

W491 Exploring the Oil Palm Transcriptome: Mechanisms Underlying Reproductive Development

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Oil palm (*Elaeis guineensis*) reproductive development includes original characteristics examined by our research group using multidisciplinary approaches, including large-scale transcriptome sequencing. Building on our research on flower development, in particular the roles of MADS-box genes, flower sex determination, fruit development and ripening are being investigated. The oil palm is monoecious, but described as temporally dioecious given that separate male and female inflorescences occur on the same palm at different times. To examine this character, transcriptome analysis of male and female flowers at early stages of development at which time sex is determined was performed. Once the female flower is pollinated, fruit development is initiated followed by ripening. The oil palm has an extraordinarily oil rich fleshy mesocarp, and presents an original model to examine the ripening regulatory networks in a monocot fruit. In addition, the mesocarp is also the richest dietary source of provitamin A. We have examined the transcriptomic basis of these two remarkable characters during mesocarp maturation and ripening. During ripening, a large increase in ethylene coincides with a coordinated regulation of ethylene biosynthesis and signaling transcripts, most notably, type VII ethylene response factor genes. Furthermore, MADS-box genes, including those encoding AGL2/SEPALLATA, AGAMOUS and GLOBOSA/PISTILLATA-like proteins, and their coordinated expression in the mesocarp, suggest differences between dicot and monocot fruit ripening. Finally, the final stage of ripening involves cell separation events in the base of the fruit. Overall, the data derived were used to construct a model to describe the maturation and ripening of the oil palm fruit.

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