THE DUAL ORIGIN OF CULTIVATION IN COCONUT AND ITS IMPLICATIONS FOR BREEDING

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[Logos of AGAP, Cirad, and ANU]
Introducing the tree of life

Food
- Immature nuts (meat and water)
- Mature nuts (grated meat, milk, copra oil, virgin oil)
- Terminal bud (Millionaire’s salad)
- Sap (Palm wine, spirit, Sugar, vinegar)
- Others…

Non food
- Oil (Soap, cosmetics, biodiesel, dynamite)
- Palms (roofs etc.)
- Wood (Construction, furniture)
- Shell (Coal, Husk (Doormats, Carpets, ropes, geotextile)
- Roots (medicinal)
- Etc.
Malayan Yellow Dwarf
Pluridisciplinary approach

- Molecular markers
  - RFLP, AFLP, DArT, Microsatellites
  - Molecular taxonomy
- Plant morphology
  - Especially fruit morphology
- Palaeobotany
  - Fossils
- Linguistics
  - Names for “coconut” or various coconut parts
- History
  - Austronesian, arab and european navigations
Microsatellite diversity studies

- 1322 individuals
- 140 origins
- 32 producing countries
- 10 SSR markers
- Statistical analyses
  - Structure
  - AMOVA
  - GeneClass 2

Distribution of genetic diversity in coconut

Legend:
- **I**: "Indo-Atlantic"
- **P**: "PNG"
- **P**: "Pacific" (<80% Dwarf, Panama, PNG, or S. Pacific)
- **D**: "Dwarf"
- **P**: "S. Pacific"
- **P**: "Panama"
- **I/P**: "Admixed" (20% < Indo-Atlantic <80%)

Navigation routes:
- Austronesians
- Arabs
- Europeans
# Genetic distances

## (RFLP Nei 1978 )

<table>
<thead>
<tr>
<th>Coconut 21 RFLP</th>
<th>Oil Palm 37 RFLP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pacific 228 indiv. S.E. A. Melanesia, Polynesia, Panama</td>
<td>• E. o. 245 indiv. Peru, Brazil, French Guyana, Central America, Suriname</td>
</tr>
<tr>
<td>Indo-Atlantic. 40 indiv.</td>
<td>• E. g. 38 indiv. Africa</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>Cocos nucifera</th>
<th>Elaeis spp</th>
</tr>
</thead>
<tbody>
<tr>
<td>Min</td>
<td>Max</td>
<td>Min</td>
</tr>
<tr>
<td>Between Indo-Atlantic and Pacific</td>
<td>0.493</td>
<td>0.695</td>
</tr>
<tr>
<td>Within Pacific</td>
<td>0.023</td>
<td>0.309</td>
</tr>
</tbody>
</table>

Based on RFLP, SSR, AFLP suggest 2 (sub-)species, No fertility barrier!

Based on RFLP and AFLP, $E. g.$ is within the range of variation of $E. o.$ But $F_1$ partially sterile!
Synthetic representation of diversity of fruit morphology

Higher% water
Lower% meat

Higher fruit weight
Lower% husk

S.E. Asia
South Pacific
Indo-Atlantic
Introgressed I. A.

Ref: Harries 1978
Lethal yellowing field testing

(Case of Jamaica, after Been 1981)

South-east Asian and related populations tend to behave better and more consistently than populations from the rest of the world. Indo-Atlantic populations are susceptible.
Challenges for coconut breeding

- Large seeded tree crop
  - Requires large surfaces
  - Long generation time
  - Low prolificacy
  - Limits genetic progress

- Smallholder crop
- Multipurpose crop
- Generally poor acceptance of high producing hybrids

**Structure of Genetic Diversity**
AMOVA (10 SSR markers)

- Within regions: 52%
- Between regions: 15%
- Between subspecies: 33%
Mapping “large spectrum” QTLs for coconuts

Principle

Dwarf

Pacific Tall

Indo-Atlantic Tall

Hybrid

Mapping population

Treated as haploids (Dwarfs are uniform)
Lethal disease in Tanzania

- All populations studied:
  - 33% South-east Asian alleles,
  - 67% Indian alleles
- North: Arabo-persian influence (mid 19th century)
  - Disease appeared earlier
  - Partial resistance detected
- South German influence (Late 19th – early 20th century)
  - Disease appeared later
  - No known resistance

- Approach:
  - High throughput genotyping
  - Identify geographic variations
  - Locate loci under selection
  - Search for putative R-genes
Detecting genes under selection in farmer’s fields

Simulated data. s=1.25. 32 generations. Initial frequency: 0.33

Selection

No selection

Random fluctuation, Autocorrelation due to LD

Peek

Resistance QTL
### Stakeholders
- Not directly involved but
- Likely to benefit from the project
- Willing to support the project
- From support letters to financing

### Actors in coconut breeding
- Mainly coconut breeding organizations
- Willing to plant trials with their own planting material
- Possibly interested in training in genomic breeding

### Partners of the sequencing projects
- Organizations involved in genomics research
- Identified for their potential contribution to coconut sequencing project
In conclusion

- Molecular studies reveal a major subdivision between Indo-Atlantic and Pacific populations
- Breeding programs should take advantage of this genetic structure
- Sequencing coconut genome will help
- Large SNP marker sets are needed
  - Between sub-species polymorphism should be given priority
- Anticipate different varietal output
  - Dwarf x Tall population hybrids
  - Composite varieties
  - Improved traditional varieties Tall and Dwarfs
Thank you

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  - Ken Olsen WUSTL
  - Cogent network

- And workshop organizers