

## Development and Characterization of *Elaeis oleifera* Microsatellite Markers (Pembangunan dan Pencirian Penanda Mikrosatelit *Elaeis oleifera*)

NOORHARIZA MOHD ZAKI\*, ISMANIZAN ISMAIL, ROZANA ROSLI,  
TING NGOOT CHIN & RAJINDER SINGH

### ABSTRACT

Ten *Elaeis oleifera* microsatellite markers were developed and characterised from 1500 sequences of the *E. oleifera* genomic library. The markers were utilised to assess the genetic diversity of *E. oleifera* germplasm collections from four South American countries (Colombia, Costa Rica, Panama and Honduras). The number of alleles per-locus varied from 2 to 11 and the observed and expected heterozygosity ranged from 0.0685 to 0.9853 and 0.1393 to 0.8216 respectively. Majority of the markers showed transferability to *Elaeis guineensis* while two markers showed transferability across *Arecaceae* taxa. These *E. oleifera* microsatellite markers are expected to become useful tools to determine the population structure and conservation of *E. oleifera* populations.

**Keywords:** *E. oleifera*; genomic; microsatellite; transferability

### ABSTRAK

Sebanyak sepuluh penanda mikrosatelit genomik *Elaeis oleifera* telah dibangunkan dan dicirikan daripada sejumlah 1500 klon di dalam perpustakaan genomik *E. oleifera*. Keupayaan penanda yang dibangunkan ini digunakan bagi menganalisis kepelbagaian genetik di dalam koleksi germplasma dari empat negara di Amerika Selatan (Colombia, Costa Rica, Panama dan Honduras). Bilangan alel per-locus yang dicerap adalah di dalam lingkungan 2 hingga 11 manakala heterozigositi yang dicerap dan dijangka adalah masing-masing 0.0685 hingga 0.9853 dan 0.1393 hingga 0.8216. Majoriti penanda mikrosatelit menunjukkan kebolehpindahan kepada *Elaeis guineensis* manakala dua penanda berjaya menunjukkan kebolehpindahan merentasi takson famili *Arecaceae*. Penanda-penanda mikrosatelit yang berjaya dibangunkan ini di jangka dapat menjadi penanda dalam menentukan struktur populasi dan pemuliharaan populasi *E. oleifera*.

**Kata kunci:** *E. oleifera*; genomik; kebolehpindahan; mikrosatelit

### INTRODUCTIONS

The oil palm belongs to the genus *Elaeis* and comprises of two species; the economically important *E. guineensis*, native to Africa and *E. oleifera*, found in Central and South America. The *E. oleifera* species is seen as a promising genetic resource and is currently being used in oil palm breeding programs for the development of inter-specific hybrids. The agronomic traits in *E. oleifera* that have attracted the attention of oil palm breeder includes slow trunk growth, improved oil quality (Moretzsohn et al. 2002) and resistance to disease such a *Fusarium* wilt and lethal yellowing (Hardon & Tan 1969)

Microsatellite markers are being widely applied for studies such as genome mapping, marker assisted selection of crop plants and molecular ecology studies. The development of microsatellite markers will be very valuable for genetic studies of oil palm. This is especially, so, since microsatellite markers show co-dominant inheritance, multiallelic in nature, abundant,

allow extensive genome coverage and can be detected using PCR. Microsatellites also appear to be the most promising molecular marker system for understanding the population genetic structure and gene flow (Singh et al. 2008).

Molecular marker studies on oil palm have mainly focused on the commercial *E. guineensis* although some studies have been reported for *E. oleifera* (Moretzsohn et al. 2002; Singh et al. 2008). The limited studies on *E. oleifera* have either used neutral markers such as random amplified polymorphic DNA (RAPD) or microsatellite markers developed from *E. guineensis* (Bilotte et al. 2001; Singh et al. 2008). Thus, in this study, we report the development of genomic microsatellite markers from *E. oleifera* and their application in characterizing four *E. oleifera* germplasm collections. We also investigated the transferability of the microsatellite loci to the other species of the same genus and across palm taxa, respectively.

TABLE 1. Characterisation of the 10 *E.oleifera* genomic microsatellite loci based on 75 individuals from 4 countries in South America

Locus	Primer pair sequence (5'-3')	Probe Database UID	Ta (°C)	Repeat motif	Size (bp)	A <sub>o</sub>	H <sub>o</sub>	H <sub>e</sub>	P-values
sMo00018	F: TTAATGAGAGAGAGAGGAC R: TGGAGCCATGAGAAAGAGTA	9947963	54	(CT) <sub>14</sub>	242-252	3	0.2778	0.4507	0.0146
sMo00020	F: CCTTCTCCTCCTCCTTTTG R: CCTCCCTCCCTCTCACCAATA	9947964	58	(AG) <sub>15</sub>	182-208	9	0.6338	0.8216	0.0092
sMo00027	F: TTACAGTTGAGGCAGTATGTCAAT R: CTGTAIGTCAAAACCTTCTGCAC	9947965	50	(TC) <sub>14</sub>	184-213	6	0.4533	0.6674	0.0003
sMo00128	F: TAGCTCCAACAGTTGCCTTAT R: GGTCCCGTCTTAIGATTTAFTCT	9947966	56	(AAT) <sub>12</sub>	182-203	6	0.4167	0.7071	0.0001
sMo00129	F: TTAGTATGGGTGTCATAAGTGG R: GCTTCCAGCTCCTCTTCTTACC	9947967	56	(TTC) <sub>13</sub>	212-232	7	0.3378	0.7032	0.0000
sMo00130	F: TAAGCAAAAAGATCAGGCACCTC R: GGCTGGTGAAAATAAGTTTACAAAAG	9947968	56	(AAG) <sub>11</sub>	173-214	11	0.9853	0.8068	1.0000
sMo00132	F: ATAGCCAGAGGGCAAAACTGT R: GCAACACACGGGACTCAAAAATA	9947969	56	(TTA) <sub>13</sub>	159-180	2	0.0685	0.1393	0.1433
sMo00134	F: TCCCAATAGTCGTTACAAACCAG R: GATTAGCAAAAAGGGCAAAAAGG	9947970	56	(ATTA) <sub>6</sub>	252-256	2	0.1944	0.4753	0.0000
sMo00138	F: AGGGTTGTCGCTCCAATTTAT R: GGCATCTTTTGTGACCTGTAGAAG	9947971	56	(TTTTC) <sub>6</sub>	180-194	3	0.1200	0.3588	0.0000
sMo00152	F: GGAACAAGGACAAGAAAGAAA R: TGTATCAAGCCTCAAGTATCTGG	9947972	56	(AC) <sub>6</sub> (AG) <sub>11</sub>	245-256	2	0.2319	0.4999	0.0000

Notes: A<sub>o</sub> - number of alleles detected; H<sub>o</sub> - observed heterozygosity; H<sub>e</sub> - expected heterozygosity

P-values &lt;0.05 indicates significant deviation from Hardy-Weinberg equilibrium



Singh et al. (2008) for the microsatellites developed from the *E. guineensis* expressed sequence tags (ESTs) collections.

#### CONCLUSION

This preliminary study we believe is the first report of SSR markers from *E. oleifera*. The markers will be useful tools for genetic and evolutionary studies in oil palm. The transferability across oil palm species and taxa reveals the suitability of *E. oleifera* genomic SSR markers for comparative genetic studies in the Arecaceae family.

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- Noorhariza Mohd Zaki\*, Rozana Rosli, Ting Ngoot Chin & Rajinder Singh  
Malaysian Palm Oil Board  
6, Persiaran Institusi  
Bandar Baru Bangi  
43000 Kajang, Selangor, Malaysia
- Ismanizan Ismail  
Pusat Pengajian Biosains dan Bioteknologi  
Fakulti Sains dan Teknologi  
Universiti Kebangsaan Malaysia  
43600, Bangi, Selangor, Malaysia
- Institut Biologi Sistem (INBIOSIS)  
Universiti kebangsaan Malaysia  
43600, Bangi, Selangor, Malaysia

\*Corresponding author; email: hariza@mpob.gov.my

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