



Genetic diversity in coconut

L. Baudouin, P. Lebrun,
A. Berger, F. Bonnot

Early bearing and productive palms: hybrids



An important issue: Disease resistance

■ Non-limitative list

- Lethal yellowing
- Cadang Cadang
- Vanuatu CFD
- Phytophthora

■ Resistance trial

- In most cases, it is impossible to inoculate the disease
- Results are difficult to interpret

■ Alternative option

- Identify resistance factors in active epidemic spots



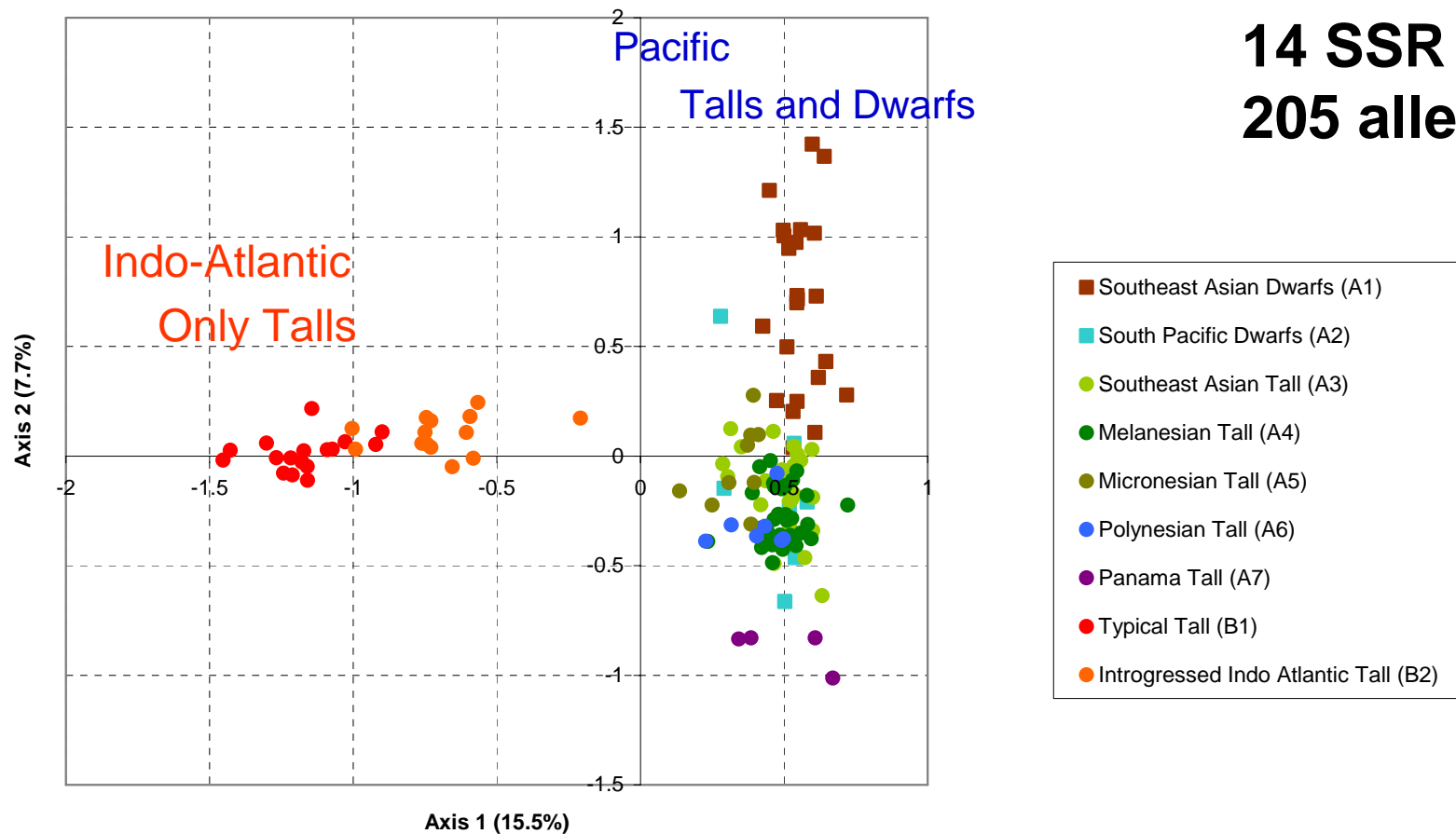
Perspectives of molecular breeding and association mapping

- For multitrait breeding
 - Particularly with a long life cycle
- For disease resistance
 - Identifying resistance traits in affected regions
- Availability of high throughput markers
 - DArT

Genetic diversity in coconut

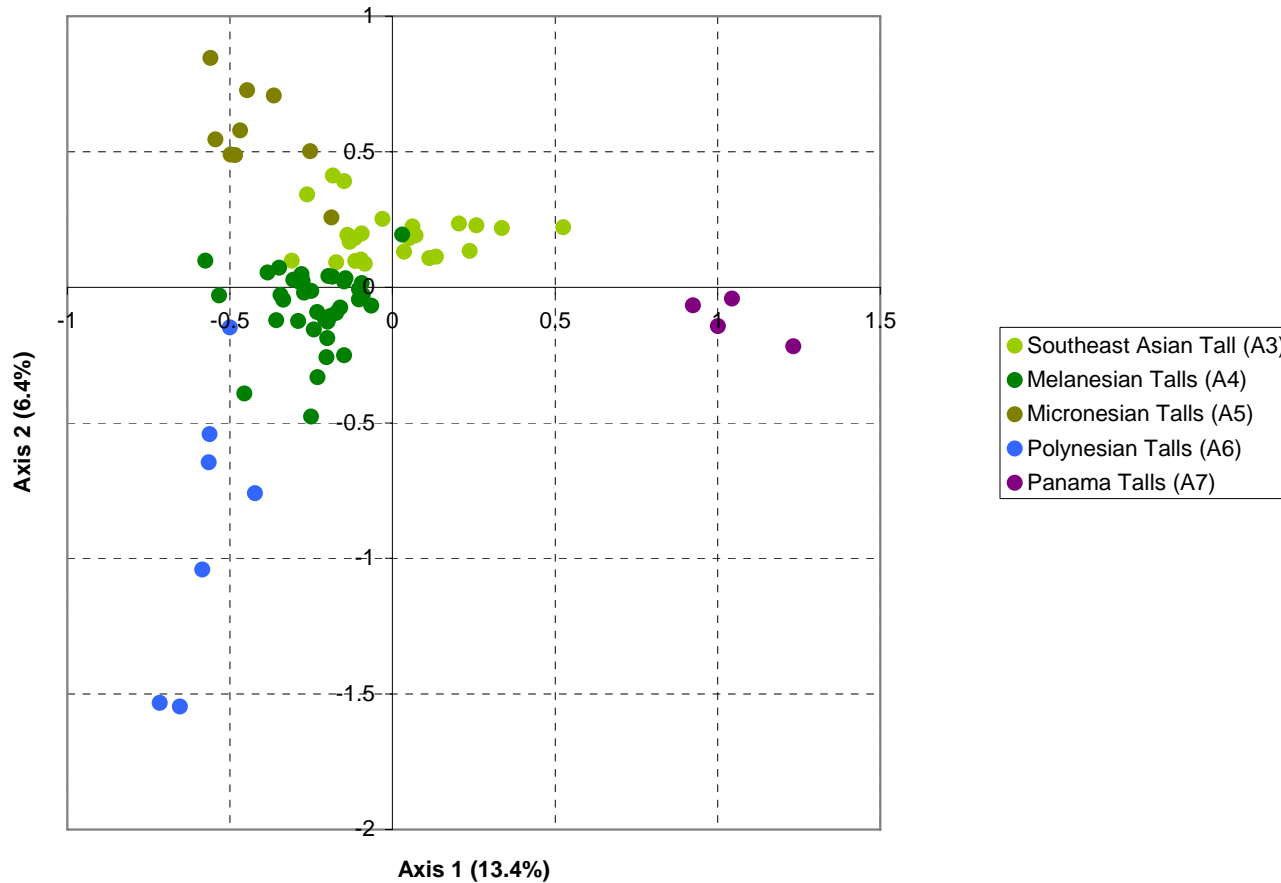
Factorial component analysis (all cultivars)

14 SSR loci
205 alleles

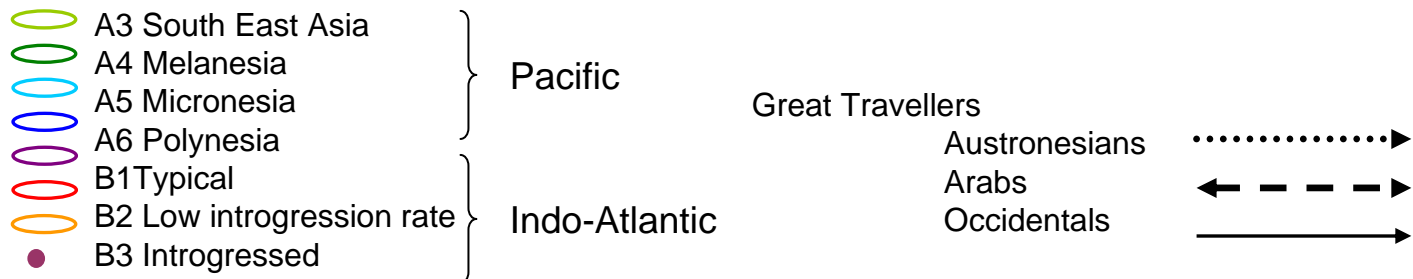
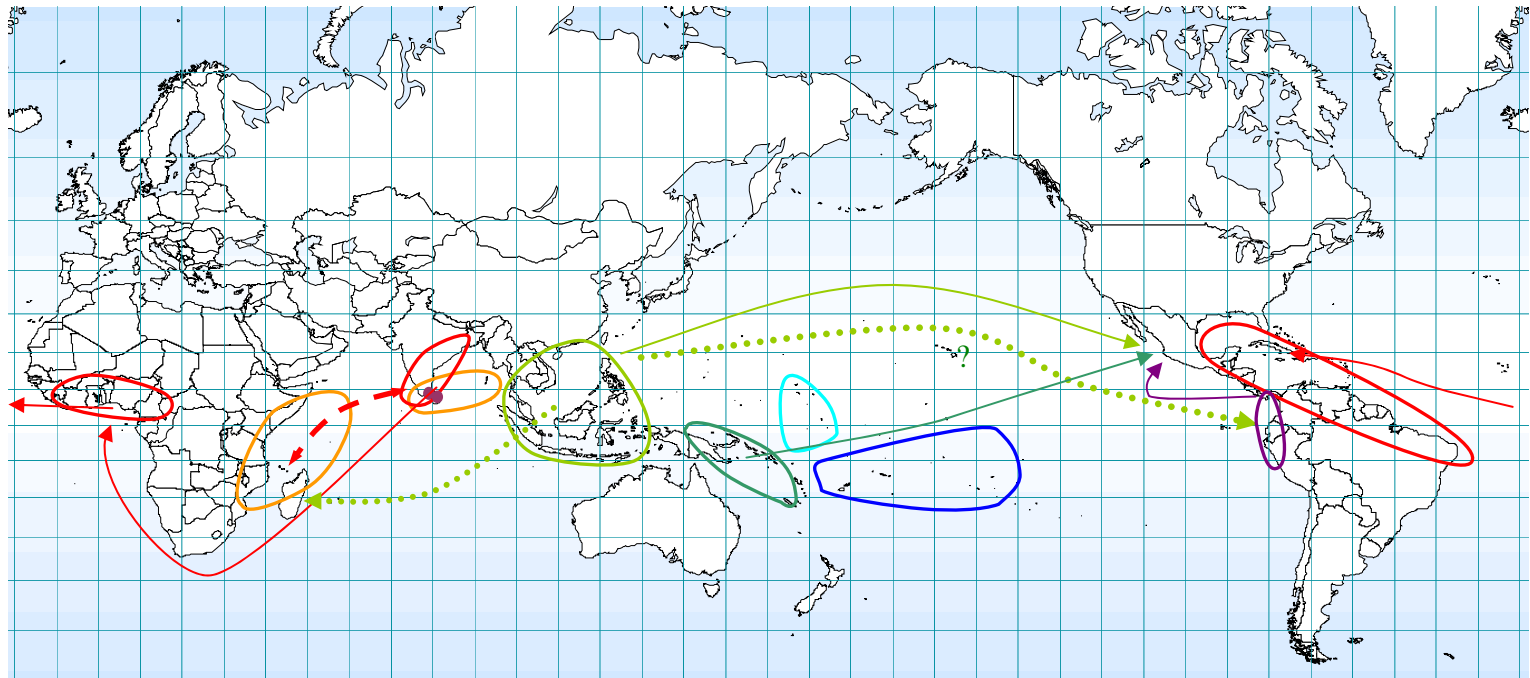



Genetic diversity among Pacific Tall cultivars

FCA Pacific Tall



Geographic repartition of Tall coconut genetic diversity





« Tier 2 » project

456 trees x 13 (14) SSR loci \longrightarrow 1000 x 22

80%

completed by september



Assessment of LD in coconut

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Objectives

- Assessing the feasibility of association mapping in coconut
 - Selecting 9 closely linked microsatellite pairs
 - Studying LD for paired and non-paired loci
 - Collecting individuals from a breeding population (Vanuatu) and analysing them

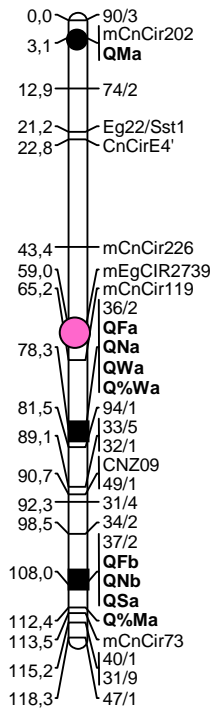


DNA collection from the entire world

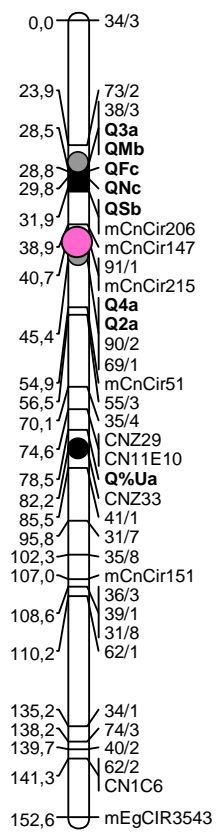
- More than 2000 individuals
- Studied with 14 reference microsatellites
 - Kit for coconut cultivar identification
- Large number of cultivars
- Some with more than 100 individuals
 - Panama, Mozambique, Vanuatu, Brazil

Linkage map

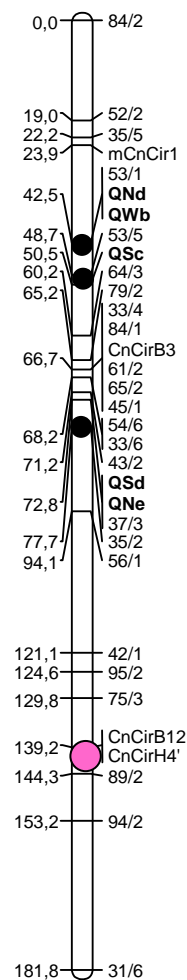
LG:1



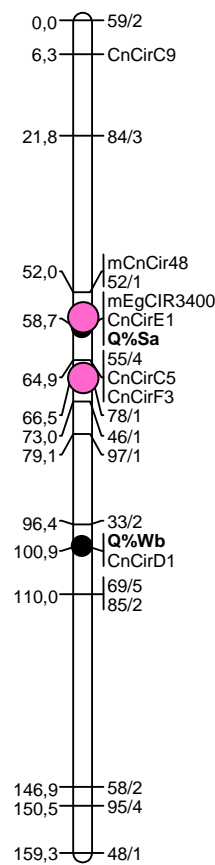
LG:2



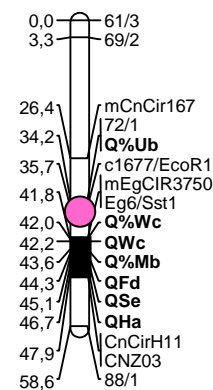
LG:3



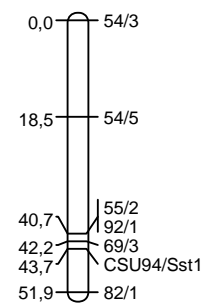
LG:4



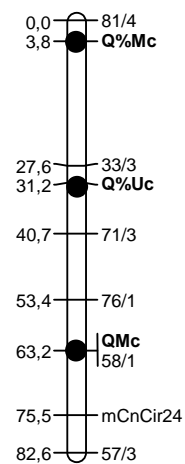
LG:5



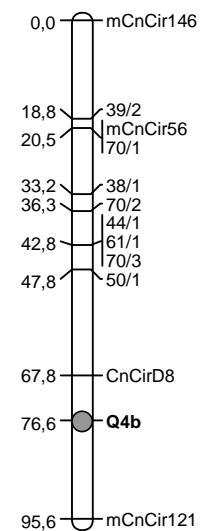
LG:6



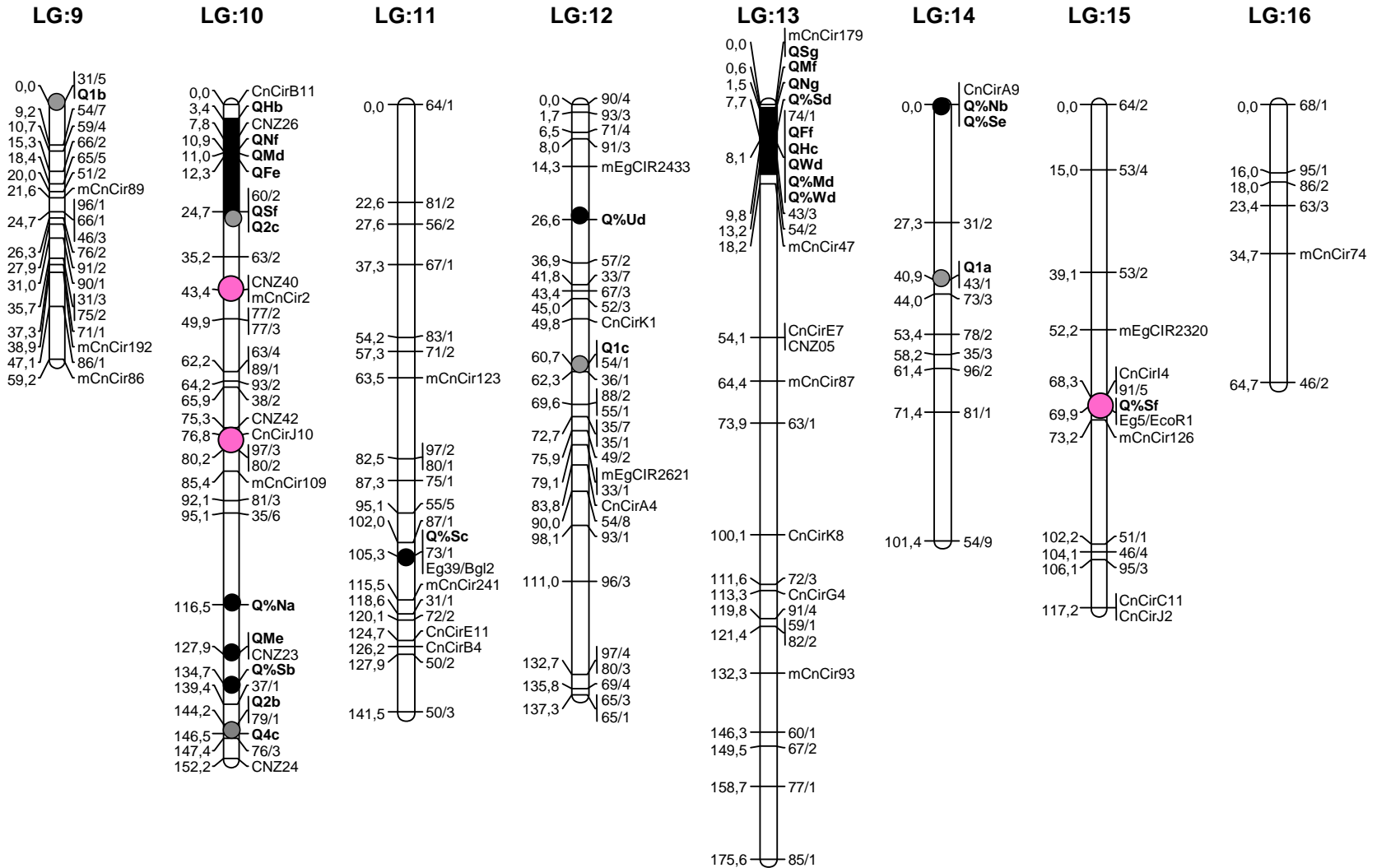
LG:7



LG:8



Linkage map



New markers for testing LD

Locus	location		distance	rate of	number of	from	to	range	entropy	diversity
			cM	realization	alleles	(bp)	(bp)	(bp)	bits/gene	
EgCIR2739	LG 1	59	6.2	94%	25	207	257	50	3.1	0.796
CnCIR119		65.2		59%	15	212	240	28	3.0	0.836
CnCIR147	LG 2	38.9	7.0	75%	14	225	253	28	2.7	0.787
CnCIR206		31.9		92%	22	101	157	56	3.3	0.863
EgCIR3400	LG 4	57.8	0.0	73%	14	148	178	30	2.7	0.805
CnCIRE1		57.8	7.1	82%	8	235	255	20	2.4	0.795
CnCIRF3	LG 4	64.9	0.0	22%	22	383	419	36	3.3	0.858
CnCIRC5		64.9	0.0	59%	25	106	162	56	3.8	0.909
EgCIR3750	LG 5	41.8	6.1	95%	9	137	159	22	1.6	0.546
CnCIRH11		47.9		85%	24	155	221	66	3.3	0.866
CnZ03		47.9	0.0	96%	10	89	153	64	1.2	0.422
CnZ40	LG10	43.4	4.5	83%	19	142	194	52	3.2	0.862
CnCIR2		43.4		91%	24	228	288	60	2.8	0.726
CnZ42	LG10	75.3	1.5	87%	18	160	212	52	2.4	0.707
CnCIRJ10		76.8		0%						
CnCIRI4	LG15	68.3	4.9	90%	3	305	309	4	0.5	0.193
CnCIR126		73.2		94%	7	193	210	17	0.5	0.177

Results

- Two loci on LG 3

	Brazil					Mozambique							Panama				
	218	226	230			218	226	230	232	234	236		218	226	230		
157	0.1	0	8.3	8.4													
159	0.7	0.1	57.8	58.6	159	0	0	47.6	0.2	1.8	0.7	50.3	135	0.2	12.9	0	13.1
161	0.3	0	4.2	4.5	161	0	0	10.9	0.1	4.8	0.8	16.6	141	0.2	1.1	0	1.3
163	0	0	0.8	0.8	163	0.1	0	7.2	2.6	0.8	0	10.7	163	0.1	0	0.6	0.7
169	0	0	0.4	0.4	165	0	0	1	0	0	0	1	165	0.9	31.5	0	32.4
173	17.3	0	2.7	20	173	0.4	1	0.1	0	0	0	1.5	171	2.4	0.1	0	2.5
177	0	6.3	0.1	6.4	177	0	8.2	0	0	0	0	8.2	173	48.6	1.1	0.1	49.8
179	0	0.4	0	0.4	179	0	9.6	0	0	0	0	9.6		52.4	46.7	0.7	99.8
181	0	0	0.4	0.4	181	0	0	1.9	0	0	0	1.9					
	18.4	6.8	74.7	99.9		0.5	18.8	68.7	2.9	7.4	1.5	99.8					
	LOD score in favour of linkage disequilibrium model :																
	67.5					49.0							51.3				
	Mutual information																
	39.5 %					30.5 %							46.1 %				

Results

Three loci on LG4

		Mutual information			LOD
Brazil					
	EgCIR3400	CnCIRE1	0.355	12.7 %	14.27
	CnCIRE1	CnCIRC5	0.146	4.4 %	4.13
	EgCIR3400	CnCIRC5	0.293	7.4 %	-0.22
Vanuatu					
	EgCIR3400	CnCIRE1	0.311	9.7 %	8.21
	CnCIRE1	CnCIRC5	0.507	10.8 %	8.75
	EgCIR3400	CnCIRC5	1.413	28.5 %	21.32
Panama					
	EgCIR3400	CnCIRE1	0.419	18.4 %	18.72
	CnCIRE1	CnCIRC5	0.456	13.1 %	12.79
	EgCIR3400	CnCIRC5	0.607	21.8 %	15.18
Mozambique					
	EgCIR3400	CnCIRE1	0.851	23.3 %	23.47
	CnCIRE1	CnCIRC5	0.458	9.1 %	18.49

Results

Two loci on LG5

			Mutual information		LOD
Brazil					
	CnCIRH11	CnZ03	0.285	11.0 %	17.877
Vanuatu					
	CnCIRH11	CnZ03	0.000	0.0 %	-3.094
Panama					
	CnCIRH11	CnZ03	0.156	11.6 %	7.8192
Mozambique					
	CnCIRH11	CnZ03	0.272	8.1 %	4.0281

Discussion

- LD analysis method seems to work satisfactorily
- LD was found preferentially at paired loci
 - But it was not always the case
 - Moderate LD at unpaired loci
 - No LD at paired loci
- Cautions
 - These are preliminary results
 - Populations are composite (subdivision, Wahlund effect?)

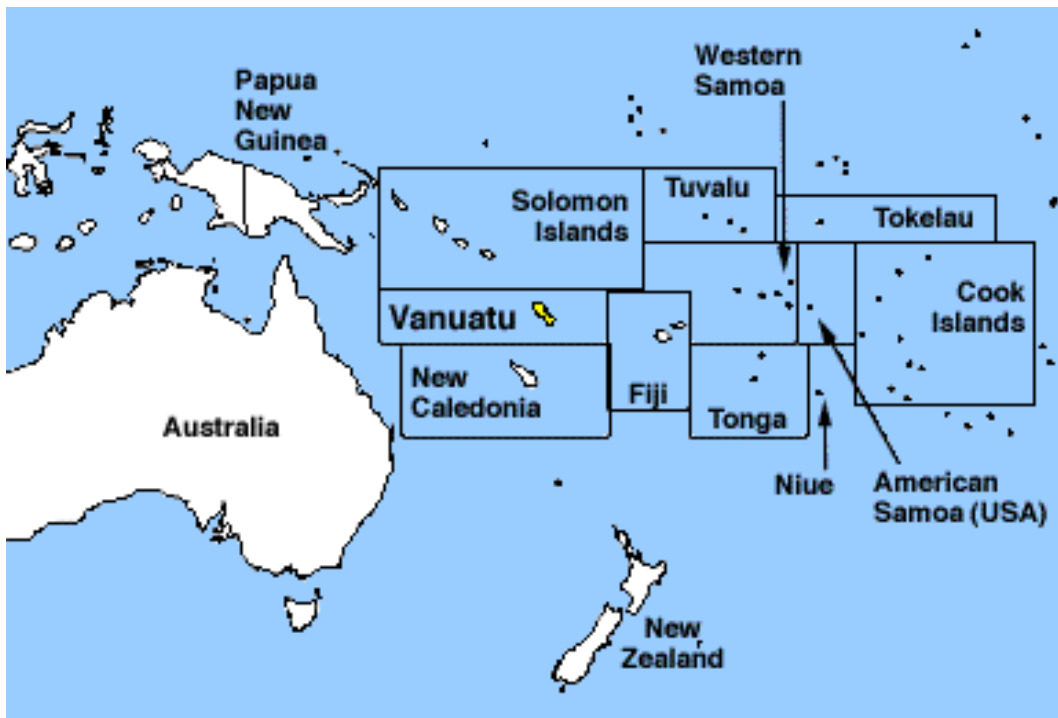
Population structure, phenotypic information and association studies in long generation crops

Coconut in Vanuatu
Luc Baudouin



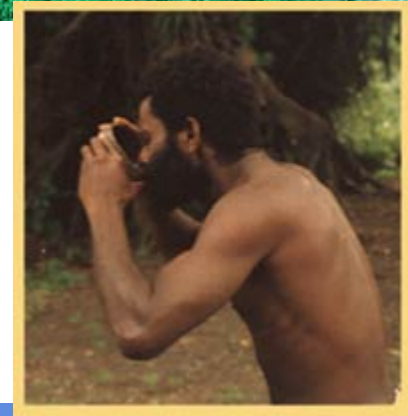
Location

- Archipelago
- 166° E, 16°N
- About 700 km from N to south



Importance

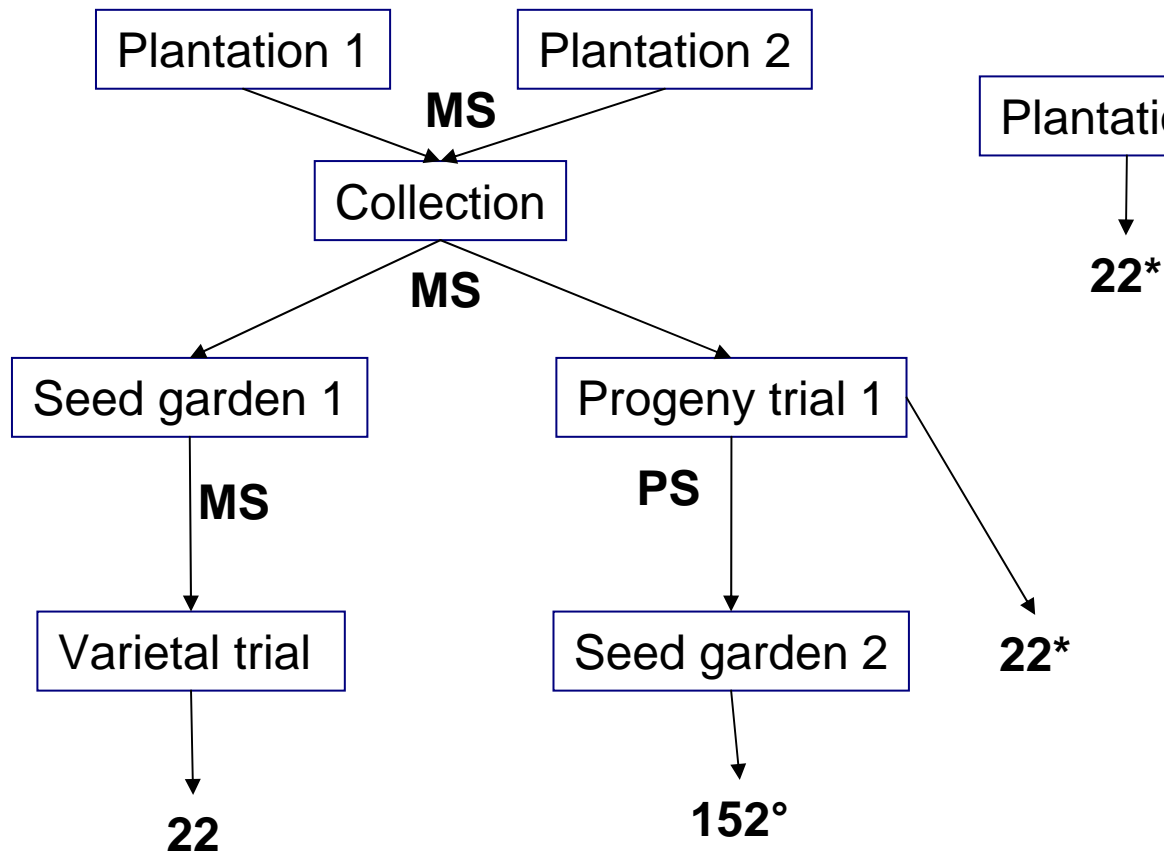
- Coconut is often the only source of monetary income in remote islands of Vanuatu
- It forms the largest part of the daily fat uptake
- It is part of the local culture (kastom)
- For breeders and conservationists, it is a major source of diversity



Constraints

- Presence of a viral disease, which is lethal to almost all foreign cultivars (coconut foliar decay)
- High cost of improved seed production AND transportation.

Sampling



*progeny by open
pollination (tall trees)
°Pedigrees are partially
known

Observations

- In accordance with the “stantech” manual
- Fruit and bunch return
 - Number of bunches
 - Number of fruits
- Fruit component analysis
 - Fruit weight
 - Nut weight
 - Husk weight
 - Shell weight
 - Meat weight
 - Water weight
- Ease of removing albumen from the shell (1 to 4)
- Stem measurements
 - Stem circumference at 20cm
 - Stem circumference at 1.5m
 - Plant height
 - Internode length
- Leaf measurement
 - Petiole length
 - Petiole width
 - Petiole thickness
 - Rachis length
 - Number of leaflets
 - Leaflet width
 - Leaflet length

Plans (achieved by september)

- 200 trees (219 extracted)
- 13 reference (COGENT) SSRs
+ 17 SSR loci on seven linkage groups
providing 15 couples of linked markers
(0 to 7.1 cM)
(ongoing)

Collaborating institutions

- Coconut Research Institute, Sri Lanka
- Vanuatu Agricultural Research and Training Center, Vanuatu
- Agropolis-CIRAD, France

- Training in Montpellier on molecular markers
 - Tiata Sileye, VARTC (three weeks in November)
 - Dr Champa Kumari Bandanarayake, CRI (three months, September to November)

- Connection with other projects
 - Genetic structure in coconut: “Tier 2 genotyping” and “LD analysis”
 - DArT development