

Genetic and Epigenetic, diversity in African Plantains

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CIRAD

TAG MEETING 2006





● French



● French Horn



● False Horn



Messiatso

Mutant de type French issu de
Mbouroukou N°1



Mbouroukou N°1

Type Faux Corne

Fruits de couleur vert-jaune avant
maturité

The plantain paradox

- African plantain have been classified into the same group but are very diverse for agronomical traits of interest.
- Are they genetically similar? or do they are issued from different origins ?

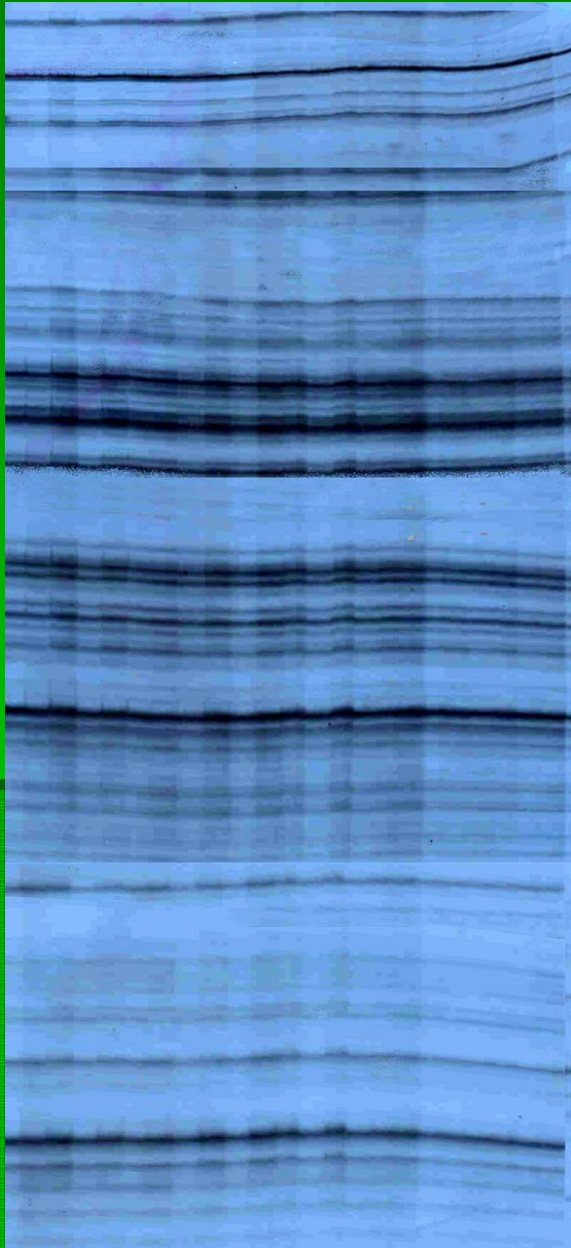
The answers of molecular markers ?

- Isozymes, RFLP, SSR and DArT
- DNA methylation studies through MSAP analysis

Isozymes and RFLPs

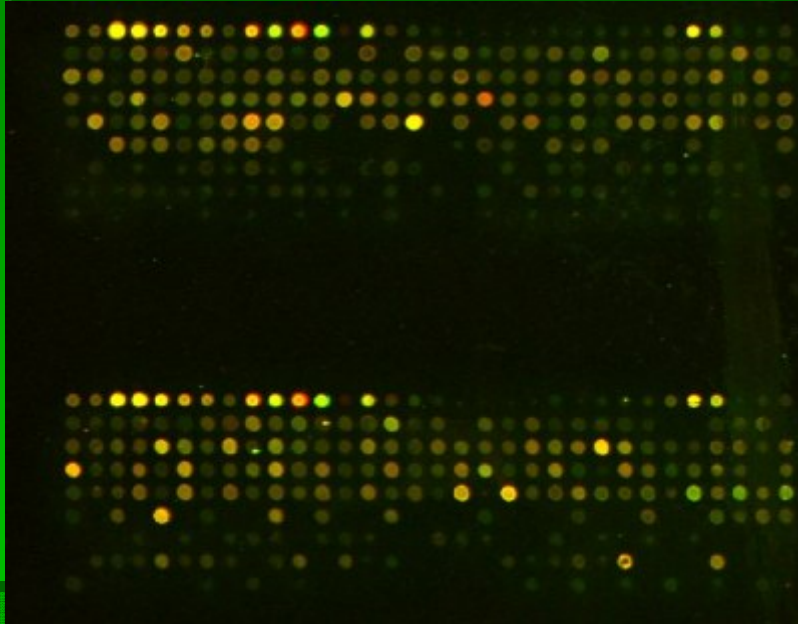
- No differences within plantain group with isozymes.
 - No difference between 5 clones using RFLP with mitochondrial, chloroplastic or nuclear probes. (F. Carreel, PhD 1994)
-
- Suspect a same origin, but small samples do not allow to conclude

AFLP



- 0 polymorphism/260 markers/4 plantains (Ude et al., 2002)
- 78 polymorphic markers/15 primer pairs, 750? markers /25 plantains (Ude et al., 2003)
- 1 polymorphic marker /8 primer pairs 633 markers /30 plantains (Noyer et al., 2005)
- Needs for technical homogenization but the same genetic background is confirmed

DArT



373 DArT markers (PstI/TaqI) 187 banana genotypes.

1 marker and missing data

4 markers

35 markers

0 | 0.05

- Partial view of Neighbor Joining tree based on Sokhal & Michener index calculated from the 373 best DART markers



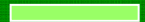


- DART markers confirm AFLP results
- African plantains have a very narrow genetic basis
- Fingerprint techniques cannot really distinguish efficiently amongst African plantain group.



SSRs



Microsatellites Markers

Primer Name	Polymorphic	Number of alleles ¹			
25-26	no	3	27 plantains		3 plantains
33-34	No	3			
103-104	No	2			
91-92	No	2			
93-94	No	3			
36-38	No	2			
125-126	yes	3			
129-130	No	2			
105-108	yes	2			
101-102	No	2			

Plantains are very heterozygous

Plantains are issued from a single original cross

Since original cross, no additional sexuality

- Another type of diversity exists :
« epigenetic diversity »
- This concern some characters which are transmitted to sexual or vegetative offspring but not in a Mendelian manner.

- Very less is known about epigenetic traits but DNA methylation is often tightly linked to epigenetic traits (even if it is not clear if methylation is a cause, a consequence or a « collateral damage »).
- In banana, most of methylation pattern is transmitted through vegetative propagation (suckers) or micro propagation

Do methylation polymorphism exists amongst plantain ?

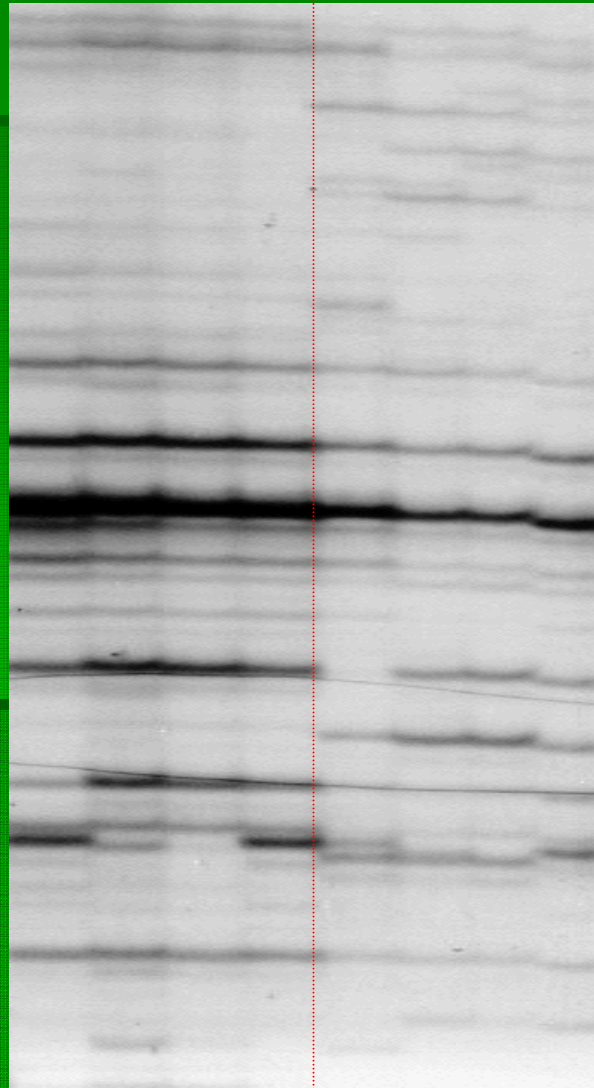
Are methylation patterns transmitted in banana progenies ?

MSAP

- « Methylation sensitive amplification polymorphism »
- Based on the same principle as AFLP
- Compare the profile obtained from the SAME sample treated with both isoschyzomers (HpaII/MspI)
- Provide information on the methylation status of the internal Cytosine of CCGG sites: C^mCGG or CCGG

HpaII

Msp I



CCGG

C^mCGG

C^mCGG

CCGG

CCGG

CCGG

CCGG

C^mCGG

CCGG

CCGG

- 30 plantains have been studied using 8 MSAP primer pairs representing 633 CCGG sites throughout the banana genome.
- 15 loci were found to be polymorphic

Factorial analysis: Axes 1 / 3



French



French Horn



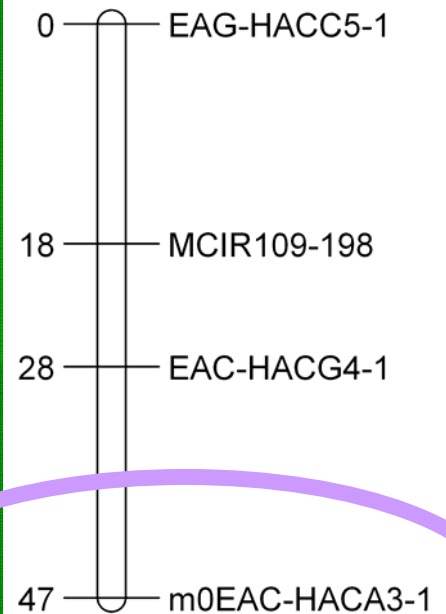
False Horn



True Horn

Genetic mapping of tetraploid x diploid banana using SSRs, AFLP and MSAP markers

- Despite technical problems due to ploidy of the cross and size of the population, methylation markers are transmitted through sexual cross in banana.



Conclusion and Prospects

- African plantain originate from an ancestral single cross involving heterozygous parents. No additional cross has been involved.
- Fingerprint techniques are not efficient to differentiate amongst plantains
- SSR markers due to high mutation rate could help

- Analysis of DNA Methylation polymorphism is an helpful technique for diversity analysis in groups with very low genetic diversity
- Future work could include
 - Study of SSR polymorphism within plantain group.
 - Study of the epigenetic diversity under selection pressure.
 - Diversity analysis with gene targeted markers.

Acknowledgements

Darts : A.M.Risterrucci, J.-C. Glaszmann, A. killian

SSRs : A. Bouet, J.L. Noyer

AFLPs and Methylation : S. Causse, J.L. Noyer,
G. Noumbissie, D. Bienvenue, T. Palama

And special thanks to CARBAP and Kodjo
TOMEKPE