Article AR2029

DOI: HTTPS://DOI.ORG/10.23910/IJBSM/2019.10.6.2029

International Journal of Bio-resource and Stress Management

December 2019

Crossref

Print ISSN 0976-3988
Online ISSN 0976-4038

IJBSM 2019, 10(6):636-644

Research Article *Natural Resource Management*

Genetic Variability, Correlation and Path Analysis Study on Snap Melon (*Cucumis melo* L. var. *momordica*) Farmer's Varieties

Pasha S. G.*, S. Marker and Sarath Chandra G.

Dept. of Genetic and Plant breeding, Naini Agriculture Institute, SHUATS, Prayagraj, U.P. (211 007), India

Open Access

Corresponding Author

Pasha S. G.
e-mail: 130806agr214@gmail.com

Citation: Pasha et al., 2019. Genetic Variability, Correlation and Path Analysis Study on Snap Melon (*Cucumis melo* L. var. *momordica*) Farmer's Varieties. International Journal of Bio-resource and Stress Management 2019, 10(6):636-644. HTTPS://DOI.ORG/10.23910/IJBSM/2019.10.6.2029

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

Acknowledgement: The Authors are sincerely grateful to the Hon'ble Vice-Chancellor, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj and to PPV-FRA, Ministry of Agriculture and farmer Welfare Government of India for providing the necessary facilities to complete my research work.

Abstract

The present investigation was carried out to assess the genetic variability, correlation and path analysis for yield and its component traits in 15 Snap melon farmer's varieties of Eastern Uttar Pradesh for 17 quantitative characters during *Kharif*- 2018. Analysis of variance showed significance differences for all the quantitative traits at 1% and 5% level of significance. Indicating considerable amount of genetic variation in different farmer's varieties of Eastern Uttar Pradesh. The low difference between GCV and PCV depicted that a little or no influence of environment on the expression of the various quantitative traits. High heritability coupled with high genetic advance was depicted by for fruit weight at average followed by number of seeds fruit^{-1} and 100 seed weight, indicating a predominance of additive gene effects and the possibilities of effective selection based on these traits for snap melon improvement. Therefore, these traits may be used as selection indices for genetic improvement of Snap melon farmer's varieties. Node at first female flower appearance followed by number of fruits plant^{-1}, fruit length, fruit diameter, fruit flesh thickness and fruit weigh at average show positive significant correlation and direct effect on yield plant^{-1} further proves their genetic worth for selection breeding through pure line/ pedigree method.

Keywords: Variability parameters, correlation coefficient, path analysis, snap melon

1. Introduction

Snap melon (*Cucumis melo* L. var. *momordica*) belongs to family Cucurbitaceae with chromosome number (2n=2x=24) is a tropical old-world cucurbit species (Somkuwar et al., 1997). India being one of the secondary centers of origin of Cucumis melo, is rich in its feral and cultivated forms which comprise nearly 40 species (Whitaker and Davis, 2008) and Africa was suggested to be the region of domestication of melon based on the availability of many specimens of wild Cucumis (Koli and Murthy, 2013). A modest gene bank of snap melon has been established in the Department of Vegetable Crops, Punjab Agricultural University, Ludhiana, India (Dhillon et al., 2009). A wide range of variability is met from Gujarat in the west to West Bengal in the east (Seshadri and More, 2002). It is very popular in arid and semi arid regions (Hazra et al., 2011). It is also cultivated in other countries of Southeast Asia, for instance Myanmar (Yi et al., 2009) and Vietnam.

Indian snap melon accessions have been reported to be a good source for disease and insect pest resistance, and many of them are used as

Article History

RECEIVED in 28th August 2019 RECEIVED in revised form 15th December 2019 ACCEPTED in final form 23rd December 2019

reference accessions world widely (Cohen et al., 2003) and are good sources of nutrients, vitamin C, sugars, minerals and dietary fibers. A 100g edible fruit of snap melon contains 15.6g carbohydrates, 18.6 mg vitamin-C, 0.3 g protein, 95.7% moisture (Peter and Hazra, 2012) and provides 74.0 kcal energy (Goyal and Sharma, 2009). However, the fruits can be stored for 2-3 weeks (Kumar et al., 2013).

It is cultivated as a mixed crop along with maize, sorghum and pearl millet in rainy season or as a sole crop in summer season (Seshadri and More, 2009). The mature fruits of snap melon are peeled off; sun dried and preserved which is locally known as khelra (Pareek and Samadia, 2002). Snap melon are commonly called 'Phut,' which means 'to split.' Fruit cracking is either longitudinal or starting in the middle of fruit, though in some instances only skin peeling (longitudinal or random) occurs (Dhillon et al., 2007).

The understanding of genetic variability present in a given crop species for the traits under improvement is imperative for the success of any plant breeding program. Heritability is in conjunction with high Genetic advance as percent of mean would be more useful in predicting the resultant effect in the selection of the best genotypes for yield and its attributing traits (Pandey et al., 2009). Coefficient of correlations is the measure of level of the relationship between two or more traits related to yield. Path coefficient was estimated to find out the association and quantify the direct and indirect influence of one character upon another. Yield in snap melon is the product of several interrelated traits, so a successful breeding programme depends largely upon the information on the genetic variability and correlation of desired quantitative traits with yield. Therefore, an assessment was made about the performance of various economic traits and the extent of variability, heritability, expected genetic advance and interrelationship of yield components in snap melon was measured.

2. Materials and Methods

Fifteen farmer's varieties of Snap melon were obtained from local farmers of Eastern Uttar Pradesh and are grown in a Randomized Block Design with three replications during *Kharif*- 2018 at Field Experimentation Centre of the Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (Allahabad), U.P. Standard cultural practices were followed and recommended dose of fertilizers were given to raise a good crop.

The observations were recorded on five random plants for each treatment in each replication for node at first female flower appearance, node at first male flower appearance, days to first female flower opening, days to first male flower opening, vine length, number of nodes per vine, days to first harvest (DAS), number of fruits per plant, fruit length (cm), fruit diameter (cm), seed cavity length (cm), seed cavity breadth (cm), number of seeds per fruit, fruit flesh thickness (cm), 100 seed weight (g), average fruit weight (kg) and yield per plant. The data collected were subjected to Analysis of Variance as suggested by Panse and Sukhatme (1967). Genotypic Coefficient of Variation and Phenotypic Coefficient of Variation was calculated by using the procedure suggested by Burton (1952). Heritability in broad sense was computed by using the formula given by Burton and Devane (1953). The genetic advance for selection intensity at 5% was calculated by the formula given by Johnson et al. (1955). Correlation coefficients were determined as suggested by Al-Jibouri et al. (1958). The Path Coefficient analysis was done according to Dewey and Lu (1959).

2. Results and Discussion

The mean sum of squares due to the treatments showed significant differences among all the genotypes at 5% level of significance and 1% level of significance for all the characters. Indicating that these varieties were genetically variant from each other and similar findings were reported by Pandey et al, (2009) in snap melon.

The magnitude of GCV and PCV in (Table 1) were found high (>20) for yield plant^{-1}, fruit weight at average, 100 seed weight, fruit flesh thickness, number of seeds per fruit^{-1}, fruit length and node at first female flower appearance. The higher phenotypic coefficient of variation (PCV) than those of genotypic coefficient of variation (GCV) indicated the predominant role of environment on the expression of these traits and low GCV and PCV were recorded for days to first female flowering opening. A little possibility of improvement of these characters through selection could be used during crop improvement program. Therefore, response to direct selection may be effective in improving these traits. Similar findings were reported by Tomar et al. (2008), Samadia et al. (2009) in snap melon.

Heritability in broad sense was found to be high (>60%) for all the characters except for node at first male flower appearance followed by number of nodes per vine and number of fruits per plant. Characters showing high heritability indicate that they are less influenced by environment and there could be of greater correspondence between phenotypic and breeding values and there is a scope for improvement in these characters through direct selection.

High heritability (>60%) coupled with high genetic advance as percent mean (>30%) was recorded for fruit weight at average (99.85% and 143.79%) followed by number of seeds fruit^{-1} (99.11% and 16.09%), 100 seed weight (90.33% and 42.94%), fruit length (86.84% and 58.57%), yield plant^{-1} (85.71% and 150.43%), seed cavity length (81.69% and 31.58%), fruit diameter (78.85% and 37.36%), fruit flesh thickness (78.58% and 49.95%) and node at first female flower appearance (69.45% and 44.57%). Therefore indicating a predominance of additive gene effects and the possibilities of effective selection

Table 1: Estimates of range, mean, coefficient of variation, heritability, genetic advance, genetic advance as % of mean

Characters	Range	Mean	Coefficient of Variation		Heritability (bs) %	Genetic advance (GA)	Genetic advance as % of mean
			GCV	PCV			
Node at 1st female flower appearance	3.00-8.00	4.85	25.96	31.15	69.45	2.16	44.57
Node at 1st male flower appearance	2.25-4.10	3.11	16.91	24.73	46.78	0.74	23.83
Days to 1st female flower opening	29.30-41.20	36.21	9.18	10.62	74.72	5.92	16.34
Days to 1st male flower opening	23.50-36.40	29.52	13.73	14.55	89.13	7.88	26.71
Vine length	161.17-268.00	226.92	14.44	15.20	90.23	64.13	28.26
Number of nodes vine^{-1}	19.00-28.00	22.09	9.40	16.01	34.46	2.51	11.37
Days to 1st harvest	60.00-81.70	68.04	12.33	13.05	89.27	16.33	24.00
Number of fruits plant^{-1}	2.00-5.00	2.87	18.07	43.42	17.32	0.44	15.49
Fruit length	10.00-26.00	17.60	30.51	32.74	86.84	10.31	58.57
Fruit diameter	13.00-28.00	20.95	20.42	23.00	78.85	7.83	37.36
Seed cavity length	5.00-8.90	7.18	16.96	18.76	81.69	2.27	31.58
Seed cavity breadth	3.60-5.70	4.56	14.11	15.37	84.27	1.22	26.68
Number of seeds fruit^{-1}	163.00-939.00	414.91	56.61	56.86	99.11	481.67	116.09
Fruit flesh thickness	1.70-4.00	2.80	27.36	30.86	78.58	1.40	49.95
100 seed weight	1.01-2.04	1.46	21.93	23.08	90.33	0.63	42.94
Fruit weight at average	0.11-1.63	0.64	69.85	69.90	99.85	0.91	143.79
Yield plant^{-1}	1.55-6.17	1.98	78.87	85.19	58.71	3.85	150.43

can be conducted based on these traits for crop improvement program. Similar findings were reported in Snap melon by Joseph (2012), Muddarsu and Venkat (2013), in cucumber by Ene et al., (2016), in Melon by Malik (2012), in Muskmelon by Tomar et al. (2008) and in Watermelon by Choudhary et al., (2012)Thus these characters offer the best possibility of improvement through selection procedures.

For achieving rational improvement in yield and its related parameters, knowledge on mechanism of correlation, cause and effect relationship provides a basis for formulating suitable selection methods for the yield.

In this present investigation in (Table 2) node at first female flower appearance (rg= 0.565**, rp= 0.417**), days to first female flower opening (rg=0.177*, rp= 0.125*), vine length (rg=0.335*, rp= 0.310*), number of fruits plant^{-1} (rg=0.892**, rp=0.626**), fruit length (rg=0.561**, rp= 0.537**), fruit diameter (rg=0.783**, rp=0.656**), seed cavity breadth (rg=0.480**, rp= 0.438**), fruit flesh thickness (rg=0.675**, rp= 0.589**) and fruit weight at average (rg=0.944**, rp=0.876**) had shown significant positive correlation with yield per plant at both phenotypic and genotypic levels representing that any improvement in these traits will increase the yield in snap melon. These observations are in conformity with the findings of Reddy et al., (2007) and Pandey et al., (2009) in snap melon.

Whereas, days to first harvest (DAS) (rg=-0.397**, rp= -0.359*) showed significant negative correlation with yield per plant at both phenotypic and genotypic levels representing that any improvement in these traits would reduce the yield in snap melon. The expression of yield depends upon a number of yield contributing traits. It is not always independent in their action but may be inter-linked. The selection practiced for one character may simultaneously bring change in the other related character. Thus the information of the magnitude and direction of association between the component characters is essential for the improvement in the desirable direction.

The estimates of correlation coefficient mostly indicated inter-relationship of different characters; however it did not furnish the information on cause and effect. Under such situation path analysis would help the breeder to identify the index of selection. Path coefficient analysis was conducted in order to study the direct and indirect effect of individual components characters on dependent variable .i.e., yield in snap melon. Study of path coefficient enables the breeder to concentrate on the variables which show high direct effect on yield. The genotypic and phenotypic correlation coefficients of yield with other traits were further partitioned into direct and indirect effects and results are presented in (Table 3).

Path analysis reveals the direct and indirect effects of characters on yield (Table 3). From the study, it is revealed that the characters i.e., node at first female flower appearance (G=0.192, P=0.123), number of fruits plant^{-1} (G=0.173, P=0.380), fruit length (G=0.276, P=0.068), fruit diameter

Table 2: Phenotypic (rp) and Genotypic (gp) correlation coefficient between yield and its component traits of snap melon

Characters		NFFA	NMFA	DFFO	DMFO	VL	NNV	DH	NFP	FL	FD	SCL
Node at 1st female flower appearance	rg	1.00	0.352*	0.530**	-0.073	-0.085	0.223	0.017	0.737**	0.200	0.356*	0.294*
	rp	1.00	0.090	0.355*	-0.085	-0.046	0.079	0.037	0.264	0.108	0.315*	0.131
Node at 1st male flower appearance	rg		1.00	-0.031	-0.108	-0.206	-0.146	0.296*	0.880**	-0.355*	0.104	0.280
	rp		1.00	-0.078	-0.039	-0.154	-0.182	0.177	0.170	-0.165	0.068	0.219
Days to 1st female flower opening	rg			1.00	0.067	0.085	0.051	-0.269	0.078	0.371*	0.037	-0.044
	rp			1.00	0.067	0.061	0.037	-0.228	-0.003	0.248*	-0.023	0.016
Days to 1st male flower opening	rg				1.00	0.137	0.601**	0.581**	-0.542**	-0.020	-0.544**	-0.075
	rp				1.00	0.140	0.411**	0.506**	-0.247	-0.021	-0.474**	-0.046
Vine length	rg					1.00	0.718**	-0.538**	-0.136	0.706*	0.310*	0.513*
	rp					1.00	0.391**	-0.460**	-0.008	0.620*	0.282	0.450**
No. of nodes vine^{-1}	rg						1.00	0.210	-0.124	0.120	-0.237	0.124
	rp						1.00	0.126	-0.193	0.102	-0.205	0.137
Days to 1st harvest	rg							1.00	-0.462**	-0.711*	-0.706**	-0.403*
	rp							1.00	-0.174	-0.616*	-0.564**	-0.374*
Number of fruits plant^{-1}	rg								1.00	-0.108	0.831**	0.504*
	rp								1.00	0.067	0.354*	0.139
Fruit length	rg									1.00	0.564**	0.470*
	rp									1.00	0.486**	0.390**
Fruit diameter	rg										1.00	0.363*
	rp										1.00	0.334*
Seed cavity length	rg											1.00
	rp											1.00
Seed cavity breadth	rg											
	rp											
No. of seeds fruit^{-1}	rg											
	rp											
Fruit flesh thickness	rg											
	rp											
100 seed weight	rg											
	rp											
Fruit weight at average	rg											
	rp											
Yield plant^{-1}	rg											
	rp											

NFFA: Node at 1st female flower appearance; NMFA: Node at 1st male flower appearance; DFFO: Days to 1st female flower opening; DMFO: Days to 1st male flower opening; VL: Vine length; NNV: Number of nodes vine^{-1}; DH: Days to 1st harvest; NFP: Number of fruits plant^{-1}; FL: Fruit length; FD: Fruit diameter; SCL: Seed cavity length

Table 2: Continue...

Characters		SCB	NSF	FFT	SW	FWA	YP
Node at 1st female flower appearance	rg	0.340*	0.307*	0.227	-0.065	0.338*	0.565**
	rp	0.321*	0.246	0.146	-0.085	0.285	0.417**
Node at 1st male flower appearance	rg	0.592**	0.241	-0.390**	0.036	0.143	0.391
	rp	0.312*	0.188	-0.089	-0.021	0.097	0.230
Days to 1st female flower opening	rg	-0.086	-0.025	0.297*	-0.034	0.071	0.177*
	rp	-0.074	-0.033	0.238	-0.042	0.059	0.125*
Days to 1st male flower opening	rg	0.067	0.174	-0.072	-0.042	-0.157	-0.122
	rp	0.055	0.163	0.006	-0.048	-0.145	-0.092
Vine length	rg	0.241	0.044	0.462**	-0.325	0.401**	0.335*
	rp	0.216	0.044	0382**	-0.292	0.380*	0.310*
No. of nodes vine^{-1}	rg	0.280	-0.054	-0.178	-0.572*	-0.150	-0.046
	rp	0.143	-0.031	-0.186	-0.302*	-0.093	-0.093
Days to 1st harvest	rg	0.058	-0.091	-0.565**	0.249	-0.473**	-0.397**
	rp	0.027	-0.092	-0.498**	0.220	-0.448**	-0.359*
Number of fruits plant^{-1}	rg	0.576**	0.594**	0.048	0.021	0708**	0.892**
	rp	0.302*	0.245	0.044	0.037	0.298*	0.626**
Fruit length	rg	0.102	0.316*	0.881**	-0.214	0.685**	0.561**
	rp	0.111	0.303*	0.696**	-0.184	0.638**	0.537**
Fruit diameter	rg	0.472**	0.530**	0.763**	-0.173	0.857**	0.783**
	rp	0.442**	0.461**	0.563**	-0.174	0.760**	0.656**
Seed cavity length	rg	0.298*	0.125	0.346*	-0.579*	0.482	0.527
	rp	0.213	0.118	0.274	-0.513*	0.429**	0.433**
Seed cavity breadth	rg	1.00	0.413**	0.127	-0.386*	0.426**	0.480**
	rp	1.00	0.374*	0.042	-0.338*	0.397**	0.438**
No. of seeds fruit^{-1}	rg		1.00	0.458**	-0.138	0.654	0.686
	rp		1.00	0.404**	-0.132	0.650	0.630
Fruit flesh thick-ness	rg			1.00	0.015	0.864**	0.675**
	rp			1.00	-0.016	0.766**	0.589**
100 seed weight	rg				1.00	-0.063	-0.003
	rp				1.00	-0.057	-0.001
Fruit weight at average	rg					1.00	0.944**
	rp					1.00	0.876**
Yield plant^{-1}	rg						1.00
	rp						1.00

NSF: Number of seeds fruit^{-1}; FFT: Fruit flesh thickness; SW: 100 seed weight; FWA: Fruit weight at average; YP: Yield plant^{-1}; **: Significance at (p=0.01) and * Significance at (p=0.05) level

(G=0.028, P=0.056), fruit flesh thickness (G=0.282, P=0.063) and fruit weight at average (G=0.903, P=0.678) showed positive direct effect on grain yield at the both phenotypic (P) and genotypic (G) levels indicating the effectiveness of direct selection, Therefore these traits can be selected for crop improvement program. These observations were similarly reported in Snap melon by Pandey et al., (2009), Joseph (2012), Muddarsu and Venkat (2013) and Reddy et al. (2007), in Muskmelon by Nagri et al,. (2009), Choudhary et al,. (2004), Pandey et al. (2003), and Tomar et al. (2008), in Sweet melon by Ibrahim and Ramadan (2013) and in Watermelon by Choudhary et al. (2012).

The components of residual effect of path analysis in yield and its components traits is 0.0252 at genotypic level and 0.0378 at phenotypic level. The lower residual effect indicated that the characters chosen for path analysis were adequate, appropriate and further indicated that characters included in this study were effective for improving the yield.

Table 3: Direct (diagonal) and indirect (off diagonal) effect of different traits on yield of Snap melon

Characters		NFFA	NMFA	DFFO	DMFO	VL	NNV	DH	NFP	FL	FD	SCL	SCB
Node at 1st female flower appearance	G	0.192	0.054	-0.037	-0.014	0.006	0.012	-0.002	0.128	0.055	-0.010	-0.014	-0.028
	P	0.123	0.008	0.011	-0.010	-0.001	-0.001	-0.002	0.100	0.007	-0.018	0.012	-0.001
Node at 1st male flower appearance	G	0.067	-0.154	0.002	-0.021	0.014	-0.008	-0.042	0.152	-0.098	-0.003	-0.014	-0.048
	P	0.011	-0.090	-0.002	-0.005	-0.004	0.001	-0.011	0.065	-0.011	-0.004	0.020	-0.001
Days to 1st female flower opening	G	0.102	-0.005	0.069	0.013	-0.006	0.003	0.038	0.014	0.102	-0.001	0.002	0.007
	P	0.044	-0.007	-0.030	0.008	0.001	0.000	0.014	-0.001	0.017	0.001	0.001	0.000
Days to 1st male flower opening	G	-0.014	-0.017	-0.005	-0.191	-0.009	0.032	-0.082	-0.094	-0.005	0.016	0.004	-0.005
	P	-0.010	-0.004	0.002	-0.118	0.003	-0.003	-0.031	-0.094	-0.001	0.026	-0.004	0.000
Vine length	G	-0.016	-0.032	-0.006	0.026	-0.067	0.038	0.076	-0.024	0.195	-0.009	-0.025	-0.020
	P	-0.006	-0.014	0.002	0.017	0.023	-0.003	0.028	-0.030	0.042	-0.016	0.040	-0.001
No. of nodes vine^{-1}	G	0.043	-0.023	-0.004	0.115	-0.048	-0.052	-0.030	-0.022	0.033	0.007	-0.006	-0.023
	P	0.010	-0.016	0.001	0.048	0.009	-0.007	-0.008	-0.073	0.007	0.011	0.012	-0.001
Days to 1st harvest	G	0.003	0.046	0.019	0.111	0.036	0.011	-0.141	-0.080	-0.196	0.020	0.020	-0.005
	P	0.005	0.016	-0.007	0.060	-0.011	-0.001	-0.061	-0.066	-0.042	0.031	-0.033	0.000
Number of fruits plant^{-1}	G	0.141	0.136	-0.005	-0.103	0.009	-0.007	0.065	0.173	-0.030	-0.024	-0.024	-0.047
	P	0.032	0.015	0.000	-0.029	0.000	0.001	0.011	0.380	0.005	-0.020	0.012	-0.001
Fruit length	G	0.038	-0.055	-0.026	-0.004	-0.047	0.006	0.101	-0.019	0.276	-0.016	-0.023	-0.008
	P	0.013	-0.015	0.007	-0.002	0.014	-0.001	0.038	0.025	0.068	-0.027	0.035	0.000
Fruit diameter	G	0.068	0.016	-0.003	-0.104	-0.021	-0.012	0.100	0.144	0.155	0.028	-0.018	-0.038
	P	0.039	0.006	-0.001	-0.056	0.006	0.001	0.035	0.135	0.033	0.056	0.030	-0.002
Seed cavity length	G	0.056	0.043	0.003	-0.014	-0.034	0.007	0.057	0.087	0.130	-0.010	-0.048	-0.024
	P	0.016	0.020	0.000	-0.005	0.010	-0.001	0.023	0.053	0.026	-0.019	0.089	-0.001
Seed cavity breadth	G	0.065	0.091	0.006	0.013	-0.016	0.015	-0.008	0.100	0.028	-0.013	-0.014	-0.082
	P	0.039	0.028	-0.002	0.006	0.005	-0.001	-0.002	0.115	0.008	-0.025	0.019	-0.004
No. of seeds fruit^{-1}	G	0.059	0.037	0.002	0.033	-0.003	-0.003	0.013	0.103	0.087	-0.015	-0.006	-0.034
	P	0.030	0.017	-0.001	0.019	0.001	0.002	0.006	0.093	0.021	-0.026	0.011	-0.002
Fruit flesh thickness	G	0.044	-0.060	-0.021	-0.014	-0.031	-0.009	0.080	0.008	0.243	-0.022	-0.017	-0.010
	P	0.018	-0.008	0.007	0.001	0.009	0.001	0.030	0.017	0.047	-0.031	0.025	0.000
100 seed weight	G	-0.012	0.006	0.002	-0.008	0.022	-0.030	-0.035	0.004	-0.059	0.005	0.028	0.031
	P	-0.010	-0.002	-0.001	-0.006	-0.007	0.002	-0.013	0.014	-0.012	0.010	-0.046	0.001
Fruit weight at average	G	0.065	0.022	-0.005	-0.030	-0.027	-0.008	0.067	0.123	0.189	-0.024	-0.023	-0.035
	P	0.035	0.009	0.002	-0.017	0.009	0.001	0.027	0.114	0.043	-0.042	0.038	-0.002

NFFA: Node at 1st female flower appearance; NMFA: Node at 1st male flower appearance; DFFO: Days to 1st female flower opening; DMFO: Days to 1st male flower opening; VL: Vine length; NNV: Number of nodes vine^{-1}; DH: Days to 1st harvest; NFP: Number of fruits plant^{-1}; FL: Fruit length; FD: Fruit diameter; SCL: Seed cavity length; SCB: Seed cavity breadth; P=Phenotypic level and G= Genotypic level, Genotypic path (Residual effect=0.0252) and Phenotypic path (Residual effect=0.0378)

Table 3: Continue...

Characters		NSF	FFT	SW	FWA	YP
Node at 1st female flower appearance	G	-0.011	-0.064	-0.007	0.306	0.565^{**}
	P	0.016	-0.010	-0.010	0.193	0.417^{**}
Node at 1st male flower appearance	G	-0.008	0.110	0.004	0.129	0.391
	P	0.012	0.006	-0.002	0.066	0.230
Days to 1st female flower opening	G	0.001	-0..084	-0.003	0.064	0.177^{*}
	P	-0.002	-0.016	-0.005	0.040	0.125^{*}
Days to 1st male flower opening	G	-0.006	0.020	-0.004	-0.142	-0.122
	P	0.010	0.000	-0.006	-0.098	-0.092
Vine length	G	-0.002	-0.130	-0.033	0.362	0.335^{*}
	P	0.003	-0.027	-0.034	0.258	0.310^{*}
No. of nodes vine^{-1}	G	0.002	0.050	-0.058	-0.136	-0.046
	P	-0.002	0.013	-0.035	-0.063	-0.093
Days to 1st harvest	G	0.003	0.159	0.025	-0.427	-0.397^{**}
	P	-0.006	0.035	0.025	-0.304	-0.359^{*}
Number of fruits plant^{-1}	G	-0.021	-0.014	0.002	0.640	0.892^{**}
	P	0.015	-0.003	0.004	0.202	0.626^{**}
Fruit length	G	-0.011	-0.248	-0.022	0.619	0.561^{**}
	P	0.019	-0.048	-0.021	0.433	0.537^{**}
Fruit diameter	G	-0.018	-0.215	-0.017	0.774	0.783^{**}
	P	0.029	-0.039	-0.020	0.515	0.656^{**}
Seed cavity length	G	-0.004	-0.098	-0.058	0.435	0.527
	P	0.007	-0.019	-0.059	0.291	0.433^{**}
Seed cavity breadth	G	-0.014	-0.036	-0.039	0.385	0.480^{**}
	P	0.024	-0.003	-0.039	0.269	0.438^{**}
No. of seeds fruit^{-1}	G	-0.035	-0.129	-0.014	0.590	0.686
	P	-0.063	-0.028	-0.015	0.441	0.630
Fruit flesh thick-ness	G	-0.016	0.282	0.001	0.780	0.675^{**}
	P	0.025	0.069	-0.002	0.520	0.589^{**}
100 seed weight	G	0.005	-0.004	-0.101	-0.057	-0.003
	P	-0.008	0.001	-0.116	-0.039	-0.001
Fruit weight at average	G	-0.023	-0.243	-0.006	0.903	0.944^{**}
	P	0.041	-0.053	-0.007	0.678	0.876^{**}

NSF: Number of seeds fruit^{-1}; FFT: Fruit flesh thickness; SW: 100 seed weight; FWA: Fruit weight at average; YP: Yield plant^{-1}; P=Phenotypic level and G= Genotypic level, Genotypic path (Residual effect=0.0252) and Phenotypic path (Residual effect=0.0378)

4. Conclusion

Characters like node at first female flower appearance followed by number of fruits plant^{-1}, fruit length, fruit diameter, fruit flesh thickness and fruit weight at average showed positive significant correlation and direct effect on yield plant^{-1} further proves their genetic worth for selection breeding through pure line/ pedigree method.

5. Acknowledgement

The Authors are sincerely grateful to the Hon'ble Vice-Chancellor, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj and to PPV-FRA, Ministry of Agriculture and farmer Welfare Government of India for providing the necessary facilities to complete my research work.

6. References

Al-Jibouri, A., Miller, P. A., Robinson, H. F., 1958. Genotype and environmental variation and co-variation in upland crops of interspecific orgin. Agronomy Journal 50, 477–483.

Burton, G.W., 1952. Quantitative Inheritance of Grasses. Proceeding. 6th International Grassland Congress 1, 277–-283.

Burton, G. W., Devane., 1953. Estimation of Heritability in Tall Fescue Festula arundnacea from replicated clonal material. Agronomy Journal 45, 478–481.

Choudhary, B.R., Fageria, M.S., Dhaka, R.S., 2004. Correlation and path coefficient analysis in musk melon (Cucumis melo L.). Indian Journal of Horticulture 61(2), 158–162.

Choudhary, B.R., Kumar, S., Sharma, S.K., 2012. Genetic variability and inter-trait association in muskmelon (Cucumis melo L.) under arid conditions. International Conference on Sustainable Agriculture for Food and Livelihood Security, 473–474.

Choudhary, B.R., Pandey, S., Singh, P.K., 2012. Morphological diversity analysis among watermelon (Citrullus lanatus (Thunb) Mansf.). Progressive Horticulture 44(2), 321–326.

Cohen, Y., Meron, I., Zurial, S., 2003. A new pathotype of pseudoperenospora cubensis causing downey mildew in cucurbits in Israel. PhytoParasitica 31, 452–466.

Dewey, D.R., Lu, K.H., 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal 51, 515–518.

Dhillon, N.P.S., Ranjana, R., Singh, K., Eduardo, I., Monforte, A. J., Pitrat, M., Dhillon, N.K., Singh, P.P., 2007. Diversity among landraces of Indian snap melon (Cucumis melo L.var. momordica). Genetic Resources and Crop Evolution 54, 1267–1283

Dhillon, N.P.S., Singh, J., Fergany, M., Monforte, A.J., Sureja, A.K., 2009. Phenotypic and molecular diversity among landraces of snap melon (Cucumis meloL. var. momordica) adapted to the hot and humid tropics of Eastern India. Plant Genetic Resource 7, 291–300.

Ene, C.O., Ogbonna, P.E., Agbo, C.U., Chukwudi, U.P., 2016. Studies of phenotypic and genotypic variation in sixteen cucumber genotypes. Chilean Journal of Agriculture Research 76(3), 307–313.

Goyal, M., Sharma, S.K., 2009. Traditional Wisdom and value addition prospects of arid foods of desert of North-West India. Indian Journal of Traditional Knowledge 8, 581–585.

Hazra, P., Chattopadhyay, A., Karmakar, K., Dutta, S., 2011. Modern Technology in Vegetables Production, New India Publishing Agency, Pitam Putra, New Delhi, 413.

Ibrahim, E.A., Ramadan, A.Y., 2013. Correlation and Path coefficient analysis in sweet melon (*Cucumis melo* L. var. Aegyptiacus) under irrigated and drought conditions. Pakistan Journal of Biological Science 16(13), 610–616.

Johnson, H.W., Robison, H.F., Comstock, R.E., 1955. Estimates of genetic and environmental variability in soyabean. Agronomy Journal 47, 314–318.

Joseph, P.T., 2012. Performance analysis of snap melon (cucumis melo var. momordica duth. & full.).Msc (Agri.) thesis, college of horticulture Vellanikkara, Kerala, 1–132.

Koli, S.P., Murthy, H.K., 2013. Estimation of phenotypic divergence in a collection of Cucumis melo from Kerala state, Southern India. Agricultural Sciences, 4(7A).

Kumar, R., Ameta, K.D., Dubey, R.B., Pareek, S., 2013. Genetic variability, correlation and path analysis in sponge gourd. African Journal of Biotechnology 12(6), 539–543.

Malik, A.A., 2012. Analysis of genetic diversity of Indian melon (Cucumis melo L.) land races and its comparison with global reference melon populations. Ph.D(Vegetable crops) thesis, Punjab Agricultural University, Ludhiana, 5–158.

Muddarsu, V., 2013. Study on genetic variability on snap melon(Cucumismelo L.var momordica) through physio-chemical traits and seed protein profiling. M.sc(Agri) thesis. College of Horticulture and Forestry Central Agriculture University, Phasigha.

Nagri, P.K., Raut, V.U., Wagh, A.P., Chandan, P.M., Dod, V.N., 2009. Variability, correlation and path analysis studies in musk melon (abstract). International Conference on Horticulture. 9–12.

Pandey, S., Kashya, S.K., Aastik, J., Choudhary, B.R., Sanjeev, K., Singh, D.K., Mathura, R., 2009. Inter-trait association and genetic variability assessment in snap melon (Cucumis melo L. var. momordica). Indian Journal of Plant Genetic Resources, 22(2), 113–116.

Pandey, S., Rai, M., Ram, D., Singh, B., Chaubey, P.K., 2003. Component analysis in snap melon (*Cucumis melo* L. var. *momordica*). Journal of Vegetable Science 30(1), 64–67.

Panse, V.G., Sukhatne, P.V., 1967. Statistical methods for agricultural workers, 2nd Edition ICAR New Delhi, 361.

Pareek, O.P., Samadia, O.K., 2002. For arid Zone farmers-Promising indigenous cucurbit varieties. Indian Journal of Horticulture 47(2), 15-8.

Peter, K.V., Hazra, 2012. Handbook of Vegetables. Thomson Press Limited, New Delhi,. 359.

Reddy, A.N.K., Munshi, A.D., Behera, T.K., Sureja, A.K., 2007. Correlation and path analysis for yield and biochemical characters in snap melon (*Cucumis melo* L. var. *momordica*). Subrao Journal of Genetics and Breeding 39(1), 65–72.

Samadia, D.K., More, T.A., Khan, H., Choudhary, M.L., 2009. Breeding musk melon for high temperature conditions of arid region. Abstract, International Conference on Horticulture, 58.

Seshadri, V.S., More, T.A., 2002. Indian Land Races in (*Cucumis melo* L.). Acta Horti, 651, 172–174.

Seshadri, V. S., More, T. A., 2009. Cucurbit Vegetables- Botany, Production and Utilization, Stadium Press Private

Limited, New Delhi, 482.

Somkuwar, R.G., More, T.A., Mehra, R.B., 1997. Correlation and path coefficient analysis in musk melon. Indian Journal of Horticulture Science 54(4), 312–316.

Tomar, R.S., Kulkarni, G.U., Kakade, D.K., 2008. Genetic analysis in musk melon (*Cucumis melo* L.). Journal of Horticulture Science 3(2), 112–118.

Whitaker, T.W., Davis, G.N., 2008. Cucurbits: Botany, Cultivation and Utilization, Ajay Book Service, New Delhi, 249.

Yi, S.S., Akashi, Y., Tanaka, K., Cho, T.T., Khaing, M.T., Yoshino, H., Nishida, H., Yamamoto, T., Kato, K., 2009. Molecular analysis of genetic diversity in melon landraces (*Cucumis melo* L.) from Myanmar and their relationship with melon germplasm from East and South Asia. Genetic Resources of Crop Evolution 56, 1149–1161.