Genome Organization and Diversity of Major Satellite DNAs in Banana (Musa spp.)

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- Bananas are giant perennial tropical plants within genus Musa
- Most of cultivated clones originated from natural inter- and intra-individual crosses of two wild diploid species: M. acuminata (A genome) and *M. balbisiana* (B genome) Previous study showed closely related nature of A and B genomes, including highly similar repetitive DNA fraction •454 sequncing of *M. acuminata* 'Calcutta4' enable to identify two different satellites DNA sequences in the nuclear genome

Studied accessions		
Accession name	ITC code	Genome constitution
Calcutta4	0249	AA
Long Tavoy	0283	AA
Maia Oa	0728	AA
DH Pahang	1511	AA
Tuu Gia	0610	AA
Cameroun	0246	BB
Honduras	0247	BB
Tani	1120	BB
Pisang Klutug Wulung		BB
Musa schizocarpa	0560	SS
Musa schizocarpa	1002	SS
Obino l'Ewai	0109	AAB
Maritú	0639	AAB
3 Hands Planty	1132	AAB
Pelipita	0472	ABB
Balonkawe	0473	ABB
Ato	0820	AS
Tonton Kepa	0822	AS
Umbubu	0854	AT

Materials and Methods



- Satellite DNAs consist of thousands or even millions of tandemly arranged repetitive units in head-to-tail orientations
- Satellite DNAs show specific banding pattern on chromosomes and may be genus- or speciesspecific

- > Doleželová M, Valárik M, Swennen R, Horry JP, Doležel J. 1998. Physical mapping of the 18S-25S and 5S ribosomal RNA genes in diploid bananas. Biol Plant 41:497-505. > Hřibová E, Neumann P, Matsumoto T, Roux N, Macas J, Doležel J. 2010. Repetitive part of the banana (Musa acuminata) genome investigated by low-depth 454 sequencing. BMC Plant Biol 10: 204

Results

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Fluorescence in situ hybridization of satellite CL18 and CL33





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Examples of Idiograms



DIPLOID ACCESSIONS

(A) Localization of CL18 (red) and CL33 (green) on chromosomes of 'Long Tavoy'. (B) Localization of 5S rDNA (red) and CL18 (green) on chromosomes 'Maia Oa'. (C) Localization of 5S rDNA (red) and CL33 (green) on chromosomes of 'Long Tavoy'. (D) Localization of CL18 (red) and LINE element (green) on chromosomes of 'Tuu Gia'. (E) Localization of 5S rDNA (red) and CL18 (green) on chromosomes of 'Pisang Klutuk Wulung'. (F) Localization of BAC clone 2G17 (red) and 5S rDNA (green) on chromosomes of 'Cameroun'. (G) Localization of BAC clone 2G17 (red) and CL18 (green) on chromosomes of 'Tani'. **(H)** Localization of 45S rDNA (red) and 5S rDNA (green) on chromosomes of M. schizocarpa. (I) Localization of 5S rDNA (red) and CL33 CL18 (red) and CL33 (green) on chromosomes of M. schizocarpa. (K) Localization of CL18 (red) and 5S rDNA (green) on chromosomes of *M. schizocarpa*. Chromosomes were counterstained with DAPI (blue). Bar = 5 μ m. CL18 is marked by long arrow, CL33 is marked by short arrow.

HYBRID ACCESSIONS

(A) Localization of CL18 (red) and CL33 (green) on chromosomes of 'Maritú'. (B) Localization of CL18 (red) and 5S rDNA (green) on chromosomes of 'Maritú'. (C) Localization of 5S rDNA (red) and CL33 (green) on chromosomes of 'Maritú'. (D) Localization of CL18 (red) and BAC clone 2G17 (green) on chromosomes of 'Pelipita'. (E) Localization of CL18 (red) and 5S rDNA on chromosomes of 'Pelipita'. (F) Localization of CL18 (red) and CL33 (green) on chromosomes of 'Ato'. (G) Localization of CL18 (red) and 5S rDNA (green) on chromosomes of 'Tonton Kepa'. (H) Localization of CL18 (red) and CL33 (green) on chromosomes of 'Umbubu'. (I) Localization of 5S rDNA (red) and CL33 (green) on chromosomes of 'Ato'. (J) Localization of CL18 (red) and CL33 (green) on chromosomes of *M. schizocarpa*. (J) Localization of (green) on chromosomes of 'Tonton Kepa'. (K) Localization of 5S rDNA (red) and CL18 (green) on chromosomes of 'Umbubu'. Chromosomes were counterstained with DAPI (blue). Bar = 5 μ m. CL18 is marked by long arrow, CL33 is marked by short arrow.







(A) Consensus sequence of CL33-like satellite was reconstructed from all obtained sequences units of all analyzed species and is displayed as sequence logo. (B)Neighbor-Joining tree constructed from a Jukes-Cantor distance matrix and rooted to the midpoint shows diversity of individual types of CL33-like repetitive units obtained from all studied species.

Conclusions

- Genomic distribution of satellite sequences CL18 and CL33, 5S rDNA, 45S rDNA and BAC clone 2G17 was established in a set of Musa species and cultivated clones
- The use of CL18, CL33, 5S rDNA, 45S rDNA and BAC clone 2G17 as probes for FISH increased the number of chromosomes which could be identified in *Musa*
- Different patterns of probe co-localization in *M. acuminata* sp. and *M.* balbisiana sp. enabled determination of genomic constitution in their interspecific hybrids
- For the first time, diversity of satellite sequences CL18 and CL33 was analyzed at molecular level
- Sanger sequencing of both satellites revealed extensive conservation within and between the evaluated accessions
- No genome-specific sub-types of satellite repetitive unit were found in A and B Musa genomes

CL18-like TOTHOR AND REAL AND R satellite TI CAN TAGANTAGANTA DA ANTA TANAN ANA TANAN ANA TANAN A ANA TANAN ANA TANAN TANAN TANAN TANAN TANAN TANAN TANAN • Repetitive units is ~ 2 kb long Two parts of the sequence unit ATHEITTH TREET C. HIGE TIG TANATTIKKTC TIG TTANATATTIKA ATHEITTE TIC TIC TIC TIKANA TAYA ANA CE CORRECT ANA ANT CHITA ANA ANT TA ANA ANT CHITA ANA ANA ANT CHITA ANA ANT CHITA ANA ANT CHITA ANA ANA ANA ANA ANA were sequenced Sequencing of *M. acuminata* 'TuuGia' and *M. schizocarpa* did not result in the sequences similar to part 1 TTATA ACATTIC CITE TACCAL COL AN OLOCICY OTAGANA CA ACCOMATGANITE ANTICA OTTE TACA GACANTA TAC TOACONTATA TO COMPANY OF A TOTATA TATA ACATOR OF A TOTATA ACTIVITY ACANOR OF A TOTATA ACANOR OF A TOTATA ACTIVITY ACANOR OF A TOTATA ACANOR OF ACANOR OF A TOTATA ACANOR OF ACANOR OF A TOTATA ACANOR OF ACANO Sequences of AS hybrid panana clones homologous to part 1 of CL18-like repeat contained a long deletion Sequences homologous to part 2 of CL18-like repetitive units were not identified in hybrid banana clone '3 Hands Planty' CHANNER CATCHINATIAN CHANNEL AND CHANNEL CCHATTICCACTACAAAAGTAGACCAACACA ECKCTARTEG, NATCHOTTCHANCHT, CTATAANA GAALGTATAATACTTATAGTIGCCCATG ATAAACTACCATTCHCAATTA Consensus sequences of both parts of CL18-like satellite were reconstructed from all analyzed species and are displayed as sequence logo (Part1 – A; Part2 – C). Neighbor-Joining trees 2941444 4244146414641464144411 14 GATAGALATATITIGTICAACTITIATACATTICACTI 410041 TAAATATAATATAATATAATATATATATATA constructed from a Jukes-Cantor distance matrix and rooted to the ATTVICTORIATANA AN CAACHING AS CAAA MOTCHA CLITTAL OT SHOULDAN AS TO CAAL AT ATTAL AT AN AN AN AN AN AN AN AN AN diversity of midpoint show reconstructed parts of CL18-like A TCCL ALCHARGE GARCARCHINE A LANDARA TALANDAR ON AND CHERCENAL AND THE SCHULT ACADEMIC AND A STANDARD AND THE SCHULT AND A STANDARD AND A STAN satellite units obtained from all studied species (Part1 – B; Part2 – D).



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