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Regulatory mechanisms underlying oil palm mesocarp maturation and functional specialization in lipid and carotenoid metabolism

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The lipid-rich fleshy mesocarp tissue of the oil palm (Elaeis guineensis) fruit is not only the main source of edible oil for the world, but it is also the richest dietary source of provitamin A. This study examines the transcriptional basis of these two outstanding metabolic characters in the oil palm mesocarp. Morphological, cellular, biochemical, and hormonal features defined key phases of mesocarp development. A 454 pyrosequencing derived transcriptome was then assembled for the developmental phases preceding and during maturation, when high rates of lipid and carotenoid biosynthesis occur. A total of 2,629 contigs with differential representation revealed coordination of metabolic and regulatory components. Further analysis focused on the fatty acid and triacylglycerol assembly pathways and during carotenogenesis. Notably, a contig similar to the Arabidopsis (Arabidopsis thaliana) seed oil transcription factor WRINKLED1 was identified with a transcript profile coordinated with those of several fatty acid biosynthetic genes and the high rates of lipid accumulation, suggesting some common regulatory features between seeds and fruits.

Regulatory mechanisms underlying oil palm mesocarp maturation and functional specialization in lipid and carotenoid metabolism

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Introduction

The monocotyledonous oil palm (*Elaeis guineensis*) fruit is a drupe whose thick fleshy mesocarp is exceptionally rich in oil (80% dry mass), making this species the highest oil-yielding crop in the world. The mesocarp is also especially abundant in carotenoids, and crude palm oil is the richest dietary source of provitamin A. Our objective was to provide a basis to understand the molecular regulation and coordination of TAG and carotenoid biosynthesis during oil palm mesocarp maturation and ripening compared with those found in seeds and non-oily fruit.

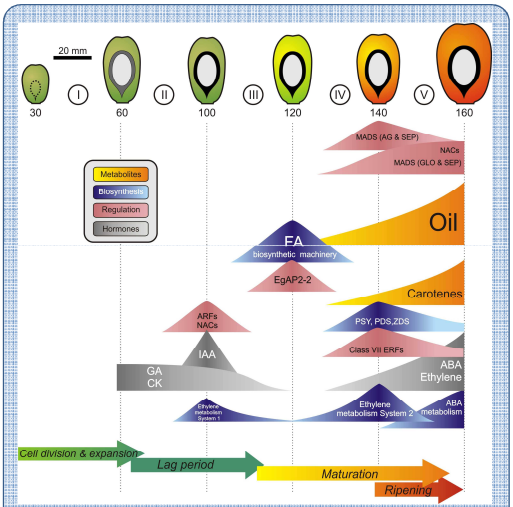

Figure 1. Scheme representing the major events that occur during the phases of mesocarp development.

Fruit development

- Morphological, histological, and biochemical (hormones, lipids) analyses were used to define phases of oil palm fruit development, maturation, and ripening (Fig. 1)
- Phase IV, between 120 and 140 DAP, is characterized by the onset of lipid and carotenoid accumulation
- Very low amounts of all hormones examined, including auxin, GA and cytokinin, ABA, and ethylene, were detected during phase IV
- Oil accumulates within subcellular spherical organelles (10–15 µm in diameter, six to 12 per mesocarp cell) that occupy the whole volume of the cells (Fig. 2)
- Mesocarp cells also contain distinct regions, presumably chromoplasts, with high carotenoid concentrations (Fig. 2)
- This detailed morphological, histological and biochemical description of fruit development enabled to chose the stages for transcriptome 454 pyrosequencing

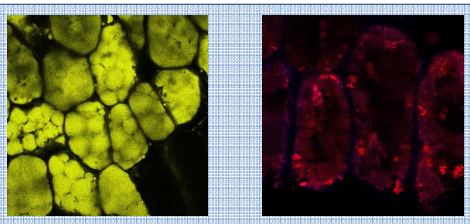

Figure 2. Confocal microscopy of mesocarp oil (left) and β-carotene (right)

Oil biosynthesis

- The core FA synthetic machinery of the oil palm mesocarp is remarkably coordinated at the transcriptional level (Fig. 3)
- The transcription peak of FA biosynthetic genes coincided with the onset of oil accumulation
- A transcript encoding a transcription factor similar to WRINKLED1 Is highly expressed in the mesocarp during FA biosynthesis
- Canonical AW elements were found in several transcripts encoding enzymes involved in glycolysis and FA synthesis
- FA synthesis in the plastid and TAG assembly in the ER seem to be governed by two different transcriptional programs
- The last acylating step of TAG assembly may involve several complementary routes

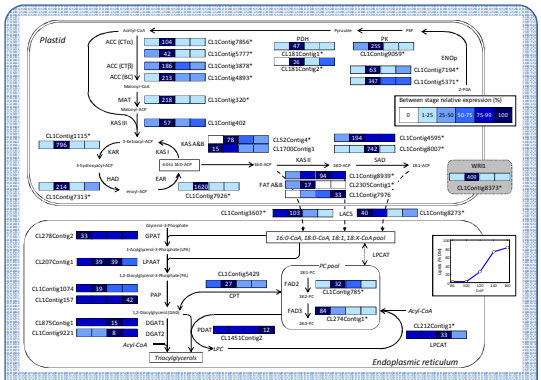

Figure 3. FA synthesis and TAG assembly in the oil palm mesocarp as reconstructed from the 454 pyrosequencing transcriptome. Gene expression levels at 100, 120, 140, 160 DAP are indicated with colored bars. *=significant differential expression

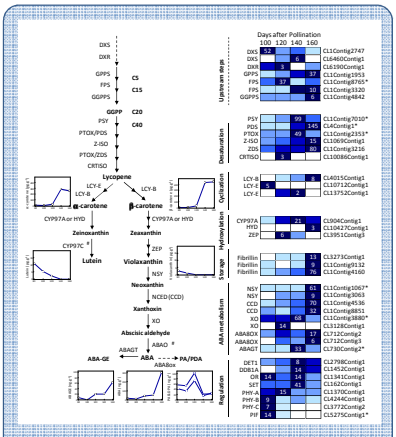

Figure 4. Carotenoid and ABA biosynthetic pathways with related metabolites and transcripts present during mesocarp development

Carotene biosynthesis

- The massive carotene accumulation precedes ABA biosynthesis (Fig. 4)
- Phytoene synthase (PSY) an phytoene desaturase (PDS) are likely the key players for carotenoid accumulation
- Genes involved in the desaturation steps and carotenoid storage show a fine coordinated transcriptional activation
- Downstream steps involved in the cyclization of lycopene toward carotenes and upstream isoprenoid synthesis appear to be poorly regulated at the transcriptional level
- Chloroplasts and chromoplasts share a common repertoire of carotenogenesis regulators

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