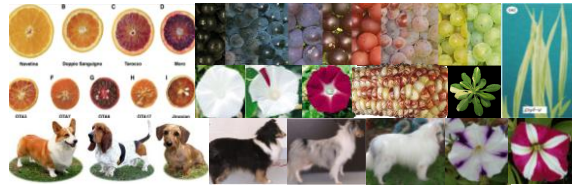


Transposable elements in the *C. canephora* genome

Coffee Genome Consortium



Introduction



15% to 85% of plant genomes are TEs

Deep impact of TEs on plant genes and genomes:

neo-formation of genes, gene mutation, perturbation of gene regulation, chromosome structure and genome size variations

Central role of TEs in Plant Gene and Genome Evolution

Buella et al., 2012; Goto-Yamanoto K., Hirochika H., 2004; Tagami et al., 2005; Tsukahara et al., 2009

Introduction

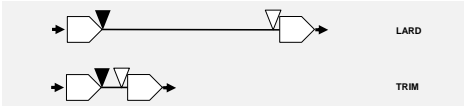
Class I - Copy and Paste mechanisms via a RNA molecule

Autonomous LTR Retrotransposons



Families
Ty3/gypsy
Ty1/copia

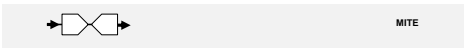
Non-autonomous



Class II - Cut and Paste mechanisms via a DNA molecule



TIR DNA Transposon

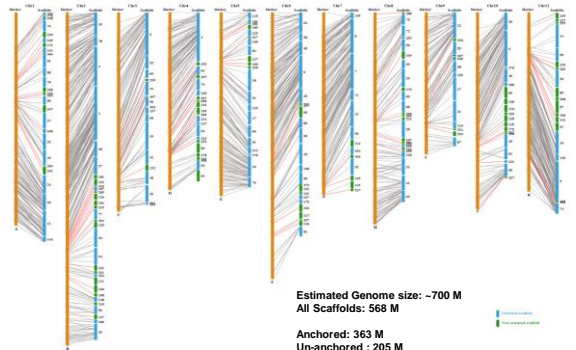


MITE

Introduction

The *C. canephora* draft genome (DH 200-94) sequence from the Coffee Genome Consortium

90X genome coverage have been produced: 25,216 contigs & 13,345 scaffolds

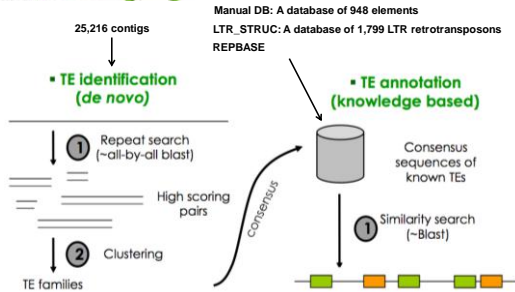
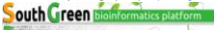


Estimated Genome size: ~700 M
All Scaffolds: 568 M
Anchored: 363 M
Un-anchored : 205 M

Annotation of TEs in the Robusta genome with REPET

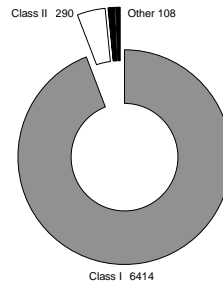
The REPET package (v2.1) <https://urgi.versailles.inra.fr/Tools/REPET>

Véronique Jamilloux



Annotation of TEs in the Robusta genome with REPET

TE identification (de novo) An initial database of 6,812 references (V1.0)

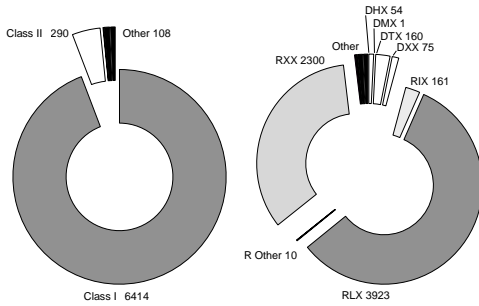


High representation of RLX and RXR predicted elements

Wicker et al., 2007

Annotation of TEs in the Robusta genome with REPET

TE identification (de novo) An initial database of 6,812 references (V1.0)



High representation of RLX and RXX predicted elements

Wicker et al., 2007

Annotation of TEs in the Robusta genome with REPET

TE annotation: Overview of *C. canephora* genome TE composition (V1.0) 500,000 GFF lines

Pseudomolecule	Non-autonomous										Total %
	RLG	RLC	RXX	RIX	RSX	DTX	DNX	DHX	XXX		
chr1	17.37	6.13	9.58	1.82	0.08	2.70	1.19	0.78	2.06	41.71	
chr2	14.16	5.14	8.07	1.35	0.08	3.07	0.95	0.41	2.01	35.24	
chr3	18.42	6.44	8.70	1.73	0.06	2.95	1.32	1.12	2.07	42.81	
chr4	16.04	6.51	9.07	1.65	0.08	2.83	1.06	0.54	1.96	39.74	
chr5	19.03	7.02	9.48	2.10	0.07	2.74	1.23	0.71	1.98	44.36	
chr6	15.58	5.72	8.90	1.54	0.08	3.06	0.99	0.58	1.91	38.36	
chr7	15.41	5.36	8.67	1.40	0.08	2.91	1.06	0.85	2.21	37.95	
chr8	16.26	6.17	10.10	1.93	0.08	3.04	1.17	0.71	2.12	41.58	
chr9	20.56	6.53	10.24	2.11	0.08	2.68	1.69	0.44	1.87	46.2	
chr10	16.27	6.20	8.74	1.79	0.07	3.14	1.32	0.49	1.93	39.95	
chr11	19.08	7.10	10.88	2.02	0.07	2.69	1.02	0.63	1.87	45.36	
chrUn	37.38	8.15	14	1.73	0.04	1.57	0.2	0.49	1.09	64.65	
Total %	24.14	6.84	10.92	1.73	0.07	2.43	0.80	0.59	1.68	49.2	

LTR Retrotransposons

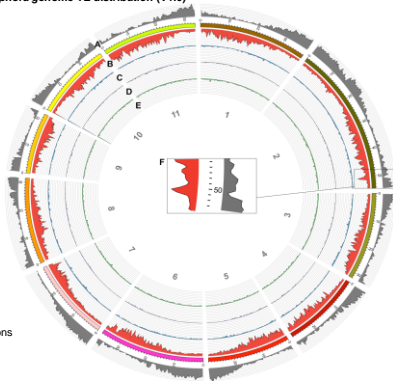
Class I

Class II

LTR Retrotransposons represent 42% of the *C. canephora* genome

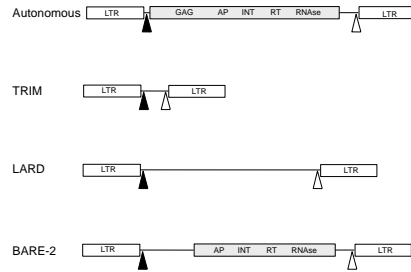
Annotation of TEs in the Robusta genome with REPET

Overview of *C. canephora* genome TE distribution (V1.0)

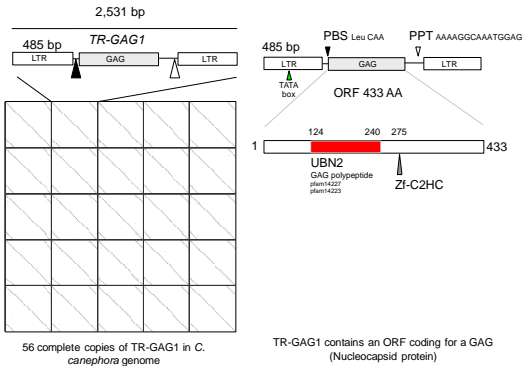


A Genes
B LTR Retrotransposons
C LINES
D Transposons
E MITEs

Non autonomous LTR retrotransposons: Life with a GAG



Non autonomous LTR retrotransposons: Life with a GAG

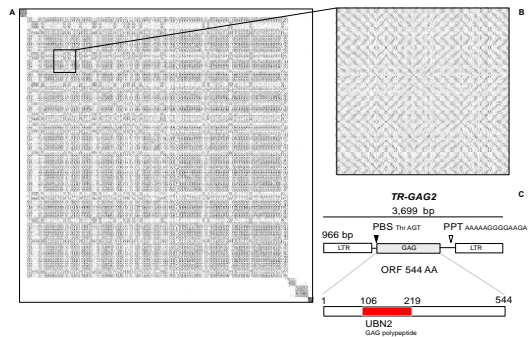


56 complete copies of TR-GAG1 in *C. canephora* genome

TR-GAG1 contains an ORF coding for a GAG (Nucleocapsid protein)

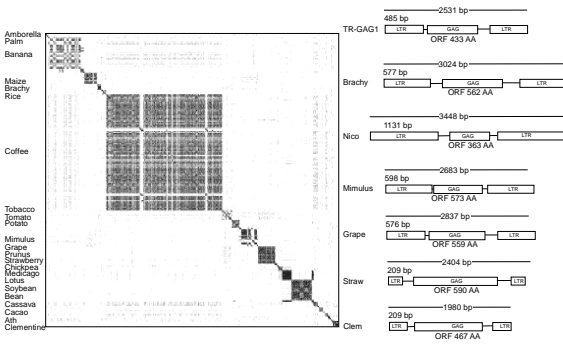
TR-GAG1 is a new family of non autonomous elements in Robusta genome

Non autonomous LTR retrotransposons: Life with a GAG



Five new TR-GAG families, of which TR-GAG2 shows a high copy number in Coffee

Non autonomous LTR retrotransposons: Life with a GAG



TR-GAG is a conserved structure in numerous plant genomes

Outlooks

- Improve TE annotation (V 2.0)
- Improve the detection and identification of Non-autonomous LTR retrotransposons
- Study in details the chromosomal distribution of TE and their localization near or inside (intron) coding regions
- Understand the impact of TE on gene expression : To study TE expression and to identify TE cassettes (co-transcription) using RNAseq data
- Study the activity of TR-GAG elements and detect their mobility

Acknowledgements

Coffee genome consortium



- Nestlé (Tours, France)
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- Univ. of Buffalo (USA)
- ENEA (Italy)
- Embrapa-Cenargen (Brazil)
- Univ. of Trieste (Italy)
- Univ. of Queensland (Australia)

Transposable elements



EVODYN: Romain Guyot, Thomas Gayraud, Clara Zaremski, Peria Hamon, Serge Hamon, **Alexandre de Kochko**

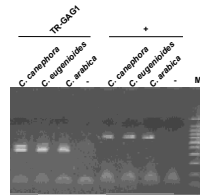
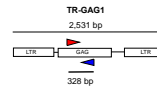
DIVA: Philippe Lashermes, Alexis Dereeper
ID: Stéphanie Bocs

Veronique Vanilloux

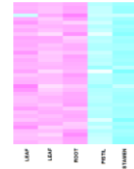


<http://coffee-genome.org>

Non autonomous LTR retrotransposons: Life with a GAG



C. canephora RNAseq



Rogério Fernandes de Souza

TR-GAG1 is expressed in Coffee species