

Research article

Deciphering The Traits Association And Path Coefficient Analysis Among Yield Attributing Traits Of Snap Melon (*Cucumis melo* var. *momordica*) Genotypes

ABSTRACT

An investigation was carried out at the University of Horticultural Sciences, Bagalkot, Karnataka, during the Rabi season of 2021. The experiment employed a randomized complete block design with two replications and aimed to assess twenty-five snap melon genotypes alongside three check varieties, sourced from various regions in India. Seventeen yield-related traits were observed for each genotype, and the mean data was utilized for subsequent analysis. The study on trait associations revealed that genotypic correlations exhibited higher values compared to their respective phenotypic counterparts, indicating stronger, consistent correlations independent of environmental factors. Notably, yieldplant⁻¹ exhibited positive and significant correlations with vine length, number of fruits vine⁻¹, fruit weight, length of fruit, fruit circumference, and flesh thickness at both genotypic and phenotypic levels. Path coefficient analysis unveiled that the total number of fruits plant⁻¹ and average fruit weight exerted positive direct effects on yieldplant⁻¹. Consequently, the study suggests that selection based on traits such as number of fruits⁻¹ plant and average fruit weight would be effective for enhancing yield in snap melon.

Key words: *Cucumis melo*, Correlation coefficient, Path analysis and Snap melon

1. INTRODUCTION

Snapmelon (*Cucumis melo* var. *momordica*) is a summer season crop of the family Cucurbitaceae and originated in India, it is popularly known as 'phoot or phut' which means to crack as the fruit tends to split either from the middle or longitudinally. Some other synonym is phootkakar[1]. Snapmelon is a grown mainly in tropical and sub-tropical regions of the world and also grown to limited parts of the temperate regions, which have relatively long summer. In India, it is widely cultivated in the states of Gujarat, Rajasthan, Haryana, Punjab, West Bengal, Uttar Pradesh and few areas of North Eastern states [2]. It is a monoecious crop and fruit colour ranges from creamish yellow to orange. Snap melon is a multipurpose crop, the immature tender fruits of snapmelon are cooked or pickled and ripened low sugared fruits are eaten as salad. Fruits are rich in quality and its juice is gaining popularity as squash, due to its wide medicinal application. It is used as a good summer drink since it reduces heat from the body. Fruits are perishable and can be stored for 2-4 days at room temperature. However, in cold store at 2-4 °C and 85-90 % RH the fruits can be stored for 2-3 weeks [3].

Knowledge on degree of association between yield and its component traits is very important in selecting suitable plant type, because yield is a complex character is governed by polygenic system. Additionally, it is significantly impacted by changes in the environment. Correlation study examines the inherent relationship between different traits, and helps in the identification of specific traits that can be targeted for enhancing yield. However, using the correlation coefficient to determine the association between characters does not give a precise indication of the relative importance of direct and indirect influences on yield. To address this issue, path coefficient analysis technique was developed [4]. This approach effectively breaks down the correlation coefficient into measures of direct and indirect effects on yield. By doing so, it allows for a more detailed examination of specific traits that contribute to a given correlation. Snap melon is an unexploited from breeding point of view. Hence, the study was conducted to assess the nature and magnitude of association among yield and its related traits in order to identify high-yielding snapmelon genotypes.

2. MATERIALS AND METHODS

2.1 Experimental materials and procedure

The investigation took place in the vegetable science experimental block at the UHS, Bagalkot, Karnataka, during the rabi season of 2020-21. Bagalkot district is located in the northern part of Karnataka, has black soil, it retains moisture and rich in minerals. The geographical location lies at 16°12'N, 75°45'E the average elevation above mean sea level of this area reaches approximately 610 m. Climate is warm and dry throughout the year. Different snapmelon genotypes were collected from diverse locations of India and evaluated for their performance. The best performed twenty-five genotypes (Table 1), alongside three check varieties were selected for the genotype assessment. The experimental design employed was a RCBD with two replications. Seedlings were initially cultivated in plug trays and subsequently transplanted to the primary field with a spacing of 2m × 1m after a 14-day period. Appropriate cultural practices were implemented to ensure the robust growth and establishment of the crop. Observations were meticulously recorded for seventeen traits, at different vegetative and fruiting stage of the crop.

Table 1: Details of genotypes of snap melons used in the study.

Sl. No.	Lines	Source
1	L ₁ (HUB - 1)	Lakhamapura, Badami taluk, Bagalkote district.
2	L ₂ (HUB - 2)	Sattari, Goa.
3	L ₃ (HUB - 3)	S. D. Patak, Ramdurg Belgaum district
4	L ₄ (HUB - 4)	Salcete, Goa.
5	L ₅ (HUB - 5)	Dapoli, Maharashtra.
6	L ₆ (HUB - 6)	Hireshellikeri, Bagalkote.
7	L ₇ (HUB - 8)	Dodamarg, Maharashtra.
8	L ₈ (HUB - 9)	Santhosh awti, SathihalaBasavanaBagevadi.
9	L ₉ (HUB - 10)	Katageri, Badami taluk
10	L ₁₀ (HUB - 11)	Kundargi, Bagalkote.
11	L ₁₁ (HUB - 14)	Rampur, Bagalkote.
12	L ₁₂ (HUB - 15)	Haveli, Bagalkote.

13	L ₁₃ (HUB - 16)	Kallapur, Nargunda
14	L ₁₄ (HUB - 18)	Bailhongal, Belgaum
15	L ₁₅ (HUB - 19)	Cancona, Goa.
16	L ₁₆ (HUB - 20)	Murnal, Bagalkote.
17	L ₁₇ (HUB - 21)	Mankani, Bagalkote.
18	L ₁₈ (HUB - 22)	Gokak, Belgaum
19	L ₁₉ (HUB - 24)	Mudhol, Bagalkote.
20	L ₂₀ (HUB - 25)	Mannur, Sindagi.
21	L ₂₁ (HUB - 31)	Belgaum
22	L ₂₂ (HUB - 35)	Gadag
23	L ₂₃ (HUB - 42)	Ramdurga
24	L ₂₄ (HUB - 46)	Haveli, Bagalkote.
25	L ₂₅ (HUB - 49)	Bagalkote.
26	L ₂₆ (AHS - 10)	CIAH, Bikaner.
27	L ₂₇ (AHS - 82)	CIAH, Bikaner.
28	L ₂₈ (Pusa Shandar))	IARI New Delhi

2.2 Traits association and path coefficient analysis

The correlation study was computed using the method described by Al-Jibourieet *al.*, [5] which involves analysing variance and covariance matrices. This allows for the partitioning of total variability into replications, genotypes and errors. By utilizing genotypic and phenotypic correlation coefficients, we were able to determine their direct and indirect contributions on vine yield per unit. The direct and indirect effects were then derived following the methodology proposed by Dewey and Lu [6].

3. RESULT AND DISCUSSION

3.1 Correlation analysis

Correlations study helps in determining the real components of yield, which is a complex character. Selection for yield on the basis of phenotypic performance is usually not very efficient, hence it can be done on the basis of its component characters. Associations between various agronomical traits with yield and among each other is of major interest to the plant breeder from a practical view point, since selection involved two or more characters. Yield is a complex character contributed by many commonly related components. Hence information on the nature and magnitude of the relationship of individual yield component to the final yield and interrelationships among themselves would play a fundamental role for the identification of characters, which would influence the economic traits [7].

The present correlation study showed that the genotypic correlations had higher values compared to their respective phenotypic correlation coefficients in most cases (Table 2). This indicates the less influence of the environment on the expression of the trait[8]. Yield plant⁻¹ was found to be positively and significantly associated with average fruit weight ($r_g = 0.779$, $r_p = 0.522$), fruit circumference ($r_g = 0.735$, $r_p = 0.345$), fruit length ($r_g = 0.584$, $r_p = 0.327$), flesh thickness ($r_g =$

0.579, $r_p=0.412$), number of fruits vine⁻¹ ($r_g = 0.475$, $r_p = 0.289$) and vine length ($r_g = 0.365$, $r_p = 0.274$) at both genotypic and phenotypic levels (Table 2). These results showed the importance of above traits in determining the fruit yield, since they had certain inherent relationship with yield. Similar findings were reported in oriental prickling melon [9]; bitter gourd [10]; snapmelon [11]; muskmelon [12] and in cucumber [13]. Node of first male flower appearance ($r_g=-0.102$, $r_p=-0.061$), node of first female flower appearance ($r_g=-0.038$), days to first male flower ($r_g=-0.064$, $r_p=-0.118$), days to first female flower ($r_g=-0.019$, $r_p=-0.006$), number of female flowers vine⁻¹ ($r_g=-0.127$, $r_p=-0.028$) and days to first harvest ($r_g=-0.401$, $r_p=-0.233$) were recorded negative correlation with yield⁻¹ vine (Table 2), these results were similar to the findings of [14] and [15] in cucumber and [11] in oriental pickling melon. In the present study number of fruits⁻¹ vine was negatively correlated with average fruit weight ($r_g=-0.26$, $r_p=-0.142$) (Table 2) alike result has also been reported earlier in musk melon [16]. The trait average fruit weight was positively significantly correlated with circumference of the fruit ($r_g=0.812$, $r_p=0.636$), fruit length ($r_g=0.782$, $r_p=0.722$) and fruit flesh thickness ($r_g=0.773$, $r_p=0.691$) and in turn fruit weight has direct effect on overall yield ($r_g = 0.779$, $r_p = 0.522$) (Table 2). Hence, in order to select genotypes having higher fruit yield one should consider parameters having higher vine length, number of fruits vine⁻¹, average fruit weight, fruit length, fruit circumference and fruit flesh thickness.

Table 2. Genotypic (G) and phenotypic (P) correlation coefficient among yield and its component traits in snap melon.

		VL	IL	NB/V	NFMF	NFFF	DFMF	DFFF	NMF	NFF	DFFS	DFH	NF/V	AFW	FL	FT	FC	FY/V
VL	G	1.000	0.144	0.387**	-0.155	-0.097	-0.356**	-0.513**	-0.159	0.030	-0.447**	-0.050	0.550**	0.045	-0.195	0.088	0.215	0.365**
	P	1.000	0.121	0.310*	-0.105	-0.106	-0.254**	-0.370**	-0.135	0.012	-0.317*	-0.034	0.441**	0.065	-0.146	0.102	0.126	0.274*
IL	G		1.000	-0.045	0.312*	0.359**	0.514**	0.11	0.034	-0.371**	0.173	0.011	-0.07	0.242	0.435**	0.223	0.242	0.186
	P		1.000	-0.069	0.149	0.289*	0.263**	0.062	-0.004	-0.194*	0.099	-0.038	-0.048	0.158	0.205*	0.197*	0.138	0.226*
NB/V	G			1.000	-0.037	-0.054	0.057	-0.358**	-0.247	-0.259	-0.266*	0.081	0.309*	-0.005	0.099	0.015	0.291*	0.088
	P			1.000	0.001	0.029	0.037	-0.193*	-0.01	-0.117	-0.119	0.003	0.161	-0.046	0.041	0.02	0.193*	0.11
NFMF	G				1.000	0.527**	0.753**	0.458**	0.415**	-0.320*	0.321*	0.139	-0.144	-0.018	-0.09	0.283*	-0.052	-0.102
	P				1.000	0.401**	0.622**	0.335*	0.298*	-0.229*	0.266*	0.197*	-0.107	-0.006	-0.045	0.230*	-0.043	-0.061
NFFF	G					1.000	0.414**	0.602**	0.377**	0.053	0.686**	0.455**	-0.375**	0.261	0.271*	0.494**	0.368**	-0.038
	P					1.000	0.254**	0.429**	0.262**	0.158	0.446**	0.282*	-0.273*	0.114	0.078	0.381**	0.129	0.031
DFMF	G						1.000	0.536**	0.281*	-0.370**	0.461**	0.008	-0.437**	0.144	0.186	0.161	0.127	-0.064
	P						1.000	0.334*	0.246**	-0.249**	0.289*	0.058	-0.336*	0.138	0.235*	0.162	0.106	-0.118
DFFF	G							1.000	0.548**	0.246	0.985**	0.283*	-0.585**	0.393**	0.276*	0.334*	0.276*	-0.019
	P							1.000	0.344**	0.162	0.725**	0.146	-0.350**	0.268*	0.171	0.273*	0.151	-0.006
NMF	G								1.000	0.168	0.651**	-0.189	-0.079	0.204	0.028	0.192	0.17	0.063
	P								1.000	0.092	0.363**	-0.036	-0.043	0.07	0.06	0.042	0.077	0.129
NFF	G									1.000	0.168	0.128	-0.039	-0.007	-0.083	-0.035	-0.207	-0.127
	P									1.000	0.11	0.024	-0.095	-0.053	-0.135	-0.01	-0.055	-0.028

DFFS	G	1.000	0.225	-0.493**	0.396**	0.268*	0.289*	0.295*	0.043
	P	1.000	0.074	-0.314*	0.349**	0.198*	0.239*	0.214*	0.016
DFH	G		1.000	0.02	-0.528**	-0.278*	-0.188	-0.216	-0.401**
	P		1.000	-0.021	-0.333*	-0.197*	-0.16	-0.079	-0.233*
NF/V	G			1.000	-0.26	-0.381**	-0.211	-0.277*	0.475**
	P			1.000	-0.142	-0.235*	-0.168	-0.154	0.289*
AFW	G				1.000	0.782**	0.773**	0.812**	0.779**
	P				1.000	0.722**	0.691**	0.636**	0.522**
FL	G					1.000	0.631**	0.841**	0.584**
	P					1.000	0.538**	0.546**	0.327*
FT	G						1.000	0.672**	0.579**
	P						1.000	0.506**	0.412**
FC	G							1.000	0.735**
	P							1.000	0.345**
FY/V	G								1.000
	P								1.000

*and ** indicate significant at 5 and 1 per cent probability

VL=Vine length (cm)

NFFF = Node of 1st female flower

NFF = No. of female flower

AFW = Averg. fruit weight (g)

FY/V = Fruit yield vine⁻¹ (kg)

IL=Internodal length (cm)

DFMF = Days to 1st male flower

DFFS = Days to first fruit set

FL = Fruit length (cm)

NOB/V=No. of branches vine⁻¹

DFFF = Days to 1st female flower

DFH = Days to first fruit harvest

FT = Flesh thickness (mm)

NFMF = Node of 1st male flower

NMF = No. of male flower

NF/V = No. of fruits vine⁻¹

FC = Fruit circumference (cm)

2.2 Path coefficient analysis

The fruit yield being a complex trait, depends on several other yield related traits. While some of these traits directly contribute to the yield and others were indirectly influence the yield by affecting the behaviour and growth of other components. Hence, it is important to understand how yield is influenced by other related traits. Correlation studies reveal the positive and negative associations between different characters and their interrelationships. However, it does not provide information about the extent and nature of the contribution of the related traits to yield. Path coefficient analysis, on the other hand, offers a more comprehensive understanding of the relationships between different traits. It considers both the direct and indirect effects of various yield components. By determining the interrelationships between yield and its components, plant breeders can easily identify the traits that have the greatest impact on yield.

In the present study genotypic path analysis revealed that number of fruits⁻¹ plant (1.535) exhibited the highest positive direct effect on fruit yield followed by average fruit weight (1.269) and fruit circumference (0.9741) (Table 3, Figure 1). Fruits plant⁻¹ and average fruit weight were also showed positive and significant correlation with yield plant⁻¹ (Table 2). This suggest that direct selection based on fruitsplant⁻¹ and average fruit weight could significantly enhance the yield plant⁻¹. The results are accordance with the report of cucumber [17, 18, 19, 13] and snapmelon [11]. Fruit circumference (0.9741), days to first harvest (0.6632), node to first female flower appearance (0.3591), days to first female flower appearance (0.2230), number of male flowers (0.1867) and number of female flowers (0.0036) were also exhibited positive direct effect on fruit yield. However, days to first fruit set (-1.249), number of branches vine⁻¹ (-0.991), node to first male flower appearance (-0.8574), internodal length (-0.6588), flesh thickness (-0.2534), vine length (-0.2208) and fruit length (-0.1398) had negative direct effect on yield. Similar report was also observed in snap melon [20].

Table 3. Genotypic path coefficient analysis for sixteen yield components on fruit yield vine⁻¹ in snap melon.

	VL	IL	NOB/V	NFMF	NFFF	DFMF	DFFF	NMF	NFF	DFFS	DFH	NF/V	AFW	FL	FT	FC	rG
VL	-0.2208	-0.0318	-0.0855	0.0343	0.0215	0.0786	0.1132	0.0351	-0.0068	0.0988	0.0111	-0.1214	-0.0099	0.0432	-0.0194	-0.0475	0.365**
IL	-0.0949	-0.6588	0.0299	-0.2055	-0.2366	-0.3388	-0.0727	-0.0222	0.2442	-0.1139	-0.0071	0.0458	-0.1595	-0.2863	-0.1467	-0.1591	0.186
NOB/V	-0.3840	0.0450	-0.9914	0.0366	0.0539	-0.0568	0.3546	0.2447	0.2576	0.2638	-0.0798	-0.3068	0.0049	-0.0978	-0.0145	-0.2880	0.088
NFMF	0.1330	-0.2674	0.0317	-0.8574	-0.4517	-0.6458	-0.3927	-0.3562	0.2742	-0.2754	-0.1188	0.1233	0.0157	0.0772	-0.2425	0.0449	-0.102
NFFF	-0.0349	0.1289	-0.0195	0.1892	0.3591	0.1486	0.2161	0.1352	0.0193	0.2464	0.1632	-0.1346	0.0935	0.0973	0.1773	0.1321	-0.038
DFMF	-0.5823	0.8415	0.0938	1.2326	0.6773	0.6364	0.8764	0.4594	-0.6057	0.7547	0.0130	-0.7155	0.2362	0.3039	0.2640	0.2075	-0.064
DFFF	-0.0627	0.0135	-0.0437	0.0560	0.0736	0.0655	0.1223	0.0670	0.0302	0.1246	0.0345	-0.0716	0.0481	0.0337	0.0409	0.0338	-0.019
NMF	-0.0297	0.0063	-0.0461	0.0776	0.0703	0.0524	0.1023	0.1867	0.0315	0.1215	-0.0353	-0.0147	0.0381	0.0051	0.0358	0.0317	0.063
NFF	0.0001	-0.0013	-0.0009	-0.0012	0.0002	-0.0013	0.0009	0.0006	0.0036	0.0006	0.0005	-0.0001	0	-0.0003	-0.0001	-0.0007	-0.127
DFFS	0.5592	-0.2160	0.3326	-0.4014	-0.8575	-0.5765	-1.2735	-0.8132	-0.2099	-1.2499	-0.2808	0.6155	-0.4944	-0.3346	-0.3613	-0.3684	0.043
DFH	-0.0333	0.0071	0.0534	0.0919	0.3014	0.0053	0.1874	-0.1253	0.0847	0.1490	0.6632	0.0130	-0.350	-0.1843	-0.1244	-0.1435	-0.401**
NF/V	0.8438	-0.1067	0.4750	-0.2208	-0.5753	-0.6712	-0.8982	-0.1209	-0.0601	-0.7560	0.030	1.5350	-0.3989	-0.5852	-0.3235	-0.4249	0.475**
AFW	0.0571	0.3073	-0.0063	-0.0232	0.3306	0.1832	0.4993	0.2588	-0.0084	0.5022	-0.670	-0.3299	1.2695	0.9928	0.9806	1.0312	0.779**
FL	0.0274	-0.0607	-0.0138	0.0126	-0.0379	-0.0260	-0.0385	-0.0038	0.0116	-0.0374	0.0388	0.0533	-0.1093	-0.1398	-0.0882	-0.1176	0.584**
FT	-0.0223	-0.0564	-0.0037	-0.0717	-0.1251	-0.0409	-0.0847	-0.0486	0.0087	-0.0733	0.0475	0.0534	-0.1958	-0.1599	-0.2534	-0.1703	0.579**
FC	0.2095	0.2353	0.2830	-0.0511	0.3583	0.1235	0.2693	0.1652	-0.2020	0.2871	-0.2108	-0.2697	0.7912	0.8194	0.6544	0.9741	0.735**
rG	0.365**	0.1860	0.088	-0.102	-0.038	-0.064	-0.019	0.063	-0.127	0.043	-0.401**	0.475**	0.779**	0.584**	0.579**	0.735**	1

Residual effect = 0.200 Bold diagonal figure indicate direct effect

rG = Genotypic correlation coefficient of fruit yield/vine

VL=Vine length (cm)

IL=Internodal length (cm)

NOB/V=No. of branches vine⁻¹ NFMF = Node of 1st male flower

NFFF = Node of 1st female flower

DFMF = Days to 1st male flower

DFFF = Days to 1st female flower NMF = No. of male flower

NFF = No. of female flower

DFFS = Days to first fruit set

DFH = Days to first fruit harvest NF/V = No. of fruits vine⁻¹

AFW = Averg. fruit weight (g)

FL = Fruit length (cm)

FT = Flesh thickness (mm) FC = Fruit circumference (cm)

FY/V = Fruit yield vine⁻¹ (kg)

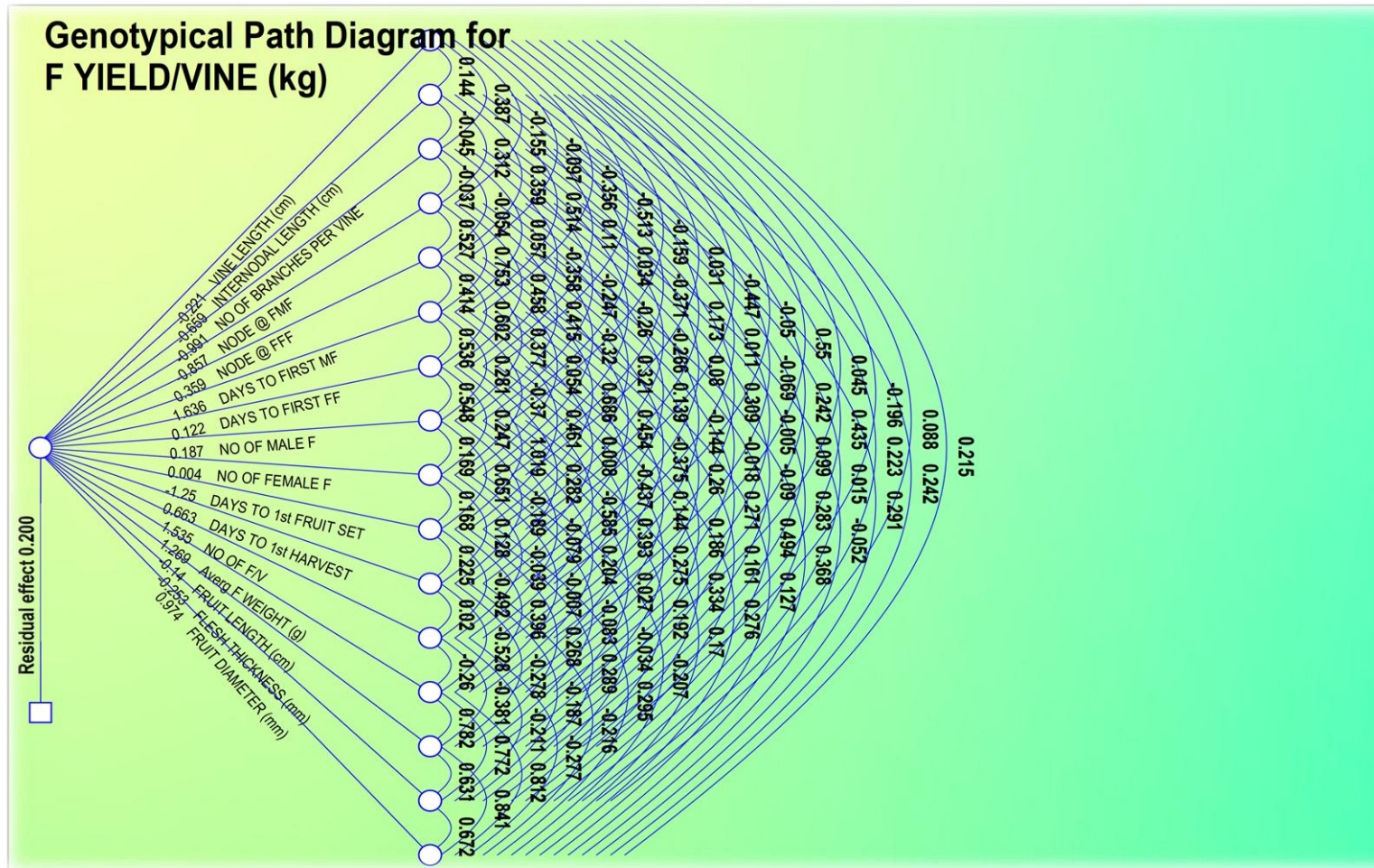


Fig 1. Path coefficient analysis for sixteen yield components on fruit yield per vine in snap melon at genotypic level.

4.CONCLUSION

The findings of the present investigation led to the conclusion that the selection of a high yielding type with good quality is possible amongst the genotypes studied. The traits number of fruits per plant, average fruit weight, and fruit circumference played a significant role in determining the fruit yield of snapmelon because of its direct positive effect and positive correlation with fruit yield.

5.ACKNOWLEDGMENT

The authors are thankful to Collage of Horticulture, Bagalkot for providing necessary facilities to carrying out the present investigation.

References:

1. Dhillon NPS, Ranjana R, Singh K, Eduardo I, Monforte and AJ, Pitrat *et al.* Diversity among landraces of Indian snapmelon (*Cucumis melo* var. *momordica*). *Genet. Resour. Crop Evol.* 2007;54(6):1267-1283.
2. Hazara P, Chattopadhyay A, Karmakar K and Dutta S. *Modern technology in vegetable production*. New India Pub. Agency, New Delhi. 2011; pp. 413
3. Kumar S, Kumar D, Kumar R, Thakur KS and Dogra BS. Estimation of genetic variability and divergence for fruit yield and quality traits in cucumber (*Cucumis sativus* L.) in North-Western Himalayas. *J. Plant Sci.* 2013;1(2):27-36.
4. Wright S. Correlation and causation. *J. Agri. Res.* 1921;20: 557-580.
5. Al-Jibouri HA, Miller PA and Robinson HF. Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin 1. *Agron. J.* 1958;50(10):633-636.
6. Dewey DR and Lu K. A Correlation and path-coefficient analysis of components of crested wheatgrass seed production 1. *Agron. J.* 1959; 51(9):515-518.
7. Nadarajan N, Manivannan N and Gunasekaran M. *Quantitative genetics and biometrical techniques in plant breeding*. Kalyani Publishers. New Delhi. 2005;pp. 258
8. Said EM and Fatiha H. Genotypic variation in fruit characters in some genotypes of watermelon cultivated in Morocco. *Int. J. Agron. Agric. Res.* 2015;6:130-37
9. Babu RR, Rao NH and Reddy RVSK. Correlation and path analysis in oriental pickling melon (*Cucumis melo* L. var. *conomon*) genotypes. *The J. Res. PJTSAU*, 2014;42(3):62-66.
10. Khan MH, Bhuiyan SR, Saha KC, Bhuyin MR and Ali ASMY. Variability, correlation and path coefficient analysis of bitter gourd (*Momordica charantia* L.). *Bangladesh J. Agri. Res.* 2015;40(4): 607-618.
11. Pasha SG, Marker S and Chandra GS. Genetic variability, correlation and path analysis study on Snap melon (*Cucumis melo* L. var. *momordica*) farmer's varieties. *Int. J. Bio-resour. Stress Manag.* 2019;10(6):636-644.
12. Mamatha, R. M.; Allolli, T. B.; Chittapur, R. B.; Gunnaiah, R.; Ganiger, V. M.; Lokesh, M. S. and Gopali, J. B. (2023). Character association study in the botanical groups of *Cucumis melo*. *The Pharma Innov. J.*, **12**(9): 1616-1619
13. Rani, R.; Dogra, B. S.; Singh, S. P.; Kumari, S. and Sharma, P. (2023). Variability and character association studies for yield and yield contributing characters in cucumber (*Cucumis sativus*) under low hills of Himachal Pradesh. *Indian J. Agric. Sci.*, **93**(7): 801-805.
14. Afangideh U and Uyoh EA. Genetic variability and correlation studies in some varieties of cucumber (*Cucumis sativus* L.). *Jordan J. Agril. Sci.* 2007;3(4):376-384.

15. Sharma S, Kumar R, Chatterjee S and Raj H. Correlation and path analysis studies for yield and its attributes in cucumber (*Cucumis sativus* L. *Int. J. Chem. Stud.* 2018;**6**(2):2045-2048.
16. Reddy BPK, Begum H, Sunil N, Reddy MT, Babu JD and Reddy RSK. Correlation and path coefficient analysis in muskmelon (*Cucumis melo* L.). *Suranaree J. Sci. Tech.* 2013;20(2):135-149.
17. Ene CO, Ogonna PE, Agbo CU and Chukwudi UP. Studies of phenotypic and genotypic variation in sixteen cucumber genotypes. *Chilean J. Agril. Res.* 2016;76(3):307-313.
18. Ahirwar CS, Singh DK and Kushwaha ML. Assessment of genetic variation in cucumber (*Cucumis sativus* L.) germplasm on correlation, path analysis and cluster analysis. *Chem. Sci. Rev. Lett.* 2017;6(23):1886-1893.
19. Khedkar, P. D.; Janeja, H. S.; Delvadiya, I. R. and Talekar, N. (2022). Interrelationship among elite germplasm of cucumber (*Cucumis sativus* L.) at genotypic and phenotypic level. *Eco. Env. and Cons.* 29 (January Suppl. Issue): 2023; pp. (S511-S516).
20. Muddarasu, V. R.; Dubey, R. K. R.; Vikas, S.; Garima, U.; Barun, S.; Pandey, A. K. and Singh, J. P. (2015). Variability, interrelationship and path analysis for yield improvement in snapmelon (*Cucumis melo* L. var *momordica*). *Int. J. Basic App. Agril. Res.*, **13**: 300-308.