monforte et al. [38] found no heterosis for soluble solid concentration, from negative to positive heterosis for fruit weight and diameter, and a general positive heterosis for ovary shape and fruit length.

Many agronomic traits in melon, such as fruit weight, size, and quality, are complex and polygenic [5,10]. In such cases, dominance interactions among alleles at different loci can contribute significantly to the superior phenotypic expression of these traits in the  $F_1$  hybrids. Additionally, epistatic interactions between different genes can further enhance the performance of hybrids by creating beneficial gene combinations that are not present in the parental lines [8].

Traits of interest in melon breeding are yield, biotic and abiotic stress resistance, fruit shape and size, taste, and nutritional value (sugar and antioxidants). Yield and fruit quality stand out as pivotal characteristics in melon breeding programs, particularly in optimizing early greenhouse production. Improving fruit quality presents a multifaceted challenge, encompassing external attributes such as size, shape, and netting, as well as internal factors such as color and flavor. Fruit flavor, in particular, is influenced by various elements, including aromatic profile, flesh texture, and total soluble solids content (commonly denoted as TSS or °Brix), which directly correlates with sugar concentration and serves as a reliable indicator of internal quality [14,21,39].

Genotypes that presented the highest negative general combining abilities for precocity were the most desirable. These genotypes were P3 and P5. The selection of parents based on their combining ability, and understanding of the genetic control of key traits, ensures the efficiency of a breeding program [40]. In the current study, good general combiners for fruit quality (TSS, fruit length, diameter, and cavity) were the parents P3, and P6. However, P3 had a negative GCA for TSS. The good combiners for fruit weight were P1, P3, and P4.

Specific combining ability effects are useful to identify specific crosses with desirable traits [40]. In our study, the best specific crosses for fruit weight were  $1 \times 3$  and  $3 \times 4$ . These had low TSS. The crosses  $1 \times 3$ ,  $1 \times 5$ ,  $3 \times 6$ , and  $5 \times 7$  were selected for their precocity. The best crosses for high TSS were  $1 \times 3$ ,  $1 \times 5$ ,  $2 \times 6$ , and  $4 \times 6$ . It could be concluded that parent 3 could be considered the best combiner for breeding most traits. The crosses ( $1 \times 3$ ), ( $2 \times 6$ ), and ( $4 \times 6$ ) achieved high (SCA) effects for most of the studied traits. Evaluation of heterosis (%) revealed that hybrid  $P1 \times P3$  can be considered as the best-performing hybrid for average fruit weight, TSS, and precocity which also exhibiting the highest positive and significant SCA effect for these traits.

For the selection of superior parents, we suggest that parental inbred line P3, which exhibited the maximum significant GCA in the desirable direction for all the traits except for TSS. This inbred line is a good combiner for fruit weight. P1 and P3 showed high heterosis in fruit weight, cavity diameter, rind thickness, fruit length, TSS, and diameter and are a good combination of parents if we want big fruits and relatively early ripening. Moreover, favorable heterosis over the better parent was found for the precocity of maturity, fruit weight, and fruit diameter. Thus, there is the potential to generate superior new varieties in hybrid production.

When selecting superior parents for future crosses in breeding programs, taking correlations between traits into consideration is important. Indeed, the negative correlations observed, in our study, between precocity and fruit weight, length, and cavity diameter highlight a trade-off between early ripening and fruit size in breeding programs. While early ripening may be advantageous for certain market preferences or climatic conditions, it often results in smaller fruits, potentially impacting market acceptance and yield potential. Thus, breeding programs aiming for early-ripening cultivars must carefully balance this trade-off, emphasizing the importance of maintaining desirable fruit characteristics. In this context, index selection in improving several traits simultaneously could be advantageous

as reported recently [41,42]. Understanding the genetic basis of fruit traits and their interaction with environmental factors is crucial for optimizing breeding strategies.

Moreover, the high correlation among fruit length, weight, and cavity diameter suggests a common genetic control over these traits. This underscores the significance of elucidating the genetic mechanisms underlying fruit development and ripening processes. Leveraging this knowledge, we can design targeted breeding programs to manipulate specific genetic loci associated with desirable fruit traits while considering other essential agronomic characteristics. Additionally, incorporating biochemical analyses could provide insights into the physiological mechanisms contributing to the observed phenotypic traits in melon. Molecular analyses offer powerful tools to uncover the genetic basis of complex traits and enhance selection accuracy.

Combining biochemical and molecular analyses with traditional breeding methods can create a more holistic approach to melon improvement, leading to the development of superior hybrids with greater efficiency. While our study primarily focused on evaluating  $F_1$  hybrids, further exploration of less performant  $F_1$  hybrids in the segregant generation could offer insights into trait segregation and recombination, potentially leading to the development of improved varieties.

## 5. Conclusions

The current study determined the combining ability and heterosis for quality traits in melon to select promising parental lines for breeding and selection of hybrids with farmer-preferred traits for genetic advancement and cultivar release. We explored the various components of combining ability, including the GCA and SCA, and the implications they have on fruit characteristics and yield in the melon breeding program. This will guide the efforts in developing melon cultivars with superior potential, thereby contributing to the sustainability and prosperity of melon production in Tunisia and worldwide. The parental line P3 could be utilized as a good combiner to obtain desirable segregates for improving different traits. Also, the hybrid  $P1 \times P3$  can be released for commercial cultivation after further evaluation in multiple locations for multiple years.

**Supplementary Materials:** The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/horticulturae10070724/s1>, Table S1: Mean performance of parents and their  $F_1$  for the studied traits; Table S2: ANOVA table reporting the significant effect of the genotype on phenotypic variance for each evaluated trait; Table S3: Estimation of general combining ability (GCA) effects of parental lines in the  $F_1$  generation for the evaluated traits; Table S4: Mid-parent and better-parent heterosis (%) values (MPH and BPH, respectively) for the evaluated traits.

**Author Contributions:** Conceptualization and methodology, H.C.-R. and A.H.A.M.G.; formal analysis, L.K., H.C.-R. and A.H.A.M.G.; results validation, H.C.-R., L.K. and A.H.A.M.G.; writing—original draft preparation, H.C.-R.; writing—review and editing, H.C.-R., L.K., A.H.A.M.G., O.F. and A.G.-C. All authors have read and agreed to the published version of the manuscript.

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**Data Availability Statement:** The raw data supporting the conclusions in this study will be made available on request from the corresponding author.

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## References

1. Garcia-Mas, J.; Benjak, A.; Sanseverino, W.; Bourgeois, M.; Mir, G.; González, V.M. The Genome of melon (*Cucumis melo* L.). *Proc. Natl. Acad. Sci. USA* **2012**, *109*, 11872–11877. [[CrossRef](#)] [[PubMed](#)]
2. Pitrat, M. Melon genetic resources: Phenotypic diversity and horticultural taxonomy. In *Genetics and Genomics of Cucurbitaceae*; Grumet, R., Katzir, N., Garcia-Mas, J., Eds.; Springer: New York, NY, USA, 2016; pp. 1–36. [[CrossRef](#)]
3. Manchali, S.; Kotamballi, N.; Chidambara, M.V.; Bhimanagoud, S.P. Nutritional composition and health benefits of various botanical types of melon (*Cucumis melo* L.). *Plants* **2021**, *10*, 1755. [[CrossRef](#)] [[PubMed](#)]
4. Maietti, A.; Tedeschi, P.; Stagno, C.; Bordiga, M.; Travaglia, F.; Locatelli, M.; Arlorio, M.; Brandolini, V. Analytical traceability of melon (*Cucumis melo* var *reticulatus*): Proximate composition, bioactive compounds, and antioxidant capacity in relation to cultivar, plant physiology state, and seasonal variability. *J. Food. Sci.* **2012**, *77*, C646–C652. [[CrossRef](#)] [[PubMed](#)]
5. Chikh-Rouhou, H.; Abdedayem, W.; Solmaz, I.; Sari, N.; Garcés-Claver, A. Melon (*Cucumis melo* L.): Genomics and Breeding. In *Smart Plant Breeding for Vegetable Crops in Post-Genomics Era*; Singh, S., Sharma, D., Sharma, S.K., Singh, R., Eds.; Springer: Singapore, 2023; pp. 25–52. [[CrossRef](#)]
6. El-Sayed, A.; Gharib, A.H.A.M.; El-Tahawey, M.A.F.A. Heterosis and combining ability in melon (*Cucumis melo* L.). *Menoufia J. Plant Prod.* **2019**, *4*, 429–441. [[CrossRef](#)]
7. Fasahat, P.; Rajabi, A.; Rad, J.M.; Derera, J. Principles and utilization of combining ability in plant breeding. *Biom. Biostat. Int. J.* **2016**, *4*, 00085. [[CrossRef](#)]
8. Napolitano, M.; Terzaroli, N.; Kashyap, S.; Russi, L.; Jones-Evans, E.; Albertini, E. Exploring heterosis in melon (*Cucumis melo* L.). *Plants* **2020**, *9*, 282. [[CrossRef](#)] [[PubMed](#)]
9. Feng, S.; Chen, X.; Wu, S.; Chen, X. Recent advances in understanding plant heterosis. *Agric. Sci.* **2015**, *6*, 1033–1038. [[CrossRef](#)]
10. Barros, A.K.D.A.; Nunes, G.H.D.S.; Queiróz, M.A.D.; Pereira, E.W.L.; Costa Filho, J.H. Diallel analysis of yield and quality traits of melon fruits. *Crop Breed. Appl. Biotechnol.* **2011**, *11*, 313–319. [[CrossRef](#)]
11. Neto, J.G.C.; Ferreira, K.T.C.; De Aragão, F.A.S.; Antônio, R.P.; De Sousa Nunes, G.H. Potential of parents and hybrids experimental of the yellow melon. *Cienc. Rural* **2020**, *50*, e20190452. [[CrossRef](#)]
12. Feyzian, E.; Dehghani, H.; Rezai, A.; Jalali Javaran, M. Diallel cross analysis for maturity and yield-related traits in melon (*Cucumis melo* L.). *Euphytica* **2009**, *168*, 215–223. [[CrossRef](#)]
13. Tomar, R.S.; Bhalala, M.K. Heterosis studies in muskmelon (*Cucumis melo* L.). *J. Hortic. Sci.* **2006**, *1*, 144–147. [[CrossRef](#)]
14. Kaur, S.; Sharma, S.P.; Sarao, N.K.; Deol, J.K.; Gill, R.; Abd-Elsalam, K.A.; Alghuthaymi, M.A.; Hassan, M.M.; Chawla, N. Heterosis and Combining Ability for Fruit Yield, Sweetness,  $\beta$ -Carotene, Ascorbic Acid, Firmness and Fusarium Wilt Resistance in Muskmelon (*Cucumis melo* L.) Involving Genetic Male Sterile Lines. *Horticulturae* **2022**, *8*, 82. [[CrossRef](#)]
15. Gvozdanovic-Varga, J.; Vasic, M.; Milic, D.; Cervenski, J. Diallel cross analysis for fruit traits in watermelon. *Genetika* **2011**, *43*, 163–174. [[CrossRef](#)]
16. Hallauer, A.R. History, contribution, and future of quantitative genetics in plant breeding: Lessons from maize. *Crop Sci.* **2007**, *47*, 4–19. [[CrossRef](#)]
17. Luan, F.; Sheng, Y.; Wang, Y.; Staub, J.E. Performance of melon hybrids derived from parents of diverse geographic Origins. *Euphytica* **2010**, *173*, 1–16. [[CrossRef](#)]
18. Hassan, W.H.A.; Gad, A.A.; El-Salam, M.M.A.; Ismail, H.E.M. Gene action and heterosis of muskmelon. *Zagazig J. Agric. Res.* **2018**, *45*, 1953–1961. [[CrossRef](#)]
19. Chikh-Rouhou, H.; Gómez-Guillamón, M.L.; Garcés-Claver, A. Melon germplasm from Tunisia with immense breeding value. *Cucurbit Genet. Coop. Rep.* **2021**, *44*, 7–12.
20. Chikh-Rouhou, H.; Mezghani, N.; Mnasri, S.; Mezghani, N.; Garcés-Claver, A. Assessing the genetic diversity and population structure of a Tunisian melon (*Cucumis melo* L.) collection using phenotypic traits and SSR molecular markers. *Agronomy* **2021**, *11*, 1121. [[CrossRef](#)]
21. Chikh-Rouhou, H.; Tlili, I.; Ilahy, R.; R'him, T.; Sta-Baba, R. Fruit quality assessment and characterization of melon genotypes. *Int. J. Veg. Sci.* **2021**, *27*, 3–19. [[CrossRef](#)]
22. Chikh-Rouhou, H.; Garcés-Claver, A.; Kienbaum, L.; Ben Belgacem, A.M.; Gómez-Guillamón, M.L. Resistance of Tunisian melon landraces to *Podosphaera xanthii*. *Horticulturae* **2022**, *8*, 1172. [[CrossRef](#)]
23. Chikh-Rouhou, H.; Gómez-Guillamón, M.L.; González, V.; Sta-Baba, R.; Garcés-Claver, A. *Cucumis melo* L. germplasm in Tunisia: Unexploited sources of resistance to Fusarium Wilt. *Horticulturae* **2021**, *7*, 208. [[CrossRef](#)]
24. Chikh-Rouhou, H.; Ben Belgacem, A.M.; Sta-Baba, R.; Tarchoun, N.; Gómez-Guillamón, M.L. New Source of resistance to *Aphis gossypii* in Tunisian melon genotypes using phenotypic and molecular marker approaches. *Phytoparasitica* **2019**, *47*, 405–413. [[CrossRef](#)]
25. Chikh-Rouhou, H.; Garcés-Claver, A.; Sta-Baba, R.; González, V.; Daami-Remadi, M. Screening for Resistance to Race 1 of *Fusarium oxysporum* f.sp *melonis* in Tunisian melon cultivars using molecular markers. *Commun. Agric. Appl. Biol. Sci.* **2018**, *83*, 87–92.
26. Kacem, K.; Chikh-Rouhou, H. Preliminary selection and phenotypic characterization of melon landraces exhibiting resistance to powdery mildew. *Int. J. Phytopathol.* **2022**, *11*, 115–123. [[CrossRef](#)]
27. Griffing, B. Concept of general and specific combining ability in relation to diallel crossing systems. *Aust. J. Biol. Sci.* **1956**, *9*, 463–493. [[CrossRef](#)]

28. Covarrubias-Pazarán, G. Genome assisted prediction of quantitative traits using the R package sommer. *PLoS ONE* **2016**, *11*, e0156744. [[CrossRef](#)] [[PubMed](#)]
29. Baker, R.J. Issues in diallel analysis. *Crop Sci.* **1978**, *18*, 533–536. [[CrossRef](#)]
30. Zhu, J. Methods of predicting genotype value and heterosis or offspring of hybrids. *J. Biomath.* **1993**, *8*, 32–44.
31. Russell, L.; Singmann, H.; Love, J.; Buerkner, P.; Herve, M. Emmeans: Estimated Marginal Means, aka Least-Squares Means. 2018. Available online: <https://rdrr.io/cran/emmeans/man/emmeans.html> (accessed on 15 January 2024).
32. Schloerke, B.; Cook, D.; Larmarange, J.; Briatte, F.; Marbach, M.; Thoen, E.; Elberg, A.; Crowley, J. GGally: Extension to 'ggplot2'. R Package Version 2.2.1. 2024. Available online: <https://github.com/ggobi/ggally> (accessed on 15 January 2024).
33. Wickham, H. *ggplot2 (Elegant Graphics for Data Analysis)*; Springer: Cham, Switzerland, 2016; pp. 1–260. [[CrossRef](#)]
34. Akanksha, A.; Jaiswal, H.K. Combining ability studies for yield and quality parameters in basmati rice (*Oryza sativa* L.) genotypes using diallel approach. *Electron. J. Plant Breed.* **2019**, *10*, 9–17. [[CrossRef](#)]
35. Christie, B.R.; Shattuck, V.I. The diallel cross: Design, analysis, and use for plant breeders. In *Plant Breeding Reviews*; Wiley: New York, NY, USA, 2010; pp. 9–36.
36. Melgoza, F.A.G.; Escalante, F.B.; Río, A.J.L.; Benítez, A.L.; Mendoza, A.B.; Torres, A.N.R.; Martínez, R.H.; Aranda, C.A.B. Diallel analysis for yield and quality characteristics in melon. *J. Exp. Agric. Int.* **2022**, *44*, 29–36. [[CrossRef](#)]
37. Nerson, H. Heterosis in fruit and seed characters of muskmelon. *Asian Aust. J. Plant Sci. Biotechnol.* **2012**, *6*, 24–27.
38. Monforte, A.J.; Iban, E.; Silvia, A.; Pere, A. Inheritance mode of fruit traits in melon: Heterosis for fruit shape and its correlation with genetic distance. *Euphytica* **2005**, *144*, 31–38.
39. Paris, M.; Staub, J.E.; McCreight, J.D. Determination of fruit sampling location for quality measurements in melon (*Cucumis melo* L.). *Cucurbit Genet. Coop. Rep.* **2003**, *26*, 12–17.
40. Rukundo, P.; Shimelis, H.; Laing, M.; Gahakwa, D. Combining Ability, Maternal Effects, and Heritability of Drought Tolerance, Yield and Yield Components in Sweet potato. *Front. Plant Sci.* **2017**, *7*, 1981. [[CrossRef](#)] [[PubMed](#)]
41. Adewumi, A.S.; Asare, P.A.; Adejumobi, I.I.; Adu, M.O.; Taah, K.J.; Adewale, S.; Mondo, J.M.; Agre, P.A. Multi-Trait Selection Index for Superior Agronomic and Tuber Quality Traits in Bush Yam (*Dioscorea praehensilis* Benth.). *Agronomy* **2023**, *13*, 682. [[CrossRef](#)]
42. Gomes, D.A.; Alves, I.M.; Maciel, G.M.; Siquieroli, A.C.S.; Peixoto, J.V.M.; Pires, P.S.; Medeiros, I.A. Genetic dissimilarity, selection index and correlation estimation in a melon germplasm. *Hortic. Bras.* **2021**, *39*, 46–51. [[CrossRef](#)]

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