Palm species have mesocarp and seed tissues particularly rich in lipids with a broad variation in fatty acid (FA) composition, and constitute an outstanding model to identify the molecular determinants of oil biosynthesis. As a preliminary step, we used a transcriptomic approach to reconstruct the FA and triacylglycerol biosynthetic (TAG) pathways during oil palm mesocarp development. The results indicate that de novo formation of FA in the plastid was remarkably coordinated at the transcriptional level, in contrast to TAG assembly in the endoplasmic reticulum. Interestingly, a contig similar to the Arabidopsis seed oil transcription factor WRINKLED1 was identified with a transcript profile coordinated with those of several FA biosynthetic genes and the onset of lipid accumulation, suggesting some common regulatory features between oily seeds and fruits. We are currently applying this approach to decipher the basis of the high laurate and linoleate content of the oil palm kernel and embryo oils, respectively. In the future, we aim to elucidate the very high variability for the FA composition of the mesocarp oil in the Arecaceae family using a similar strategy.

What Newton did not discover about falling palm fruit

The oil palm (*Elaeis guineensis*), a monocotyledonous species in the family Arecaceae, has not only an extraordinarily oil rich fleshy mesocarp, and presents an original model to examine the ripening regulatory networks in a monocot fruit tissue. The final stage of ripening involves cell separation events in specialized tissue layers between the mesocarp and pedicel that leads to fruit shedding and seed dispersal. A two-stage abscission process involving primary and adjacent abscission zones (AZs), plus high levels of unmethylated pectin and polygalacturonase (PG) activity in the AZ, warrant further investigation. We have examined in more detail the abscission processes of the oil palm fruit using a multidisciplinary approach and have discovered other originalities underlying oil palm fruit shedding. Overall, the data provide a basis to compare with the well-studied dicot model fruit species, and suggest some conservation but also diversification has occurred in these processes between monocots and eudicots.