

Correlation Studies in Inter-botanical Cross of Melon Kashi Madhu (*Cucumis melo* var. *chandalak*) × IC632170 (*Cucumis melo* var. *momordica*)

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ABSTRACT: The evaluation of melon (*Cucumis melo* L.) genotypes was carried out under polyhouse conditions at farmer's field in Pavagada taluk, Tumkur District during summer 2021 following Augmented block design. The objective of the experiment was to determine the yield components which can be used for genetic improvement of yield hence correlation study was undertaken among F₂ population in inter-botanical cross of Kashi Madhu × IC632170 (Snapmelon). The correlation study revealed that yield per plant had a highly significant and positive correlation with ovary length, fruit length, fruit width, flesh thickness, seed cavity and average fruit weight. The correlation study has uncovered the relationship between the yield and yield attributing traits mainly viz., fruit width, flesh thickness and average fruit weight. The results indicated that selection for higher yield through these traits would be effective.

Keywords: *Cucumis melo* L., Kashi Madhu, Snapmelon, F₂ population, Correlation and Yield.

INTRODUCTION

Melons (*Cucumis melo* L., 2n = 24) are one of the important horticultural crops grown worldwide with an area of 1.04 Mha and production of 27.5 million tonnes. Melon belongs to the family Cucurbitaceae. Although East Africa was believed to be the centre of origin of melon, the recent literature suggests the Asiatic origin (Schaefer *et al.*, 2009; Sebastian *et al.*, 2010). India is one of the areas of melon diversification and several melon landraces are cultivated in different geographical locations (Fergany *et al.*, 2011; Reddy *et al.*, 2016; Shivapriya *et al.*, 2021). Southwest and Central Asia comprising southern Russia, Afghanistan, Pakistan are the primary centres of melon diversity, whereas, secondary centres of diversity are proclaimed to be China, Korea and the Iberian Peninsula (Esquinas-Alcazar and Gulick 1983).

Melons exhibit very wide genetic variation among the different botanical groups with respect to fruit related traits such as shape, size, colour, texture, taste and composition and resistance to diseases and pest (Pitrat, 2016). The cross-compatibility between different botanical groups of melon (Mathew *et al.*, 1986) and

wide genetic variability would provide breeders, vast potential for exchange of genes between them and aid in improvement of melon cultivars (Deakin *et al.*, 1971).

In the present study, representative lines of two botanical groups of melon (*chandalak* and *momordica*) were used. *Chandalak* melons of North India are known for their sweet fruits and Kashi Madhu, a high yielding sweet melon with attractive orange pulp is a selection from a local landrace "Mau" melon of Uttar Pradesh (Pandey *et al.*, 2008). Snapmelon (*momordica*) is of Indian origin and known for its multiple disease resistant genes (Pitrat and Besombes 2008, Pitrat, 2016; Liu *et al.*, 2010; Manchali *et al.*, 2019). The very short post-harvest life and fruit bursting nature of snapmelon hinders its large-scale cultivation but in Kerala, it is being cultivated at commercial scale for juice industry (Pareek *et al.*, 1999).

In the realm of crop improvement, knowledge of the linkage and correlation between various horticultural traits is crucial (Taha *et al.*, 2003). Further, yield is a complex trait and depended on other associated traits. Correlation studies helps for deciding which trait contribute towards productivity traits positively or

negatively among genotypes. With this background present study was taken to assess the correlation present among the traits in inter-botanical cross of melon.

MATERIAL AND METHODS

The parental lines, Kashi Madhu (male) and IC632170 (female) were crossed to obtain F₁ and selfed to produce F₂ seeds. The F₁ and F₂ generation seeds were developed under polyhouse condition at the Regional Horticultural Research and Extension Centre, University of Horticultural Sciences campus, GKVK, Bengaluru. The parents and F₁ were replicated six times. The evaluation of parents, F₁ and 201 F₂ generations were conducted under polyhouse conditions at farmer's field in the B. K. village, Nagalamadike hobli, Pavagada taluk, Tumkur District during summer 2021 following Augmented block design. The spacing of 45 × 60 cm was followed. Drip irrigation and mulching system were adopted to conserve soil moisture and control weeds. Plant protection measures were taken to achieve healthy growth of vines.

The data were recorded from each genotype for fifteen quantitative traits viz., Days to first female flowering (DFF), Ovary length (OL), Ovary width (OW), Days to first fruit maturity (DFM), Fruit length (FL), Fruit width (FW), Flesh thickness (FT), Seed cavity (SC), Seed length (SL), Seed width (SW), Average fruit weight (AFW), Total number of fruits per plant (TNF), Yield per plant (YLD), Total Soluble Solids (TSS) and pH. The correlation co-efficient among all possible character combinations were estimated employing formula of Al- Jibourie *et al.* (1958).

RESULTS AND DISCUSSION

Phenotypic correlation of yield attributing traits associated to fruit yield in F₂ generation derived from the inter-botanical cross of Kashi Madhu × IC632170 are presented in Table 1. The Days to first female flowering was positive and significantly correlated to days to first fruit maturity (0.675). The ovary length was significantly and positively correlated to ovary width (0.327), fruit length (0.415), fruit width (0.196), flesh thickness (0.187) and average fruit weight (0.377). The trait ovary width positively and significantly correlated with fruit width (0.240) and seed cavity (0.222), whereas, days to first fruit maturity correlated to seed length (0.165) and seed width (0.177). The fruit length was significantly and positively correlated to fruit width (0.504), flesh thickness (0.401), seed cavity (0.228), average fruit weight (0.633) and negatively and significantly correlated to total number of fruits per plant (-0.253). The trait fruit width significantly and positively correlated to flesh thickness (0.484), seed cavity (0.483) and average fruit weight (0.513). The flesh thickness was positively and significantly correlated to seed length (0.144) and average fruit weight (0.501), while, seed cavity significantly and positively correlated to seed length (0.469) and average fruit weight (0.338). The yield per plant had significant and positive correlation with ovary length (0.271), fruit length (0.530), fruit width (0.386), flesh thickness (0.415), seed cavity (0.317) and average fruit weight (0.826).

Table 1: Correlation coefficients of yield attributing traits associated to fruit yield in F₂ generation derived from the inter-botanical cross Kashi Madhu × IC632170.

	DFF	OL	OW	DFM	FL	FW	FT	SC	SL	SW	AFW	TNF	YLD	TSS	pH
DFF	1.000														
OL	-0.017	1.000													
OW	-0.012	0.327**	1.000												
DFM	0.675**	-0.037	-0.015	1.000											
FL	0.057	0.415**	0.065	0.004	1.000										
FW	-0.041	0.196**	0.240**	-0.080	0.504**	1.000									
FT	0.004	0.187**	0.043	-0.033	0.401**	0.484**	1.000								
SC	0.028	0.054	0.222**	0.013	0.228**	0.483**	0.111	1.000							
SL	-0.098	-0.014	0.019	0.165*	-0.089	0.036	0.144*	0.183**	1.000						
SW	-0.100	-0.002	0.041	0.177*	-0.074	-0.063	0.013	0.015	0.469**	1.000					
AFW	0.006	0.377**	0.138	-0.063	0.633**	0.513**	0.501**	0.338**	0.052	-0.016	1.000				
TNF	-0.136	0.160*	-0.053	-0.073	-0.253**	0.180*	-0.187**	-0.072	0.059	0.095	-0.396**	1.000			
YLD	-0.089	0.271**	0.065	-0.085	0.530**	0.386**	0.415**	0.317**	0.075	0.048	0.826**	0.065	1.000		
TSS	-0.051	-0.040	-0.085	-0.067	0.033	0.010	0.043	0.095	0.021	-0.003	0.054	0.035	0.077	1.000	
pH	0.140*	0.028	-0.037	-0.081	-0.026	-0.042	-0.115	0.039	-0.072	0.024	-0.065	0.234**	0.069	0.232**	1.000

DFF: Days to first female flowering
FW: Fruit width
AFW: Average fruit weight

OL: Ovary length
FT: Flesh thickness
TNF: Total number of fruits

OW: Ovary width
SC: Seed cavity
YLD: Yield per plant

DFM: Days to fruit maturity
SL: Seed length
TSS: Total Soluble Solids

FL: Fruit length
SW: Seed width

The fruit length was positively and significantly correlated to fruit width, flesh thickness and seed cavity in intervarietal hybrids of Mangalore melon. In a study carried out using 13 different melon lines indicated a positive correlation of yield with earliness and positive and significant correlation of yield with primary branches, whereas non-significant coefficients of correlation indicate that selection for different traits could be done simultaneously and independently (Taha *et al.*, 2003). Simple correlation among 49 melon genotypes indicated significant and positive relation between yield and fruit weight, flesh diameter (Rad *et al.*, 2010). The character days to first female flowering showed negative significant with number of fruits per plant and total sugar content in the present study. Similar results observed in eight Muskmelon hybrids (Shivaprasad *et al.*, 2017).

The average fruit weight was associated with fruit length and seed cavity (Khomphet *et al.*, 2022). The yield was positively and significantly correlated to fruit diameter, fruit length and flesh thickness in musk melon (Nanthakumar *et al.*, 2021). Similar positive association was reported in other studies for fruit yield with fruit weight and fruit length in oriental pickling melon (Ramana, 2000). Positive association of fruit yield with seed cavity width and total soluble solids (Reddy *et al.*, 2007 in snapmelon; Mehta *et al.*, 2009 in musk melon) fruit weight, fruit length, fruit girth, flesh thickness and seed cavity (Babu *et al.*, 2013). The flesh thickness was positively associated to fruit width in intervarietal hybrids of Mangalore melon (Kumbar *et al.*, 2021).

CONCLUSIONS

The correlation study at phenotypic level in F₂ population exhibited significant and positive association of yield per plant with fruit length, fruit width, flesh thickness, seed cavity and average fruit weight. Hence selection of anyone of these traits enhances the performance of yield per plant.

FUTURE SCOPE

The F₂ population can be advanced further to get a stable and homozygous RILs and to isolate superior lines for yields, early maturity and shelf life.

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Conflict of Interest. None.

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