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Genetic study for yield and quality traits in infra-specific mapping population of melon

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ABSTRACT

Heritability, inter-relationship and path coefficient studies were performed in an infra-specific cross between Snapmelon (*Cucumis melo* var. *momordica*) and muskmelon (*Cucumis melo* L.) to produce an array of 249 F3 families. A pattern of moderate to high, broad sense heritability was estimated for yield attributing fruit traits. Fruit weight exhibited highest heritability (90.3%) while ovary length and diameter showed lowest heritability. Positive and significant correlation of yield was found with fruit weight, number of fruits per plant, Fruit quality traits ascorbic acid content (Vitamin C) and fruit flesh pH showed positive correlation. Path analysis showed significant positive direct effect of number of fruits per plant and fruit weight on yield. Study on allelic interaction of fruit traits during early generation will allow selection of better inbred lines and variety development reducing the cost of advancement, space and time required for inbreeding large size population.

Keywords: *Cucumis melo* var. *momordica*, Ascorbic acid, Fruit weight, Path analysis, Correlation, Yield traits, Infra-specific cross, Population, TSS.

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INTRODUCTION

Melon is a popular fruit, consumed fresh and processed in various desserts and sweetmeats all over world. Melon fruit contains 10% carbohydrates, 90% water and other minerals, it is good source of Vitamins, folic acid, β-carotene and potassium and melon seeds are rich in oil and protein (Adekunle and Oluwa 2008). Snapmelon are group of melons native to India; it contains high degree of disease resistant and ascorbic acid content (Vitamin C), fruits are sour in taste and generally used in preparation of pickles and salad (Dhillon et al. 2009).

Conservation of wild gene pool and traditionally grown Indian *Cucumis* landraces are of economic interest for introgression into elite germplasm and beneficial for crop improvement. The genetic study of partition's components attributable to different causes and the relative magnitude of these components are important to determine genetic properties of the population (Falconer 1989). Hence heritability, correlation, path analysis for yield and associated traits within population would be helpful approach to define earlier generation selection and reduction in population size to avoid the cost of advancement, space and time required for inbreeding large size population (Silva et al. 2010). In an infra-specific hybridization of snapmelon (*Cucumis melo* var. *momordica*) crossed to subspecies muskmelon (*Cucumis melo* L.) there is wide variation (Garg et al. 2007). The segregating generations results rare recombination of genes expressing superior, inferior or similar phenotypic traits to the parents.

The present study was undertaken to evaluate genetic variation in F3 families of an infra specific population, identification of yield contributing traits to determine the relationship among the traits and their association with yield of melon.

MATERIAL AND METHODS

Experimental site and plant materials. Field experiments were performed at Indian Institute of Vegetable Research, Varanasi (82.52^{o} E longitude and 25.10^{o} N latitude, at an elevation of 128.93 m from mean sea level in the centre of indo-gangetic plain) on sufficiently drained sandy loam soils. The infra-specific cross was made between Muskmelon x Snapmelon cultivars (Kashi Madhu × B-159). 'Kashi Madhu' is an improved cultivar with yellow colored, round, fruit having a musky aroma and sweet and juicy flesh (Pandey et al. 2008a). 'B-159' is a Snapmelon accession, fruits are long, less sweet, with a thin rind that bursts at maturity (Pandey et al. 2008b).

Experimental design. Seed from parents (P1, P2), F1, and 249 selected F3 genotypes were grown over 2 consecutive years, in a randomized block design (RCBD). The experiment provided minimum chances of plant competition (i.e., within row spacing) which is a major factor that can affect melon productivity (Maynard and Scott 1998). Standard cultural practices were used. The fruit characters measured were polar circumference of fruit (FL), equatorial circumference of fruit (FD), flesh thickness (FT), fruit weight (FW), number of fruit per plant (NOF), pedicel length (PL), total soluble solids (TSS), fruit flesh acidity (pH), ascorbic acid content (AA), ovary length (OL), ovary diameter (OD), and total yield per plant (YPP) in F3 inbred lines. Five fully ripened fruits were randomly collected from parental lines, F1's, and from at least 10 plants of each F3 family for measurement. Flesh pH of fruit was measured using an electronic pH meter and ascorbic acid (mg/100 g) of melon fruit was measured by a titrimetric method (Ranganna 1977) in replications.

Data analysis. Each trait was recorded and averaged for assessment of mean performance of F3 genotypes. Statistical analysis was performed using SPSS software (ver. 16.0, IBM Corporation, U.S.A). A genotypic coefficient of variation (GCV), phenotypic coefficients of variation (PCV) and broad sense heritability was estimated by the procedure of Burton and DeVane (1952) and Hanson et al. (1956). The Genetic advance (GA) and genetic advance as percent of mean (GAM) for each character was calculated according to Johnson et al. (1955). Correlation and path coefficient analysis were done by mean data of all F3 families according to Al-Jibouri et al. (1958) and Dewey and Lu (1959).

RESULTS AND DISCUSSION

Genetic variation. Genetic variations within population were calculated using frequency distribution of fruit traits (Table 1). Ascorbic acid content exhibited a wide range of variation in F3 population while narrow range of variation was found for ovary length (1.0-3.6). A reduction in variance of F3 occurred for ovary length, ovary diameter followed by flesh thickness, flesh pH, yield per plant, number of fruit per plant, pedicel length, total soluble solids, fruit weight, ascorbic acid, equatorial circumference of fruit and polar circumference of fruit. Skewness was positive for all characters except fruit flesh pH, showing negative skewness (-0.88).

In this study, the genetic parameters were used to access variability among fruit traits in infra-specific mapping melon melon population; earlier variability has been studied (Vijay 1987, Pandey et al. 2005).

Table 1. Descriptive statistics of fruit characters in melon.

Character	OL[a]	OD	FL	FD	FW	NOF	FT	PL	TSS	pH	AA	YPP
Grand Mean	1.69	1.95	33.71	29.72	530.17	3.13	1.72	3.36	4.10	5.88	5.20	1.72
Standard deviation	0.34	0.30	9.68	7.40	249.4	1.0	0.62	1.10	1.24	0.93	2.92	1.0
Variance	0.11	.09	93.8	54.8	6.22	1.14	0.39	1.21	1.56	0.87	8.56	1.04
Skewness	1.31	2.94	0.38	0.30	2.22	0.48	3.20	0.81	0.73	-0.88	1.07	2.55
Kurtosis	4.78	17.4	1.77	1.34	9.76	0.22	17.7	0.47	0.00	2.3	0.69	10.3
SE ±	0.33	0.30	0.27	0.27	0.78	0.64	0.27	0.62	0.76	0.51	0.98	0.41

Abbreviations of fruit traits [a] OL,OD,FL, FD, FW, NOF, FT, PL, TSS, pH, AA,YPP(Ovary Length, Ovary Diameter, Fruit Length, Fruit Diameter, Fruit Weight, Number of Fruits Per Plant, Flesh Thickness, Pedicel Length, Total Soluble Solids, Flesh pH, Ascorbic Acid, Yield Per Plant).

Table 2. Genetic variability of fruit characters in melon.

Character	Range		Variability		Heritability (%)		Genetic advance (%)	Genetic advance as percent of mean
	Min	Max	PCV	GCV				
OL [b] (cm)	1	3.6	28.31	15.18	28.7	L [a]	2.80	16.5
OD (cm)	1.2	3.9	20.20	7.23	12.8	L	10.0	5.12
FL (m)	2.1	74.3	31.83	30.20	90.0	H	19.19	56.9
FD (m)	1.9	54.3	24.77	21.96	78.6	H	11.92	40.10
FW (kg)	1.16	2.03	58.20	55.31	90.3	H	57.4	98.1
NOF	1.0	7.0	40.67	31.90	61.5	M	16.2	51.7
FT (cm)	0.9	6.1	34.43	28.15	66.8	M	8.2	47.6
PL (cm)	0.9	6.8	37.88	30.34	64.2	M	16.8	50.0
TSS (%)	1.0	7.8	35.83	27.59	59.3	M	18.0	43.9
pH	1.0	7.6	17.25	13.45	60.8	M	12.7	21.5
AA (g/100 g)	1.1	16.3	59.31	54.59	84.7	H	53.9	93.6
YPP (kg)	0.2	7.33	78.70	73.06	86.2	H	24.1	94.1

[a] Lower (L) <30, Medium (M) >30- <70, High (H) >70 (Kumar et al. 2009).

[b] OL,OD,FL, FD, FW, NOF, FT, PL, TSS, pH, AA,YPP(Ovary Length, Ovary Diameter, Fruit Length, Fruit Diameter, Fruit Weight, Number of Fruits Per Plant, Flesh Thickness, Pedicel Length, Total Soluble Solids, Flesh pH, Ascorbic Acid, Yield Per Plant).

The positive skeweness within population for fruit traits indicated dominant allelic interaction while flesh thickness skewed towards negative showed a central tendency of lesser dominance or additive nature. Negative skewness for fruit quality traits like flesh pH is an expected result (Preetha and Raveendra 2008). Selection of highly heritable traits in early generations was reported by Vivekanandan et al. (1992).

The estimate of GCV value was higher compared to PCV value for all characters. A high GCV occurred for YPP, followed by FW, AA, NOF, PL, FL, FT, TSS, pH, OL and OD (Table 2). The estimate of PCV value was high for YPP followed by AA, FW, NOF, PL, TSS, FT, FL, OL, FD, and OD; the lowest value was for flesh pH. Heritability was divided into 3 categories Lower <30, Medium >30- <70 and High (H) >70 (Kumar et al. 2009). The result showed high heritability for FL, FD, FW, AA and YPP; low for OL and OD, and medium for the NOF, FT, PL, TSS and flesh pH. High genetic advance was found for FW, AA, YPP, FL, TSS, PL, NOF, pH, FD, OD and FT showed low genetic advance. The results for genetic advance as percent of mean were significant and highest for FW followed by YPP, AA, FL, PL, NOF, FT, TSS, FD, pH, OL and least for OD. Pure lines can be attained by direct phenotypic selection. High genetic variance and high heritability of FL and FD in this study fits the hypothesis that predicts highly heritable polygenic control of fruit shape in melon (Kalloo et al. 1983, Monforte et al. 2004).

High heritability followed by high genetic advance and generation advance as percent of mean values of fruit weight and number of fruit per plant indicated good variation in these characters and consequently better chances of improving yield through selection generation by generation. Heritability was also high for fruit weight and number of fruits per plant when studied in other genotypes of muskmelon (Lippert and Hall 1982, Rastogi and Deep 1990, Rakhi and Rajmony 2005). The low heritability of TSS would be due to complex nature of this trait which involves metabolic process in sugar accumulation compared to other morphological traits other environmental factors like temperature, humidity and nutrition affect sugar accumulation during ripening of fruit (Park et al. 2004). The low heritability of quality traits in F3 generation indicated that selection of these traits may be postponed till advanced generations when genotypes will be homozygous.

Table 3. Inter-trait correlation coefficient of yield and contributing fruit traits in melon.

Trait	OD [a]	FL	FD	FW	NOF	FT	PL	TSS	pH	AA	YPP
OL	0.199	0.163	-0.066	0.143	0.250	0.033	0.225	-0.090	-0.161	-0.056	0.261
OD		-0.262	0.159	-0.104	0.160	-0.057	0.032	0.015	0.164	0.193	-0.025
FL			0.115	0.319	0.145	-0.242	0.317	-0.355	-0.504*	-0.209	0.322
FD				0.055	-0.004	0.120	-0.166	0.186	0.234	0.064	0.046
FW					0.252	-0.419*	0.471*	-0.333	-0.505*	-0.276	0.879**
NOF						-0.195	0.163	-0.199	-0.289	-0.103	0.620**
FT							-0.564**	0.379	0.568**	0.323	-0.401**
PL								-0.449*	-0.712**	-0.359	0.455**
TSS									0.658**	0.299	-0.344
pH										0.463*	-0.550**
AA											-0.261

**,* Significant at 1% and 5% levels, respectively

[a] OL,OD,FL, FD, FW, NOF, FT, PL, TSS, pH, AA,YPP(Ovary Length, Ovary Diameter, Fruit Length, Fruit Diameter, Fruit Weight, Number of Fruits Per Plant, Flesh Thickness, Pedicel Length, Total Soluble Solids, Flesh pH, Ascorbic Acid, Yield Per Plant).

Table 4. Phenotypic direct diagonal and indirect effects of fruit characters on yield in melon.

Trait	OL [a]	OD	FL	FD	FW	NOF	FT	PL	TSS	pH	AA
OL	**0.035**[b]	-0.009	0.000	0.000	0.047	0.048	0.001	0.001	0.000	0.003	0.000
OD	0.020	**-0.016**	0.000	0.000	-0.028	0.010	0.001	0.000	0.001	-0.002	0.000
FL	0.003	0.002	**-0.001**	0.001	0.219	0.054	-0.003	0.003	-0.004	0.014	0.001
FD	-0.002	-0.001	0.000	**0.005**	0.039	-0.006	0.002	-0.002	0.002	-0.006	0.000
FW	0.002	0.001	0.000	0.000	**0.735**	0.076	-0.006	0.004	-0.004	0.014	0.001
NOF	0.003	0.000	0.000	0.000	0.114	**0.491**	-0.002	0.001	-0.002	0.006	0.000
FT	0.001	-0.001	0.000	0.001	-0.214	-0.056	**0.018**	-0.005	0.004	-0.015	-0.001
PL	0.004	0.000	0.000	-0.001	0.266	0.037	-0.007	**0.012**	-0.004	0.018	0.001
TSS	0.000	-0.001	0.000	0.001	-0.183	-0.052	0.005	-0.004	**0.015**	-0.015	-0.001
pH	-0.003	-0.001	0.000	0.001	-0.282	-0.077	0.008	-0.006	0.006	**-0.036**	-0.001
As. A	-0.001	-0.001	0.000	0.000	-0.173	-0.032	0.004	-0.003	0.003	-0.012	**-0.004**

Residual value 0.0801

[a] OL,OD,FL, FD, FW, NOF, FT, PL, TSS, pH, AA,YPP(Ovary Length, Ovary Diameter, Fruit Length, Fruit Diameter, Fruit Weight, Number of Fruits Per Plant, Flesh Thickness, Pedicel Length, Total Soluble Solids, Flesh pH, Ascorbic Acid, Yield Per Plant)

[b] Bold value are direct diagonal effect on yield per plant.

Correlation coefficient. Genotypic correlation was higher than phenotypic correlation, indicating a low influence due to environment and the expression of characters being mainly due to genetic factors (Table 3). Yield was positively and significantly correlated with FW, NOF and PL while negatively and significantly, correlated with FT and flesh pH. AA was positively correlated with flesh pH and flesh pH was positively correlated with other two traits FT and TSS. The study showed a negative correlation of fruit quality traits flesh pH with other morphological traits FL, FW and PL. Similarly another quality trait TSS was found negatively correlated with PL. Genotypic correlations were higher in magnitude than their respective phenotypic correlations in this generation due to fixation of recombination and segregation in earlier F2 generation through selfing (Pandey et al. 2010). These findings are supported by the previous study of culinary melon landraces (Rakhi and Rajmony 2005).

Path coefficient analysis. The path analysis of the mapping population (Table 4) deduced direct and indirect effects showed highest positive direct effect on YPP was exerted by FW and NOF followed by OL, FT, AA, FD and TSS. The fruit traits OD, flesh pH and FL had negative direct diagonal and indirect effects on yield at genotypic and phenotypic levels. Pedicel length had a negative direct effect on yield at the genotypic level; ascorbic acid content had a negative significant effect on yield. Path coefficient analysis showed FW had direct effect on yield while FT, TSS, AA and FD had indirect effects on yield. Recurrent observations of FW on yield were found in F2 generation of this infra specific mapping population suggesting improved fruit yield (Pandey et al. 2011). Feyzian et al. (2009) also found a direct effect of FW on yield in diallel crossing program of melon.

CONCLUSION

Melon is a commercial crop grown in large part of India. The present genetic study revealed potential variation among fruit traits which can be exploited for

future melon improvement. Fruit shape trait (length and width) were found as highly heritable polygenic character with dominant allelic interaction and played an important role in increasing yield. Furthermore correlation and path analysis explicitly indicated that number of fruit per plant, fruit weight, ascorbic acid, TSS and flesh pH, are important selection indices for high yielding good quality melon genotypes. Evaluation of developed genetic population for quality and yield traits through correlation and path analysis is recommended for future utility of the melon.

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