Estimation of Heterosis for Yield and Yield contributing Traits among intraspecific Hybrids of *Cucumis melo*

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ABSTRACT: Melo is a species of the extremely complex genus *Cucumis* in the cucurbitaceae family, with a chromosome number of 2n=24. With respect to fruit characteristics like fruit shape, size, color, texture, taste and nutritional composition, the species *melo* exhibits considerable morphological variation. Local cultivars of *melo* are low in moisture content, nutrients and keeping quality, hence the taxonomic groups of *Cucumis melo* are crossed to improve the local cultivars. In the current study, 30 hybrids were developed by crossing 5 lines with 6 testers in a line-tester fashion. Hybrids were then assessed along with parents in a randomized complete block design (RCBD) with two replications. UHSCS-9 × Mudicode Local and UHSCS-12 × Arka Siri hybrids performed better for the yield and its related traits with maximum heterosis over the better parent. These crosses can be exploited in crop improvement by generating transgressive segregants.

Keywords: Hybrids, Relative heterosis, Heterobeltiosis, Yield, melo.

INTRODUCTION

Melon, which belongs to the family Cucurbitaceae and has the chromosomal number 2n=24, is one of the most genetically diverse species and a significant vegetable crop in the genus *Cucumis*. Although the origin of the melon is thought to be in Africa, central Asia, Iran, India, Turkmenistan, Tajikistan, Transcaucasia, and Uzbekistan are seen to be the key centers of variation, along with China and Afghanistan (Zhu *et al.,* 2016). It is grown around the world in moderate and warm climates (Biswas, 2006). Melons include a spectrum of phytochemicals that might have a number of health benefits (Manchali *et al.,* 2021). Melons are a rich source of beta carotene and vitamin C, low in fat, sodium, and cholesterol, and contain a number of essential nutrients, including potassium.

The species *C. melo* is highly polymorphic taxon has intense diversification, significant physiological, morphological and molecular variation encircling a great number of horticultural varieties or groups (Lija and Beevy 2021; Manasherova and Cohen 2022). *C. melo* is regarded as the species in the genus *Cucumis*

with the greatest degree of polymorphism (Whitaker and Davis 1962; Bates and Robinson 1995). According to Kirkbride (1993); Thakur *et al.* (2019) there are two subspecies of muskmelon that can be distinguished based on the amount of pubescence on the ovary: *C. melo* subsp. *melo* (*cantaloupe, reticulates, adana, chandalak, ameri, inodorus, flexuosus, chate, tibish, dudaim*), and *C. melo* subsp. *agrestis* (*conomon, makuwa, chinensis, acidulus* and *momordica* groups). Melons are a reliable source of beneficial horticultural features and disease and insect resistance. *C. melo* var. *momordica* has a high level of resistance to yellow mosaic virus, downy mildew, and fusarium wilt. var. *chate* is a good source of earliness, whereas var. *acidulus* and *indorus* have a good shelf life for several months. Regarding fruit color, var. *makuwa* is a reliable source (Pitrat, 2000). Despite possessing a number of favorable features, these botanical groups of melons have not been exploited in crop improvement programs. Cross ability among these botanical groups provides an opportunity to exploit hybrid vigour on commercial scale. Hence, the current experiment was conducted to

determine extent of heterosis in 30 intraspecific hybrids.

MATERIAL AND METHODS

Six testers (Arka Siri, AHS-10, Long melon, BCMCR-1, Mudicode local, UHSCS-77) and five lines (UHSCS-9, UHSCS-12, UHSCS-39, UHSCS-44 and UHSCS-56) were crossed in line × tester mating design. The developed 30 hybrids and 11 parents were evaluated in RCBD with two replications during *kharif* season at the experimental plot of College of Horticulture, Bagalkot. Observations were recorded on five randomly selected plants for the traits like vine length (m), internodal length (cm), number of primary branches per plant, fruit length (cm), fruit diameter (cm), average fruit weight (g), number of fruits per plant and total yield per plant (kg). Statistical analysis was performed using the INDOSTAT statistical package. Heterosis is the percentage of increase or decrease in the performance of F1 hybrid with respect to yield and yield attributes over mid-parent (relative heterosis) and superior parent (heterobeltiosis). Heterosis was computed for yield and yield related characters using the formula as follows,

$$\text{Mid-parent heterosis (MPH) per cent} = \frac{\text{F1} - \text{MP}}{\text{MP}} \times 100$$

Where,
F1 = Mean value of F1 hybrid
MP = Average of two parents involved in the cross

$$\text{Better parent heterosis (BPH) per cent} = \frac{\text{F1} - \text{BP}}{\text{BP}} \times 100$$

Where,
F1 = Mean value of F1 hybrid
BP = Mean value of superior parent of the particular cross

RESULT AND DISCUSSION

A. Vine length
The mid parental heterosis was varied from -30.80% (UHSCS-56 × UHSCS-77) to 18.93% (UHSCS-44× Arka Siri) and better parental heterosis was varied from -43.25% (UHSCS-56× Arka Siri) to 0.63% (UHSCS-44 × AHS-10). Only one hybrid UHSCS-44 × Arka Siri showed significantly positive (18.93%) heterosis over mid parent and none of the hybrid shown significantly positive heterosis over better parent (Table 1). These results are consistent with those obtained by Glala *et al.* (2010); Duradundi *et al.* (2018); Shoura *et al.* (2023) in muskmelon.

B. Internodal length
Negative heterosis is preferred for this attribute. The magnitude of mid parent heterosis ranged from -4.18 % (UHSCS-39 × Mudicode Local) to 30.43 % (UHSCS-44 × Arka Siri) and none of the crosses found superior over mid parent in desirable direction. Better parent heterosis was varied between -15.28% (UHSCS-9 × Arka Siri) and 27.88 % (UHSCS-39 × BCMCR-1) and two hybrids (UHSCS-9 × Arka Siri and UHSCS-39× Mudicode Local) out of thirty hybrids showed significant negative heterosis over better parent (Table 1).

C. Number of primary branches per plant
The heterotic range with respect to number of primary branches produced in a plant over mid parent and better parent ranged from -8.30% (UHSCS-9 × UHSCS-77) to 40.65% (UHSCS-9 × Mudicode Local) and -28.25% (UHSCS-44 × Arka Siri) to 17.05% (UHSCS-12 × AHS-10) respectively. Fourteen and one hybrid showed significant positive heterosis over mid parent and better parental values, respectively (Table 1). These results are in accordance to Saha *et al.* (2022); Shoura *et al.* (2023) in muskmelon.

D. Fruit length
Significant and positive heterosis is preferred for fruit length. Sixteen hybrid combinations among thirty hybrids expressed significant and positive heterosis over mid parent. The magnitude of mid parental heterosis was found highest in the cross combination UHSCS-39 × Arka Siri (49.25%) and lowest in the cross UHSCS-39 × Long melon (-21.07%). The better parent heterosis with respect to this trait varied significantly from -42.43% (UHSCS-39 × Long melon) to 38.07% (UHSCS-39 × UHSCS-77). Five hybrids among thirty combinations showed significant and positive heterosis over better parent. Highest better parental heterosis (more than 30%) was observed in UHSCS-39 × UHSCS-77 (38.07%), UHSCS-39 × AHS-10 (37.84%) and UHSCS-39 × Arka Siri (37.51%) (Table 2). Result was in line with findings of Kamer *et al.* (2015); Selim (2019); Badami *et al.* (2020); Saha *et al.* (2022) in musk melon.

E. Fruit diameter
With respect to fruit diameter the magnitude of mid parental heterosis varied significantly between -13.85% (UHSCS-9 × Long melon) and 55.08% (UHSCS-12 × Arka Siri) and twenty-two cross combinations exhibited significant heterosis in positive direction. The degree of heterosis over the better parent was varied from -27.92% (UHSCS-39 × Long melon) to 11.96% (UHSCS-39 × Arka Siri) and none of the hybrid combinations showed significant and positive heterosis over better parent (Table 2). The results are similar with the findings of Singh and Vashisht (2018); El-Sayed *et al.* (2019); Tak *et al.* (2017); Kaur *et al.* (2022) in musk melon.

F. Average fruit weight
Highest mid parental heterosis was exhibited by the cross UHSCS-12 × Arka Siri (255.90%) followed by UHSCS-9 × Arka Siri (230.17%) and lowest in the hybrid combination UHSCS-56 × Long melon (-7.78%). Out of thirty hybrids twenty-five hybrids exhibited significant and positive heterosis over mid parent with respect to average fruit weight. Better parental values for this trait varied greatly among the hybrids and it varied from -36.71% (UHSCS-56 × BCMCR-1) to 134.59% (UHSCS-12 × Arka Siri). Sixteen hybrids showed significant heterosis over better parent in positive direction (Table 2). The results are in agreement with the findings of Singh and Vashisht (2018); Shoura *et al.* (2023) in muskmelon; Selim

(2019) in Egyptian melon and Pornsuriya *et al.* (2013) in thai and cantaloupe melons.

G. Number of fruits per plant

Three cross combinations found significantly superior to mid parent and the highest mid parental value was noticed in the cross combination UHSCS-9 × Long melon (42.12%), whereas lowest in UHSCS-39 × Arka Siri (44.42%). Over better parent this trait ranged between -62.03% (UHSCS-39 × Arka Siri) and 30.00% (UHSCS-9 × Long melon) and only one cross combination across thirty hybrids found significantly superior over better parent (Table 3). Suzy *et al.* (2020), Magawry and Shaban (2021); Shoura *et al.* (2023) in muskmelon.

H. Total yield per plant

Maximum mid parental values for total yield per plant was found in the hybrid combination UHSCS-9 × Mudicode Local (295.10%) and minimum in UHSCS-

56 × BCMCR-1 (-20.44%). Twenty-three hybrids expressed significant and positive heterosis over mid parent and fifteen hybrids displayed superiority over better parent in desirable direction. Better parental values with respect to this trait varied considerably between -42.48% (UHSCS-56 × BCMCR-1) and 208.27% (UHSCS-12 × Arka Siri). UHSCS-12 × Arka Siri (208.27%) followed by UHSCS-9 × Mudicode Local (178.76%) and UHSCS-56 × AHS-10 (175.28%) found superior over better parent (Table 3). The obtained results are in the same direction with those exhibited by El-Sayed *et al.* (2019), in muskmelon; Selim (2019) in Egyptian melon; Pornsuriya *et al.* (2013) in thai and cantaloupe melons; Napolitano *et al.* (2020) in melon intraspecific hybrids, Glala *et al.* (2010) in the intraspecific hybrids of sweet melon and muskmelon, Khairiya *et al.* (2023) in sponge urd and Chandramouli *et al.* (2023) in bottle gourd.

Table 1: Estimates of heterosis (%) over mid parent and better parent for growth parameters.

Sr. No.	Crosses	Vine length		Internodal length		Number of primary branches	
		MP	**BP**	**MP**	**BP**	**MP**	**BP**
1.	UHSCS-9 × Arka Siri	-13.17	-35.07 **	-2.39	-15.28 **	-1.57	-24.38 **
2.	UHSCS-9 × AHS-10	-5.56	-13.88 *	20.12 **	8.99	-4.31	-19.47 **
3.	UHSCS-9 × Long melon	-11.69	-13.73	0.87	-2.25	7.67	-17.28 **
4.	UHSCS-9 × BCMCR-1	-30.12 **	-31.67 **	11.26 *	4.38	3.00	-14.57 *
5.	UHSCS-9 × Mudicode Local	-15.22 *	-21.04 **	26.54 **	25.83 **	40.65 **	9.81
6.	UHSCS-9 × UHSCS-77	-12.10	-20.30 **	28.07 **	27.71 **	-8.30	-19.47 **
7.	UHSCS-12 × Arka Siri	-11.45	-33.28 **	14.85 **	0.17	26.32 **	2.83
8.	UHSCS-12 × AHS-10	5.72	-2.60	10.59 *	0.85	30.10 **	17.05 *
9.	UHSCS-12 × Long melon	-28.28 **	-29.16 **	5.95	3.24	26.32 **	2.83
10.	UHSCS-12 × BCMCR-1	-20.80 **	-23.40 **	18.67 **	11.93 *	28.50 **	13.80
11.	UHSCS-12 × Mudicode Local	1.70	-4.27	13.65 **	12.39 *	34.44 **	11.40
12.	UHSCS-12 × UHSCS-77	-5.33	-13.28	-1.41	-2.23	9.09	2.83
13.	UHSCS-39 × Arka Siri	3.68	-19.09 *	13.29 *	4.52	34.51 **	8.33
14.	UHSCS-39 × AHS-10	3.15	-0.34	21.87 **	17.94 **	12.52	0.00
15.	UHSCS-39 × Long melon	-0.24	-3.91	25.03 **	20.54 **	17.23 *	-5.58
16.	UHSCS-39 × BCMCR-1	-10.13	-17.12 *	28.30 **	27.88 **	14.29 *	0.00
17.	UHSCS-39 × Mudicode Local	-23.59 **	-24.49 **	-4.18	-10.83 *	28.83 **	5.58
18.	UHSCS-39 × UHSCS-77	-11.70	-15.20	11.68 *	4.19	13.39 *	5.50
19.	UHSCS-44 × Arka Siri	18.93 *	-9.69	30.43 **	24.14 **	-2.91	-28.25 **
20.	UHSCS-44 × AHS-10	8.05	0.63	26.00 **	26.00 **	-5.43	-23.94 **
21.	UHSCS-44 × Long melon	-6.18	-6.25	27.63 **	19.22 **	0.09	-26.03 **
22.	UHSCS-44 × BCMCR-1	-28.56 **	-31.67 **	14.75 **	10.71	4.07	-17.42 **
23.	UHSCS-44 × Mudicode Local	-20.03 **	-23.91 **	17.72 **	6.28	13.04 *	-15.20 **
24.	UHSCS-44 × UHSCS-77	-8.86	-15.62 *	9.88	-0.56	3.90	-13.05 *
25.	UHSCS-56 × Arka Siri	-20.69 **	-43.25 **	27.85 **	14.07 *	6.24	-19.07 **
26.	UHSCS-56 × AHS-10	-2.12	-15.97 *	29.49 **	20.96 **	-0.04	-16.71 **
27.	UHSCS-56 × Long melon	-14.83 *	-22.08 **	9.58	9.58	6.24	-19.07 **
28.	UHSCS-56 × BCMCR-1	-28.76 **	-31.95 **	15.17 **	11.38 *	15.91 *	-4.79
29.	UHSCS-56 × Mudicode Local	-27.60 **	-36.62 **	-1.79	-5.33	23.30 **	-4.57
30.	UHSCS-56 × UHSCS-77	-30.80 **	-40.91 **	-6.30	-9.44	4.15	-9.50
	S.E. Difference	0.195	0.226	0.392	0.453	0.343	0.396
	CD (0.05)	0.400	0.461	0.801	0.925	0.701	0.810
	CD (0.01)	0.538	0.622	1.080	1.247	0.945	1.091

Table 2: Estimates of heterosis (%) over mid parent and better parent for fruit yield parameters.

Sr. No.	Crosses	Fruit length		Fruit diameter		Average fruit weight	
		MP	BP	MP	BP	MP	BP
1.	UHSCS-9 × Arka Siri	13.35	-5.75	28.12 **	-9.20	230.17 **	128.17 **
2.	UHSCS-9 × AHS-10	19.14 *	13.98	30.88 **	-5.85	96.68 **	23.84 **
3.	UHSCS-9 × Long melon	-0.80	-21.49 **	-13.85	-24.44	10.51	10.42
4.	UHSCS-9 × BCMCR-1	30.48 **	22.25 **	45.26 **	6.56	97.04 **	18.75 **
5.	UHSCS-9 × Mudicode Local	35.68 **	30.11 **	38.94 **	-0.66	153.69 **	52.88 **
6.	UHSCS-9 × UHSCS-77	21.68 *	5.12	19.30	-15.86	133.64 **	53.59 **
7.	UHSCS-12 × Arka Siri	19.82 *	-4.73	55.08 **	9.67	255.90 **	134.59 **
8.	UHSCS-12 × AHS-10	21.87 **	10.49	48.93 **	6.90	144.27 **	48.51 **
9.	UHSCS-12 × Long melon	11.47 *	-7.77	-12.06	-22.63	57.58 *	44.31
10.	UHSCS-12 × BCMCR-1	4.05	-7.49	34.20 **	-1.77	29.34 **	-24.27 **
11.	UHSCS-12×Mudicode Local	-2.99	-11.85	24.33 *	-11.29	101.77 **	18.13 **
12.	UHSCS-12 × UHSCS-77	33.58 **	10.07	27.98 **	-9.92	187.27 **	81.29 **
13.	UHSCS-39 × Arka Siri	49.25 **	37.51 **	52.07 **	11.96	183.90 **	89.33 **
14.	UHSCS-39 × AHS-10	48.10 **	37.84 **	27.38 **	-4.68	117.08 **	33.12 **
15.	UHSCS-39 × Long melon	-21.07 **	-42.43 **	-13.48	-27.92	43.26	34.09
16.	UHSCS-39 × BCMCR-1	22.84 **	16.71	25.67 *	-3.94	44.77 **	-14.63*
17.	UHSCS-39 ×Mudicode Local	16.94 *	8.59	41.84 **	5.43	58.39 **	-13.20
18.	UHSCS-39 × UHSCS-77	43.43 **	38.07 **	5.43	-22.78 **	78.46 **	13.76
19.	UHSCS-44 × Arka Siri	11.32	-2.27	38.47 **	-0.41	137.19 **	65.91 **
20.	UHSCS-44 × AHS-10	11.42	9.21	41.29 **	3.20	119.09 **	39.20 **
21.	UHSCS-44 × Long melon	3.65	-21.68 **	-4.90	-18.32	24.69	22.17
22.	UHSCS-44 × BCMCR-1	16.71 *	16.49	37.68 **	2.62	35.69 **	-17.61 **
23.	UHSCS-44 × Mudicode Local	-8.37	-20.80	16.14	-15.70	101.57 **	22.39 **
24.	UHSCS-44 × UHSCS-77	7.22	-8.16	21.84 *	-12.80	36.91 **	-9.05
25.	UHSCS-56 × Arka Siri	30.83 **	5.16	23.81 *	-7.80	132.33 **	64.88 **
26.	UHSCS-56 × AHS-10	24.90 **	14.72	25.87 **	-4.68	145.78 **	57.86 **
27.	UHSCS-56 × Long melon	2.21	-16.39 **	-6.27	-22.99	-7.78	-11.80
28.	UHSCS-56 × BCMCR-1	2.63	-7.58	33.36 **	3.22	3.30	-36.71 **
29.	UHSCS-56 × Mudicode Local	6.91	-1.57	25.81 *	-5.37	44.79 **	-11.29
30.	UHSCS-56 × UHSCS-77	-0.57	-17.12 *	23.01 *	-8.88	34.24 **	-9.69
	S.E. Difference	1.498	1.729	0.585	0.675	36.264	41.874
	CD (0.05)	3.063	3.537	1.196	1.381	74.168	85.642
	CD (0.01)	4.128	4.767	1.612	1.861	99.957	115.420

Table 3: Estimates of heterosis (%) over mid parent and better parent for fruit yield parameters.

Sr. No.	Crosses	Number of fruits per plant		Total yield per plant	
		MP	BP	MP	MP
1.	UHSCS-9 × Arka Siri	-33.31 *	-51.78 **	159.13 **	145.49 **
2.	UHSCS-9 × AHS-10	16.18	-7.59	184.54 **	105.20 **
3.	UHSCS-9 × Long melon	42.12 **	30.00 **	76.49 *	73.28
4.	UHSCS-9 × BCMCR-1	-13.64	-27.67 *	111.45 **	38.92 **
5.	UHSCS-9 × Mudicode Local	5.00	-19.65	295.10 **	178.76 **
6.	UHSCS-9 × UHSCS-77	-15.71	-29.66 *	121.32 **	61.11 **
7.	UHSCS-12 × Arka Siri	-22.89	-44.46 **	245.26 **	208.27 **
8.	UHSCS-12 × AHS-10	30.30 *	3.15	288.49 **	169.70 **
9.	UHSCS-12 × Long melon	15.92	6.65	100.44 *	85.02
10.	UHSCS-12 × BCMCR-1	-11.93	-26.61 *	49.53 *	-4.62
11.	UHSCS-12 × Mudicode Local	-14.06	-34.52 **	128.93 **	55.79 **
12.	UHSCS-12 × UHSCS-77	-4.44	-20.65	208.89 **	116.28 **
13.	UHSCS-39 × Arka Siri	-44.42 **	-62.03**	120.45 **	102.63 *
14.	UHSCS-39 × AHS-10	-6.67	-30.69**	182.26 **	99.63 **
15.	UHSCS-39 × Long melon	-0.50	-0.99	74.89	66.40
16.	UHSCS-39 × BCMCR-1	-10.83	-30.69 **	79.61 **	16.23
17.	UHSCS-39 × Mudicode Local	-33.38 **	-52.18 **	57.86 *	9.33
18.	UHSCS-39 × UHSCS-77	-27.60 *	-43.91 **	70.74 **	21.84
19.	UHSCS-44 × Arka Siri	-38.46 **	-56.99 **	89.32 **	79.73 *
20.	UHSCS-44 × AHS-10	-3.80	-26.56 *	160.19 **	101.67 **
21.	UHSCS-44 × Long melon	19.17 *	15.00	54.33	41.55
22.	UHSCS-44 × BCMCR-1	-32.89 **	-46.24 **	13.85	-20.84
23.	UHSCS-44 × Mudicode Local	-12.41	-35.48 **	146.86 **	86.53 **
24.	UHSCS-44 × UHSCS-77	-23.70	-39.09 **	14.91	-9.96
25.	UHSCS-56 × Arka Siri	-39.04 **	-58.22 **	77.15 *	58.28
26.	UHSCS-56 × AHS-10	5.24	-21.54 *	238.13 **	175.28 **
27.	UHSCS-56 × Long melon	-4.90	-5.00	-7.69	-20.12
28.	UHSCS-56 × BCMCR-1	-37.93 **	-51.55 **	-20.44	-42.48 **
29.	UHSCS-56 × Mudicode Local	-18.85	-41.53 **	58.34 **	25.39
30.	UHSCS-56 × UHSCS-77	-27.04 *	-43.24 **	10.47	-9.00
	S.E. Difference	0.866	1.000	0.447	0.516
	CD (0.05)	1.771	2.045	0.914	1.055
	CD (0.01)	2.387	2.756	1.231	1.422

CONCLUSIONS

The hybrids UHSCS-39 × UHSCS-77 (fruit length), UHSCS-12 × Arka Siri (average fruit weight), UHSCS-9 × Long melon (number of fruits per plant) and UHSCS-9 × Mudicode Local (total yield per plant) were best performing for the yield and its related traits with maximum heterosis and can be exploited for crop improvement. Nutrient content, moisture and keeping quality of the hybrids have been improved significantly when compared to parents (Local cultivars).

FUTURE SCOPE

UHSCS-9 × Mudicode Local and UHSCS-12 × Arka Siri can be further assessed for their stability to confirm their potentiality and their adaptability to different agro-climatic conditions. Desirable hybrid combinations are advanced through inbreeding or through backcrossing to develop inbred lines having desirable traits.

REFERENCES

Badami, K., Daryono, B. S., Amzeri, A. and Khoiri, S. (2020). Combining ability and heterotic studies on hybrid melon (*Cucumis melo* L.) populations for fruit yield and quality traits. *Sabrao Journal of Breeding and Genetics, 52*(4), 402-417.

Bates, D. M. and Robinson, R. W. (1995). Cucumbers, melons and water-melons. In: Smartt J, Simmonds N. W., Editors. *Evolution of Crop Plants. 2nd edn.* Harlow, UK: Longman; 89-96.

Biswas, P. K. (2006). Encyclopaedia of Medicinal Plants. Vol. III, New Delhi, Dominant Publishers and Distributors, 584-585.

Chandramouli, B., Reddy, R. V. S. K., Balakrishna, B., Rao, M. P. and Umakrishna, K. (2023). Studies on heterosis and inbreeding depression for yield and yield related traits in bottle gourd (*Lagenaria siceraria* (Mol.) Standl.). *Biological Forum-An International Journal, 15*(6), 395-398.

Duradundi, S. K., Gasti, V. D., Mulge, R., Kerutagi, M. G. and Masuthi, D. A. (2018). Heterosis studies in muskmelon (*Cucumis melo* L.) for growth, earliness and yield traits. *International journal of chemical studies, 6*(4), 3079-3086.

El-Sayed, A. A., Amani, H., Gharib and ElTahawey, M. A. F. A. (2019). Heterosis and combining ability in melon (*Cucumis melo* L.). *Menoufia Journal of Plant Production, 4*(10), 429–441.

Glala, A. A., Saleh, S. A., Sawaan, O. M. and Omar, N. M. (2010). Developing new promising galia melon F1 hybrids by utilizing some Egyptian melon genetic resources. In *IV International Symposium on Cucurbits, 871,* 157-164.

Kamer, A., Mona, M. E., Yousry, M. and Gamal, A. M. E. (2015). Heterosis and heritability studies for fruit characters and yield in melon (*Cucumis melo* L.). *Middle East Journal of Applied Sciences, 5*(1), 262-273.

Kaur, S., Sharma, S. P., Sarao, N. K., Deol, J. K., Gill, R., Abd-Elsalam, K. A., Alghuthaymi, M. A., Hassan, M. M. and Chawla, N. (2022). Heterosis and combining ability for fruit yield, sweetness, β-carotene, ascorbic acid, firmness and fusarium wilt resistance in muskmelon (*Cucumis melo* L.) involving genetic male sterile lines. *Horticulturae, 8*(82), 1-24.

Khairiya, P., Singh, J. P. and Singh, D. (2023). Heterosis Analysis for Growth and Yield Attributes in Sponge Gourd [*Luffa cylindrica* (Roem) L.]. *Biological Forum-An International Journal, 15*(5), 441-449.

Kirkbride, J. H. (1993). Biosystematic monograph of the genus *Cucumis* (Cucurbitaceae). Parkway Publishers, Boone, NC, USA.

Lija, M. and Beevy, S. S. (2021). A review on diversity of melon. *Plant Science Today, 8*(4), 995-1003.

Magawry, N. A, E. and Shaban W. I. (2021). Genetic Study on powdery mildew resistance and some economic traits in melon (*Cucumis melo). Horticultural Science, 10*(1), 31-39.

Manasherova, E. and Cohen, H. (2022). A collection of melon (*Cucumis melo*) fruit cultivars with varied skin appearances provide insight to the contribution of suberin in periderm formation and reticulation. *Plants, 11*(10), 1336.

Manchali, S., Murthy C., K. N., Vishnuvardana and Patil, B. S. (2021). Nutritional composition and health benefits of various botanical types of melon (*Cucumis melo* L.). *Plants, 10*(9), 1755.

Napolitano, M., Terzaroli, N., Kashyap, S., Russi, L., Evans, E. J. and Albertini, E. (2020). Exploring heterosis in melon (*Cucumis melo* L.). *Plants, 9*(2), 5-19.

Pitrat, M., Hnanelt, P. and Hammer, K. (2000). Some comments on intra-specific classification of cultivars of melon. *Proc. Cucurbitaceae. Acta Horticulturae, 510,* 29-36.

Pornsuriya, P., Pornsuriya, P. and Teerasakulchol, S. (2013). Heterosis of three-way crosses between Thai melon and cantaloupe. *Journal of Applied Sciences Research, 9,* 6111-6114.

Saha, K., Choudhary, H., Munshi, A. D. and Singh, A. K. (2022). Heterosis and combining ability for yield traits and its relationship with gene action in muskmelon (*Cucumis melo*). *Indian journal of agricultural science, 92*(5), 602–606.

Selim, M. A. M. (2019). Heterosis and combining ability for some fruit quality traits of Egyptian melon inbred lines using line × tester analysis. *Egyptian Journal of Agricultural Research, 7*(1), 317-342.

Shoura, E. A., Mohamed, G. Z. and Shafike, N. E. (2023). Assessment of heterosis, combining ability and genetic variance for some economical traits in melon (*Cucumis melo* L.). *Journal of Plant Production, 14,* 201-209.

Suzy, M. Abdelaziz A. A., El-Eslamboly, S. A. and AbdEl-Nabi H. M. D. (2020). A study of the genetic behaviour of some genotypes of melon (*Cucumis melo* L.). *Plant Archives, 20*(2), 5381-5387.

Tak, S., Kaushik, R. A., Ameta, K. D., Dubey, R. B., Rathore, R. S. and Nath, A. (2017). Combining ability studies on cucumber and snapmelon hybrids. *International Journal of Current Microbiology and Applied Sciences, 6*(6), 942-949.

Thakur, H., Sharma, S. and Thakur, M. (2019). Recent trends in muskmelon (*Cucumis melo* L.) research: An overview. *The Journal of Horticultural Science and Biotechnology, 94*(4), 533-547.

Vashisht, V. K., Sehgal, G., Lal, T. and Gaikwad, A. K. (2010). Combining ability for yield and yield

attributing traits in muskmelon. *Crop Improvement*, *37*, 34-36.

Whitaker, T. W. and Davis. G. N. (1962). Cucurbits: Botany, cultivation, and utilization. *Interscience Publishers*, New York.

Zhu, H., Guo, L., Song, P., Luan, F., Hu, J., Sun, X. and Yang, L. (2016). Development of genome-wide SSR markers in melon with their cross-species transferability analysis and utilization in genetic diversity study, Molecular *Breeding*, *36*, 153-167.

How to cite this article: Mamatha R.M., T.B. Allolli, Rekha B. Chittapur, Raghavendra Gunnaiah, Vasant M. Ganiger, M.S. Lokesh and Jnaneshwar B. Gopali (2023). Estimation of Heterosis for Yield and Yield contributing Traits among intraspecific Hybrids of *Cucumis melo*. *Biological Forum – An International Journal, 15*(9): 358-363.