Mechanisms of haplotype divergence at the RGA08 NBS-LRR locus in wild banana: *Musa balbisiana*

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Banana is a giant herb

A bunch of fruits, composed of hands and fingers

a pseudo stem formed of tightly packed leaves

Vegetative propagation through suckers
An important plant with complex genetics

**Genus** *Musa*

*Musa acuminata*  *Musa balbisiana*

Diploid/triploid cultivars

100 billions of tons production

90 billions of tons local consumption
Bananas belong to a sister group of Poales.

Poales (9,002,614)
- POACEAE: Agrostis, Avena (oats), Festuca, Brachypodium, Lolium, Aegilops, Hordeum, Oryza (rice), Dendrocalamopsis (bamboo), Leymus, Panicum (switchgrass), Pennisetum Secale, Triticum, Eleusine (finger millet), Saccharum (sugarcane), Sorghum, Zea (maize);
- BROMELIACEAE: Ananas (pineapple)
- Dasyphygionales (43)
- Zingiberales (63,581)
  - MUSICACEAE: Musa, ZINGIBERACEAE: Zingiber (ginger), Curcuma (turmeric)
  - Commelinales (388)
  - Arecales (6,404)
  - ARECACEAE: Cocos (coconut), Elaeis (oil palm)
- Asparagales (65,450)
  - ALLIACEAE: Allium; ASPARAGACEAE: Asparagus; AGAVACEAE: Agave, Yucca;
  - AMARYLLIDACEAE: Lycoris; HYACINTHACEAE: Hyacinthus; IRIDACEAE: Crocus, iris;
  - ORCHIDACEAE: Phalaenopsis (moth orchid)
  - Liliales (5,315)
  - ALSTROEMERIACEAE: Alstroemeria;
  - LILIACEAE: Lilium
- Pandanales (683)
  - VELLOZIACEAE: Xerophyta (resurrection plant)
- Dioscoreales (635)
  - DIOSCOREACEAE: Dioscorea (wild yams)
- Petrosaviales (21)
- Alismatales (6,997)
  - ARECACEAE: Zantedeschia (arum lily), Lemna (duckweed)
- Acorales (9,858)
  - ACORACEAE: Acorus
Comparative genomics of banana

- 9 out of 17 BAC clones with partial synteny
- traces of synteny retained over 120 million years of divergence

Lescot et al. BMC Genomics 2007
Comparative genomics within the Musaceae

- high level of synteny
- intergenic regions are variable

Lescot et al. BMC Genomics 2007
Musa diversity: the *Musa balbisiana* genome

- *Musa balbisiana*: wild diploid species $x = 11$
- Involved in the genomic composition of cultivars (plantain)
- High vigor and disease resistance
- Two genomic regions identified and sequenced containing multiple RGAs: 226kb and 252Kb
- Genetic mapping $\rightarrow$ allelic regions
- Flanking gene-rich regions (90 kb) are highly conserved
- Haplotype divergence: 1 My (Musa A/B: 4.6 My)
- TEs participate to haplotype divergence (2 indels, 5.3 kb)
- Complex pattern in the RGA cluster, higher TE density
The MARGA08 gene family

- 31 NB-LRR genes of the same family (average identity > 80%)
- 2 clades
- 9 Allelic pairs
- Evolution through tandem and inverted gene duplication, segment duplication, TE activity, diversifying selection
- Differential expansion of the two RGAs clades on the two DNA strands and between haplotypes
- 21 kb size difference between the haplotypes at this locus.
Conclusion

- One of the largest single family RGA cluster identified in plants.

- High sequence conservation in gene rich regions of *M. balbisiana*

- Recent TE activity contributes to sequence divergence

- Considerable variation exist between haplotypes of one plant in the repertoire of RGA

- The “MUSATRACT” ANR funded banana genome sequencing project is ongoing (Genoscope, CIRAD and GMGC). Sequencing of the doubled haploid Pahang clone (*M. acuminata*, genome A).
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Thank you for your attention
### GENOME EVOLUTION BY POLYPLOIDIZATION: BACKCROSS ENHANCES DNA SEQUENCE RESTRUCTURING IN TRITICALE

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### CONSTRUCTION OF AN SSR-BASED LINKAGE MAP FOR CYNARA CARDUNCULUS

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### SEX-DEPENDENT DIFFERENCES IN TRANSCRIPTION OF TRANSPOSABLE ELEMENTS IN A DIOECIOUS PLANT SPECIES

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### MECHANISMS OF HAPLOTYPE DIVERGENCE AT THE RGA08 NBS-LRR LOCUS IN WILD BANANA (MUSA BALBISIANA)

Genome structure, evolution and comparative genomics

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