

Oil Palm Crop Improvement: Role of Biotechnology in the Present Scenario

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Editorial

Oil Palm (*Elaeis guineensis*) is a cross-pollinated crop with the female and male inflorescences being produced in alternate cycles. It produces approximately 5–8 metric tons of crude palm oil and 0.4–0.8 metric tons of kernel oil per hectare per annum. The major palm oil-importing countries are India, China, Netherlands, and Pakistan. The palm oil has a major share in the world edible oils. Also there is a high scope in increasing the oil palm yield to a greater extent. The breeding efforts to improve the varieties with high fresh fruit bunches (FFB) yields is major concern to increase palm oil productivity. Reduced height increment, drought tolerance, superior oil quality, pest and disease tolerance, as well as precocity are also important considerations. Although traditional plant breeding based on phenotypic selection is very effective, it has suffered from several limitations for complex traits. The advancement of omic technologies like integrated genomics, transcriptomics, and proteomic analyses can elucidate the relationships between genotype and phenotype. The first draft genome sequence of African oil palm *E. guineensis*, was published by Singh [1] using a combination of Roche/454 GS FLX Titanium (Roche/454) and Sanger bacterial artificial chromosome end sequencing.

Though the genome sequence of oil palm available, the applications for its use till now is limited. To exploit this the rapid advances in DNA sequencing technology have made whole-genome sequencing (WGS) both technically and economically feasible. Association mapping in oil palm, however, is not reported often may be due to several reasons. But in oil palm association mapping may offer a valuable technology to identify the genetic loci of important traits. The CK et al. [2] performed GWAS for oil-to-dry-mesocarp content on 2045 genotyped *tenera* palms using 200K SNPs and found that 80 loci were

significantly associated with oil-to-dry mesocarp yield ($P \leq 10^{-4}$), and three key signals were found. In oil palm, vegetative propagation is made possible only via tissue culture. Oil palm tissue culture is unique, undergoing callusing and embryogenesis processes, which had been rigorously attempted between the 1960s and 1970s. Though tissue culture is successful in few laboratories, till now the technology is not versatile to use by any one, since most of the protocols are patented. There is a need to relook into oil palm tissue culture to make it profitable. Genetic engineering also achieved in some instances to overcome the limitations of conventional breeding to achieve objectives that would be difficult or impossible by traditional means. Attempts are in progress for transforming traits such as disease or pest resistance and quality traits such as oil composition. In Malaysia, the main goal for genetic engineering of oil palm is to increase oleic acid content at the expense of palmitic acid. Besides increasing oleic acid, modification of fatty acid composition (unsaturation vs. saturation) and production of novel high-value products have also been targeted. Genome editing has been a widely used technology in animals and to some extent in plants for manipulation of any gene or cell of any living organism. This could be effectively used in oil palm for editing desirable genes using customized nucleases carrying sequence-specific DNA-binding domains to target specific DNA sequences.

References

1. Singh R, Ong Abdullah M, Low ETL, Manaf MAA, Rosli R, et al. (2013) Oil palm genome sequence reveals divergence of interfertile species in old and new worlds. *Nature* 500: 335-339.
2. The CK, Ong AL, Kwong QB, Apparow S, Chew FT, et al. (2016) Genome-wide association study identifies three key loci for high mesocarp oil content in perennial crop oil palm. *Sci Rep* 6: 19075.