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RESEARCH ARTICLE

Genetic variability studies on yield attributing traits in Palmyrah (*Borassus flabellifer* L.): Implications for crop improvement

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Abstract

Palmyrah is a dioecious palm, which is known for its resilience in arid and semi-arid environments. It is used to produce numerous edible and non-edible products. The association among yield-related traits and their pattern of influence are useful in evaluating and planning the selection criteria for desirable traits. The aim of this study was to examine the genetic variability and character association among the Palmyrah genotypes. A total of thirty accessions of Palmyrah were used for this study. Eleven traits contributing to growth and yield were recorded and analysed for genetic variability, correlation and path analysis. The number of bunches, single fruit weight and fruit yield per palm recorded the higher estimates of GCV and PCV. Among the eleven traits, 10 traits showed high heritability and GAM, whereas the trunk girth showed high heritability and moderate GAM. Fruit yield per palm exhibited positive correlation with trunk girth, number of bunches, number of fruits per bunch and single fruit yield. Path coefficient analysis revealed that the traits like number of bunches and single fruit weight had a positive and high direct effect on fruit yield per palm. Based on these results, Palmyrah improvement programme could be accelerated by selecting the variables that have a stronger correlation to fruit yield per palm and moderate to high estimates of PCV, GCV, heritability and high genetic advancement.

Keywords: correlation; fruit yield; Palmyrah; path analysis; variability

Introduction

Palmyrah is a dioecious palm belonging to Arecaceae family. It is known for its ecological contributions and extensive utility in traditional and modern applications. It is predominantly found in the southern states of India, *viz.,* Tamil Nadu, Andhra Pradesh, Telangana, Odisha and Bihar. This palm is often referred to as "Kalpa Vriksha," due to its extensive utility across various sectors. Each part of Palmyrah palm is valuable, from the fruit to underground tuber, its leaves and trunk, all contributing to its economic significance in rural communities (1, 2). The Palmyrah tuber is rich in carbohydrates, starch and vital minerals, rendering it an important food source. The pulp of the fruit is rich in nutrients, offering vitamins A and C and is used in a variety of traditional foods and drinks (3,4). The detection of bioactive substances such as 5-Hydroxymethylfurfural in the haustorium powder suggests its capability in addressing disorders like anaemia and hypoxia (5). Palmyrah palm is recognized as an important crop for enhancing climate resilience in farming. Its environmental benefits, economic contributions and wider adaptability makes it a vital resource for communities dealing with the challenges posed by climate change. Promoting the cultivation and sustainable management of Palmyrah palms could significantly improve food security and ecological health in adverse climatic conditions. So, there is a great scope for developing palm varieties with respect to the desirable traits like high yield, dwarfness, precocity in bearing, etc.

Understanding the genetic variability and trait association among Palmyrah accessions is crucial for enhancing the yield and sustainability of the palm in adverse environments. By studying the genetic variability, researchers can identify genotypes with desirable characteristics such as high degree of early bearing, fruit yield with drought tolerance and improved fruit quality. This knowledge is particularly valuable in breeding programs aimed at developing cultivars with desirable traits.

The improvement of crop is heavily dependent on the nature and magnitude of available genetic variability, heritability and the incorporation of preferred traits into new varieties. The efficiency of breeding programmes can be boosted when there is a significant variability within the existing germplasm, enabling the plant breeder to create new varieties or improve existing ones more rapidly (6). Therefore, the knowledge of genetic estimates is necessary for crop improvement, which provides information for selection. Measurement of genetic variability can be accomplished with the help of genetic estimates such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as percent mean (GAM). Hence, before beginning any crop improvement programme, it is important to characterize the genetic background of Palmyrah and breeding values (7).

Yield, a complex polygenic trait, derives from multiple interactions between yield- contributing traits that can be assessed by correlation coefficients which reveal the interrelationship among different traits and identify the key characteristics on which the selection can be based for enhancing the genetic potential of crops (8). Nevertheless, in correlation studies, indirect associations can become more complex and confusing. Path analysis prevents this issue by assessing the direct impact of one trait on another by breaking down a specific correlation coefficient into its direct and indirect effect components (9, 10).

Path coefficient analysis acts as a valuable method for assessing both direct and indirect traits of association and enables a comprehensive exploration of specific traits that contribute to a particular correlation. It reveals the details on the magnitude and direction of both direct and indirect effects of the yield components (11). Nonetheless, the absence of data regarding the relationship between yield and its contributing traits is believed to hinder the crop improvement of Palmyrah. Hence, the present investigation was aimed on gathering sufficient information regarding the extent of variability and genetic relationship of yield and yield -related characteristics in Palmyrah.

Additionally, understanding these genetic correlations could facilitate the development of more efficient and sustainable Palmyrah cultivation strategies, potentially leading to enhanced yields and improved economic outcomes for farmers and industries relying on this versatile palm.

The genetic factors influencing growth and yield traits in Palmyrah particularly in terms of correlation and path analysis remain largely unexplored, presenting a significant gap in this economically important palm species. This shortfall can hamper the development of targeted breeding programs for improved productivity. To overcome this research gap, the objective of this study was framed to examine the genetic variability, correlation and path analysis of growth and yield traits in Palmyrah.

Materials and Methods

This study was conducted at Palmyrah Research Station, Tamil Nadu Agricultural University during 2023 and 2024. The experimental site was situated at an elevation of 40 metres above mean sea level and 8°22 N latitude and 78° E. Thirty female accessions, each 31 years old were selected and evaluated. A randomized block design with two replication per treatment was used to determine their trait relationship. From each accession, a sample of three individuals were randomly selected per replication to perform morphometric analysis. Eleven traits, seven vegetative and four reproductive traits *viz.,* Plant height (PH), Trunk Girth (TG), Leaf Length (LL), Number of Leaflets per leaf (LL/L), Petiole Length (PL), Petiole Girth (PG), Number of Fruit Bunches (NB), Number of Fruits per Bunch (NF/B), Single Fruit Weight (SFW), Fruit Girth (FG) and Fruit Yield per Palm (FY) were recorded. Parameters related to the fruit were measured at the harvest stage. All the measurements were recorded for two successive years.

Data analysis

The pooled data were subjected to different statistical analysis. The genotypic coefficient of variation and phenotypic coefficient of variation (12), Heritability in a broad sense (h^2) (13) and Genetic advance (14) were examined. The simple correlation between different characters at both genotypic and phenotypic levels was computed among the traits (15). Simple Pearson's correlation coefficients were calculated from mean values of the parameters and these coefficients were utilized to estimate path coefficients (16) through Agricolae R package.

Categorization of variability parameters

GCV and PCV were classified as low (0 -10 %), moderate (10 - 20 %) and high (>20 %) (17). The heritability in broad sense values was categorized as low (Less than 50 %), moderate (50 - 75 %) and high (More than 75 %) (14). The range of genetic advance was characterized as per cent of mean values *viz.,* low (Less than 10 %), moderate (10-20 %) and high (More than 20 %) (14).

Results and Discussion

The examination of variability indices, such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as a percent of the mean, revealed the presence of variability in Palmyrah genotypes.

Phenotypic coefficient of variance and genotypic coefficient of variance

For ease of understanding, coefficients of variation were categorized as genotypic and phenotypic. The minor discrepancy between phenotypic and genotypic coefficients of variation is due to a minimal environmental impact, indicating that the phenotype closely represents the genotype. Studies on the genetic parameters in Palmyrah genotypes showed that the phenotypic coefficient of variation was slightly greater than the genotypic coefficient of variation across all the traits, indicating that the influence of environment had a limited impact on the genotype in the expression of those traits. Higher GCV and PCV values (Table 1 and Fig. 1) were observed for number of bunches (32.71 and 33.23, respectively), single fruit weight (33.21 and 33.87 respectively) and fruit yield per palm (59.81 and 60.13 respectively). A similar trend of genetic variability was identified in studies on Coconut (18). In Arecanut, (19) High GCV and PCV values were observed for fresh fruit weight and fresh nut yield.

Heritability and genetic advance as per cent of mean

Understanding the heritability is crucial to determine whether phenotypic differences among individuals are due to genetic differences or environmental factors. The data pertaining to heritability and GAM is represented in Table 1 and Fig. 2. High heritability combined with high genetic advance as percent mean was observed for plant height (89.40 % and 32.24), number of leaflets per leaf (92.80 % and 26.62), petiole length (92 % and 30.73), petiole girth (95.20 % and 38.86), number of bunches (96.80 % and 66.33), number of fruits per bunch (92.40 % and 32.86), single fruit weight (96.10 % and 67.10), fruit yield per palm (98.90 % and 122.58) and moderate genetic advance for trunk girth (19.03). This signifies the dominance of additive genes, which might be recognized as a u feature for selection (18). Research pertaining to significant heritability and genetic advance as percent mean in nut yield, nut weight, dehusked nut weight and moderate genetic advance for copra weight in Coconut was reported (20). Fruit weight, dehusked nut weight, kernel weight, shell weight and plant height recorded a direct impact on the copra production per palm in Coconut, demonstrating great heritability and genetic progress (21).

Gene action studies

The present investigation demonstrated high heritability along with high genetic advance as percent of mean for traits such as plant height, number of leaflets per leaf, petiole length, petiole girth, number of bunches, number of fruits per bunch, single fruit weight and fruit yield per palm. High heritability and moderate genetic advance as percent of mean was observed for trunk girth. The recognition of such traits which may be attributed to additive gene action, would provide possibilities for selection in early generations.

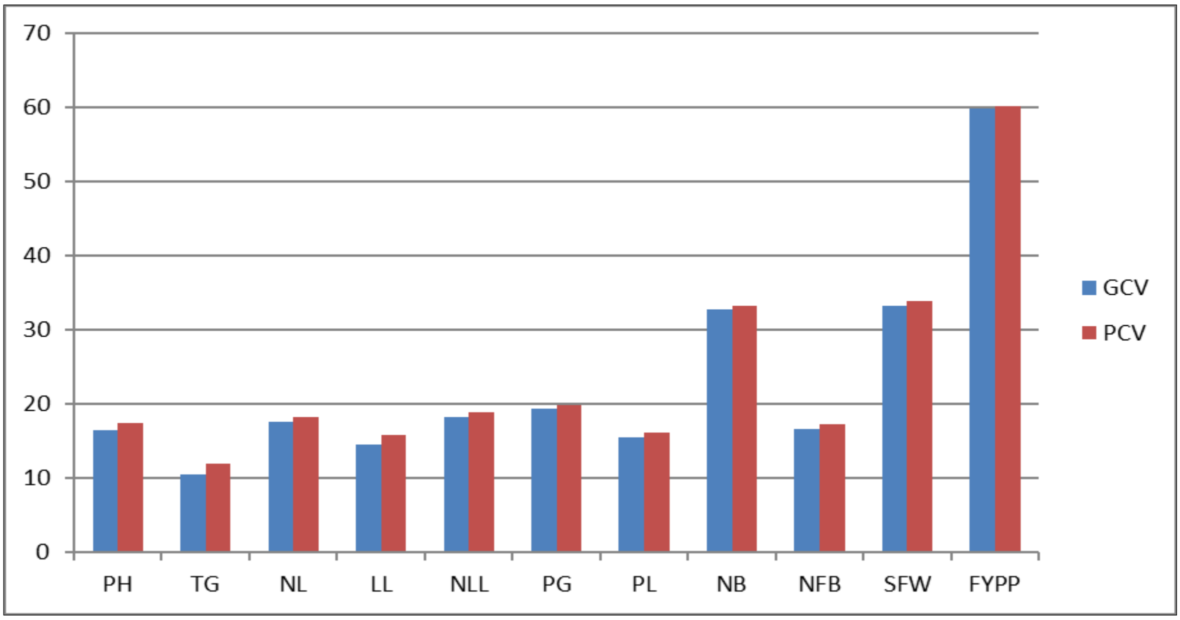

Fig. 1. GCV and PCV for morphological traits in Palmyrah.

Table 1. Genetic estimates of yield related traits in Palmyrah genotypes

Trait	Minimum	Maximum	Mean	GCV	PCV	Heritability (%)	GAM
PH	5.26	9.86	6.91	16.55	17.49	89.40	32.24
TG	116.87	203.40	153.73	10.51	11.95	77.20	19.03
NL	19.56	43.99	30.39	17.53	18.24	92.30	34.72
LL	142.23	326.90	202.20	14.56	15.76	85.30	27.72
NLL	48.33	110.18	73.40	18.27	18.96	92.80	36.27
PG	28.54	41.79	28.09	19.33	19.81	95.20	38.86
PL	88.92	185.42	117.46	15.54	16.20	92.00	30.73
NB	5.57	20.23	11.79	32.71	33.23	96.80	66.33
NFB	5.59	13.31	10.00	16.58	17.25	92.40	32.86
SFW	416.92	1950.96	977.00	33.21	33.87	96.10	67.10
FYPP	23.81	298.77	123.69	59.81	60.13	98.90	122.58

GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; GAM: Genetic advance as percent mean; SFW: Single fruit weight; PH: Plant height; TG: Trunk Girth; NL: Number of leaves; FYPP: Fruit yield per palm; LL: Leaf Length; NLL: Number leaflet per leaf; PG: Petiole girth; PL: Petiole length; NB: Number of bunches; NFB: Number of fruits per bunch

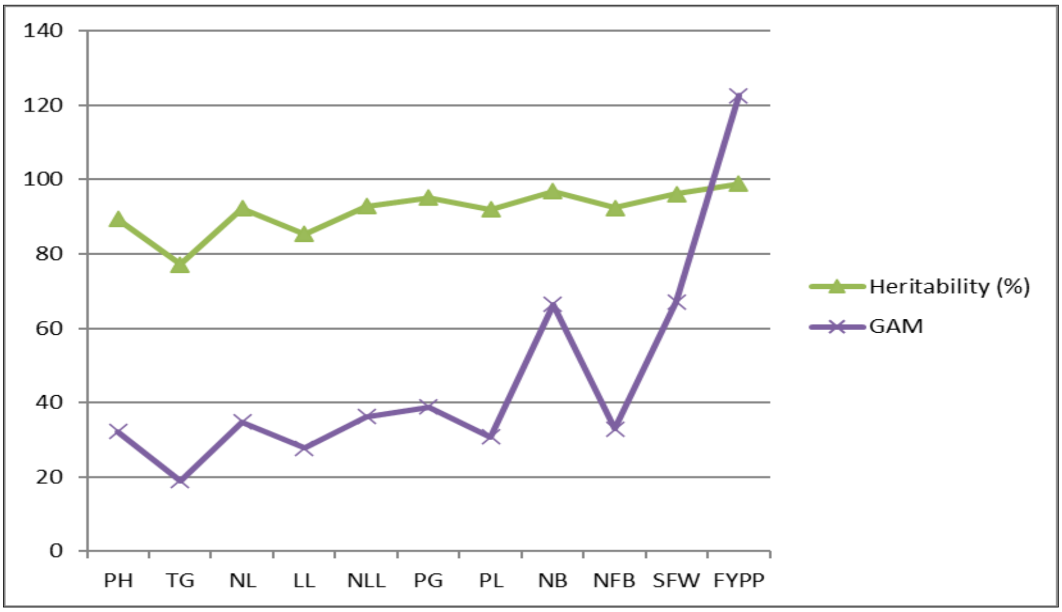

Fig. 2. Heritability and GAM for morphological traits in Palmyrah.

Correlation

Simple correlations between the characters, when analysed over 30 accessions, revealed both positive and negative correlations at varying magnitudes (Table 2 and Fig. 3).

The -value varies between 0 and 1 in this study (21). Examining the association between any trait pair is an indirect way of enhancing the yield of the plants. A trait pair with a correlation coefficient of +1 indicates a perfect positive correlation, implying that enhancing one of the traits would simultaneously improve the other. A correlation coefficient of -1 explains a negative correlation, indicating that if one trait is improved the other one will be affected negatively and if the correlation coefficient is zero signifies no relationship between the traits.

In this study, the correlation coefficient ranged from -0.05 (between NLL and NF) to 0.86 (between NB and FYPP). Trunk girth (0.41), number of bunches (0.86), number of fruits per bunch (0.56) and single fruit weight were positively correlated and can therefore be considered as major contributing traits to the fruit yield per plant. In contrast, significant positive correlation was observed between the number of functional leaves, length of leaf and petiole length with nut yield in coconut (20).

The number of fruits per bunch showed positive correlation with fruit yield per palm (0.56), number of bunches per palm (0.50), single fruit weight (0.16) and trunk girth (0.030). A positive correlation was exhibited between the number of nuts produced per palm and various factors, including the number of leaves per year, number of spadices, number of female flowers per inflorescence, number of female flowers per spikelet and number of spikelets per spadix in coconut (22).

The number of bunches showed a strong perfect positive correlation with the fruit yield per palm, whereas the trunk girth and number of fruits per bunch showed moderate positive correlation. Single fruit weight showed significant positive correlation with fruit yield per plant (0.74), plant height (0.49), trunk girth (0.68) and number of bunches (0.38). Therefore, the traits positively correlating with fruit yield per palm can be emphasized in the Palmyrah breeding programme. Based on the results, it could be concluded that improvement of trunk girth, number of bunches, number of fruits and single fruit weight would ultimately lead to an increase in fruit yield per palm.

Table 2. Simple correlation among the various biometric traits in Palmyrah genotypes

	FYPP	PH	TG	NL	LL	NLL	PG	PL	NB	NF	SFW
FYPP	1										
PH	0.12	1									
TG	0.41*	0.57***	1								
NL	-0.11	0.23	0.22	1							
LL	0.33	0.46*	0.41*	0.37*	1						
NLL	0.17	-0.14	0.15	-0.16	0.24	1					
PG	0.13	0.26	0.26	0.25	0.42*	0.14	1				
PL	0.13	0.45*	0.23	0.3	0.66****	-0.14	0.57**	1			
NB	0.86****	-0.09	0.18	-0.1	0.27	0.35	0.08	0.1	1		
NF	0.56**	-0.21	0.03	-0.2	-0.21	-0.05	-0.08	-0.31	0.50**	1	
SFW	0.74****	0.49**	0.68****	0.07	0.50**	0.01	0.21	0.32	0.38*	0.16	1

Significance: $p < 0.001^{****}$, $p < 0.01^{***}$, $p < 0.1^{**}$, $p < 0.5^{*}$

FYPP: Fruit Yield Per Palm; PH: Plant Height; TG: Trunk Girth; NL: Number of Leaves; LL: Leaf Length; NLL: Number of Leaflets per leaf; NB: Number of Branches; PL: Petiole Length; NB: Number of Branches; SFW: Single fruit weight; PG: Petiole Girth

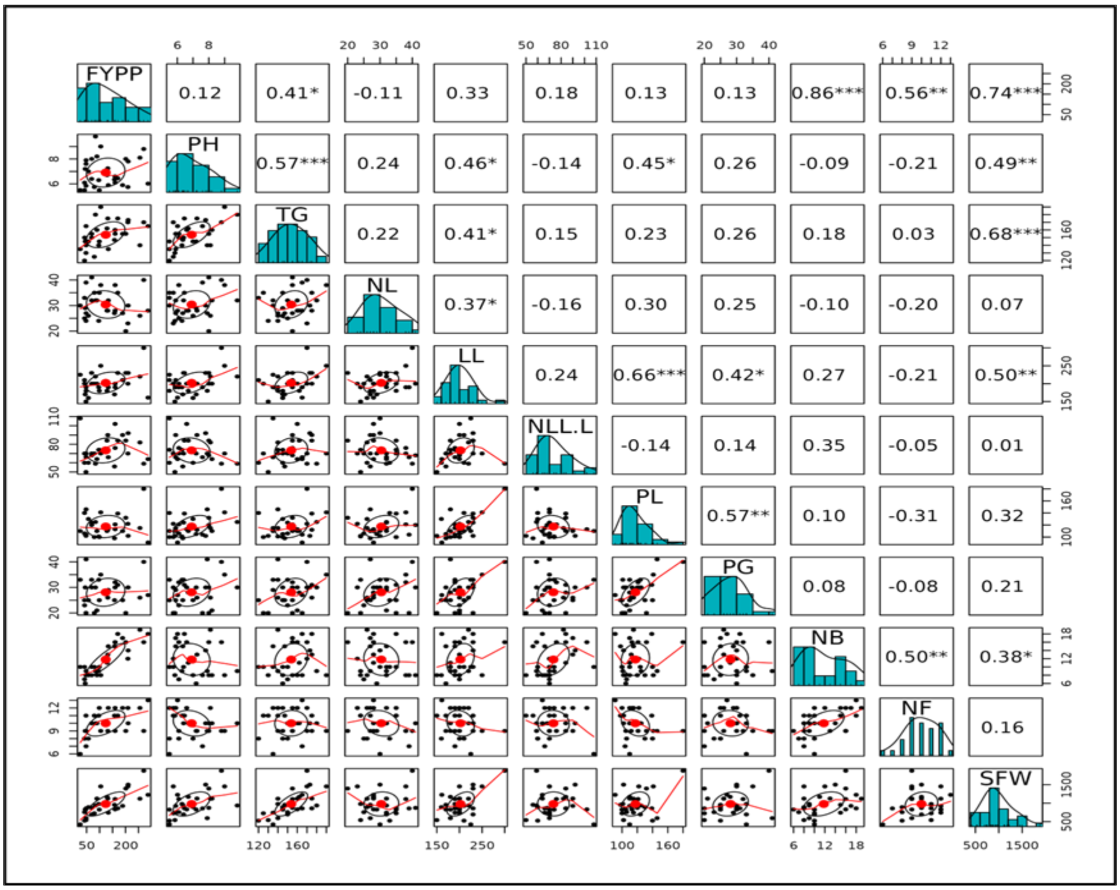

Fig. 3. Correlation paris plot for 11 yield components in Palmyrah.

Path analysis

The direct degree of correlation between the yield and its components are vital for identifying the key traits, which can be considered as a strategy for crop improvement in the breeding program. Consequently, these correlation findings were explored further through path coefficient to find the interrelationships among the traits. The findings revealed that there was a significant interrelationship among the different vegetative and yield characteristics. All the traits demonstrated their relationship with fruit yield either through direct or indirect effect.

The path coefficient analysis is presented in Table 3 and Fig. 4. Based on the path coefficient analysis results, number of bunches (0.628) exhibited high and positive direct effect on fruit yield per palm followed by single fruit yield (0.517), number of fruits per palm (0.128), petiole girth (0.064) and leaf length (0.036). These characters also showed positive correlation with fruit yield per palm. Thus, the selection of these characters simultaneously would bring out improvement in fruit yield per palm of Palmyrah. The traits *viz.,* plant height (-0.003), trunk girth (-0.043), number of leaves (-0.056), number of leaflets per leaf (-0.078) and petiole length (-0. 108) showed negative direct effects. The selection for these characters simultaneously would bring out improvement in fruit yield of Palmyrah. The results agree with the studies conducted in Oil palm where, the number of bunches had positive direct effect (0.181) on its fresh fruit bunch (23). In Coconut, the number of functional leaves exerted the maximum direct effect on nut yield / palm followed by petiole length and length of leaf (20). Similar trend was also observed in studies conducted on Oil palm (24).

Table 3. Simple path analysis among the various biometric traits in Palmyrah genotypes

PH	-0.003	-0.024	-0.013	0.017	0.011	0.017	-0.049	-0.058	-0.027	0.255	0.125
TG	-0.002	-0.043	-0.013	0.015	-0.012	0.017	-0.025	0.116	0.004	0.351	0.409
NL	-0.001	-0.01	-0.056	0.014	0.012	0.016	-0.033	-0.062	-0.026	0.035	-0.111
LL	-0.001	-0.017	-0.021	0.036	-0.019	0.027	-0.072	0.168	-0.027	0.257	0.330
NLL	0	-0.006	0.009	0.009	-0.078	0.009	0.016	0.221	-0.007	0.003	0.175
PG	-0.001	-0.011	-0.014	0.015	-0.011	0.064	-0.062	0.05	-0.011	0.106	0.126
PL	-0.001	-0.01	-0.017	0.024	0.011	0.036	-0.108	0.065	-0.039	0.166	0.127
NB	0	-0.008	0.006	0.01	-0.028	0.005	-0.011	0.628	0.063	0.198	0.864
NF	0.001	-0.001	0.012	-0.008	0.004	-0.005	0.033	0.312	0.128	0.082	0.557
SFW	-0.001	-0.029	-0.004	0.018	-0.001	0.013	-0.035	0.241	0.02	0.517	0.740

Residual effects: 0.023

FYPP: Fruit Yield Per Palm; PH: Plant Height; TG: Trunk Girth; NL: Number of Leaves; LL: Leaf Length; NLL: Number of Leaflets per leaf; PG: Petiole Girth; NF: Number of fruits per bunch; PL: Petiole Length; NB: Number of Branches; SFW: Single fruit weight

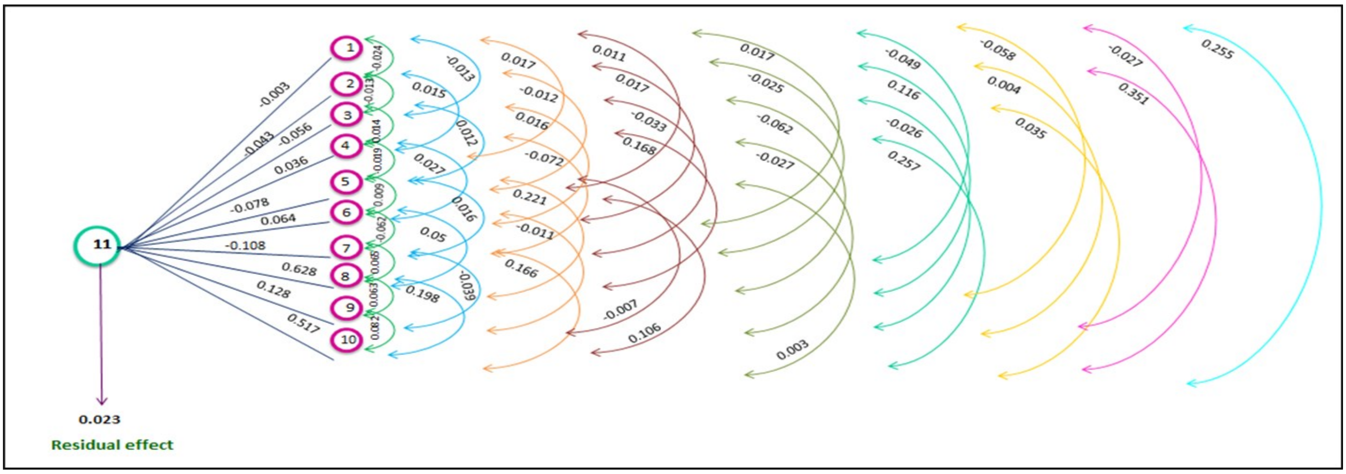

Fig. 4. Path diagram of yield related characters in Palmyrah accessions.

1. Plant Height; 2. Trunk Girth; 3. Number of Leaves; 4. Leaf Length; 5. Number of Leaflets per leaf; 6. Petiole Girth; 7. Petiole Length; 8. Number of fruits per bunch; 9. Number of Branches; 10. Single fruit weight; 11. Fruit Yield Per Palm

Conclusion

This study concluded the influence of analyzing genetic variability, heritability and path coefficients that identified desirable traits for the improvement of fruit yield of Palmyrah. High heritability and genetic advance for the traits, *viz.,* number of bunches, single fruit weight and fruit yield per palm, highlighted their potential as selection criteria in breeding programmes. The positive correlation and high direct effects of these traits on fruit yield, as revealed by path coefficient analysis, further affirmed their importance in genetic enhancement strategies. These findings provided valuable insights for accelerating Palmyrah improvement programs, enabling the development of high-yielding and climate-resilient genotypes. Future research focusing on additional genetic and molecular tools could further augment these efforts, ensuring sustainable cultivation practices and enhanced economic outcomes for communities reliant on this versatile palm.

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Authors' contributions

PA carried out the genetic studies, participated in the data collection, data analysis and drafted the manuscript. RSP participated in the design of the study and performed the statistical analysis and edited the manuscript. VR and MAP participated in the data analysis. NMB and MR participated in design of the study. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

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