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Genetic Determinism of the Fatty Acid Composition of Palm Oil in *Elaeis* (*E. guineensis* Jacq. and *E. oleifera* (H.B.K) Cortès) by Genetic Mapping and Differential Expression Analysis of Candidate Genes

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Room: Towne

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In this study of the International Oil Palm Genome Projects (OPGP) Consortium, an *Elaeis* interspecific pseudo-backcross of first generation (*E. oleifera* x *E. guineensis*) x *E. guineensis* allowed tracing segregating alleles from both *Elaeis* genomes. Nineteen quantitative trait loci (QTLs) associated to palm oil fatty acid proportions compared to 16 QTLs of same traits in an intra-specific oil palm cross evidenced common or specific QTLs in *E. guineensis* and *E. oleifera*. Genes related to palm oil fatty acids were investigated using full-length cDNA libraries and mRNA extracts from the mesocarp of developing fruits in each *Elaeis* species represented by four genetic pools. Expression of 113 key *Elaeis* genes or putative regulation factors of *de novo* fatty acid and triacylglycerol pathways were characterized at species level by *in silico* transcript profiling and Real Time RT-qPCR analysis. Genes were mapped on the pseudo-backcross using 180 intra-gene SNP markers. Forty-eight genes were differentially expressed between *Elaeis* species, with 94% over expressed in *E. guineensis*. The EgAP2-2 (*WR11-like*) transcription factor might influence the start of the *de novo* fatty acid pathway by main action only on the MAT and KAS III genes, as independent in expression from other genes