In this study of the International Oil Palm Genome Projects (OPGP) Consortium, an Elaeis interspecific pseudo-backcross of first generation (E. oleífera 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. oleífera. 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 (WRI1-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.