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PIGMENTS AND FLAKE COLOUR DIVERSITY IN JACKFRUIT (*Artocarpus heterophyllus* LAM): BIOSYNTHESIS AND APPLICATIONS

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ABSTRACT

Jackfruit (*Artocarpus heterophyllus* Lam.) pulp displays an unusually wide colour range, from pale cream and yellow through deep yellow and saffron to orange and orange-red. This diversity is increasingly recognised as a biochemically meaningful trait, not merely a descriptive one. Carotenoid profiling by HPLC-PDA-MS/MS has identified eighteen carotenoids in jackfruit pulp. All-trans-lutein and all-trans-β-carotene are the dominant components, with total concentrations that vary considerably between batches (de Faria *et al*., 2009). Comparative studies of accessions differing in flake colour report that deep-yellow flakes tend to accumulate more flavonoids and show higher antioxidant activity, whereas orange-red flakes are comparatively richer in β-carotene and phenolic acids (Natta *et al*., 2023). Germplasm surveys from Karnataka similarly associate orange and orange-red accessions with elevated carotenoid and lycopene concentrations (Karunakaran *et al*., 2025). An integrated transcriptome-metabolome comparison of light-yellow, yellow and orange cultivars has extended these observations to the molecular level, reporting differential accumulation of 32 carotenoids and 25 flavonoids alongside differential expression of biosynthetic genes spanning both pathways (Liang *et al*., 2026). Pigment accumulation also changes through fruit development, tracking the transition from chlorophyll-dominated immature tissue to carotenoid-rich ripe pulp. CIE L*ab** colourimetry captures these changes quantitatively and correlates with direct pigment analysis without substituting for it. This review synthesises evidence on jackfruit pigment chemistry, biosynthesis and molecular regulation, genotypic and developmental variation, colour-pigment relationships, nutritional and processing significance and breeding implications. Findings directly supported by primary data are distinguished throughout from those that remain associative or require further verification. Persistent gaps include the restricted number of genotypes examined in molecular studies, incomplete standardisation of sampling and analytical methods, limited bioaccessibility data and the near-total absence of studies linking individual pigments to instrumental colour across diverse germplasm. Closing these gaps through cording phenotyping, chromatographic and metabolomic profiling, transcriptomic and marker-assisted selection would support the identification of jackfruit genotypes that combine distinctive colour with enhanced nutritional and processing quality.

Key words : *Artocarpus heterophyllus*, Jackfruit, Pulp colour, Carotenoid, Lutein, β-carotene, Flavonoids, Pigment biosynthesis, CIE L*ab**, Metabolomic, Transcriptomics.

Introduction

Jackfruit (*Artocarpus heterophyllus* Lam., family Moraceae) is the largest tree-borne fruit in cultivation. It has been a food crop across South and Southeast Asia for a long time and the pulp, seeds and other fruit components are consumed fresh or processed into a wide range of products. Beyond its agronomic importance, jackfruit has drawn growing scientific attention for a phytochemical composition that includes carotenoids, flavonoids, phenolic acids, vitamins and minerals (Baliga *et al*., 2011; Ranasinghe *et al*., 2019). Among these constituents, the pigments are distinctive because they determine the visual appearance of the edible pulp, and they also carry nutritional antioxidant significance. The

species is generally considered to have originated in the Western Ghats of India, and it is the most important commercial member of a genus of more than 70 species (Karunakaran *et al*., 2024).

One of the most conspicuous features of the species is the range of colour shown by its edible flakes. Depending on genotype, maturity and growing conditions, pulp colour can vary from cream or pale yellow through deep yellow and saffron to orange and orange-red depending on genotype, maturity and growing conditions (Ranasinghe *et al*., 2019; Liang *et al*., 2026). The variation is not simply cosmetic. Colour classes have repeatedly been linked to differences in the accumulation of bioactive compounds (Natta *et al*., 2023; Liang *et al*., 2026) and carotenoids in particular account for much of the yellow to orange spectrum. The first detailed chromatographic survey of jackfruit carotenoids used HPLC coupled to photodiode-array and tandem mass-spectrometric detection. It identified eighteen carotenoids, fourteen of them reported in the species for the first time. All-trans-lutein (24-44% of the identified fraction) and all-trans-â-carotene (24-30%) were the principal components. Total carotenoid content varied roughly four-fold between the three fruit batches examined, from 34.1 µg/100 g to 129.0-150.3 µg/100 g (de Faria *et al*., 2009).



Fig. 1 : Diversity of flake colour in Jackfruit.

Pigmentation in jackfruit is not restricted to carotenoids. Flavonoids and other phenolic compounds also differ among tissues and genotypes and they may contribute both to colour and to antioxidant capacity. A comparative evaluation of fifteen clonal accessions with contrasting flake colours found that deep-yellow flakes carried the highest flavonoid content, antioxidant activity, ascorbic acid and α-glucosidase-inhibitory activity, while orange-red flakes were distinguished by the highest β-carotene and total phenolic content together with the strongest α-amylase and β-glucosidase-inhibitory activity and the highest concentrations of sinapic acid, ferulic acid and quercetin (Natta *et al*., 2023). These results show that colour classes differ not only in pigment quantity, but in the composition of the broader phytochemical prolife.

The nutritional relevance of these pigments follows from their chemistry. β-carotene is a provitamin A carotenoid. Lutein and other xanthophylls, by contrast, are of interest mainly for their antioxidant properties rather than vitamin A activity. The nutritional value of a given jackfruit sample therefore depends on which carotenoids are present and in what proportion, not on total carotenoid content alone. Carotenoids have been documented in jackfruit for several decades, but most of the earlier literature was descriptive, it reported total carotenoid or flavonoid content or antioxidant capacity without resolving how genotype, biosynthesis and visible colour relate to one another.

The gap has begun to close with the application of transcriptomics and metabolomics. An integrated analysis comparing jackfruit cultivars with light yellow, yellow and orange pulp identified 32 differentially accumulated carotenoids and 25 differentially accumulated flavonoids among the three phenotypes. It also found differential expression of genes spanning both the carotenoid pathway (*PSY, PDS, ZDS, LCYE, LUT5, ZEP* and *VDE*) and the flavonoid pathway (*PAL, C4H, 4CL, F3H, FLS, ANS* and *ANR*) (Liang *et al*., 2026). In recent study, specific numerical findings are treated throughout this review as an important but not yet independently replicated line of evidence. The general picture it supports that pulp colour reflects coordinated shifts across multiple metabolite classes rather than the level of one pigment is nonetheless consistent with the broader biochemical literature summarised below.

Colour is also a practical trait. It influences consumer acceptance, offers a low-cost criterion for germplasm screening and may guide the selection of pigment-rich genotypes for fresh consumption, natural colourants or functional-food applications. Carotenoids are chemically labile; however, their retention through maturation, handling and processing is governed by temperature, oxygen, light and storage duration (Saxena *et al*., 2012), so any practical use of jackfruit pigments must consider stability alongside initial concentration.

This review draws together the fragmented literature on jackfruit pigment chemistry, biosynthesis, genotypic and developmental variation, instrumental colour measurement, postharvest behaviour and breeding relevance. Where a finding rests on a single, not-yet-

replicated source, or where a cited value could not be independently confirmed against the original publication, this is stated explicitly rather than left implicit. The aim is an evidence-graded synthesis, not merely a descriptive synthesis.

Colour Diversity in Jackfruit

Flake colour is among the most commonly used points of variation used to describe jackfruit germplasm. It spans white or cream, pale yellow, yellow, deep yellow, orange and coppery orange-red pulp. Germplasm surveys consistently record this range. A characterisation of jackfruit genotypes in North-East India described white, yellow, orange and coppery-red flake types and proposed that flake characteristics may track specific patterns of photosynthate partitioning within the tree, alongside broader morphological variability (Dey, 2024; Karunakaran *et al*., 2025).

Colour class and biochemical composition move together. In an evaluation of white, yellow and orange flaked varieties, orange flakes carried higher carotenoid and total soluble solids content and had the softest texture. White flakes were firmest and yellow flakes fell between the two (Balamaze *et al*., 2019). A parallel pattern emerges from Indian germplasm, among 94 seedling-originated accessions evaluated in southern Karnataka, orange and orange-red types were enriched in carotenoids and lycopene relative to paler accessions with two representative accessions: the orange JT-04 (5.83 mg/100g carotenoids, 1.12 mg/100g lycopene). Colour intensity clearly does not scale with either compound in a simple, linear way (Karunakaran *et al*., 2025). A comparable colour-biochemistry association was reported among fifteen clonal accessions from eastern India, where colour groups diverged in flavonoid and carotenoid content as much as in appearance. Deep yellow flakes recorded the highest flavonoid concentration, antioxidant activity, ascorbic acid and α-glucosidates inhibition, whereas orange-red flakes exhibited the highest β-carotene and phenol contents, together with greater inhibition of α-amylase and β-glucosidase (Natta *et al*., 2023).

Southern Karnataka and Tumakuru (Tumkur) district in particular, is one of the richest documented sources of flake-colour variation in India. Karunakaran *et al*. (2025) selected Tumakuru as their main study area because its range of climatic zones and ecological conditions coincides with marked variability in fruit traits and they describe Chelur hobli in Gubbi taluk as the largest jackfruit belt in southern Karnataka. Of the seedling-origin accessions they classified from Tumakuru and Bengaluru Rural districts, 15 had yellow, 18 yellow-orange, 37 orange and 23 orange-red flakes; the orange-red class, which tended to carry more carotenoids and lycopene, came mostly from Gubbi taluk. An independent survey of elite dessert types in four Karnataka districts also drew most of its selections from Tumkur district, with bulb colour ranging from cream through light yellow and yellow to orange (Suneel *et al*., 2023). Surveys of the traditional jackfruit-growing tracts of southern Karnataka carried out by ICAR-IIHR between 2014 and 2018 identified two farmer-selected varieties with coppery-red flakes, 'Siddu' and 'Shankara' (Karunakaran, 2019), both maintained by farmers in Tumakuru district. A later study examined the economic viability of conserving such red-fleshed types on farm and consumer preferences for them (Karunakaran *et al*., 2026).

The molecular basis for these associations has begun to be examined directly. Comparing cultivars with light yellow, yellow and orange pulp, an integrated transcriptome-metabolome study reported differential accumulation of 32 carotenoids and 25 flavonoids. This indicates that colour differences arise from coordinated shifts across many metabolites, not from a single dominant pigment (Liang *et al*., 2026). The finding is consistent with and extends an earlier chromatographic

Table 1 : Associations reported between jackfruit flake colour and pigment/biochemical composition.

Flake colour	Major pigment/ biochemical association	Reference
White	White flakes were firmest	Balamaze *et al*. (2019)
Orange	Orange flakes were softest and associated with higher carotenoids and total soluble solids	
Deep yellow	Highest flavonoids, antioxidant activity, ascorbic acid;	Natta *et al*. (2023)
Orange red	highest β-carotene, phenolics, sinapic/ferulic acid, quercetin	
Orange	5.83 mg/100 g carotenoids, 2.26 mg/100 g lycopene	Karunakaran *et al*. (2025)
Orange-red	4.43 mg/100 g carotenoids, 1.12 mg/100 g lycopene	
White to deep orange coloured	Significant variability in total carotenoids and total flavonoids among genotypes	Dey (2024)

demonstration that jackfruit carotenoids are derived from a compositionally complex mixture rather than being dominated by one compound (de Faria *et al.*, 2009). Taken together, the available evidence supports treating jackfruit pulp colour as an outcome of genotype, developmental stage, biosynthetic activity and growing environment acting jointly, rather than as a fixed visual label. Colour class and pigment concentrations are consistently associated, so colour can serve as a rapid, low-cost first pass in germplasm evaluation. It cannot substitute for chemical analysis, two accessions in the same colour class can carry different absolute pigment loads as JT-04 and JG-14 illustrate. Analytically similar total carotenoid values can also correspond to visually distinct pulp if the underlying carotenoid mixtures differ in composition.

Table 2 : Carotenoid, flavonoid and phenolic contents of *Artocarpus heterophyllus*.

Pigments	Variety	References
Total carotenoids	34.1 to 150.3 µg/100 g	de Faria *et al*. (2009)
	0.49 to 5.83 mg/100 g FW	Karunakaran *et al*. (2025)
	1.63 to 4.75 mg/100 g	Hazarika *et al*. (2025)
	Up to 3131.88 µg/100 g	Gomez *et al*. (2024)
	4.4 to 20.6 mg/kg	Kaur *et al*. (2024)
β-Carotene	0.62 to 0.91 µg/g DW	Liang *et al*. (2026)
	244.84 IU	Garcia-Mateos (2021)
α-Carotene	0.36 to 0.86 µg/g DW	Liang *et al*. (2026)
Lycopene	0.24 µg/g DW	Liang *et al*. (2026)
	0.04 to 2.26 mg/100 g FW	Karunakaran *et al*. (2025)
Lutein	0.21 to 3.05 µg/g DW	Liang *et al*. (2026)
Zeaxanthin	12.04 to 24.00 µg/g DW	Liang *et al*. (2026)
Violaxanthin	0.05 to 0.68 µg/g DW	Liang *et al*. (2026)
Neoxanthin	0.10 to 0.19 µg/g DW	Liang *et al*. (2026)
Total flavonoids	1.62 to 12.97 mg CE/100 g	Karunakaran *et al*. (2025)
	34.11 to 188.01 mg CE/100 g	Cheng *et al*. (2025)
	12.9 to 30.3 mg QE/kg	Kaur *et al*. (2024)
	9.86 mg QE/100 g FW	Garcia-Mateos (2021)
Naringenin chalcone	0.02 to 0.56 nmol/g DW	Liang *et al*. (2026)
Taxifolin	0.05 to 2.18 nmol/g DW	Liang *et al*. (2026)
Eriodictyol	0.04 to 1.71 nmol/g DW	Liang *et al*. (2026)
Catechin	0.61 to 1.31 nmol/g DW	Liang *et al*. (2026)
Apigenin	0.01 to 3.40 nmol/g DW	Liang *et al*. (2026)
Luteolin	0.01 to 0.51 nmol/g DW	Liang *et al*. (2026)
Total phenols	14.23 to 77.60 mg GAE/100g FW	Karunakaran *et al*. (2025)
	46.87 to 235.45 mg GAE/100g FW	Cheng *et al*. (2025)
	365.3 to 738.6 GAE/kg	Kaur *et al*. (2024)
	58.44 mg GAE/100 g FW	Garcia-Mateos (2021)
	7.69 mg GAE/g DW	Pu *et al*. (2023)

Pigments associated with Jackfruit Pulp colour

The colour of jackfruit pulp reflects the combined presence of several structurally distinct classes of pigment and pigment-related metabolites. Carotenoids are the best characterised and provide the principal chemical basis for the yellow-to-orange spectrum. Flavonoids and other phenolics vary substantially among colour types and contribute to the broader phytochemical profile, though their direct optical role is less well established. Chlorophylls dominate immature, green tissue and are progressively lost during ripening. These three pigment classes differ markedly in chemistry, biosynthetic origin and probable contribution to visible colour, so they are treated separately below, and their relative importance to hue and intensity should not be assumed to be interchangeable.

Carotenoids

Carotenoids are lipid-soluble isoprenoid pigments. They are divided into two groups: hydrocarbon carotenes (eg., α- and β-carotene, lycopene) and oxygenated xanthophylls (*e.g.*, lutein, zeaxanthin, violaxanthin. In plants, they participate in photosynthesis and photoprotection. In the diet, several members of the class carry provitamin A or antioxidant activity. The reference characterization of the jackfruit carotenoid fraction remains the HLC-DA-MS/MS survey of de Faria *et al*. (2009). It resolved eighteen compounds, including lutein, β-carotene, α-carotene, β-cryptoxanthin, neoxanthin and violaxanthin derivatives and showed that no single pigment dominates the profile. all-trans-lutein (24-44%) and all-trans-β-carotene (24-30%) were

the largest fractions, with all-trans-neoxanthin, 9-cis-neoxanthin and 9-cis-violaxanthin each contributed smaller but consistent shares. Total carotenoid content differed roughly four-fold among the three batches analyzed (129.0-150.3 µg/100 g), a spread the authors attributed to genetic and/or agronomic factors rather than analytical variability.

An earlier survey of jackfruit genotypes with cream, light yellow, dark yellow, red and orange pulp reported markedly higher carotinoid concentration in red and orange types than in paler ones. β-carotene, α-carotene and lycopene all varying substantially among genotypes (Shyamalamma *et al*., 2017). Most recent metabolomic work reinforces the qualitative point that colour differences reflect the carotenoid mixture as a whole rather than a single compound. Comparing light-yellow, yellow and orange cultivars, Liang *et al*. (2026) reported 32 differentially accumulated carotenoids, with zeaxanthin together with violaxanthin dipalmitate prominent in the orange phenotype. Carotenoid and lycopene concentration recorded across Karnataka germplasm tracked colour intensity in orange and orange-red accessions, though not in strict proportion to hue (Karunakaran *et al*., 2025).

β-carotene

β-carotene is nutritionally significant as a provitamin A carotenoid and is closely linked to orange colour development. Among fifteen clonal accessions differing in flake colour, the orange-red type had the highest β-carotene concentrations, while paler accessions had less (Natta *et al*., 2023). Biosynthetically, β-carotene arises from cyclisation of lycopene by lycopene β-cyclase and is itself the precursor of oxygenated derivatives such as â-cryptoxanthin and zeaxanthin. Liang *et al*. (2026) reported differential expression of genes governing this branch among contrasting-colour cultivars. This is consistent with, though not proof of, a regulatory role for these genes in the observed pigment differences.

Lutein and other xanthophylls

Lutein is the single largest component of the jackfruit carotenoid fraction identified by de Faria *et al.* (2009) and is associated mainly with yellow rather than orange hue. Metabolomic comparison across colour phenotypes similarly places lutein alongside zeaxanthin in the light-yellow and yellow groups (Liang *et al*., 2026). Neoxanthin and violaxanthin derivatives, also detected by de Faria *et al*. (2009), are pathway products or intermediates rather than end-point pigments in the classical scene and the identification of an esterified form, violaxanthin dipalmitate, has been identified as a metabolite associated with the orange phenotype (Liang *et al*., 2026). This illustrates why total-carotenoid measurements, which do not distinguish esterified from free forms, can obscure biologically relevant differences.

Lycopene

Lycopene is the acyclic precursor from which both carotene branches derive. It occurs in jackfruit pulp at concentrations that are generally modest relative to lutein and â-carotene, but it varies considerably among genotypes. Higher concentrations have been reported in red and orange pulp than in cream or yellow pulp (Shyamalamma *et al*., 2017) and independently in orange and orange-red Karnataka accessions relative to paler ones (Karunakaran *et al*., 2025). Several carotenoids co-vary with colour; lycopene should be read as one contributor among several rather than as the determinant of red-orange hue in jackfruit.

Flavonoids and other phenolic pigments

Flavonoids are a chemically diverse group: flavones, flavonols, flavanones, chalcones and related structures. Their contribution to the visible colour of jackfruit pulp is considerably less well established than that of the carotenoids, even though their concentrations clearly differ among colour classes. Among fifteen clonal accessions, deep-yellow flakes carried the highest flavonoid content and antioxidant activity, while orange-red flakes were instead distinguished by higher β-carotene and phenolic content (Natta *et al*., 2023). This pattern that associates flavonoid abundance with one colour class; it does not demonstrate that flavonoids themselves produce that colour.

The most direct evidence linking flavonoid metabolism to pulp-colour phenotype comes from Liang *et al*. (2026). They reported 25 differentially accumulated flavonoids among light-yellow, yellow and orange cultivars. Naringenin chalcone, eriodictyol and taxifolin were enriched in the light-yellow cultivar, phlorizin in the yellow cultivar and apigenin and luteolin in the orange cultivar, alongside differential expression of PAL, C4H, 4CL, F3H, FLS, ANS and ANR. These findings describe an association between specific flavonoids and specific colour phenotypes. They show that any of these compounds is the optical chromophore responsible for the observed hue. Differential accumulation alongside differential gene expression is best read as evidence of coordinated metabolic reprogramming rather than direct proof of a colour-determining role for individual flavonoids. Further pigment-specific spectroscopic work would be needed to settle which, if any, flavonoids contribute directly to jackfruit pulp colour, as opposed to simply co-varying

with it.

Chlorophylls and the green-to-yellow/orange transition

Chlorophylls dominate immature jackfruit tissue and are progressively degraded during ripening, a pattern general to fleshy fruit in which the loss of green pigment unmasks carotenoids that were already present or newly synthesised. Chlorophyll turnover has not been characterised in jackfruit pulp with the same resolution as carotenoid accumulation. The transition from green to yellow-orange pulp is well documented descriptively, but the precise temporal relationship between chlorophyll loss and individual carotenoid gain remains an open question rather than an established sequence.

Relative contribution of pigment classes

Considered together, the evidence indicated that jackfruit pulp colour is a multicomponent biochemical trait. Carotenoids provide the strongest and most direct chemical basis for the yellow-to-orange range. Flavonoid and phenolic metabolism vary alongside colour and contribute to the broader phytochemical differences between colour classes, but a direct optical role for specific flavonoids remains to be demonstrated. Chlorophyll loss underlies the initial green-to-coloured transition, without yet being resolved at the level of individual pigments. Visual classification is therefore useful for rapid, low-cost phenotyping. Establishing the biochemical basis of any particular colour phenotype, however requires chromatographic pigment profiling, ideally combined with the kind of metabolomic comparison used by Liang *et al.* (2026).

Biosynthesis and Molecular Regulation of Pigments in Jackfruit

Carotenoid pathway

Carotenoid biosynthesis proceeds through the plastidial isoprenoid pathway. Geranylgeranyl diphosphate is converted to phytone by phytone synthase (*PSY*), then desaturated and isomerised via phytoene desaturase (*PDS*) and ζ-catotene desaturase (*ZDS*) to lycopene, the pathway's major branch point. From lycopene, lycopene β-cyalase directs flux towards β-carotene and its hydroxylated derivatives, including zeaxanthin. Lycopene ε-cyclase (*LCYE*) initiates the alternative branch towards α-carotene and ultimately, lutein. Further epoxidation and de-epoxidation reactions, involving zeaxanthin epoxidase (*ZEP*) and violaxanthin de-epoxidase (*VDE*), interconvert xanthophylls within the so-called xanthophyll cycle. The sequence can be summarised as GGPP → phytoene → ζ-carotene → lycopene → α-/β-carotene →

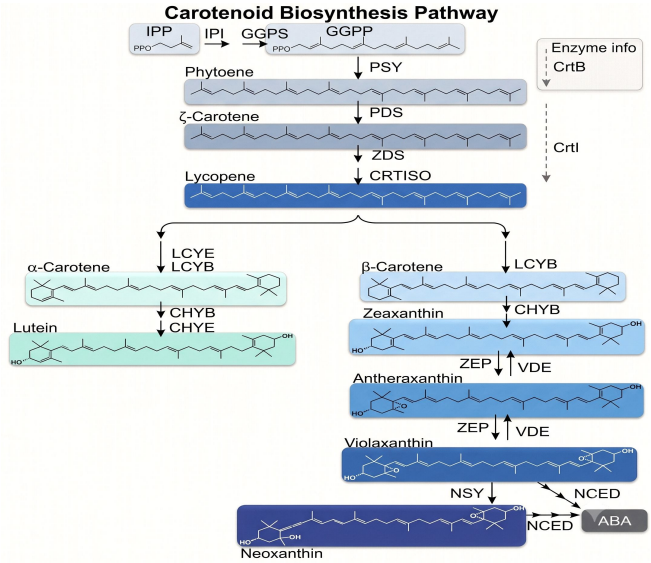


Fig. 2 : Carotenoid Biosynthesis Pathway.

xanthophylls, which carotenoids predominate in a given tissue is largely determined by the relative activity of each branch, rather than by flux through the pathway as a whole.

The diversity of carotenoids that de Faria *et al.* (2009) resolved in jackfruit pulp spanning both the α- and β-carotene branches and multiple xanthophyll derivatives indicates that the pathway is broadly active in this species rather than being restricted to a single terminal product. Liang *et al.* (2026) reported differential expression of *PSY, PDS* and *ZDS* among cultivars with light yellow, yellow and orange pulp, consistent with a role for early pathway regulation in the observed pigment differences. Differential transcript abundance does not by itself prove these genes are the proximate cause of the colour difference, however, this is generally true of transcriptomic evidence. Carotenoid concentration also depends on downstream conversion, sequestration in chromoplasts, esterification and degradation, none of which is captured by expression data alone. Downstream of lycopene, *LCYE* and *LUT5* were likewise differentially expressed among the three colour phenotypes. This is consistent with the observed differences in lutein and related xanthophyll accumulation (Liang *et al.*, 2026). Differential expression of *ZEP* and *VDE* points to altered activity of the xanthophyll cycle as a further contributor to the final pigment mixture.

Flavonoid pathway

Flavonoid biosynthesis begins within general phenylpropanoid metabolism. Phenylalanine ammonia-lyase (PAL) generates cinnamic acid, which is then modified via cinnamate 4-hydroxylase (*C4H*) and 4-coumarate-CoA ligase (*4CL*). Chalcone synthase (*CHS*)

then forms the chalcone backbone, from which chalcone isomerase (*CHI*), flavanone 3-hydroxylase (*F3H*), flavonol synthase (*FLS*), anthocyanidin synthase (*ANS*) and anthocyanidin reductase (*ANR*) generate the diverse flavonoid end-products. In jackfruit, Liang *et al.* (2026) reported differential expression of *PAL, C4H, 4CL, F3H, FLS, ANS* and *ANR*, alongside 25 differentially accumulated flavonoids, among the three colour phenotypes. This indicates substantial reprogramming of the pathway between phenotypes. However, a direct optical contribution from individual flavonoids remains unconfirmed.

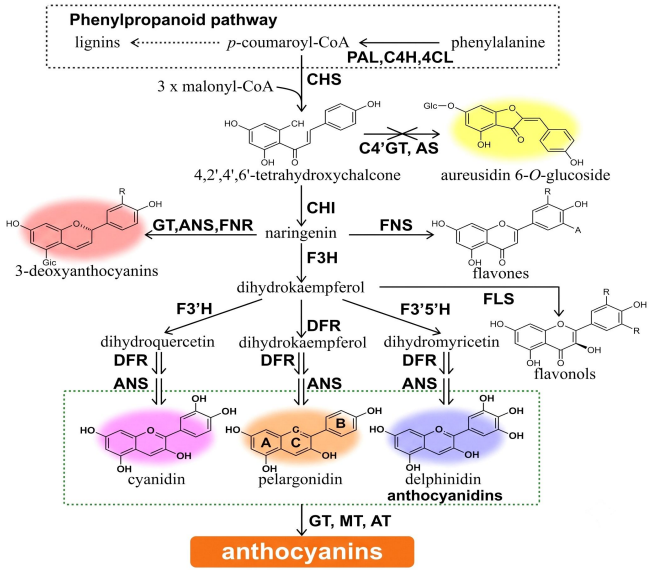


Fig. 3 : Flavonoid Biosynthesis Pathway.

Coordinated regulation and its limits

The central finding of the transcriptome-metabolome comparison by Liang *et al.* (2026) is that carotenoid and flavonoid metabolism shift together across colour phenotypes, rather than one pathway varying independently of the other. This supports a model in which jackfruit pulp colour is the outcome of coordinated, multi-pathway metabolic regulation, not the product of a single gene or pigment. The model does not demonstrate that any specific gene causes a specific colour outcome, since gene expression is only one determinant of final pigment concentration alongside of precursor supply, competing pathway flux, transport, sequestration and turnover. It also rests on one recent study of comparing three cultivars, so its generality across the wider genetic diversity of cultivated jackfruit has not yet been tested.

Molecular characterisation of pigment regulation in jackfruit remains far more limited than in tomato, citrus or mango, where gene function has been confirmed through mutant analysis, transformation or gene editing. No such functional validation yet exists for the jackfruit candidate genes discussed above. Their identification through differential expression provides a starting point rather than a settled mechanism. Progress will depend on combining expression data with enzyme assays, metabolite quantification and eventually functional tests, applied across a germplasm base substantially larger than the handful of genotypes examined to date.

Genotypic Variation in Pigment composition and Pulp colour

Jackfruit germplasm varies widely in fruit and flake traits and pulp colour, from cream through yellow, deep yellow, orange and orange-red among the most visible of these. Molecular surveys confirm that this phenotypic range has a genetic correlate. An SSR-based analysis of twenty genotypes differing in pulp colour found six of twenty-two markers polymorphic and resolved three principal that broadly separated cream and yellow pulp genotypes from orange and red pulp types (Kavya *et al.*, 2019).

Carotenoid variation among genotypes

Total carotenoid content differs substantially among genotypes and tracks pulp intensity in a general, non-linear way. In an early comparative survey, Orange- and red-fleshed genotypes carried markedly more carotenoids than cream- or yellow-fleshed once, with β-carotene, α-carotene and lycopene all varying independently among genotypes (Shyamalamma *et al.*, 2017). Most recent, independently verified data from Karnataka germplasm illustrate the same qualitative pattern without the same numerical uncertainty. Orange accession JT-04 (5.83 mg/ 100g carotenoids, 2.26 mg/ 100 g lycopene) and orange-red accession JG-14 (4.43 mg/100g carotenoids, 1.12 mg/ 100 g lycopene) both exceeded paler accessions in the same survey. The two accessions also differ from one another, which shows that colour intensity and pigment concentration are correlated but not interchangeable measures (Karunakaran *et al.*, 2025).

Germplasm from north-east India extends this picture beyond the southern dry zone. Hazarika *et al.* (2025) evaluated 25 indigenous accessions sampled from natural populations at 25 locations in four districts of Mizoram (Aizawl, Kolasib, Mamit and Champhai). Carotene, estimated spectrophotometrically at 452 nm, ranged from 1.63 mg/100 g (MZU-HAMP-JS-1) to 4.57 mg/100 g (MZU-HAMP-JS-7 and JS-11), with a mean of 2.93 mg/ 100 g and a coefficient of variation of 24.06%. Carotene was one of 15 of the 25 traits with a CV above 20%. It loaded on the first principal component (27.85% of total variance) together with fruit diameter, flake traits, TSS and shelf life, it was positively correlated with non-

Table 3 : Genotypic variation reported in jackfruit pigment composition and pulp colour.

Colour class examined	Key findings	References
Cream, Yellow Orange, Red	SSR analysis (6/22 polymorphic markers) resolved clusters broadly separating cream/yellow from orange/red genotypes)	Kavya *et al*. (2019)
Cream, Light yellow, Dark yellow, Red, Orange	Higher β-carotene, α-carotene and lycopene in red/orange pulp	Shyamalamma *et al*. (2017)
Yellow, Deep yellow, Orange, Orange-red	Orange-red: highest β-carotene/phenolics; Deep yellow: highest flavonoids/antioxidant activity	Natta *et al*. (2023)
Pale yellow to orange-red	Orange/ orange red accessions showed elevated carotenoid and lycopene concentrations	Karunakaran *et al*. (2025)
Light yellow, yellow, orange	32 carotenoids and 25 flavonoids differentially accumulated; 13 biosynthetic genes differentially expressed	Liang *et al*. (2026)
Yellow	SSR: 26 of 30 primers amplified 216 loci with mean PIC of 0.728, genetic similarity of 55-85%	Naik *et al*. (2026)

reducing sugars. The two highest-carotene accessions also had the highest TSS (25.20 and 26.33 °Brix), sugar:acid ratio (79.01 and 80.65) and ascorbic acid (26.40 and 27.82 mg/100 g) and among the longest shelf lives (12.00 and 13.33 days). In this population, high carotene content did not come at the expense of dessert quality.

A methodological caution applies when these surveys are compared with chromatographic data. The totals obtained by whole-extract spectrophotometry in the two Indian surveys (0.49–5.83 mg/100 g in Karunakaran *et al*., 2025; 1.63–4.57 mg/100 g in Hazarika *et al*., 2025) are roughly one to two orders of magnitude higher than the summed individual carotenoids quantified by HPLC in the study of de Faria *et al*. (2009) (34.1–150.3 µg/100 g). Genotype, maturity, extraction and the difference between measuring absorbance of a whole extract and summing resolved chromatographic peaks may all contribute. Different carotenoids absorb light differently, two genotypes with similar total carotenoid content can therefore still differ in hue if their carotenoid mixtures differ in composition, a point underscored by the metabolomic finding that light-yellow, yellow and orange cultivars differ as much in which carotenoids accumulate as in how much (Liang *et al*., 2026).

Flavonoid and phenolic variation

Genotypic variation extends to the non-carotenoid fraction. Among fifteen clonal accessions, deep-yellow flakes carried the highest â-carotene, total phenolics, sinapic acid, ferulic acid and quercetin (Natta *et al*., 2023). This pattern indicates that jackfruit colour classes correspond to distinct biochemical profiles rather than to a single axis of "more or less pigments." It does not show that any individual flavonoid determines the observed colour. Most biochemical surveys, including this one, quantify groups of related compounds rather than testing the optical contribution of single metabolites, so the distinction between association and causation remains important when interpreting these results.

Molecular evidence for genotype-linked pigment variation

The clearest current molecular evidence for genotype-dependent pigment variation comes from the comparison of light-yellow, yellow and orange cultivars by Liang *et al*. (2026). It identified 32 differentially accumulated carotenoids and 25 differentially accumulated flavonoids, with distinct metabolite signatures for each phenotype: naringenin chalcone, eriodicyol, taxifolin, zeaxanthin and lutein associated with the light-yellow cultivar; phlorizin and lutein with the yellow cultivar and apigenin, luteolin, zeaxanthin and violaxanthin dipalmitate with the orange cultivar. Thirteen genes spanning the carotenoid and flavonoid pathways were also differentially expressed (*PSY, PDS, ZDS, LCYE, LUT5, ZEP, VDE, PAL, C4H, 4CL, F3H, FLS, ANS, ANR*).

Colour as a screening criterion and its limits

The recurring association between pulp colour and pigment content gives visual classification real, practical value as a first-pass screening tool in large germplasm collections, where exhaustive chemical analysis of every accession is rarely feasible. It should not be used as a proxy for quantitative pigment data. The same broad colour category can arise from different combinations of pigments; colour perception itself is affected by maturity and lighting. As the JT-04/JG-14 comparison illustrates, visually similar accessions can differ appreciably in

Table 4 : Genes associated with carotenoid and flavonoid biosynthesis differentially expressed among contrasting pulp colour cultivars.

Gene	Pathway/enzyme function	Relevance to pigmentation
PSY	Phytoene synthase; first step of carotenoid biosynthesis	Controls entry of flux into the carotenoid pathway
PDS	Phytoene desaturase	Converts phytoene toward downstream carotenoids
ZDS	ζ-Carotene desaturase	Contributes to formation of lycopene precursors
LCYE	Lycopene ε-cyclase	Directs flux toward the α-carotene/lutein branch
LUT5	Carotenoid ε-ring hydroxylase	Involved in lutein/xanthophyll formation
ZEP	Zeaxanthin epoxidase	Converts zeaxanthin towards violaxanthin
VDE	Violaxanthin de-epoxidase	Reverses ZEP activity within the xanthophyll cycle
PAL	Phenylalanine ammonia-lyase	Entry point into phenylpropanoid/flavonoid metabolism
C4H	Cinnamate 4-hydeoxylase	Phenylpropanoid pathway
4CL	4-Coumarate-CoA ligase	Generates activated phenylpropanoid intermediates
F3H	Flavanone 3-hydroxylase	Early committed step in flavonoid biosynthesis
FLS	Flavonol synthase	Formation of flavonols
ANS	Anthocyanidin synthase	Downstream flavonoid-pathway enzymes
ANR	Anthocyanidin reductase	Formation of flavan-3-ol related compounds

measured pigment content (Karunakaran *et al*., 2025).

Implications for breeding

Genotypic variation in pigment composition is, in principle, exploitable for breeding genotypes with defined nutritional or processing characteristics, for example, selecting for high β-carotene as a provitamin A source, or for stable orange colour for fresh-market appeal. The candidate genes identified by Liang *et al*. (2026) are a reasonable starting point for marker development, but given that they derive from only three cultivars, functional validation and evaluation across broader germplasm are prerequisites before they can be used with confidence in marker-assisted selection.

Changes in Pigment composition during Fruit Development and Ripening

Carotenoid accumulation during maturation

Jackfruit pulp is typically pale or greenish in early development and becomes progressively yellow, golden or orange as maturation proceeds, a transition generally attributed to combined chlorophyll loss and carotenoid accumulation, as in other fleshy fruit. Total carotenoid content has been reported to increase through successive maturity stages in jackfruit (Shamla *et al*., 2019), and an approximately two-fold increase in pulp carotenoid-related colour from harvest to the ripe stage has also been described in older literature on the species, cited here as reported in the secondary source through which it reached the present review rather than verified (Selvaraj and Pal, 1989).

Instrumental evidence for the green to coloured transition

Quantitative colour measurement corroborates the qualitative picture. In jackfruit genotypes followed across four maturity stages. A comparison of tropical Australian jackfruit genotypes found that orange-fleshed accessions had lower L, higher positive a* and lower hue angle, together with higher carotenoid content and ascorbic acid, confirming that the yellow to orange transition is captured consistently by these instrumental parameters across independent genotype sets (Kaur *et al*., 2024a, 2024b).

Divergent behaviour of flavonoids and phenolics

Not every phytochemical class increases alongside carotenoids during ripening. Total phenolic and flavonoid content declined over the same period that total carotenoids rose in one maturity-stage study (Shamla *et al*., 2019), indicating that fruit maturation involves a reorganisation of the phytochemical profile rather than a uniform increase in all pigment-associated compounds. The correspondingly deeper colour of ripe jackfruit should not be read as evidence that antioxidant capacity as a whole rises in step with visible colour intensity.

Postharvest continuation of colour development and its non-uniformity

As jackfruit is climacteric, pigment development can continue after harvest if fruit is picked at a mature but not fully ripe stage. Chemical and colour changes

documented in cultivar J3 during ripening included significant shifts in colour alongside increases in soluble solids and sugars. This indicates that pigment development proceeds in step with, rather than independently of, the broader ripening programme (Ong *et al*., 2006). Ripening is also not spatially uniform: differences in hue have been reported between the upper and lower portions of the same fruit, with the upper region appearing to colour earlier. This has a direct methodological consequence for pigment studies. Sampling position should be standardised and reported, since inconsistent sampling could introduce apparent "genotype" differences that are in fact within-fruit developmental differences.

Genotype × maturity interaction

Genotypes differ in baseline pigment composition and maturation modifies that composition further. Comparisons of carotenoid concentration across studies are only meaningful when maturity stage, cultivar and analytical method are matched or explicitly accounted for.

Relationship Between Pulp Colour, pigment concentration and Instrumental Colour parameters

Instrumental measurement as a complement to visual classification

Visual description of jackfruit pulp colour, such as white, light yellow, yellow, deep yellow, saffron, orange, and orange-red, is useful but inherently subjective. It is sensitive to illumination, sample condition and observer judgement. The CIE L*a*b* system offers an objective alternative: L records lightness, a the green-to-red axis and b the blue-to-yellow axis, with chroma (C*) describing saturation and hue angle (h°) describing dominant colour tone.

Colour parameters and pigment accumulation

Orange-fleshed jackfruit consistently shows lower L, higher positive a and lower hue angle than yellow-fleshed material and these differences track measured carotenoid content (Kaur *et al*., 2024a, 2024b). The relationship is biologically coherent: chlorophyll loss and carotenoid accumulation in chromoplast-containing tissue jointly drive both the visual and the instrumental signal, but its strength is not expected to be identical across genotypes, because carotenoid mixtures that differ in composition can produce different colour outcomes at a given total concentration.

Two genotypes with comparable total carotenoid content can still differ visibly if xanthophylls (which favour yellow) predominate in one and carotenes such as â-carotene (which favours orange) predominate in the other. The metabolomic comparison of light-yellow, yellow and orange cultivars supports exactly this point, associating distinct pigment combinations, not merely different total amounts, with each phenotype (Liang *et al*., 2026). Instrumental colourimetry is consequently best regarded as a rapid phenotyping tool suited to screening large numbers of samples. Chromatographic or mass-spectrometric analysis remains necessary wherever the identity and quantity of individual pigments must be established with confidence.

Validated colour pigment models

No validated, broadly applicable model currently links CIE L*a*b* parameters to individual jackfruit carotenoids across diverse germplasm. The positive associations reported to date (Kaur *et al*., 2024a, 2024b) come from single studies with a limited number of genotypes and have have not been tested for generality across maturity stages, growing environments or wider genetic backgrounds. Developing and validating such models, ideally using regression or multivariate approaches applied to genotype panels that include simultaneous colourimetry, chromatographic pigment profiling and where feasible, metabolomics, would substantially increase the efficiency of germplasm screening, but this remains a research target rather than an established capability.

Nutritional, Functional and Industrial significance

Nutritional relevance of jackfruit pigments

Jackfruit pigments carry nutritional significance beyond their visual role. β-carotene contributes provitamin A activity, while lutein and other xanthophylls are of interest mainly for antioxidant rather than vitamin A function. These compounds differ in the proportions reported across genotypes and colour classes (de Faria *et al*., 2009), so the nutritional profile of a given sample depends on carotenoid composition rather than total carotenoid content alone (Ranasinghe *et al*., 2019). Selecting for intensely coloured pulp may therefore raise the concentration of some bioactive compounds without guaranteeing improvement in any specific nutritional endpoint.

Colour as a quality and maturity indicator

Pulp colour ranks alongside sweetness, texture and aroma as a trait consumers use to judge jackfruit quality. It also changes measurably and progressively through maturation, which gives it practical value as one indicator of ripeness. Colour development varies among cultivars, though, so it is best used alongside other maturity indices like soluble solids, firmness, and aroma rather than in isolation (Kaur *et al*., 2024a). Colour alone does not

guarantee appeal. In a sensory evaluation of Karnataka dessert types, some orange-bulbed selections scored no higher for colour and appearance than paler types, apparently because panellists also judged bulb integrity (Suneel *et al*., 2023). At the same time, the effort invested in conserving and marketing coppery-red farmer varieties such as 'Siddu' and 'Shankara' (Karunakaran, 2019; Karunakaran *et al*., 2026) suggests that distinctive flake colour is itself treated as a commercial trait.

Colour diversity as a screening tool for functional-food development

Colour groups differ biochemically in documented way: deep-yellow accessions are rich in flavonoids and antioxidant activity, while orange-red accessions are rich in β-carotene and phenolics (Natta *et al*., 2023). This suggests that colour phenotype could guide the initial selection of genotypes intended for functional-food development. Promising colour groups should however, be confirmed by direct chemical analysis rather than accepted based on colour alone; the metabolomic evidence for compositionally distinct, rather than early more-or-less concentrated, pigment profiles across colour phenotypes reinforces this caveat (Liang *et al*., 2026).

Jackfruit as a natural colourant source

Plant-derived colourants as alternatives to synthetic dyes extend naturally to carotenoid-rich fruit such as jackfruit (Sigurdson *et al*., 2017). The carotenoid profile documented by de Faria *et al*. (2009) established the chemical basis for such use. Total carotenoid concentrations reported for jackfruit pulp are comparatively modest relative to established commercial carotenoid sources suggest that dedicated industrial-scale pigment extraction is not yet an obviously competitive application. A more realistic near-term use is dual-purpose exploitation of pigment-rich pulp in beverages, purees, bakery products and other foods where the fruit's intrinsic colour is itself desirable.

Colour and pigment stability through processing

Carotenoids are chemically labile, so their practical value depends on stability during handling and processing as well as on initial concentration. Hot-air drying of jackfruit bulb slices at 50-70°C measurably degrades both colour and total carotenoids. The two changes follows different kinetic orders: first order for total carotenoids and for the Hunter Lxb colour term and zero-order for total colour difference and non-enzymatic browning. Carotenoid degradation also shows higher temperature sensitivity than the colour parameters measured (Saxena *et al*., 2012). Pigment loss and visible colour loss do not respond identically to temperature. Colour measurements can therefore under- or overestimate actual carotenoid degradation depending on processing conditions and periodic chemical verification remains advisable wherever colour is used as a proxy for pigment retention.

Value-added applications and sustainable utilisation

Jackfruit pulp is increasingly investigated as a raw material for beverages, dried products, purees and other formulated foods. Naturally pigmented, orange or deep-yellow pulp offers colour without reliance on added colourants. Realising this potential in practice requires evaluating pigment stability under the specific thermal, oxidative and storage conditions each product entails, rather than assuming that fresh-fruit colour will be retained. More broadly, jackfruit processing generates substantial peel, core and seed by-products. Recovering pigments or other bioactive fractions from these streams is an area of active interest in the wider circular-bioeconomy literature on fruit valorisation, though jackfruit-specific data on pigment recovery from processing residues remain limited. The presence of a carotenoid in raw jackfruit pulp does not guarantee equivalent absorption after digestion, since bioaccessibility depends on the food matrix, co-ingested lipid processing and molecular structure (Melendez-Martinez *et al*., 2021).

Genetic Regulation and Breeding prospects

Genetic basis of colour variation

The existence of discrete, heritable colour classes, together with the molecular clustering demonstrated by SSR analysis (Kavya *et al*., 2019), supports treating jackfruit pulp colour as a genetically influenced trait rather than one determined solely by environment or maturity. Genotypes differing in colour also differ in the relative abundance of individual carotenoids and flavonoids rather than only in total pigment load (Liang *et al*., 2026). Colour phenotype should therefore be understood as the composite outcome of several metabolic processes rather than the product of a single gene.

Candidate genes and their current evidentiary status

The genes most directly implicated in jackfruit pulp colour variation to date and *PSY, PDS, ZDS, LCYE, LUT5*, *ZEP* and *VDE* in the carotenoid pathway and *PAL, C4H, 4CL, F3H, FLH, ANS* and *ANR* in the flavonoid pathway. They were identified through differential expression among light-yellow, yellow and orange cultivars in a single transcriptome-metabolome study (Liang *et al*., 2026). Differential expression alone does not establish causal control of colour, as none of these genes has yet been functionally validated in jackfruit through transformation, silencing or gene editing, and the three-

cultivar design of the source study leaves open whether the same genes explain colour variation across the species' wider genetic diversity.

Molecular markers

SSR markers have already distinguished jackfruit genotypes by pulp-colour classes (Kavya *et al*., 2019), showing that molecular tools can complement morphological and biochemical characterisation. Clustering by overall genetic relatedness is not the same as identifying a marker linked to a specific pigment-biosynthesis gene; realising marker-assisted selection for colour or pigment traits will require combining SNP or SSR genotyping with quantitative pigment phenotyping in a genome-wide association framework, which has not yet been carried out in jackfruit. Two recent SSR studies show what such marker panels can already deliver. In eleven elite Karnataka accessions selected for flake colour and quality, 20 microsatellite loci amplified 192 alleles (mean 9.6 per locus; mean PIC 0.761). Five highly informative loci (JKSSR5, JKSSR12, JKSSR15, JKSSR20 and JKSSR21) were proposed as a minimal set for fingerprinting varieties (Karunakaran *et al*., 2025). Genotypes within a single colour class can still differ widely: among 25 yellow-flaked genotypes, 26 of 30 SSR primers amplified 216 loci, the mean PIC was 0.728 and pairwise genetic similarity ranged from 55 to 85% (Naik *et al*., 2026).

Breeding considerations

Pulp colour cannot be bred in isolation from other fruit-quality traits. A commercially useful genotype must combine acceptable colour with adequate soluble solids, texture, flavour, low latex level and good shelf life, so a genotype selected purely for high carotenoid content could still be commercially unsuitable if these other traits are unfavourable. As understanding of pigment metabolism matures, breeding selection principles move from broad visual categories toward defined biochemical targets, such as elevated β-carotene or lutein. This shift depends on the marker validation described above, which remains a future rather than a current capability. Some encouragement comes from the Mizoram survey, in which the accessions highest in carotene were also among the best for TSS, sugar:acid ratio, ascorbic acid and shelf life (Hazarika *et al*., 2025). Pigment content and dessert quality need not be traded off, at least in that population. The eleven elite Karnataka accessions identified by Karunakaran *et al*. (2025) are conserved in farmers' fields and in the National Active Germplasm Repository at ICAR-IIHR, Bengaluru, which gives breeders access to documented coloured-flake, high-carotenoid material.

Postharvest stability and Processing effects

Postharvest pigment dynamics

Carotenoid biosynthesis can continue after harvest in fruit picked at physiological maturity. Total carotenoid content has been reported to roughly double between the mature and ripe eating stages (Selvaraj and Pal, 1989). Beyond this initial postharvest increase, prolonged storage promotes oxidation, isomerisation and other degradative changes typical of highly unsaturated carotenoid molecules, so the relationship between storage duration and pigment content is better described as rise-then-decline than as monotonic in either direction (Ngamwonglumlert *et al*., 2020; Melendez-Martinez *et al*., 2023).

Storage and minimal processing

Minimally processed jackfruit bulbs, pretreated and packaged under modified-atmosphere conditions, retained higher levels of total carotenoids, phenolics, flavonoids and ascorbic acid after 35 days at 6°C than untreated controls (Saxena *et al*., 2009). Pretreatment and packaging choices therefore materially affect pigment retention during cold storage, independent of the fruit's initial pigment load. Fresh-cut jackfruit is particularly vulnerable to enzymatic browning and moisture loss once cellular tissue is disrupted. Combinations of calcium chloride, ascorbic acid and modified-atmosphere packaging have each been associated with improved colour and carotenoid retention in this context.

Drying and thermal processing

Hot-air drying of jackfruit bulb slices at 50, 60 and 70°C decreases Hunter L and b values while increasing the *a* value. Total carotenoid degradation and the Hunter L×b colour term both follow first-order kinetics, while total colour difference and non-enzymatic browning follow zero-order kinetics. Total carotenoid content correlates strongly with the L×b term ($R^2 \geq 0.979$) under these specific drying conditions (Saxena *et al*., 2012). The activation energy for carotenoid degradation (55.61 kJ/mol) substantially exceeds that for the colour parameters measured in the same study (27.21 – 29.96 kJ/mol). Colour loss and carotenoid loss respond differently to temperature and a given change in measured colour should not be assumed to represent a proportional change in carotenoid content, particularly when extrapolating beyond the specific drying conditions tested. More broadly, thermal processing can either degrade carotenoids through heat-driven oxidation or increase their measured extractability by disrupting plant tissue. The net effect reported for a given food system depends on the balance between these two opposing mechanisms

(Melendez-Martinez *et al*., 2023), a distinction that has not yet been resolved specifically for jackfruit.

Genotype-dependent processing outcome

Genotypes differ substantially in initial pigment concentration and composition, so identical processing treatments are unlikely to produce identical pigment or colour outcomes across genotypes; a genotype with high initial β-carotene may retain visually acceptable orange colour despite degrading proportionally as much as a lower-pigment genotype that shows more obvious fading. This genotype-dependence has not been systematically studied in jackfruit processing research, which has generally treated the raw material as biochemically uniform.

Emerging processing technologies

Reviews of jackfruit processing describe a range of thermal and non-thermal approaches: retort processing, microwave treatment, irradiation, high-pressure processing, pulsed electric fields, ultrasound, supercritical fluid extraction, freezing and hurdle technology, with non-thermal methods of particular interest for pigment-sensitive applications because they reduce the thermal burden associated with carotenoid oxidation (Nelluri *et al*., 2022). Encapsulation is a further approach under investigation for protecting labile pigments from oxygen and light exposure in food systems generally; jackfruit-specific studies establishing whether its carotenoids can be extracted and stabilised at commercially useful concentrations were not identified.

Research Gaps and Future perspective

Several limitations recur across the literature synthesised in this review and taken together, define the priorities for future work.

Restricted genotype coverage in molecular studies

The most detailed molecular evidence currently available – the transcriptome-metabolome comparison identifying differentially accumulated carotenoids, flavonoids and biosynthetic genes, rests on three cultivars (Liang *et al*., 2026). Whether the same metabolites and genes explain colour variation across the much broader diversity documented in germplasm surveys (e.g., 94 accessions in Karunakaran *et al*., 2025; 20 genotypes in Kavya *et al*., 2019) has not been tested and should not be assumed. Regional collections such as the Tumakuru and Mizoram populations (Karunakaran *et al*., 2025; Hazarika *et al*., 2025) would be natural starting points for such work.

Total-pigment measurements obscure compositional differences

Much of the older literature reports total carotenoids or total flavonoid content rather than individual compounds, which can mask biologically and visually important differences in composition. Comprehensive LC-MS/MS profiling of individual carotenoids, including esters, cis/trans isomers and oxidation products, across a wider genotype set would address this directly.

No validation colour-pigment prediction model

Instrumental colourimetry correlates with pigment content in the individual studies reviewed here (Kaur *et al*., 2024a, 2024b), but no model linking L, a, b*, chroma or hue angle to specific carotenoid concentrations has been validated across genotypes, maturity stages or growing environments.

Genotype × environment interactions are essentially uncharacterised

Most available studies evaluate genotypes within a single site and season, leaving genetic and environmental contributions to pigment variation confounded; multi-location, multi-season trials are needed before pigment traits can be considered stable breeding targets.

Candidate genes lack functional validation

The carotenoid and flavonoid pathway genes discussed, but none of them has been functionally confirmed in jackfruit through transformation, silencing or editing.

Sampling and analytical methods are not standardised

Differences in fruit maturity, sampling position within the fruit, extraction solvent, analytical platform and reporting basis complicate direct comparison across studies and may explain some of the numerical discrepancies flagged. Standardised protocols would materially improve comparability of future work.

Bioaccessibility and bioavailability are unaddressed

No specific jackfruit data on carotenoid bioaccessibility or bioavailability after digestion were identified; in vitro digestion models would be a reasonable starting point before undertaking human studies.

Processing and storage stability data are incomplete at the level of individual pigments

Existing postharvest and processing studies largely report total carotenoids or aggregate colour parameters rather than the fate of individual compounds such as lutein, â-carotene, neoxanthin or violaxanthin derivatives during drying, freezing, canning or minimal processing.

Sustainable pigment recovery from processing by-products remains speculative for jackfruit specifically

Although, the broader circular-bioeconomy literature supports recovering carotenoids from fruit-processing residues in general, jackfruit-specific feasibility data were not identified.

Conclusion

Jackfruit exhibit substantial diversity in pulp colour, ranging from pale yellow to deep yellow and saffron to orange and orange-red, reflecting variation in its complex pigment composition. Carotenoids, particularly lutein, β-carotene and other xanthophylls, constitute an important component of this colour diversity, while differences in flavonoid and phenolic profiles, further distinguish colour phenotypes. Recent transcriptomic and metabolic evidence has provided important molecular perspective by demonstrating coordinate differences in carotenoid- and flavonoid associated metabolise and biosynthetic genes among differently coloured jackfruit cultivars. However, these molecular associations remain to be validated across larger and genetically diverse germplasm collections before specific pathways or genes can be considered definitive determinants of pulp colour.

Pulp colour also changes dynamically during fruit maturation and ripening, accompanying chlorophyll degradation and changes in carotenoid accumulation. Instrumental colour measurements, particularly CIE L*a*b* parameters, provide a useful quantitative means of characterising these changes, but they should complement rather than replace direct pigment analysis. The substantial genotypic variation reported for colour and pigment-related biochemical traits indicates that pulp colour can serve as a useful preliminary phenotypic indicator during germplasm evaluation, while biochemical and molecular analysis provide the precision required for characterising the underlying variation. Surveys in Tumakuru district of Karnataka and in Mizoram show that much of this variation is still held in seedling-origin trees on farms and in natural stands, and that it includes accessions combining high carotenoid content with good dessert quality (Karunakaran *et al*., 2025; Hazarika *et al*., 2025).

Beyond its value as a quality trait, jackfruit pigment diversity has nutritional, functional and technological significance. Carotenoids contribute to antioxidant properties and, in the case of provitamin-A carotenoids, nutritional value, while pigment-rich colour phenotypes may provide opportunities for the development of natural colourants and value-added products. Also, pigment stability is influenced by maturation, processing and storage conditions, emphasising the need to understand the relationship between pigment chemistry and colour retention through the post-harvest chain. Future research should therefore integrate standardised colour phenotyping with quantitative pigment analysis, metabolomics, transcriptomics and genomic approaches across diverse germplasm and environments. Such integrated approaches could improve understanding of the biological basis of jackfruit colour diversity and support the selection and breeding of genotypes with desirable colour, nutrition and processing attributes.

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