



**UNIVERSITI PUTRA MALAYSIA**

***CONSTRUCTION OF OIL PALM (*Elaeis guineensis* Jacq.) GENETIC  
LINKAGE MAP AND MAPPING OF YIELD-RELATED QUANTITATIVE  
TRAIT LOCI***

**FAKHRUR RAZI BIN MOHD SHAHA**

**FS 2022 1**



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**By**

**FAKHRUR RAZI BIN MOHD SHAHA**

**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia,  
in Fulfillment of the Requirement for the Degree of Master of Science**

**December 2020**

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Abstract of the thesis presented to the Senate of Universiti Putra Malaysia in fulfilment of the requirement for the Degree of Master of Science

**CONSTRUCTION OF OIL PALM (*Elaeis guineensis* Jacq.) GENETIC LINKAGE MAP AND MAPPING OF YIELD RELATED QUANTITATIVE TRAIT LOCI**

By

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**December 2020**

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**Faculty: Science**

Oil palm (*Elaeis guineensis* Jacq.) is one of the major oil-producing crops that provide great nutritional value and high economic returns. Genotyping-by-sequencing (GBS) provides a platform to accelerate the discovery of single nucleotide polymorphisms (SNP) and insertion and deletions (InDel) markers for the construction of a genetic linkage map. The genetic linkage map facilitates the identification of quantitative trait loci (QTL) associated with the trait of interest. Together these approaches will speed up the process in identifying markers for marker-assisted selection (MAS) in oil palm breeding programmes. A total of 112 full sibling mapping population from a cross of a Deli *dura* and a Serdang *pisifera* was used in this study. Reduced representation libraries (RRL) of 112 F1 progeny and the two parents were sequenced, and the reads were mapped against *E. guineensis* reference genome. A total of 2.5 million SNPs and 153,547 InDels were identified. However, only a subset of 5,278 markers comprising 4,838 SNPs and 440 InDels were informative for the construction of linkage map. The sixteen linkage groups spanned 2,737.6 cM for the maternal map and 4,571.6 cM for the paternal map with the average marker densities of one marker per 2.9 cM and 2.0 cM, respectively. Phenotypic data were correlated with polymorphic markers to discover markers flanking QTL regions for fresh-fruit-bunch yield (FFB), oil yield (OY), oil-to-bunch (O/B), oil-to-dry mesocarp (O/DM), oil-to-wet mesocarp (O/WM), mesocarp-to-fruit (M/F), kernel-to-fruit (K/F), shell-to-fruit (S/F), and fruit-to-bunch (F/B) ratio. Two significant QTLs for M/F were detected with PVE value of 20.6% and 23.9%, four markers for K/F were detected with PVE value range from 19.4% to 25.6%, and a marker for S/F was successfully detected with PVE value of 18.1%. The QTL peaks detected for K/F, M/F and S/F were significant with the logarithm of odds (LOD) value ranging from 4.51 to 6.24, which surpassed the genome-wide LOD threshold. Meanwhile, the allele effect analysis showed alleles associated with these three traits could contribute to the trait improvement from 4.6% to 20.7%. These findings, including a dense linkage map and identification of significant QTL regions associated with K/F, M/F and S/F that could be applied in MAS in the oil palm breeding programme. In addition, these approaches using the oil palm genetic linkage map and QTL analysis could fast-track the process of

generating new oil palm varieties as compared to the oil palm conventional breeding method.



Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Master Sains

**PEMBINAAN PETA RANGKAIAN GENETIK BAGI KELAPA SAWIT (*Elaeis guineensis* Jacq.) SERTA PENENTUAN LOKUS BERCIRI KUANTITATIF YANG BERKAIT DENGAN HASIL KELAPA SAWIT**

Oleh

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Kelapa sawit (*Elaeis guineensis* Jacq.) merupakan salah satu daripada tanaman penghasilan-minyak utama yang memberikan nilai nutrisi besar dan pulangan ekonomi yang tinggi. Genotip-secara-penjujukan (GBS) memberikan satu kaedah untuk mempercepatkan penemuan penanda polimorfisme nukleotida tunggal (SNP) dan penanda penyisipan dan penghapusan (InDel) untuk membina peta rangkaian genetik. Peta rangkaian genetik memudahkan pengenalpastian lokus ciri kuantitatif (QTL) berkaitan dengan ciri yang diingini. Bersama-sama pendekatan ini dapat mempercepatkan proses mengenal pasti penanda untuk pemilihan berbantuan-penanda (MAS) dalam program pembiakbakaan kelapa sawit. Sebanyak 112 populasi pemetaan saudara kandung daripada kacukan Deli *dura* dan Serdang *pisifera* telah digunakan dalam kajian ini. Pengurangan perwakilan perpustakaan (RRL) untuk 112 progeni F1 bersama dengan dua induknya telah diujukkan dan bacaannya dipetakan terhadap genom rujukan *E. guineensis*. Sebanyak 2.5 juta SNP dan 153,547 InDel telah dikenalpasti. Walau bagaimanapun, sejumlah 5,278 penanda merangkumi 4,838 SNP dan 440 InDel adalah bermaklumat untuk pembinaan peta rangkaian genetik. Enam belas kumpulan rangkaian genetik merangkumi 2,737.6 cM bagi peta induk ibu dan 4,571.6 cM bagi peta induk bapa dengan purata kepadatan penanda masing-masing untuk satu penanda per 2.9 cM dan 2.0 cM. Data fenotipik berkorelasi dengan penanda polimorfisme untuk penemuan penanda mengapit kawasan QTL untuk hasil buah tandan segar (FFB), hasil minyak (OY), nisbah minyak kepada tandan (O/B), nisbah minyak kepada mesokarp kering (O/DM), nisbah minyak kepada mesokarp segar (O/WM), nisbah mesokarp kepada buah (M/F), nisbah isirong kepada buah (K/F), nisbah tempurung kepada buah (S/F), dan nisbah buah kepada tandan (F/B) telah dikaji untuk mengenalpasti kawasan QTL yang bererti. Dua QTL bererti untuk M/F telah dikenalpasti dengan nilai PVE 20.6% dan 23.9%, empat QTL bererti untuk K/F telah dikenalpasti dengan nilai PVE antara 19.4% hingga 25.6%, dan satu QTL bererti untuk S/F telah berjaya dikenalpasti dengan nilai PVE adalah 18.1%. Puncak QTL bererti yang dikenalpasti untuk K/F, M/F and S/F adalah bererti dengan nilai algoritma ganjil (LOD)

antara 4.51 hingga 6.24 yang melebihi nilai ambang bagi LOD keseluruhan-genom. Sementara itu, analisis kesan alel menunjukkan alel yang berkaitan dengan ketiga-tiga ciri ini dapat menyumbang kepada penambahbaikan ciri antara 4.5% hingga 20.7%. Hasil penemuan ini termasuklah peta rangkaian genetik padat dan pengenalpastian kawasan QTL bererti berkaitan dengan K/F, M/ F dan S/F yang dapat diaplikasikan dalam MAS program pembiakbakaan kelapa sawit. Disamping itu, pendekatan ini menggunakan peta rangkaian genetik dan analisis QTL dapat mempercepatkan proses untuk penghasilan varieti baharu kelapa sawit berbanding dengan kaedah pembiakbakaan konvensional kelapa sawit.

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This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted to fulfil the requirement for the degree of Master of Science. The members of the Supervisory Committee were as follows:

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- The research conducted and the writing of this thesis was under our supervision;
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## LIST OF ABBREVIATIONS

AFLP	Amplified fragment length polymorphism
BC	Backcrosses
cM	centimorgan
CRoPS	Complexity reduction of polymorphic sequences
CW	Chromosome wide
DH	Double haploid
DNA	Deoxyribonucleic acid
D X P	<i>Dura X pisifera</i>
EFSA	European Food Safety Authority
EST	Expressed sequence tag
F <sub>1</sub>	The first filial generation of offspring
F <sub>2</sub>	The second filial generation of offspring
FFB	Fresh fruit bunch
FELDA	Malaysia's Federal Land Development Authority
FOA	Food and Agriculture Organization of the United Nation
F/B	Fruit to bunch ratio
GBS	Genotyping by Sequencing
GW	Genome wide
InDel	Insertion and Deletion
IPOA	Indonesia Palm Oil Association
kb	Kilo base-pair
K/F	Kernel to fruit ratio
LD	Linkage disequilibrium
LN	Liquid nitrogen



LOD	Logarithm of odds
MAB	Marker assisted breeding
MAS	Marker assisted selection
M/F	Mesocarp to fruit ratio
ML	Maximum likelihood
MPOB	Malaysia Palm Oil Board
NIL	Near-isogenic line
OY	Oil yield
O/B	Oil to bunch ratio
O/DM	Oil to dried mesocarp ratio
O/WM	Oil to wet mesocarp ratio
PCA	Principle component analysis
PCR	Polymerase chain reaction
PVE	Phenotypic variance explained
QTL	Quantitative trait loci
RIL	Recombinant inbred line
RAD-seq	Restriction-site associated DNA sequencing
RAPD	Random amplified polymorphic DNA
RE	Restriction enzyme
RFLP	Restriction fragment length polymorphism
RRL	Repeat representation library
RSPO	Roundtable on Sustainability Palm Oil
SNP	Single nucleotide polymorphism
SPSS	Statistical Package for the Social Science
SSR	Simple sequence repeats
S/F	Shell to fruit ratio

UTR

Untranslated region



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# CHAPTER 1

## INTRODUCTION

### 1.1 Background of the study

Oil palm, *Elaeis guineensis* Jacq., is one of the major oil-producing crops. There are two main globally commercialized species of oil palm which are *E. guineensis* and *E. oleifera*. The former originates from West Africa; meanwhile, the latter is from South or Central America (Corley & Tinker, 2016). In Southeast Asia where the main global producing countries are situated, the planting material of *E. guineensis* is more favourable. There are three different fruit types of oil palm available, comprising of *dura*, *pisifera* and *tenera*. Generating *tenera* from *dura* and *pisifera* as a planting material is one of the major breakthroughs in the oil palm breeding program. *Tenera* has higher oil yielding compared to its parents and resulted in 30% of the yield increment (Corley & Tinker, 2006).

Breeding progress for yield improvement in major crops, however, is still at low rate which is about 1 - 2% per annum (Soh, 2004; OECD/FAO, 2019). It has been reported an almost stagnant yield of the oil palm performance in Malaysia from 2003 to 2018 which was different for soybean, rapeseed and sunflower which showed yield increment of 6 - 62% for the similar period of time (Oil World, 2019). In fact, the best selection of plant for yield improvement should be done at later cycle when unstable genotypes, low heritability and differential plant competitive abilities may be observed at the early cycle (Soh, 2004). Such breeding pipeline should be challenging to be applied in the perennial crops compared to the annual crop. Oil palm which is a perennial crop has a life span of up to 40 years (Khusairi et al., 2019). This could take a long-term investment to generate new oil palm generation with some yield improvement.

Due to the oil palm longevity and the time taken to produce new variety using the conventional breeding approach, Marker Assisted Breeding (MAB) could fast track the oil palm breeding process. The generation time to produce a new cross with a trait of interest could reduce from 8 - 10 years in the conventional breeding method to just 4 - 5 years using DNA markers approach (Corley, 2017). In addition, molecular marker techniques have been introduced to give a better resolution at the molecular level while maintaining a similar objective in improving a valuable trait in a species. DNA markers could be applied to select progenies inheriting a desired trait prior to field planting.

Dissecting a potential DNA marker associated with a trait-of-interest from a genomic pool should be done before applying in marker-assisted breeding program. Oil yield which is a complex trait and controlled by multiple genes is very challenging to be identified by the marker associated with this trait. However, QTL analysis could be feasible to identify DNA region associated with oil yield or oil yield-related trait. Initially, the construction of genetic linkage map should be performed once significant markers have been identified. The significant markers can be shortlisted from various

types of markers including RFLP, RAPD, AFLP, SSR and SNP. For the yield improvement, these marker technologies have been successfully applied in various plant species to discover polymorphic markers which are used for the construction of genetic linkage map before the identification of QTL regions.

Recently, mining DNA markers using next generation sequencing (NGS) approaches is more feasible and affordable for many institutes as the sequencing cost reduces. This technology is able to produce genome wide markers. For oil palm, Pootakham et al. (2015) and Bai et al. (2017) currently reported the construction of dense oil palm genetic linkage maps using NGS platform would pave to the QTL identification. Similar approaches also found to be useful in various plant species; prominently sugarcane (Balsalobre et al., 2017), soybean (Liu et al., 2017), wheat (Gao et al., 2015), and alfalfa (Zhang et al., 2019). Leveraging this marker technology in the oil palm breeding program could not only reduce the time taken to produce new variety but also could possibly unlock the oil palm yield improvement in the near future.

## 1.2 Problem statements and justification of the study

Oil palm has a huge potential advantage to remain as a major edible oil source for a global need. However, there is a yield gap between the current yield performance in our local crop compared to the potential yield of this crop which is 18.5 t/ha (Corley, 2006). Due to fact that oil palm is a narrow genetic diversity, Malaysian Palm Oil Board (MPOB) has begun to collect oil palm germplasm since 1973 with the objective to broadening oil palm's genetic base through introgression and breeding (Rajanaidu et al., 2017). A total of 21 traits have been collected, including yield and its components, bunch quality characters and vegetative traits (Rajanaidu et al., 2017). Among them, yield and its components such as fresh fruit bunch (FFB) and oil yield (OY), and bunch quality characters, including oil to bunch ratio (O/B), oil to dry mesocarp ratio (O/DM), oil to wet mesocarp ratio (O/WM), mesocarp to kernel ratio (M/F), kernel to fruit ratio (K/F), shell to fruit ratio (S/F), and fruit to bunch ratio (F/B) are influencing factors for oil palm yield production.

Therefore, this study was initiated to embark on the potential DNA markers associated with yield production traits in oil palm cross, Deli *dura* and Serdang *pisifera*. Many oil palm genetic linkage maps have been published (Pootakham et al., 2015; Bai et al., 2017); however, none of the publications had been reported using this cross with the NGS technique to discover polymorphic markers. Thus, this study could discover new DNA regions in the oil palm genome which are associated with a trait of interest, particularly in oil yield-related traits that could be applied in MAS to enhance the oil palm yield performances.

### 1.3 The objectives of this study

There are three main objectives of this study:

1. to employ Genotyping by Sequencing (GBS) technique to discover genome-wide SNP and InDel markers in oil palm,
2. to construct a high-density oil palm genetic linkage map using SNP and InDel markers, and
3. to identify quantitative trait loci (QTL) regions associated with oil palm fresh fruit bunch (FFB), oil yield (OY) and yield-related components, including oil-to-bunch (O/B) ratio, oil-to-dry mesocarp (O/DM) ratio, oil-to-wet mesocarp (O/WM) ratio, mesocarp-to-fruit (M/F) ratio, kernel-to-fruit (K/F) ratio, shell-to-fruit (S/F) ratio and fruit-to-bunch (F/B) ratio.

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