Diversity analysis and correlation study of fruit physical, biochemical characters and antioxidant properties of some palmyrah palm (*Borassus flabellifer* L.) genotypes under Western dry tract of West Bengal

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ABSTRACT

The present study investigates the diversity in fruit morphology, biochemical composition, and antioxidant attributes of eighteen naturally occurring palmyrah palm genotypes growing under the western dry tract of West Bengal, India. The selected region, characterized by lateritic soils and semi-arid climate, supports a wide range of seedling progenies exhibiting considerable phenotypic variation. Fruit morphological evaluation of eighteen seedling progenies (each considered as treatments for mean, variance analysis) of palmyrah palm from different locations of western dry tract of West Bengal in the year 2023-24 and 2024-25 revealed pronounced differences among genotypes in fruit size, shape, and pulp content. Fruit weight varied from 787.2 g to 2381.7 g, and pulp content ranged between 369.8 g and 1340.5 g, indicating substantial potential for yield improvement. Biochemical analyses also displayed significant variability, with total soluble solids (TSS) ranging from 15.7°Brix to 22.0°Brix, total sugars from 13.7% to 20.1%, and ascorbic acid from 19.4 to 46.7 mg 100 ⁻¹ g fresh pulp. Antioxidant activity (DPPH radical scavenging) spanned from 45.2% to 77.3%, strongly correlating with phenolic and ascorbic acid contents. Correlation analysis demonstrated that fruit weight was highly associated with pulp content (r = 0.963), while TSS showed strong positive relations with reducing sugars (r = 0.904) and TSS: acidity ratio (r = 0.842). The results highlight the existence of broad genetic variability within the regional germplasm and identify genotypes such as PPG-17, PPG-12, and PPG-13 as promising candidates for both table and processing purposes. Overall, the findings provide a scientific basis for selection, conservation, and genetic improvement of palmyrah palm for enhanced fruit quality and antioxidant potential under dry land conditions.

Keywords: Bioactive compounds, diversity, fruit morphology and quality, palmyrah palm,

INTRODUCTION

The palmyrah palm (*Borassus flabellifer* L.) is a hardy, multipurpose tree belonging to the family Arecaceae (Palmae). It is a dioecious, long-lived species native to the Indian subcontinent and widely distributed across South and Southeast Asia (Gnanavelrajah *et al*., 2025). Within the genus *Borassus*, which comprises about five species, *B. flabellifer* is the most economically important. It thrives in hot, dry, and semi-arid regions owing to its deep root system, drought tolerance, and ability to grow in poor soils and commonly known as “toddy palm” or “ice-apple palm” (Jayaraj *et al*., 2025). The palm not only contributes to the ecological stability of arid landscapes but also serves as a source of food, fibre, timber,

and income for rural communities, earning it the title of "tree of life" (Rao *et al*., 2021).

Owing to its wide utility and adaptability, palmyrah forms an integral part of the socio-economic fabric of dry-land ecosystems like as many other minor fruits (Deb *et al*., 2024; Mukherjee *et al*., 2023). Nutritionally, the fruit pulp and sap are rich in carbohydrates, sugars, vitamins, minerals, and phenolic compounds, exhibit antioxidant and antimicrobial properties. The fibrous mesocarp is a good source of dietary fibre, while the hardened endosperm (palmyrah nut) provides starch for industrial applications (Penkey *et al*., 2025). Despite these valuable attributes, organized cultivation and systematic research on this species remain minimal. Most palms grow naturally through seed propagation, leading to a highly heterogeneous population structure.

The genetic diversity of palmyrah palm represents an important resource for future crop improvement and conservation. Being a cross-pollinated and dioecious species, each seedling is genetically unique, contributing to wide variability in fruit size, shape, pulp yield, and biochemical composition. Characterizing this variation is essential for identifying superior genotypes for breeding, propagation, and commercial use (Sridevi *et al*., 2020). A broad genetic base also enhances the adaptability of the species to climatic fluctuations and environmental stresses. In India, palmyrah is mainly found in Tamil Nadu, Andhra Pradesh, Odisha, West Bengal, and parts of Gujarat and Maharashtra (Vanitha *et al*., 2025). Within West Bengal, its natural population is concentrated in the western dry tract covering Birbhum, Bankura, and West Burdwan districts. This region, characterized by lateritic soils, high summer temperatures, and low rainfall, provides a favourable environment for the species. Here, palmyrah exists mostly as scattered seedling progenies along field boundaries and wastelands. Over generations, natural regeneration and open pollination have led to the evolution of a diverse genetic pool, yet this remains largely undocumented. The region's palms may therefore represent an unexplored reservoir of genetic variability in fruit morphology and pulp quality, possessing potential for selection and improvement.

The present investigation was undertaken to assess the genetic diversity among seedling progenies of palmyrah palm from the western dry tract of West Bengal using fruit morphological and quality parameters. The specific objectives were to document the variation in fruit traits among different seedling populations in Birbhum, West Burdwan, and Bankura districts; analyze the relationships among fruit morphology and pulp quality attributes; and identify promising genotypes with desirable characteristics for propagation and conservation. By elucidating the extent of variability within natural populations, this study aims to highlight the hidden potential of palmyrah genetic resources in West Bengal and provide a scientific basis for their systematic improvement, value addition, and sustainable utilization.

MATERIALS AND METHODS

The present investigation was conducted during the fruiting season of 2023–24 and 2024-25 in the western dry tract of West Bengal, India, covering three major districts like Birbhum, Bankura, and West Bardhaman. These districts represent a typical semi-arid ecosystem characterized by lateritic to sandy loam soils, erratic rainfall, and high summer temperatures exceeding 40°C. The region supports a rich natural population of palmyrah palm, which thrives under minimal management. Eighteen mature, fruit-bearing female palms of seedling origin were randomly selected from naturally growing populations in these districts, ensuring representation of diverse phenotypes. Each selected palm of different locations was treated as a distinct genotype and designated as Palmyrah Palm Genotype (PPG-1 to PPG-18) (Table 1). From each genotype, fully mature fruits were randomly

harvested at the ripening stage when the exocarp turned deep yellowish-brown and the pulp attained full sweetness. Care was taken to collect fruits of uniform maturity and to avoid mechanical damage during harvesting and transport. The collected fruits were washed, cleaned, and analyzed immediately after harvest to minimize compositional changes. Each genotype was considered as one biological replicate, and all determinations were performed in triplicate.

Fruit morphology was assessed following standard descriptors used for palm species considering five randomly selected fruits from each genotype to get average value for each parameter. The parameters recorded included polar diameter (cm), equatorial diameter (cm), fruit weight (g), fruit volume (ml), cap diameter (cm), single seed weight (g), pulp content (g), and pomace content (g). The shape index was calculated as the ratio of polar to equatorial diameter to express the overall fruit form. All dimensional traits were measured using a digital Verniercaliper, while fruit weight and seed weight were determined using an electronic balance with ±0.01 g precision. Fruit volume was recorded by water displacement in a graduated cylinder. Pulp and pomace weights were determined after separating the edible mesocarp manually from the fibrous residue. The data were expressed as mean values from three independent measurements per genotype.

The biochemical composition of fruit pulp (from composite samples of five fruits from each palmyrah palm) was determined using fresh, homogenized samples. The following parameters were analyzed: **Total Soluble Solids (TSS):** Measured with a digital refractometer (Atago, Japan) and expressed in degrees Brix (°B). **Total sugar and reducing sugar:** Estimated using the anthrone and DNS methods, respectively, and expressed as percentage of pulp fresh weight (Lane and Eynon ,1923).**Titratable acidity:** Determined by titration with 0.1 N NaOH using phenolphthalein as indicator and expressed as percent citric acid equivalent (AOAC, 1990). **TSS: Acidity Ratio**: Calculated as the ratio of total soluble solids to acidity, serving as an indicator of palatability. **Ascorbic acid content:** Estimated by the 2,6-dichlorophenol indophenol visual titration method and expressed as mg ascorbic acid per 100 g pulp (Rangana, 1986). **Total phenol content**: Determined using the Folin–Ciocalteu reagent and expressed as mg gallic acid equivalents (GAE) per 100 g pulp (Dewanto *et al.*, 2002). **Antioxidant activity:** Measured as percent DPPH radical scavenging activity following the method of (Brand-Williams *et al.,* 1995) and expressed as percentage inhibition. All analyses were performed under controlled laboratory conditions, and each parameter was measured in triplicate to ensure reliability. The instruments were calibrated prior to each set of measurements.

Data collected for all morphological and biochemical parameters were subjected to statistical analysis to assess the extent of variability among genotypes. Descriptive statistics (mean, range, standard deviation, and coefficient of variation) were calculated for each trait. One-way analysis of variance (ANOVA) was performed to test the significance of differences among genotypes. To explore interrelationships among fruit traits, Pearson's correlation coefficients were computed between selected important morphological and biochemical variables.

RESULTS AND DISCUSSION

Morphological characters

All morphological or fruit physical parameters are presented in Table 2 in the current study. **The polar diameter** of fruits ranged from 40.1 cm in PPG-2 to 56.9 cm in PPG-8, while the **equatorial diameter** varied between 35.3 cm (PPG-2) and 52.3 cm (PPG-16). The significantly wide range in these parameters suggests variable fruit shapes and degrees of fruit expansion among genotypes. The **shape index**, calculated as

the ratio of polar to equatorial diameter, fluctuated between 0.92 (PPG-15) and 1.14 (PPG-4 and PPG-8). Values close to 1.00 indicated near-spherical fruits, while higher indices implied slightly elongated forms. The significantly maximum shape index in PPG-4 and PPG-8 reveals their tendency towards an oblong structure, whereas PPG-15 and PPG-3 exhibited more flattened shapes. **Fruit volume**, a major determinant of marketable size, displayed pronounced variation, ranging from 770.6 ml (PPG-2) to 2354.3 ml (PPG-17). Genotypes PPG-4, PPG-7, PPG-12, PPG-13, and PPG-17 produced markedly larger fruits (> 2000 ml), while PPG-2 and PPG-6 bore smaller ones. A similar trend was observed for **fruit weight**, which ranged from 787.2 g in PPG-2 to 2381.7 g in PPG-17. The strong correspondence between fruit volume and weight indicates the uniform density of fruit tissues among genotypes. **Cap diameter**, another important indicator of fruit base expansion, varied between 8.6 cm in PPG-2 and 14.2 cm in PPG-8, suggesting genetic differences in fruit morphology and pedicel attachment. Heavier fruits generally exhibited larger cap diameters, as observed in PPG-7, PPG-8, PPG-13, and PPG-17. The **single seed weight** ranged from 169.2 g (PPG-2) to 334.5 g (PPG-4), reflecting significant variability in seed development and fruit–seed ratio. Genotypes such as PPG-4, PPG-8, and PPG-13 had heavier seeds, while PPG-2 and PPG-6 recorded lower values, implying a greater proportion of pulp relative to seed mass in these accessions. **Pulp content**, which directly influences the fruit's edible yield, varied widely from 369.8 g in PPG-6 to 1340. 5 g in PPG-17. The significantly highest pulp yield in PPG-17, followed by PPG-9, PPG-12, and PPG-13, indicates their potential utility in pulp-based product development. Conversely, the lowest pulp content in PPG-2 and PPG-6 denotes comparatively poor mesocarp development. **Pomace content** (residual fibrous material) ranged from 43.3 g (PPG-2) to 156.8 g (PPG-17), showing a consistent increase with fruit size and pulp mass. Genotypes producing higher pomace content, such as PPG-17 and PPG-12, also possessed thicker fruit walls and denser fibrous structures, traits that may be advantageous for breeding programs targeting bio-fiber extraction.

Marked differences in fruit dimensions, weight, and pulp content among the genotypes demonstrate strong genotypic control over fruit development. The pronounced variation in fruit weight and volume observed across the studied genotypes aligns with previous findings in other perennial palms, where differential assimilate partitioning and mesocarp development are key determinants of fruit size (Garcia-Inza *et al*., 2014). The strong positive relationship between fruit weight and pulp content observed in this study indicates that larger fruits generally allocate more biomass to the mesocarp, the edible portion of the fruit. This relationship highlights the potential of using fruit weight as an indirect selection criterion for identifying high-yielding genotypes (Mori and Cipriani, 2023). Similarly, the strong association between fruit and seed weight reflects coordinated development, suggesting that the genotypes differ in resource allocation efficiency between seed and pulp tissues (Wetzstein *et al*., 2011).

Biochemical composition and quality attributes

The biochemical composition of fruits exhibited wide and statistically meaningful variations among the eighteen palmyrah palm genotypes, confirming the existence of substantial genotypic diversity for fruit quality traits (Table 3). Parameters such as total soluble solids (TSS), sugars, acidity, and antioxidant components revealed clear differentiation, reflecting the nutritional and processing potential of the germplasm.

The total soluble solids (TSS), which reflect soluble carbohydrate accumulation and overall sweetness, ranged from 15.7°Brix in PPG-16 to 22.0°Brix in PPG-17. Genotypes PPG-12 (21.5°Brix), PPG-8

(20.8°Brix), and PPG-13 (20.1°Brix) also recorded higher values, suggesting superior sweetness and flavour intensity. Conversely, PPG-11 and PPG-16 displayed significantly lower TSS, implying comparatively bland taste. These variations may arise from differences in carbohydrate metabolism and fruit maturity at harvest, emphasizing their importance in genotype selection for table or processing purposes. A similar trend was observed in **total sugar content**, which varied between 13.7% (PPG-11) and 20.1% (PPG-17). Genotypes exhibiting significant higher total sugars, such as PPG-12, PPG-8, and PPG-13, correspondingly possessed elevated TSS values, indicating a strong positive association between the two parameters. The lowest sugar concentration in PPG-11 and PPG-16 suggests lower photosynthetic assimilate partitioning into fruit pulp. **Reducing sugars**, which largely determine sweetness perception and fermentation efficiency, fluctuated between 10.6% (PPG-6) and 17.2% (PPG-17). The high reducing sugar levels in PPG-17, PPG-12, and PPG-13 denote enhanced enzymatic conversion of non-reducing sugars, contributing to their higher palatability. On the contrary, PPG-6 and PPG-11 recorded lower reducing sugars, which could influence the sensory appeal and suitability of these genotypes for processing into sweet products. The **titratable acidity** ranged from 0.22% in PPG-7 to 0.37% in PPG-16, indicating significant variable acid–sugar balance across genotypes. Fruits with lower acidity, such as PPG-7, PPG-8, and PPG-12, were correspondingly higher in TSS, yielding a favourable **TSS: acidity ratio**, a key indicator of flavour quality. The highest TSS: acidity ratio (88.0) was recorded in PPG-17, followed by PPG-7 (87.7) and PPG-12 (86.0), highlighting their superior sweetness and consumer acceptability. By contrast, PPG-16 exhibited the lowest ratio (42.4) due to its relatively high acidity, producing a less balanced flavour profile. **Ascorbic acid content** varied extensively, from 19.4 mg/100 g in PPG-11 to 46.7 mg/100 g in PPG-10. The relatively higher ascorbic acid concentration in PPG-10 indicates its greater antioxidant potential and nutritional superiority, while PPG-11 and PPG-16 showed significant lower values, signifying reduced vitamin C accumulation. Interestingly, genotypes with moderate TSS and sugar levels, such as PPG-10 and PPG-7, maintained higher ascorbic acid content. Considerable diversity was also recorded for **phenolic content**, which ranged from 23.4 mg GAE/100 g in PPG-11 to 45.8 mg GAE/100 g in PPG-10. Elevated phenol levels in PPG-10, PPG-17, and PPG-5 indicate their potential as rich sources of natural antioxidants and their suitability for value-added nutraceutical applications. On the other hand, PPG-6, PPG-11, and PPG-16 exhibited comparatively lower phenolic concentrations. The **antioxidant activity**, measured through DPPH radical scavenging, ranged from 45.2% in PPG-11 to 77.3% in PPG-17. The strong antioxidant capacity recorded in PPG-17, PPG-7, and PPG-5 corresponds with their elevated phenolic and ascorbic acid contents, demonstrating a synergistic effect of both classes of compounds. The relatively lower antioxidant activity in PPG-11 and PPG-16 suggests a deficiency in these bioactive metabolites.

Biochemical characterization further revealed substantial variation in total soluble solids (TSS), sugar fractions, acidity, and antioxidant constituents. High TSS and sugar levels in genotypes such as PPG-17 and PPG-12 indicate superior sweetness and better consumer preference. The close association between TSS and reducing sugar content suggests a shared metabolic pathway in carbohydrate accumulation during ripening (Durán-Soria *et al*., 2020). Similar patterns have been reported in date palm and coconut, where sugar enrichment during fruit maturation results from increased enzymatic hydrolysis of polysaccharides and conversion of organic acids into soluble sugars (Sharif, 2019). Acidity levels varied considerably among genotypes, influencing the overall taste and sugar–acid ratio (TSS: acidity), which serves as a reliable indicator

of flavour balance. Genotypes with high TSS: acidity ratios were generally more palatable and suitable for fresh consumption. The inverse relationship between TSS and acidity observed in some genotypes may be attributed to progressive utilization of organic acids as respiratory substrates during ripening (Durán-Soria *et al*., 2020). Antioxidant parameters, including ascorbic acid and phenolic content, also displayed pronounced differences. Fruits rich in these compounds exhibited enhanced antioxidant activity, suggesting a synergistic effect of vitamin C and phenolics in quenching free radicals. This relationship is consistent with earlier observations in tropical fruits such as mango and date palm, where phenolic metabolism contributes significantly to antioxidant defence mechanisms. The high phenol and ascorbic acid contents in certain genotypes imply their potential utility in functional food development and nutraceutical industries (Nowak *et al*., 2018).

Correlation analysis among important morphological and biochemical parameters

Correlation analysis among the studied traits of palmyrah palm genotypes revealed several significant positive relationships, indicating close interdependence between morphological and biochemical parameters influencing fruit quality and yield potential (Table 4 and figure 1). Fruit weight exhibited a very strong and positive association with pulp content (r = 0.963) and seed weight (r = 0.838), suggesting that heavier fruits tend to possess higher edible pulp mass as well as larger seeds. This relationship confirms that fruit size is a reliable indicator of potential pulp yield. A moderately high correlation of fruit weight with the TSS: acidity ratio (r = 0.644) and ascorbic acid (r = 0.551) further implies that larger fruits generally maintain better sweetness–acidity balance and vitamin C content. Among biochemical parameters, total soluble solids showed an exceptionally high positive correlation with reducing sugar (r = 0.904) and TSS: acidity ratio (r = 0.842), reflecting that sweetness and flavour balance are largely governed by sugar accumulation. The significant correlation of TSS with antioxidant activity (r = 0.618) suggests that higher sugar concentration may accompany enhanced antioxidant potential. Phenol content showed a notable positive correlation with antioxidant activity (r = 0.666) and ascorbic acid (r = 0.631), confirming the combined contribution of phenolics and vitamin C to the total antioxidant capacity of palmyrah fruits. Similarly, shape index was moderately correlated with TSS (r = 0.562) and TSS: acidity ratio (r = 0.610), indicating that more elongated fruits may possess comparatively sweeter pulp. Overall, the correlation pattern highlights that selection for higher fruit weight and TSS will simultaneously enhance pulp yield, sweetness, and antioxidant potential. These inter-trait relationships provide a valuable basis for identifying superior genotypes for both nutritional quality improvement and commercial exploitation.

Correlation analysis provided valuable insight into the interdependence of morphological and biochemical traits. The strong positive correlation between fruit weight and pulp content reinforces the importance of size-related parameters as indicators of yield potential. Similarly, the high correlation between TSS and reducing sugars confirms that sweetness is largely governed by the accumulation of simple carbohydrates (Lenucci *et al*., 2022). The association of TSS with antioxidant activity suggests that sugar metabolism may also influence the synthesis of secondary metabolites, possibly through shared metabolic intermediates (Elhadi *et al*., 2023). Furthermore, the positive correlation between phenol content and antioxidant activity confirms that phenolic compounds are major contributors to the antioxidant potential of palmyrah fruits (Ouamnina *et al*., 2024).

Collectively, these findings emphasize the complex interplay between fruit morphology, biochemical composition, and antioxidant metabolism. The observed trait

associations provide a foundation for selection strategies targeting both high yield and superior fruit quality. Genotypes such as PPG-17, PPG-12, and PPG-13, which exhibited large fruits, high pulp recovery, elevated sugar concentration, and strong antioxidant capacity, represent promising candidates for breeding programs and commercial exploitation.

CONCLUSION

The study revealed significant genotypic variability among palmyrah palm accessions in terms of fruit morphology and biochemical composition. Strong associations between fruit weight, pulp content, and sugar traits highlight the potential for simultaneous improvement of yield and quality through targeted selection. Genotypes such as PPG-17, PPG-12, and PPG-13 demonstrated superior performance in sweetness and antioxidant potential and size as well as pulp content, indicating their suitability for large-scale cultivation and processing. The positive correlations among sugars, acids, and antioxidant compounds underscore an integrated metabolic regulation influencing fruit quality. Overall, the findings provide a scientific basis for identifying elite genotypes and developing breeding strategies aimed at enhancing productivity, nutritional value, and industrial utilization of palmyrah palm in diverse growing environments.

CONFLICT OF INTEREST STATEMENT

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

REFERENCES:

AOAC (Association of Official Analytical Chemists). 1990. Official Methods of Analysis Vol-I (15th Edition) Ed: Kenneth Helrich, AOAC, Virginia, pp:83.

Brand-Williams, W., Cuvelier, M. E. and Berset, C. 1995. Use of a free radical method to evaluate antioxidant activity, *LWT - Food Sci. Tech.*, **28**(1):25-30.

Deb, P., Mukherjee, P. K. and Das, P. 2024. Morpho-biochemical characterization of pomelo (*Citrus grandis* L.) accessions and assessment of bioactive compounds under western part of West Bengal, *Int. J. Min. Fruit Med. Arom. Plants*, **10**(1):112-124. https://doi.org/10.53552/ijmfmap.10.1.2024.112-124.

Dewanto, V., Wu, X., Adom, K. K., and Liu, R. H. 2002. Thermal processing enhances the nutritional value of tomatoes by increasing total antioxidant activity. *J. Agric. Food Chem*., **50** (10): 3010–3014.

Durán-Soria, S., Pott, D. M., Osorio, S. and Vallarino, J. G. 2020. Sugar signaling during fruit ripening, *Front. Plant Sci*., **28**:11:564917. https://doi.org/10.3389/fpls.2020.564917.

Elhadi, M. Y., Ornelas-Paz, J. J., Jeffrey, K. B., García-Solís, P. and Celis, M. E. M. 2023. The contribution of mango fruit (*Mangifera indica* L.) to human nutrition and health, *Arabian J. Chem*., **16**(7):104860.https://doi.org/10.1016/j.arabjc.2023.104860.

Garcia-Inza, G., Castro, D., Hall, A.J. andMaria, R. 2014. Responses to temperature of fruit dry weight, oil concentration, and oil fatty acid composition in olive (*Olea europaea* L. var. 'Arauco'), *Eur. J. Agron*., **54**: 107–115. https://doi.org/10.1016/j.eja.2013.12.005.

Gnanavelrajah, N., Theepika, S., Karthigesu, J. and Raveendran, S. 2025. Palmyrah (*Borassus flabellifer*) palm land-use system: A potential key tool for

enhancing carbon stock and floristic diversity in a dry zone tropical landscape. *Trees, Forests and People*, **20**: 100827.https://doi.org/10.1016/j.tfp.2025.100827.

Jayaraj, D., Irene Vethomoni, P., Auxcilia, J., Manivannan, N., Manivannan, M. I. and Anand, M. 2025. Integrative potential of palmyrah (*Borassus flabellifer*) in climate mitigation and pharmaceutical innovation, *Plant Sci. Tod*., **4**: 9103. https://doi.org/10.14719/pst.9103

Lane, J. H. and Eynon, L. 1923. Methods for determination of reducing and non-reducing sugars. *J. Sci*., **42**: 32-37.

Lenucci, M. S., Tornese, R., Mita, G. and Durante, M. 2022. Bioactive compounds and antioxidant activities in different fractions of mango fruits (*Mangifera indica* L., cultivar Tommy Atkins and Keitt), *Antioxidants (Basel)*. **11**(3):484. https://doi.org/10.3390/antiox11030484.

Mori, D. G. and Cipriani, G. 2023. Marker-assisted selection in breeding for fruit trait improvement: A review, *Int. J. Mol. Sci.*, **24**(10): 8984. https://doi.org/10.3390/ijms24108984.

Mukherjee, P. K., Deb, P., Kumar, M. and Mondal, A. 2023. Studies on morpho-biochemical changes of longan [*Euphoria longana* (Lour) Steud.] fruit during fruit growth and development for determination of maturity, *Int. J. Min. Fruit Med. Arom. Plants*, **9**(2): 177-184. https://doi.org/10.53552/ijmfmap.9.2.2023.177-184.

Nowak, D., Gośliński, M., Wojtowicz, E. and Przygoński, K. 2018. Antioxidant properties and phenolic compounds of vitamin C-rich juices, *J. Food Sci*., **83**(8):2237-2246. https://doi.org/10.1111/1750-3841.14284.

Ouamnina, A., Alahyane, A., Elateri, I., Boutasknit, A. and Abderrazik, M. 2024. Relationship between phenolic compounds and antioxidant activity of some moroccan date palm fruit varieties (*Phoenix dactylifera* L.): A two-year study, *Plants*, **13**(8): 1119. https://doi.org/10.3390/plants13081119.

Penkey, Y., Pavan, S. and Geetha, G. 2025. Palmyrah Palm: A Sustainable Crop for a Healthier Future. *Agri Articles*, **5**: 1179-1180.

Ranganna, S. 1986. Handbook of Analysis and Quality Control of Fruit and Vegetable Products. 2nd Edition, Tata McGrow-Hill Education, New York.

Rao, M. C. S., Swami, D. V., Ashok, P., Nanda S. P. and Rao, B. B. 2021. Scope, nutritional importance and value addition in palmyrah (*Borassus flabellifer* L.): an under exploited crop,*In*: Bioactive compounds - biosynthesis, characterization and applications, Intech Open, London, 2021, *Eds*: Leila Queiroz Zepka and Tatiele Casagrande do Nascimento and Eduardo Jacob-Lopes, chapter: 12. https://doi.org/10.5772/intechopen.97501.

Sharif, H. A. B. M. 2019. Glucose, TSS and nutrient content of dates, mango, apple and banana: A comparative study, *Int. J. Biosci. Biochem*., **1**: 18-20. https://doi.org/10.33545/26646536.2019.v1.i1a.6.

Sridevi T. R., Arunachalam, R., Chandrakumar, M.,Parthasarathi, G. and Nisha, R. 2020. Potential review on palmyra (*Borassus flabellifer* L.). *Adv. in Res*., **2020**: 29-40. https://doi.org/10.9734/air/2020/v21i930229.

Vanitha, K., Ragavan, T., Gurusamy, A., Prabhakaran, J., Arthirani, B., Rani, A., Somasundaram, S., Dhanasekaran, S. K. and Bhargavi, M. B. 2025. Health benefits and neutracuticle properties of palmyra palm - A forgotten treasure, *Plant Sci. Tod*., **7**: 7398.https://doi.org/10.14719/pst.7398

Wetzstein, H., Zhang, Z., Ravid, N. and Wetzstein, M. 2011. Characterization of attributes related to fruit size in pomegranate, *Hort Sci.*, **46**: 908-912. https://doi.org/10.21273/HORTSCI.46.6.908.

Table 1: Geographical position of different palmyrah palm genotypes in three districts of West Bengal.

Sl. No.	Address	Latitute (ºN)	Longitude (ºE)
1.	Atgram, Nalhati, Birbhum	24.25	87.85
2.	Bhagabatipur, Nalhati, Birbhum	24.27	87.77
3.	Hazarpur, Sadinpur, Birbhum	24.23	87.83
4.	MaraBasahar, Hansan, Birbhum	24.19	84.84
5.	Dangram, Rampurhat, Birbhun	24.16	87.80
6.	Sahapur, Tarapith, Birbhum	24.10	87.82
7.	Kharasinpur, Mallarpur, Birbhum	24.05	87.73
8.	Beluti, Kotasur, Birbhum	23.94	87.75
9.	Muradihi, Sainthia, Birbhum	23.93	87.69
10.	Kaferpur, Kirnahar, Birbhum	23.78	87.88
11.	Nohana, Ahmadpur, Birbhum	23.80	87.70
12.	Bahadurpur, Bolpur, Birbhum	23.65	87.62
13.	Barabani, Asansol, West Burdwan	23.70	87.02
14.	Banshra, Ranigunj, West Burdwan	23.63	87.14
15.	Pandabeshwar, West Burdwan	23.69	87.25
16.	Unanshila, Ragunathpur, Bankura	23.51	86.71
17.	Gangajalghati, Bankura	23.45	87.06
18.	Kochdihi, Sonamukhi, Bankura	23.29	87.37

Table 2: Fruit physical characters of different palmyrah palm genotypes under western dry tract of West Bengal:

Palmyrah palm genotype (PPG)	Polar diameter(cm)	Equatorial diameter (cm)	Shape index	Fruit volume (ml)	Fruit weight (g)	Cap diameter (cm)	Single seed weight (g)	Pulp content (g)	Pomace content (g)
PPG-1	46.4	47.5	0.97	1480.5	1476.5	12.7	212.7	724.3	76.6
PPG-2	40.1	35.3	1.13	770.6	787.2	8.6	169.2	404.4	43.3
PPG-3	42.4	44.8	0.94	1210.2	1198.7	11.8	208.7	513.0	61.1
PPG-4	52.8	46.4	1.14	2340.5	1894.6	12.4	334.5	791.7	101.7
PPG-5	47.7	45.2	1.05	1450.0	1444.8	12.2	233.8	628.1	117.4
PPG-6	42.3	40.7	1.03	820.4	1019.6	11.7	197.6	369.8	59.9
PPG-7	54.7	50.4	1.08	2180.7	2049.3	13.5	260.2	1150.4	119.5
PPG-8	56.9	50.1	1.14	2000.2	2147.1	14.2	325.5	1047.9	125.3
PPG-9	55.3	50.3	1.09	2064.3	2178.5	9.7	289.8	1311.3	143.6
PPG-10	49.4	47.0	1.05	1813.6	1942.9	11.8	241.4	1069.5	121.7
PPG-11	47.2	48.2	0.97	1985.5	1740.4	13.3	220.7	962.1	118.5
PPG-12	54.1	51.4	1.05	2156.8	2217.7	12.4	262.1	1261.6	150.2
PPG-13	51.7	46.9	1.10	2202.4	2256.1	13.1	301.6	1239.9	144.8
PPG-14	46.6	47.8	0.97	1679.5	1519.4	9.7	239.2	730.4	72.1
PPG-15	42.0	45.5	0.92	1853.2	1748.2	11.8	251.5	893.6	102.4
PPG-16	49.5	52.3	0.94	1748.1	1899.6	12.0	246.7	1044.3	117.5
PPG-17	53.8	50.6	1.06	2354.3	2381.7	13.1	295.4	1340.5	156.8
PPG-18	54.1	49.2	1.10	2076.9	2154.3	12.3	302.3	1113.1	137.2
Mean	49.28	47.20	1.04	1788.20	1780.9	12.0	255.1	921.9	109.4
CV	15.61	18.69	16.96	20.23	24.8	11.51	17.3	22.3	32.4

Table 3: Fruit biochemical characters and antioxidant activity of different palmyrah palm genotypes under western dry tract of West Bengal:

Palmyrah palm genotype (PPG)	Total soluble solids (^{o}Brix)	Total sugar (%)	Reducing sugar (%)	Acidity (%)	TSS: Acidity ratio	Ascorbic acid content (mg/100g)	Phenol content (mgGAE/100g)	Antioxidant activity (% DPPH)
PPG-1	16.3	14.1	11.5	0.30	54.3	22.4	36.5	61.6
PPG-2	19.6	16.5	14.4	0.32	61.2	26.6	39.6	67.4
PPG-3	18.2	16.6	13.7	0.35	52.0	21.7	26.2	50.8
PPG-4	17.8	14.2	11.9	0.29	61.3	27.3	37.7	58.9
PPG-5	19.5	16.3	13.3	0.33	59.0	25.7	40.1	65.4
PPG-6	17.6	13.7	10.6	0.30	58.6	24.4	25.8	49.0
PPG-7	19.3	17.4	13.1	0.22	87.7	34.9	37.4	71.3
PPG-8	20.8	18.9	14.8	0.25	83.2	32.5	32.0	65.6
PPG-9	19.4	16.4	13.4	0.24	80.8	30.2	26.7	57.0
PPG-10	16.2	15.5	12.7	0.27	60.0	46.7	45.8	51.5
PPG-11	15.9	13.7	11.2	0.33	48.1	19.4	23.4	45.2
PPG-12	21.5	19.3	16.5	0.25	86.0	35.9	31.6	50.1
PPG-13	20.1	18.6	14.5	0.24	83.7	32.4	34.3	57.6
PPG-14	16.5	14.8	11.7	0.28	58.9	27.1	27.7	48.9
PPG-15	18.3	16.3	13.4	0.29	63.1	25.3	32.8	55.3
PPG-16	15.7	14.5	10.9	0.37	42.4	21.7	25.3	48.5
PPG-17	22.0	20.1	17.2	0.25	88.0	34.6	42.1	77.3
PPG-18	18.4	16.0	13.5	0.26	70.7	31.9	35.7	64.6
Mean	18.5	16.2	13.2	0.28	66.6	28.9	33.3	58.1
CV	10.1	11.7	13.3	14.1	14.2	22.4	18.9	15.1

Table 4: Pearson Correlation coefficients of important fruit morphological and biochemical characters of palmyrah palm genotypes:

Parameters	Shape index	Fruit weight	Seed weight	Pulp content	TSS	Reducing sugar	TSS: Acidity ratio	Ascorbic acid	Phenol	Antioxidant activity
Shape index	1.000									
Fruit weight	0.277	1.000								
Seed weight	0.504*	0.838	1.000							
Pulp content	0.223	0.963*	0.692	1.000						
TSS	0.562	0.370	0.398	0.366	1.000					
Reducing sugar	0.400	0.438	0.345	0.469	0.904*	1.000				
TSS:Acidity	0.610*	0.644	0.588	0.648*	0.842*	0.754*	1.000			
Ascorbic acid	0.507	0.551	0.406	0.562	0.387	0.501	0.636*	1.000		
Phenol	0.470	0.153	0.162	0.124	0.303	0.403	0.313	0.631*	1.000	
Antioxidant activity	0.559	0.220	0.307	0.198	0.618	0.542	0.569	0.293	0.666*	1.000

*5% level of significance

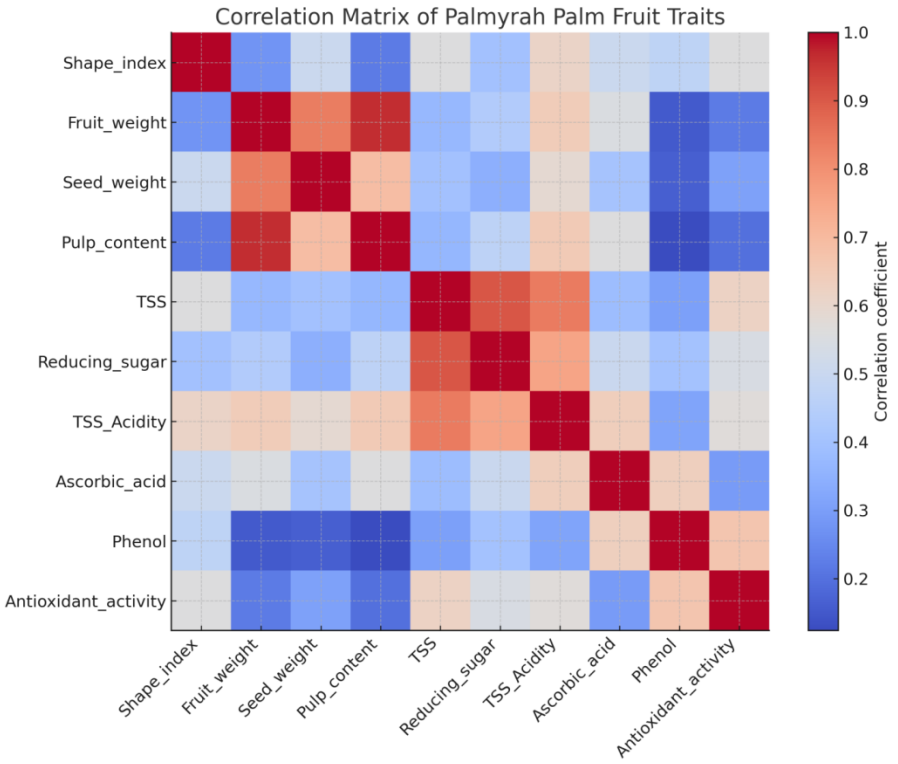

Figure 1: Correlation heat map of important fruit morphological and biochemical characters of palmyrah palm genotypes