



UNIVERSITI PUTRA MALAYSIA

***DETERMINATION OF GENETIC DIVERSITY AND INBREEDING LEVEL
IN DELI DURA AND AVROS ADVANCED BREEDING MATERIALS IN OIL
PALM (ELAEIS GUINEENSIS JACQ.) USING MICROSATELLITE
MARKERS***

TAY CHEE CHUN

FBSB 2016 10



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By

TAY CHEE CHUN

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

June 2016

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Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfillment of the requirement for the degree of Master of Science

DETERMINATION OF GENETIC DIVERSITY AND INBREEDING LEVEL IN DELI DURA AND AVROS ADVANCED BREEDING MATERIALS IN OIL PALM (*Elaeis guineensis* Jacq.) USING MICROSATELLITE MARKERS

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June 2016

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Intensive selections in breeding have led to a narrowed genetic diversity in oil palm. Although uniformity is favorable to breeders, loss of genetic diversity may lead to deleterious consequences. Thus, background knowledge on genetic diversity in advanced breeding material of oil palm (*Elaeis guineensis* Jacq.) is critical for crop improvement. The objectives of the study are to evaluate the genetic diversity in the advanced breeding materials, Deli dura and AVROS populations, and to determine the levels of inbreeding in these populations using CIRAD's Simple Sequence Repeat (SSR) markers. The parental populations evaluated here were 186 palms from 8 Dx D/D-selfs Deli dura and 188 palms from 8 Tx T/T-selfs AVROS progenies sourced from Agency 1 and Agency 2. Ekona population was included as control. Genotyping was done by using 32 SSR markers which produced 230 alleles among the 17 oil palm progenies. The number of alleles scored per SSR primer ranged between 4 to 11. The average number of alleles per locus was 7.1875. The expected heterozygosity (H_e) and observed heterozygosity (H_o) among the populations were 0.7063 and 0.5270, respectively. Genetic distance values were calculated. The dendrogram resulting from the Neighbour-Joining clustering analysis revealed that the 17 populations were clustered into 3 main clusters namely Deli dura, AVROS and Ekona populations. The AVROS cluster was further divided into two sub-clusters according to Agency. The Deli dura cluster was sub-clustered based on the cross type i.e. Dx D and D-selfs. The two different generations of AVROS provided an overview of the inbreeding level in the AVROS population. AVROS from Agency 2 had inbreeding coefficient of 0.0336 compared to AVROS from Agency 1 which was -0.0810. The inbreeding value indicated that Agency 2 AVROS had lower heterozygosity compared to Agency 1. The genetic variability revealed via SSR markers on the advanced breeding populations

provide a better understanding to the breeder and the information can guide them in decision making during the inbred lines development.



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

**PENENTUAN KEPELBAGAIAN GENETIK DAN TAHAP PEMBIAKBAKAAN
DALAM BAHAN PEMBIAKAN MAJU DELI DURA DAN AVROS BAGI
KELAPA SAWIT (*Elaeis guineensis* Jacq.) MENGGUNAKAN PENANDA
MIKROSATELIT**

Oleh

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Pemilihan yang intensif dalam pembiakbakaan kelapa sawit telah membawa kepada kepelbagaian genetik yang semakin sempit. Walaupun keseragaman penting untuk peladang, tetapi kehilangan kepelbagaian genetik boleh membawa kepada akibat yang parah. Oleh itu, pengetahuan latarbelakang ke atas kepelbagaian genetik dalam bahan pembiakbakaan maju kelapa sawit (*Elaeis guineensis* Jacq.) adalah kritikal untuk penambahbaikan tanaman. Objektif kajian ini adalah untuk menilai kepelbagaian genetik dalam bahan-bahan pembiakbakaan maju, Deli dura dan AVROS, dan untuk menentukan tahap pembiakbakaan dalam populasi ini menggunakan penanda molekul (SSR) dari CIRAD. Populasi yang dinilai terdiri daripada 186 pokok Deli dura dari 8 progeni DxD / D-selfs dan 188 pokok AVROS dari 8 progeni TxT / T-selfs diperolehi daripada Agensi 1 dan Agensi 2. Populasi Ekona telah digunakan sebagai kawalan. Penjenisan gen telah dilakukan dengan menggunakan 32 penanda molekul SSR yang menghasilkan 230 alel antara 17 populasi kelapa sawit. Bilangan alel untuk setiap SSR berbilang antara 4 hingga 11. Purata bilangan alel setiap lokus adalah 7.1875. Heterozigositi dijangka (H_e) dan heterozigositi diperhati (H_o) di kalangan populasi adalah 0.7063 dan 0.5270, masing-masing. Nilai jarak genetik telah dikira. Dendrogram dari analisis kelompok, Neighbour-Joining telah menunjukkan bahawa 17 populasi telah dikelompokkan ke dalam 3 kelompok utama iaitu Deli dura, AVROS dan Ekona populasi. Progeni AVROS telah dikelompokkan kepada 2 sub-kelompok mengikut agensi. Kelompok Deli dura telah bercabang dengan lanjut berdasarkan jenis jujukan iaitu DxD dan D-selfs. Kedua-dua generasi yang berbeza bagi AVROS telah memberi gambaran keseluruhan tahap pembiakbakaan dalam populasi AVROS. AVROS daripada Agensi 2 mempunyai pekali pembiakbakaan 0.0336 berbanding AVROS daripada Agensi 1 yang mempunyai -0.0810. Nilai pembiakbakaan ini menunjukkan

bahawa AVROS daripada Agensi 2 mempunyai heterozigositi yang lebih rendah berbanding dengan Agensi 1. Kesimpulannya, kepelbagaian genetik yang didedahkan melalui penggunaan penanda molekul (SSR) terhadap populasi pembiakbakaan maju telah memberi peladang kefahaman yang lebih baik dan informasi ini dapat memberi garis panduan kepada mereka semasa membuat keputusan untuk pembangunan pembiakbakaan.



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I certify that a Thesis Examination Committee has met on 29th June 2016 to conduct the final examination of TAY CHEE CHUN on his thesis entitled "Determination of Genetic Diversity and Inbreeding Level in Deli Dura and AVROS Advanced Breeding Materials in Oil Palm (*Elaeis guineensis* Jacq.) Using Microsatellite Markers " in accordance with the Universities and University Colleges Act 1971 and the Constitution of the Universiti Putra Malaysia [P.U.(A) 106] 15 March 1998. The Committee recommends that the student be awarded the Master of Science.

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LIST OF ABBREVIATIONS

°C	Degree celsius
AFLP	Amplified fragment length polymorphism
AVROS	Algemene Vereniging van Rubberplanters ter Oostkust van Sumatra
bp	Base pairs
CE	Capillary electrophoresis
CIRAD	Centre International de Reseaux Agriculture and Development
cm	centimeter
CPO	Crude palm oil
D × P	<i>dura</i> × <i>pisifera</i>
DNA	Deoxyribonucleic acid
dNTPs	Deoxynucleoside triphosphate
Gb	Gigabase
GBS	Genotyping-by-sequencing
GDP	Gross domestic product
GENP	Genting Plantations
Ha	Hectare
H _e	Expected heterozygosity
H _o	Observed heterozygosity
HWE	Hardy-Weinberg Equilibrium
MAS	Marker assisted selection
MgCl ₂	Magnesium chloride
mL	milliliter
mM	millimole
MPOB	Malaysian Palm Oil Board
MRRS	Modified reciprocal recurrent selection
μL	microliter
μM	micromole
Na	Observed number of alleles
NCM1	North Carolina Model 1

NGS	Next generation sequencing
PCR	Polymerase chain reaction
PIC	Polymorphic information content
PORIM	Palm Oil Research Institute of Malaysia
PORLA	Palm Oil Registration and Licensing Authority
QTL	Quantitative trait loci
R&D	Research and development
RAPD	Randomly Amplified Polymorphic DNA
RFLP	Restriction Fragment Length Polymorphism
SNP	Single Nucleotide Polymorphism
SSR	Simple Sequence Repeats
T	<i>tenera</i>
U	Units (of an enzyme)
URT	Ulu Remis Tenera
UV	Ultra Violet
V	volts

CHAPTER 1

INTRODUCTION

The African oil palm (*Elaeis guineensis* Jacq.) is an oil crop that is native to Africa. As the world's leading oil crop, oil palm produces 29.8% of the total vegetable oils and fats surpassing soybean 22.5% (Oil World 2013). It yields 5 to 15 times more oil per hectare as compared to rapeseed or soybean. In 2012, the estimated global oil palm planted area was 14.8 million ha that produced 53.67 million tonnes of crude palm oil (CPO). In 2014, the oil palm planted area in Malaysia was 5.39 million ha producing 19.67 million tonnes of palm oil. The great economic value generated by palm oil export has changed the oil palm from its ornamental status to that of a cash crop.

In Malaysia, oil yield has increased fourfold in the last 50 years, half of this being attributable to genetic improvement of the planting material (Lee *et al.*, 1990). However, the study showed that selection for this improvement reduced the coefficient of variation for fruit bunch yield by nearly half. Intensive breeding from a narrow genetic base is leading to limited variation within the elite material, potentially reducing the rate of future breeding progress. Efforts to broaden the genetic variability of the current oil palm advanced breeding populations are crucial to enable the breeders to exploit the genetic potentials in order to produce planting materials that are high yielding with better oil quality and high tolerance to pests and diseases. Musa and Gurmit (2008) has indicated great potential for improvement through the introgression of selected palms from the MPOB germplasm into the advanced dura and tenera lines which reduced palm height (Isa *et al.*, 2008) and improved oil palm yield and fruit qualities (Junaidah *et al.*, 2008).

Conventional breeding takes several years for oil palm improvement due to the fact that it is perennial oil crop with a long generation cycle of breeding. These led to slow progress and hamper the release of high yielding planting materials. However, there are various molecular techniques that are available today which provide a powerful tool to facilitate crop improvement and selection. Molecular markers have been exploited in oil palm research over the last two decades in areas such as DNA fingerprinting using restriction fragment length polymorphism (RFLP) (Cheah *et al.*, 1996). According to Corley (2005), the employment of molecular markers has allowed illegitimate crosses to be identified and legitimate individuals to be determined. In addition, molecular markers are able to detect genetic variability (Billotte *et al.*, 2005), genome mapping and Quantitative Trait Loci (QTL) detection for Marker Assisted Selection (MAS) (Billotte *et al.*, 2010).

With the advancement of biotechnology and oil palm genome sequencing, molecular markers were developed and are available in the public domain. Microsatellite marker

or Simple Sequence Repeat (SSR) is one of the molecular markers that are in abundance which is well utilised for genetic diversity studies (Norziha *et al.*, 2008; Singh *et al.*, 2008). It has great advantages over other markers systems due to its high polymorphism and wide distribution of the loci within the genome (Vignal *et al.*, 2002). Besides, SSR is a co-dominant marker which is ideal for diversity measurements and is highly reproducible through the Polymerase Chain Reaction (PCR). Hamblin *et al.* (2007) reported that SSRs performed better to assign the inbreds to sub-populations as compared to Single Nucleotide Polymorphism (SNPs) in their research to evaluate the genetic diversity in a set of public maize inbreds. Besides microsatellite markers, there are reports of other molecular markers such as restriction fragment length polymorphism (RFLP) of ribosomal DNA (Rajanaidu *et al.*, 1989), random amplified polymorphic DNA (RAPD) (Shah *et al.*, 1994), and amplified fragment length polymorphism (AFLP) (Kularatne, 2000).

The Malaysian advanced breeding materials particularly the Deli population and AVROS population have been subjected to extensive selection since the 1930s (Maizura *et al.*, 2009). Breeding and selection for crop improvement using these populations by breeders had led to narrowed genetic diversity as shown by various reports (Lee *et al.*, 1990; Hayati *et al.*, 2004; Maizura *et al.*, 2006). The majority of the studies were carried out using germplasms and not many focused on advanced breeding materials. Besides, no comparison of different generations of materials was carried out previously. Thus, an understanding on the genetic diversity of the advanced breeding populations at the molecular level is of importance for breeders to exploit the remaining genetic potential for crop improvement. The findings from this study could serve as supplementary information for the breeders during their crossing design enabling more precise decisions on the selection of parental materials for seed production and inbred line development.

The objectives of the current study were:

1. To determine the genetic diversity in the advanced breeding materials, Deli and AVROS populations, for future breeding and improvement.
2. To determine the levels of inbreeding across different generations in the advanced breeding populations.
3. To utilise SSR markers as a tool to investigate the occurrence of illegitimate palms among the progenies of specific crosses.

REFERENCES

- Abdullah, N., Yusop, M.R., Ithnin, M. & Saleh, G. 2008, "Genetic variation among oil palm parent genotypes and their progenies based on microsatellite markers", *Journal of oil palm Research*, vol. 20, no. 2, pp. 533-541.
- Adin, A., Weber, J., Montes, C.S., Vidaurre, H., Vosman, B. & Smulders, M. 2004, "Genetic differentiation and trade among populations of peach palm (*Bactris gasipaes* Kunth) in the Peruvian Amazon—implications for genetic resource management", *Theoretical and Applied Genetics*, vol. 108, no. 8, pp. 1564-1573.
- Allou, D., Adon, B. & Sangare, A. 2008, "Molecular variability from two selection of BRT10 population in an inbreeding program of oil palm (*Elaeis guineensis* Jacq.) in Côte d'Ivoire", *African Journal of Biotechnology*, vol. 7, no. 20.
- Arias, D., Montoya, C., Rey, L. & Romero, H. 2012, "Genetic similarity among commercial oil palm materials based on microsatellite markers", *Agronomía Colombiana*, vol. 30, no. 2, pp. 188-195.
- Arias, D., Ochoa, I., Castro, F. & Romero, H. 2014, "Molecular characterization of oil palm *Elaeis guineensis* Jacq. of different origins for their utilization in breeding programmes", *Plant Genetic Resources*, vol. 12, no. 03, pp. 341-348.
- Bakoumé, C., Wickneswari, R., Siju, S., Rajanaidu, N., Kushairi, A. & Billotte, N. 2015, "Genetic diversity of the world's largest oil palm (*Elaeis guineensis* Jacq.) field genebank accessions using microsatellite markers", *Genetic Resources and Crop Evolution*, vol. 62, no. 3, pp. 349-360.
- Barcelos, E., Amblard, P., Berthaud, J. & Seguin, M. 2002, "Genetic diversity and relationship in American and African oil palm as revealed by RFLP and AFLP molecular markers", *Pesquisa Agropecuária Brasileira*, vol. 37, no. 8, pp. 1105-1114.
- Beirnaert, A.D.F. & Vanderweyen, R. 1941, *Contribution à l'étude génétique et biométrique des variétés d'Elaeis guineensis Jacquin*, East African Standard.
- Billotte, N., Jourjon, M., Marseillac, N., Berger, A., Flori, A., Asmady, H., Adon, B., Singh, R., Nouy, B. & Potier, F. 2010, "QTL detection by multi-parent linkage mapping in oil palm (*Elaeis guineensis* Jacq.)", *Theoretical and Applied Genetics*, vol. 120, no. 8, pp. 1673-1687.

- Billotte, N., Marseillac, N., Risterucci, A., Adon, B., Brottier, P., Baurens, F., Singh, R., Herran, A., Asmady, H. & Billot, C. 2005, "Microsatellite-based high density linkage map in oil palm (*Elaeis guineensis* Jacq.).", *Theoretical and Applied Genetics*, vol. 110, no. 4, pp. 754-765.
- Billotte, N., Risterucci, A., Barcelos, E., Noyer, J., Amblard, P. & Baurens, F. 2001, "Development, characterisation, and across-taxa utility of oil palm (*Elaeis guineensis* Jacq.) microsatellite markers", *Genome*, vol. 44, no. 3, pp. 413-425.
- Bruford, M.W., Cheesman, D.J., Coote, T., Green, H.A., Haines, S.A., O'Ryan, C. & Williams, T.R. 1996, "Microsatellites and their application to conservation genetics", *Molecular genetic approaches in conservation*, , pp. 278-297.
- Cadalen, T., Boeuf, C., Bernard, S. & Bernard, M. 1997, "An intervarietal molecular marker map in *Triticum aestivum* L. Em. Thell. and comparison with a map from a wide cross", *Theoretical and Applied Genetics*, vol. 94, no. 3-4, pp. 367-377.
- Cheah, S.C., LCL Rahimah, A., Aberlenc-Bertossi, F.A., Adon, H., Amblard, B., Beule, P., Billote, T., Durand-Gasselien, N., Duval, T. & Flori, Y. 1996, *Quality control process for oil palm tissue culture using DNA probes*, .
- Chin, C. 1999, "FELDA oil palm planting materials", *Seminar on sourcing of oil palm planting materials for local and overseas joint-ventures* July 22-23 Subang Jaya, Malasia PORIM-ASGARD, .
- Clark, R.M., Schweikert, G., Toomajian, C., Ossowski, S., Zeller, G., Shinn, P., Warthmann, N., Hu, T.T., Fu, G., Hinds, D.A., Chen, H., Frazer, K.A., Huson, D.H., Scholkopf, B., Nordborg, M., Ratsch, G., Ecker, J.R. & Weigel, D. 2007, "Common sequence polymorphisms shaping genetic diversity in *Arabidopsis thaliana*", *Science (New York, N.Y.)*, vol. 317, no. 5836, pp. 338-342.
- Cochard, B., Adon, B., Rekima, S., Billotte, N., de Chenon, R.D., Koutou, A., Nouy, B., Omoré, A., Purba, A.R. & Glazsmann, J. 2009, "Geographic and genetic structure of African oil palm diversity suggests new approaches to breeding", *Tree genetics & genomes*, vol. 5, no. 3, pp. 493-504.
- 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*, vol. 142, no. 1-2, pp. 169-196.

- Corley, R. 2005, "Illegitimacy in oil palm breeding-a review.", *Journal of Oil Palm Research*, vol. 17, no. 1, pp. 64-69.
- Corley, R. 1998, "What is the upper limit to oil extraction ratio?", *International Conference on Oil and Kernel production in oil palm. A global perspective* September 27-28 Kuala Lumpur, Malaysia PORIM, .
- Corley, R. & Tinker, P. 2003, "Vegetative propagation and biotechnology", *The oil palm*, vol. 4, pp. 201-215.
- Dransfield, J., Uhl, N.W., Asmussen, C.B., Baker, W.J., Harley, M.M. & Lewis, C.E. 2005, "A new phylogenetic classification of the palm family, Arecaceae", *Kew Bulletin*, , pp. 559-569.
- Emanuelli, F., Lorenzi, S., Grzeskowiak, L., Catalano, V., Stefanini, M., Troggio, M., Myles, S., Martinez-Zapater, J.M., Zyprian, E., Moreira, F.M. & Grando, M.S. 2013, "Genetic diversity and population structure assessed by SSR and SNP markers in a large germplasm collection of grape", *BMC plant biology*, vol. 13, pp. 39-2229-13-39.
- Evanno, G., Regnaut, S. & Goudet, J. 2005, "Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study", *Molecular ecology*, vol. 14, no. 8, pp. 2611-2620.
- Excoffier, L., Estoup, A. & Cornuet, J.M. 2005, "Bayesian analysis of an admixture model with mutations and arbitrarily linked markers", *Genetics*, vol. 169, no. 3, pp. 1727-1738.
- Falush, D., Stephens, M. & Pritchard, J.K. 2003, "Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies", *Genetics*, vol. 164, no. 4, pp. 1567-1587.
- Futaayama DJ (1986) *Evolutionary Biology*, 2nd edn. Sinauer Associates Inc. Sunderland, MA
- Garcia, A.A., Benchimol, L.L., Barbosa, A.M., Geraldi, I.O., Souza Jr, C.L. & Souza, A.P.d. 2004, "Comparison of RAPD, RFLP, AFLP and SSR markers for diversity studies in tropical maize inbred lines", *Genetics and Molecular Biology*, vol. 27, no. 4, pp. 579-588.

- Gascon JP, Noiret JM, Meunier J (1969) Effets de la consanguinité chez *Elaeis guineensis* Jacq. *Oleagineux* 24:603–607
- Godt, H.J. & Hamrick, J. 1989, "Allozyme diversity in plant species", *Plant population genetics, breeding and genetic resources*, , pp. 43-63.
- Hama-Ali, E.O., Alwee, Sharifah Shahrul Rabiah Syed, Tan, S.G., Panandam, J.M., Ling, H.C., Namasivayam, P. & Peng, H.B. 2015, "Illegitimacy and sibship assignments in oil palm (*Elaeis guineensis* Jacq.) half-sib families using single locus DNA microsatellite markers", *Molecular biology reports*, vol. 42, no. 5, pp. 917-925.
- Hamblin, M.T., Warburton, M.L. & Buckler, E.S. 2007, "Empirical comparison of simple sequence repeats and single nucleotide polymorphisms in assessment of maize diversity and relatedness", *PloS one*, vol. 2, no. 12, pp. e1367.
- Hamrick, J.L. & Godt, M. 1996, "Effects of life history traits on genetic diversity in plant species", *Philosophical Transactions of the Royal Society of London B: Biological Sciences*, vol. 351, no. 1345, pp. 1291-1298.
- Hardon, J. 1970, "Inbreeding in populations of the oil palm (*Elaeis guineensis* Jacq.) and its effect on" selection.", *Oléagineux*, vol. 25, pp. 449-456.
- Hartley, C. 1977, "The oil palm (*Elaeis guineensis*)", Longmans Londres.
- Hartley, C. 1988, "The oil palm (*Elaeis guineensis*)", Longmans Scientific and Technical Publ, New York.
- Hayati, A., Wickneswari, R., Maizura, I. & Rajanaidu, N. 2004, "Genetic diversity of oil palm (*Elaeis guineensis* Jacq.) germplasm collections from Africa: implications for improvement and conservation of genetic resources", *Theoretical and Applied Genetics*, vol. 108, no. 7, pp. 1274-1284.
- Heather Kowalski, First draft of oil palm genome completed by Synthetic Genomics Inc and Asiatic Centre for Genome Technology, 2008, <http://www.syntheticgenomics.com/210508.html> (accessed 21 May 2008)
- Henson, I. 1991, "Age-related changes in stomatal and photosynthetic characteristics of leaves of oil palm (*Elaeis guineensis* Jacq)", *Elaeis*, .

- Huang, X., Wei, X., Sang, T., Zhao, Q., Feng, Q., Zhao, Y., Li, C., Zhu, C., Lu, T. & Zhang, Z. 2010, "Genome-wide association studies of 14 agronomic traits in rice landraces", *Nature genetics*, vol. 42, no. 11, pp. 961-967.
- Isa, Z., Ong, K., Norasyikin, I. & Suboh, O. 2008, "Performance of MPOB-Nigerian population 12 at Kulim—an update", *Proceedings of the 3rd Seminar on Performance of PS1 and PS2 Materials and Elite Germplasm. Malaysian Palm Oil Board, Selangor*, pp. 139.
- Isa, Z.A., Suboh, O, Azhar, D and Norasyikin I. 2013, "Performance of Dami DXP planted in inland soil in Tereh Utara, Kulim Plantation", *Proceedings of the International Seminar on Oil Palm Breeding – Yesterday, Today and Tomorrow. Malaysian Palm Oil Board, Selangor*, pp. 40-63
- Jeennor, S. & 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 genetics & genomes*, vol. 10, no. 1, pp. 1-14.
- Jonah, P., Bello, L., Lucky, O., Midau, A. & Moruppa, S. 2011, "Review: the importance of molecular markers in plant breeding programmes", *Global Journal of Science Frontier Research*, vol. 11, no. 5.
- Joshi, S.P., Ranjekar, P.K. & Gupta, V.S. 1999, "Molecular markers in plant genome analysis", *Curr Sci*, vol. 77, no. 2, pp. 230-240.
- Junaidah, J., Chin, C., Rafii, M. & Syuhada, W. 2008, "Performance and utilization of MPOB-Nigerian oil palm materials in FELDA", *Proceedings of the 3rd Seminar on Performance of MPOB PS1 and PS2 Materials and Elite Germplasm*, pp. p73.
- Karkkainen, K., Koski, V. & Savolainen, O. 1996, "Geographical variation in the inbreeding depression of Scots pine", *Evolution*, , pp. 111-119.
- Kašička, V. 2014, "Recent developments in capillary and microchip electrophoresis of peptides (2011–2013)", *Electrophoresis*, vol. 35, no. 1, pp. 69-95.
- Kochert, G. 1994, "RFLP technology" in *DNA-based markers in plants* Springer, , pp. 8-38.
- Kong, L., Bai, J., & Li, Q. (2014). Comparative assessment of genomic SSR, EST–SSR and EST–SNP markers for evaluation of the genetic diversity of wild and cultured Pacific oyster, *Crassostrea gigas* Thunberg. *Aquaculture*, 420, S85-S91.

- Kularatne, R. 2000, *Assessment of genetic diversity in natural oil palm (Elaeis guineensis Jacq.) using amplified fragment length polymorphism markers*, .
- Kularatne, R., Shah, F. & Rajanaidu, N. 2000, "Estimation of genetic diversity in some African germplasm collection of oil palm(*Elaeis guineensis* Jacq) as detected by AFLP markers", *Asia-Pacific Journal of Molecular Biology and Biotechnology*, vol. 8, no. 1, pp. 27-36.
- Lee, C. & Yeow, K. 1985, "Progress in breeding and selection for seed production at HMPB Oil Palm Research Station.", *Planter (Malasia)*, .
- Lee, C., Yong, Y., Donough, C., Chiu, S., Soh, A., Rajanaidu, N., Basri, M., Pamin, K. & Muluk, C. 1990, "Selection progress in the Deli dura population.", *Proceedings of workshop on progress of oil palm breeding populations, Permatang Siantar, Sumatra, Indonesia, 25 November 1988*. Palm Oil Research Institute of Malaysia, , pp. 81.
- Lui, K. & Muse, S. 2005, "PowerMarker: integrated analysis environment for genetic marker data", *Bioinformatics*, vol. 21, no. 9, pp. 2128-2129.
- Luyindula, N., Mantantu, N., Dumortier, F. & Corley, R. 2005, "Effects of inbreeding on growth and yield of oil palm", *Euphytica*, vol. 143, no. 1-2, pp. 9-17.
- Lynch, M. & Walsh, B. 1998, *Genetics and analysis of quantitative traits*, Sinauer Sunderland, MA.
- Maizura, I., Norziha, A., Rafii, M.Y. Saleh, G. 2009. Relationship between Genetic Distance of Oil Palm Parental Palms and Performance of Their Progenies based on Microsatellite Markers. Paper presented in GSAS Seminar (19th June 2009) at MPOB, HQ.
- Maizura, I., Rajanaidu, N., Zakri, A. & Cheah, S. 2006, "Assessment of genetic diversity in oil palm (*Elaeis guineensis* Jacq.) using restriction fragment length polymorphism (RFLP)", *Genetic Resources and Crop Evolution*, vol. 53, no. 1, pp. 187-195.
- Maria, M., Clyde, M. & Cheah, S. 1995, "Cytological analysis of *Elaeis guineensis* (tenera) chromosomes.", *Elaeis*, vol. 7, no. 2, pp. 122-131.
- Morin, P.A., Luikart, G. & Wayne, R.K. 2004, "SNPs in ecology, evolution and conservation", *Trends in Ecology & Evolution*, vol. 19, no. 4, pp. 208-216.

- MPOB 2014. Statistics compiled by Malaysian Palm Oil Board Retrieved 31 Dec, 2014, from <http://bepi.mpob.gov.my/index.php/statistics/production.html>
- MPOB. Overview of the Malaysian Oil Palm Industry 2014. Oil Palm Bulletin ISBN/ISSN of 1511-7448.
- Musa, B. & Gurmit, S. 2008, "Utilization of MPOB germplasm at United Plantations", *Proceedings of the 3rd Seminar on Performance of PS1 and PS2 Materials and Elite Germplasm. Malaysian Palm Oil Board, Selangor*, pp. 43.
- Nei, M. 1972, "Genetic distance between populations", *American naturalist*, , pp. 283-292.
- Noh, A., Rafii, M., Saleh, G., Kushairi, A. & Latif, M. 2012, "Genetic performance and general combining ability of oil palm Deli dura x AVROS pisifera tested on inland soils", *The Scientific World Journal*, vol. 2012.
- Ooi, S., Hardon, J. & Phang, S. 1973, "Variability in the Deli dura breeding population of the oil palm (*Elaeis guineensis* Jacq.). I. Components of bunch yield.", *Malaysian Agricultural Journal*, vol. 49, no. 2, pp. 112-121.
- Oil World 2013 ISTA Mielke GmbH No. 7, Vol 56, Hamburg Feb 16th
- Pamin, K., Hutomo, T. & Purba, A. 1995, "Performance of growth, yield and oil quality of *E. guineensis* × *E. oleifera* hybrids and their backcross", *Proceedings of seminar on worldwide performance of DxP, interspecific hybrids and clones, Barranquilla, Colombia*, pp. 5.
- Penner, G.A., Lee, S.J., Bezte, L.J. & Ugali, E. 1996, "Rapid RAPD screening of plant DNA using dot blot hybridization", *Molecular Breeding*, vol. 2, no. 1, pp. 7-10.
- Phillips, R.M., Bair, E., Lawrence, D.S., Sims, C.E. & Allbritton, N.L. 2013, "Measurement of protein tyrosine phosphatase activity in single cells by capillary electrophoresis", *Analytical Chemistry*, vol. 85, no. 12, pp. 6136-6142.
- Pritchard, J.K., Stephens, M. & Donnelly, P. 2000, "Inference of population structure using multilocus genotype data", *Genetics*, vol. 155, no. 2, pp. 945-959.

- Purba, A., Noyer, J., Baudouin, L., Perrier, X., Hamon, S. & Lagoda, P. 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", *Theoretical and Applied Genetics*, vol. 101, no. 5-6, pp. 956-961.
- Quagliaro, G., Vischi, M., Tyrka, M. & Olivieri, A.M. 2001, "Identification of wild and cultivated sunflower for breeding purposes by AFLP markers", *The Journal of heredity*, vol. 92, no. 1, pp. 38-42.
- Rajanaidu, N., Ainul, M.M., Kushairi, A. and Din, A. 2013, "Historical review of oil palm breeding for the past 50 years-Malaysian journey", *Proceedings of the International Seminar on Oil Palm Breeding – Yesterday, Today and Tomorrow. Malaysian Palm Oil Board, Selangor*, pp. 11-28
- Rajanaidu, N., Rao, V., Hassan, A.H. & Ong, A. 1989, "Genetic resources-new developments in oil palm breeding.", *Elaeis*, vol. 1, no. 1, pp. 1-10.
- Ren, J., Chen, L., Sun, D., You, F.M., Wang, J., Peng, Y., Nevo, E., Beiles, A., Sun, D. & Luo, M. 2013, "SNP-revealed genetic diversity in wild emmer wheat correlates with ecological factors", *BMC evolutionary biology*, vol. 13, no. 1, pp. 1.
- Rohlf, F. 2005, "NTSYS-pc: Numerical taxonomy and multivariate analysis system, Version 2.2. New York", .
- Rosenquist, E. 1986, "The genetic base of oil palm breeding populations", *International Workshop on Oil Palm Germplasm and Utilisation, Bangi, Selangor (Malaysia), 26-27 Mar 1985*IPMKSM, .
- Saghai Maroof, M.A., Biyashev, R.M., Yang, G.P., Zhang, Q. & Allard, R.W. 1994, "Extraordinarily polymorphic microsatellite DNA in barley: species diversity, chromosomal locations, and population dynamics", *Proceedings of the National Academy of Sciences of the United States of America*, vol. 91, no. 12, pp. 5466-5470.
- Semagn, K., Bjørnstad, Å. & Ndjiondjop, M. 2006, "An overview of molecular marker methods for plants", *African Journal of Biotechnology*, vol. 5, no. 25.
- Seng, T., Saad, S.H.M., Chin, C., Ting, N., Singh, R.S.H., Zaman, F.Q., Tan, S. & Alwee, Sharifah Shahrul Rabiah Syed 2011, "Genetic linkage map of a high yielding FELDA Deli× Yangambi oil palm cross", *PLoS One*, vol. 6, no. 11, pp. e26593.

- Shah, F., Rashid, O., Simons, A. & Dunsdon, A. 1994, "The utility of RAPD markers for the determination of genetic variation in oil palm (*Elaeis guineensis*)", *Theoretical and Applied Genetics*, vol. 89, no. 6, pp. 713-718.
- Sime Darby, Sime Darby makes important discovery in oil palm genome, 2009, <http://www.simedarby.com/media/press-release/sime-darby-makes-important-discovery-in-oil-palm-genome> (accessed 12 May 2009)
- Singh, N., Choudhury, D.R., Singh, A.K., Kumar, S., Srinivasan, K., Tyagi, R., Singh, N. & Singh, R. 2013, "Comparison of SSR and SNP markers in estimation of genetic diversity and population structure of Indian rice varieties", *PLoS One*, vol. 8, no. 12, pp. e84136.
- Singh, R., Tan, S.G., Panandam, J.M., Rahman, R., Ooi, L.C., Low, E.L., Sharma, M., Jansen, J. & Cheah, S. 2009, "Mapping quantitative trait loci (QTLs) for fatty acid composition in an interspecific cross of oil palm", *BMC Plant Biology*, vol. 9, no. 1, pp. 1.
- Singh, R., Zaki, N.M., Ting, N., Rosli, R., Tan, S., Low, E.L., Ithnin, M. & Cheah, S. 2008, "Exploiting an oil palm EST database for the development of gene-derived SSR markers and their exploitation for assessment of genetic diversity", *Biologia*, vol. 63, no. 2, pp. 227-235.
- Soh, A., Vanialingam, T., Taniputra, B. & Pamin, K. 1981, "Derivatives of the Dumpy palm--some experimental results", *Planter*, 1981, ISSN: 0032-0951.
- Taeprayoon, P., Tanya, P., Lee, S. & Srinives, P. 2015, "Genetic background of three commercial oil palm breeding populations in Thailand revealed by SSR markers", *Australian Journal of Crop Science*, vol. 9, no. 4, pp. 281.
- Ting, N., Zaki, N.M., Rosli, R., Low, E.L., Ithnin, M., Cheah, S., Tan, S. & Singh, R. 2010, "SSR mining in oil palm EST database: application in oil palm germplasm diversity studies", *Journal of genetics*, vol. 89, no. 2, pp. 135-145.
- Van Inghelandt, D., Melchinger, A.E., Lebreton, C. & Stich, B. 2010, "Population structure and genetic diversity in a commercial maize breeding program assessed with SSR and SNP markers", *Theoretical and Applied Genetics*, vol. 120, no. 7, pp. 1289-1299.

- Vignal, A., Milan, D., SanCristobal, M. & Eggen, A. 2002, "A review on SNP and other types of molecular markers and their use in animal genetics", *Genetics Selection Evolution*, vol. 34, no. 3, pp. 275-306.
- Vos, P., Hogers, R., Bleeker, M., Reijans, M., van de Lee, T., Hornes, M., Frijters, A., Pot, J., Peleman, J. & Kuiper, M. 1995, "AFLP: a new technique for DNA fingerprinting", *Nucleic acids research*, vol. 23, no. 21, pp. 4407-4414.
- Wahid, M.B., Abdullah, S.N.A. & Henson, I. 2005, "Oil palm—achievements and potential", *Plant Production Science*, vol. 8, no. 3, pp. 288-297.
- Wang, K., Jiang, D., Sims, C.E. & Allbritton, N.L. 2012, "Separation of fluorescently labeled phosphoinositides and sphingolipids by capillary electrophoresis", *Journal of Chromatography B*, vol. 907, pp. 79-86.
- Wang, J. & Santure, A.W. 2009, "Parentage and sibship inference from multilocus genotype data under polygamy", *Genetics*, vol. 181, no. 4, pp. 1579-1594.
- Weir, B.S. & Cockerham, C.C. 1984, "Estimating F-statistics for the analysis of population structure", *evolution*, , pp. 1358-1370.
- Weir, B.S. & Cockerham, C. 1996, "Genetic data analysis II: Methods for discrete population genetic data. Sinauer Assoc", *Inc., Sunderland, MA, USA*, .
- Weising, K., Nybom, H., Pfenninger, M., Wolff, K. & Kahl, G. 2005, *DNA fingerprinting in plants: principles, methods, and applications*, CRC press.
- WengWah, L., BihHua, K., SooHeong, B., KiaLing, C., ChongHee, L., & SuanChoo, C. (2014). Sequencing for super seeds. *Planter*, 90(1057), 261-274.
- Wright, S. 1978, *Evolution and the genetics of populations: a treatise in four volumes: Vol. 4: variability within and among natural populations*, University of Chicago Press.
- Yu, R. H., Wang, Y. L., Sun, Y., & Liu, B. (2012). Analysis of genetic distance by SSR in waxy maize. *Genetics and Molecular Research*, 11(1), 254-260.

BIODATA STUDENT

Tay Chee Chun was born on 24th February 1986 in Johor, Malaysia. He obtained his BSc. in Biotechnology and Management from National University of Malaysia (UKM). During his final year project, he carried out research on gene cloning of *Fatty Acid Thioesterase (FAT)* from *Capsicum frutescens* with aim to identify the component of capsaicinoid that contribute the pungency as the presence of the *FAT* is correlated to the degree of pungency. After earning his bachelor's degree, Chee Chun joined ACGT in June 2008 and later was seconded to Genting AgTech Sdn Bhd (GAT), a subsidiary company of Genting Plantations Berhad (GENP). Since joining GAT, Chee Chun has been involved in projects related to linkage mapping and population genetic studies for oil palm. His interest includes molecular genetics and oil palm breeding. He is currently involved in oil palm breeding and marker assisted selection activities. In 2014, he was given the opportunity to pursue a Master's degree in Plant Biotechnology at Universiti Putra Malaysia (UPM) under the sponsorship of GENP. He has spent two years studying the genetic diversity and inbreeding level of different generation of oil palm advanced breeding materials under the supervision of Prof. Tan Soon Guan and Assoc. Prof. Dr. Mohd. Puad Abdullah.

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