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Exploring Genetic Variability and Cause-effect Relationship for Yield and its Contributing Traits in Brinjal (*Solanum melongena* L.)

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ABSTRACT

The experiment was conducted with sixteen distinct brinjal (*Solanum melongena* L.) genotypes during October, 2018 to February, 2019 at Horticultural Research cum Instructional farm under All India Coordinated Research Project (AICRP) on vegetable crops at Uttar Banga Krishi Viswavidyalaya, Pundibari of Cooch Behar district in West Bengal (736 165), following randomized block design to analyze genetic variability, correlation, and path coefficients to identify traits influencing fruit yield. Significant genetic variability among all traits indicated ample scope for effective selection in the breeding programme. High heritability (>60%) coupled with substantial genetic advance (>20%) found for traits like fruit yield, fruit weight, and fruits plant^{-1} suggested the presence of strong additive gene action, which favoured direct selection. Correlation analysis identified positive associations of fruit yield with the number of branches plant^{-1}, fruits plant^{-1}, and fruit weight, while infested branches plant^{-1} negatively impacted yield. Path analysis revealed fruits plant^{-1} (0.606) and the number of branches plant^{-1} (0.564) had the highest direct effects on fruit yield, supported by strong positive correlations. Other traits like fruit diameter (0.545), days to 50% flowering (0.370), fruit weight (0.200), and phenol content (0.194) contributed positively. Negative direct effects of fruit length, fruit girth, and days to maturity indicated limited influence on fruit yield. A low residual effect (0.0463) validated the adequacy of selected traits in capturing genetic variability. The study emphasized the number of branches plant^{-1} and fruits plant^{-1} were critical traits for yield improvement, providing a robust framework for developing high-yielding, brinjal genotypes for sustainable cultivation.

KEYWORDS: Brinjal, eggplant, genetic variability, correlation coefficient, path analysis

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1. INTRODUCTION

Brinjal or eggplant (*Solanum melongena* L.) is a widely cultivated and well-liked Solanaceous vegetable crops in India (Shilpa et al., 2018). India is considered as the primary centre of origin for brinjal (Vavilov, 1931; Mishra et al., 2023) and also poor man's crop because of its great importance, demand, popularity and availability (Thingujam et al., 2016; Biradar et al., 2023). Brinjal is mostly grown for use in cuisine and it serves as an excellent supplier of several nutrients, vitamins, minerals and phenols with cardio-protective benefits (Pohl et al., 2019; Bushra et al., 2022). India's diverse climate, geography and being centre of origin for brinjal, have given rise to a wide variety of brinjal genotypes, with different colours, fruit morphology, fruit quality, and culinary properties (Barik et al., 2021). Apart from culinary applications, brinjal has numerous medicinal benefits including advantages for individuals with diabetes, (Gangadhara et al., 2021; Mishra et al., 2023; Kantyal et al., 2024), liver issues, and toothaches (Shukla and Naik, 1993; Akanksha et al., 2023). The rising recognition of eggplant's diverse health benefits has resulted in a notable and steady growth in its demand in recent years (Thota and Delvadiya, 2024). The fruits are abundant in calcium, magnesium, and phosphorus, and fatty acids (Dhankhar and Singh, 1984; Akanksha et al., 2023), which is potential for enhancing various traits to meet diverse consumer preferences (Barik et al., 2021).

The success of any crop improvement programme relies on the availability and effective utilization of genetic variability within the plant material, which serves as a foundation for plant breeding efforts (Paramanik et al., 2023). To optimize this potential, it is essential to partition variability into heritable and non-heritable components by estimating genotypic (GCV) and phenotypic (PCV) coefficients of variation, enabling breeders to better understand phenotypic traits prior to selection (Siva et al., 2020; Thomas et al., 2022). Heritability plays a crucial role for plant breeders in identifying and selecting potential genotypes for genetic improvement (Singh et al., 2024). It also helps in understanding the connections between phenotypic and genotypic characteristics under diverse environmental conditions (Sujin et al., 2017). The effectiveness of selection is enhanced by heritability and genetic advance as a percentage of the mean, aiding in evaluating the transferability of desirable traits to progeny (Nihad et al., 2021; Mahla et al., 2024). These parameters are critical for assessing genetic variability in germplasm, and the inheritance of traits ensures a more accurate and efficient breeding strategy (Kumar et al., 2016). Thus, a comprehensive inquiry into the genetic nature of variability is fundamental to the success of any crop improvement programme.

Direct selection is often unsuitable because it is influenced by multiple environmental factors (Sivakumar et al., 2016). It is also essential to identify the additional component factors that may be used to increase fruit yield. Understanding the relationship between yield and its contributing traits are important, that can be explained using correlation and path coefficient analysis in developing high-yielding varieties with wider adaptability. The trait association derived from the correlation coefficient assists in evaluating the relative influence of various component traits on yield and path analysis partitions these relationship into direct effects or indirect effects, thereby identifying the major traits that can influence the yield (Dewey and Lu, 1959; Faysal et al., 2022; Jangala et al., 2022). Hence, based on these considerations, this study was conducted to analyse and understand the association, cause and effect of the relationship between the different yield and its attributing traits.

2. MATERIALS AND METHODS

The current experiment was conducted during October, 2018 to February, 2019 at Horticultural Research cum Instructional farm under All India Coordinated Research Project (AICRP) on vegetable crops at Uttar Banga Krishi Viswavidyalaya, Pundibari of Cooch Behar district in West Bengal (736 165), India. The field experiment involved sixteen genotypes of brinjal and was conducted in a randomized block design (RBD) with three replications. Seedlings were transplanted after 30 days, maintaining a spacing of 75×60 cm^2. All recommended cultural practices were followed as per requirement. Observations were taken from five randomly tagged plants in each replication for the number of branches $plant^{-1}$ and infested branches $plant^{-1}$. For the fruit-based traits, fruits $plant^{-1}$, fruit weight (g), fruit length (cm), fruit girth (cm), fruit diameter (cm), and phenol content (mg g^{-1}) data were collected from 10 fruits. Other traits like days to 50% flowering, days to maturity and fruit yield were recorded on a per plot basis and the fruit yield was estimated by the transformation of the per-plot (replication) yield into tonne ha^{-1}. Anonymous (1994) software was used for statistical analysis. The analysis of variance was conducted according to (Gomez and Gomez, 1984). The observed mean data were analyzed, and variability parameters such as the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were determined using the method proposed by Burton and De Vane (1953). Heritability estimates were derived using the approaches of Burton and De Vane (1953) and Allard (1960), while genetic advance was computed based on the methodology proposed by Johnson et al. (1955). Additionally, correlation coefficients were calculated using the formula described by Johnson et al. (1955). The Path-coefficient analysis was performed to split the genotypic correlation coefficient into direct and indirect effects as suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

3. RESULTS AND DISCUSSION

3.1. Analysis of variance (ANOVA)

The analysis of variance (ANOVA) (Table 1) showed significant differences in the mean sum of squares across the eleven traits under this study, indicating the presence of considerable genetic divergence and sufficient variability among the sixteen genotypes. Therefore, it suggested that there was ample opportunity for the selection of different traits to utilize in the brinjal improvement programme. The presence of significant difference among the brinjal genotypes for the characters days to 50% flowering, number of branches plant^{-1}, infested branches plant^{-1}, fruits plant^{-1}, fruit weight, fruit length, fruit girth, fruit diameter, days to maturity, phenol content and fruit yield were also reported by Madhavi et al. (2015); Uddin et al. (2021); Lintu and Namboodiri (2023); Susmitha et al. (2023); Tabasum et al. (2024); Vasa et al. (2025).

Table 1: Analysis of variance (ANOVA) for different traits in Brinjal

Sources of variation	Degrees of freedom	Mean sum of squares				
		Days to 50% flowering	No. of branches plant^{-1}	Infested branches plant^{-1}	Fruits plant^{-1}	Fruit weight (g)
Replication	1	0.281	8.508	0.389	1.531	75.461
Genotypes	15	44.231**	34.563**	5.383**	125.623**	18394.466**
Error	15	0.815	0.409	0.826	5.790	374.353

Table 1: Continue...

Sources of variation	Degrees of freedom	Mean sum of squares					
		Fruit length (cm)	Fruit girth (cm)	Fruit diameter (cm)	Days to maturity	Phenol content (µg g^{-1})	Fruit yield (t ha^{-1})
Replication	1	0.525	0.151	0.131	0.500	2359199.250	0.007
Genotypes	15	26.337**	42.083**	4.972**	19.858**	3322079.473**	364.873**
Error	15	1.871	0.210	0.140	0.500	8305.185	4.184

*: Significant at (p=0.05) probability level, **: Significant at (p=0.01) probability level

3.2. Genetic variability in brinjal genotypes

In Table 2, the duration for days to 50% flowering ranged from 69.00 to 84.00 days, with an average value of 76.469 days (Shinde et al., 2012). Number of branches plant^{-1} varied between 10.60 and 24.40, with a mean of 16.722 (Abrham et al., 2024; Nagar et al., 2024). The extent of infested branches plant^{-1} ranged from 6.32 to 13.60, averaging 9.783 (Pugalendhi et al., 2010). Fruits plant^{-1} was observed to range from a minimum of 15.20 to a maximum of 47.20, with a mean value of 29.231 (Kumar et al., 2012; Singh et al., 2024). Fruit weight ranged from 142.1 g to 488.0 g, with an average of 281.156 g (Singh et al., 2024). Fruit length was recorded between 10.50 cm and 27.50 cm, with a mean of 17.297 cm (Singh et al., 2024). Fruit girth varied from 11.00 cm to 25.80 cm, averaging 17.675 cm (Kumar et al., 2012). Fruit diameter ranged from 3.50 cm to 9.90 cm, with a mean diameter of 5.73 cm (Singh et al., 2024). Days to maturity ranged from 106.00 to 119.00 days, with an average of 111.563 days (Chaudhary et al., 2017). Phenol content in fruits varied from 3358.92 µg g^{-1} to 7565.99 µg g^{-1}, with an average of 5430.472 µg g^{-1} (Shaheen et al., 2013) Fruit yield varied between 25.43 t ha^{-1} and 67.21 t ha^{-1}, with an average yield of 43.83 t ha^{-1} (Chaudhary et al., 2017, Akhtar et al., 2019).

3.2.1. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV)

Variability parameters, such as genotypic (GCV) and phenotypic coefficient of variation (PCV), were commonly used to evaluate genetic variability. These parameters provide insight into the extent of variability within a population, with GCV and PCV values were categorized as high (>20%), moderate (10–20%) or low (<10%) (Sivasubramanian and Madhavamenon, 1973). The PCV and GCV values for the studied genotypes were presented in Table 2. The analysis revealed that GCV values were consistently lower than PCV values for all traits, with minimal differences between the two, suggested a low environmental influence and a high genetic contribution to phenotypic expression. High GCV and PCV values were recorded for fruit weight (33.761% and 34.110%), fruit yield (30.639% and 30.817%), fruit diameter (27.130% and 27.519%), fruits plant^{-1} (26.481% and 27.113%), fruit girth (25.888% and 25.952%), number of branches plant^{-1} (24.713% and 24.860%), phenol content (23.703% and

Table 2: Estimates of mean, range, variance, heritability and genetic advance for different traits of brinjal genotypes

Traits	Mean	Range	PCV (%)	GCV (%)	Heritability (broad sense) (%)	Genetic Advance as % of mean
Days to 50% Flowering	76.469	69.00–84.00	6.150	6.093	98.200	12.435
Number of branches plant^{-1}	16.722	10.60–24.40	24.860	24.713	98.800	50.606
Infested branches plant^{-1}	9.783	06.32–13.60	16.769	15.428	84.700	29.242
Fruits plant^{-1}	29.231	15.20–47.20	27.113	26.481	95.400	53.278
Fruit weight (g)	281.156	142.10–488.00	34.110	33.761	98.000	68.837
Fruit length (cm)	17.297	10.50–27.50	20.980	20.221	92.900	40.148
Fruit girth (cm)	17.675	11.00–25.80	25.952	25.888	99.500	53.195
Fruit diameter (cm)	5.73	03.50–09.90	27.519	27.130	97.200	55.098
Days to maturity	111.563	106–119	2.824	2.789	97.500	5.672
Phenol Content (μg g^{-1})	5430.472	3358.92–7565.99	23.733	23.703	99.800	48.768
Fruit yield (t ha^{-1})	43.83	25.43–67.21	30.817	30.639	98.900	62.754

PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation

23.733%), and fruit length (20.221% and 20.980%). These traits exhibited a wider range of variation, indicating greater potential for enhancement through selection. The high GCV and PCV estimates for fruit weight, fruit yield, and fruits plant^{-1} align with the earlier findings of Madhavi et al. (2015); Shilpa et al. (2018); Sindhuja et al. (2020); Uddin et al. (2021); Thomas et al. (2022). Similarly, high GCV and PCV values for fruit diameter, number of branches plant^{-1}, and fruit length also corresponded to the observations of Nilakh et al. (2017); Thomas et al. (2022). Additionally, the results for fruit girth and phenol content are consistent with the findings of Rani et al. (2023). Infested branches plant^{-1} exhibited moderate GCV and PCV values (15.428% and 16.769%), while low GCV and PCV values were recorded for days to 50% flowering (6.093% and 6.150%) and days to maturity (2.789% and 2.824%), consistent with the findings of Siva et al. (2020) and Balasubramaniyam et al. (2021).

3.2.2. Heritability and genetic advance

The extent of variability was indicated by GCV and PCV, but the proportion of variability passed on to the offspring can only be assessed through heritability and genetic advance parameters. Heritability in the broad sense often failed to accurately reflect the inheritance of traits, as only the additive genetic variance was passed down through generations. Consequently, relying solely on heritability in the broad sense might lead to incorrect conclusions about the effectiveness of selection for a given trait. Evaluating heritability in conjunction with genetic advance as a percentage of the mean provided a more precise understanding of the contribution of additive and non-additive components to the trait. Broad-sense heritability varied from 84.700% to 99.800%, with nearly all traits exhibiting heritability exceeding 60% (Table 2). High genetic gain, expressed as genetic advance as a percentage of the mean (>20%), was observed for fruit weight (68.837%), fruit yield (62.724%), fruit diameter (55.098%), fruits plant^{-1} (53.278%), fruit girth (53.195%), number of branches plant^{-1} (50.606%), phenol content (48.768%), fruit length (40.148%), and infested branches plant^{-1} (29.242%). Moderate genetic advance as a percentage of the mean was recorded for days to 50% flowering (12.435%), while low genetic advance was noted for days to maturity (5.672%). High heritability combined with substantial genetic gain was observed for fruit weight, fruit yield, fruit diameter, fruits plant^{-1}, fruit girth, number of branches plant^{-1}, phenol content, fruit length, and infested branches plant^{-1}. This suggested the dominance of additive gene action, indicating significant potential for enhancing these traits through selection. Shilpa et al. (2018) reported that fruit weight and fruit yield exhibited high heritability along with a high genetic advance, making them reliable selection criteria for yield improvement. Siva et al. (2020) highlighted the strong genetic influence on fruit diameter and number of branches plant^{-1}, suggesting that these traits respond well to selection. Thomas et al. (2022) demonstrated that phenol content and fruit girth showed substantial heritability and genetic gain, indicating their stability across generations. Pardhi et al. (2025) emphasized that infested branches plant^{-1} and fruit length exhibited significant heritability, underscoring their importance in breeding programs for improved fruit quality and resistance to pest infestation.

3.3. Correlation analysis

For a successful breeding programme, it was essential to first identify the relationships among various yield and growth traits before making selections. Correlation coefficient analysis was a valuable tool for determining the strength and direction of associations between different traits. In this study, the genotypic correlation among sixteen genotypes was analyzed, with the relationships between fruit yield and other traits presented in Table 3.

The genotypic correlations between fruit yield and other traits revealed both positive and negative associations. Days to 50% flowering exhibited significant positive correlations with infested branches plant^{-1} (0.551), fruit length (0.431) and days to maturity (0.540), but a negative correlation with fruits plant^{-1} (-0.369). The number of branches plant^{-1} showed highly significant positive correlation with fruit weight (0.817), fruit yield (0.863), and fruits plant^{-1} (0.350). Infested branches plant^{-1} had a significant positive correlation with days to maturity (0.762), fruit girth (0.420), and fruit length (0.416) but displayed significant negative correlations with fruits plant^{-1} (-0.351), fruit weight (-0.407), and fruit yield (-0.447). Fruits plant^{-1} were positively correlated with fruit weight (0.644), fruit length (0.362), and fruit yield (0.538), but negatively correlated with fruit diameter (-0.349). Fruit weight demonstrated a strong positive correlation with fruit yield (0.969) and phenol content (0.376). Fruit length showed high positive correlations with fruit girth (0.405) and phenol content (0.382). Additionally, fruit girth exhibited a highly significant positive correlation with fruit diameter (0.939). Hence, traits such as the number of branches plant^{-1}, fruits plant^{-1}, and fruit weight should be prioritized to improve fruit yield. Conversely, an increase in infested branches plant^{-1} is likely to lead to reduced fruit yields. These results align with previous studies on brinjal. Prabhu and Natarajan (2008) reported that the number of branches plant^{-1} and fruit weight had a strong positive association with fruit yield. Thangamani and Jansirani (2012) emphasized the role of fruits plant^{-1} in yield improvement. Sivakumar et al. (2016) observed that fruit girth and fruit weight contributed significantly to yield variation. Rameshkumar et al. (2021) highlighted the direct effects of fruit length and fruit weight on yield. Thomas et al. (2022) further confirmed that traits viz. the number of branches plant^{-1} and fruit yield exhibited significant positive correlation and high heritability and genetic advance, making them ideal for selection. Chetan et al. (2023) reinforced these findings, demonstrating that fruit-related traits viz. number of branches plant^{-1}, fruits plant^{-1}, and fruit weight play a crucial role in enhancing brinjal productivity.

Table 3: Genotypic correlation between yield and its attributing traits in brinjal

Traits	Days to 50% Flowering	No. of branches plant^{-1}	Infested branches plant^{-1}	Fruits plant^{-1}	Fruit weight (g)	Fruit length (cm)	Fruit girth (cm)	Fruit diameter (cm)	Days to maturity	Phenol content (µg g^{-1})
No. of branches plant^{-1}	-0.137									
Infested branches plant^{-1}	0.551**	-0.164								
Fruits plant^{-1}	-0.369*	0.350*	-0.351*							
Fruit weight (g)	-0.337	0.817**	-0.407*	0.644**						
Fruit length (cm)	0.431*	0.208	0.416*	0.362*	0.019					
Fruit girth (cm)	0.114	0.077	0.420*	-0.280	-0.118	0.405*				
Fruit diameter (cm)	0.058	0.106	0.236	-0.349*	-0.074	0.218	0.939**			
Days to maturity	0.540**	-0.083	0.762**	-0.211	-0.136	0.078	0.138	0.082		
Phenol content (µg g^{-1})	-0.117	0.282	-0.009	0.193	0.376*	0.382*	0.230	0.116	-0.303	
Fruit yield (t ha^{-1})	-0.297	0.863**	-0.447*	0.538**	0.969**	0.055	-0.068	0.016	-0.202	0.340

*: Significant at (p=0.05) probability level, **: Significant at (p=0.01) probability level

3.4. Path analysis

Path analysis was a statistical method used to partition the correlation coefficient into direct and indirect effects of an independent variable. It provided valuable insights into the influence of various yield-contributing traits on overall yield. Understanding these direct and indirect impacts on a dependent variable, such as fruit yield plant^{-1}, was crucial for formulating an effective selection strategy.

In this study, path analysis was performed using fruit yield as the dependent variable, while traits such as days to 50% flowering, number of branches plant^{-1}, infested branches plant^{-1}, fruits plant^{-1}, fruit weight, fruit length, fruit girth, fruit diameter, days to maturity, and phenol content were treated as independent variables. Each trait showed both direct and indirect effects, as summarized in Table 4.

The results (Table 4) revealed that fruits plant^{-1} had the highest direct effect (0.606) on fruit yield, followed by the number of branches plant^{-1} (0.564), fruit diameter (0.545), days to 50% flowering (0.370), fruit weight (0.200) and phenol content (0.194). Among these traits, only the number of branches plant^{-1}, fruits plant^{-1} and fruit weight exhibited the highest direct effects along with significant positive correlations with fruit yield. This indicates that selection based on these two traits would effectively enhance fruit yield. Khurana et al. (1988) and Randhawa et al. (1989) reported that the number of branches plant^{-1} had a strong positive influence on fruit yield. Mishra and Mishra (1990) and Mandal and Dana (1992) found that fruit weight contributed significantly to yield improvement. Kalda et al. (1996) highlighted the importance of fruits plant^{-1} in determining overall productivity. More recently, Sivakumar et al. (2016) and Rameshkumar et al. (2021) reaffirmed these relationships, emphasizing that direct selection for these traits viz. number of branches plant^{-1}, fruits plant^{-1} and fruit weight could lead to substantial yield gains in brinjal.

The number of branches plant^{-1} not only had the highest direct effect (0.564) but also showed a significant positive correlation with fruit yield (0.863). It further contributed positively through indirect effects from traits such as infested branches plant^{-1} (0.212), fruit weight (0.163), fruit diameter (0.058), days to maturity (0.015), and phenol content (0.055). Conversely, negative indirect effects were observed for days to 50% flowering (-0.051), infested branches plant^{-1} (-0.017), fruit length (-0.112), and fruit girth (-0.024). Traits such as fruit length, fruit girth, and days to maturity exhibited negative direct effects on fruit yield, suggesting they had minimal direct influence on yield plant^{-1}.

The residual effect was found to be very low (0.0463), indicating that the analysis captured most of the variability present among the brinjal genotypes across the eleven traits.

Table 4: Direct (diagonal) and indirect (off-diagonal) effects of different traits on fruit yield of brinjal

Traits	Days to 50% flowering	No. of branches plant^{-1}	Infested branches plant^{-1}	Fruits plant^{-1}	Fruit weight (g)	Fruit length (cm)	Fruit girth (cm)	Fruit diameter (cm)	Days to maturity	Phenol content (μg g^{-1})	Correlation with fruit yield
Days to 50% flowering	0.370	-0.077	0.056	-0.224	-0.067	-0.232	-0.036	0.032	-0.096	-0.023	-0.297
No. of branches plant^{-1}	-0.051	0.564	-0.017	0.212	0.163	-0.112	-0.024	0.058	0.015	0.055	0.863**
Infested branches plant^{-1}	0.204	-0.092	0.102	-0.213	-0.081	-0.224	-0.133	0.128	-0.136	-0.002	-0.447*
Fruits plant^{-1}	-0.137	0.197	-0.036	0.606	0.129	-0.195	0.089	-0.190	0.038	0.038	0.538**
Fruit weight (g)	-0.125	0.461	-0.041	0.390	0.200	-0.010	0.037	-0.044	0.024	0.073	0.969**
Fruit length (cm)	0.159	0.117	0.042	0.220	0.004	-0.538	-0.129	0.119	-0.014	0.074	0.055
Fruit girth (cm)	0.042	0.043	0.043	-0.170	-0.024	-0.218	-0.317	0.512	-0.025	0.045	-0.068
Fruit diameter (cm)	0.022	0.060	0.024	-0.212	-0.015	-0.117	-0.298	0.545	-0.015	0.023	0.016
Days to maturity	0.200	-0.047	0.078	-0.128	-0.027	-0.042	-0.044	0.045	-0.178	-0.059	-0.202
Phenol content (μg g^{-1})	-0.043	0.159	-0.001	0.117	0.075	-0.206	-0.073	0.063	0.054	0.194	0.340

*: Significant at (p=0.05) probability level; **: Significant at (p=0.01) probability level; Residual effect: 0.0463

Sivakumar et al. (2016) reported that fruit weight and fruits plant^{-1} exhibited strong direct effects on fruit yield, suggesting their importance as selection criteria in breeding programs. Jhangta et al. (2017) found that the number of branches per plant had a high positive correlation with yield, emphasizing its role in productivity improvement. Mangi et al. (2017) demonstrated that direct selection for fruit weight and number of branches plant^{-1} could effectively enhance overall fruit yield. Rameshkumar et al. (2021) highlighted the significance of fruits plant^{-1} in determining total yield potential, reinforcing its importance in selection strategies. Chaudhary et al. (2024) observed that fruit girth and fruit weight had strong direct effects on yield, making them key contributors to genetic improvement. Singh et al. (2024) confirmed that multiple yield-related traits, particularly fruits plant^{-1} and fruit weight, played crucial roles in improving brinjal productivity.

4. CONCLUSION

The study highlighted significant genetic variability, and assessed heritability, genetic advance, correlation and path analysis, emphasizing to identify the potential traits to improve yield. High heritability and genetic advance for fruit yield, fruit weight, and fruits plant^{-1} suggested additive gene action and favouring selection. Correlation and path analysis identified fruits plant^{-1} and the number of branches plant^{-1} as major traits with the highest positive direct effects on fruit yield. These findings provided critical insight for the brinjal breeding programme quite comprehensively.

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