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# Genetic variability, correlation and path analysis for yield and its attributes in sweet corn (*Zea mays* L. Var. *saccharata*)

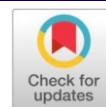
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## ABSTRACT

Assessment of genetic variability is very essential for breeding programs aimed at the improvement of a desirable trait. The present investigation was carried out with 14 inbreds along with 04 checks evaluated in RBD design with three replications during Kharif 2024. Due to few composites and hybrids the sweet corn cultivation is limited to small areas in India which necessitated the importance of developing sweet corn hybrids to meet the market demands with consumer preferences. Analysis of variance among sweet corn genotypes revealed that all yield and yield-related traits were significant. Higher mean value in the desirable direction for most of the traits under consideration was depicted by Misthi & CMVL Sweet Corn 1 checks and genotypes viz., SSCML 7, SSCML 8 & SSCML 9. Higher estimates of GCV, PCV, heritability, and genetic advance were observed for the traits viz., weight of green cob with husk, weight of green cob without husk and sweet corn length indicating the role of additive gene action. Priority should be given to these traits in formulating selection strategies on the basis of these characters to realize better gains by selection. Association study reveals that Plant height, weight of green cob with husk, sweet corn length and sweet corn girth exhibited significant correlation in desirable direction with weight of green cob without husk. Days to fifty per-cent tasseling and silking depicted a negative significant association with green cob weight without husk indicating that the selection of an early flowering trait with less ASI among genotypes will show a positive impact on green cob weight. These attributes could be considered for the selection of high-yielding sweet corn genotypes in formulating a breeding program.

**Keywords:** Additive gene action, Correlation, Genetic advance, Genetic variability, Heritability, Path analysis, Sweet Corn

## Introduction

Sweet corn (*Zea mays* L. var. *saccharata*) also called as sugar corn, is one of the most valuable grain crops planted worldwide across various environments. Sweet corn contains nutrients such as starch, sugar, water-soluble polysaccharides, proteins, vitamins, zeaxanthin, lutein and carotenoids [1]. There is limited genetic diversity in hybrid sweet corn along with several undesirable traits, like low germination, poor seedling vigour and highly susceptible to pests and diseases [2]. The performance of sweet corn hybrid is influenced strongly by genotype as well as environmental factors [3]. The recessive mutation at the sugary locus tends to accumulate 2-4 times more sugar (i.e. about 12 to 14%) in the endosperm which is highly water-soluble, making sweet corn different from normal corn [4]. Therefore, it is very essential to evaluate the genetic variation of the traits associated with yield.

Sweet corn is categorised into five groups on the basis of gene mutation in the endosperm. The first category includes allelic mutations at a sugary locus (*su1*) which is in normal sweet corn. It produces a high amount of sugar with a very high starch conversion rate after harvest if not provided with a cold storage

facility (Singh, 2014). In the second category i.e. sweet corn cultivars with a mutation in the *shrunken2* (*sh2*) gene there is high sugar accumulation with a low starch conversion rate which was observed in super sweet corn cultivars and was suitable for long-distance transports and the development of extra sweet corn cultivars. The third category comprises of sweet corn cultivars with a mutation at *se* locus in *su1* genetic background which made sweet corn more sugar-enhanced corns, tender with extended shelf life and high sugar levels than field corn. The fourth category includes a combination of mutations viz., *su1*, *sh2*, and *se* which led to the development of synergistic corn with balanced sugars and tenderness [5]. The fifth category comprises of augmented *shrunken* sweet corn, a new generation of *shrunken* sweet corn which is *shrunken* like super sweet corn and tender, juicy like sugar enhanced (*se*) types. Apart from tenderness and sweetness, sweet corn cultivation gained importance among Indian farmers for green fodder and green ear yield. However, to date only a few composites and hybrids were developed by the public and private sectors respectively [6] which has confined sweet corn cultivation to small areas in India by both farmers and private sectors to meet the rising market demand. This scenario necessitated the importance of developing sweet corn hybrids to meet the market demands with consumer preferences.

The amount of variation in the genetic makeup of plants within a population or between populations is known as genetic variability which is influenced by several factors like mutation, gene flow, crossing over and polyploidy.

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Breeding strategies for the improvement of any trait depends upon the understanding of the genetic variability of a population [7].

Sweet corn yield is influenced by several yield-contributing quantitative traits. Therefore, association studies among these traits are important to select elite genotypes in the breeding program. Correlation describes the degree of relationship between two variables and facilitates in indirect selection of traits. It measures the relationship between two variables, with correlation coefficients ranging from -1 to +1, where 0 indicates no correlation [8, 9]. Assessing correlations among traits is useful in designing and evaluating plant breeding programs, as a positive correlation between two traits implies that increasing one will likely improve the other. When more variables are involved, the correlation co-efficient alone does not provide a clear picture of the since correlation is affected by a third [10].

Therefore, Path analysis becomes the most valuable statistical technique to establish the true relationship between variables in terms of cause and effect. Partitioning of correlation co-efficient into direct effect and series of indirect effects on dependent character is called path analysis which assesses the cause-effect relationship for an effective indirect selection. It is widely used in plant breeding to determine the relative importance of each parameter and to differentiate between direct and indirect effects on outcomes [11, 12]. Thus, association studies help in establishing the degree and direction of a relationship between variables which is important for formulating breeding procedures. Also, the knowledge of the association between yield and its related traits improves the efficiency of indirect selection. Thus, the present investigation was taken up to determine the relationship between yield and its related traits using correlation and path analysis for the selection of potential inbred lines of sweet corn.

### Materials and Methods

The experiment was conducted at the college farm, BAC Sabour during Kharif 2024 in RBD with three replications. A total of 14 inbreds along with 04 checks were evaluated for 09 quantitative traits viz., days to fifty percent tasseling, days to fifty percent silking, plant height, ear height, weight of green cob with husk, wt. of green cob without husk, sweet corn length, sweet corn girth and TSS. Data was recorded from five plants per row. A recommended package of practices was adopted to raise healthy crops.

### Result and Discussions

From the analysis of variance of sweet corn genotypes, all yield and yield-related traits were significant among the genotypes. From the mean table (table 1) it can be depicted that the days to fifty percent tasseling ranged from 52.67 to 60.67 with the mean value of 56.00. Mishti was the best check for days to fifty percent tasseling (55.33) while, the genotypes SSCML 8 (52.67), SSCML 2 (53.00) and SSCML 7 (53.33) flowered early. Days to fifty percent silking ranged from 56.33 to 64.00 with an average value of 60.04. Mishti was the best check for days to fifty percent silking (59.67), while in genotypes SSCML 8 (56.63), SSCML 2 (57.00) and SSCML 7 (57.00), there was early silk emergence as compared to the other genotypes under study. Plant height ranged from 108.83 cm to 154.33 cm having mean of 128.57. Mishti was the best check depicting plant height of 154.33 cm while among inbreds SSCML 8 (127.67) & SSCML 11 (126.67) depicted higher plant height. Ear height ranged from 42.00 to 83.00 (average 58.43).

The genotypes SSCML 10 (57.67) & SSCML 9 (55.00) depicted more ear height while the best check was ASKH 4 (63.00). The range of weight of green cob with husk (Kg) was from 18.92 to 9.17 with mean value of 12.82. Mishti (18.92) was the best check while, the genotypes SSCML 7 (14.75) and SSCML 8 (14.43) depicted higher mean value for weight of green cob with husk. A Similar trend was noted for the eight of green cob without husk (Kg). It ranged from 14.15 to 4.13 with an average of 7.09 Kg. Mishti (14.15) was the best check while the best genotypes were SSCML 7 (7.81) and SSCML 8 (7.55). Sweet corn length ranged from 19.02 to 9.06 having mean value of 12.13 cm. CMVL Sweet corn was the best check depicting the maximum cob length of 19.02 cm while the genotypes SSCML 5 (12.61), SSCML 8 (12.55) and SSCML (12.44) depicted more cob length than other genotypes included in the study. Sweet corn girth ranged from 4.52 to 2.73 with an average value of 3.56. Mishti (4.52) was the best check while, SSCML 11 (3.96) and SSCML 7 (3.68) were the best genotypes depicting higher cob girth. The total soluble solids (TSS) value ranged from 19.22 to 15.35 along with a mean value of 17.94. CMVL Sweet corn 1 (18.50) was the best check for TSS while the genotypes SSCML 3 (19.22) and SSCML 10 (19.00) depicted higher TSS. For most of the traits under consideration, Mishti & CMVL Sweet Corn 1 was the best check, while genotypes viz., SSCML 7, SSCML 8 & SSCML 9 performed well for most of the traits under consideration [13, 14, 15].

GCV and PCV (table 2) estimates were higher for the weight of green cob with husk, weight of green cob without husk and sweet corn length while, it was medium for traits viz., days to fifty percent tasseling, days to fifty percent silking, plant height, Ear height and sweet corn girth and low for total soluble solids. Heritability was higher for all the traits under consideration. The genetic advance was higher for plant height, ear height, weight of green cob with husk, weight of green cob without husk, sweet corn length and sweet corn girth. It was medium for traits days to fifty percent tasseling and days to fifty percent silking while, low for total soluble solids. The high, medium and low PCV and GCV values indicate the potentiality with which the characters express. However, GCV is considered to be more useful than PCV for assessing variability since it depends on the heritable portion of variability. Low to moderate GCV and PCV values indicated the influence of the environment on these traits and limited scope for improvement by selection. Heritability estimates are the true indicators of genetic potentiality of the genotypes which can be used as a tool for selection. However, heritability estimates when considered in conjunction with the predicted genetic gain form a reliable tool for selection. They indicate the expected genetic advance of a character in response to the certain selection pressure imposed on them. These findings clearly indicate that the traits having higher heritability coupled with genetic advance are governed by additive gene action, therefore selection can be directly done on the basis of these traits viz., plant height, ear height, weight of green cob with husk, weight of green cob without husk, sweet corn length and sweet corn girth. Priority should be given to these traits in formulating selection strategies on the basis of these characters to realize better gains by selection [13, 14, 15, 16, 17].

The knowledge of inter-relationships present among various characters is necessary when selection for simultaneous improvement of these traits is applied. If two favourable characters are associated, selection for one character will automatically be good enough for the other. Correlation analysis revealed that days to fifty percent tasseling depicted positive and significant correlation with days to fifty percent silking

(1.00) and ear height (0.40) while, significant and negative correlation was found with weight of green cob without husk (-0.36), sweet corn length (-0.38) and sweet corn girth (-0.41). Days to fifty percent silking depicted a positive and significant correlation with ear height (0.41) while negative and significant association was found with weight of green cob without husk (-0.33), sweet corn length (-0.35) and sweet corn girth (-0.37). Plant height exhibited positive and significant association with weight of green cob with husk (0.53), weight of green cob without husk (0.73), sweet corn length (0.58) and sweet corn girth (0.74). Ear height manifested positive and significant association with weight of green cob with husk (0.30). Weight of green cob with husk depicted positive and significant association with weight of green cob without husk (0.88), sweet corn length (0.74), sweet corn girth (0.73) and total soluble solids (0.27). Weight of green cob without husk exhibited positive and significant association with sweet corn length (0.77) and sweet corn girth (0.97). Sweet corn length manifested positive and significant association with sweet corn girth (0.79) and total soluble solids (0.41). However, based on the present study, it can be said that more emphasis will have to be given for plant height, weight of green cob with husk, sweet corn length and sweet corn girth since these depicted significant correlation in the desirable direction with weight of green cob without husk [7, 15, 16, 17, 18, 19, 20, 21, 22, 23]. Days to fifty percent tasseling and silking depicted a negative significant association with green cob weight without husk indicating that the selection of an early flowering trait with less ASI among genotypes will show positive impact on green cob weight [16]. The non-significant association of TSS with green cob weight without husk indicates the scope of developing hybrids having higher yield along with higher sugar content [16].

Path coefficient analysis provides a more realistic picture of the inter-relationship of various characters with seed yield per plant since, seed yield is the complex character influenced by a number of inter-related component traits. Days to fifty percent tasseling showed negative direct effect on weight of green cob without husk (-0.61) and it was negatively and significantly associated with weight of green cob without husk (-0.36). It exhibited a positive indirect effect *via*, plant height (0.04), weight of green cob with husk (0.11), sweet corn length (0.23) and sweet corn girth (0.25). Days to fifty percent silking showed positive direct effect on weight of green cob without husk (0.51) and was negatively and significantly associated with the weight of green cob without husk (-0.33). It exhibited a positive indirect effect *via*, days to fifty percent tasseling (0.52), ear height (0.21) and total Soluble Solids (0.61). Plant height depicted a positive direct effect on weight of green cob without husk (0.05) and was positively and significantly associated with weight of green cob without husk (0.73). It exhibited a positive indirect effect *via*, ear height (0.03), weight of green cob with husk (0.03), Sweet corn length (0.31), Sweet corn girth (0.04) and total Soluble Solids (0.01). Ear height exhibited positive direct effect on the weight of green cob without husk (0.18) and was non-significantly associated with weight of green cob without husk (0.73). It exhibited a positive indirect effect *via*, days to fifty percent

tasseling (0.07), days to fifty percent silking (0.67), plant height (0.01), weight of green cob with husk (0.05) and total Soluble Solids (0.04).

The weight of green cob with husk had a positive direct (0.36) and significant correlation (0.88) with the weight of green cob without husk. The positive indirect effect was depicted by the traits *viz.*, plant height (0.19), ear height (0.11), sweet corn length (0.26), sweet corn girth (0.26) and total soluble solids (0.98). Sweet corn length exhibited a positive direct effect (0.07) and significant correlation (0.77) with the weight of green cob without husk. It depicted a positive indirect effect *via*, plant height (0.04), weight of green cob with husk (0.05), sweet corn girth (0.57) and total Soluble Solids (0.03). Sweet corn Girth manifested positive direct effect (0.56) and significant correlation (0.79) with weight of green cob without husk. It exhibited positive indirect effect *via*, plant height (0.41), weight of green cob with husk (0.41), sweet corn length (0.44) and total Soluble Solids (0.09). Total soluble solids had a negative direct effect (-0.16) and non-significant correlation. So from the above findings, emphasis on traits *viz.*, plant height, weight of green cob with husk, sweet corn length and sweet corn girth should be given in formulating breeding strategies [22, 24, 25, 26, 27]. The highest positive direct effect was depicted by sweet corn girth indicating the direct selection on the basis of this trait will be effective. Higher negative direct impact was depicted by days to fifty percent tasseling which implies that an increase in days to fifty percent tasseling will have direct impact on cob weight without husk [28, 29]. This clearly indicates that some traits are of prime importance in selection for improvement of green cob yield and needs to be considered in formulating breeding strategies for higher yield.

## Conclusion

The evaluation of genetic variability among fourteen genotypes revealed significant differences in yield and its attributes. The PCV for all the observed traits were higher than GCV indicating the notable influence of the environment on the expression of the trait. Higher heritability coupled with higher genetic advance was exhibited by the traits *viz.*, plant height, ear height, weight of green cob with husk, weight of green cob without husk, sweet corn length and sweet corn girth. Priority should be given to these traits in formulating selection strategies on the basis of these characters to realize better gains by selection. However, based on the correlation and path analysis, it can be said that more emphasis will have to be given for traits such as plant height, weight of green cob with husk, sweet corn length and sweet corn girth since these depicted significant correlation with higher direct effect in desirable direction with weight of green cob without husk. Therefore these traits can be considered for the selection of sweet corn genotype to realize increased green cob yield.

**Conflict of interest:** The authors declare no conflict of interests.

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Table 1: Mean values of 18 sweet corn genotypes for nine quantitative traits during kharif 2024

Name of Genotypes	Days to Fifty percent Tasseling	Days to Fifty percent Silking	Plant Height (cm)	Ear Height (cm)	Wt. of green cob with husk (kg)	Weight of green cob without husk (kg)	Sweet Corn Length (cm)	Sweet Corn Girth(cm)	Total Soluble Solids (%)
SSCML 1	57.33	61.33	116.00	48.50	11.26	5.02	11.43	3.36	18.17
SSCML 2	53.00	57.00	117.00	42.00	10.74	4.93	9.09	3.31	15.35
SSCML 3	54.00	58.00	114.33	49.33	10.10	4.84	12.03	3.62	19.22
SSCML 4	54.33	58.67	108.83	43.83	10.11	4.53	11.75	3.40	17.72
SSCML 5	54.67	59.33	118.00	46.00	14.37	7.84	12.61	3.36	18.73
SSCML 6	59.33	62.67	113.00	48.00	10.19	5.81	11.31	3.57	18.23
SSCML 7	53.33	57.00	120.33	50.33	14.75	7.81	12.47	3.68	18.52
SSCML 8	52.67	56.33	127.67	52.67	14.43	7.55	12.55	3.03	18.67
SSCML 9	56.33	60.67	120.00	55.00	11.92	5.61	12.44	3.57	15.53
SSCML 10	60.67	64.33	112.67	57.67	11.31	4.35	9.85	2.73	19.00
SSCML 11	56.00	60.67	126.67	51.67	13.73	6.85	11.68	3.96	17.55
SSCML 12	59.33	63.00	120.00	45.00	10.35	4.92	9.23	3.26	16.97
SSCML 13	55.00	59.67	120.00	50.00	9.17	4.13	9.06	3.01	18.23
SSCML 14	58.33	62.00	116.00	51.00	10.41	5.71	10.23	3.20	18.23
Mishti (C)	55.33	59.67	154.33	54.33	18.92	14.15	13.92	4.52	17.93
ASKH 1 (C)	56.00	60.33	152.33	57.33	13.75	8.86	13.21	3.72	18.12
ASKH 4 (C)	56.67	60.67	143.00	63.00	18.03	12.42	16.43	4.41	18.18
CMVL Sweet Corn 1(C)	56.00	60.67	152.00	47.00	17.15	12.32	19.02	4.36	18.50
Mean	56.02	60.12	125.12	50.71	12.82	7.09	12.13	3.56	17.94
Maximum	52.67	56.33	108.83	42.00	9.17	4.13	9.06	2.73	15.35
Minimum	60.67	64.33	154.33	63.00	18.92	14.15	19.02	4.52	19.22
SE ±	1.02	0.77	1.07	0.76	0.75	0.90	1.15	0.91	0.81
C.D. 5%	2.96	2.23	3.10	2.24	2.18	2.61	3.19	2.61	2.34
C.V. %	4.08	3.16	3.78	2.87	2.85	3.55	4.39	3.63	3.25

SE: Standard error, C. D. : critical difference, C.V.: Coefficient of variance

Table 2: Genetic Parameters for nine quantitative traits evaluated during kharif 2024

Genetic parameters	Days to Fifty percent Tasseling	Days to Fifty percent Silking	Plant Height (cm)	Ear Height (cm)	Wt. of green cob with husk (kg)	Weight of green cob without husk (kg)	Sweet Corn Length (cm)	Sweet Corn Girth(cm)	Total Soluble Solids (%)
Genetic Coefficient of Variation	11.76	13.25	10.79	17.69	25.05	34.58	21.43	13.90	5.56
Phenotypic Coefficient of Variation	14.54	14.27	11.01	18.35	25.89	34.81	21.75	14.04	6.34
Heritability (%)	68.76	69.01	95.95	92.93	93.66	98.69	97.08	98.02	76.95
Genetic Advance	8.59	10.08	27.89	20.53	7.51	6.39	5.68	1.04	1.80
Genetic Advance as percent of Mean	16.43	15.14	21.77	35.13	49.94	70.75	43.49	28.35	10.05

Table 3: Genotypic correlation coefficient of weight of green cob without husk with other characters in eighteen sweet corn genotypes during kharif 2024

Characters	Days to Fifty percent Tasseling	Days to Fifty percent Silking	Plant Height (cm)	Ear Height (cm)	Wt. of green cob with husk (kg)	Weight of green cob without husk (kg)	Sweet Corn Length (cm)	Sweet Corn Girth(cm)
Days to Fifty percent Silking	1.00**							
Plant Height (cm)	-0.07	-0.01						
Ear Height (cm)	0.40**	0.41*	0.04					
Wt. of green cob with husk (kg)	-0.18	-0.15	0.53**	0.30*				
Weight of green cob without husk (kg)	-0.36**	-0.35*	0.73**	0.18	0.88**			
Sweet Corn Length (cm)	-0.38**	-0.35**	0.58**	-0.08	0.73**	0.77**		
Sweet Corn Girth(cm)	-0.41**	-0.37**	0.74**	-0.04	0.73*	0.94**	0.79**	
Total Soluble Solids (%)	0.07	0.12	0.09	0.24	0.27*	0.12	0.41**	0.16

**Table 4: Genotypic Path coefficient of weight of green cob without husk with other characters in eighteen sweet corn genotypes during kharif 2024**

Characters	Days to Fifty percent Tasseling	Days to Fifty percent Silking	Plant Height (cm)	Ear Height (cm)	Wt. of green cob with husk (Kg)	Sweet Corn Length (cm)	Sweet Corn Girth(cm)	Total Soluble Solids (%)
Days to Fifty percent Tasseling	<b>-0.61</b>	0.52	-0.03	0.07	-0.06	-0.03	-0.24	-0.01
Days to Fifty percent Silking	-0.61	<b>0.51</b>	-0.01	0.7	-0.05	-0.03	-0.21	-0.02
Plant Height (cm)	0.04	-0.01	<b>0.05</b>	0.01	0.19	0.04	0.41	-0.01
Ear Height (cm)	-0.24	0.21	0.02	<b>0.17</b>	0.11	-0.01	-0.02	-0.37
Wt. of green cob with husk (Kg)	0.11	-0.08	0.03	0.05	<b>0.36</b>	0.05	0.41	-0.04
Sweet Corn Length (cm)	0.23	-0.18	0.03	0.01	0.26	<b>0.07</b>	0.49	-0.07
Sweet Corn Girth(cm)	0.25	-0.19	0.04	-0.01	0.26	0.57	<b>0.56</b>	-0.03
Total Soluble Solids (%)	0.04	0.06	0.04	-0.04	0.10	0.029	0.88	<b>-0.16</b>

## References

- Junpatiw, A., Lertrat, K., Lomthaisong, K., Tangwongchai, R. (2013). Effects of steaming, boiling and frozen storage on carotenoid contents of various sweet corn cultivars. *International Food Research Journal*. 20(5): 2219-2225
- Abe, A., Adelegan, C.A. (2019). Genetic variability, heritability and genetic advance in shrunken-2 super-sweet corn (*Zea mays L. saccharata*) populations. *Journal of Plant Breeding and Crop Science*. 11(4): 100-105. doi: 10.5897/JPBCS2018.0799.
- Szareski, V.J., Carvalho, I.R, Kehl, K., de Pelegrin, A.J., Nardino, M., Demari, G.H., Barbosa, M.H., Lautenchleger, F., Smaniotto, D., Aumonde, T.Z., Pedó, T., Souza, V.Q. (2018). Interrelations of characters and multivariate analysis in corn. *Journal of Agricultural Science*. 10: 187-194. doi: 10.5539/jas.v10n2p187.
- VaniPraveena, M., Talekar, S.C., Kachapur, R.M. and Harlapur, S.I. (2021). Elite general and specific combiners for high sugar content and green ear yield in sweet corn (*Zea mays L. saccharata*). *J. Farm Sci.*, 34 (1): 10-14.
- Szymanek, M, Tana's, W. and Kassar, F.H. (2015). Kernel carbohydrates concentration in sugary-1, Sugary enhanced and shrunken sweet corn kernels. *Agric. Agric. Sci. Procedia*, 7: 260–264.
- Khanduri, A., Hossain, F, Lakhera, P.C. and Prasanna, B.M. (2011). Effect of harvest time on kernel sugar concentration in sweet corn. *Indian J. Genet. Plant Breed.*, 71(3): 231.
- Niji, M.S., Ravikesavan, R., Ganesan, K.N and Chitdeshwari, T. (2018). Genetic variability, heritability and character association studied in sweet corn (*Zea mays L. saccharata*). *Electron. J. Plant Breed.*, 9(3): 1038- 1044.
- Popet, P., Eksomtramage, T., Anothai, J. and Khomphet, T. (2022). Correlation and path analysis in commercial tenera oil palms collected from Southern Thailand. *Indian Journal of Agricultural Research*. 56(4): 485-488. doi: 10.18805/IJARE.A-631.
- Schober, P., Schwarte, L.A. (2018). Correlation coefficients: Appropriate use and interpretation. *Anesthesia and Analgesia*. 126(5): 1763-1768. doi: 10.1213/ANE.0000000000002864.
- Bello, O.B., Abdulmalik, S.Y., Afolabi, M.S. and Ige, S.A. (2010). Correlation and path co-efficient analysis of yield and agronomic characters among open pollinated maize varieties and their F1 hybrids in a diallel cross. *Afr. J. Biotechnol.*, 9 (18): 2633-2639.
- Bhanu, N.A., Singh, M.N., Tharu, R., Saroj S.K. (2017). Genetic variability, correlation and path coefficient analysis for quantitative traits in chickpea genotypes. *Indian Journal of Agricultural Research*. 51(5): 425-430. doi: 10.18805/IJARE.A-4687.
- Valenzuela, S., Bachmann, I. (2017). Path analysis. In: *The International Encyclopedia of Communication Research Methods*. John Wiley and Sons. doi: 10.1002/9781118901731.iecrm0181.
- Ambresh, H., Lingaiah, B., Renuka, M. and Jyothi, K. (2017). Phenotypic and genotypic correlation co-efficient studies in tomato (*Solanum lycopersicum L.*) for yield and quality traits. *Inter. J. Curr. Microbiol. Appl. Sci.*, 6 : 2287-2292
- Suresh, D., Kachapur, R.M., Talekar, S.C. and Gurumurthy, R. (2021). Genetic variability and trait association studies in maize (*Zea mays L.*). *J. Farm Sci.*, 34(2) : 122-125.
- Khomphet, T. (2024). Genetic Variability, Correlation and Path Analysis of Agronomic Traits and Yield Components of Thai Sweet Corn. *Indian Journal of Agricultural Research*. doi: 10.18805/IJARE.AF-886.
- Suhaisini, B., Ravikesavan, R. and Yuvaraja, A. (2016). Genetic variability and correlation among yield and yield contributing traits in sweet corn. *Madras Agric. J.*, 103 (10-12) : 293-296.
- Aman, J., Bantte, K., Alamerew, S. and Sbhatu, D.B. (2020). Correlation and path co-efficient analysis of yield and yield components of quality protein maize (*Zea mays L.*) hybrids at Jimma, western Ethiopia. *Int. J. Agron*, 1-7.
- Sadaiah, K., Reddy, V.N. and Kumar, S.S. (2013). Correlation studies for yield and yield contributing characters in sweetcorn (*Zea mays L. saccharata*). *Int. J. Agric. Innov. Res.*, 2 (2) : 145-148.
- Gazal, A., Nehvi, F., Lone, A.A. and Dar, Z.A. (2017). Assessment of genetic variability of a set of maize inbred lines for drought tolerance under temperate conditions. *Int. J. Curr. Microbiol. App. Sci*, 6 (12): 2380-2389.

20. Rajwade, J.K., Jagadev, P.N., Lenka, D. and Gupta, S. (2018). Correlation and path co-efficient studies on elite genotypes of maize inbred lines. *J. Pharmacogn. Phytochem.*, 7 (2) : 2765-27671.
21. Chinthiya, A., Ganesan, K.N., Ravikesavan, R. and Senthil, N. (2019). Combining ability and association studies on different yield contributing traits for enhanced green cob yield in sweet corn (*Zea mays con Varsaccharata*). *Electron. J. Plant Breed.*, 10 (2): 500- 511.
22. Olawamide, D.O and Fayeun, L.S. (2020). Correlation and path coefficient analysis for yield and yield components in late maturing provitamin a synthetic maize (*Zea mays L.*) breeding lines. *J. Exp. Agric. Int.*, 42 : 64-72.
23. VaniPraveena, M., Talekar, S. C. and Kachapur, R. M. (2022). Studies on correlation and path co-efficient analysis of single cross hybrids in sweet corn. *Internat. J. Plant Sci.*, 17 (2): 173-179, DOI: 10.15740/HAS/IJPS/17.2/173-179, Copyright@ 2022:HindAgri-Horticultural Society.
24. Begum, S., Ahmed, A., Omy, S.H., Rohman, M.M. and Amiruzzaman, M. (2016). Genetic variability, character association and path analysis in maize (*Zea mays L.*). *Bangladesh J. Agric. Res.*, 41(1): 173-182.
25. Chavan, S., Bhadru, D., Swarnalatha, V. and Mallaiah, B. (2020). Studies on genetic parameters, correlation and path analysis for yield and yield attributing traits in sweet corn (*Zea mays L. saccharata*). *Int. J. Curr. Microbiol. App. Sci.*, 9 (7) : 1725-1734
26. Yahaya, M.S., Bello, I. and Unguwanrimi, A.Y. (2021). Correlation and path-co-efficient analysis for grain yield and agronomic traits of maize (*Zea mays L.*). *Science World J.*, 16 (1) : 10-13.
27. Reddy, P.R.K., Talekar, S.C., Naidu, G. and Harlapur, S.I. (2021). Estimation of genetic variability, correlation and path coefficient analysis in early segregating generation of maize (*Zea mays L.*). *J. Farm Sci.*, 34 (4) : 357-360.
28. Talekar, S.C., Viswanatha, K.P. and Lohithaswa, H.C. (2017). Assessment of genetic variability, character association and path analysis in F2 segregating population for quantitative traits in chickpea. *Int. J. Curr. Microbiol. App. Sci.*, 6 (12) : 2184-2192.
29. Hosamani, M., Kuchanur, P.H., Swamy, N. and Karajgi, D.S. (2018). Studies on phenotypic correlation and path coefficient analysis of grain yield and its component traits in maize (*Zea mays L.*) hybrids. *J. Pharmacogn. Phytochem.*, 7 (5) : 1374-1377.