UNIVERSITI PUTRA MALAYSIA

DNA MARKERS AND MAPPING OF QUANTITATIVE TRAIT LOCI FOR YIELD AND BUNCH QUALITY IN DELI DURA X YANGAMBI PISIFERA OIL PALM (Elaeis guineensis Jacq.) POPULATION

SENG TZER YING

IB 2015 12

DNA MARKERS AND MAPPING OF QUANTITATIVE TRAIT LOCI FOR YIELD AND BUNCH QUALITY IN DELI DURA X YANGAMBI PISIFERA OIL PALM (*Elaeis guineensis* Jacq.) POPULATION

By

SENG TZER YING

Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in Fulfilment of the Requirements for the Degree of Doctor of Philosophy

July 2015

Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfilment of the requirements for the Degree of Doctor of Philosophy

DNA MARKERS AND MAPPING OF QUANTITATIVE TRAIT LOCI FOR YIELD AND BUNCH QUALITY IN DELI DURA X YANGAMBI PISIFERA OIL PALM (*Elaeis guineensis* Jacq.) POPULATION

By

SENG TZER YING

July 2015

Chair : Assoc. Prof. Faridah Qamaruz Zaman, PhD
Faculty : Institute of Bioscience

Increased modern farming of the oil biosynthesis efficient oil palm, *Elaeis guineensis* Jacq., has propelled it to be the world's largest source of edible oil today. However, further oil yield improvement by conventional breeding is increasingly limited by lengthy time and costs due to long reproductive cycles, large plant size and an evaluation period of 10-15 years. Molecular tools which allow rapid, large scale evaluation over a short time, independent of plant age, will be particularly valuable in the face of such constraints. Towards such a goal, the aim of this particular study was to construct a genetic linkage map of a high yield oil palm population using DNA markers and to identify Quantitative Trait Loci (QTLs) related to oil yield components. This was followed by configuration of Quantitative Trait Alleles (QTA) with favourable and unfavourable effects on their respective oil yield components. The mapping population was a high-yielding Felda breeding cross, coded DA41, represented by 118 progeny palms. Besides the genotypic data generated in this study, phenotypic data of 21 yield components were available from ongoing field trials. The DNA markers employed for genotype data were microsatellites (SSR), Amplified Fragment Length Polymorphism (AFLP) and Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP) markers. A total 804 segregating marker loci (489 SSRs, 307 AFLPs and 8 PCR-RFLP) were used for final linkage analysis and map construction. The map of DA41 (ARK86D X ML161P) was 2398.8 cM long with 512 marker loci (368 SSRs, 135 AFLPs and 9 PCR-RFLPs), at an average 32 markers and a range of 15-59 markers per linkage group, and an average map density of 5 cM. The linkage group length was 77.5 cM to 223 cM, with an average of 150 cM. Taking the yield components phenotype data on board resulted in the detection of 164 QTLs associated with oil yield components. The QTLs had an average confidence region of 15.4 cM and no marker interval exceeded 50 cM. In the DA41 population, cumulative QTL effects increased in tandem with the number of QTL markers, matching the QT+ allele for each of the traits tested.

The many QTLs detected per trait suggested that the traits studied are polygenic with many genes of individual small effects on independent loci. However, the scope of the study did not rule out or rule in epistasis between different QTLs affecting a particular trait. Furthermore, several QTLs probably also show pleiotropic effects as seen by QTL clustering of inter-related traits on almost all the linkage groups, confirming the complexity of the genetic architecture of not only oil yield but also its components in the oil palm. The overall picture suggests that certain regions of the chromosomes are richer in the genes that affect the expression of a particular yield component trait and encompass pleiotropic, epistatic and heterotic effects. Hence, it will not be surprising if a large proportion of the identified additive effects from QTLs actually arise from digenic interactions between loci. For practical applications from this work, it will be necessary to test these yield component QTLs in a broader array of genetic backgrounds and in different environments. Also, more closely linked markers or flanking markers to the QTLs should be sought because recombinations between the markers and QTLs can occur when transferring the results from one population to another. Clearly, while this study has generated results that can be used in initial marker-assisted selection (MAS) for oil palm breeding, such as in population selection and enrichment, more detailed knowledge of marker-trait association will further contribute to more precise applications.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia
sebagai memenuhi keperluan untuk Ijazah Doktor Falsafah

PETANDA-PETANDA DNA DAN MENGENALPASTI LOKUS SIFAT KUANTITATIF BAGI HASIL DAN MUTU TANDAN KELAPA SAWIT (*Elaeis guineensis* Jacq.) PADA POPULASI DELI *DURA* X YANGAMBI *PISIFERA*

Oleh

SENG TZER YING

Julai 2015

Pengerusi : Prof. Madya Faridah Qamaruz Zaman, PhD
Fakulti : Institut Biosains

Peningkatan pertanian secara moden kelapa sawit *Elaeis guineensis* Jacq yang bercekap biosintesis minyak, telah menjadikannya tanaman minyak yang paling lumayan di dunia hari ini. Walau bagaimanapun, hasil kelapa sawit secara pembiakan konvensional yang memakan masa dan mahal. Ini disebabkan kitaran pembiakan yang panjang, saiz pokok yang besar dan tempoh penilaian yang lama (10-15 tahun). Kaedah molekular membolehkan penilaian skala besar dalam masa yang singkat tanpa bergantung kepada factor umur pokok. Tujuan kajian ini adalah untuk membina peta rangkaian genetic kelapa sawit berhasil tinggi dengan menggunakan penanda DNA (asid deoksiribonukleik) serta mengenalpasti Lokus Sifat Kuantitatif (QTLs) yang berkaitan dengan komponen hasil minyak. Analisis lanjut untuk konfigurasi QTA yang mempunyai kesan meningkat/menurun terhadap komponen hasil minyak turut diuji. Kacukan Felda DA41 yang berminyak tinggi terpilih bagi uji-kaji ini, sebanyak 118 pokok. Selain daripada data genotipik yang dihasilkan dalam penelitian ini, data fenotipik daripada 21 komponen hasil juga sedia-ada. Penanda DNA digunakan untuk data genotipik adalah mikrosatelit (SSR), Polimorfisme panjang fragmen teramplifikasi (AFLP) dan Reaksi berantai polymerase-Polimorfisme Panjang Berkas Restriksi (PCR-RFLP). Sejumlah 804 penanda lokus (489 SSRs, 307 AFLPs and 8 PCR-RFLPs) telah digunakan untuk analisis rangkaian dan pembinaan peta akhir. Peta DA41 (ARK86D X ML161P) adalah 2398.8 cM dengan 512 penanda lokus (368 SSRs, 135 AFLPs and 9 PCR-RFLPs), dengan purata penanda lokus 32 dan pada lingkungan penanda lokus 15-59 dalam setiap rangakaian kumpulan, dan purata densiti peta adalah 5 cM. Rangakaian kumpulan sepanjang 77.5 cM to 223 cM, dengan puratanya 150 cM. Sebanyak 164 QTLs yang berkaitan dengan komponen hasil minyak telah dikesan. QTLs mempunyai kepastian dalam linkungan 15.4 cM dan tiada selang penanda melebihi 50cM. Dalam DA41, kesan terkumpul QTL meningkat apabila bilangan penanda QTL padan dengan allele QT+ untuk semua sifat yang diuji. Banyak QTLs yang dikesan

bagi setiap sifat mengesahkan bahawa sifat yang dikaji memang dikawal oleh banyak gen mempunyai kesan individu yang kecil terhadap lokus bebas. Walaubagaimanapun, epistasis antara QTLs juga perlu diambil-kira menyebabkan hubungan yang lebih komplek antara QTLs dan jumlah ekspresi suatu sifat. Malah QTLs mungkin memberi kesan pleiotropic, dimana mereka mengawal sifat berkait yang berbeza, walaupun mempunyai kedudukan kromosom yang sama/dekat. QTL yang berkelompok sebegini dilihat dalam hampir kesemua kromosom , mengesahkan kerumitan seni-bina genetik yang mengawal hasil dan komponennya dalam kelapa sawit. Kelompok ini menggambarkan kawasan-kawasan tertentu dalam kromosom yang lebih kaya dengan gen yang memberi kesan terhadap ekspresi suatu sifat komponen tertentu. Kajian ini mengesahkan warisan kompleks pada sifat-sifat komponen hasil yang merangkumi kesan pleiotropic, epistatic dan heterotic pada QTLs hasil minyak. Oleh itu, tidak mengejutkan jika sebahagian besar kesan tambahan QTLs yang dikenalpasti juga disebabkan oleh interaksi digenic antara lokus dalam kelapa sawit juga. Lebih banyak eksperimen perlu dijalankan menggunakan pokok kelapa sawit yang mempunyai sumber genetik dan persekitaran yang berbeza, bagi menguji QTLs hasil. Selain itu, penanda rapat atau penanda pengapit bagi QTL diperlukan dalam kajian seterusnya. Ini disebabkan penggabungan semula yang mungkin berlaku dalam populasi lain antara penanda dan QTLs. Walaupun kajian ini berjaya menjana hasil yang boleh digunakan dalam proses pemilihan berasaskan penanda (marker-assisted selection, MAS), pengetahuan yang lebih terperinci dalam assosiasi penanda-sifat akan meningkatkan penggunaannya.

ACKNOWLEDGEMENTS

I gratefully acknowledge the support, guidance and also encouragement of my chair supervisor, Assoc. Prof. Dr. Faridah Qamaruz Zaman. A special thank you goes to all co-supervisors, Prof. Tan Soon Guan, Dr. Rajinder Singh and Dr. Sharifah Shahrul Rabiah Syed Alwee, for their supervision and valuable comments that helped towards the completion of this study. Sincere thanks go to Dr. Enrique Ritter, Dr. Norbert Billotte, Ms. Ting Ngoot Chin, for assisting in my discovery of the research field, sharing their professional knowledge, giving valuable comments and constant encouragement.

My appreciation also extends to my laboratory colleagues in FGV Biotechnology Centre (FBC), especially Mrs. Jamilah Ismail, Mrs. Siti Hawa and Ms. Nurul Hafiza Ramli whose heartfelt support, patience, and assistance allowed the work to be completed successfully. I would like to thank all FBC staff for their helpfulness and willingness to share, thus making it possible to complete this work. Deep gratitude also goes to Mr. Chin Cheuk Weng, Mr. Nasruddin Mohamad, Mr. Mohd. Latif Kamarudin, Mr. Nardeman Samin and Mr. Yahor and the administration at breeding station, Pusat Penyelidikan Pertanian Tun Razak, Pahang for providing breeding materials.

Especial thanks go to Mr. Chang Kwong Choong (Andy) for editing my thesis and for the enduring encouragement. My special thanks go to a group of friends out of the lab, for their invaluable friendship, help, understanding, love and care. I wish to express my deepest gratitude and appreciation to my parents Seng Hoi Lum and Sing Mooi and also my siblings for their understanding, encouragement and endless love throughout my study. Last but not least, I thank my husband, Vengeta Rao, for a life of love, joy and courage. Also, my indebtedness to my two sons, Chenna and Manu, who were always so tolerant of the time that it took to finish this work and for their never failing love and support.

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

Faridah Bt. Qamaruz Zaman, PhD
Associate Professor
Institute of Bioscience
Universiti Putra Malaysia
(Chairperson)

Tan Soon Guan, PhD
Professor
Faculty of Biotechnology and Biomolecular Sciences
Universiti Putra Malaysia
(Member)

Rajinder Singh A/L Harminder Singh, PhD
Group Leader of Genomics Group
Advanced Biotechnology and Breeding Centre (ABBC)
Malaysian Palm Oil Board (MPOB)
(Member)

Sharifah Shahrul Rabiah Syed Alwee, PhD
Chief Executive Officer
Felda Global Ventures Research and Development Sdn. Bhd.
(Member)

BUJANG BIN KIM HUAT, PhD
Professor and Dean
School of Graduate Studies
Universiti Putra Malaysia

Date:

Declaration by graduate student

I hereby confirm that:

- this thesis is my original work
- quotations, illustrations and citations have been duly referenced
- the thesis has not been submitted previously or comcurrently for any other degree at any institutions
- intellectual property from the thesis and copyright of thesis are fully-owned by Universiti Putra Malaysia, as according to the Universiti Putra Malaysia (Research) Rules 2012;
- written permission must be owned from supervisor and deputy vice – chancellor (Research and innovation) before thesis is published (in the form of written, printed or in electronic form) including books, journals, modules, proceedings, popular writings, seminar papers, manuscripts, posters, reports, lecture notes, learning modules or any other materials as stated in the Universiti Putra Malaysia (Research) Rules 2012;
- there is no plagiarism or data falsification/fabrication in the thesis, and scholarly integrity is upheld as according to the Universiti Putra Malaysia (Graduate Studies) Rules 2003 (Revision 2012-2013) and the Universiti Putra Malaysia (Research) Rules 2012. The thesis has undergone plagiarism detection software

Signature: ________________________ Date: __________________

Name and Matric No: Seng Tzer Ying (GS22332)

Declaration by Members of Supervisory Committee

This is to confirm that:

- the research conducted and the writing of this thesis was under our supervision;
- supervision responsibilities as stated in the Universiti Putra Malaysia (Graduate Studies) Rules 2003 (Revision 2012-2013) were adhered to.

Signature: ____________________________
Name of Chairman of Supervisory Committee: Faridah Bt. Qamaruz Zaman, PhD, Assoc. Prof

Signature: ____________________________
Name of Member of Supervisory Committee: Tan Soon Guan, PhD, Prof

Signature: ____________________________
Name of Member of Supervisory Committee: Rajinder Singh A/L Harminder Singh, PhD

Signature: ____________________________
Name of Member of Supervisory Committee: Sharifah Shahrul Rabiah Syed Alwee, PhD

TABLE OF CONTENTS

CHAPTER

LIST OF TABLES

LIST OF FIGURES

LIST OF APPENDICES

LIST OF ABBREVIATIONS

Most of the abbreviations used are standard. However, attention is drawn to the following:

χ^2	Chi square values
ABI	Applied Biosystems (Perkin Elmer)
ABW	Average bunch weight
ACCase	Acetyl CoA-carboxylase
ACS	American Chemical Society
AFLP	Amplified Fragment Length Polymorphism
AMD	Average marker density
AMP-PCR	anchored microsatellite primered PCR
Ao	number of alleles observed per locus
AP-PCR	Arbitrarily Primed Polymerase Chain Reaction
ASAP	Allele-Specific Associated Primers
AVROS	Algemeene Vereniging van Rubberplanters ter Oostkust van Sumatra
BAC	Bacterial Artificial Chromosomes
BC	Backcross
BNO	Bunch numbers
BPRO	Breeding Populations of Restricted Origin
BSA	Bovine serum albumin
BWT	Bunch weight
BWT	Bunch Weight (kg)
CAP	Cleaved Amplified Polymorphic Sequence
CIM	composite interval mapping
CIRAD	Centre International Recherche Agricola et Developpement
cM	centiMorgan
CM	markers common to both parents
CRoPS	Complexity Reduction of Polymorphic Sequences
CTAB	Hexadecyltrimethyl ammonium bromide
D x T	*dura* x *tenera* cross
D	*dura* form
DAF	DNA Amplification Fingerprinting
DES	descent from P1: ARK86D or P2: ML161P
DNA	Deoxyribonucleic acid
dNTPs	deoxynucleotide triphosphates
DPF	Dry Pericarp-to-Fruit (%)
E	expected number
e.g.	for example
EDTA	Ehtylenediaminetetraacetic acid
eQTLs	expression QTLs
EST	Expressed Sequence Tags
EtBr	Ethidium Bromide
etc.	and the others
F(null)	null allele estimated frequency
F/B	ratio of total fruit weight to bunch weight

F_1	First cross / Filial 1
F_2	Intercross between two F_1
FAC	Fatty acid composition
FAM	5-carboxyfluorescein (ABI fluorescent label – blue)
FASSB	FELDA Agricultural Services Sdn. Bhd.
FB	Fruit-to-Bunch (%)
FELDA	Federal Land Development Authority Malaysia
FFA	free fatty acid
FFB	fresh fruit bunch
FIB	Fibre-to-Bunch (%)
FIPS	Family and individual palm selection
FIWP	Fibre-to-Wet Pericarp (%)
GBS	Genotyping by-sequencing
GCA	General Combining Ability
GDP	Gross Domestic Product
GLM	Generalized linear model
GMO	Genetically modified organisms
H_{exp}	expected heterozygosity
H_{obs}	observed heterozygosity
HVR	Hypervariable Regions
HWE	Hardy-Weinberg equilibrium
I-C	interval length (confidence)
INEAC	Institut National pour l'Etude Agronomique du Congo
IP1	individual markers (parent 1 specific)
IP2	individual markers (parent 2 specific)
IRD	Infrared dye
IRHO	Institut de Recherches pour les Huiles et Oleagineux
ISA/ISSR	Inter SSR Amplification
IV	iodine value
JOE	(ABI fluorescent label – green)
KB	Kernel-to-Bunch (%)
KF	Kernel-to-Fruit (%)
KLM	Kuala Lumpur Melanocca
KY	kernel yield
LGs	linkage groups
LiCl	Lithium chloride
LOD	logarithm-of-the-odds
M/B	Mesocarp-to-bunch
M/F	mesocarp-to-fruit
MABW	Mean Average Bunch Weight From Pool Over Years Weight
MAS	Marker-Assited Selection
MB	Molecular breeding
MBNO	Mean Bunch Number Weight from Pool Over Years Weight
MFFB	Mean Fresh Fruit Bunch from Pool Over Years Weight
MFW	Mean fruit weight
MFW	Mean Fruit Weight (g)
MIM	multiple interval mapping
MKW	Mean Kernel Weight

MPOB	Malaysia Oil Palm Board
MP-PCR	Microsatellite (repeat)-primed PCR
MPW	Mean Pericarp Weight
MRRS	Modified reciprocal recurrent selection
MSW	Mean Shell Weight
Na_2OAc	Sodium acetate
NaCl	Sodium chloride
NaOH	Sodium hydroxide
NE-1P	average non-exclusion probability for one candidate parent
NE-PP	average non-exclusion probability for a candidate parent pair
NGS	Next Generation Sequencing
NH_4OAc	Ammonium Acetate
NIFOR	Nigerian Institute for Oil Palm Research
Nig	*Nigrescens*
NIL	Near Isogenic Lines
O	observed number
O/F	oil-to-fruit
O/M	oil-to-mesocarp
O/WM	oil-to-wet mesocarp
OB	Oil-to-Bunch (%)
OD	Optical Density
ODP	Oil-to-Dry Pericarp (%)
OWP	Oil-to-Wet Pericarp (%)
OY	oil yield
P	*pisifera* form
p	Probability
PCR	Polymerase Chain Reaction
pers. comm.	Personal communication
PIC	Polymorphism Information Content
PIR	Protein Identification Resource
PKO	Palm kernel oil
PNG	Papua New Guinea
POS	position of QTL from left flanking marker of the interval
PRL	probability for Null hypothesis of no QTL
PV	phenotypic variance
PVP	Polyvinylpyrrolidone
PVP-40	Polyvinylpyrrolidone with molecular weight 40,000
“q”	derived from male parent
“Q”	derived from female parent
QT+	quantitative trait plus
QTA	Quantitative Trait Allele
QTL	Quantitative Trait Loci
r	recombination estimates
R^2	coefficient of determination
RAD	Restriction Site Associated DNA
RAMP	Randomly Amplified Microsatellite Polymorphism
RAPD	Random Amplified Polymorphic DNA
RE	Restriction Endonuclease

Rf	Restorer genes
RFLP	Restriction Fragment Length Polymorphism
RFs	recombination frequencies
RFU	Relative Fluorescent Units
RGAs	resistances gene analogues
RIL	Recombinant Inbred Line
RNA	Ribonucleic Acid
RNAase	Ribonuclease
ROX	Internal size standard (ABI fluorescent label – red)
rpm	revolutions per minute
S/F	shell-to-fruit
SAMPL	Selective Amplification of Microsatellite Polymorphic Loci
SCA	Specific Combining Ability
SCAR	Sequence Characterization Amplified Region
sCIM	simplified composite interval mapping
SCMV	Sugarcane Mosaic Virus
SDS	Sodium Dodecyl Sulphate
SF	Shell-to-Fruit (%)
sh	Shell gene
SM	single/simple marker analysis
SNP	Single Nucleotide Polymorphisms
SPAR	Single Primer Amplification Reaction
SPP	number of spikelets per panicle
SPSS	SPSS statistical software packages
SSR	Simple Sequence Repeat
STMS	Sequence-Tagged Microsatellite Sites
STR	Short Tandem Repeats
STS	Sequence Tagged Sites
T x T	*tenera* x *tenera* cross
T	*tenera* form
TAE	Tris-acetate EDTA
TAMRA	(ABI fluorescent label – yellow)
TBE	Tris-borate EDTA
TE	Tris-EDTA
TGW	1,000 grain weight
TM	total number of markers for linkage group
Tris	Tris (hydromethyl) methylamine
UV	Ultraviolet
V0	mean value of the trait across all palms without the band
V1	mean value of the trait across all palms with the band
Vdif (V1-V0)	difference between the mean
Vir	*Virescens*
VNTR	Variable Number Tandem Repeat
WAIFOR	West African Institute for Oil Palm Research
WFI	Water-to-Fiber (%)
WM/F	wet mesocarp-to-fruit
WPF	Wet Pericarp-to-fruit (%)
WWP	Water-to-Wet Pericarp (%)

CHAPTER 1

AN OVERVIEW

1.1 Introduction

The oil palm, *Elaeis guineensis* Jacq., is the world's most productive oil crop and has been an important crop for mankind for more than 5000 years (Zeven, 1967). The cultivation has contributed greatly to the economic development of otherwise backward rural areas by providing cash employment and higher earnings over the traditional, largely sustenance, agriculture. Palm oil is an important export commodity in some of the countries where the crop is grown, and is the second largest contributor to Malaysia's Gross Domestic Product (GDP). Besides Malaysia, oil palm cultivation has expanded rapidly in other parts of South East Asia, especially Indonesia, and, to a smaller extent, Africa and South and Central America.

Although the oil palm is the most productive oil crop, from intrinsic high oil yields coupled with breeding and agronomic improvements, the national Malaysian yield has stagnated for the past 20 years with fresh fruit bunch (FFB) production at ~20t/ha/yr, palm oil at ~4t/ha/yr and palm kernel (KY) ~1.0 t/ha/yr (Malaysian Palm Oil Board, 2013). With the rapid expansion of the world population particularly in the third world where dietary fat intake is still very low, edible oils and fats consumption is likely to increase tremendously, prompting increased production. For this to happen, simply expanding the area cultivated would be the easiest, but practically difficult for want of land and the increasingly strident calls for conservation. For example, in 2010 it was estimated that any future expansion in the oil palm area in Malaysia would only be to 1.3M ha (Malaysian Prime Minister's Department, 2010). This leaves the only option of increasing yield to solve this problem. There certainly has been yield improvement over, say, the last 50 years – about 70 percent due to breeding improvement and 30 percent due to better agronomic practices (Rosenquist, 1985; Davidson 1993; Corley and Tinker, 2003). The most important single breeding effort for yield improvement was the gain in bunch oil content from 16% (in the Dura type of oil palm) to 26% (in the tenera or DxP type) following discovery of the shell thickness gene and subsequent universal adoption of DxP planting materials (Hardon *et al.*, 1985, 1987). Following the advances with the shell gene, further yield gains were made through classical breeding for better duras and pisiferas to cross, i.e., with good general combining ability (GCA) and specific combining ability (SCA). Oil production as high as 14.9 t/ha/year from FFB yield of 45 t/ha/year and oil content of 35 percent have been recorded in experimental plantings (Rajanaidu and Kushairi, 2003). These impressive experimental yields are, nevertheless, still below the theoretical maximum of 18.2 t/ha/yr oil from 45t FFB (Corley 1983, 1985, 1998).

As noted above, classical oil palm breeding is time consuming and costly - due to long generation cycles, large plant size and an evaluation period of 10-15 years. For such crops, the new science of molecular breeding (MB) - using molecular markers to facilitate the breeding process (Mohan *et al.*, 1997; Hash and Bramel-Cox, 1999; Kumar, 1999) – beckons. Having markers for characters with easily detectable phenotypes can simplify the recovery of genes of interest linked to the traits, hence the vogue for Marker-Assisted Selection (MAS). MAS generally refers to using molecular markers, near to, or flanking, to a gene which effect on the phenotype is of interest, to identify and then select for/against the gene (Kumar, 1999). The markers are thus signposts for the whereabouts of the gene and indicate the part of the genome to manipulate, i.e., where to introduce/remove genes in the crop (Hash and Bramel-Cox, 1999; Young, 1999; Mackill, 2003). Once a gene is tagged with a marker, pre-selection for the gene (through the marker) can be made in even very young seedlings. Only the plants with the marker/trait of interest are retained/rejected. Furthermore, MAS can greatly reduce the number of breeding cycles by offering greater precision in palm selection in each cycle. The key to accelerating oil palm breeding through MAS is genetic linkage information, usually presented as linkage maps.

As maybe gathered from the above, oil yield is the most important economic trait in oil palm, hence the search for marker(s) for the shell gene which has veered most mapping work to *tenera* x *tenera* (Mayes *et al.*, 1997; Singh *et al.*, 2005), *dura* x *tenera* (Rhode, 2003; Billotte *et al.*, 2005) and *tenera* x *pisifera* (Moretzsohn *et al.*, 2000) crosses. However, away from the shell thickness hunt, direct higher oil yield in the oil palm (as opposed to more oil from less shell), like in most other crops, is a composite trait which final expression is the sum of a number of components that result in higher FFB yield and better fruit quality traits for oil in the bunch (Sparnaaij *et al.*, 1963). Thus, direct oil yield in oil palm is a complex trait under polygenic control, multiplicativly interrelated and highly influenced by the environment. Therefore, while a useful first step, MAS, based merely on markers for the single gene of shell thickness alone, is unlikely to contribute much to oil yield of the crop.

Hence, the main aims of this study are to detect and map QTLs affecting the oil yield components in oil palm and in passing, re-assess the interrelationships between oil yield and its components. The study was preceded by a survey of the genetic variation in existing potential mapping populations to obtain an indication of the potential improvement possible through breeding, and to identify suitable planting materials for mapping. The availability of reliable phenotype data for the traits of interest (oil yield components), from FASSB recording, for all selected individual palms in the proposed mapping population, was obviously also a key requirement. Three molecular marker assay systems with a slew of advantages – AFLPs, RFLPs and SSRs - were employed to genotype the mapping population.

1.2 Objectives

The objectives of this study were:

i) To select of mapping population and survey the genetic variation of oil yield components in the population.
ii) To identify polymorphic AFLPs, RFLPs and SSRs markers.
iii) To construct genetic linkage maps for both parental palms, ARK86 and ML161 and construct a high density map by integrating both parental maps
iv) To identify markers possibly associated with the quantitative traits linked to the oil yield components in oil palm.
v) To determine the allelic configurations of each QTL and their specific effects (positive or negative) on the trait and compute the cumulative effects of all the QTL+ alleles for each trait.

REFERENCES

Ahiekpor, E. S. S. and Yap T. C. (1982). Heritability, correlation and path coefficient analyses of some oil palm breeding populations in Malaysia. In E. Pushparajah and P.S. Chew (Ed.), *The oil palm in agriculture in the eighties, Vol. 1* (pp. 47–54). Kuala Lumpur: Incorps. Soc. Planters.

Ajmone-Marsan, P., Monfredini, G., Ludwing, W. F., Melchinger, A. E., Franceschini, P., Pagnotto, G., Motto, M. (1995). In an elite cross of maize a major quantitative trait locus controls one-fourth of the genetic variation for grain yield. *Theor. Appl. Genet.,* 90: 415–424.

Ariffin, D. (2000). Major diseases of oil palm. In Y. Basiron, B. S. Jalani, and K. W. Chan (Ed.), *Advances in oil palm research* (pp. 596–622). Kuala Lumpur: Malaysian Palm Oil Board.

Ariffin, D., Idris Seman, A. and Marzuki, A. (1995) Development of a technique to screen oil palm seedlings for resistance to Ganoderma. In *Proceedings of the 1995 PORIM National Oil Palm Conference on Technology in Plantation: The Way Forward,* Palm Oil Res. Inst. Malaysia, KualaLumpur, pp.132–141.

Arnedo-Andrés, M. S., Gil-Ortega, R., Luis-Arteaga, M. and Hormaza, J. I. (2002) Development of RAPD and SCAR markers linked to the *Pvr4* locus for resistance to PVY in pepper (*Capsicum annuum* L.). *Theor. Appl. Genet.,* 105: 1067-1074.

Ashburner, G. R., Thompson, W. K. and Halloran, G. M. (1997). RAPD analysis of South Pacific coconut palm populations. *Crop Sci.* 37: 992-997.

Ataga, C. D. and Fatokun, C. A. (1989). Disc polyacrylamide gel electrophoresis of pollen proteins in the oil palm (*Elaeis*). *Euphytica,* 40(1-2):83-88

Austin, D. F., Lee, M. (1996). Comparative mapping in F2:3 and F6:7 generations of quantitative trait loci for grain yield and yield components in maize. *Theor. Appl. Genet.,* 92(7):817-26. doi: 10.1007/BF00221893.

Baird, N. A., Etter, P. D., Atwood, T. S., Currey, M. C., Shiver, A. L., Lewis Z. A., Selker, E. U., Cresko, W. A. and Johnson, E. A. (2008). Rapid SNP discovery and genetic mapping using sequenced RAD markers. *PLoS ONE,* 3(10): e3376. doi:10.1371/journal.pone.0003376

Bakoumé, C., Wickneswari, R., Rajanaidu, N., Kushairi, A., Amblard, P., and Billotte, N. (2007). Allelic diversity of natural oil palm (*Elaeis guineensis* Jacq.) populations detected by microsatellite markers:

implication for conservation. *Plant Genet Resour: Characterization and Utilization.* 5(2):104–107

Barbazuk, W. B., Emrich S. J., Chen, H. D., Li, L., and Schnable, P. S. (2007). “SNP discovery via 454 transcriptome sequencing. *Plant J.,* 51(5):910–918

Barcelos, E., Second, G., Kahn, F., Amblard, P., Lebrun, P., and Sequin, M. (1999). Molecular markers applied to the analysis of genetic diversity and to the biogeography of Elaeis (Palmae). In A. Menderson and F. Borchsenius, (Ed.), *Evolution, Variation and Classification of Palm* (pp.191–201) New York: New York Botanical Garden

Barcelos, E., Amblard, P., Berthaud, J. and Seguin, M. (2002). Genetic diversity and relationship in American and African oil palm as revealed by RFLP and AFLP molecular markers. *Pesq. Agropec. Brasil*, 37:1105–1114

Barcelos, E., Miranda-Santos M. D., Elizabeth, M. and Varoncellos, C. (1986). Phenotypic variation in natural populations of Caiaue, *Elaeis oleifera*, H.B.K. Cortes, in the Brazilian Amazon. In: Proc. Int. Workshop *‘Oil palm germplasm and utilisation’*, (pp. 102–116). Kuala Lumpur: Palm Oil Res. Inst. Malaysia.

Bartoš, J., Sandve, S. R., Kölliker, R., Kopecký, D., Christelová, P., Stočes, S., Ostrem, L., Larsen, A., Kilian, A., Rognli, O. A., and Doležel, J. (2011). Genetic mapping of DArT markers in the Festuca Lolium complex and their use in freezing tolerance association analysis. *Theor. Appl. Genet.,* 122(6):1133-1147. Doi: 10.1007/s00122-010-1518-z. Epub 2011 Jan 7.

Bates, G. W. (1992). Molecular analysis of nuclear genes in somatic hybrids. *Physiol. Plant.* 85: 308-314.

Baudouin, L. and Durand-Gasselin, T. (1991). Genetic transmission of characters linked to oil yields in oil palm by cloning results for young palms. *Oléagineux,* 46: 313–320

Beavis, W. D. (1998). QTL analyses: power, precision, and accuracy. In A. H. Paterson (Ed.) *Molecular issection of complex traits* (pp. 145–162). New York: CRC Press.

Beavis, W. D. (1994). The power and deceit of QTL experiments: lessons from comparative QTL studies. In D. B. Wilkinson (Ed.) *49th Ann Corn Sorghum Res Conf. Am Seed Trade Assoc.* (pp. 250-266). Chicago: IL.

Becker, J., Vos, P., Kuiper, M., Salamini, F., Heun, M. (1995). Combined mapping of AFLP and RFLP markers in barley. *Mol Gen Genet.,* 249: 65-73.

Beirnaert, A. and Vanderweyen, R. (1941). Contribution a l'étude génétique et biométrique des variétés d'*Elaeis guineensis* Jacquin. *Publication Institute National Etude Agronomie Congo Belge. Serie. Science,* 27: 1-101

Bernardo, R., and Yu, J. (2007). Prospects for genome-wide selection for quantitative traits in maize. *Crop Sci.,* 47: 1082-1090.

Bevan, J. W. L., Fleming, T. and Gray, B. S. (1966). *Planting techniques for oil palms in Malaysia.* Kuala Lumpur: Incorporated society of Planters.

Billotte, N., Jourjon, M. F., Marseillac, N., Berger, A., Flori, A., Asmady, H., Adon, B., Singh, R., Nouy, B., Potier, F., Cheah, S. C., Rohde, W., Ritter, E., Courtois, B., Charrier, A. and Mangin, B. (2010). QTL detection by multi-parent linkage mapping in oil palm (*Elaeis guineensis* Jacq.). *Theor. Appl. Genet.,* 120(8): 1673-1687

Billotte, N., Risterucci, A. M., Barcelos, E., Noyer, J. L., Amblard, P., Baurens, F. C. (2001). Development, characterisation, and across-taxa utility of oil palm (*Elaeis guineensis* Jacq) microsatellite markers. *Genome,* 44:413–425

Billotte, N., Marseillac, N., Risterucci, A. M., Adon, B., Brottier, P., Baurens, F.C., Singh, R., Herrán, A., Asmady, H., Billot, C., Amblard, P., Durand-Gasselin, T., Courtois, B., Asmono, D., Cheah, S. C., Rohde, W., Ritter, E. and Charrier, A. (2005). Microsatellite-based high density linkage map in oil palm (*Elaeis guineensis* Jacq.). *Theor. Appl. Genet.,* 110: 754-765.

Blaak, G. (1965) Breeding and inheritance in the oil palm. Part III: Yield selection and inheritance. *J, Niger. Inst. Oil Palm Res,* 4, 262-283

Blaak, G., Sparnaaij, L. D. and Menendez, T. (1963). Breeding and inheritance in oil palm, Part II. Methods of bunch analysis. *J. W. Afr. Inst. Oil Palm Res,* 4:146 –155

Bostein, D., White, R. L., Skolnik, M. and Davis, R. W. (1980). Construction of a genetic linkage map in man using restriction fragment length polymorphism. *The American Journal of Human Genetics,* 32: 314-331.

Boutin-Ganache, I., Raposo, M., Raymond, M., Deschepper, C. F. (2001). M13-tailed primers improve the readability and usability of microsatellite analyses performed with two different allele-sizing methods. *BioTechniques*, 31:24-28

Breton, F., Hasan, T., Hatiadi, Z., Lubis, A. U. and De Franqueville, H. (2005). Characterization of parameters for the development of an early screening test for basal stem rot tolerance in oil palm progenies. In

Proceedings of the PIPOC 2005. (pp.167–183). KualaLumpur: Malaysian Palm Oil Board.

Breure, C. J. and Corley R.H.V. (1983). Selection of oil palms for high density planting. *Euphytica,* 32: 177–186

Breure, C. J. (1986). Parent selection for yield and bunch index in the oil palm in West New Britain. *Euphytica,*35: 65–72

Breure, C. J., Rosenquist, E. A., Konimor, J. and Powell, M. S. (1986). Oil palm introductions to Papua New Guinea and the formulation of selection methods at Dami Oil Palm Research Station. In A. C. Soh, N. Rajanaidu, and M. Nasir (Ed.), *Int. Workshop on Oil Palm Germplasm and Utilization* (pp. 189–193). Kuala Lumpur: Palm Oil Res. Inst. Malaysia.

Breure, C. J. and Soebagjo, F. X. (1991). Factors associated with occurrence of crown disease in oil palm (*Elaeis guineensis* Jacq) and its effect on growth and yield. *Euphytica,* 54: 55-64.

Broekmans, A. F. M. 1957. Growth flowering and yield of the oil palm in Nigeria. *Journal of West African Institue of Oil Palm Resarch,* 2:187–220.

Brooker, R. J. (1999). *Genetics Analysis and Principles.* California: Benjamin/Cumming, Menlo Park.

Buckler, E. S., Holland, J. B., Bradbury, P. J., Acharya, C. B., Brown, P. J., Browne, C., Ersoz, E., Flint-Garcia, S., Garcia, A., Glaubitz, J. C., Goodman, M. M., Harjes, C., Guill, K., Kroon, D. E., Larsson, S., Lepak, N. K., Li, H., Mitchell, S. E., Pressoir, G., Peiffer, J. A., Rosas, M. O., Rocheford, T. R., Romay, M. C., Romero, S., Salvo, S., Sanchez-Villeda, H., da Silva, H. S., Sun, Q., Tian, F., Upadyayula, N., Ware, D., Yates, H., Yu, J., Zhang, Z., Kresovich, S., McMullen, M. D. (2009). The genetic architecture of maize flowering time. *Science,* 325(5941):714-718.

Budiman, M. A., Singh, R., Low, E. T. L., Nunberg, A., Citek, R., Rohlfing, T., Bedell, J. A., Lakey, N. D., Martienssen, R. A., Cheah, S. C. (2005). Sequencing of the oil palm genespace. In: Proceedings of PIPOC 2005 international palm oil congress. Agriculture, biotechnology and sustainability conference, Kuala Lumpur, 25–29 Sept 2005, pp 628–639

Burotowski, S. (1994). The basics of basal transcription by RNA polymerase II. *Cell.* 77: 1-3.

Burstin, J., Marget, P., Huart, M., Moessner, A., Mangin, B., Duchene, C. Desprez, B., Munier-Jolain, N., Duc, G. (2007). Developmental genes have pleiotropic effects on plant morphology and source capacity, eventually impacting on seed protein content and productivity in pea. *Plant Physiol.* 144: 768–781. www.plantphysiol.org/cgi/doi/10.1104/pp.107.096966.

Caetano-Anollés, G. (1998). Review and interpretation: DNA analysis of Turfgrass genetic diversity. *Crop Sci.* 38: 1415-1424.

Caetano-Anolles, G. B., Bassam, B. J. and Gresshoff, P. M. (1991). DNA amplification fingerprinting using very short arbitrary oligonucleotide primers. *Biotechonology.* 9: 553-557.

Chan, K. W. and Lim K. C. (1982). Quantification of the effects of legume establishment and maintenance on yield of oil palm. In E. Pushparajah and P.S. Chew (Ed.), *The oil palm in agriculture in the eighties, Vol. 2* (pp. 301–314). Kuala Lumpur: Incorps. Soc. Planters.

Chan, K. W. (1972). *The effects of plant growth substances on fruit induction, development and fruit abscission in the oil palm* (*Elaeis guineensis* Jacq.). Thesis, University of Malaya, Kuala Lumpur.

Chan, K. W., Alwi, A., and Liau, S. S. (1989). The long-term influence of weevil pollination on yield production pattern of oil palm in Guthrie Estates in Malaysia. Proceedings from *the 1989 PORIM International Palm Oil Development Congress – Agriculture Conference.* (pp.133-143). Kuala Lumpur.

Chapas, L. C., Tinker, P. B., and Ziboh, C. O. (1957). The determination of the oil content of oil palm fruit. *J. W. Afr. Inst. Oil Palm Res.,* 2: 230–236.

Cheah, S. C., Siti Nor Akmar, A., Ooi, L. C. L., Rahimah, A. R. and Madon, M. (1993). Detection of DNA variability in the oil palm using RFLP probes. In Y. Basiron *et al.* (Eds.). Proceedings from *1991 PORIM Int. Palm Oil Conf. – Agriculture* (pp. 144–150), Kuala Lumpur: Palm Oil Res. Inst. Malaysia.

Cheah, S. C. (2000). Biotechnological strategies for improving plantation tree crops: the oil palm – a case study. In: Proceedings of the International Planters Conference. 17–20 May 2000, Kuala Lumpur,pp.59–76.

Cheah, S. C. (1990). Restriction fragment length polymorphism (RFLP) in the oil palm. Paper presented at Third National Molecular Biology Seminar. 25–26 September 1990, Serdang, Malaysia.

Cheah, S. C., Sambanthamurthi, R., Siti Nor Akmar, A., Abrizah, O., Manaf, M. A. A., Umi Salamah, R. and Parveez, G. K. A. (1995). Towards genetic engineering of oil palm. In J. C. Kader and P. Mazliak (Eds.).

Plant Lipid Metabolism (pp. 570–572). Netherlands: Kluwer Academic Publishers.

Chen, G. D., Li, H. B., Zheng, Z., Wei, Y. M., Zheng, Y. L., McIntyre, C. L., Zhou, M. X., and Liu, C. J. (2012). Characterization of a QTL affecting spike morphology on the long arm of chromosome 3H in barley (*Hordeum vulgare* L.) based on near isogenic lines and a NIL-derived population*. Theor. Appl. Genet.,* 125: 1385–1392.

Cheong, P. L., Koh, S. J., Cheah, S. C., and Singh, R. (2006). Analysis of tissue culture-derived regenerants using methylation sensitive AFLP. *Asia-Pacific J. Mol. Biol. Biotechnol.* 14(2): 47-55

Chin, C. W. (1988). Outlook on fertile pisifera breeding. In: Proc. 1987 Int. Oil Palm Conf. ‘Progress and prospects’ (Ed. by A. Halim Hassan *et al.*), pp. 107–111, Palm Oil Res. Inst. Malaysia, Kuala Lumpur.

Chin, C. W. and Shuhaimi, S. (2000). *Utilisation of PORIM’s Nigerian germplasm as potential planting materials in FELDA Agricultural Services Sdn Bhd (FASSB)’s breeding programme.* Paper presented at Int. Symp. ‘Oil palm genetic resources and utilization’, Malaysian Palm Oil Board, Kuala Lumpur. 8–10 June 2000.

Chin, C.W. and shuhaimi, S. (1999). *Felda oil palm planting materials.* In Proc. 1996 Seminar “ Sourcing of Oil Palm Planting Materials for Local and Overseas Ventures’ (Rajanaidu, N and Jalani, B S, eds.). Palm Oil Research Institute of Malaysia, Kuala Lumpur, pp. 71-90.

Chin, C. W., Shuhaimi, S., Nasaruddin, M. M. and Ng, W. J. (2003). Performance of Nigerian Introgressed Genetic Materials at FELDA. In *Proceedings of the Seminar on Progress of PS1 and PS2 Planting Materials and Release of Elite Germplasm to the Industry.* Malaysian Palm Oil Board; 2003:48-64.

Chin, C. W., Ng, W. J., Junaidah, J., Suhaimi, S. and Mohd. Nasruddin, M. (2005). Developing high oil yield DxP: The Felda Experience. Proceedings from the 2005 National Seminar on Advances in Breeding and Clonal Technologies for Super Yielding Planting Material.

Cho, Y. G., McCouch, S. R., Kuiper, M., Kang, M. R., Pot, J., Groenen, J. T. M., and Eun, M. Y. (1998). Integrated map of AFLP, SSLP and RFLP markers using a recombinant inbred population of rice (Oryza sativa L.). *Theor. Appl. Genet.,* 97: 370–380

Choong, C. Y., Shah, F. H., Rajanaidu, R. and Zakri, A. H. (1996). Isozyme variation of Zairean oil palm (*E. guineensis* Jacq.) germplasm collection. *Elaeis,* 8: 45–53.

Chua, B. H., Maizura, I., Rajinder, S., Tan, S. G., Faridah, Q. Z. and Cheah, S. C. (2005). Evaluation of EST-SSR for Assessing Genetic Diversity of African Palm (*Elaeis guineensis*) and American Palm (*Elaeis oleifera*). In: Proceedings of the 2005 Conference on Biotechnology of Plantation Commodities. Malaysian Palm Oil Board, Kuala Lumpur, pp.287–294.

Chua, K. L., Singh, R. and Cheah, S. C. (2001). Construction of oil palm (*Elaeis guineensis* Jacq.) linkage maps using AFLP markers. In: Proceeding 2001 International Oil Palm Congress – Agriculture. Pp 461-465. Malaysian Palm Oil Board, Kuala Lumpur.

Chutimanitsakun, Y., Nipper, R. W., Cuesta-Marcos, A., Cistué, L., Corey, A., Filichkina, T., Johnson, E. A., and Hayes, P. M. (2011). Construction and application for QTL analysis of a Restriction Site Associated DNA (RAD) linkage map in barley. *BMC Genomics,* 12(4). Doi: 10.1186/1471-2164-12-4.

Clegg, A. J. (1973). An analysis of damage incurred by oil palm bunches during handling and transport. In R.L. Wastie and D. A. Earp, (Eds), *Advances in Oil Palm Cultivation*. (pp. 421-429) Kuala Lumpur: Incorporated Society of Planters.

Cochard B., Durand-Gasselin T., Amblard P., Konan E. and Gogor S. (1999). Performance of adult oil palm clones. In: Preprints, 1999 PORIM Int. Palm Oil Conf., pp. 12–22, Palm Oil Res. Inst. Malaysia, Kuala Lumpur.

Cochard, B., Adon, B., Rekima, S., Billotte, N., de Chenon, R.D., Koutou, A., Nouy, B., Omore, A., Purba, A. R., Glazsmann, J. C. and Noyer, J. L. (2009). Geographic and genetic structure of African oil palm diversity suggests new approaches to breeding. *Tree Genet. Genomes,* 5:493–504

Cohen, J., (1988). *Statistical Power and Analysis for the Behavioral Sciences, 2nd ed.* Hillsdale, NJ: Lawrence Erlbaum Associates.

Collard, B. C. Y. and Mackill, D, J. (2008). Marker assisted selection: an approach for precision plant breeding in the twenty-first century. *Philos Trans R Soc Lond Ser B Biol Sci,* 363: 557–572

Collard, B., Jahufer, M., Brouwer, J., Pang, E. (2005). An introduction to markers, quantitative trait loci (QTL) mapping and marker-assisted selection for crop improvement: The basic concepts. *Euphytica,* 142(1–2):169-196.

Collard, B. C. Y., Jahufer, M. Z. Z., Brouwer, J. B. and Pang, E. C. K. (2005). An introduction to markers, quantitative trait loci (QTL) mapping and marker-assisted selection for crop improvement: The basic concepts. *Euphytica,* 142(12), 169–196

Coltman, D. W. (1999). Male reproductive success in a promiscuous mammal: behavioural estimates compared with genetic paternity. *Mol Ecol,* 8(7):1199–1209.

Coque, M. and Gallais, A. (2006). Genomics regions involved in response to grain yield selection at high and low nitrogen fertilization in maize. *Theor. Appl. Genet.,* 112: 1205–1220

Corley, R. H. V. and Gray, B. S. (1976b). Yield and yield components. In R.H.V. Corley, J.J. Hardon and B.J. Wood research (Eds.), *Oil palm* (pp. 77–86). Amsterdam: Elsevier

Corley, R. H. V. and Lee, C. H. (1992). The physiological basis for genetic improvement of oil palm in Malaysia. *Euphytica,* 60, 179–184

Corley, R. H. V. (1977b). Oil palm yield components and yield cycles. In D.A. Earp and W. Newall (Eds.), *International developments in oil palm* (pp. 116–129). Kuala Lumpur: Incorp. Soc. Planters.

Corley, R. H. V. (1983). Potential productivity of tropical perennial crops. *Expl Agric.,* 19, 217–237

Corley, R. H. V. (1985). Yield potentials of plantation crops. In: Potassium in the agricultural systems of the humid tropics, Proc*. 19th Colloquium Int. Potash Inst.,* (pp. 61–80), Int. Potash Inst., Berne.

Corley, R. H. V. (1998). What is the upper limit to oil extraction ratio? In: Proc. 1996 Int. Conf. ‘Oil and kernel production in oil palm – a global perspective’ (Ed. by N. Rajanaidu, I.E. Henson and B.S. Jalani), pp. 256–269, Palm Oil Res. Inst. Malaysia, Kuala Lumpur

Corley, R. H. V., and Stratford, R. (1998). Biotechnologies and Oil Palm: Opportunities and Future Impact. International Palm Oil Conference. Commodity of the past, today and future. Nusa Dua Bali. September 23-25. pp. 1-19

Corley, R. H. V., Ng M. and Donough, C. R. (1995a). Effects of defoliation on sex differentiation in oil palm clones. *Expl Agric.,* 31, 177–189.

Corley, R. H. V. (2005). Illegitimacy in oil palm breeding – a review. *J. Oil Palm Res.,* 17: 64-69

Corley, R. H. V. and Tinker, P. B. (2003). *The Oil Palm* (4^{th} ed.). Blackwell Science Ltd, USA. 1-460 pp.

Danan, S., Jean-Baptiste, V., and Véronique, L. (2011). Construction of a potato consensus map and QTL meta-analysis offer new insights into the genetic architecture of late blight resistance and plant maturity traits, BMC Plant Biology, 11: 16 Doi:10.1186/1471-2229-11-16

Darvasi, A., Weinreb, A., Minke, V., Weller, J. I. and Soller, M. (1993). Detecting marker-QTL linkage and estimating QTL gene effect and map location using a saturated genetic map. *Genetics,* 134: 943–951.

Davidson, L. (1993) Management for efficient, cost-effective and productive oil palm plantations. In: Proc. 1991 PORIM International Palm Oil Conference – Agriculture (Ed. By Y. Basiron *et al.*), pp. 153–167, Palm oil Research Institute of Malaysia, Kuala Lumpur, pp 153–167

Dawson, I. K., Simons, A. J., Waugh, R. and Powell, W. (1995). Diversity and genetic differentition among sub-populations of *Gliciridia sepium* revealed by PCR-based assays. *Heredity,* 74: 10-18.

De Almeida, S. C. A., Belchior, C. R., Nascimento, M. V. G., Vieira, L. dos S. R. and Fleury, G. (2002). Performance of a diesel generator fuelled with palm oil. *Fuel.* 81: 2097–2102.

De Blank, S. (1952) A reconnaissance of the American oil palm. *Trop. Agric. Trinidad*, 29: 1–14

De Franqueville, H. and Renard, J. L. (1990) Improvement of oil palm vascular wilt tolerance. Results and development of the disease at the R. Michaux plantation. *Oléagineux,* 45: 399–405

De Franqueville, H., Asmady, H., Jacquemard, J. C., Hayun, Z., and Durand-Gasselin, T. (2001). Indications on sources of oil palm (*Elaeis guineensis* Jacq.) genetic resistance and susceptibility to *Ganoderma* sp., the cause of basal stem rot. p. 420–431. In: (Unedit.) Proc. 2001 PIPOC Int. Palm Oil Congr. Malaysian Palm Oil Board, Kuala Lumpur.

De Vienne, D. (2003). *Molecular Markers in Plant Genetics and Biotechnology.* Science Publishers Inc.

Den Herder, G., Van Isterdael, G., Beeckman, T., De Smet, I. (2010). The roots of a new green revolution. *Trends Plant Sci.,* 15:600–607.

Din, M. A., and Rajanaidu, N. (2000). Evaluation of *Elaeis oleifera* interspecifi c hybrids and backcrosses. Paper presented at international symposium on “Oil palm genetic resources and utilisation”, Malaysian Palm Oil Board, Kuala Lumpur, 8–10 June 2000.

Doebley, J., Stec, A., Hubbard, L. (1997). The evolution of apical dominance in maize. *Nature,* 386:485–8.

Doležel, J., Bartoš, J., Voglmayr, H., Greilhuber, J. (2003). Nuclear DNA content and genome size of trout and human. *Cytometry Part A.* 51A (2): 127–128.

Donough, C. R. and Law, I. H. (1988). The effect of weevil pollination on yield and profitability at Pamol Plantations. In: Proc. 1987 Int. Oil Palm Conf. ‘Progress and prospects’, (Ed. by A. Halim Hassan et al.), pp. 523–527, Palm Oil Res. Inst., Malaysia, Kuala Lumpur.

Drouaud, J., Camilleri, C., Bourguignon, P. Y., Canaguier, A., Berard, A., Vezon, D., Giancola, S., Brunel, D., Colot, V., Prum, B., Quesneville, H., Mézard, C. (2006). Variation in crossing-over rates across Chromosome 4 of Arabidopsis thaliana reveals the presence of meiotic recombination hot spots. *Genome Res.*, 16:106–114.

Dufrane, M., and Berger, J. L. (1957). Étude sur la récolte des palmeraies. *Bull. agric. Congo Belge,* 48: 581–640

Durand-Gasselin, T., Kouame, K. R., Cochard, B., Adon, B. and Amblard, P. (2000a). Diffusion variétale du palmier à huile (*Elaeis guineensis* Jacq.). *Oil Corps Gras Lipides*, 7: 203–206

Durand-Gasselin, T., Asmady, H., Flori, A., Jacquemard, J.C., Hayun Zaelani, H., Breton, F. and De Franqueville, H. (2005). Possible sources of genetic resistance in oil palm (*Elaeis guineensis* Jacq.) to basal stem rotcaused by Ganoderma boninense – prospects for future breeding. *Mycopathologia,* 159:93–100.

Durand-Gasselin, T., Hayun, S., Jacquemard, J. C., Indra, S., Adjé, I., Flori, A. and Nouy, B. (2006). *Palm Oil yield potential of oil palm (Elaeis guineensis) seeds developed in a network by CIRAD and its partners.* Presented at International Seminar on Yield Potential in Oil Palm II, Phuket, Thailand. 27-28 Nov 2006.

East, E. M. (1908). Inbreeding in corn. *In: Reports of the Connecticut Agricultural Experiments Station for Years 1907-1908* (pp. 419-428). Connecticut Agricultural Experiment Station.

Edwards, A., Civitello, A., Hammond, H. A. and Caskey, C. T. (1991). DNA typing and genetic mapping with trimeric and tetrameric tandem repeats. *The American Journal of Human Genetics,* 49: 746-756.

Edwards, M. D., Stuber, C. W. and Wendel, J. F. (1987). Molecular-marker facilitated investigations of quantitative trait loci in maize. I. Numbers, genomic distribution and types of gene action. *Genetics,* 116: 116-125.

Emberton, J., Ma, J., Yuan, Y., San Miguel, P. and Bennetzen, J. L. (2005). Gene enrichment in maize with hypomethylated partial restriction (HMPR) libraries,” *Genome Res.,* 15(10):1441–1446.

Escobar R. (1982) Preliminary results of the collection and evaluation of the American oil palm *Elaeis oleifera* (HBK, Cortes) in Costa Rica. In E. Pushparajah and Chew P.S. (Eds.), The oil palm in agriculture in the eighties, Vol. 1 (pp. 79–93). Kuala Lumpur: Incorp. Soc. Planters.

Evans, L.T. and Fischer, R. A. (1999). Yield potential: its definition, measurement, and significance. *Crop Sci.,* 39: 1544–1551.

Falconer, D. S., and Mackay, T. F. C. (1996). *Introduction to Quantitative Genetics, 4th ed.* London: Prentice Hall.

Frohman, M. A. and Martin, G. R. (1989). Cut, paste and save: New approaches to altering specific genes in mice. *Cell,* 56: 145-147.

Gardner, E. J., Simmons, M. J. and Snustad, D. P. (1991). *Principles of Genetics* (8th ed.). New York: John Wiley and Sons Inc.

Gascon J. P. and de Berchoux, C. (1963). Caractéristiques qualitatives du régime d'*Elaeis guineensis* Jacq. Quelques relations entre les dura et tenera d'une même descendance et leur application a l'amélioration des semences. *Oléagineux,* 18: 411–416

Gascon, J. P. and de Berchoux, C. (1964). Caractéristiques de la production d'*Elaeis guineensis* (Jacq.) de diverses origines et leurs croisements. Application a la sélection du palmier a huile. *Oléagineux,* 19: 75–84

Gascon, J. P., Wuidart, W. (1975). Amélioration de la production et de la qualité de l'huile d'*Elaeis guineensis* Jacq. *Oléagineux,* 30(1):1–4

Gebhardt, C., Ballvora, A., Walkemeier, B., Oberhagemann, P., and Schüler, K. (2004). Assessing genetic potential in germplasm collections of crop plants by marker-trait association: a case study for potatoes with quantitative variation of resistance to late blight and maturity type. *Mol. Breed.,* 13, 93-102.

Goff, S. A., Ricke, D., Lan, T. H., Presting, G., Wang, R., Dunn, M., Glazebrook, J., Sessions, A., Oeller, P., Varma, H., Hadley, D., Hutchison, D., Martin, C., Katagiri, F., Lange, B. M., Moughamer, T., Xia, Y., Budworth, P., Zhong, J., Miguel, T., Paszkowski, U., Zhang, S., Colbert, M., Sun, W. L., Chen, L., Cooper, B., Park, S., Wood, T. C., Mao, L., Quail, P., Wing, R., Dean, R., Yu, Y., Zharkikh, A., Shen, R., Sahasrabudhe, S., Thomas, A., Cannings, R., Gutin, A., Pruss, D., Reid, J., Tavtigian, S., Mitchell, J., Eldredge, G., Scholl, T., Miller, R. M., Bhatnagar, S., Adey, N., Rubano, T., Tusneem, N., Robinson, R., Feldhaus,, J., Macalma, T., Oliphant, A., and Briggs, S. (2002). A draft sequence of the rice genome (Oryza sativa L. ssp. japonica). *Science,* 296(5565):92-100.

Goffinet, B. and Gerber, S. (2000). Quantitative trait loci: a meta-analysis. *Genetics,* 155:463-473.

Gore, M. A., Wright, M. H., Ersoz, E. S., Bouffard, P., Szekeres, E. S., Jarvie, T. P., Hurwitz, B. L., Narechania, A., Harkins, T. T., Grills, G. S., Ware, Do. H., and Buckler, E. S. (2009). Large-Scale Discovery of

Gene-Enriched SNPs. *Plant Genome J.,* 2(2):121–133. Doi:10.3835/plantgenome2009.01.0002

Grando, M. S., Bellin, D., Edwards, K. J., Pozzi, C., Stefanini, M., and Velasco, R. (2003). Molecular linkage maps of *Vitis vinifera* L. and *Vitis riparia* Mchx. *Theor. Appl. Genet.,* 106(7):1213-24. Epub 2002 Dec 10.

Grattapaglia, D. and Sederoff, R. (1994). Genetic Linkage Maps of Eucalyptus Grandis and Eucalyptus Urophylla Using a Pseudo-Testcross: Mapping Strategy and RAPD Markers. *Genetics,* 137(4): 1121–1137.

Gray, B. S. and Bevan, J. W. L. (1969). Field factors affecting the quality of palm oil. In P.D. Turner, (Ed.), *The quality and marketing of oil palm products*. (pp. 66-74). Kuala Lumpur: Incorporated Society of Planters.

Griffiths, S., Simmonds, J., Leverington, M., Wang, Y., Fish, L., Sayers, L., Alibert, L., Orford, S., Wingen L, Snape J. (2012). Meta-QTL analysis of the genetic control of crop height in elite European winter wheat germplasm. *Mol. Breed.,* 29: 159–171.

Griffiths, A. J. F., Miller, J. H., Suzuki, D. T., Lewontin, R. C. and Gelbart, W. M. (1996). *An Introduction to Genetic Analysis.* (6th ed.). (pp. 21-143). New York: W.H. Freeman and company.

Grubbe, R. C., Radwanski, E. R. and John, M. (2000). Comparative genetics of disease resistance within the Solanaceae. *Genetics,* 155:873-887.

Gupta, P. K., Rustgi, S., Kumar, N. (2006). Genetic and molecular basis of grain size and grain number and its relevance to grain productivity in higher plants. *Genome,* 49:565–571

Häberle, J., Holzapfel, J., Schweizer, G., Hartl, L. (2009). A major QTL for resistance against Fusarium head blight in European winter wheat. *Theor. Appl. Genet.,* 119: 325–332.

Haley, C. S. and Andersson, L. (1997). Linkage mapping of quantitative trait loci in plants and animals. In P. H. Dear (Ed.), *Genome mapping–A practical approach* (pp. 49–71). New York: Oxford University Press.

Haley, C. S. and Knott, S. A. (1992). A simple regression method for mapping quantitative trait loci in line crosses using flanking markers. *Heredity,* 69: 315-324.

Hardon, J. J. and Davies, M. D. (1969). Effects of vacuum-drying on the viability of oil palm pollen. *Expl Agric.,* 5: 59–65.

Hardon, J. J. and Tan, G. Y. (1969). Interspecific hybrids in the genus *Elaeis.* I. Crossability, cytogenetics and fertility of F1 hybrids of *E. guineensis* x *E. oleifera*. *Euphytica,* 18: 372–379.

Hardon, J. J. and Thomas, R. L. (1968). Breeding and selection of the oil palm in Malaya. *Oléagineux,* 23: 85–90.

Hardon, J. J. and Turner, P. D. (1967). Observations on natural pollination in commercial plantings of oil palm (*Elaeis guineensis*) in Malaya. *Expl Agric.,* 3:105–116

Hardon, J. J., Corley, R. H. V. and Lee, C. H. (1987). Breeding and selecting the oil palm. In A. J. Abbott and R. K. Atkin (Eds.), *Improving vegetatively propagated crops* (pp. 63–81). London: Academic Press.

Hardon, J. J., Rao, V., Rajanaidu, N. (1985). A review of oil palm breeding. In G. E. Russell (Ed.), *Progress in plant breeding* (pp139–163). London: Butterworths.

Hardon, J. J. (1969). Interspecific hybrids in the genus Elaeis II. Vegetative growth and yield of F1 hybrids *E. guineensis* × *E. oleifera*. *Euphytica,* 18:380–388

Hartley, C. W. S., (1988). *The Oil Palm (Elaeis guineensis* Jacq*).* John Wiley and Sons, NY: Longman Scientific and Technical Publication.

Harun, M. H. and Noor, M. R. M. (2002). Fruit set and oil palm bunch components. *J. Oil Palm Res.,* 14(2):24-33

Hash, C. T. and Bramel-Cox, P. J. (1999). Survey of marker applications. In B. I. G. Haussmann, H.H. Geiger, D.E. Hess, C.T. Hash, and P. Bramel-Cox, (Eds.), *Application of molecular markers in plant breeding. Training manual for a seminar held at IITA, Ibadan, Nigeria, from 16-17 August 1999.* (pp. 3-12). International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Andhra Pradesh, India. http://www.icrisat.org/text/research/grep/homepage/mol/s1_1hash.pdf. Accessed on 20 September 2004.

Hayati, A., Wickneswari, R., Maizura, I. and Rajanaidu, N. (2004). Genetic diversity of oil palm (*Elaeis guineensis* Jacq.) germplasm collections from Africa: implications for improvement and conservation of genetic resources. *Theor. Appl. Genet.,* 108: 1274-1284.

Henson, I. E. (1998). The role of bunch composition in determining oil and kernel yields of oil palm. p. 151–228. In: N. Rajanaidu, I. E. Henson, and B. S. Jalani (eds.), Proc. Int. Conf. on Oil and Kernel Production in Oil Palm—A Global Perspective. Palm Oil Res. Inst. Malaysia, Kuala Lumpur.

Herrán, A., Estioko, L., Becker, D., Rodriguez, M. J. B., Rohde, W. and Ritter, E. (2000). Linkage mapping and QTL analysis in coconut (*Cocos nucifera* L.). *Theor. Appl. Genet.,* 101: 292-300.

Hittalmani, S., Girish, T. N., Biradar, H. and Maughan, P. J. (2008). Development of mapping populations: Descriptions and implications. In C. Kole (Ed.), *Principles and Practices of Plant Molecular Mapping and Breeding* (pp.69–91). Berlin, Germany: Springer-Verlag,

Hizbai, B. T., Gardner, K. M., Wight, C. P., Dhanda, R. K., Molnar, S. J., Johnson, D., Frégeau-Reid, J., Yan, W., Rossnagel, B. G., Holland, J. B., Tinker, N. A. (2012). Quantitative Trait Loci Affecting Oil Content, Oil Composition, and Other Agronomically Important Traits in Oat. *Plant Genome,* 5:164–175.

Houssou, M., J. Meunier, and Daniel, C. (1987). Breeding oil palm (*Elaeis guineensis* Jacq.) for drought tolerance. Preliminary results in Benin. In H. A. H. Hassan, P. S. Chew, B. J. Wood, and E. Pushparajah (Eds.), *Proc. 1987 Int. Oil Palm/Palm Oil Conferences. Progress and Prospects. Conference I—Agriculture.* (pp. 23–26.). Kuala Lumpur: Palm Oil Res. Inst. Malaysia,

Hua, J. P., Xing, Y. Z., Wu, W. R., Xu, C. G., Sun, X. L., Yu, S. B. and Zhang, Q. F. (2003). Single-locus heterotic effects and dominance by dominance interactions can adequately explain the genetic basis of heterosis in a neliterice hybrid. *Proc Natl Acad Sci USA,* 100:2574–2579.

Huang, X. H., Wei, X. H, Sang, T., Zhao,Q., Feng,Q., Zhao,Y., Li, C. Y., Zhu,C.R., Lu, T. T., Zhang, Z. W., Li, M., Fan, D. L., Guo, Y. L., Wang, A., Wang, L., Deng, L. W., Li, W. J., Lu, Y. Q., Weng, Q. J., Liu, K. Y., Huang, T., Zhou, T. Y., Jing, Y. F., Li, W., Buckler, E. S., Qian, Q., Zhang, Q. F., Li, J. Y., and Han, B. (2010). Genome-wide association studies of 14 agronomic traits in rice landraces. *Nature Genetics,* 42(11) 961–967.

Hunter, R. L. and Markert, C. L. (1957). Histochemicals demostration of enzymes separated by zone electrophoresis in starch gels. *Science,* 125:1294-1295.

Idris, A. S., Kushairi, A., Ismail, S. and Ariffin, D. (2005). Selection for partial resistance in oil palm to Ganoderma basal stem rot. *J. Oil Palm Res,* 16:12–18.

Isa, Z. A., Kushairi, A, Chin, C W, Sharma, M, Chia, C. C., Rajanaidu, N. and Mohd Din, A. (2005). Performance of Malaysian DxP – Third Round Evaluation. In Proc. 2005 Nat. Sem. Breed. & Clonal Tech. [Kushairi, A., Ariffin, D. and Maizura, I. eds.] Malaysian Palm Oil Board, Kuala Lumpur. 95-137.

Isa, Z. A., Kushairi, A., Mohd Din, A., Suboh, O., Junaidah, J., Noh, A., Wong, C. K. and Musa, B. A. (2011). Critical Re-Examination of the Method of Bunch Analysis in Oil Palm Breeding – An Update. Paper presented at *The International Seminar on Breeding for Sustainability in Oil Palm,* Kuala Lumpur, Malaysia. 18 November 2011.

Jaccoud, D., Peng, K., Feinstein, D., Kilian, A. (2001). Diversity arrays: a solid state technology for sequence information independent genotyping. *Nucleic Acids Res.,* 29 (4): E25. Doi:10.1093/nar/29.4.e25.

Jack, P. L., Dimitrijevic, T. A. F. and Mayes, S. (1995). Assessment of nuclear, mitocondrial and chloroplast markers in oil palm (*Elaeis guineensis* Jacq.). *Theor. Appl. Genet.,* 90: 643-649.

Jack, P. L., James, C., Prices, Z., Rance, K., Groves. L., Corley, R. H. V., Nelson, S. and Rao, V. (1998). Application of DNA markers in oil palm breeding. In A. Jatmika (Ed.), *Proceedings of the 1998 International Oil Palm Congress-Commodity of the past today and future* (pp. 315-324). Medan, Indonesia: Indonesia Oil Palm Research Institute.

Jacquemard, J. C., Meunier J. and Bonnot F. (1982). Genetic study of the reproduction of an *Elaeis guineensis* oil palm cross. In E. Pushparajah and P. S. Chew (Eds.), *The oil palm in agriculture in the eighties, Vol. 1* (pp. 19–32). Kuala Lumpur: Incorp. Soc. Planters.

Jaligot, E., Beulé, T. and Rival, A. (2002). Methylation-sensitive RFLPs: characterisation of two oil palm markers showing somaclonal variation-associated polymorphism. *Theor. Appl. Genet.,* 104: 1263–1269

Jander, G., Norris, S. R., Rounsley, S. D., Bush, D. F., Levin, I. M., and Last, R. L. (2002). Arabidopsis map-based cloning in the post-genome era. *Plant Physiol.* 129(2):440-450.

Janeja, H. S., Banga, S. S. and Lakshmikumaran, M. (2003). Identification of AFLP markers linked to fertility restorer genes for tournefortii cytoplasmic male-sterility system in Brassica napus. *Theor. Appl. Genet.,* 107: 148-154.

Jeennor, S. and Volkaert, H. (2014). Mapping of quantitative trait loci (QTLs) for oil yield using SSRs and gene-based markers in African oil palm (*Elaeis guineensis* Jacq.). *Tree Genet. Genomes,* 10 (1): 1-14

Jones, D. L. (1994). *Palms Throughout the World.* Australia: Reed Books.

Jones, C. J., Edwards, K. J., Casaglione, S., Winfield, M. O., Sala, F., van de Wiel, C., Bredemeijeijer, G., Vosman, B., Matthes, M., Daly, A., Brettscheider, R., Bettini, P., Buiatti, M., Maestri, E., Malcevschi, A., Marmiroli, N., Aert, R., Volckaert, G., Rueda, J., Linacero, R., Vasquez, A. and Karp, A. (1997). Reproducibility testing of RAPD, AFLP and SSR markers in plants by a network of European laboratories. *Mol. Breed.,* 3: 381-390.

Junaidah, J., Chin, C. W., Rafii, M. Y. and Syuhada, W. H. (2008). Performance and utilization of MPOB-Nigerian oil palm materials in FELDA. In *Proceedings of the 3rd Seminar on Performance of MPOB PS1 and PS2 Materials and Elite Germplasm*, (pp. 73-90). Malaysian Palm Oil Board.

Junaidah J., Zainudin M. H. & Chin C. W. (2009). FELDA's Experience With Wealth Creation Through Oil Palm Breeding Research And Development Of Elite Planting Materials. Proceedings of the Eighth Malaysia Congress on Genetics. Role of Genetics in Wealth Creation and Quality of Life. Pahang: 53-64

Hayashi, K., Hashimoto, N., Daigen, M., and Ashikawa, I. (2004). Development of PCR-based SNP markers for rice blast resistance genes at the Piz locus. *Theor. Appl. Genet.,* 108(7):1212–1220.

Kanawapee, N., Sanitchon, J., Srihaban, P. and Theerakulpisut, P. (2011). Genetic diversity analysis of rice cultivars (Oryza sativa L.) differing in salinity tolerance based on RAPD and SSR markers. *Electron. J. Biotechnol.*, 14(6) http://dx.doi.org/10.2225/vol14-issue6-fulltext-4

Kandemir, N., Yılmaz, G., Karan, Y. B. and Borazan, D. (2010). Development of a simple sequence repeat (SSR) marker set to fingerprint local and modern potato varieties grown in central Anatolian Plateau in Turkey. *African J. Biotechnol.,* 9(34):5516-5522. Doi: 10.5897/AJB10.573 http://www.academicjournals.org/AJB.

Kang, B. Y., Mann, I. K., Major, J. E. and Rajora, O. P. (2010). Near-saturated and complete genetic linkage map of black spruce (*Picea mariana*). *BMC Genomics,* 11:515. http://www.biomedcentral.com/1471-2164/11/515.

Kao, C. H., Zeng, Z. B. and Teasdale, R. D. (1999). Multiple interval mapping for quantitative trait loci. *Genetics,* 152(3): 1203-1216.

Karp, A. and Edwards, K. J. (1995). *DNA markers: a global overview.* In G. Caetano-Anolles and P. M. Gresshoff, (Eds.), *Protocols, Applications and Overviews.* (pp. 364) USA: Wiley-Liss Inc.

Kazan, K., Manners, J. M. and Cameron, D. F. (1993). Inheritance of random amplified polymorphic DNA markers in an interspecific cross in the genus Stylosanthes. *Genome,* 36:50-56.

Kearsey, M. J. (1998). The principles of QTL analysis (a minimal mathematics approach). *J. Exp. Bot.,* 49:1619–1623

Knapp, S. J., and W. C. Bridges. (1990). Programs for mapping quantitative trait loci using flanking molecular markers and nonlinear models. *J. Hered.,* 81:234–235.

Knapp, S. J., Bridges, W. C., and Birkes, D. (1990). Mapping quantitative trait loci using molecular marker linkage maps. *Theor. Appl. Genet.,* 79:583–592.

Kosambi, D. D. (1944). The estimation of map distance from recombination values. *Ann. Eugen.,* 12: 172–175.

Kularatne, R. S. (2000). Assessment of Genetic Diversity in Natural oil Palm (*Elaeis guineensis* Jacq.) Populations using Amplified Fragment Length Polymorphism Markers. ((Unpublished doctoral dissertation). Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia.

Kulratne, R. S., Shah, F. H. and Rajanaidu, N. (2000). Investigation on genetic diversity in African natural oil palm populations and Deli dura using AFLP markers. In N. Rajanaidu and D. Ariffin (Eds.), *Proceedings of the International Symposium on Oil Palm Genetic Resources and Utilization.* (pp. X1–X39). Kuala Lumpur: Malaysian Palm Oil Board,

Kumar, L.S. (1999). DNA markers in plant improvement: An overview. *Biotechnol. Adv.,* 17: 143-182.

Kunzel, G., Korzun, L., Meister, A. (2000). Cytologically integrated physical restriction fragment length polymorphism maps for the barley genome based on translocation breakpoints. *Genetics,* 154: 397-412.

Lai, K., Duran, C., Berkman, P. J., Lorenc, M. T., Stiller, J., Manoli, S., Hayden, M. J., Forrest, K. L., Fleury, D., Baumann, U., Zander, M., Mason, A. S., Batley, J., and Edwards, D. (2012). Single nucleotide polymorphism discovery from wheat next-generation sequence data. *Plant Biotechnol J.,* 10(6):743-9. Doi: 10.1111/j.1467-7652.2012.00718.x. Epub 2012 Jul 3.

Landegren, U., Nilsson, M., and Kwok, P. Y. (1998). Reading Bits of Genetic Information: Methods for Single-Nucleotide Polymorphism Analysis. *Genome Res.,* 8:769–776.

Lander, E. S., and Botstein, D. (1989). Mapping mendelian factors underlying quantitative traits using RFLP linkage maps. *Genetics,* 121:185–199.

Laperche, A., Devienne-Barret, F., Maury, O., Le Gouis, J., and Ney, B. (2006). A simplified conceptual model of carbon/nitrogen functioning for QTL analysis of winter wheat adaptation to nitrogen deficiency. *Theor. Appl. Genet.,* 113: 1131–1146

Latiff, A. (2000). The Biology of the Genus Elaeis. In Y. Basiron, B.S. Jalani, and K.W.Chan (Eds.), *Advances in Oil Palm Research, Volume1* (pp. 19–38). Malaysia: Malaysian Palm Oil Board (MPOB).

Lebrun, P., N'Cho, Y. P., Seguin, M., Grivet, L., and Baudouin, L. (1998b). Genetic diversity in coconut (*Cocos nucifera* L.) revealed by restriction fragment length polymorphism (RFLP) markers. *Euphytica,* 101:103–108

Lee, C. H., Yong, Y.Y., Donough, C. R. and Chiu, S.B. (1990). Selection progress in the Deli dura population. In A.C.Soh, N.Rajanaidu, H.B. Mohd Nasir, K. Paminand C. Muluk (Eds.), *Proceedings of the Workshop on Progress of Oil Palm Breeding Populations.* (pp.81–89). Kuala Lumpur: Palm Oil Res. Inst. Malaysia.

Lespinasse, D., Rodier-Goud, M., Grivet, L., Leconte, A., Legnate, H., Seguin, M. (2000). A saturated genetic linkage map of rubber tree (*Hevea spp.*) based on RFLP, AFLP, microsatellite, and isozyme markers. *Theor. Appl. Genet.,* 100:127–138.

Li, J. Z., Zhang, Z. W., Li, Y. L., Wang, Q. L., Zhou, Y. G. (2011). QTL consistency and meta-analysis for grain yield components in three generation in maize. *Theor. Appl. Genet.,* 122(4):771-782.

Li, Z. K., Pinson, S. R. M., Park, W. D., Paterson, A.H. and Stansel, J.W. (1997). Epistasis for three grain yield components in rice. *Genetics,* 145: 453–465.

Litt, M. and Luty, J. A. (1989). A hypervariable microsatellite revealed by *in vitro* amplification of a dinucleotide repeat within the cardiac muscle actin gene. *The American Journal of Human Genetics,* 44: 397-401.

Liu, B. H. (1998). Statistical Genomics: Linkage, Mapping and QTL analysis. Boca Raton, Floridah, USA: CRC Press, LLC.

Liu, T. M., Yu, T. and Xing Y. Z. (2013). Identification and validation of a yield-enhancing QTL cluster in rice (*Oryza sativa* L.). *Euphytica,* 192: 145-153

Lombard, V., Baril, C. P, Dubreuil, P., Blouet, F. and Zhang, D. (1999). Potential use of AFLP markers for the distinction of rapeseed cultivars. In "*New Horizons for an old crop*". Proceedings of the 10th International Rapeseed Congress, Canberra, Australia. http://www.regional.org.au/au/gcirc /4/587.htm. Accessed on 20 November 2004.

Low, E. T., Halimah, A., Boon, S. H., Elyana, M. S., Tan, C. Y. A., Ooi, L. C. L., Cheah, S. C., Raha, A. R., Wan, K. K., Rajinder S. (2008). Oil palm (*Elaeis guineensis* Jacq.) tissue culture ESTs: Identifying genes associated with callogenesis and embryogenesis. *BMC Plant Biology,* 8:62.

Luikart, G. and England, P. (1999). Statistical analysis of microsatellite DNA data. *Trends Ecol Evol,* 14:253– 256.

Lukowitz, W., Gillmor, C. S., and Scheible, W. D. (2000). Positional Cloning in Arabidopsis. Why It Feels Good to Have a Genome Initiative Working for You. *Plant Physiol.,* 123:795–805

Luo, L. J., Li, Z. K., Mei, H. W., Wang, D. L., Shu, Q. Y., Tabien, R., Zhong, D. B., Ying, C. S., Stansel, J. W., Khush, G. S., and Paterson, A. H. (2001). Overdominant epistatic loci are the primary genetic basis of inbreeding depression and heterosis in rice. II. Grain yield components. *Genetics,* 158:1755–1771.

Lynch, M. and Walsh, B. (1998). *Genetics and Analysis of Quantitative Traits.* Sunderland, MA: Sinauer Associates, Inc.

Ma, X. Q., Tang, J. H., Teng, W. T., Yan, J. B., Meng, Y. J. and Li, J. S. (2007). Epistatic interaction is an important genetic basis of grain yield and its components in maize. *Mol Breed,* 20:41-51.

Ma, X. F., Ross, K. and Gustafson, J.P., (2001). Physical mapping of restriction fragment length polymorphism (RFLP) markers in homoeologous groups 1 and 3 chromosomes of wheat by in situ hybridization. *Genome,* 44: 401–412.

Mackay, I. and Powell, W. (2007). Methods for linkage disequilibrium mapping in crops. *Trends Plant Sci.,* 12(2), 57-63.

Mackill, D.J. (2003). Applications of genomics to rice breeding. *IRRN.* 28: 9-15.

Madon, M., Phoon, L. Q., Clyde, M. M., Mohd, D. A. (2008). Application of flow cytometry for estimation of nuclear DNA content in *Elaeis*. *J. Oil Palm Res.,* 20:447–452

Maizura, I. Rajanaidu, N., Zakri, A. H., Cheah, S. C. (2006). Assessment of genetic diversity in oil palm (*Elaeis guineensis* Jacq.) using Restriction Fragment Length Polymorphism (RFLP). *Genet. Resour. Crop Evol,* 53:187–195.

Malaysian Palm Oil Board (MPOB). (2013). Overview of The Malaysian Oil Palm Industry 2013. Malaysian Palm Oil Board, Ministry of Plantation Industries and Commodities.

Malaysian Palm Oil Council (MPOC). (2014). Gains for palm oil 2013 performance. Global Oils and fats business magazine. 11(1):11-14

Maliepaard C., Alston, F. H., van Arkel, G., Brown, L. M., Chevreau, E., Dunemann, F., Evans, K. M., Gardiner, S., Guilford, P., van Heusden, A. W., Janse, J., Laurens, F., Lynn, J. R., Manganaris, A. G., den Nijs, A. P. M., Periam, N., Rikkerink, E., Roche, P., Ryder, C., Sansavini, S., Schmidt, H., Tartarini, S., Verhaegh, J. J., Vrielink-van Ginkel, M., King, G. J. (1998). Aligning male and female linkage maps of apple (Malus pumila Mill.) using multi-allelic markers. *Theor. Appl. Genet.,* 97: 60–73.

Maloof, J. N. (2003). QTL for plant growth and morphology. *Curr Opin Plant Biol,* 6:85–90.

Mammadov, J. A., Chen, W., Ren, R., Pai, R., Marchione, W., Yalçin, F., Witsenboer, H., Greene, T. W., Thompson, S. A., Kumpatla, S. P. (2010). Development of highly polymorphic SNP markers from the complexity reduced portion of maize (Zea mays L.) genome for use in marker-assisted breeding. *Theor. Appl. Genet.,* 121(3):577–588.

Marchini, J. and Howie, B. (2010). Genotype imputation for genome-wide association studies. *Nature Reviews Genetics*, 11(7):499–511.

Marshall, T. C., Slate, J., Kruuk, L. E. B., and Pemberton, J. M. (1998). Statistical confidence for likelihood-based paternity inference in natural populations. *Mol Ecol,* 7:639–655.

Martinez, O. and Curnow, R.N. (1992). Estimating the locations and the sizes of the effects of quantitative trait loci using flanking mapping. *Heredity,* 73: 198-206.

Mayes, C., Jack, P. L., Marshall, D. and Corley, R. H. V. (1996). Construction of a RFLP linkage map for oil palm (*Elaeis guineensis* Jacq.). *Genome,* 40,116–122.

Mayes, S., Jack, P. L. and Corley, R. H. V. (2000). The use of molecular markers to investigate the genetic structure of oil palm breeding programme. *Heredity,* 85: 288-293.

Mayes, S., Jack, P. L., Marshall, D. F. and Corley, R. H. V. (1997). The construction of an RFLP genetic linkage map for oil palm (*Elaeis guineensis* Jacq.). *Genome.* 40: 116-122.

Mayes, S., James, C. M., Horner, S. F., Jack, P. L.and Corley, R. H. V. (1997). The application of restriction fragment length polymorphism for the genetic finger printing of oil palm (*Elaeis guineensis* Jacq.). *Mol. Breed,* 2:175–180.

Maykay, T. F. C. (2001). The genetic architecture of quantitatve traits. *Annual Review of Genetics,* 35:303–339.

McCouch, S. (2004). Diversifying Selection in Plant Breeding. *PLoS Biol,* 2(10): e347. doi:10.1371/journal.pbio.0020347

McCouch, S. R., Kochert, G., Yu, Z. H., Wang, Z. Y., Khush, G. S., Coffman, W. R. and Tanksley, S. D. (1988). Molecular mapping of rice chromosomes. *Theor. Appl. Genet.,* 76: 815- 829

Menendez, T. and Blaak, G. (1964). Plant breeding division. In: *12th Annu. Rep. W. Afr. Inst. Oil Palm Res.,* pp. 49–75, Benin City.

Messmer, R., Fracheboud, Y., Banziger, M., Vargas, M., Stamp, P., Ribaut, J. M. (2009). Drought stress and tropical maize: QTL-by-environment interactions and stability of QTLs across environments for yield components and secondary traits. *Theor. Appl. Genet.,* 119:913–930

Meunier, J. and Boutin, D. (1975). L'Elaeis malanococca et l'hybride *Elaeis melanococca* × *Elaeis guineensis* Premières données. *Oléagineaux,* 30(1):5–8

Meunier, J. (1975). Le 'palmier à huile' américain *Elaeis melanococca*. *Oléagineux,* 30:51–62

Meunier, J., Gascon, J. P. and Noiret, J. M. (1970). Hérédité des caractéristiques du régime d' *Elaeis guineensis* Jacq. en Côte d'Ivoire. *Oléagineux,* 25: 377–382

Meuwissen, T. H. E., Hayes, B. J., Goddard, M. E. (2001). Prediction of total genetic value using genome-wide dense marker maps. *Genetics,* 157:1819–1829

Meyers, B. C., Tingey, S. V., and Morgante, M. (2001). Abundance, distribution, and transcriptional activity of repetitive elements in the maize genome. *Genome Res.,* 11(10):1660–1676

Miranda Santos, M. D., Barcelos, E. and Nascimento J. C. (1986). Genetic resources of *Elaeis oleifera* (H.B.K.) Cortes in the Brazilian Amazon. Proc. Int. Workshop 'Oil palm germplasm and utilisation', (pp. 95–101), Kuala Lumpur: Palm Oil Res. Inst. Malaysia.

Mohan, M., Nair, S., Bhagwat, A., Krishna, T. G., Yano, M., Bhatia, C. R. and Sasaki, T. (1997). Genome mapping, molecular markers and marker assisted selection in crop plants. *Mol. Breed.,* 3: 87-103.

Mohd Din, A., Rajanaidu, N., and Jalani, B. (2000). Performance of *Elaeis oleifera* from Panama, Costa Rica, Colombia and Honduras in Malaysia *J. Oil Palm Res.,* 12:71–80.

Montoya, C., Cochard, B., Flori, A., Cros, D., Lopes, R., Cuellar, T., Espeout, S., Syaputra, I., Villeneuve, P., Pina, M., Ritter, E., Leroy, T., and

Billotte, N. (2014). Genetic architecture of palm oil fatty acid composition in cultivated oil palm (*Elaeis guineensis* Jacq.) compared to its wild relative *E. oleifera* (H.B.K) Cortés. *PLoS One,* 9(5):e95412. Doi: 10.1371/journal.pone.0095412. eCollection 2014.

Montoya, C., Lopes, R., Flori, A., Cros, D., Cuellar, T., Summo, M., Espeout, S., Rivallan, R., Risterucci, A-M., Bittencourt, D., Zambrano, J.R., Alarcón G.W.H., Villeneuve, P., Pina, M., Nouy, B., Amblard, P., Ritter, E., Leroy, T., and Billotte, N. (2013). Quantitative trait loci (QTLs) analysis of palm oil fatty acid composition in an interspecific pseudo-backcross from *Elaeis oleifera* (H.B.K.) Cortés and oil palm (*Elaeis guineensis* Jacq.). *Tree Genetics and Genomes,* 1-19.

Moose, S. P., and Mumm, R. H. (2008). Molecular Plant Breeding as the Foundation for 21st Century Crop Improvement. *Plant Physiol.,* 147: 969–977.

Morcillo, F., Cros, D., Billotte, N., Ngando-Ebongue, G. F., Domonhédo, Pizot, M., Cuéllar, T., Espéout, S., Dhouib, R., Bourgis, F., Claverol, S., Tranbarger, T. J., Nouy, B., Arondel, V. (2013). Improving palm oil quality through identification and mapping of the lipase gene causing oil deterioration. *Nature communications,* 4. Doi 10.1038/ncomms3160.

Moretzsohn, M. C., Nunes, C. D. M., Ferreira, M. E. and Grattapaglia, D. (2000). RAPD linkage mapping of the shell thickness locus in oil palm (*Elaeis guineensis* Jacq.). *Theor. Appl. Genet.,* 100: 63-70.

Morozova, O. and Marra, M. A. (2008). Applications of next generation sequencing technologies in functional genomics. *Genomics,* 92(5):255–264.

Muralidharan, K. and Wakeland, E. K. (1993). Concentration of primer and template quality affects products in random-amplified polymorphic DNA PCR. *Biotechniques.* 14: 362-364.

Nelson, J. C., Wang, S., Wu, Y., Li, X., Antony, G., White, F. F., and Yu, J. (2011). Single-nucleotide polymorphism discovery by high-throughput sequencing in sorghum. *BMC Genomics,* 12: 352. Doi:10.1186/1471-2164-12-352

Nelson S. P. C. (1993). Producción de semillas clonal y sexual en Dami – futuros desarollos. Palmas, (Bogota) 14 (Special no.)

Ng, K. T. and Southworth, A. (1973). Optimum Time of Harvesting Oil Palm Fruit. In R. L. Wastie and D. A. Earp, (Eds.), *Advances in Oil Palm Cultivation* (pp.415-419). Kuala Lumpur: Incorporated Society of Planters.

Ngando-Ebongue, G. F., Dhouib, R., Carriere, F., Amvam Zollo, P. H., Arondel, V. (2006). Assaying lipase activity from oil palm fruit (*Elaeis guineensis* Jacq.) mesocarp. *Plant Physiol Biochem,* 44:611–617.

Noorhariza, M. Z., Ismanizan, I., Rozana, R., Ting, N. C., and Singh, R. (2010). Development and characterization of *Elaeis oleifera* microsatellite markers. *Sains Malaysia,* 39(6): 909–912.

Noorhariza, M. Z., Singh, R., and Rozana, R. (2012). *Elaeis oleifera* Genomic-SSR Markers: Exploitation in Oil Palm Germplasm Diversity and Cross-Amplification in Arecaceae. *Int. J. Mol. Sci.* 13:4069-4088. Doi:10.3390/ijms13044069

Norziha, A., Rafii, M. Y., Maizura, I., and Ghizan, S. (2008). Genetic variation among oil palm parent genotypes and their progenies based on microsatellite markers. *J. Oil Palm Res.,* 20:533–541.

Novaes, E., Drost, D. R., and Farmerieetal, W. G. (2008). High throughput gene and SNP discovery in Eucalyptus grandis,an uncharacterized genome. *BMC Genomics,* 9:312. Doi:10.1186/1471-2164-9-312. online at: http://www.biomedcentral.com/1471-2164/9/312

Obasola, C. O., Arasu, N. T. and Rajanaidu, N. (1983). Collection of oil palm genetic material in Nigeria. I. Method of collection. MARDI Report.

Oetting, W. S., Lee, H. K., Flanders, D. J., Wiesner, G. L., Sellers, T. A., and King, R. A. (1995). Linkage analysis with multiplexed short tandem repeat polymorphisms using infrared fluorescence and M13 tailed primers. *Genomics,* 30:450–458.

Okou, D. T., Steinberg, K. M., Middle, C., Cutler, D. J., Albert, T. J. and Zwick, M. E. (2007). Microarray-based genomic selection for high-throughput resequencing. *Nature Methods,* 4(11):907–909.

Okoye, M. N., Okwuagwu, C. O. and Uguru, M. I. (2009). Population Improvement for Fresh Fruit Bunch Yield and Yield Components in Oil Palm (*Elaeis guineensis* Jacq.). *American-Eurasian Journal of Scientific Research,* 4 (2): 59-63.

Okwuagwu, C. O. and Okolo, E. C. (1994). Genetic control of polymorphism for kernel-to-fruit ratio in the oil palm (*Elaeis guineensis* Jacq.). *Elaeis,* 6: 75–81.

Okwuagwu C.O. (1988). The genetic basis for the low correlation between dura and tenera fullsib shell to fruit ratio in the oil palm (*Elaeis guineensis* Jacq.). In: Proc. 1987 Int. Oil Palm Conf. ‘Progress and prospects’ (Ed. by A. Halim Hassan *et al.*), pp. 143–154, Kuala Lumpur: Palm Oil Res. Inst. Malaysia.

Okwuagwu, C. O., and Ataga, C. D. (1999). Oil palm breeding programme in Nigeria. p. 131–138. In: N. Rajanaidu and B. S. Jalani (eds.), Proc. Symp. the Science of Oil Palm Breeding, Palm Oil Res. Inst. Malaysia, Kuala Lumpur.

Okwuagwu, C. O., and Okolo, E. C. (1992). Maternal inheritance of kernel size in the oil palm (*Elaeis guineensis* Jacq.). *Elaeis,* 4:72–73.

Okwuagwu, C. O., and Okolo, E. C. (1994). Genetic control of polymorphism for kernel to fruit ratio in the oil palm (*Elaeis guineensis* Jacq.). *Elaeis,* 6:75.

Okwuagwu, C. O., Okoye, M. N., Okolo, E. C., Ataga, C. D. and Uguru, M. I. (2008). Genetic variability of fresh fruit bunch yield in Deli/dura x tenera breeding populations of oil palm (*Elaeis guineensis* Jacq.) in Nigeria. *Journal of Tropical Agriculture* 46 (1-2): 52–57

Ong, S. H., Chua, C. C., and Sow, H. P. (1981). The co-dominance theory: genetic interpretations of analyses of mesocarp oils from *Elaeis guineensis*, *Elaeis oleifera* and their hybrids. *J Am Oil Chem Soc,* 58:1032–1038.

Ooi, L. C. L., Low, E. T., and Singh, R. (2011). SNP Markers for genetic studies and prediction of monogenic traits in oil plam. MPOB information series.

Ooi, L. C. L., Ong, P. W., Maizura, I. and Singh, R. (2010). Discovery of oil palm SNPs and their application in the characterization of oil palm genetic resources and breeding materials. In: Proceedings of the national biotechnology seminar 2010, Kuala Lumpur, 24–26 May 2010.

Ooi, S.C. and Tam, T.K. (1976). The determination of the within bunch components of oil yield in the oil palm (*Elaeis guineensis* Jacq). I. Pattern of variation. Planter, Kuala Lumpur, 52, 467–475

Ooi, S. C., Da Silva, E. B., Muller A.A. and Nascimento, J. C. (1981). Oil palm genetic resources – native E. oleifera populations in Brazil offer promising sources. Pesq. Agropec. Brasil., 16, 385–395

Ooi, S. C., Hardon J. J. and Phang, S. (1973). Variability in the Deli dura breeding population of the oil palm (*Elaeis guineensis* Jacq.). I. Components of bunch yield. Malay. agric. J.,49, 112–121

Ooi, L. C. L., Maizura, I., and Singh, R. (2007). SNP Markers In Oil Palm (Elaeis spp.): Discovery And Applications. Plant and Animal Genomes XV Conference. January 13-17, 2007.Town and Country Convention Center, San Diego, CA

Osborne, D. J., Henderson, J. and Corley, R. H. V. (1992). Controlling fruit-shedding in the oil palm. Endeavour 16,173–177.

Parchman, T. L., Geist, K. S., Grahnen, J. A., Benkman, C. W., and Buerkle, C. A.. (2010). Transcriptome sequencing in an ecologically important tree species: assembly, annotation, and marker discovery," BMC Genomics 2010, 11:180 doi:10.1186/1471-2164-11-180. online at: http://www.biomedcentral.com/1471-2164/11/180

Paterson, A. H. (1996). Making genetic maps. In: Paterson AH (ed.) Genome mapping in plants, San Diego, California: Academic Press, Austin, Texas, pp. 23–39.

Paterson, A., Tanksley, S. and Sorrels, M. E. (1991). DNA markers in plant improvement. Advances in Agronomy, 44: 39–90.

Patto, M. C. V, Torres, A. M., Koblizkova, A., Macas, J., Cubero J. I. (1999). Development of a genetic composite map of Vicia faba using F2 populations derived from trisomic plants. *Theor. Appl. Genet.,* 98(5):736-743

Pawlik, D. (2002). Marker assisted breeding in the 21st Century. http://www.usask.ca/agriculture/plantsci/classes/plsc416/projects_2002/pawlin/resources/. Accessed on 18 October 2003.

Peleman, J. D. and van der Voort, J. R. (2003). Breeding by design. Trends Plant Sci. 8 (7):330-4.

Peleman, J. (1999). Application of the AFLP® technique in marker assisted breeding. In E.M. Gillet, ed., *Which DNA Marker for Which Purpose? Final Compendium of the Research Project Development, optimisation and validation of molecular tools for assessment of biodiversity in forest trees in the European Union DGXII Biotechnology FW IV Research Programme Molecular Tools for Biodiversity.* http://webdoc.sub.gwdg.de/ebook/y/1999/whichmarker/index.htm. Accessed on October 2004.

Pemberton, J. M., Albon, S. D., Guiness, F. E., Clutton-Brock, T. H., and Dover, G. A., (1992). Behavioural estimates of male mating success tested by DNA fingerprinting in a polygynous mammal. *Behav Ecol,* 3:66–75.

Perera, L., Russell, J. R., Provan, J. and Powell, W. (2001). Levels and distribution of genetic diversity of coconut (*Cocos nucifera* L.) from Sri Lanka assessed by microsatellite markers. *Euphytica,* 122: 381-389.

Pérez, T., Albornoz, J. and Dominguez, A. (1998). An evaluation of RAPD fragment reproducibility and nature. *Molecular Ecology.* 7: 1347-1358.

Petrie, M. and Kempenaers, B. (1998). Extra-pair paternity in birds: explaining variations between species and populations. Trends Ecol Evol 13(2):52–58.

Phoon, L. Q., Maria, M., Rajinder, S. and Clyde, M. M. (2005). Application of inter simple sequence repeat polymerase chain reaction (ISSR-PCR) technique in *Elaeis guineensis* Jacq. In: Proceedings of the 2005 Conference on Biotechnology of Plantation Commodities. Malaysian Palm Oil Board, Kuala Lumpur, pp.361–368.

Pillay, M. and Kenny, S. T. (1996). Random amplified polymorphic DNA (RAPD) markers in hop, Humulus lupulus: level of genetic variability and segregation in F1 progeny. *Thereotical and Applied Genetics,* 92:334-339

Prime Minister’s Department. (2010). Economic Transformation Programme: A Roadmap for Malaysia (1 Malaysia). Performance Management and Delivery Unit (PEMANDU), Putrajaya.

Purba, A. R., Noyer, J. L., Baudouin, L., Perrier, X., Hamon, S. and Lagoda, P. J. L. (2000). A new aspect of genetic diversity of Indonesian oil palm (*Elaeis guineensis* Jacq.) revealed by isoenzyme and AFLP markers and its consequences for breeding. *Theor. Appl. Genet.,* 101: 956–961.

Purseglove, J. W. (1972). Tropical Crops. Monocotyledons. Longman, London. p. 607

Queller, D. C., Strassmann, J. E., and Hugues, C. R. (1993). Microsatellites and kinship. *Trends Ecol Evol.,* 8(8):285–288.

Rafii, M. Y., Isa, Z. A., Kushairi, A., Saleh, G. B., Latif, M. A., (2013). Variation in yield components and vegetative traits in Malaysian oil palm (*Elaeis guineensis* Jacq.) dura x pisifera hybrids under various planting densities. *Industrial Crops and Products*., 46: 147–157.

Raghavan, C. and Collard, B. C. Y. (2012). Effect of small mapping population sizes on reliability of quantitative trait locus (QTL) mapping. *Afr J Biotechnol.,* 4:10661–10674.

Rajanaidu, N. (1986a). The oil palm (*Elaeis guineensis*) collection in Africa. In: Proceedings of the international workshop on “Oil palm germplasm and utilisation”. Palm Oil Research Institute of Malaysia, Kuala Lumpur, pp 59–83

Rajanaidu, N. (1986b). *Elaeis oleifera* collection in Central and South America. In: Proceedings of the international workshop on “Oil palm germplasm and utilisation”. Palm Oil Research Institute of Malaysia, Kuala Lumpur, pp 84–94

Rajanaidu, N., Kushairi, A., Rafii, M., Mohd Din, A., Maizura, I., Jalani, B. S. (2000a). Oil palm breeding and genetic resources. In: Basiron, Y., Jalani, B. S., Chan, K. W. (eds) Advances in oil palm research, vol 1. Malaysian Palm Oil Board (MPOB), Bangi, pp 171–237

Rajanaidu, N. and Jalani, B. S. (1994c). Influence of planting material on oil extraction rate (OER). In: Proc. Natn. Symp. 'Palm oil extraction rate: problems and issues' (Ed. by D. Ariffin and B.S. Jalani), pp. 53–57, Palm Oil Res. Inst. Malaysia, Kuala Lumpur

Rajanaidu, N., Jalani B.S. and Kushairi A. (1998a). Oil palm genetic resources – the development of novel planting materials. In: Proc. 1998 Int. Oil Palm Conf. 'Commodity of the past, today and the future' (Ed. by A. Jatmika *et al.*), pp. 208–220, Indonesian Oil Palm Res. Inst., Medan, Indonesia

Rajanaidu, N., Kushairi, A. and Jalani, B. S. (1998b). Variation for oil and kernel to bunch, and total economic product in oil palm germplasm and breeding materials. In: Proc. 1996 Int. Conf. 'Oil and kernel production in oil palm – a global perspective' (Ed. by N. Rajanaidu, I.E. Henson and B.S. Jalani), pp. 19–35, Palm Oil Res. Inst. Malaysia, Kuala Lumpur

Rajanaidu, N., Kushairi, A., Rafii, M., Mohd Din, A., Maizura, I. and Jalani, B. S. (2000a). Oil palm breeding and genetic resources. In: Advances in oil palm research, Vol. I (Ed. by Y. Basiron, B.S. Jalani and Chan K.W.), pp. 171–237, Malaysian Palm Oil Board, Kuala Lumpur

Rajanaidu, N., Kushairi, A., Rafii, M., Mohd Din, A., Maizura I., Isa, Z. A. and Jalani, B. S. (2000b). Oil palm genetic resources and their utilisation – a review. Paper presented at Int. Symp. 'Oil palm genetic resources and utilization', 8–10 June, Malaysian Palm Oil Board, Kuala Lumpur

Rajanaidu, N., Maizura, I. and Cheah S. C. (2000c). Screening of oil palm natural populations using RAPD and RFLP molecular markers. Paper presented at Int. Symp. 'Oil palm genetic resources and utilization', 8–10 June, Malaysian Palm Oil Board, Kuala Lumpur

Rajanaidu, N., Rao, V., Abdul Halim, H. and Ong, A. S. H. (1989). Genetic resources – new developments in oil palm breeding. Elaeis,1, 1–10

Rajanaidu, N., Rao, V., Halim Hj Hassan, A. and Ong, A. S. H. (1989). Genetic resources – new developments in oil palm breeding. *Elaeis,*1, 1–10

Rajanaidu, N. and Kushairi, A. (2003). Strategies for the development of future oil palm planting materials. ISOPB and IOPRI International Seminar. 6-9 October 2003. Medan, Indonesia.

Rajanaidu, N. and Jalani, B.S. (1994). Oil palm genetic resources – collection, evaluation, utilization and conservation. Presented at Colloquium on Oil Palm Genetic Resources. Palm Oil Res. Inst. Malaysia, Kuala Lumpur, 13 September 1994.

Rajanaidu, N. and Kushairi, A. (2003). “Strategies for the Development of Future Oil Palm Planting Materials,” Paper Presented at ISOPB Seminar on the Progress of Oil Palm Breeding and Selection, Medan, 6-9 October 2003.

Rajanaidu, N., Arasu, N. T. and Obasola, C. O. (1979). Collection of oil palm (*Elaeis guineensis* Jacq.) genetic material in Nigeria. II. Phenotypic variation of natural populations. *MARDI Res.Bull.,*7,1–27.

Rajanaidu, N., Rao, V. and Hassan, A. H. (1990). Progress of Serdang, Elmina and Serdang Avenue Deli dura breeding populations. In: A.C. Soh, N. Rajanaidu, H.B. Mohd Nasir, K. Pamin and C. Muluk (Eds.), Proceedings of the Workshop on Progress of Oil Palm Breeding Populations. Palm Oil Res. Inst. Malaysia, Kuala Lumpur, pp. 70–80.

Rajanaidu, N., Sapurah, R., Rao, V., Zakri, A. H. and Embi, M. N. (1993). Isoenzyme variation in Nigerian oil palm (*Elaeis guineensis*) germplasm. In: Proceedings of the ISOPB International Symposium on Recent Development in Oil Palm Tissue Culture and Biotechnology.KualaLumpur,Malaysia,pp.209–216.

Rajaratnam, J. A. and William, C. N. 1970. Ripeness and oil synthesis in *tenera* oil palm bunches in Malaysia. *Planter, Kuala Lumpur.* 46: 339-341.

Raman, H., Read, B. J., Brown, A. H. D. and Abbott, D. C. (1999). Molecular markers and pyramiding of multiple genes for resistance to scald in barley. In *Proceedings of the 9th Australian Barley Technical Symposium.* http://www.regional.org.au/au/abts/1999/raman3.htm. Accessed on 20 November 2004.

Rance, K. A., Mayes, S., Price, Z., Jack, P. L. and Corley R. H. V. (2001). Quantitative trait loci for yield components in oil palm (*Elaeis guineensis* Jacq.). *Theor. Appl. Genet.,* 103: 1302-1310.

Rao, V., Law I. H., Zuraini Shaharudin and Chia C. C. (1999). Ekona and AVROS – a tale of two pisiferas. Paper presented at 1999 PORIM Int. Palm Oil Congr., Kuala Lumpur

Rao, V., Soh A. C., Corley R. H. V., Lee C. H., Rajanaidu N., Tan Y.P., Chin C.W., Lim K.C., Tan S.T., Lee T.P. and Ngui M. (1983) A critical reexamination of the method of bunch quality analysis in oil palm breeding. *Palm Oil Res. Inst. Malaysia, Occ. Paper* 9, 1–28

Rao, V. (1987). Genetic variation in populations of oil palms (*Elaeis guineensis*) from Nigeria. Ph.D Thesis. University of Birmingham, Birmingham,UK.

Rao, V. (1998). Ripening in the virescens oil palm. In: Oil and kernel production in oil palm—a global perspective. In: N. Rajanaidu, I. E. Henson, and B. S. Jalani (eds.), Proc. Int. Conference. p. 226. Malaysian Palm Oil Board, Kuala Lumpur.

Rey, L., Gómez, P., Ayala, I., Delgado, W., and Rocha,. P. (2004). Colecciones genéticas de palma de aceite *Elaeis guineensis* (Jacq.) y *Elaeis oleifera* (H.B.K.) de Cenipalma: Características de importancia para el sector palmicultor. Palmas 25(4), 39-48

Rhode, W. (2003). Scientific Report 2003. (http://www.mpiz-koeln.mpg.de/~rohde/)

Richardson, D. L. (1995). The history of oil palm breeding in the United Fruit Company. ASD Oil Palm Papers, 11, 1–22

Riju, A. and Arunachalam, V. (2009). Interspecific differences in single nucleotide polymorphisms (SNPs) and indels in expressed sequence tag libraries of oil palm *Elaeis guineensis* and *E. oleifera. Nature proceedings.* http://hdl.handle.net/10101/npre.2009.3593.2

Riju, A., Chandrasekar, A. and Arunachalam, V. (2007). Mining for single nucleotide polymorphisms and insertions/deletions in expressed sequence tag libraries of oil palm. *Bioinformation,* 2:128–131.

Ritter, E., Gebhardt, C. and Salamini, F. (1990). Estimation of recombination frequencies and construction of RFLP linkage maps in plants from crosses between heterozygous parents. *Genetics,* 224:645–654

Ritter, E. and Salamini, F. (1996). The calculation of recombination frequencies in crosses of allogamous plant species with application to linkage mapping. *Genet Res.,* 67: 55-65.

Rival, A., Beule, T., Barre, P., Hamon, S., Duval, Y., and Noirot, M. (1997). Comparative fl ow cytometric estimation of nuclear DNA content in oil palm (*Elaeis guineensis* Jacq.) tissue cultures and seed derived plants. *Plant Cell Rep.,* 16:884–887.

Rohde, W., Kullaya, A., Rodriguez, J. and Ritter, E. (1995). Genetic analysis of *Cocos nucifera* L. by PCR amplification of spacer sequences separating a subset of copia-like *Eco*RI repetitive elements. *Journal of Genetics and Breeding.* 49: 179-186.

Rohde, W., Sniady, V., Herrán, A., Estioko, L., Sinje, S., Marseillac, N., Berger, A., Lebrun, P., Becker, D., Kullaya, A., Rodriguez, J., Billotte, N. and

Ritter, E. (2002). Construction and exploitation of high-density DNA marker and physical maps in the perennial tropical oil crops coconut and oil palm: from biotechnology towards marker-assisted breeding. In *Proceeding of Challenges to Organic Farming and Sustainable Land Use in the Tropics and Subtropics*, International Research on Food Security, Natural Resource Management and Rural Development University of Kassel-Witzenhausen Deutscher Tropentag, Kassel-Witzenhausen. http://www.tropentag.de/2002/abstracts/links/Rohde_8h4LNMKr.php. Accessed on 10 September 2004.

Rosenquist E. A. (1990). An overview of breeding technology and selection in *Elaeis guineensis*. In: Proc. 1989 Int. Palm Oil Dev. Conf. – Agriculture (Ed. by B.S. Jalani *et al.*), pp. 5–25, Palm Oil Res. Inst. Malaysia, Kuala Lumpur

Rosenquist, E. A. (1985). The genetic base of oil palm breeding populations. *Proceeding Palm Oil Research Institute of Malaysia.* 10: 10-27.

Rouppe van der Voort, J., Wolters P., Folkertsma, R., Hutten, R., van Zandvoort, P., Vinke, H., Kanyuka, K., Bendahmane, A., Jacobsen, E., Janssen, R., Bakker, J. (1997). Mapping of the cyst nematode resistance locus Gpa2 in potato using a strategy based on comigrating AFLP markers. *Theor. Appl. Genet.,* 95, 874–880.

Roy, R., Steffens, D. L., Gartside, B., Jang, G. Y., Brumbaugh, J. A. (1996). Producing STR locus patterns from bloodstains and other forensic samples using an infrared fluorescent automated DNA sequencer. *J Forensic Sci,* 41:418–424

Rozen, S. and Skaletsky, H. (2000). Primer3 on the WWW for general users and for biologist programmers. *Methods Mol. Biol.,* 132 365–386.

Saiki, R. K., Gelfand, D. H., Stoffel, S., Scharf, S. J., Higuchi, R. Horn, G. T., Mullis, K. B. and Erlich, H. A. (1988). Primer-directed enzymatic amplification of DNA a thermostable DNA polymerase. *Nature (London).* 239: 487-497.

Salem, K.F.M., El-Zanaty, A.M. and Esmail, R.M. (2008). Assessing wheat (Triticum aestivum L.) genetic diversity using morphological characters and microsatallite markers. *World Journal of Agricultural Sciences*. 4 (5): 538-544

Sambanthamurthi R, Sundram K, Tan Y (2000) Chemistry and biochemistry of palm oil. *Prog Lipid Res.,* 39:507–558

Sanetra, M., Henning, F., Fukamachi, S., and Meyer, A. (2009). A Microsatellite-Based Genetic Linkage Map of the Cichlid Fish, *Astatotilapia burtoni* (Teleostei): A Comparison of Genomic

Architectures Among Rapidly Speciating Cichlids. *Genetics Society of America,* DOI: 10.1534/genetics.108.089367

Schlotterer, C. and Tautz, D. (1992). Slippage synthesis of simple sequence DNA. *Nucleic Acids Research.* 22: 285-288.

Schneider, Katharina. (2005). Mapping Populations and Principles of Genetic Mapping. In The Handbook of Plant Genome Mapping , edited by P. D. G. K. Prof. Dr. Khalid Meksem: Wiley-VCH Verlag GmbH and Co. KGaA. KGaA (Weinheim): Wiley-VCH Verlag GmbH and Co. p. 1-20

Schultes, R. E. (1990). Taxonomic, Nomenclatural and ethnobotanic notes on Elias. Palm Oil Research Institute of Malaysia. *Elias.,* 2 (1) p. 172-187.

Schwarzacher, T. (1994). Mapping in plants: progress and prospects. *Current Opinion in Genetics and Development.* 4: 868-874.

Sehgal, S. A., Tahir, R. A., Nawaz, M. (2012). Molecular Characterization of Wheat Genotypes Using SSR Markers. *Int. J. Bioautomation.,* 16(2), 119-128

Semagn, K., Bjørnstad, Å. and Ndjiondjop, M. N. (2006). Principles, requirements and prospects of genetic mapping in plants. *African J. Biotechnol..* 5(25):2569-2587. Available online at http://www.academicjournals.org/AJB.

Seng T. Y., Faridah Q. Z. (2006). DNA extraction from mature oil palm leaves. *J. Oil Palm Res.,* 18: 219-224.

Seng T. Y., Siti Hawa, M. S., Chin, C. W., Ting, N. C., Singh, R., Faridah, Q. Z., Tan, S. G., Sharifah Sharul Rabiah, S. A. (2011). Genetic linkage map of a high yielding FELDA Deli x Yangambi oil palm cross. *PLoS ONE*. 6(11):e26593. doi: 10.1371/journal.pone.0026593.

Seng, T. Y., Faridah Q. Z., Ho C. L., Maizura, I., and Rao, V. (2007). Flanking AFLP markers for the *virescens* trait in oil palm. *J. Oil Palm Res.,* 19: 381-392.

Septiningsih, E. M., Trijatmiko, K. R., Moeljopawiro, S. and McCouch, S. R. (2003). Identification of quantitative trait loci for grain quality in an advanced backcross population derived from the Oryza sativa variety IR64 and the wild relative O. rufipogon. *Theor. Appl. Genet.,* 107:1433-1441.

Shah, F. H., Rashid, O., Simons, A. J. and Dunsdon, A. (1994). The utility of RAPD markers for determination of genetic variation in oil palm (*Elaeis guineensis* Jacq.). *Theor. Appl. Genet.,* 89: 713-718.

Sharma, H. C., Crouch, J. H., Sharma, K. K., Seetharama, N. and Hash, C. T. (2002). Applications of biotechnology for crop improvement: prospects and constraints. *Plant Sci.,* 163: 381–395

Sharma, M., Singh, G., San, T. T. and Singh, T. (1999). Optimizing on FFB, Oil, OER and Oil Quality. In *1999 PORIM International Palm Oil Congress (PIPOC) – Emerging technologies and opportunities in the next millennium,* ed. A. Darus, C. K. Weng and S. S. S. R. Alwee, 1-6 February 1999, pp 124-140, Palm Oil Research Institute of Malaysia (PORIM), Bangi, Malaysia.

Sharma, M., Singh, G., San, T. T and Singh, T. (1999). Optimizing on FFB, Oil, OER and Oil Quality. In *1999 PORIM International Palm Oil Congress (PIPOC) – Emerging technologies and opportunities in the next millennium,* ed. A. Darus, C. K. Weng and S. S. S. R. Alwee, 1-6 February 1999, pp 124-140, Palm Oil Research Institute of Malaysia (PORIM), Bangi, Malaysia.

Shi, J. Q., Li, R. Y., Qiu, D., Jiang, C. C., Long, Y., Morgan, C., Bancroft, I., Zhao, J. Y., Meng, J. L. (2009). Unraveling the complex trait of crop yield with QTL mapping in *Brassica napus. Genetics* 182:851-861.

Shull, G. H. (1908). "The composition of a field of maize". Reports of the American Breeders Association: 296–301.

Singh, R., Tan, S. G., Panandam, J., Abdul Rahman, R., Cheah, S. C. (2008b). Identification of cDNA-RFLP markers and their use for molecular mapping in oil palm (*Elaeis guineensis*). *Asia Pac J Mol Biol Biotechnol.,* 16:53–63

Singh, R., Tan, S G., Panandam, J., Abdul Rahman, R., Cheah, S. C. (2008c). Identification of cDNA-RFLP markers and their use for molecular mapping in oil palm (*Elaeis guineensis*). *Asia Pac J Mol Biol Biotechnol.,* 16:53–63

Singh, R., Tan, S. G., Panandam, J. M., Abdul Rahman, R., Ooi, L. C. L., Low, E. T. L., Sharma, M., Jansen, J., Cheah, S. C. (2009). Mapping quantitative trait loci (QTLs) for fatty acid composition in an interspecific cross of oil palm. *BMC Plant Biol.,* 9:114

Singh, R. (2005). Molecular markers and their applications in the construction of genetic linkage maps and analysis of monogenic and quantitative traits in oil palm. Thesis.

Singh, R. and Cheah, S. C. (1999). Analysis of the inheritance of AFLP markers in an interspecific cross of oil palm using the pseudo-testcross strategy. *J. Oil Palm Res.,* 64-73

Singh, R., Leslie Ooi, C. L. and Rahimah, A. R. (2008a). PCR-based marker for distinguishing Skin colour of oil palm fruits. MPOB Technology Transfer No. 399

Singh, R., Low, E. T. L., Ooi, L. C. L., Meilina Ong, A., Rajanaidu, N., Ting, N. C., Marhalil, M., Chan, P. L., Maizura, I., Mohamad Arif, A. M., Jayanthi, N., Chan, K. L., Rozana, R., Mohd Amin, H., Norazah, A., Muhammad, A. B., Lakey, N., Bacher, B., Brunt, A. V., Wang, C. Y., Hogan, M., He, D., MacDonald, J. D., Smith, S. W., Ordway, J. M., Martienssen, R. A. and Ravigadevi, S. (2014). The oil palm VIRESCENS gene controls fruit colour and encodes a R2R3-MYB. *Nature communications.* DOI: 10.1038/ncomms5106

Singh, R., Low, E. T. L., Ooi, L. C. L., Meilina Ong-Abdullah., Ting, N. C., Jayanthi, N., Rajanaidu, N., Mohd Din, A., Rozana, R., Mohamad Arif, A. M., Chan, K. L., Mohd Amin, H., Norazah, A., Lakey, N., Smith, S. W., Muhammad, A. B., Hogan, M., Bacher, B., Brunt, A. V., Wang, C. Y., Ordway, J. M., Ravigadevi, S. and Martienssen, R. A. (2013). The oil palm SHELL gene controls oil yield and encodes a homologue of SEEDSTICK. *Nature,* 500: 340–344.

Singh, R., Nagappan, J. and Cheah, S. C. (2004). Molecular markers towards marker-assisted selection in oil palm. Biotechnology Symposium 2004. http://www.mpiz-koeln.mpg.de/~rohde/LINK2PALM2004.html. Accessed on 11 April 2005.

Singh, R., Rahimah, A. R. and Cheah, S. C. (2006). Markers to predict skin colour of oil palm fruits. MPOB Technology Transfer No. 306.

Singh, R., Tan, S. G., Panandam, J. M, Rahimah A. R., Leslie C. L. Ooi, Low, E. T., Sharma, M., Jansen, J., and Cheah, S. C. (2009). Mapping quantitative trait loci (QTLs) for fatty acid composition in an interspecific cross of oil palm. *BMC Plant Biol.,* 9 (1): 114

Singh, R., Tan, S.G., Panandam, J. M, Sharma M, Cheah S. C. (2007). Preliminary analysis of quantitative traits loci associated with oil quality in an interspecific cross of oil palm. *Pertanika J. Trop. Agric. Sci.,* 30:31–44.

Singh, R. Noorhariza M. Z., Ting, N. C., Rozana, R, Tan,S. G., Low, E. T., Ithnin, M., and Cheah, S. C. (2008b). Exploiting an oil palm EST database for the development of gene-derived SSR markers and their exploitation for assessment of genetic diversity. *Biologia,* 63(2): 227-235

Soh, A. C. (1986). Expected yield increase with selected oil palm clones from current D×P seedling materials and its implications on clonal propagation, breeding and ortet selection. *Oleagineux,* 41:51–56.

Soh, A. C., Kee, K. K. and Goh, K. J. (2006). Research and innovation towards sustainable palm oil production. *J.Sci.Technol.Trop.,* 2,77–95.

Song, W., Pang, R., Niu, Y., Gao, F., Zhao, Y., Zhang, J., Sun, J., Shao, C., Liao, X., Wang, L., Tian, Y., Chen, S. (2012). Construction of High-Density Genetic Linkage Maps and Mapping of Growth-Related Quantitative Trail Loci in the Japanese Flounder (Paralichthys olivaceus). *PLoS ONE,* 7(11): e50404. doi:10.1371/journal.pone.0050404

Song, Q. J., Marek, L. F., Shoemaker, R. C., Lark, K. G., Concibido, V. C., Delannay, X., Specht, J. E., Cregan, P. B. (2004). A new integrated genetic linkage map of the soybean. *Theor. Appl. Genet.,* 109: 122–128.

Southworth, A. 1976. Harvesting. Pages 469-477 in R.H.V. Corley, J.J. Hardon, B.J. Wood, eds., *Developments in Crop Science (1) Oil Palm Research.* Elsevier Scientific Publishing company.

Sparnaaij, L. D. (1969). Oil palm – *Elaeis guineensis* Jacquin. In: Outlines of perennial crop breeding in the tropics (Ed. by F.P. Ferwerda and F. Wit), pp. 339–387, Veenman and Zonen, Wageningen.

Sparnaaij, L. D., Rees, A. R. and Chapas, L. C. (1963). Annual yield variation in the oil palm. *J.W. Afr. Inst. Oil Palm Res.* 4: 111–125

Speldewinde, H. V. (1968). Harvesting and harvesting methods. Pages 106-116 in P.D. Turner, ed., *Oil Palm Developments in Malaysia*. Kuala Lumpur: Incorporated Society of Planters.

Spooner, D. M. Nunez, J., Trujillo, G., Herrera, M.D.R, Guzman, F., and Ghislain, M. (2007). Extensive simple sequence repeat genotyping of potato landraces supports a major reevaluation of their gene pool structure and classification. *PNAS,* 104(49): 19398–19403

Squire, G. R. (1984b). Light interception, productivity and yield of oil palm. Internal report, Palm Oil Res. Inst. Malaysia.

Stam, P. and Van Ooijen, J. W., (1995). JoinMap™ version 2.0: software for the calculation of genetic linkage maps. Wageningen: CPRO-DLO.

Stam, P. (1993). Construction of integrated genetic maps by means of a new computer package: JoinMap. *Plant J.,* 3:739–744.

Steffens, D. L., Sutter, S. L. and Roemer, S. C. (1993). An alternate universal forward primer for improved automated sequencing of M13. *BioTechniques,* 15, 580–582.

Sun, F., Liu, P., Ye, J., Lo, L. C., Cao, S. Y., Li, L., Yue, G. H. and Wang, C. M. (2012). An approach for jatropha improvement using pleiotropic QTLs regulating plant growth and seed yield. *Biotechnology Biofuels,* 5: 42. Doi:10.1186/1754-6834-5-42

Sunnucks, P. (2000). Efficient genetic markers for population biology. *Trends Ecol. Evol.,* 15(5):199–203.\

Syed, R. A., Law, I. H. and Corley, R. H. V. (1982). Insect pollination of the oil palm: introduction, establishment and pollinating efficiency of Elaeidobious kamerunicus in Malaysia. *The Planter,* 58: 547.

Tailliez, B. and Valverde, G. (1971). Sensitivity to hurricanes of different types of oil palm crosses. *Oléagineux,* 12, 753–762

Tan, G. Y. and Rajaratnam, J. A. (1978). Genetic variability of leaf nutrient concentration in oil palm. *Crop Sci.,* 18, 548–550

Tan, K. S. and Rao, A. N. (1979). Certain aspects of developmental morphology and anatomy of oil palm. In: Histochemistry, developmental and structural anatomy of Angiosperms: a symposium, pp. 267–285

Tan, K. S. (1983). *The Botany of Oil Palm, Casual Paper on Oil Palm.* Incorporated Society of Planters, Kuala Lumpur.

Tan, Y. P., Sharma, M. and Ho, Y. W. (1995). Oil palm planting materials - current and future trends in Malaysia. Proc. of the 1995 PORIM International Palm Oil Congress: Technologies in Plantation -The Way Forward. Kuala Lumpur. pp.1-21.

Tester, M., Langridge, P. (2010). Breeding technologies to increase crop production in a changing world. *Science,* 327: 818-22.

Thomas, R. L., Seth, A. K., Chan, K. W. and Ooi, S. C. (1973). Induced parthenocarpy in the oil palm. *Ann. Bot.,* 37: 447–452

Thomas, R. L., Phang, S., Mok, C. K., Chan, K. W., Easau, P. T. and Ng, S. C. (1971). Fruit ripening in the oil palm, *Elaeis guineensis*. *Ann. Bot.,* 35: 1219-1225.

Thongthawee, S., Tittinutchanon, P. and Volkaert, H. (2010). Microsatellites for parentage analysis in an oil palm breeding population. *Thai J. Genet.,* 3(2): 172-181

Ting, N. C., Noorhariza, M. Z., Rozana, R., Low, E. T., Ithnin, M., Cheah, S. C., Tan, S. G., and Singh, R. (2010). SSR mining in oil palm EST database: application in oil palm germplasm diversity studies *J. Genet.* 89(2): 135–145

Ting, N. C., Cheah, S. C., Zamzuri, I., Tan, S. G., Faridah, Q. Z., Maizura, I. and Singh, R. (2006). Statistical mapping of quantitative trait loci controlling the time to first callusing in oil palm (Elaeis *guineensis* Jacq.) tissue culture. *Pertanika J. Trop. Agric. Sci.,* 29 (1 and 2): 35-45

Ting, N. C., Jansen, J., Nagappan, J., Ishak, Z., Chin, C. W., Tan, S. G., Cheah, S. C., Singh, R. (2013). Identification of QTLs associated with callogenesis and embryogenesis in oil palm using genetic linkage maps improved with SSR markers. *PLoS ONE,* 2013, 8(1):e53076. doi: 10.1371/journal.pone.0053076

Ting, N. C., Noorhariza, M. Z., Rozana, R., Low, E. T. L., Maizura, I., Cheah, S. C., Tan, S. G., Singh, R. (2010). SSR mining in oil palm EST database: application in oil palm germplasm diversity studies. *J. Genet.,* 89: 135–145.

Ting, N. C., Jansen, J., Mayes, S., Massawe, F., Sambanthamurthi, R., Ooi, L. C. L., Chin, C. W., Arulandoo, X., Seng, T. Y., Sharifah Shahrul Rabiah, S. A, Maizura, I., Singh, R. (2014). High density SNP and SSR-based genetic maps of two independent oil palm hybrids. *BMC Genomics*, 15(1):309. DOI:10.1186/1471-2164-15-309

Tinker, N. and Mather, D. (1995a). Methods for QTL with progeny replicated in multiple environments. *J. Quant. Trait Loci,* 1: http://probe.nalusda.gov.8000/otherdocs/jqtl/jqtl199501/jqtl199515.html.

Tinker, N. and Mather, D. (1995b). MQTL: software for simplified composite interval mapping of QTL in multiple environments. *J. Quant. Trait. Loci,* 1: http://probe.nalusda.gov:8000/otherdocs/jqtl/jqtl19958002/jqtl8016r8002.html.

Tranbarger, T. J., Dussert, S., Joët, T., Argout, X., Summo, M., Champion, A. Cros, D., Omore, A., Nouy, B., Morcillo, F. (2011). Regulatory mechanisms underlying oil palm fruit mesocarp maturation, ripening, and functional specialization in lipid and carotenoid metabolism. *Plant Physiol.,* 156(2), 564–84.

Trick, M., Long, Y., Meng, J. and Bancroft, I. (2009). Single nucleotide polymorphism (SNP) discovery in the polyploid Brassica napus using Solexa transcriptome sequencing. *Plant Biotechnol. J.,* 7(4):334–346.

Tripathi, N., Hoffmann, M., Willing, E-M., Lanz, C., Weigel, D. and Dreyer, C. (2009). Genetic linkage map of the guppy, Poecilia reticulate and quantitative trait loci analysis of male size and colour variation. *Proc. R. Soc*. B. 276:2195-2208

Truntzler, M., Barrière, Y., Sawkins, M. C., Lespinasse, D., Betran, J., Charcosset, A., Moreau, L. (2010). Meta-analysis of QTL involved in silage quality of maize and comparison with the position of candidate genes. *Theor. Appl. Genet.,* 121(8):1465-82.

Tsarouhas, V., Gullberg, U. and Lagercrantz, U. (2002). An AFLP and RFLP linkage map and quantitative trait locus (QTL) analysis of growth traits in *Salix Theor. Appl. Genet.,* 105: 277-288.

Ulloa, M., Meredith Jr, W. R., Shappley, Z. W., and Kahler, A. L. (2002). RFLP genetic linkage maps from four $F_{2.3}$ populations and a joinmap of *Gossypium hirsutum* L. *Theor. Appl. Genet.,*104: 200-208.

Univanich Palm Oil Public Company Limited. (2015). Deli x Yangambi Hybrid Seed for superior oil palm profitability. [Brochure]. Krabi, Thailand: Univanich Palm Oil Public Company Limited.

United Plantations Berhad. (2015) UP Premier Hybrid DxP Seeds. [Brochure]. Teluk Intan, Malaysia: United Plantations Berhad.

Uthaipaisanwong, P., Chanprasert, J., Shearman, J. R., Sangsrakru, D., Yoocha, T., Jomchai, N., Jantasuriyarat, C., Tragoonrung, S., Tangphatsornruang, S. (2012). Characterization of the chloroplast genome sequence of oil palm (*Elaeis guineensis* Jacq.). *Gene,* 500(2):172-80. doi: 10.1016/j.gene.(2012).03.061. Epub 2012 Apr 2.

Vales, M. I., Schön, C. C., Capettini, F., Chen, X. M., Corey, A. E., Mather, D. E., Mundt, C. C., Richardson, K. L., Sandoval-Islas, J. S., Utz, H. F., Hayes, P. M. (2005). Effect of population size on the estimation of QTL: a test using resistance to barley stripe rust. *Theor. Appl. Genet.,* 111:1260–1270.

Van Der Vossen, H. A. M. (1974). Towards more efficient selection for oil yield in the oil palm (*Elaeis guineensis* Jacq.). Ph.D. Thesis. p.107. Agricult. Univers. Wageningen.

Van Ooijen, (2004). MapQTL ® 5, Software for the mapping of quantitative trait loci in experimental populations. Kyazma B. V., Wageningen, Netherlands.

Van Orsouw, N. J., Hogers, R. C. J., Janssen, A., Yalcin, F., Snoeijers, O., Verstege, E., Schneiders, H., Van Der, H., Van Oeveren, J., Verstegen, H., Van Eijk, M. J. T. (2007). Complexity reduction of polymorphic sequences (CRoPS): a novel approach for large-scale polymorphism discovery in complex genomes. *PLoS ONE,* 2(11): e1172. doi:10.1371/journal.pone.0001172

Vanderweyen, R., Rossignol, J., and Miclotte, H. (1947). Considérations sur les teneurs en eau et en huile de la pulpe des fruits d'Elaeis. C. R. de la Semaine Agricole de Yangambi., Comm. 54, 730

Varshney, R. K. and Dubey, A. (2009). Novel genomic tools and modern genetic and breeding approaches for crop improvement. *J. Plant Biochem. Biotechnol.*, 18: 127-138.

Varshney, R. V., Hoisington, D. A., Tyagi, A. K. (2006). Advances in cereal genomics and applications in crop breeding. *Trends Biotechnol.,* 24: 490–499

Varshney, A., Mohapatra, T. and Sharma, R. P. (2004). Development and validation of CAPS and AFLP markers for white rust resistance gene in *Brassica juncea. Theor. Appl. Genet.,* 109: 153-159.

Veldboom, L. R. and Lee, M. (1994). Molecular-marker-facilitated studies of morphological traits in maize.II. Determination of QTLs for grain yield and yield components. *Theor. Appl. Genet.,* 89: 51-458

Voorrips, R. E. (2002). MapChart: Software for the graphical presentation of linkage maps and QTLs. *J. Hered.* 93: 77–78. doi: 10.1093/jhered/93.1.77

Vos, P., Hogers, R., Bleeker, M., Reijans, M., Van de Lee, T., Hornes, M., Frijters, A., Pot, J., Peleman, J., Kuiper, M. and Zabeau, M. (1995). AFLP: a new technique for DNA fingerprinting. *Nucleic Acids Res.,* 23: 4407-4414.

Wahid, M. (2009). Sequencing the oil palm genome: the beginning. Palm oil: balancing ecologics with economics. PIPOC 2009 MPOB International Palm Oil Congress, Kuala Lumpur, Malaysia. Proceedings of Agriculture, Biotechnology and Sustainability Conference, Volume I. 9-12 November 2009.

Wang, J., Yang, J., Jia, Q., Zhu, J., Shang, Y., Hua, W., and Zhou, M. X. (2014). A New QTL for Plant Height in Barley (*Hordeum vulgare* L.) Showing No Negative Effects on Grain Yield. *PLoS ONE,* 9(2): e90144. doi:10.1371/journal.pone.0090144

Wang, S., Basten, C. J., and Zeng, Z. B. (2007). Windows QTLCartographer 2.5. Department of Statistics, North Carolina State University, Raleigh, N. C. (http://statgen.ncsu.edu/qtlcart/ WQTLCart.htm)

Wang, J. L. (2008). COLONY Version 2.0 (May 2008) Manual. http://www.ege.fcen.uba.ar/materias/ecomolecular/Material/Comportamiento. Paternidad y sistemas de apareamiento/Colony/ColonyUserGuide.pdf

Welsh, J. and McClelland, M. (1990). Fingerprinting genomes using PCR with arbitrary primers. *Nucleic Acids Res.,* 18: 7213-7218

Williams, J. G. K., Kubelik, A. R., Livak, K. J., Rafalski, J. A. and Tingey, S. V. (1990). DNA polymorphism amplified by arbitrary primers are useful as genetic markers. *Nucleic Acids Res.,* 18: 6531–6535

Wonkyi-Appiah, J. B. (1987). Genetic control of fertility in the oil palm (*Elaeis guineensis* Jacq.). *Euphytica,* 36: 505–511

Wonkyi-Appiah, J. B. (1998). Oil and kernel content of OPRI materials. In: Proc. 1996 Int. Conf. 'Oil and kernel production in oil palm – a global perspective' (Ed. by N. Rajanaidu, I.E. Henson and B.S. Jalani), pp. 271–305, Palm Oil Res. Inst. Malaysia, Kuala Lumpur

Wood, B. J., Said, I., Loong, S. G., and Chew, S. C. (1984). A preliminary report on a long-term study of the effect of oil palm harvesting strategy on product recovery, including a comparison before and after weevil pollination. Proc. of the Symposium on Impact of the Pollination Weevil on the Malaysian Oil Palm Industry. Kuala Lumpur. p. 187-219.

Wu, R. L., Han, Y. F., Hu, J. J., Fang, J. J., Li, L., Li, M. L., and Zeng, Z. B. (2000). An integrated genetic map of Populus deltoides based on amplified fragment length polymorphisms. *Theor. Appl. Genet.,* 100(8):1249-1256

Xing, Y. and Zhang, Q. (2010). Genetic and molecular bases of rice yield. *Annu Rev Plant Biol.,* 61:421–42.

Yamamoto, T., Kimura, T., Shoda, M., Imai, T., Saito, T., Sawamura, Y., Kotobuki, K., Hayashi, K., Matsuta, N. (2002). Genetic linkage maps constructed by using an interspecific cross between Japanese and European pears. *Theor. Appl. Genet.,* 106, 9–18.

Yan, J. B., Tang, H., Huang, Y. Q, Zheng, Y. L. and Li, J. S. (2006). Quantitative trait loci mapping and epistatic analysis for grain yield and yield components using molecular markers with an elite maize hybrid. *Euphytica,* 149: 121–131.

Yang, J, Hu, C. C., Hu, H., Yu, R. D., Xia, Z., Ye, X. Z., and Zhu, J. (2008). QTLNetwork: mapping and visualizing genetic architecture of complex traits in experimental populations. *Bioinformatics,* 24:721-723.

Yee, C. B., Lim, K. C., Ong, E. C. and Chan, K. W. (1984). The effects of Elaeidobious kamerunicus Faust. on bunch components of *Elaeis guineensis* Jacq. Proc. Of the Symposium on Impact of the Pollination Weevil on the Malaysian Oil Palm Industry. Kuala Lumpur. p. 129-139.

Yong, Y. Y., Chin, P. P. and Chan, K. W. (1999). Guthrie Chemara planting materials. In: Proc. 1996 Seminar 'Sourcing of oil palm planting materials for local and overseas joint ventures' (Ed. by N. Rajanaidu & B.S. Jalani), pp. 91–105, Palm Oil Res. Inst. Malaysia, Kuala Lumpur.

Young, W. P., Schupp, J. M. and Keim, P. (1999). DNA methylation and AFLP marker distribution in the soybean genome. *Theor. Appl. Genet.,* 99: 785-790.

Yu, J., Hu, S., Wang, J., Wong, G. K., Li, S., Liu, B., Deng, Y., Dai, L., Zhou, Y., Zhang, X., Cao, M., Liu, J., Sun, J., Tang, J., Chen, Y., Huang, X., Lin, W., Ye, C., Tong, W., Cong, L., Geng, J., Han, Y., Li, L., Li, W., Hu, G., Huang, X., Li, W., Li, J., Liu, Z., Li, L., Liu, J., Qi, Q., Liu, J., Li, L., Li, T., Wang, X., Lu, H., Wu, T., Zhu, M., Ni, P., Han, H., Dong, W., Ren, X., Feng, X., Cui, P., Li, X., Wang, H., Xu, X., Zhai, W., Xu, Z., Zhang, J., He, S., Zhang, J., Xu, J., Zhang, K., Zheng, X., Dong, J., Zeng, W., Tao, L., Ye, J., Tan, J., Ren, X., Chen, X., He, J., Liu, D., Tian, W., Tian, C., Xia, H., Bao, Q., Li, G., Gao, H., Cao, T., Wang, J., Zhao, W., Li, P., Chen, W., Wang, X., Zhang, Y., Hu, J., Wang, J., Liu, S., Yang, J., Zhang, G., Xiong, Y., Li, Z., Mao, L., Zhou, C., Zhu, Z., Chen, R., Hao, B., Zheng, W., Chen, S., Guo, W., Li, G., Liu, S., Tao, M., Wang, J., Zhu, L., Yuan, L., Yang, H. (2002). A draft sequence of the rice genome (*Oryza sativa L. ssp. indica*). *Science,* 296(5565):79-92.

Yu, S. B., Li, J. X., Xu, C. G., Tan, Y. F., Gao, Y. J., Li, X. H., Zhang, Q. and Saghai Maroof, M. A. (1997). Importance of epistasis as the genetic basis of heterosis in an elite rice hybrid. *Proc. Natl. Acad. Sci. USA,* 94: 9226–9231

Yuan, Y., San Miguel, P. J. and Bennetzen, J. L. (2003). High-Cot sequence analysis of the maize genome. *Plant J.,* 34(2):249–255

Zabeau, M. and Vos, P. 1993. Selective restriction fragment amplification: a general method for DNA fingerprinting. European Patent Publication 92402629 (Publication no: EP 0534858 A1).

Zeng, Z. B. (1993). Theoretical basis for separation of multiple linked gene effects in mapping quantitative trait loci. *Proc. Natl. Acad. Sci. USA,* 90(23):10972-6.

Zeng, Z. B. (1994). Precision mapping of quantitative trait loci. *Genetics,* (Zeven, 1967)

Zeven, A. C. (1967). The semi-wild oil palm and its industry in Africa. Agricultural Research Reports, No. 689. Agricultural University, Wageningen, The Netherlands. http://library.wur.nl/wda/abstracts/ab412.html. Accessed on 10 March 2005.

Zhu, J., Gale, M. D., Quarrie, S., Jackson, M. T. and Bryan, G. J. (1998). AFLP markers for the study of rice biodiversity. *Theor. Appl. Genet.,* 96: 602-611.

Zieler H., Richardson, T., Schwartz A., Helge, M., Lomelin, D., Mathur, E., Cheah, S. C., Tee, T. S., Lee, W. W., Chua, K.L., Kwan, B. H., Miller, J., Koren, S., Chan, A. P., Maiti, R., Amedeo, P., Ferriera, S., Rogers, Y. H., Sutton, G., Town, C. D., and Venter, J. C. (2010). Whole-genome shotgun sequencing of the oil palm and Jatropha genomes. Plant and Animal Genomes XVIII Conference. San Diego, CA, USA.

Zulkifli, Y., Maizura, I. and Rajinder, S. (2012). Evaluation of MPOB oil palm germplasm (*Elaeis guineensis*) populations using EST-SSR. *J. Oil Palm Res.,* Vol.24 August 2012. Pg 1368-1377