fedepalma | cenipalma

21ª CONFERENCIA INTERNACIONAL SOBRE PALMA DE ACEITE

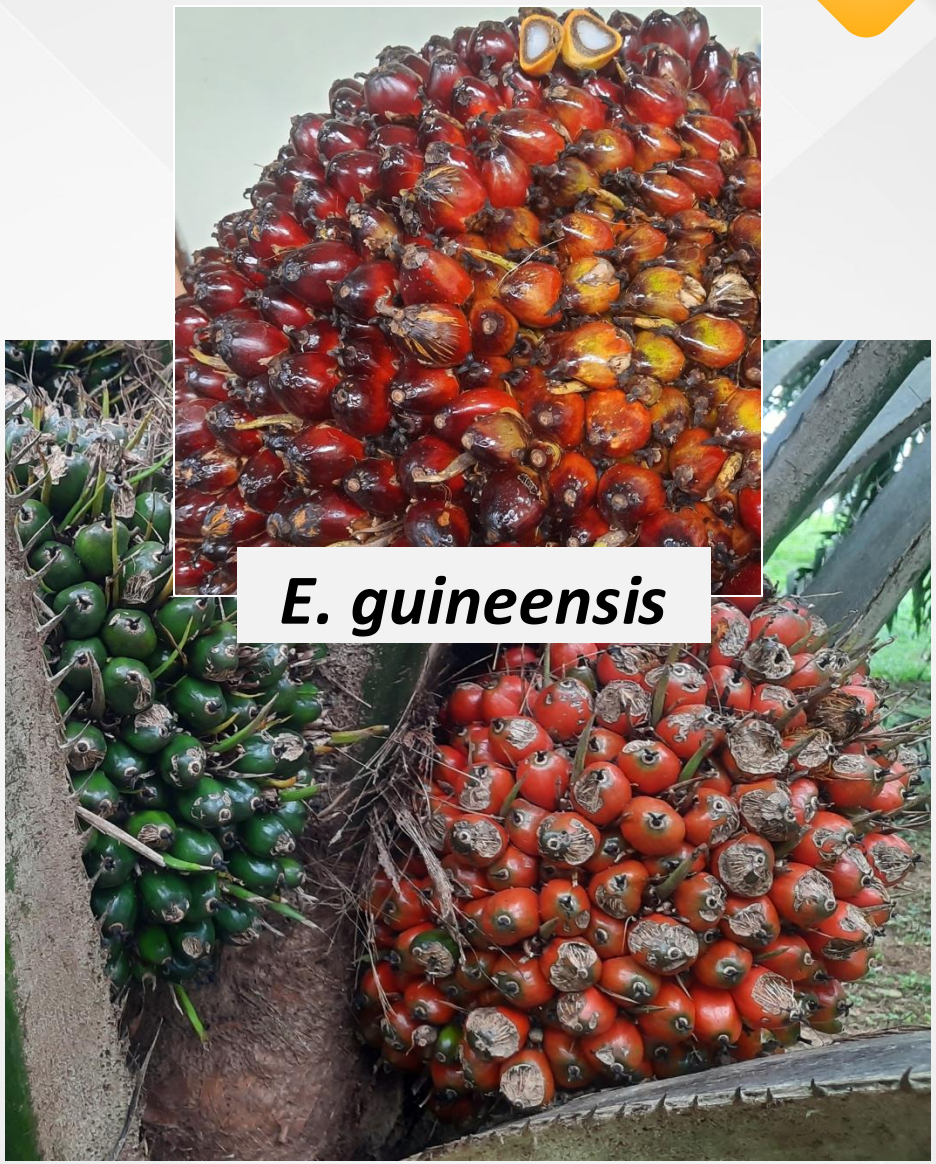
21st International Oil Palm Conference

2025

ACCELERATING THE DEVELOPMENT OF NEW OIL PALM CULTIVARS USING THE GENOMES OF *E. GUINEENSIS* AND *E. OLEIFERA*

MPOB

OIL PALM



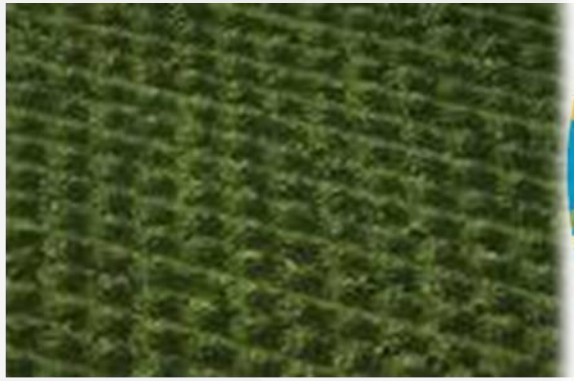
E. guineensis

E. oleifera

Source: https://www.palmpedia.net/wiki/Elaeis_oleifera

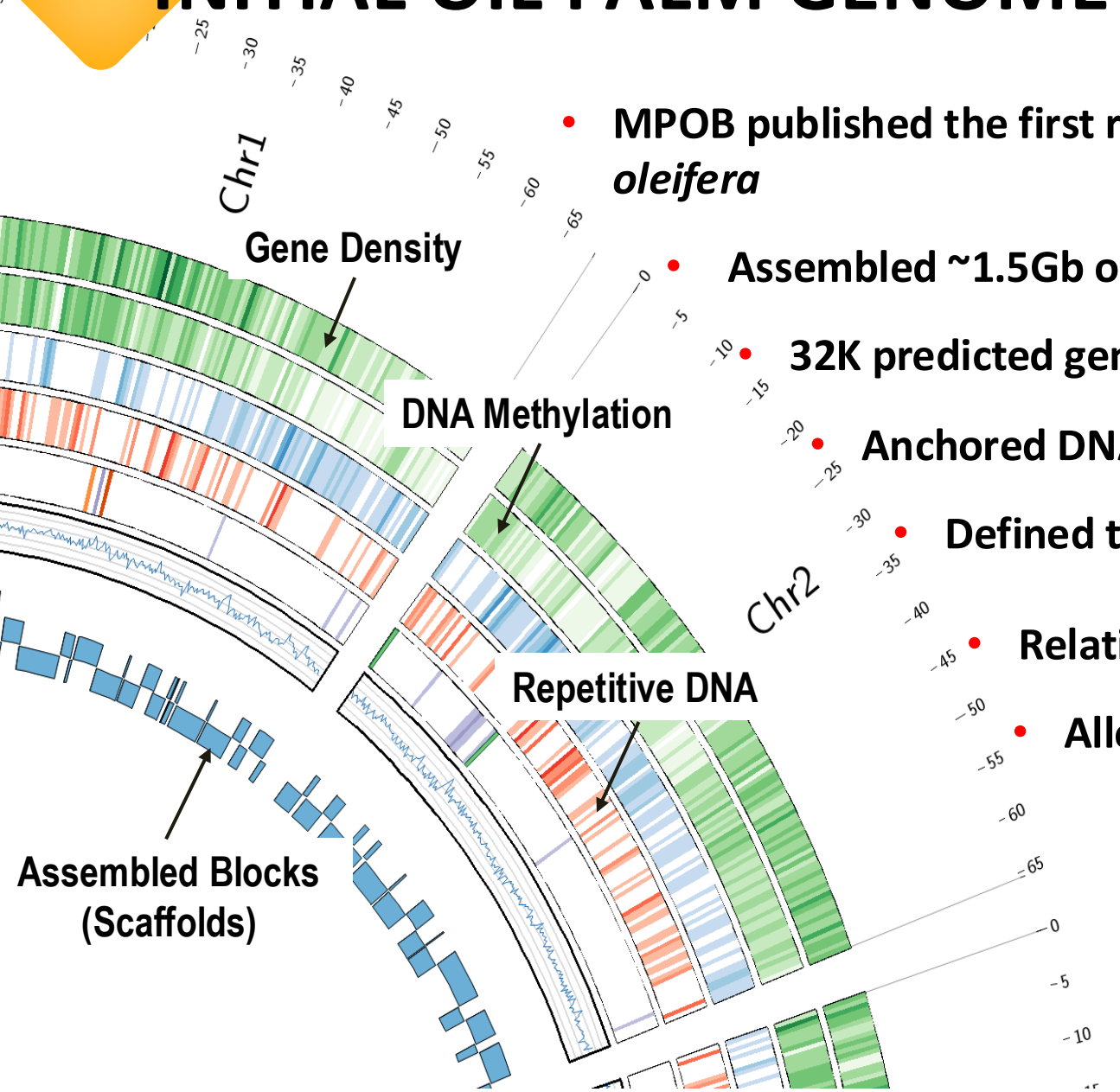
AGRICULTURE GENOMICS - ASSISTS WITH DEVELOPING NEW & IMPROVED CULTIVARS

Agricultural Genomics is the application of genomic tools to improve crops and livestock




INITIAL OIL PALM GENOME BUILDS (2013)



- MPOB published the first reference genomes for *E. guineensis* (*pisifera*) & *E. oleifera*
- Assembled ~1.5Gb of the estimated 1.8Gb *E. guineensis* genome
- 32K predicted genes
- Anchored DNA methylation density map
- Defined the repeat content of the genome
- Relatively fragmented assembly (>40K assembled blocks)
- Allowed for the discovery of the genes responsible for:
  - ✓ Fruit form phenotype (*SHELL*)
  - ✓ Fruit colour (*VIR*)
  - ✓ Mantled somaclonal abnormality (*MANTLED*)

Singh et al. (2013) *Nature* 500(7462):335-339

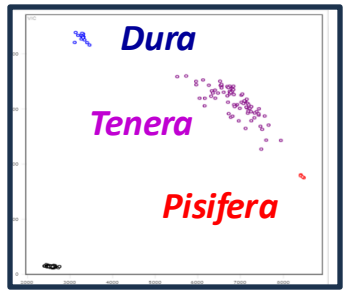
SHELL, VIRESCENS (VIR) and KARMA DNA DIAGNOSTIC ASSAYS

SHELL

MADS-box gene SEEDSTICK

Singh et al. (2013) *Nature*

SureSawit™ *SHELL ASSAY*



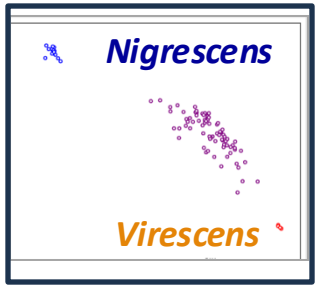
Distinguish ***Tenera*** from ***Dura*** and ***Pisifera*** palms. ***Tenera*** produces **~30% dan ~100% more oil** than ***Dura*** dan ***Pisifera***

VIR

R2R3-MYB Transcription Factor

Singh et al. (2014) *Nat. Comm.*

SureSawit™ *VIR ASSAY*



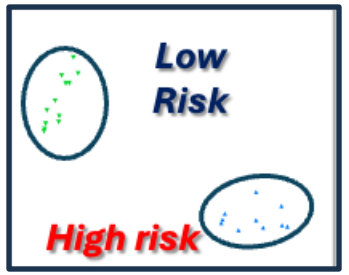
Distinguish **Virescens (VIR)** from **Nigrescens (NIG)** palms. **Virescens** fruits have **very distinct change in colour** during ripening

KARMA

Hypomethylation of KARMA retrotransposon in DEFICIENS

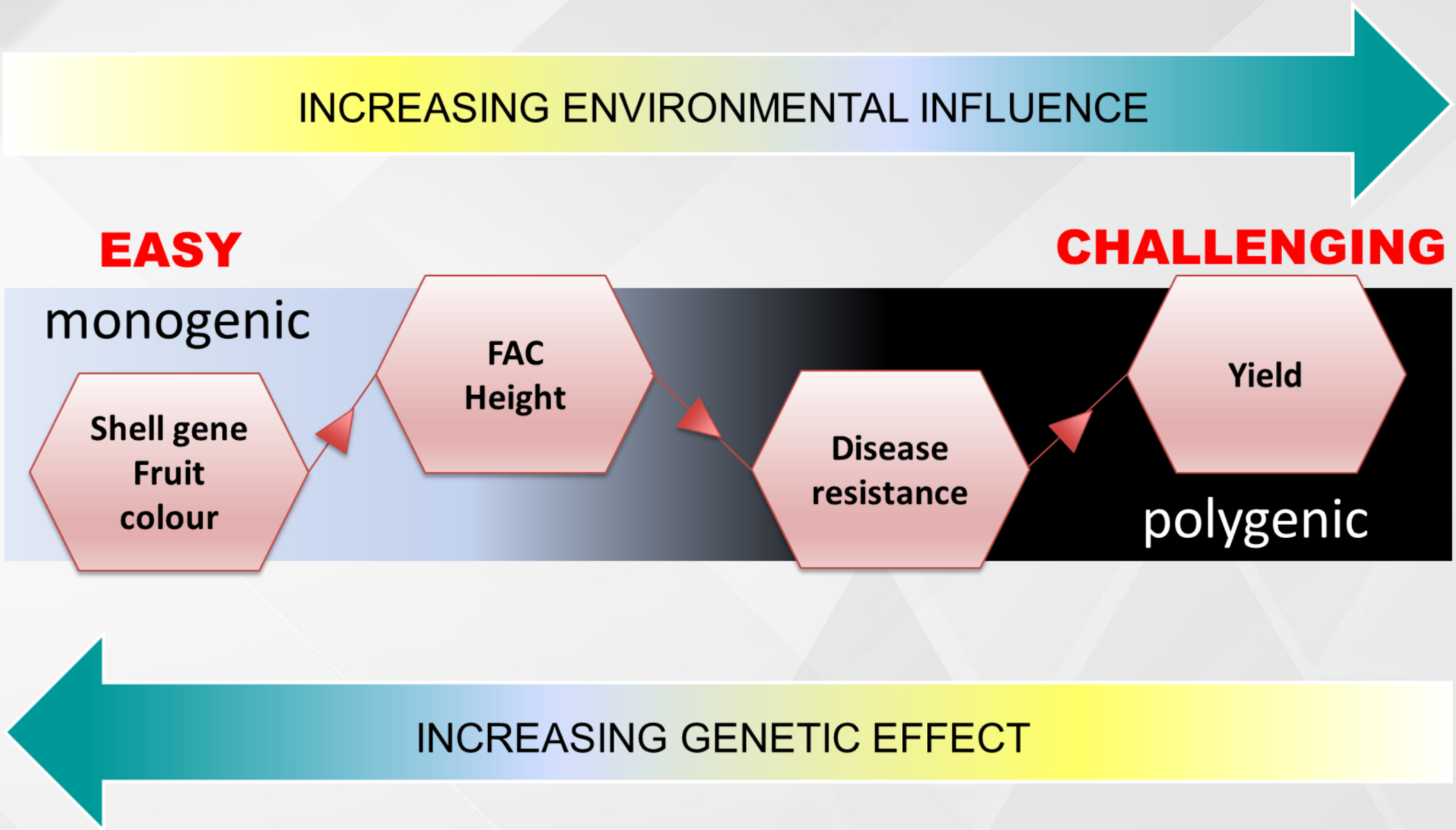
Ong-Abdullah et al. (2015) *Nature*

SureSawit™ *MANTLED ASSAY*



Determine **probability** of palms producing **MANTLED Fruits.** Mantled-free clonal palms have potential to produce **20 - 30% more oil** than seed-derived materials

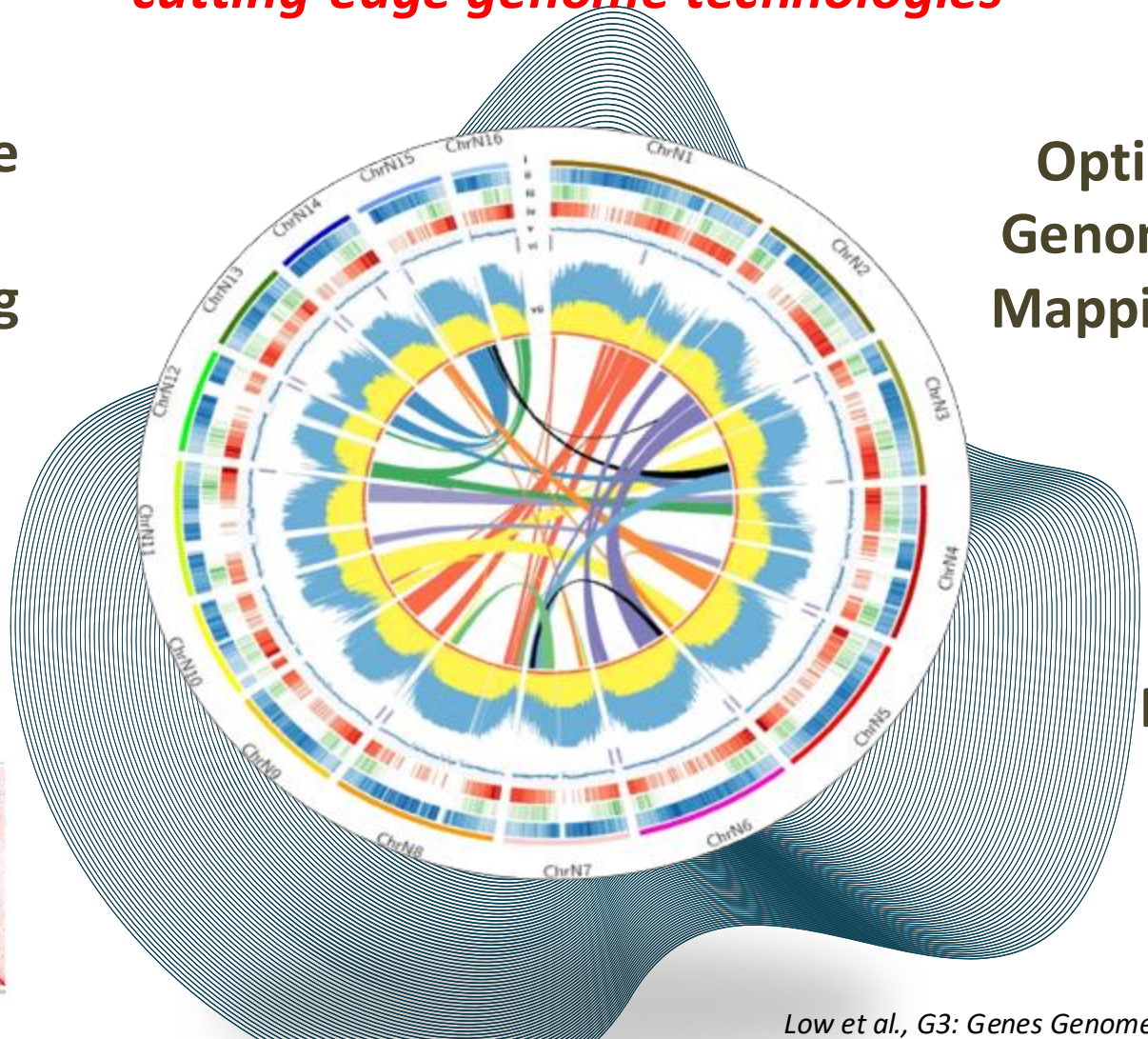
TRAITS OF INTEREST IN OIL PALM



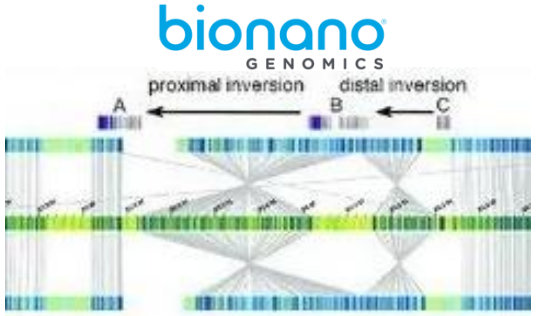
IMPROVING THE OIL PALM GENOME BUILDS

Achieving chromosome-scale assemblies involved the integration of several *cutting-edge genome technologies*

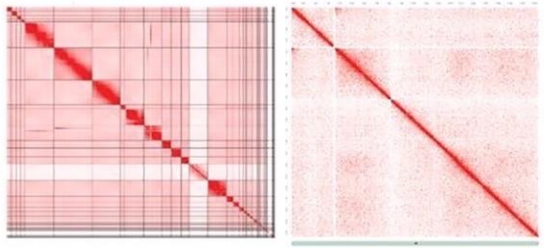
Long Range Genome Sequencing



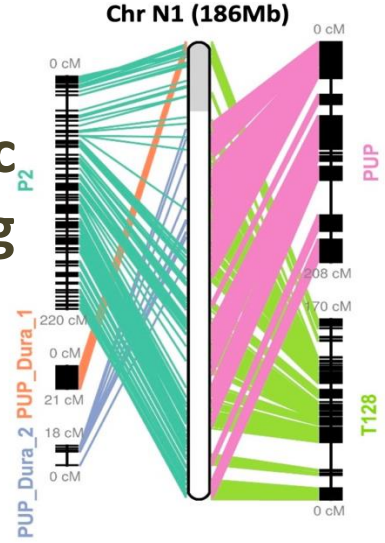
Optical Genome Mapping



Proximity Ligation Sequencing

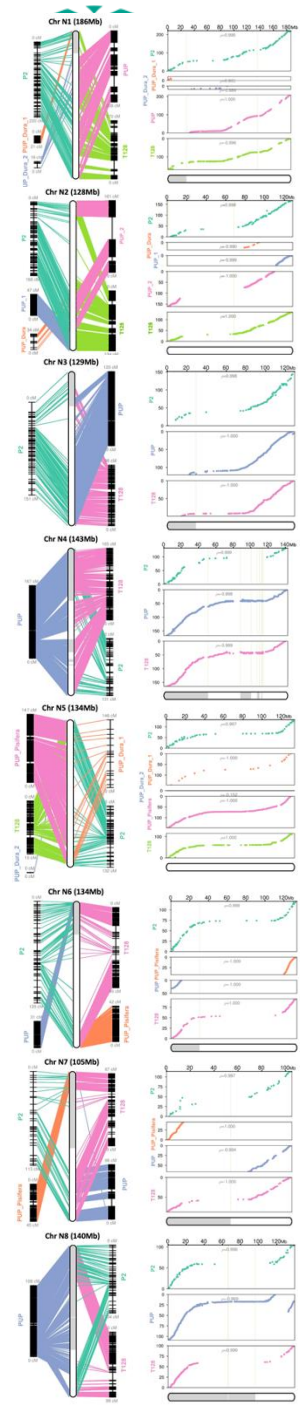


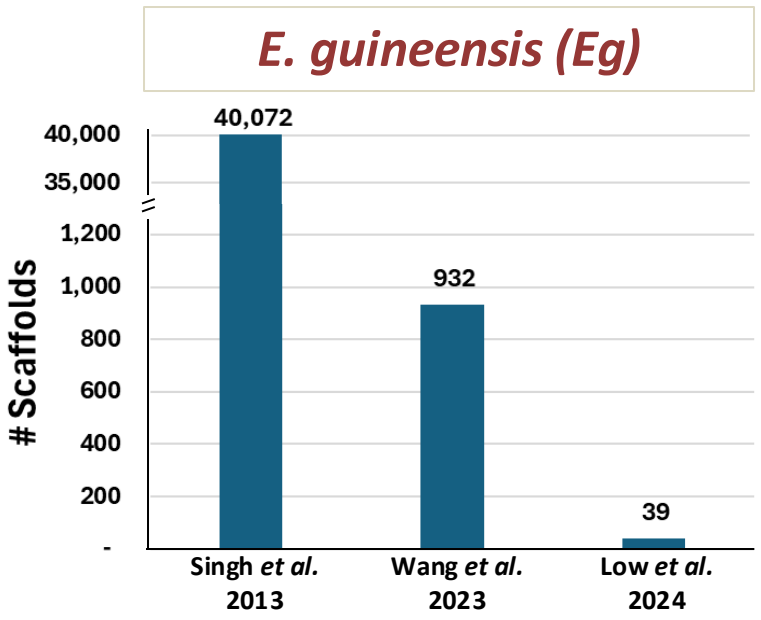
Genetic Mapping

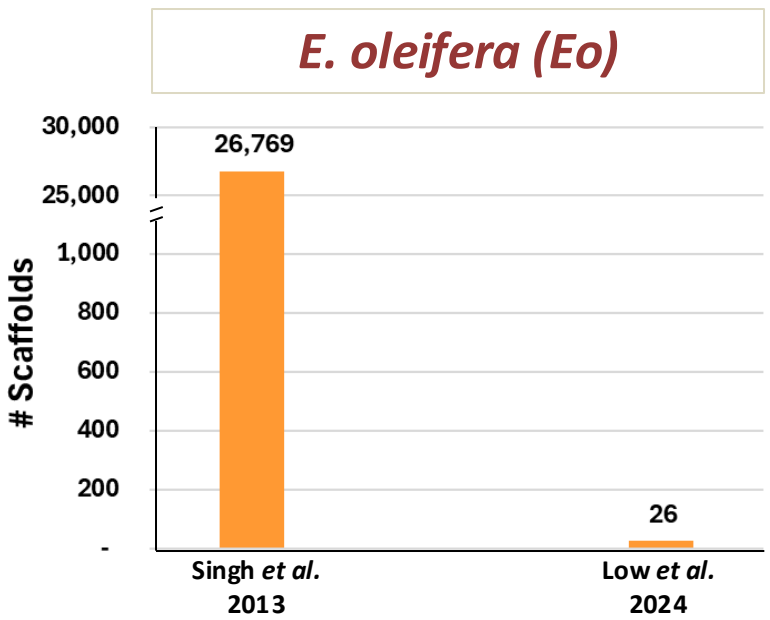


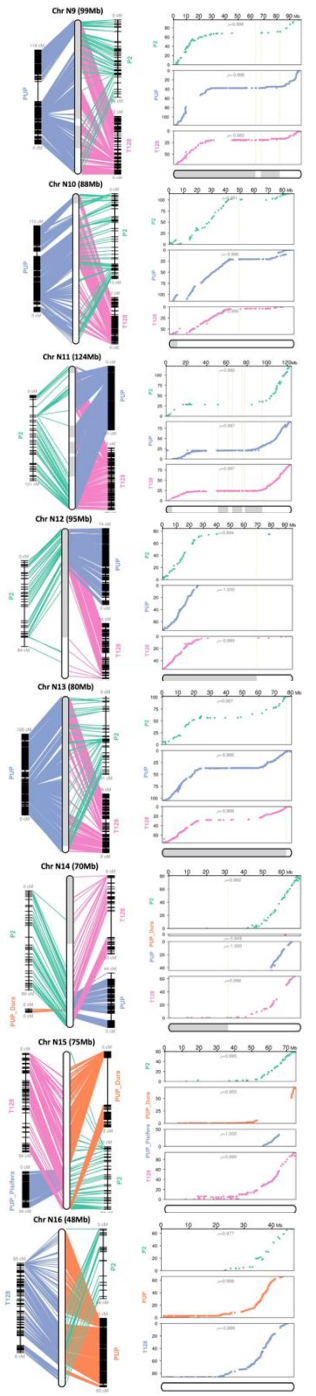
Low et al., G3: Genes Genomes Genetics 2024

OIL PALM GENOME BUILDS (2024 *vs.* 2013)





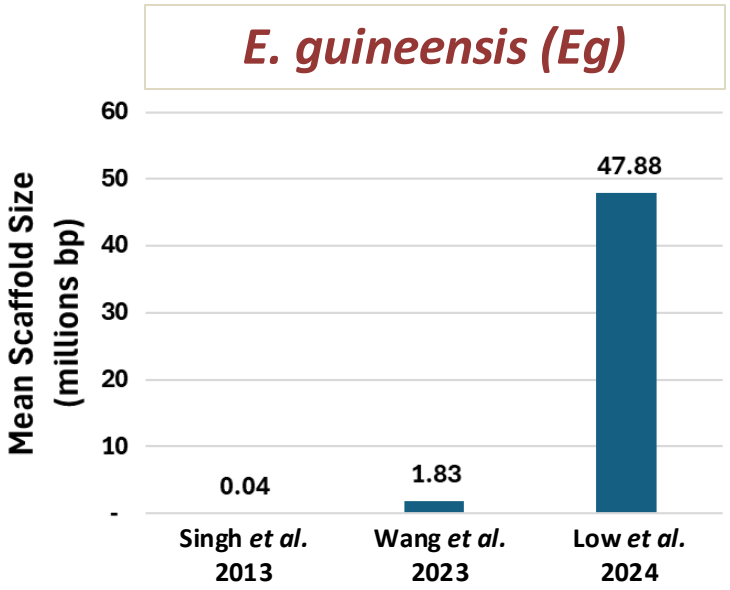


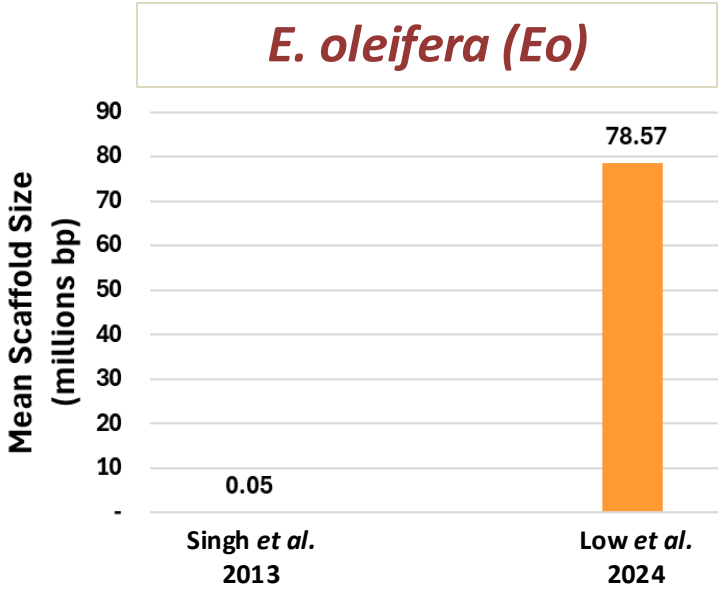


- In 2023, Temasek Life Sciences Laboratory, Singapore published an improved *Eg (dura)* reference genome;
- In 2024, MPOB published the first chromosome-scale reference genomes for both *Eg (pisifera)* and *Eo* (Low *et al.* 2024);
- ***1000-fold*** decrease in number of *Eg* and *Eo* assembled genome blocks

Low et al., G3: Genes Genomes Genetics 2024

OIL PALM GENOME BUILDS (2024 *vs.* 2013)





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Low et al., G3: Genes Genomes Genetics 2024

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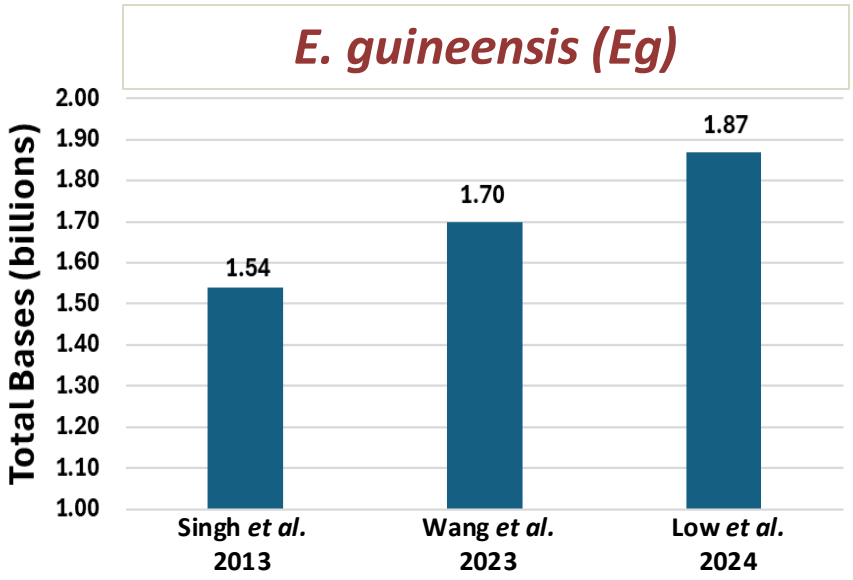

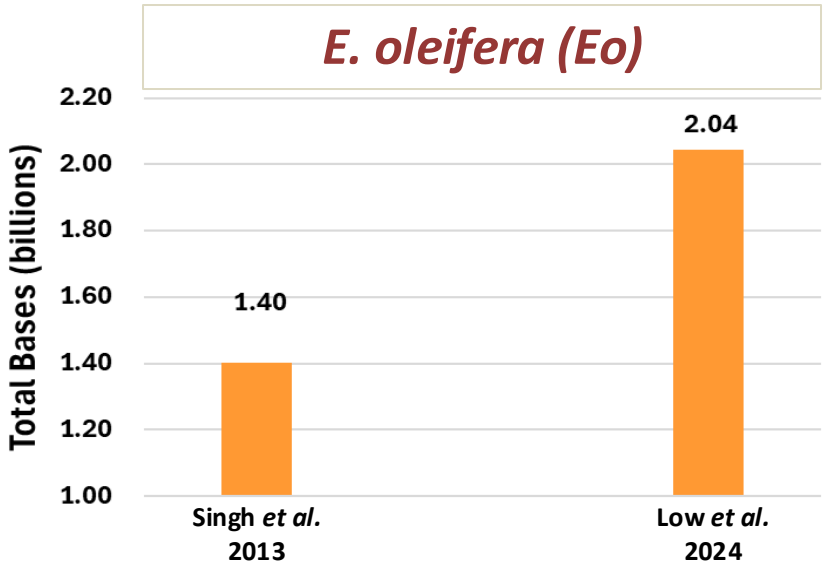

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- *1000-fold* increase in the size of *Eg* assembled blocks (*1500-fold* increase for *Eo*);
- ***330 million bp*** **added to the *Eg* genome assembly (*640 million bp* for *Eo*)**

Low et al., G3: Genes Genomes Genetics 2024

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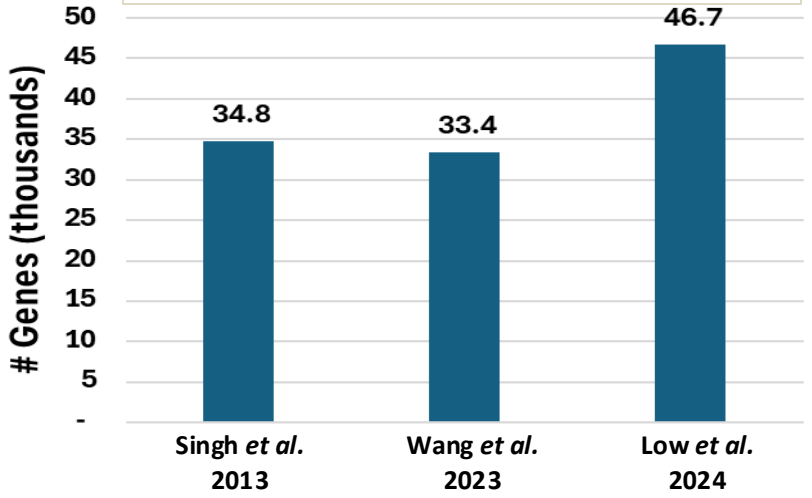

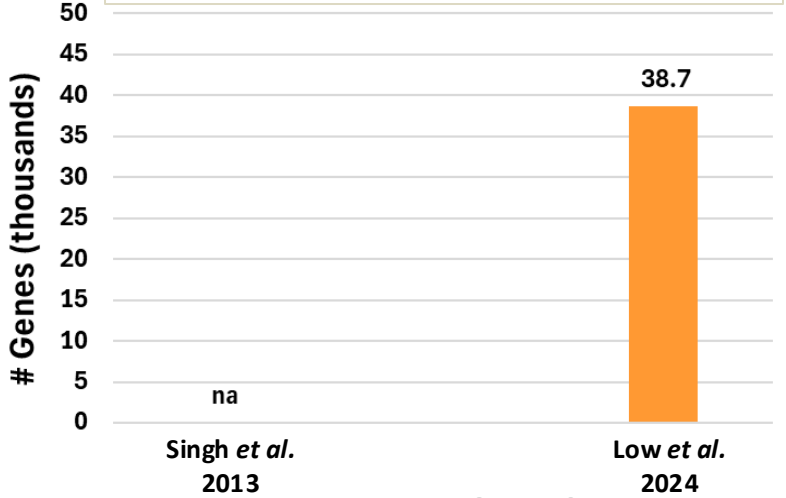

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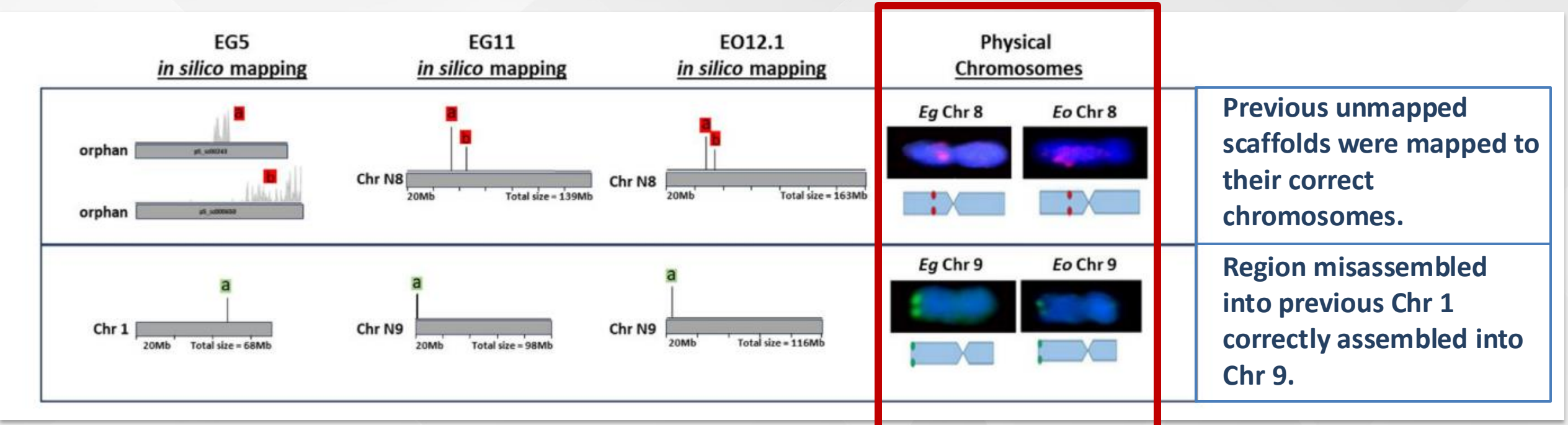
- *1000-fold* increase in the size of *Eg* assembled blocks (*1500-fold* increase for *Eo*);
- *330 million base pairs* added to the *Eg* genome assembly (*640 million base pairs* for *Eo*);
- ***11,895 additional genes*** **modeled in the *Eg* genome assembly (*38,658 genes*** **modeled for *Eo*)**
- ***Provided substantial improvements to the continuity, completeness and content of the reference genomes. The 16 oil palm pseudo-chromoses are established.***

Low et al., G3: Genes Genomes Genetics 2024

IMPROVEMENTS: CORRECTION OF MISASSEMBLIES

- **Improved assembly also led to additional corrections**



Low et al., G3: Genes Genomes Genetics 2024

NEW CHROMOSOME-SCALE GENOME ASSEMBLIES (2024)

OXFORD G3 Genes | Genomes | Genetics

G3, 2024, jkae135
https://doi.org/10.1093/g3journal/jkae135
Advance Access Publication Date: 26 June 2024
Genome Report

Chromosome-scale *Elaeis guineensis* and *E. oleifera* assemblies: comparative genomics of oil palm and other Arecaceae

Eng-Ti Leslie Low,[1] Kuang-Lim Chan,[1] Noorhariza Mohd Zaki,[1] Elizaveta Taranenko,[2] Jared M. Ordway,[2] Corey Wachmeyer,[2] Jaap Buntjer,[3] Mohd Amin Ab Halim,[1] Nik Shazana Nik Mohd Sanusi,[1] Jayanthi Nagappan,[1] Rozana Rosli,[1] Eugeniya Bondar,[2] Nadzirah Amiruddin,[1] Norashikin Sarpan,[1] Ngoot-Chin Ting,[1] Pek-Lan Chan,[1] Meilina Ong-Abdullah,[1] Marhalil Marjuni,[1] Suzana Mustaffa,[1] Norzlha Abdullah,[1] Norazah Azizi,[1] Blaire Bacher,[3] Nathan Lakey,[3] Tatiana V. Tatarinova,[2] Mohamad Arif Abd Manaf,[1] Ravigadevi Sambanthamurti,[1] Rajinder Singh[1,*]

[1]Advanced Biotechnology and Breeding Centre, Malaysian Palm Oil Board, 6 Persiaran Institusi, Bandar Baru Bangi, 43000 Kajang, Selangor, Malaysia
[2]Biology Department, University of La Verne, La Verne, CA 91750, USA
[3]Orion Genomics, 3730 Foundry Way, St. Louis, MO 63110, USA

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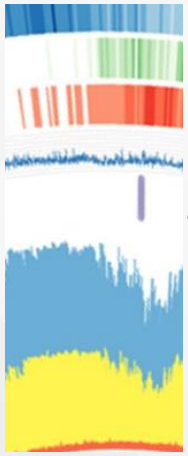
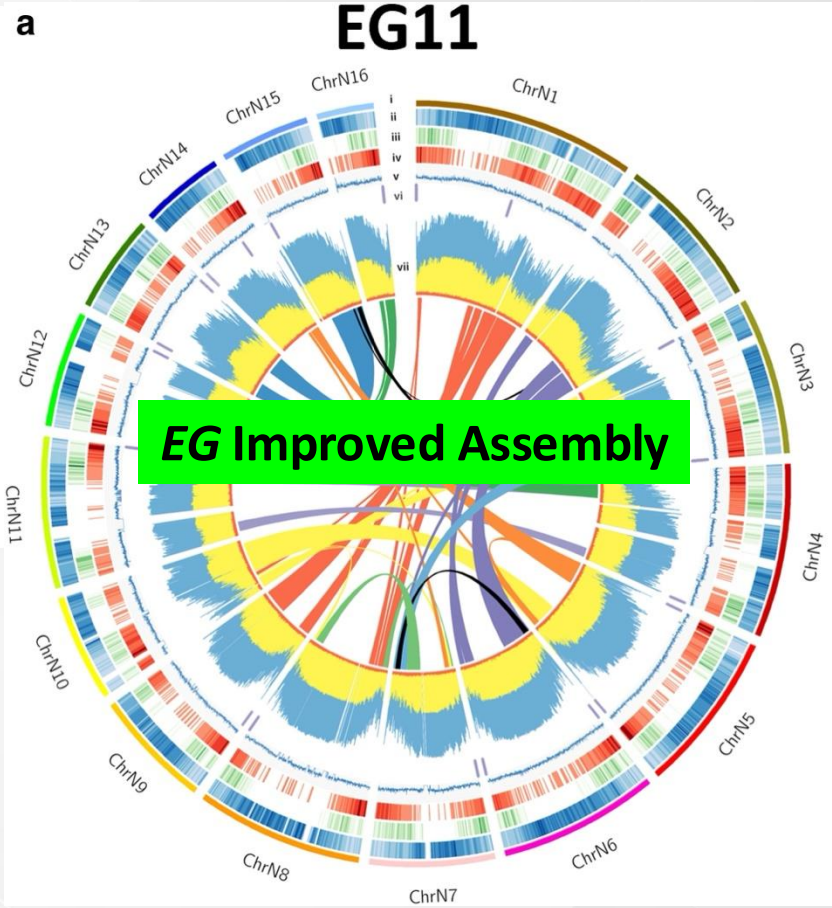
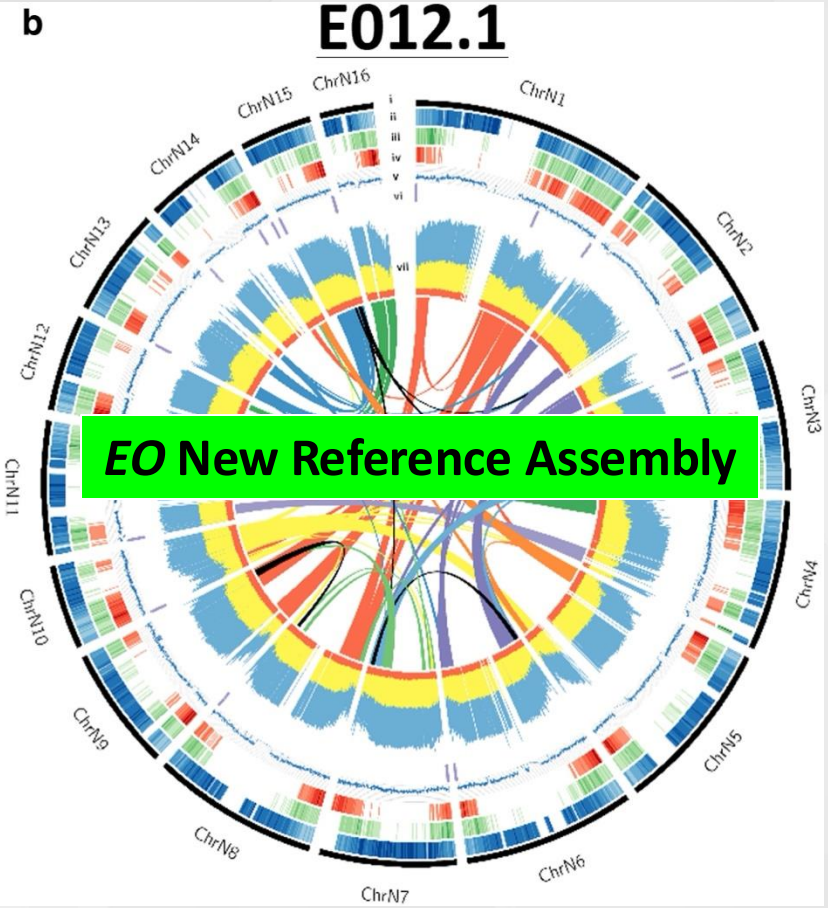
Elaeis guineensis and *E. oleifera* are the two species of oil palm. *E. guineensis* is the most widely cultivated commercial species, and introgression of desirable traits from *E. oleifera* is ongoing. We report an improved *E. guineensis* genome assembly with substantially increased continuity and completeness, as well as the first chromosome-scale *E. oleifera* genome assembly. Each assembly was obtained by integration of long-read sequencing, proximity ligation sequencing, optical mapping, and genetic mapping. High interspecific genome conservation is observed between the two species. The study provides the most extensive gene annotation to date, including 46,697 *E. guineensis* and 38,658 *E. oleifera* gene predictions. Analyses of repetitive element families further resolve the DNA repeat architecture of both genomes. Comparative genomic analyses identified experimentally validated small structural variants between the oil palm species and resolved the mechanism of chromosomal fusions responsible for the evolutionary descending dysploidy from 18 to 16 chromosomes.



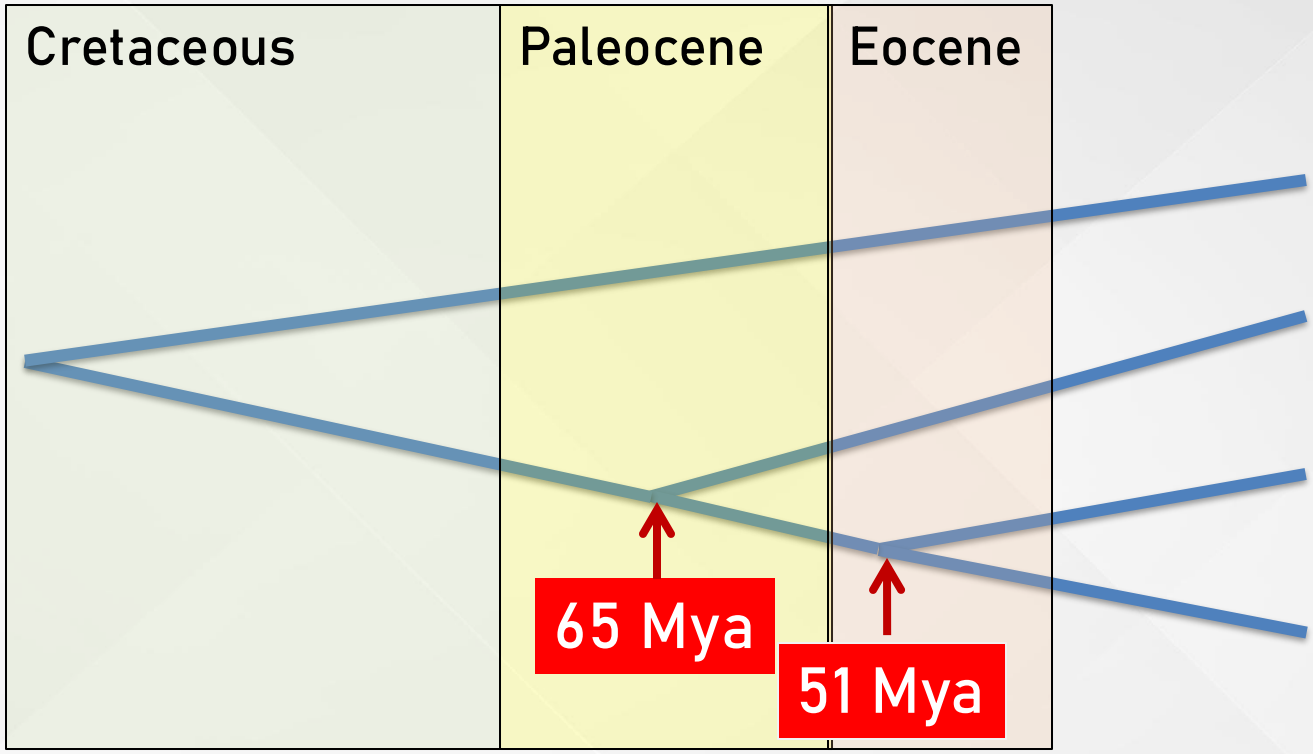
Type I retrotransposons
Type II DNA repeats
Gene Density
G + C content
Telomeric repeats
CG DNA methylation
CHG DNA methylation
CHH DNA methylation





Low et al., G3: Genes Genomes Genetics 2024

DIVERGENCE OF PALMS FROM OTHER MONOCOTS



Banana

Date Palm

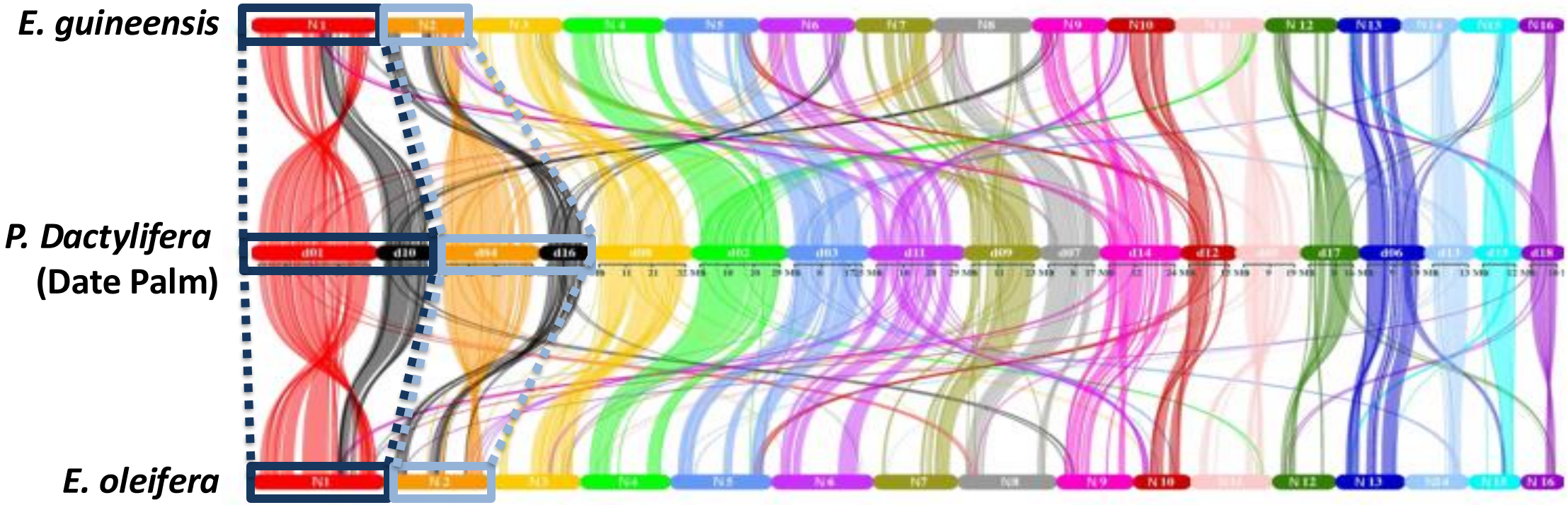
African Oil Palm

American Oil Palm

Singh et AL., 2013, Nature
Low et al., G3: Genes Genomes Genetics 2024

DESCENDING DYSPLOIDY IN OIL PALM EVOLUTION

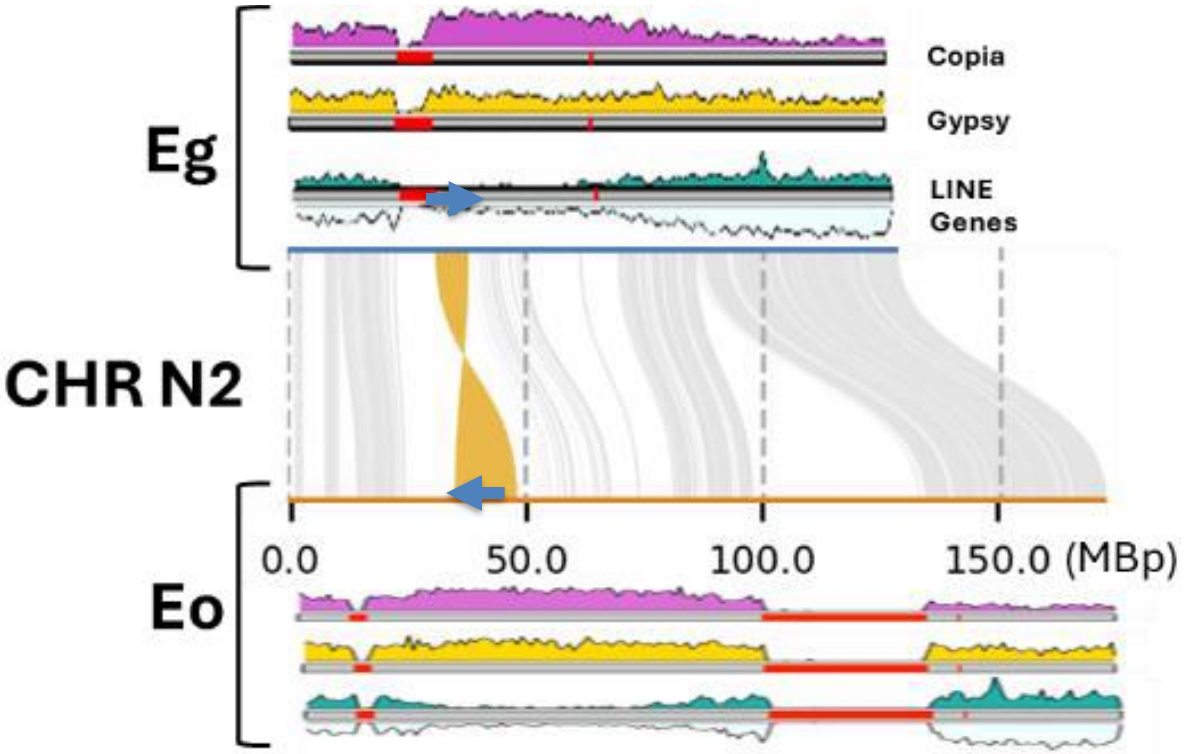
- Mostly pairwise syntenic relationships between oil palm (16 chrs) and date palm (18 chrs) chromosomes;
- Oil palm Chr 1 arose from end-to-end fusion of date palm Chrs 1 & 10, followed by additional rearrangement;
- Oil palm Chr 2 arose from end-to-end fusion of date palm Chrs 4 & 16, followed by additional rearrangement;
- Explains the descending dysploidy from 18 to 16 chrs, occurring after divergence of data palm and oil palm ~65 million years ago, but before divergence of *E. guineensis* and *E. oleifera* ~50 million years ago.



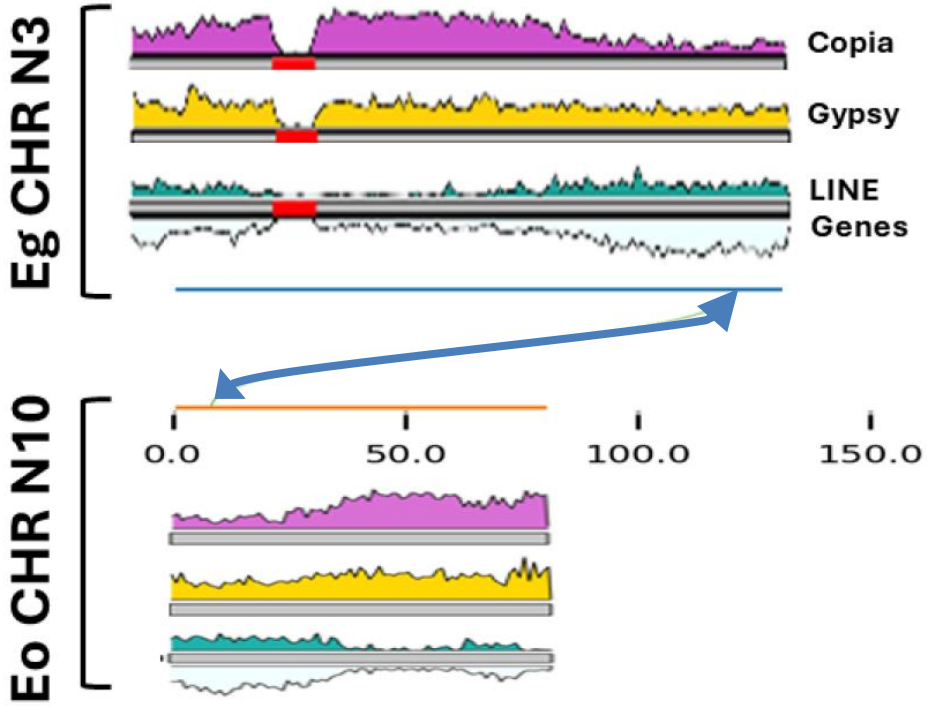
Low et al., G3: Genes Genomes Genetics 2024

STRUCTURAL VARIANTS BETWEEN TWO OIL PALM SPECIES

Inversions in one species relative to the other species



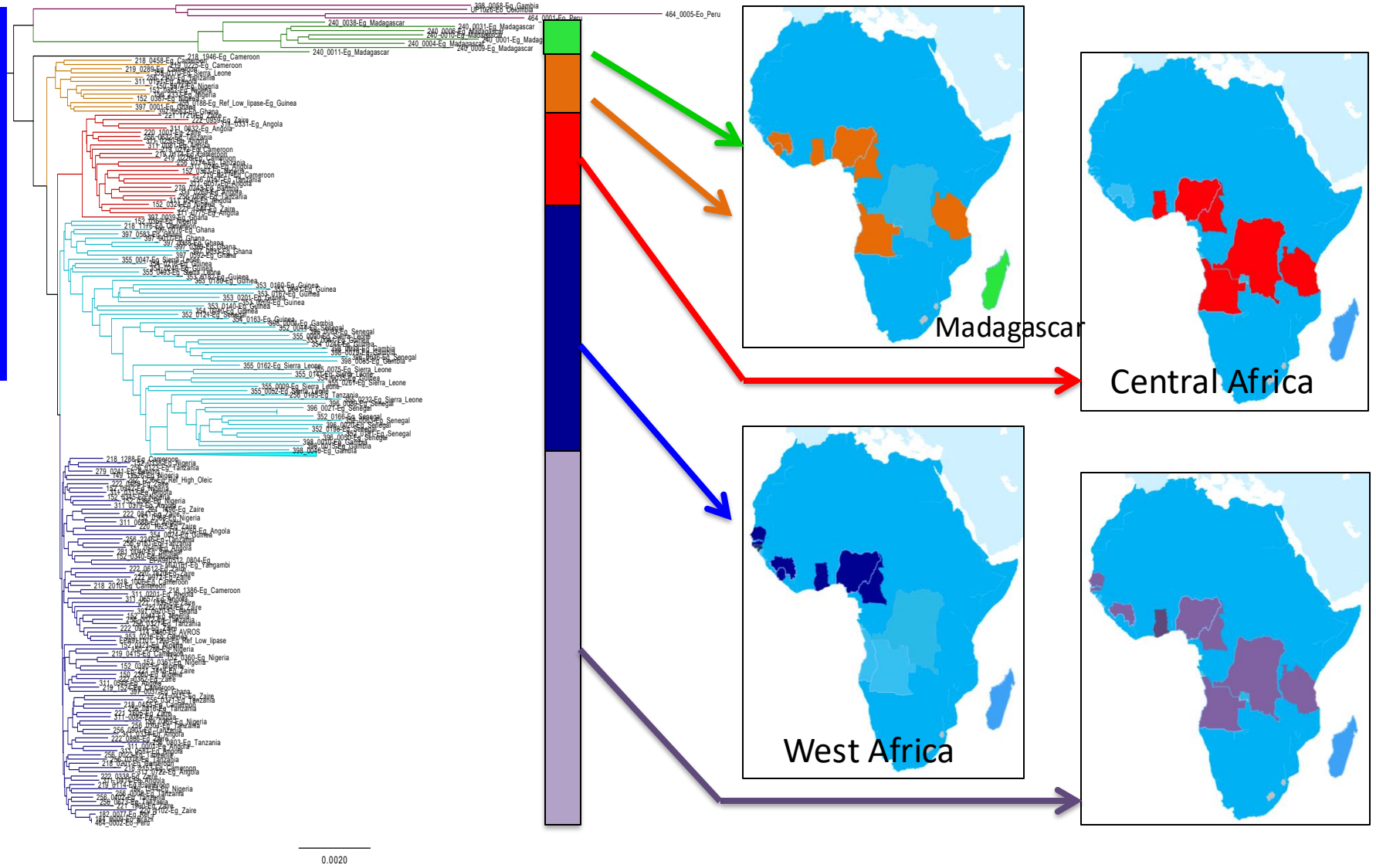
Translocations from one chromosome in one species to a different chromosome in the other species



Low et al., G3: Genes Genomes Genetics 2024

RE-SEQUENCED >300 OIL PALM GERMPLASM SAMPLES

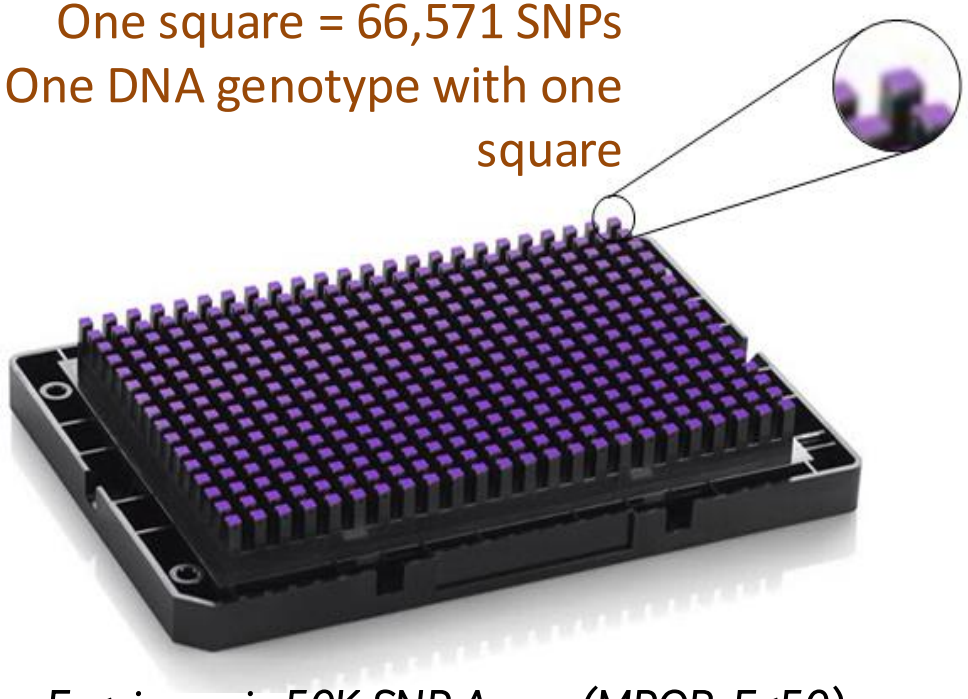
>300 *E. guineensis*, *E. oleifera* germplasm & advanced breeding lines sequenced & mined for SNPs



OIL PALM COMMUNITY ARRAY (MPOB-Eg50)

- MPOB-Eg50 is the first high-throughput optimized genotyping platform for *E. guineensis*, that is made available to oil palm scientific researchers in Malaysia as a community array.
- MPOB consolidate all samples to get a better price using the Axiom platform.

One square = 66,571 SNPs
One DNA genotype with one square



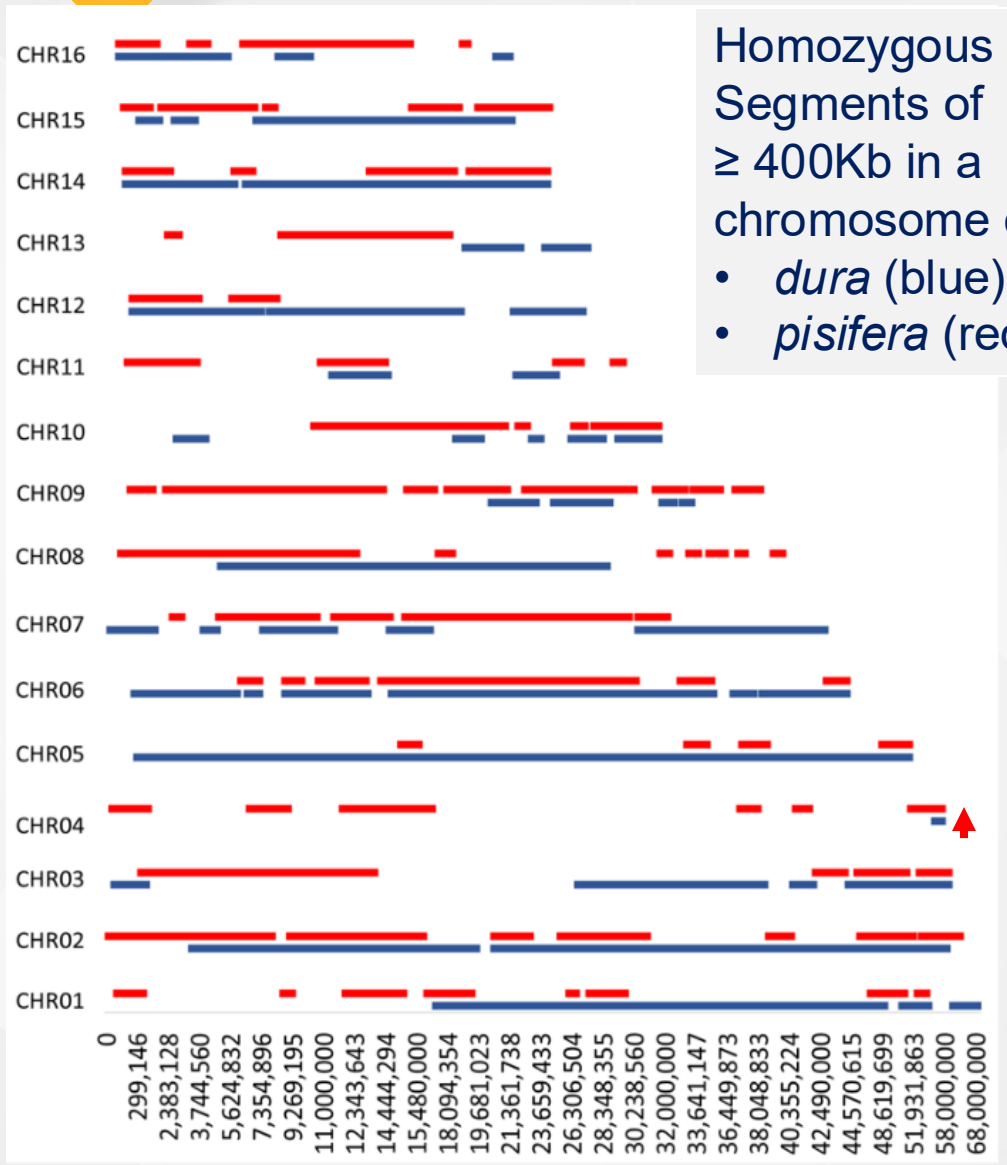
E. guineensis 50K SNP Array (MPOB-Eg50)

LAUNCHED DURING MPOB TRANSFER OF TECHNOLOGY (TOT) SEMINAR 19 JUNE 2025

APPLICATION OF MPOBEg50 SNP ARRAY

Detection of Inbreeding, Aneuploids & Polyploids

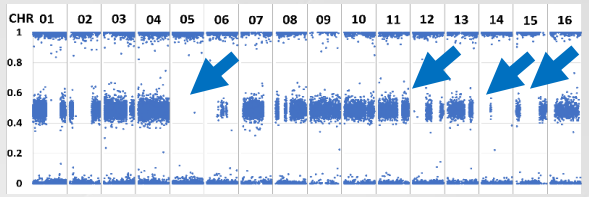
IMPACT OF IN-BREEDING MORE SEVERE NOW?



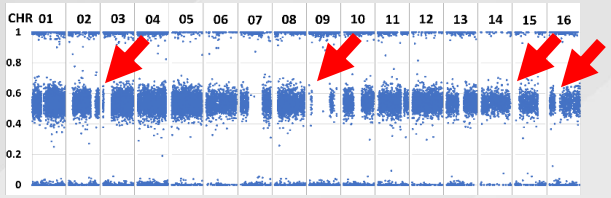
Homozygous Segments of ≥ 400Kb in a chromosome of

- *dura* (blue)
- *pisifera* (red)

Dura



Pisifera



*The Planter, Kuala Lumpur, **99** (1164): 157-170 (2023)*
DOI : https://doi.org/10.56333/tp.2023.017

Inbreeding Depression in IOI Deli *Dura* Inbred Population

MATHEWS J, NG S K, CHEW T D
IOI Research Centre, 2 km Gemencheh Batang Melaka Road, 73200 Gemencheh, Negri Sembilan Darul Khusus, Malaysia

AND

KUA K W AND GOH H L
Pamol Research Station, 8½ Miles Jalan Mersing, 86007 Kluang, Johore Darul Takzim, Malaysia

- **I**ncrease in rudimentary anther;
- **I**ncrease in bending of fronds;
- **D**ecrease FFB & BWT

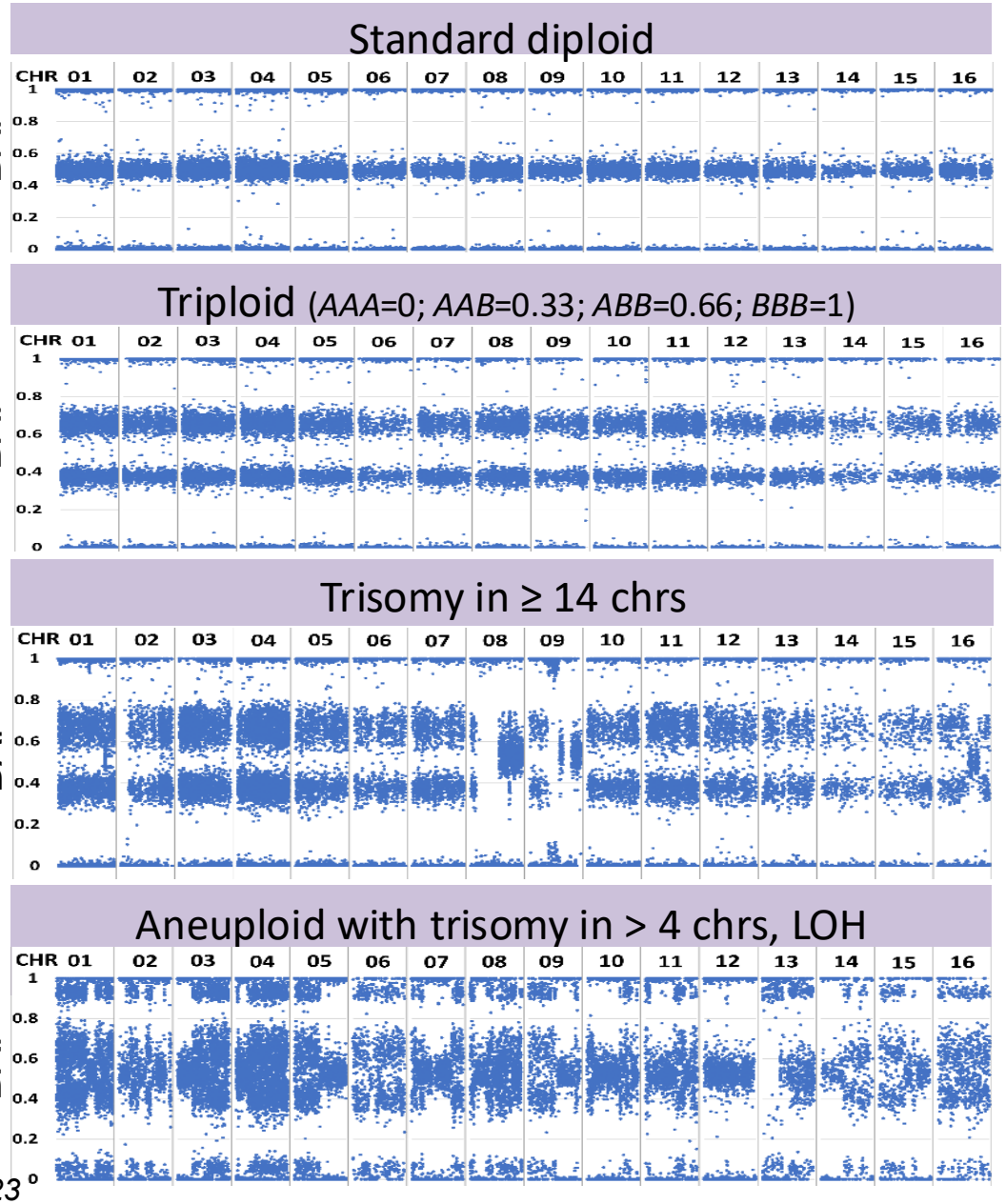
Ting et al., Scient. Horti. 2023

EXAMPLES OF CHROMOSOMAL ABERRATIONS IDENTIFIED

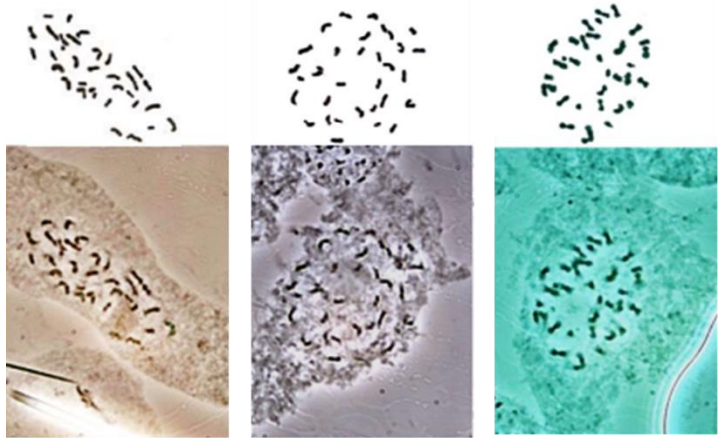
Normal (2N)

Triploid (3N)

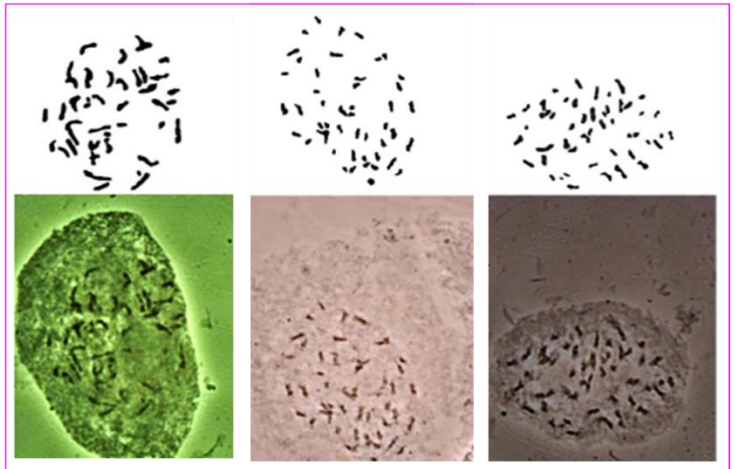
Aneuploid (2+3N)



Triploid and triploid aberrant palms confirmed via flow cytometry and chromosome counts



Dura (32) *Pisifera* (32) diploid palm (32)



694A (48) 696A (48) 678A (46 – 48)

Ting et al., Scient. Horti. 2023

APPLICATION OF GENOME INFORMATION

Widening the genetic base and improving complex traits

BREEDING STRATEGY FOR IMPROVING YIELD

Germplasm collection

Phenotypic evaluation
Genetic characterization
Marker-trait association

Introgress → Broaden the genetic base

Advanced breeding materials

Deli *dura* **AVROS *pisifera***

Improved *E. guineensis* lines	*E. oleifera*, hybrid & backcross
	

Molecular breeding

MARKER-ASSISTED SELECTION (MAS)

GENOMIC SELECTION (GS)

DEVELOPING PALMS WITH LOW HEIGHT INCREMENT & HIGH YIELD

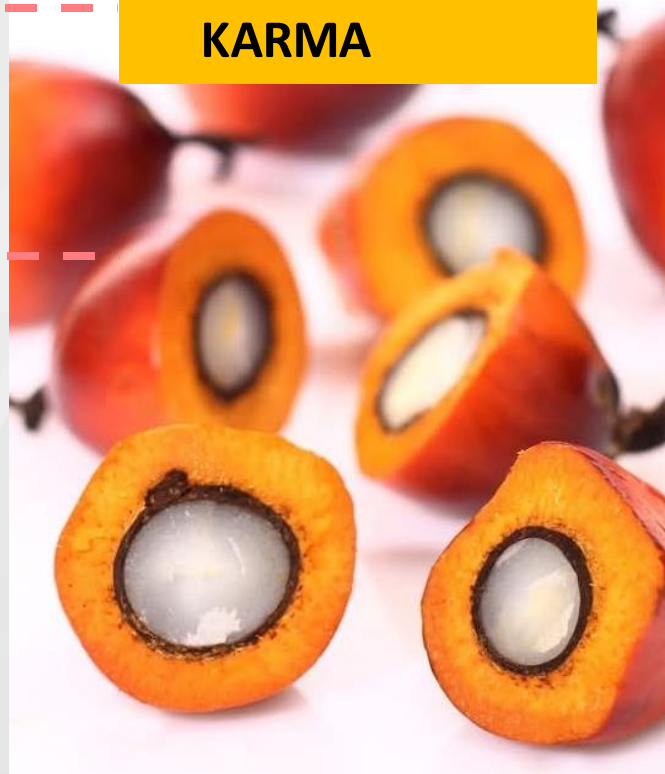
DELI *DURA*
Oil yield >5t/ha/yr
Height 45-75cm/yr

POP12 *PISIFERA*
DWARF

PS1.1 planting materials

- ✓ Oil yield 8 t/ha/yr
- ✓ Oil-to-bunch ratio 30%
- ✓ Height <30cm/yr

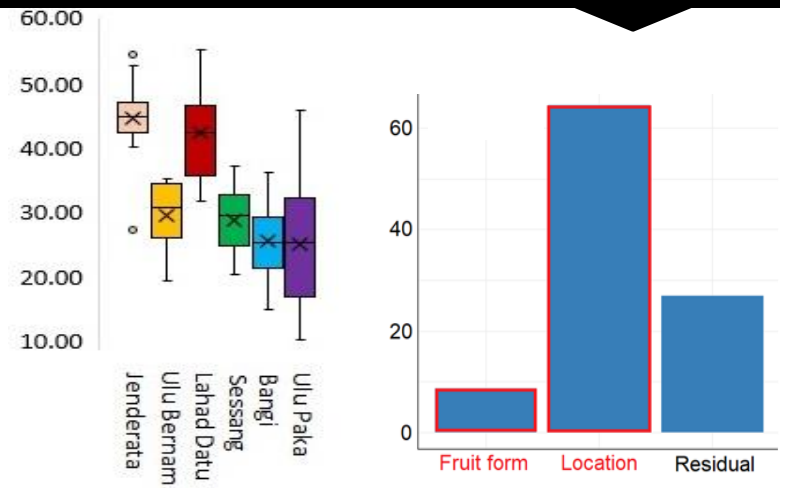
- ➢ **CLONE THE BEST PERFORMING PS 1.1 PALMS**
- ➢ **QC USING SURESAWIT™ KARMA**



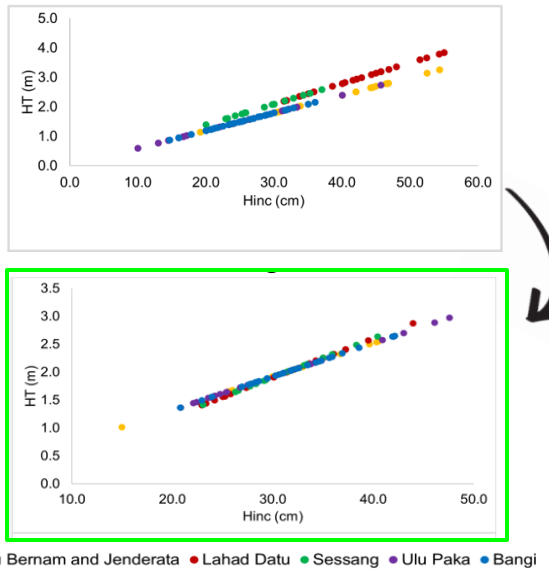
GENOMIC LOCI ASSOCIATED WITH HEIGHT- NIGERIAN BREEDING POPULATIONS

Phenotype data

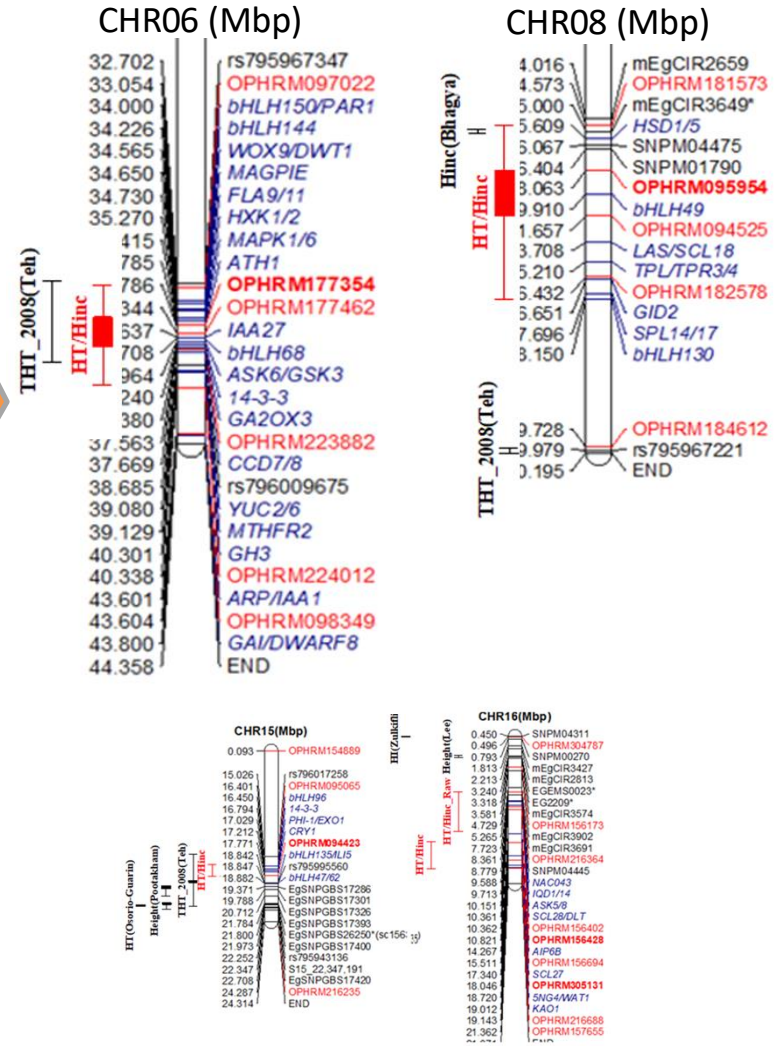
Hinc variance related to planting location (65%)



Normalization

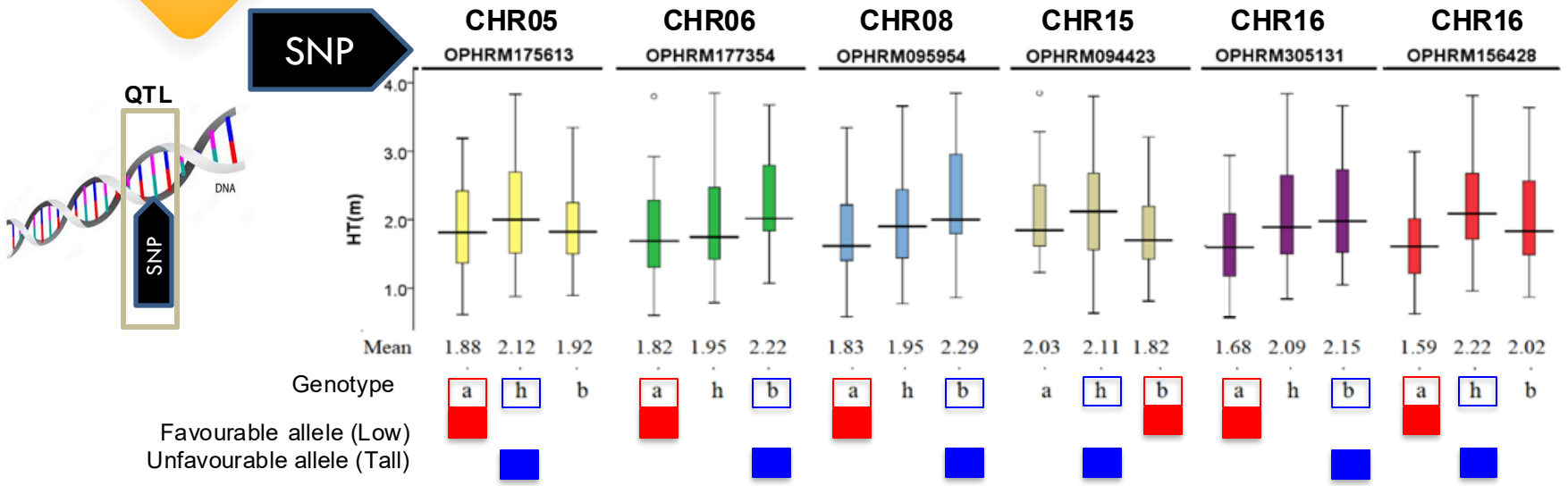


QTLs associated with height traits

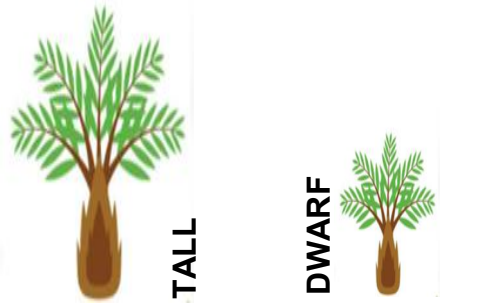


Ting et al., Physiology & Molecular Biology of Plants 2023

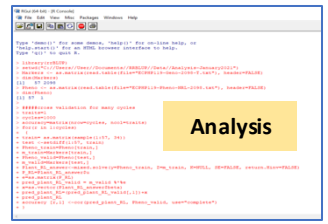
SNP LINKED QTLS ASSOCIATED WITH HEIGHT

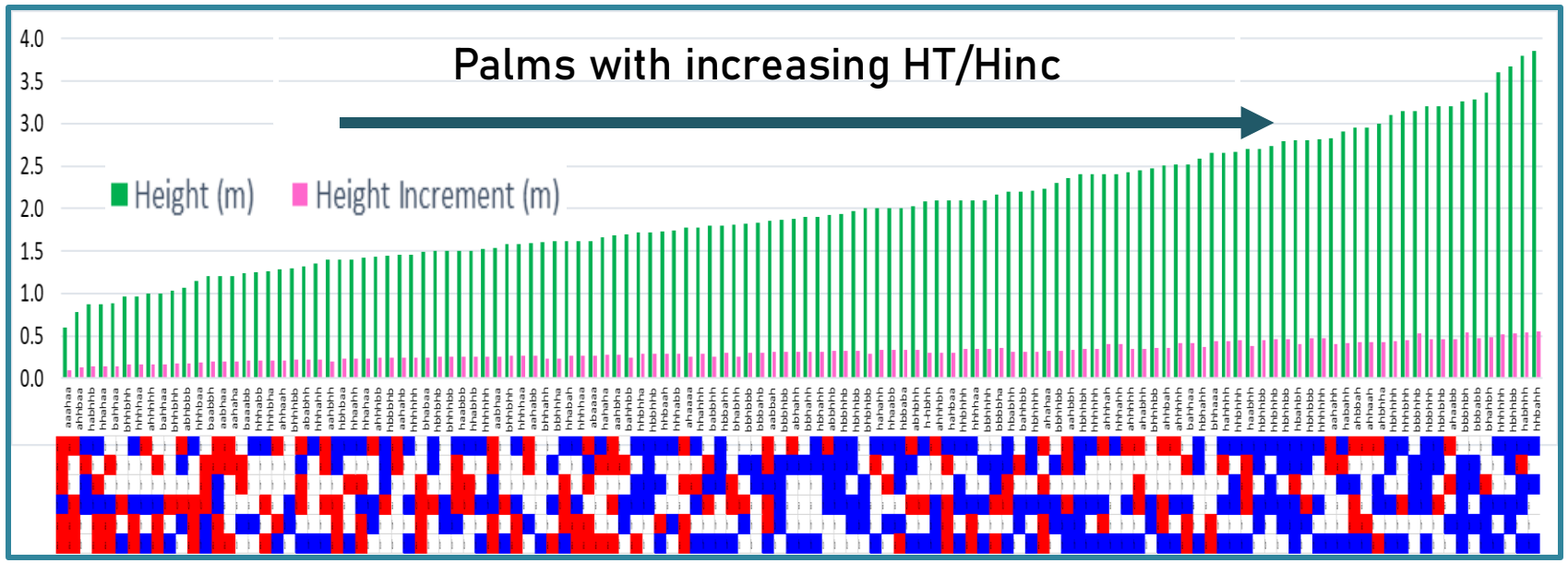


Genomic Selection



Nigerian families genotyped with SNP array





Prediction accuracies

Models	Htinc (mean ± s.e.)	RL (mean ± s.e.)
RR-BLUP	0.768±0.002	0.447±0.006
Machine Learning (Random Forest)	0.729 ± 0.005	0.447 ± 0.008
Machine Learning (Support Vector Machine)	0.765 ± 0.004	0.453 ± 0.008
Machine Learning (XGBoost)	0.751 ± 0.005	0.443 ± 0.008

Ting et al., Physiology & Molecular Biology of Plants 2023

INTERSPECIFIC HYBRID BREEDING

E. guineensis

- High yield
- Semi-saturated (50/50)

E. oleifera

- Poor yield
- Highly unsaturated
- Low height

E. oleifera x *E. guineensis*

Targets:

- High IV (>72)
- High oleic acid (C18:1>60%)
- Low palmitic acid (C16:0<25%)
- Low height increment (<30cm/year)

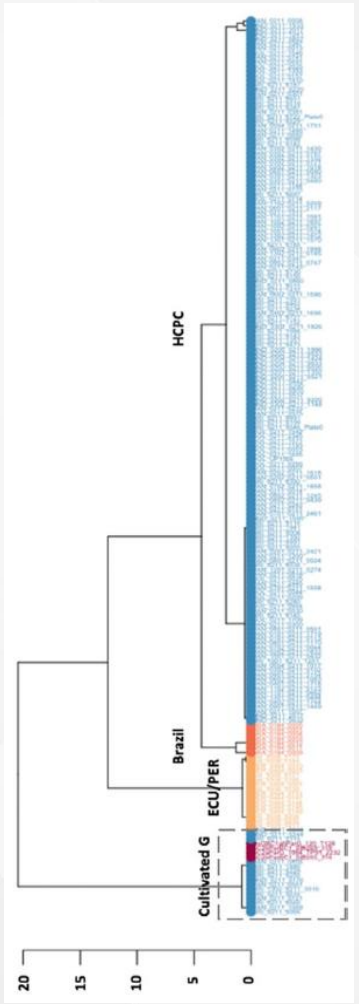
MPOB *E. OLEIFERA* GERMPLASM COLLECTIONS

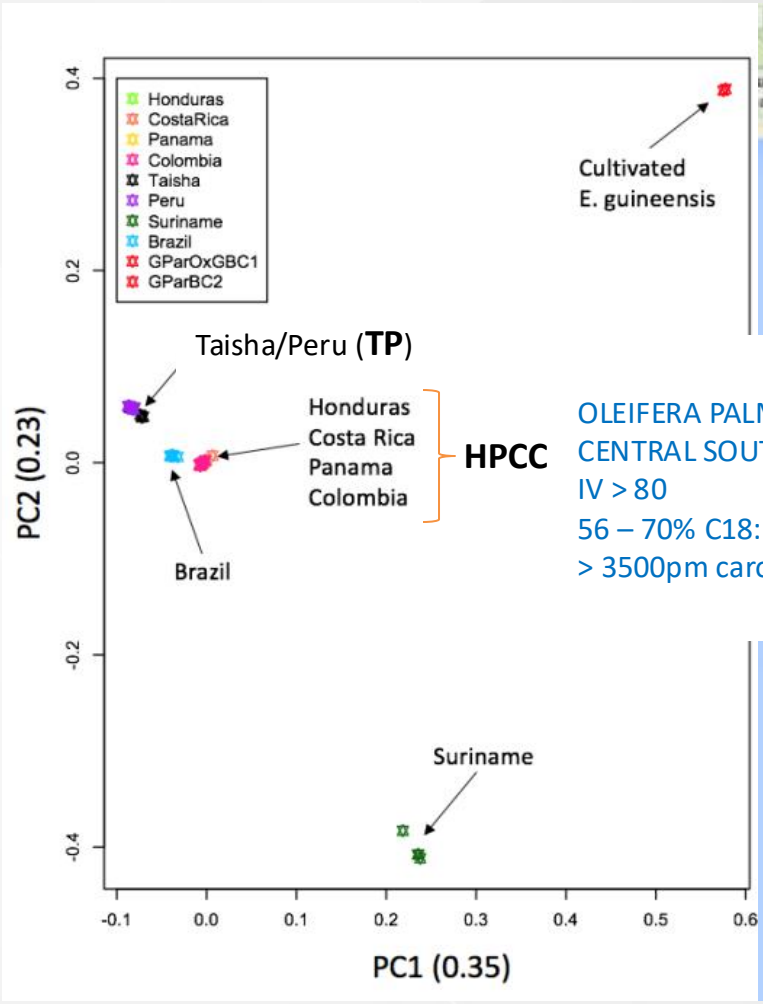
Country	Year	No. of Sites	No. of Accessions
Honduras	1982	4	14
Nicaragua	1982	9	18
Costa Rica	1982	23	61
Panama	1982	13	27
Colombia	1982	10	41
Suriname	1982	1	6
Peru	2004	2	7
Ecuador	2006	6	11

Ithnin et al., Plant Science, 2021

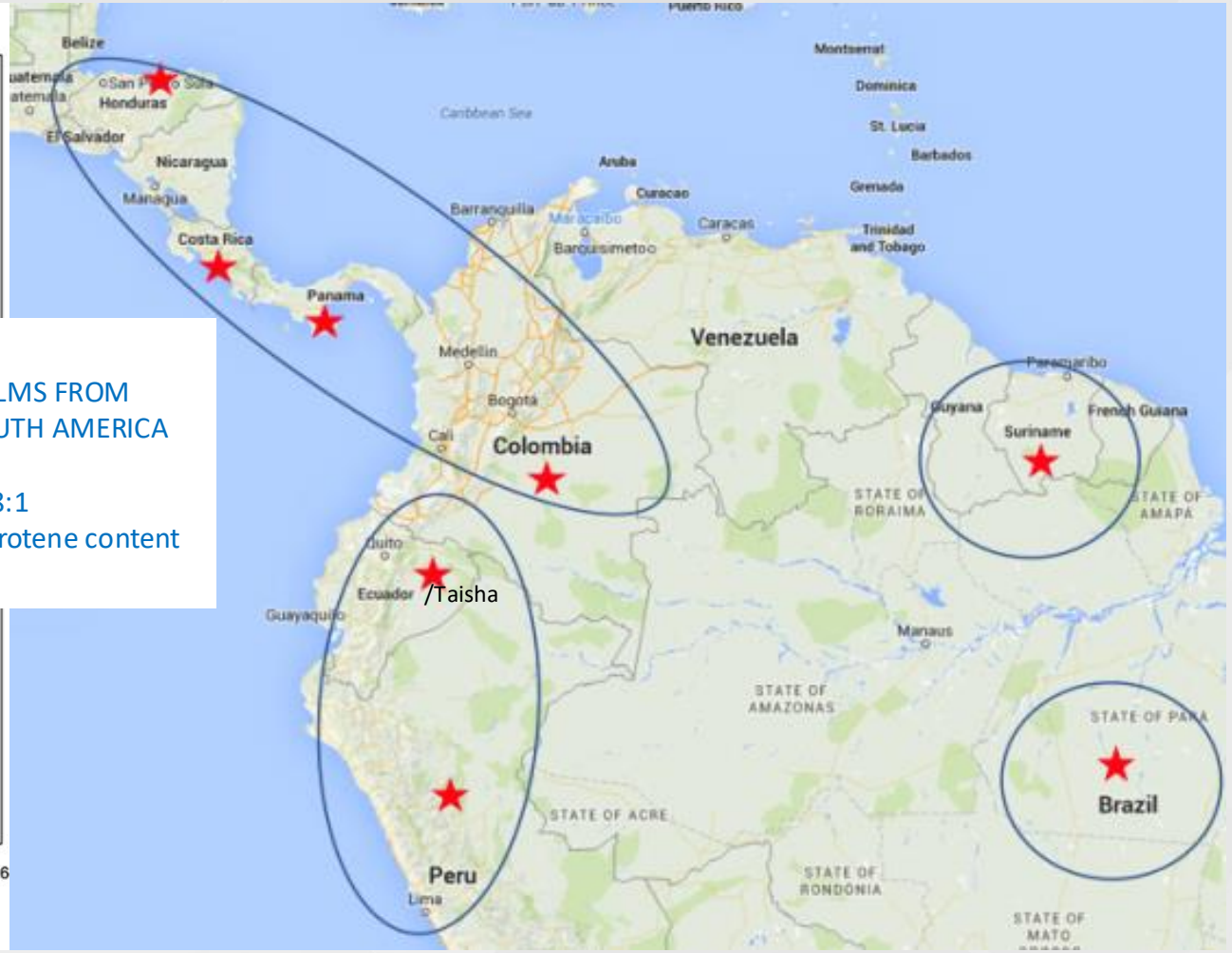
E. oleifera germplasm

GENETIC DIVERSITY ANALYSIS



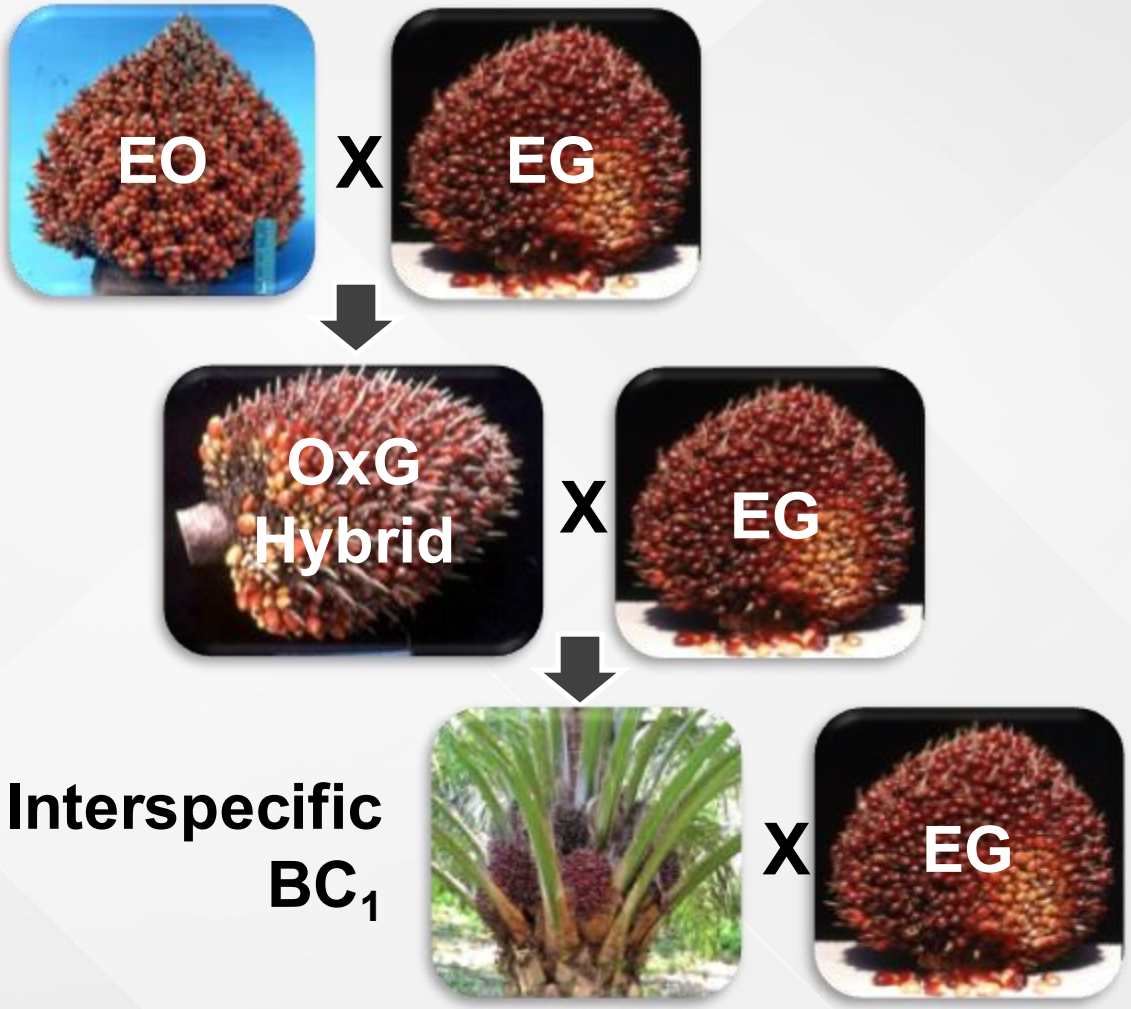


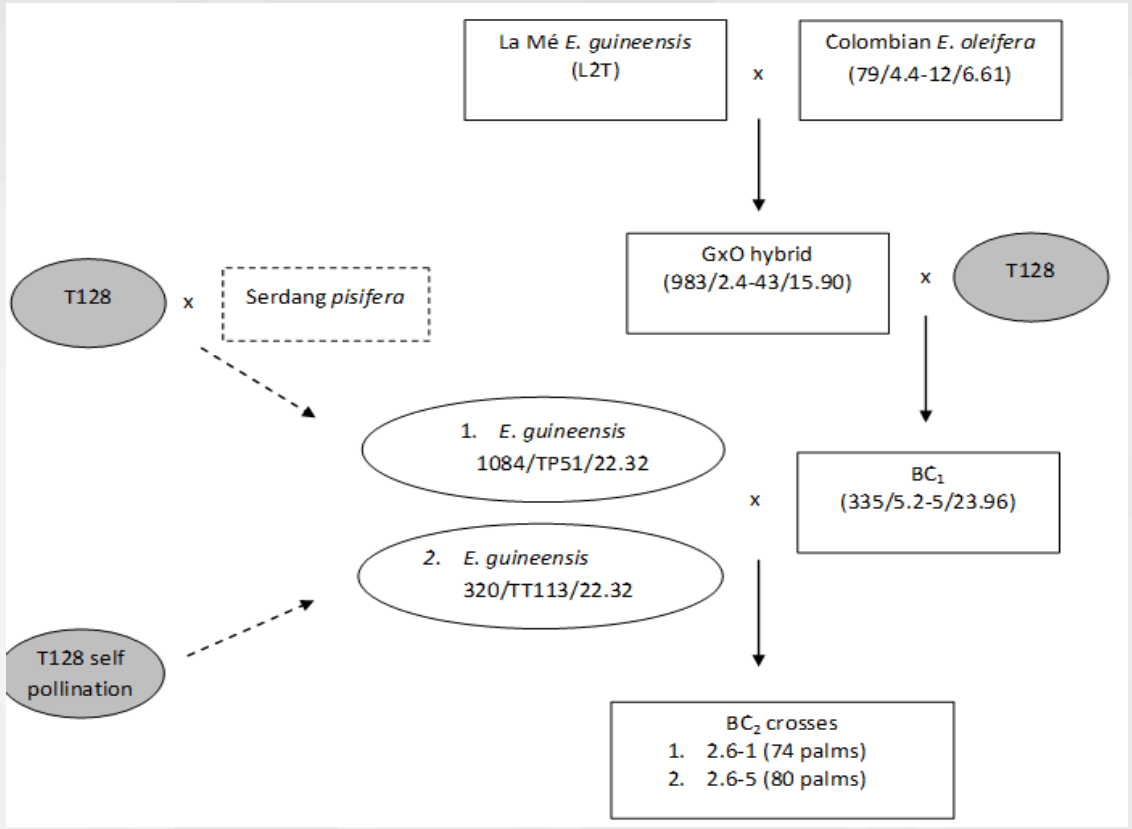
OLEIFERA PALMS FROM CENTRAL SOUTH AMERICA
IV > 80
56 – 70% C18:1
> 3500pm carotene content



EO x EG

INTERSPECIFIC BACKCROSS BREEDING



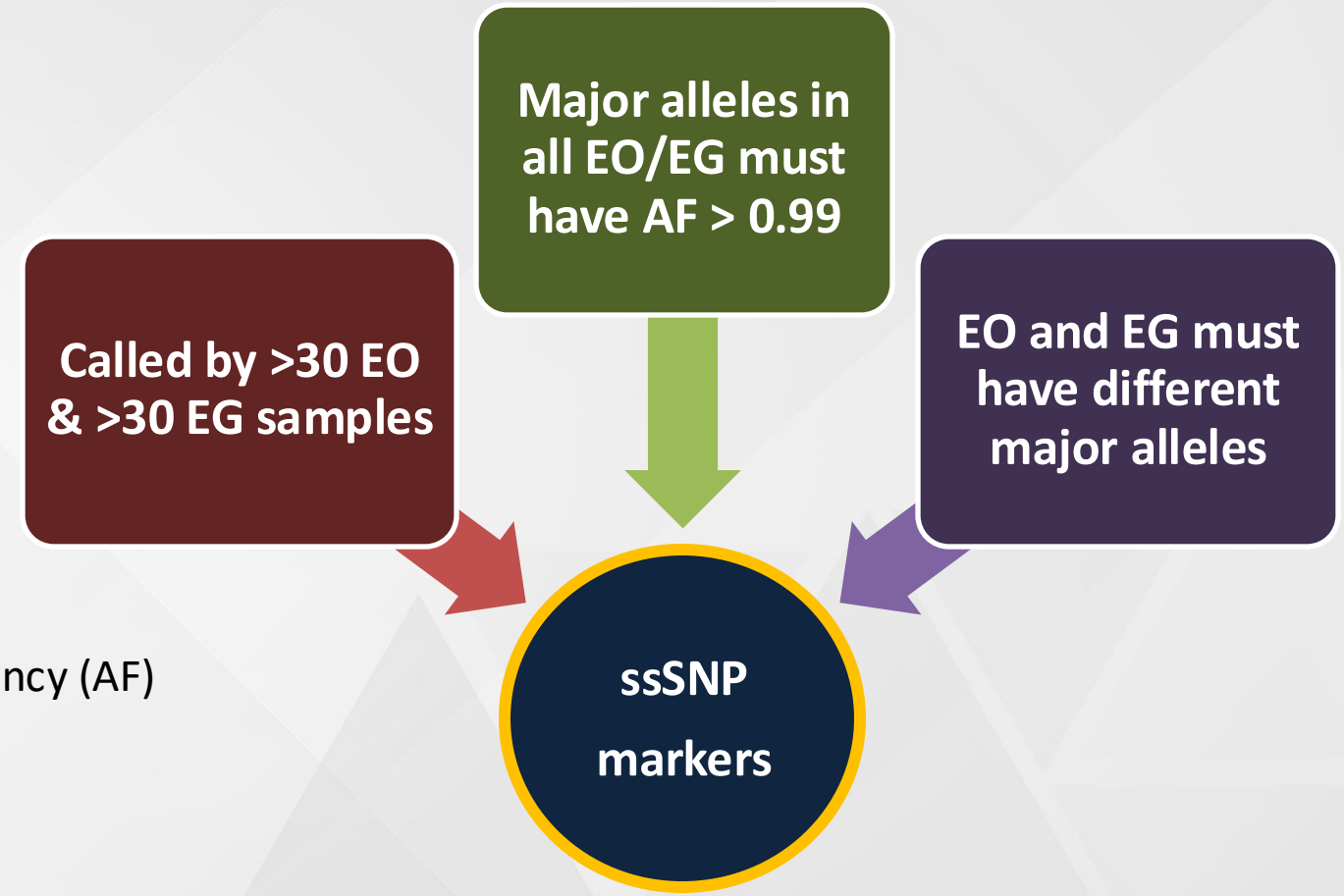


Interspecific BC_2

E. oleifera germplasm

IDENTIFICATION OF SPECIES-SPECIFIC SNPS (ssSNPs)

Species	Sample size	Number of ssSNP
EG	43	30,336
EO	184	28,862



E. guineensis (EG); *E. oleifera* (EO); Allele frequency (AF)

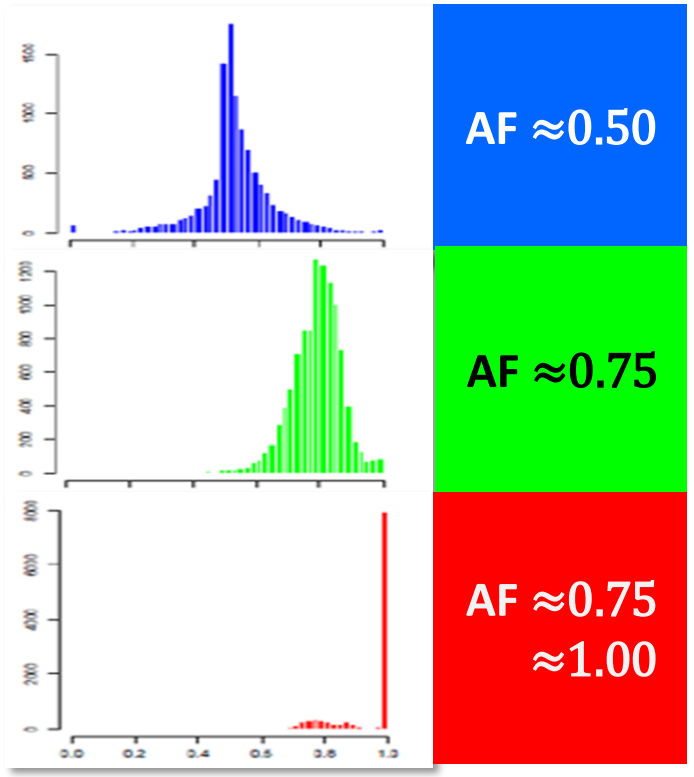
Ithnin et al., 2024, BIOCATAL AGR BIOTECH

E. oleifera (EO) & *E. guineensis* (EG) ssSNPs

ssSNPs in ● OxG ● BC_1 ● BC_2

Chromosome painting

Allele frequency (AF) histograms

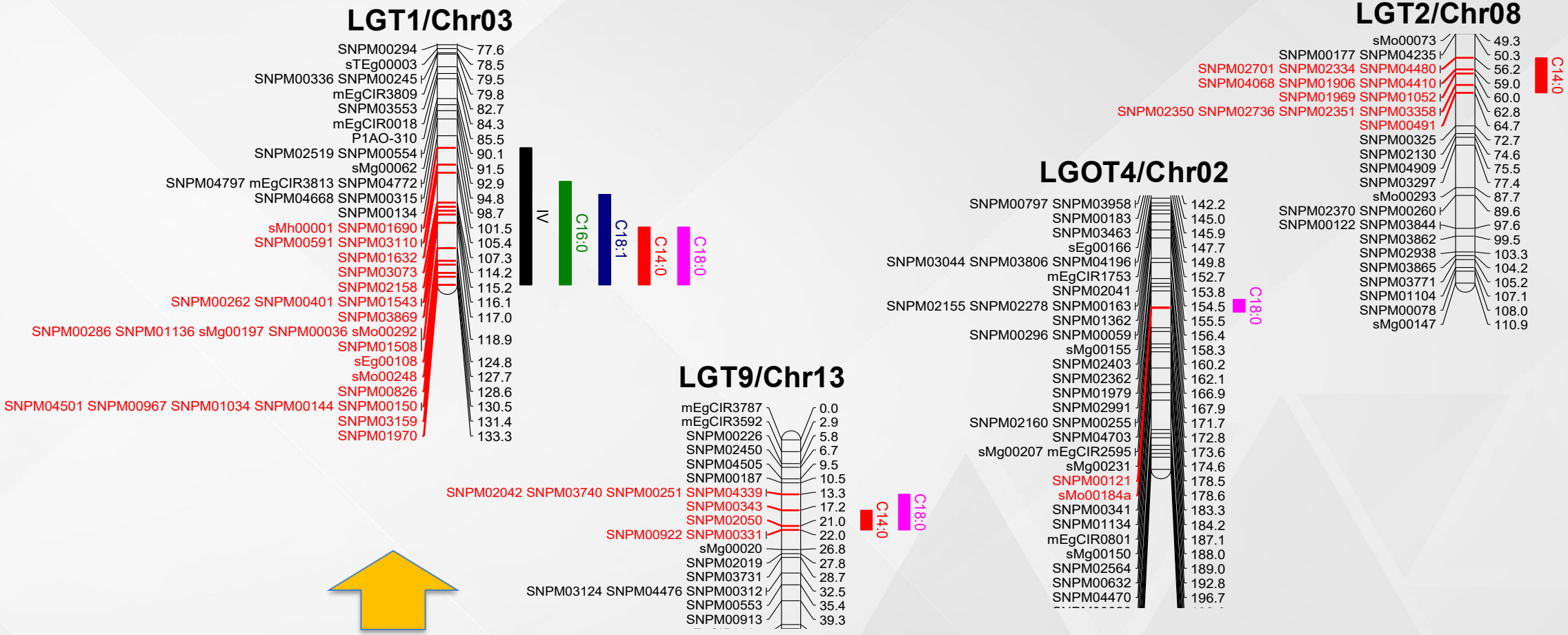


Ithnin et al., 2021, Plant Science

Ithnin et al., 2024, BIOCATAL AGR BIOTECH

EO x EG

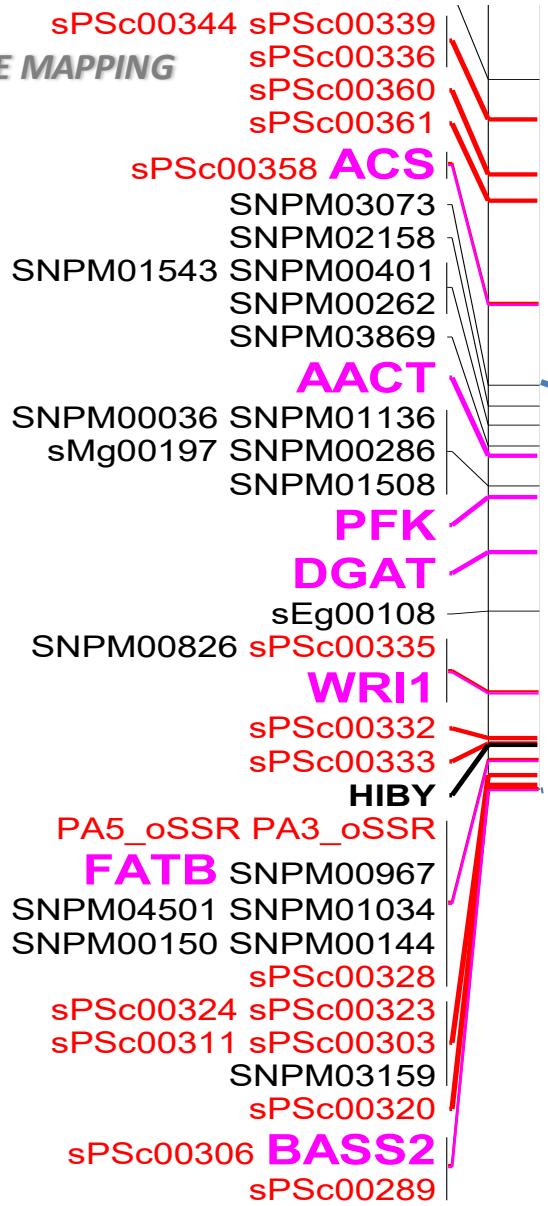
QTL MAPPING: QTLs ASSOCIATED WITH FAC



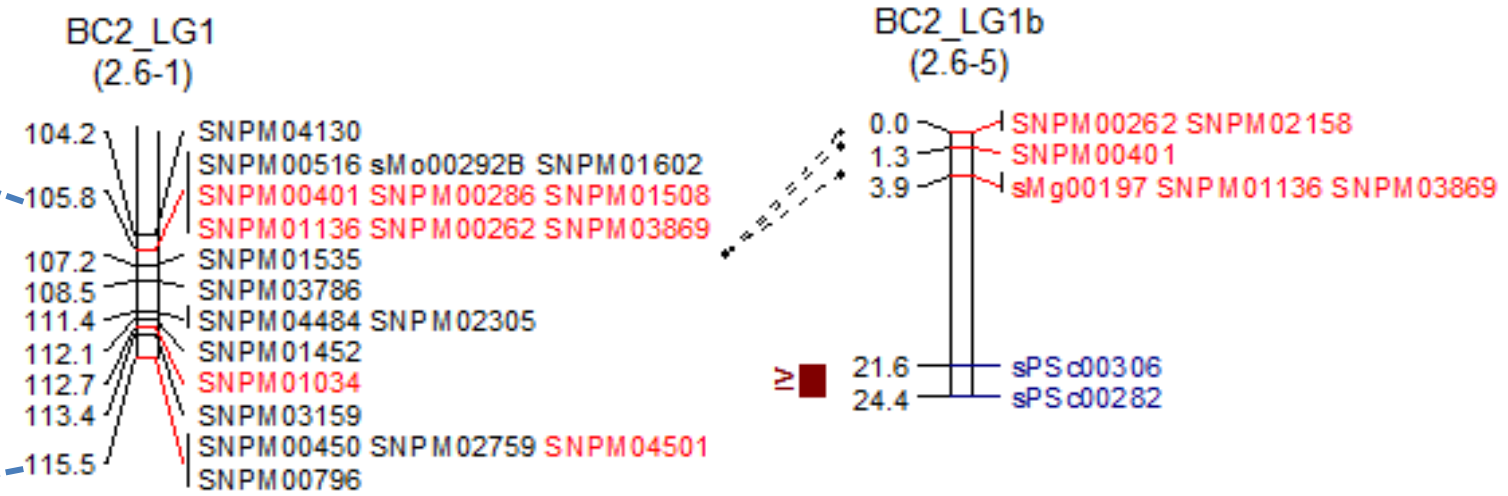
Ting et al., 2016, BMC Genomics

GENOMIC REGION ASSOCIATED WITH FAC ACROSS OxG & BACKCROSSES

GENOME MAPPING



BC_2

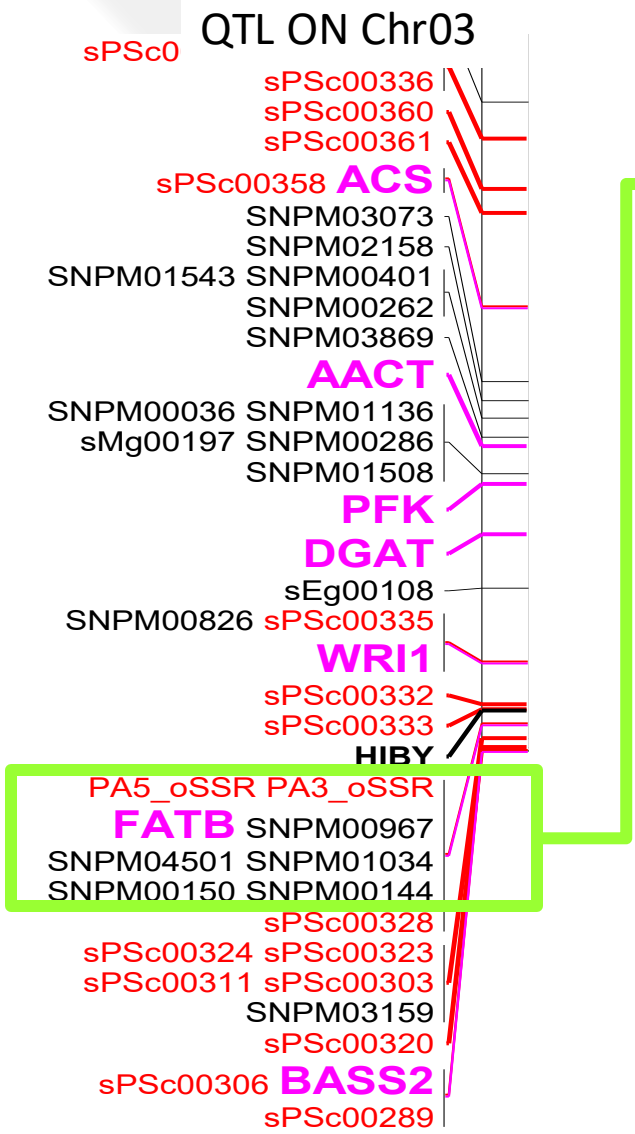


Long chain acyl-coA synthetase (**ACS**) Acetoacetyl-coA thiolase (**AACT**)
Phosphofructokinase (**PFK**) Diacylglycerol acyltransferase (**DGAT**)
Transcriptional factor **WRI 1** gene Palmitoyl–ACP thioesterase (**FATB**)
Sodium/pyruvate cotransporter **BASS2**

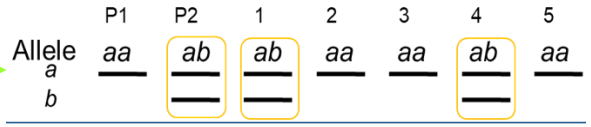
Ting et al., 2016 and 2021

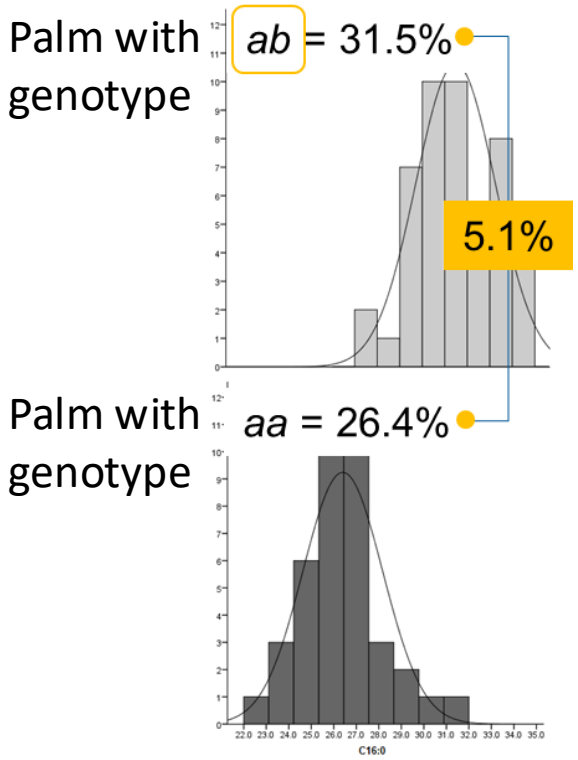
EO x EG

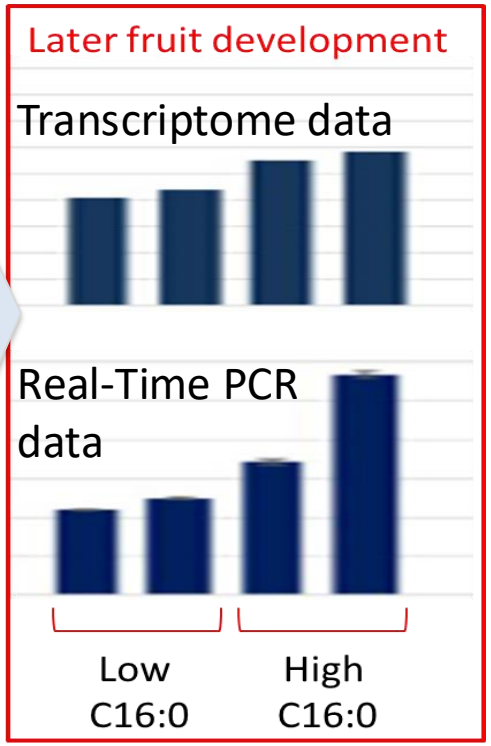
QTL MAPPING: MARKERS & GENES LINKED TO QTLs



C16:0







scientific reports

Article | Open Access | Published: 01 October 2020

Expression of fatty acid and triacylglycerol synthesis genes in interspecific hybrids of oil palm

EO x EG

Ting et al., 2020, Scientific Reports

OIL PALM IDEOTYPES TO ADDRESS YIELD GAP

CONVENTIONAL BREEDING

Meet Genetic Potential

Dwarf Palm

Vir Fruit

Long Stalk

High Oleic

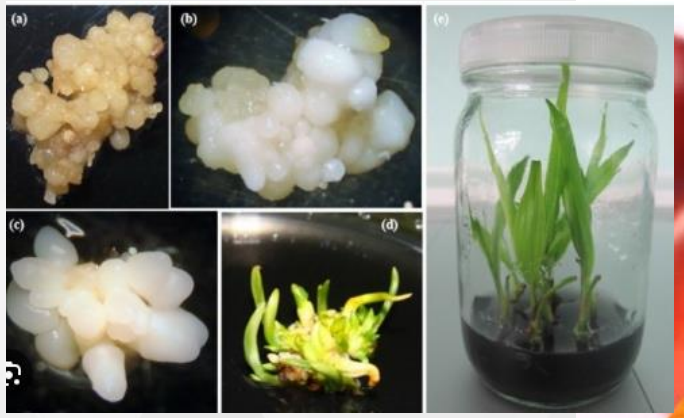
High Carotenoid

Water Use Efficiency

Disease Resistance

TISSUE CULTURE

Rapid Multiplication of Improved Planting Materials



Uniform Planting Materials

ADDRESSING THE YIELD GAP

BIOLOGICAL DATA
(Imaging (drone, GIS), plant characteristics, omics)

ENVIRONMENTAL DATA
(Rainfall, soil, topography data..)

Gemini

DATA DRIVEN
- Acquisition
- Storage
- Analytics


Image generated by Gemini

Plantation Management

GAP, mechanisation, precision agriculture

GAP required in tandem with use of improved planting material

Improved Planting Material

Conventional Breeding, Gene Editing

MUCHAS GRACIAS

21º CONFERENCIA INTERNACIONAL SOBRE PALMA DE ACEITE
21st International Oil Palm Conference