Avaliação fenotípica de uma população de *C. canephora* Conilon cultivada em altitude elevada, visando um programa de Seleção Genômica Ampla (SGA) em cafeeiro.

VIII Simpósio de Pesquisa dos Cafés do Brasil
25 – 28 de Novembro, 2013, Salvador-BA.

Alan C. Andrade
Laboratory of Molecular Genetics - LGM

alan.andrade@embrapa.br

Agricultural research - innovation - quality of life
Embrapa
Ministry of Agriculture, Livestock and Food Supply
Brazilian Government
Brasil

SGA

Fenótipo

PAI

X

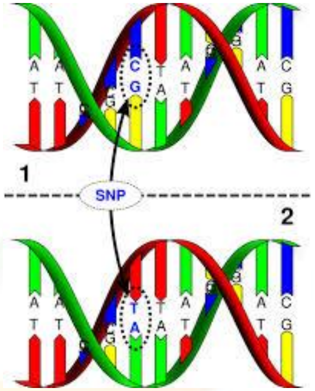
Mãe

DNA

PAI

X

Mãe



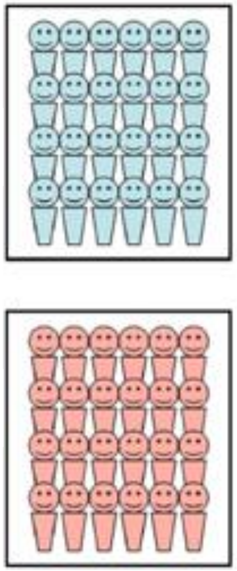
Seleção Genômica Ampla

Fenotipagem

Genotipagem

Mapeamento
(Genoma Referência)

Interesse

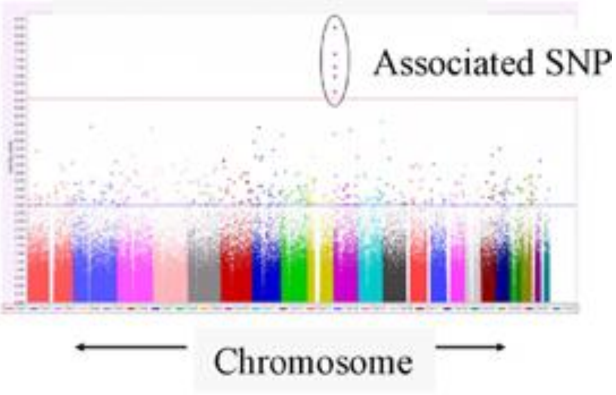


Normais

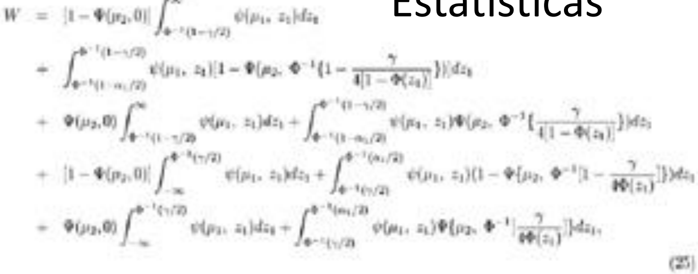
DNA

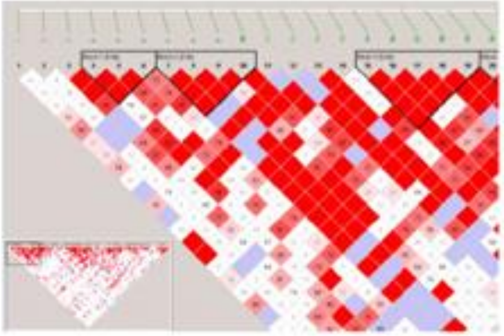
DNA Chip/GBS

Informação



Análises
Estatísticas





Desequilíbrio de Ligação

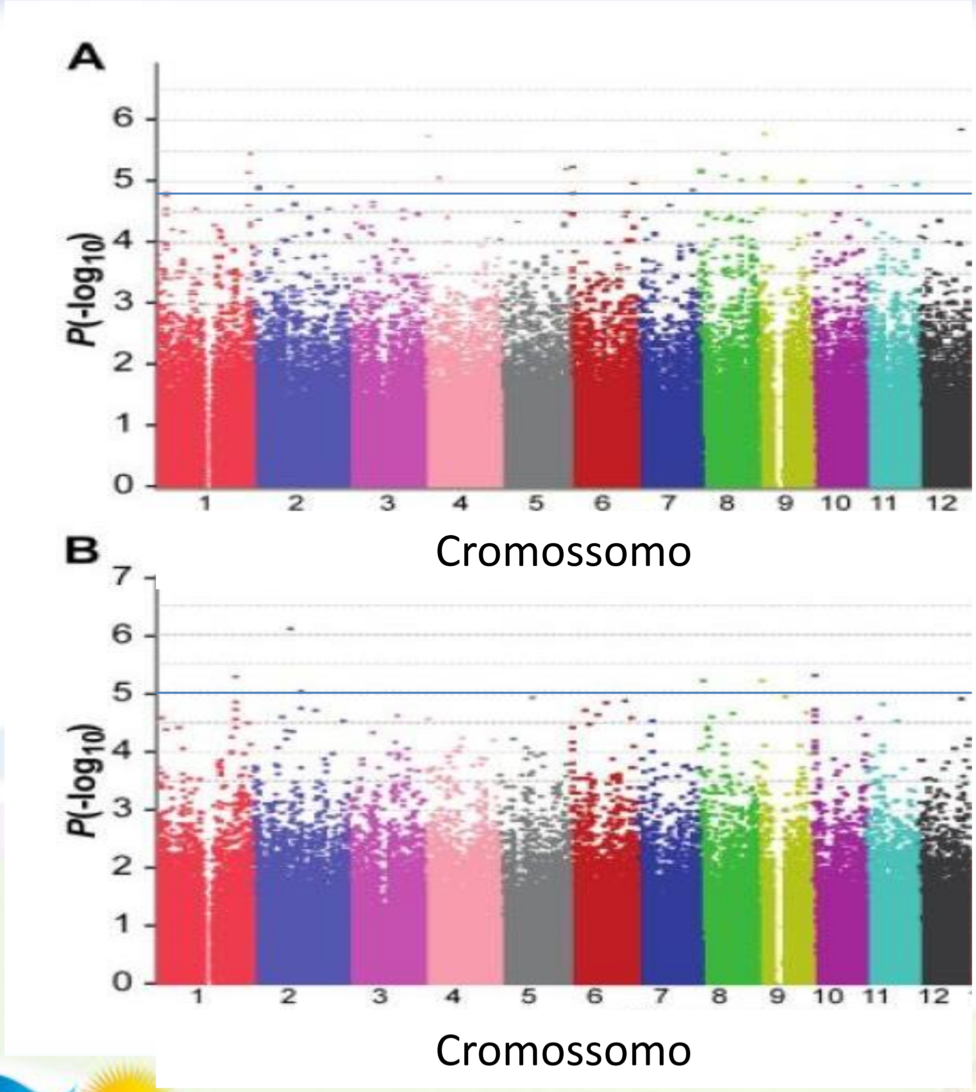
Esquema de trabalho/ Programa SGA

Material Vegetal	Seleção de indivíduos(1300) Extração de DNA
Avaliações fenotípicas	Avaliações fisiológicas(Ψam) Avaliações de campo(Produção, Vigor, SP, etc...) Avaliações de Laboratório (Parâmetros morfológicos e bioquímicos dos frutos)
Genotipagem	Mapeamento de sequencias (Grupos de diversidade, parentais) Mineração de SNPs Genotipagem
Estudos de Associação	Análises Estatísticas

Seleção Genômica Ampla

Produção

Tolerância à seca



Coffea canephora

Embrapa Cerrados, Planaltina-DF
(1.175m altitude)

População de Coffea canephora

- População de 3500 indivíduos (Março de 2008)
- Pool de sementes do campo experimental do INCAPER, contendo 48 parentais
- Introdução de híbridos do CIRAD
- (Clone 61/126 (Guinean x SG1+SG2) x A03 (SG1))

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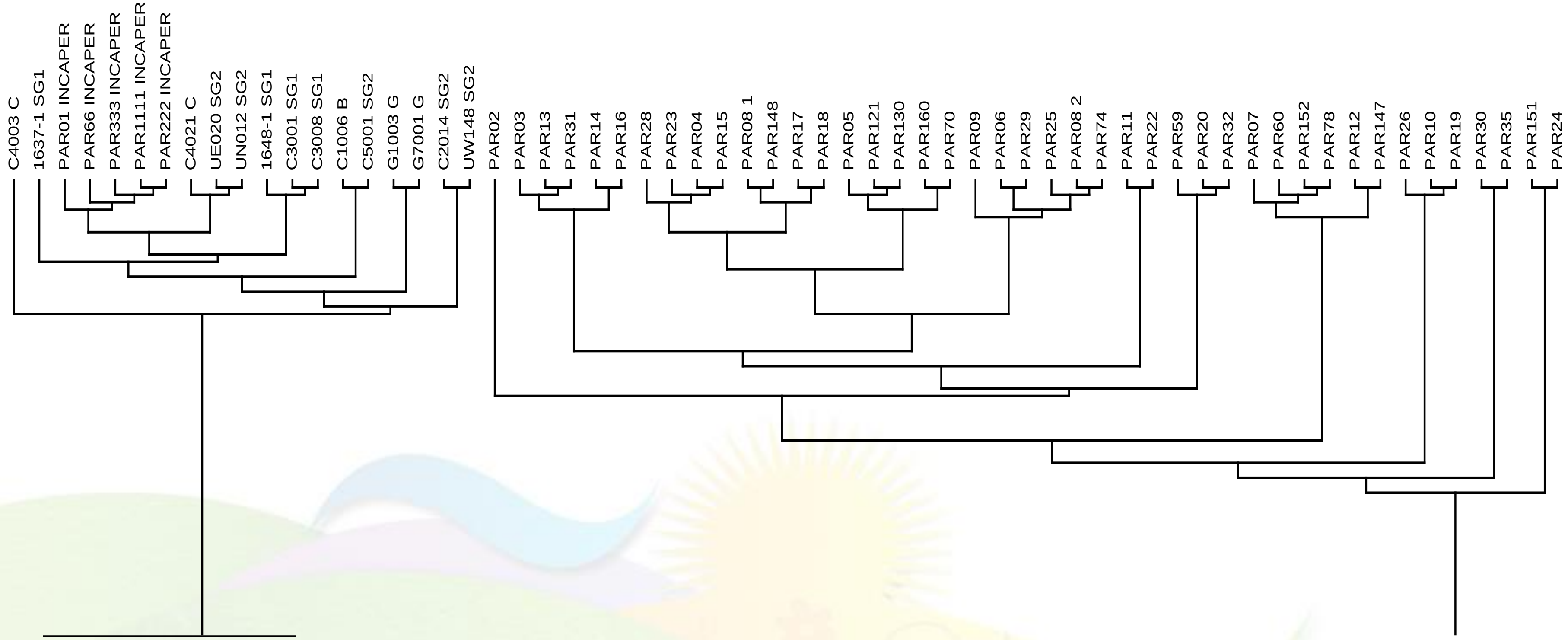
Diversidade Fenotípica

Diversidade genética

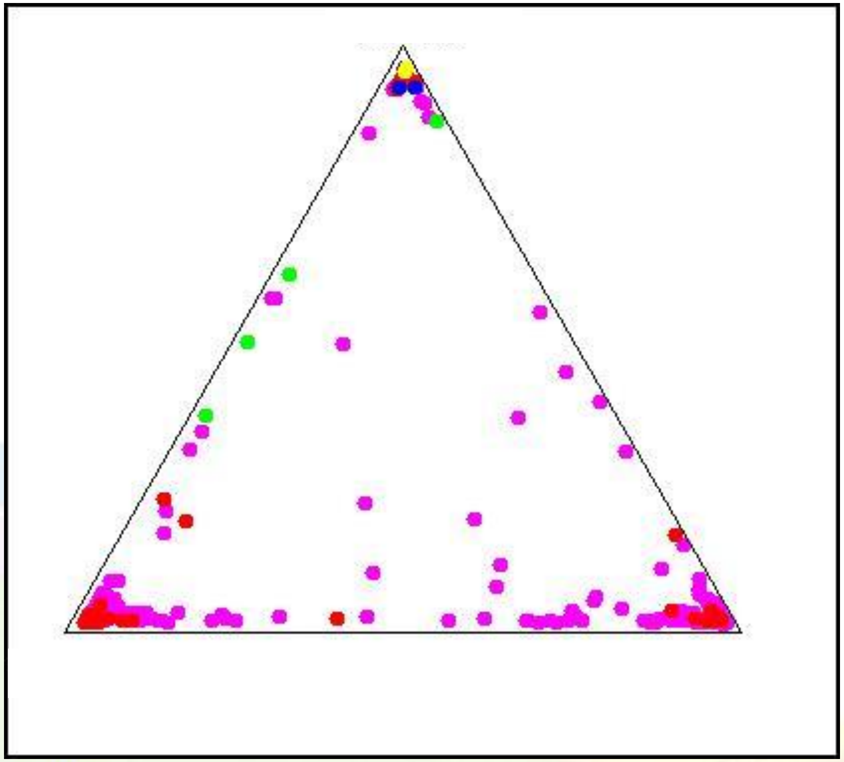
- 11 SSRs
- 48 parentais do Incaper
- 250 indivíduos

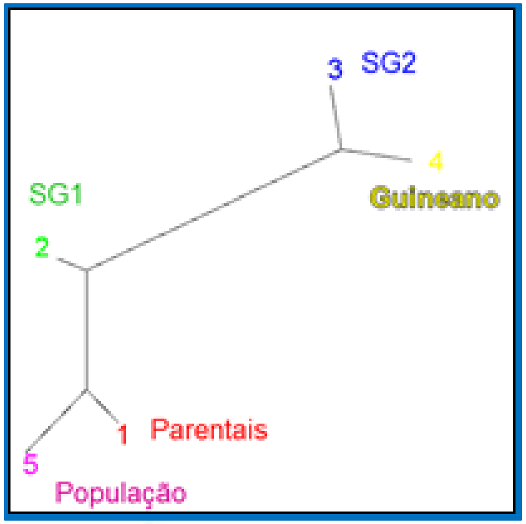
Var. 8111
Var. 8121
Var. 8131
Var. 8141-Robustão
Var. 8142 C. Vitoria



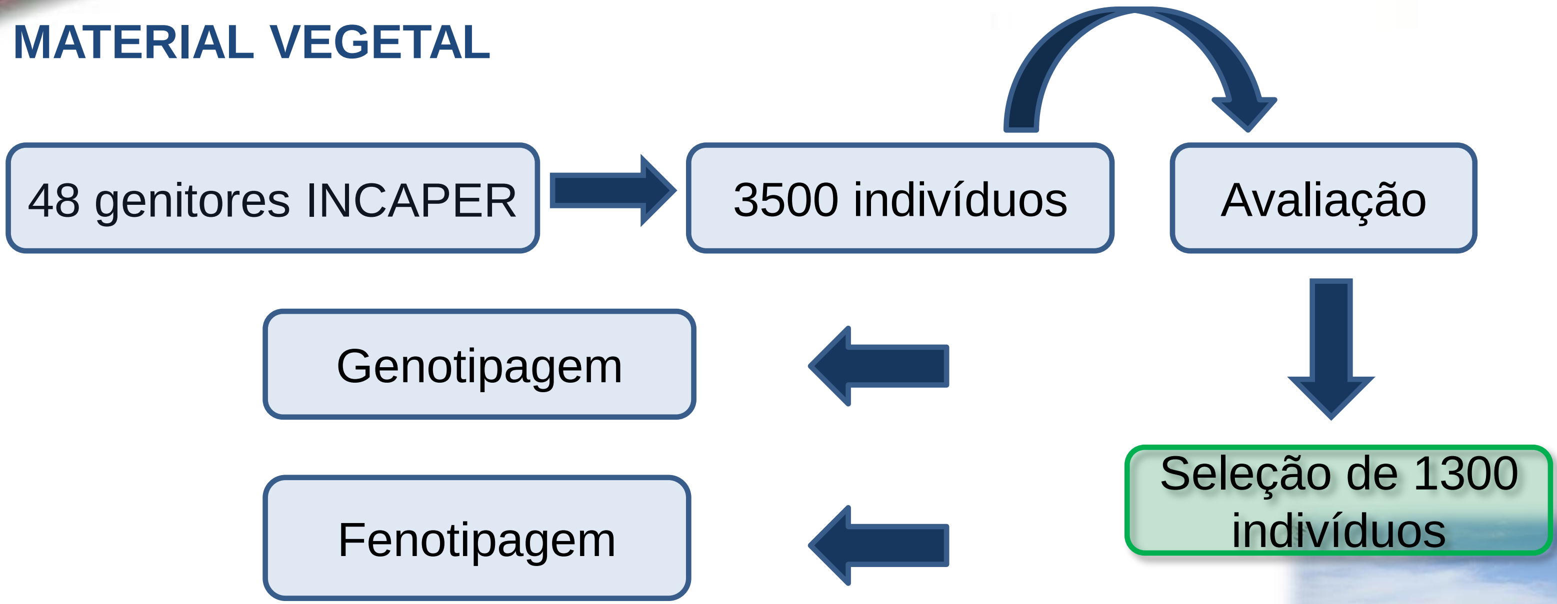
Diversidade Genética

- ● Parentais INCAPER
- ● População EMBRAPA
- ● Grupo SG1
- ● Grupo SG2
- ● Grupo Guineano





MATERIAL VEGETAL



48 genitores INCAPER

3500 indivíduos

Avaliação

Seleção de 1300 indivíduos

Genotipagem

Fenotipagem

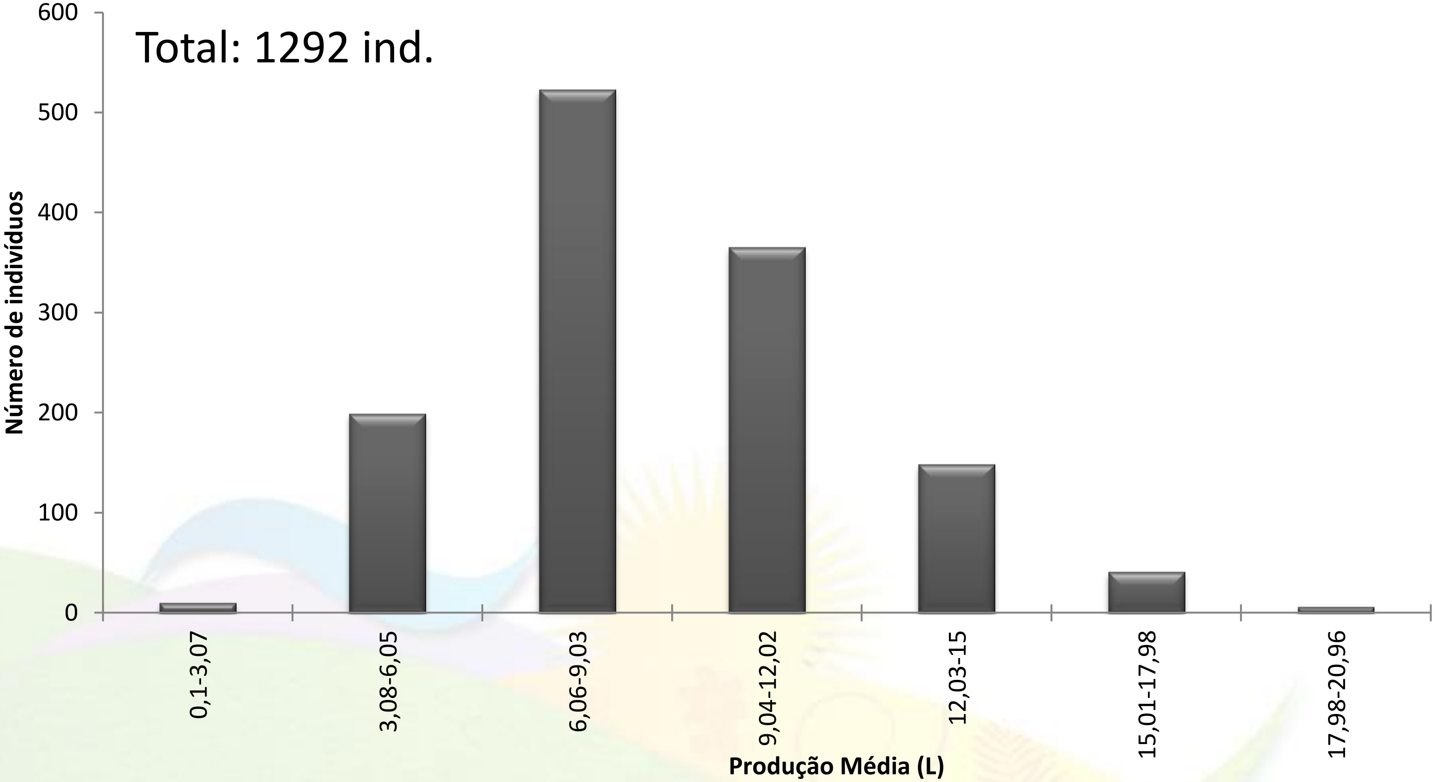
- SECA (Potencial hídrico de antemanhã-Ψam)
- Produção (2012/2013)
- Qualidade Física
    - Classificação quanto aos defeitos e impurezas
    - Peneira
    - Peso de 100 grãos
- Medida e forma dos frutos

Avaliações fenotípicas

- Produção (2011/12; 2012/13)
- Vigor, Seca de Ponteiros, Ferrugem
- Morfologia de frutos
  - (Tamanho e formato dos frutos/grãos; Peneira)
- Potencial hídrico de antemanhã (Ψam)
- Bioquímica (NIRs)

Avaliações fenotípicas

Produção (Safras 2011/12; 2012/13).



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Avaliações fenotípicas

Morfologia de frutos

Total: 1292 ind.

Planta	Medidas (cm)	E1	E2	E3	E4	E5	Média	Foto
L1P15	Área	3,1942	3,0670	3,1608	2,0485	2,8882	2,8717	
	Perímetro	10,2846	10,0100	10,0965	8,3837	9,6723	9,6894	
	Menor eixo	0,8476	0,8548	0,8979	0,6393	0,8476	0,8174	
	Maior eixo	1,1996	1,1421	1,1206	1,0200	1,0846	1,1134	
L1P49	Área	2,7595	3,0292	2,9748	2,2486	2,4950	2,7014	
	Perímetro	9,5112	9,8257	9,7624	8,5690	9,0959	9,3528	
	Menor eixo	0,8045	0,9194	0,8907	0,7327	0,7470	0,8189	
	Maior eixo	1,0918	1,0487	1,0631	0,9769	1,0631	1,0487	
L1P65	Área	2,7543	2,7689	3,3083	2,4859	2,9070	2,8449	
	Perímetro	9,4084	9,4497	10,3036	8,9968	9,6568	9,5631	
	Menor eixo	0,8476	0,8404	0,9338	0,7758	0,8763	0,8548	
	Maior eixo	1,0344	1,0487	1,1277	1,0200	1,0559	1,0573	
L2P8	Área	3,5965	3,7512	3,4234	3,1398	3,5732	3,4968	
	Perímetro	10,8373	11,0463	10,5376	10,0058	10,7474	10,6349	
	Menor eixo	0,9266	0,9553	0,9194	0,9338	0,9482	0,9367	
	Maior eixo	1,2355	1,2499	1,1852	1,0703	1,1996	1,1881	
L4P51	Área	2,5131	2,3896	2,6324	2,6324	2,7232	2,5781	
	Perímetro	8,9727	8,7076	9,1905	9,1905	9,3274	9,0777	
	Menor eixo	0,8189	0,8404	0,8332	0,8332	0,8620	0,8375	
	Maior eixo	0,9769	0,9051	1,0056	1,0056	1,0056	0,9798	

Avaliações fenotípicas

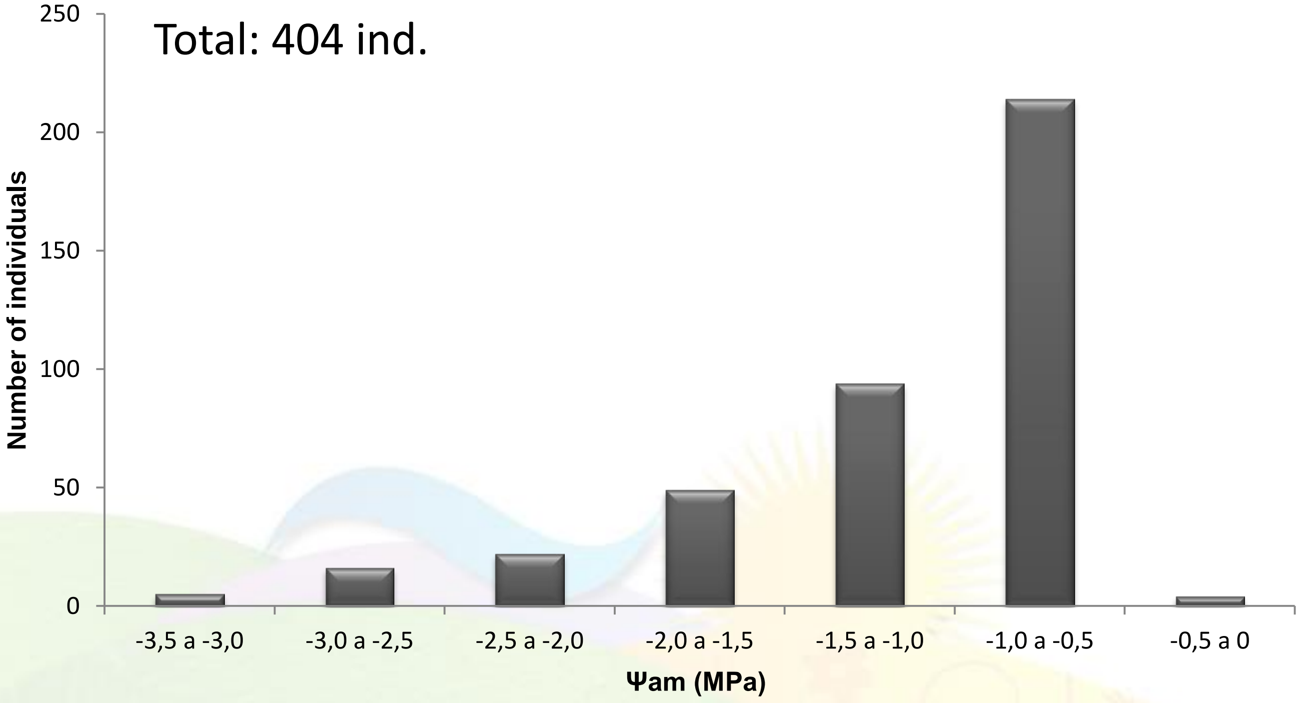
Peneira.

Total: 1292 ind.

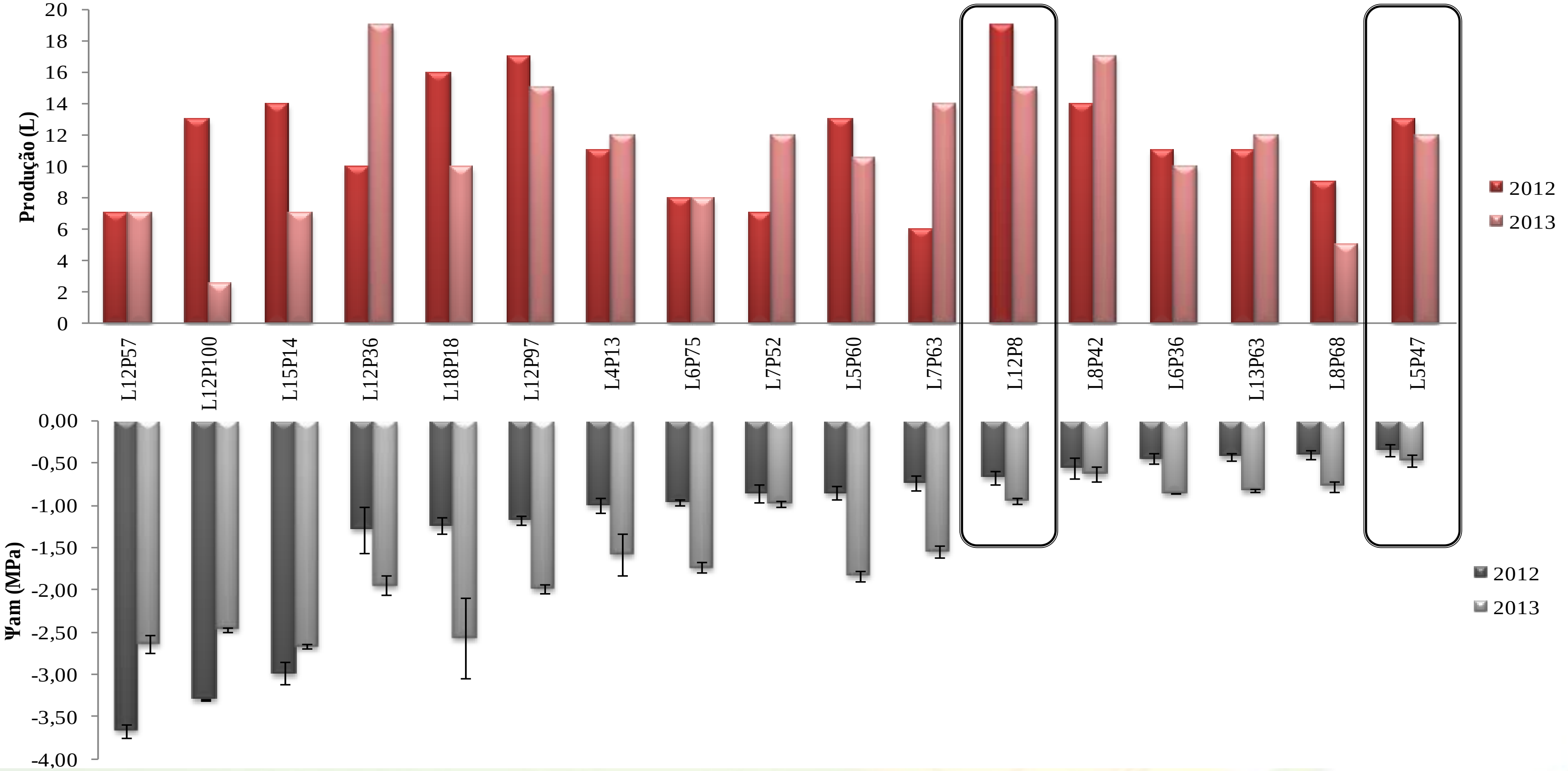
Linha	Planta	Peso inicial	Peneiras (gramas)															Peso de 100 grãos
			19	13	18	12	17	11	16	10	15	9	14	13	8	12	Final	
1	15	98,978	0,427	5,12	10,888	13,455	31,255	7,1	23,169	3,445	2,987	0,692	0,222	0,093	0,047	0	0	18,964
2	10	98,977	1,208	2,951	2,368	22,948	15,352	14,382	22,983	6,684	8,271	0,8	0,971	0,077	0	0	0	13,85
5	60	98,97	8,304	23,666	21,004	14,626	22,828	2,18	4,112	1,406	0,384	0,101	0,196	0	0	0	0	19,642
8	42	100	0,371	3,461	0,957	12,412	12,929	11,323	25,453	10,941	11,446	6,584	2,101	1,501	1,52	0,167	0	17,045
12	68	99,679	0,828	3,253	0,836	11,368	15,698	13,821	30,097	9,441	10,897	1,642	1,276	0,286	0,069	0	0	16,042
18	100	97,61	0,181	0	0,148	10,38	14,125	10,359	27,088	7,622	18,036	3,024	2,482	0,967	0,222	0,128	0,027	14,301
21	36	98,836	3,963	5,57	22,041	17,924	25,757	5,953	11,88	1,769	2,643	0,962	0,353	0,076	0	0	0,111	16,218

Avaliações fenotípicas

Ψam.



Avaliações fenotípicas



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Ministry of
Agriculture, Livestock
and Food Supply

BRAZILIAN GOVERNMENT
BRASIL

Ferramentas Genômicas

Genômica Funcional

http://www.lge.ibi.unicamp.br/cafe/

https://alanine.cenargen.embrapa.br/

Projeto Genoma Café

INICIATIVA:
Consórcio Brasileiro de Pesquisa e Desenvolvimento do Café - EMBRAPA CAFÉ
FAPESP
EMBRAPA RECURSOS GENÉTICOS E BIOTECNOLOGIA

ADMINISTRAÇÃO FINANCEIRA: INSTITUTO UNIEMP

COLABORADORES: IAC, UNICAMP, USP, UNESP, IAPAR, UFLA, UFV, EPAMIG E INCAPER.

(http://www.coffeegenome.org)

International Coffee Genome Network

Founding meeting

Paris – 4 & 5 April 2005

Coffee Genomics (*C. Canephora*)

International CanePhora Sequencing Consortium

ICSC

🇫🇷 Patrick Wincker, Benoit Bertrand, Xavier Argout, Alexander de Kochko, Philippe Lashermes

🇺🇸 Ray Ming, Victor A. Albert, Steve Rounsley, Chifumi Nagai

🇧🇷 Alan C. Andrade

🇮🇹 Giorgio Graziosi, Giovanni Giuliano

🇦🇺 Robert Henry

🇨🇦 David Sankoff

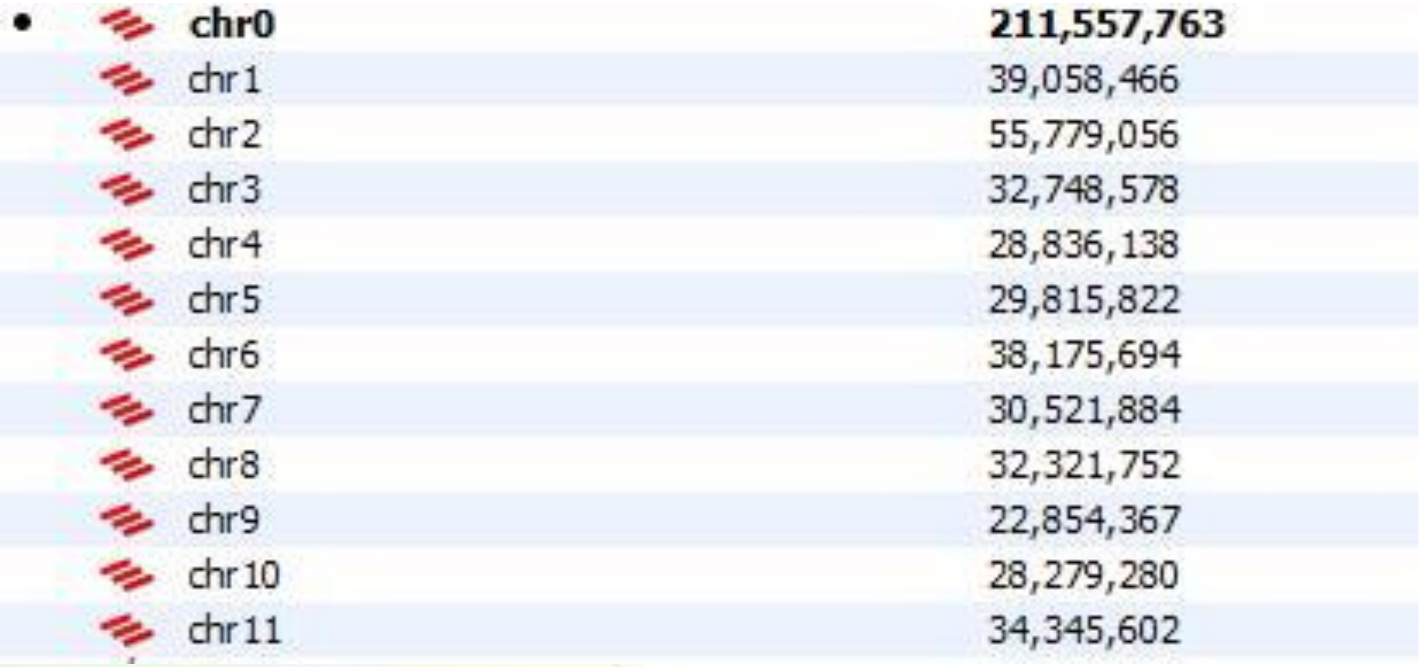
🇮🇳 Jayarama

Artigo submetido !

Coffee Genomics

ICSC

International • CanePhora • Sequencing • Consortium



	Seq. Length
• **chr0**	**211,557,763**
chr1	39,058,466
chr2	55,779,056
chr3	32,748,578
chr4	28,836,138
chr5	29,815,822
chr6	38,175,694
chr7	30,521,884
chr8	32,321,752
chr9	22,854,367
chr10	28,279,280
chr11	34,345,602

Re-sequenciamento

- Paired end

•**Libraries**

- 500 pb < fragment < 900pb 700pb
- Kit *TruSeq DNA Sample Prep* da illumina®
- Quantificada por PCR quantitativo em tempo real (qPCR)
- Adaptadores
  - Read 1

    AGATCGGAAGAGCACACGTCTGAACTCCAGTCACNNNNNNATCTCGTATGCCGTCTTCTGCTTG
  - Read 2

    AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTAGATCTCGGTGGTCGCCGTATCAT
- HiSeq2000
- Sequencing Kit SBS version 3.
- Fastq generated with Casava 1.8.2.

Re-sequenciamento

Conilons

Bulk de indivíduos

Pool	Grupo	Nº de ind.
C1	Conilon	5
C2	Conilon	1
C3	Conilon	5
C4	Conilon	4
C5	Conilon	4
C6	Conilon	5
C7	Conilon	6
C8	Conilon	2
C9	Conilon	3
C10	Conilon	4
C11	Conilon	2
C12	Conilon	3
C13	Conilon	2
C14	Conilon	2

Re-sequenciamento

Diversidade

Pool	Sub-Grupos	Grupos	Nº ind.
D1	Luki	SG1	10
D2	Niaouli	SG1	9
D3	Nana	C	10
D4	Libengue	B	9
D5	INEAC	SG2	4
D6	Erect	SG2	2
D7	Nganda	SG2	2
D8	Wild	SG2	3
D9	Pelezi	G	1
D10	Mouniandougou	G	1

Table 1 Characteristics and origins of the *C. canephora* diversity groups

Name	Origin	Diversity group	Size	Type
Nana	Central African Republic	C	92	Spontaneous
Pélézi	Ivory Coast	GP	35	Spontaneous
Guinean	Ivory Coast – Guinea	G	128	Cultivated & spontaneous
SG1 Bulk	Atlantic Coast (Gabon – Congo – Democratic Republic of Congo)	SG1	16	Cultivated & spontaneous
SG2 Bulk	Congo basin	SG2	85	Cultivated

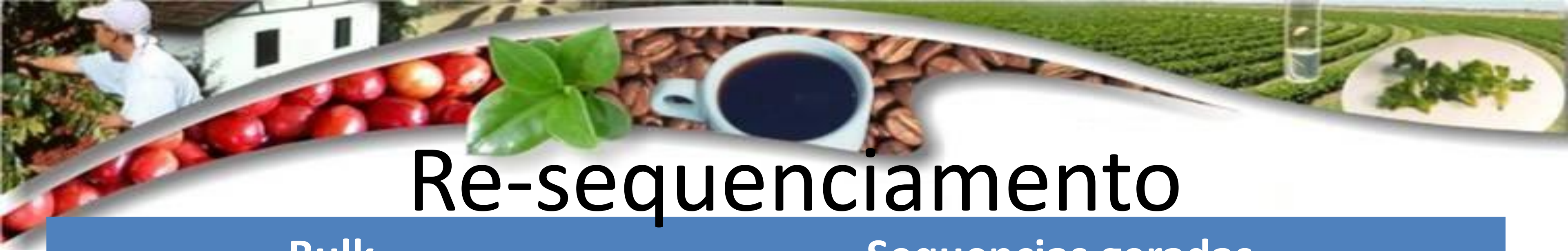
Fonte: Cubry et al, 2013

Re-sequenciamento

Bulk	Sequencias geradas
Conilon	704.388.334
Grupos de Diversidade	591.003.832

SEQUÊNCIAS MAPEADAS POR CROMOSSOMO NOS GRUPOS DE CONILON

GRUPO		C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12
SEQUÊNCIAS MAPEADAS POR CROMOSSOMO	Chr 0	22.847.673	23.266.498	26.251.519	22.920.224	26.500.581	27.815.681	17.130.483	19.537.273	22.522.141	17.383.775	17.976.528	24.389.429
	Chr 1	2.747.574	2.606.043	2.860.528	2.566.752	3.011.794	3.260.396	1.981.073	2.222.365	2.661.276	1.932.017	2.027.509	2.932.716
	Chr 2	3.745.735	3.461.916	3.694.033	3.362.678	3.978.005	4.306.896	2.622.638	2.981.014	3.600.217	2.572.280	2.672.530	3.958.483
	Chr 3	2.175.734	2.027.575	2.213.335	2.030.661	2.354.675	2.526.614	1.575.480	1.815.314	2.133.057	1.570.070	1.608.337	2.306.835
	Chr 4	1.980.196	1.878.082	2.023.810	1.828.973	2.166.485	2.310.580	1.423.346	1.602.356	1.945.111	1.406.433	1.448.269	2.111.932
	Chr 5	2.195.347	2.047.966	2.268.753	2.019.978	2.363.754	2.557.089	1.560.357	1.759.123	2.096.641	1.523.240	1.593.879	2.304.424
	Chr 6	2.584.643	2.522.983	2.728.238	2.452.092	2.891.910	3.097.469	1.897.330	2.146.752	2.586.767	1.870.663	1.949.751	2.813.507
	Chr 7	2.442.490	2.976.066	3.546.638	2.995.165	3.333.671	3.463.330	2.325.487	2.758.670	2.726.545	2.370.544	2.208.992	3.008.706
	Chr 8	2.261.443	2.186.163	2.402.402	2.162.838	2.522.483	2.802.880	1.675.104	1.884.538	2.228.929	1.610.152	1.682.928	2.536.347
	Chr 9	1.552.561	1.495.944	1.609.198	1.461.082	1.723.491	1.798.908	1.113.532	1.280.404	1.533.941	1.132.404	1.164.787	1.640.864
	Chr 10	1.915.275	1.851.555	1.990.848	1.831.830	2.122.887	2.305.051	1.396.694	1.604.950	1.915.852	1.384.972	1.441.490	2.117.205
	Chr 11	2.565.490	2.386.719	2.607.106	2.376.587	2.763.460	3.008.855	1.834.382	2.060.489	2.461.882	1.800.893	1.833.626	2.751.430
SEQUÊNCIAS MAPEADAS		49.014.161	48.707.510	54.196.408	48.008.860	55.733.196	59.253.749	36.535.906	41.653.248	48.412.359	36.557.443	37.608.626	52.871.878
SEQUÊNCIAS NÃO MAPEADAS		2.921.469	4.144.078	5.529.146	4.119.966	4.899.734	4.275.957	4.013.444	5.915.864	5.017.223	4.249.809	4.577.874	5.810.456
TOTAL DE SEQUÊNCIAS		**51.935.630**	**52.851.588**	**59.725.554**	**52.128.826**	**60.632.930**	**63.529.706**	**40.549.350**	**47.569.112**	**53.429.582**	**40.807.252**	**42.186.500**	**58.682.334**



Re-sequenciamento

Bulk	Sequencias geradas
Conilon	704.388.334
Grupos de Diversidade	591.003.832

SEQUÊNCIAS MAPEADAS POR CROMOSSOMO NOS GRUPOS DE DIVERSIDADE											
GRUPO		**D1**	**D2**	**D3**	**D4**	**D5**	**D6**	**D7**	**D8**	**D9**	**D10**
SEQUÊNCIAS MAPEADAS POR CROMOSSOMO	**Chr 0**	27.695.876	27.101.635	16.271.875	23.141.784	23.074.050	28.571.894	26.753.857	29.538.728	18.418.614	18.892.558
	Chr 1	3.431.114	3.232.529	2.017.466	2.950.498	2.763.441	3.547.441	3.299.137	3.766.199	2.173.713	2.341.398
	Chr 2	4.603.996	4.309.656	2.676.556	4.054.325	3.743.728	4.791.640	4.540.919	5.078.303	2.970.096	3.265.888
	Chr 3	2.674.003	2.527.164	1.623.370	2.377.438	2.176.914	2.774.354	2.607.283	2.966.314	1.716.333	1.836.306
	Chr 4	2.481.739	2.322.979	1.493.817	2.170.156	2.023.848	2.539.815	2.432.384	2.746.025	1.598.272	1.717.224
	Chr 5	2.671.215	2.526.554	1.596.948	2.342.968	2.176.214	2.803.213	2.639.585	3.018.461	1.735.114	1.848.829
	Chr 6	3.258.288	3.078.079	1.901.349	2.804.512	2.569.606	3.271.167	3.106.704	3.502.127	2.088.515	2.262.538
	Chr 7	3.746.639	3.312.451	1.836.496	2.518.417	2.547.593	3.260.074	2.888.482	3.354.396	1.874.394	2.171.182
	Chr 8	2.838.105	2.760.295	1.608.770	2.471.645	2.267.623	2.922.573	2.775.392	3.076.853	1.835.139	1.968.567
	Chr 9	1.949.437	1.807.508	1.170.531	1.713.601	1.600.820	1.999.471	1.924.634	2.169.494	1.294.014	1.368.028
	Chr 10	2.437.177	2.313.103	1.390.730	2.084.703	1.906.496	2.426.099	2.304.655	2.616.276	1.543.520	1.688.319
	Chr 11	3.081.853	2.980.733	1.865.377	2.667.971	2.523.213	3.233.074	3.090.200	3.405.446	2.011.636	2.137.961
SEQUÊNCIAS MAPEADAS		60.869.442	58.272.686	35.453.285	51.298.018	49.373.546	62.140.815	58.363.232	65.238.622	39.259.360	41.498.798
SEQUÊNCIAS NÃO MAPEADAS		3.988.502	11.152.922	8.002.597	4.918.534	10.100.290	5.181.175	3.473.498	5.587.170	11.452.480	5.378.860
TOTAL DE SEQUÊNCIAS		**64.857.944**	**69.425.608**	**43.455.882**	**56.216.552**	**59.473.836**	**67.321.990**	**61.836.730**	**70.825.792**	**50.711.840**	**46.877.658**

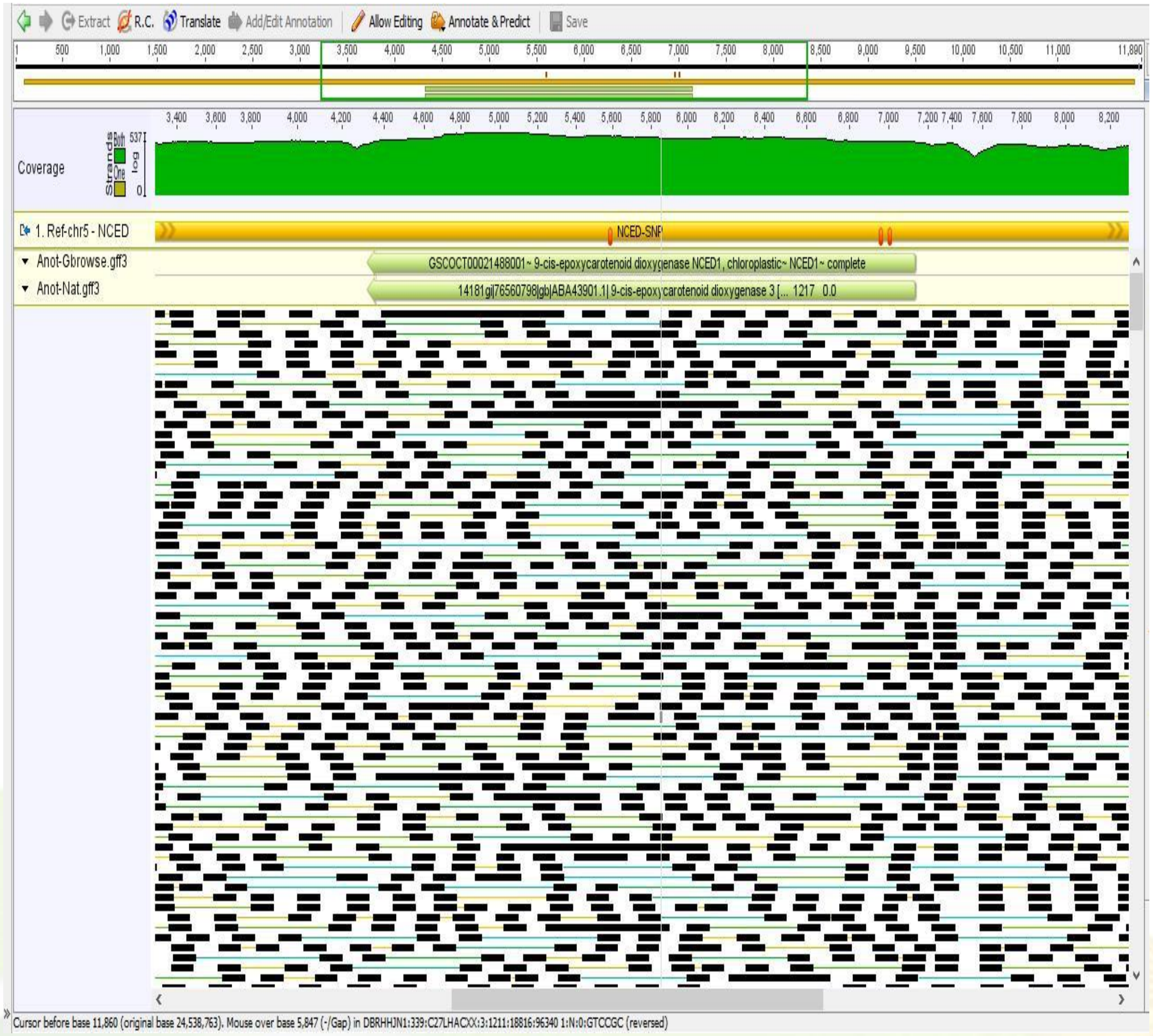
Bioinformática

Sequenciamento	Produção de sequencias
Mapeamento	Mapeamento das sequencias no genoma de referência
Refinamento	Realinhamento local; recalibração de qualidade (estimativa de *PHRED scores*)
Mineração de SNPs	Parâmetros de cobertura (> 30%); qualidade; bias na fase de leitura.

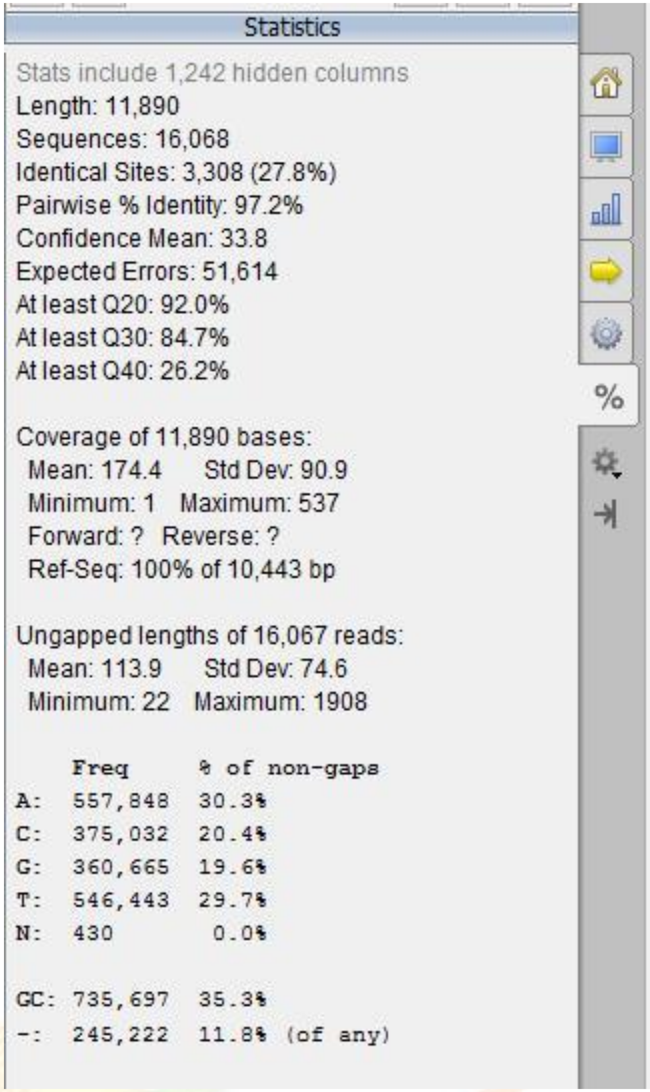
DePristo MA, et al. A framework for variation discovery and genotyping using next-generation DNA sequencing data. Nat Genet. 2011 May;43(5):491-8.

Nielsen R, Paul JS, Albrechtsen A, Song YS. Genotype and SNP calling from next-generation sequencing data. Nat Rev Genet. 2011 Jun;12(6):443-51.

Realinhamento Local



Cursor before base 11,860 (original base 24,538,763). Mouse over base 5,847 (-/Gap) in DBRHHJN1:339:C27LHACXX:3:1211:18816:96340 1:N:0:GTCCGC (reversed)



Statistics

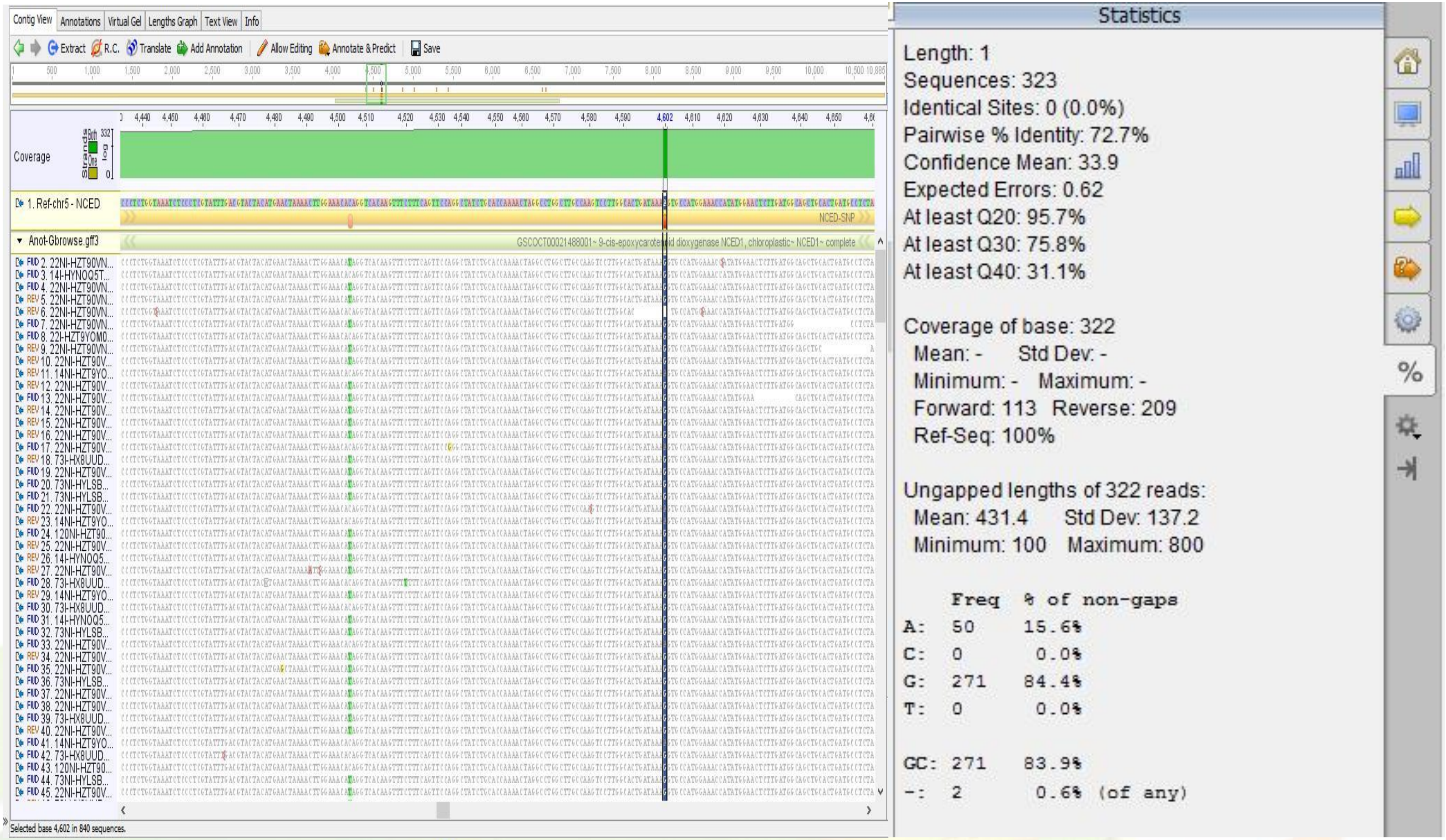
Stats include 1,242 hidden columns
Length: 11,890
Sequences: 16,068
Identical Sites: 3,308 (27.8%)
Pairwise % Identity: 97.2%
Confidence Mean: 33.8
Expected Errors: 51,614
At least Q20: 92.0%
At least Q30: 84.7%
At least Q40: 26.2%

Coverage of 11,890 bases:
Mean: 174.4 Std Dev: 90.9
Minimum: 1 Maximum: 537
Forward: ? Reverse: ?
Ref-Seq: 100% of 10,443 bp

Ungapped lengths of 16,067 reads:
Mean: 113.9 Std Dev: 74.6
Minimum: 22 Maximum: 1908

```
    Freq      % of non-gaps
A:  557,848   30.3%
C:  375,032   20.4%
G:  360,665   19.6%
T:  546,443   29.7%
N:  430        0.0%

GC: 735,697   35.3%
-:  245,222   11.8% (of any)
```

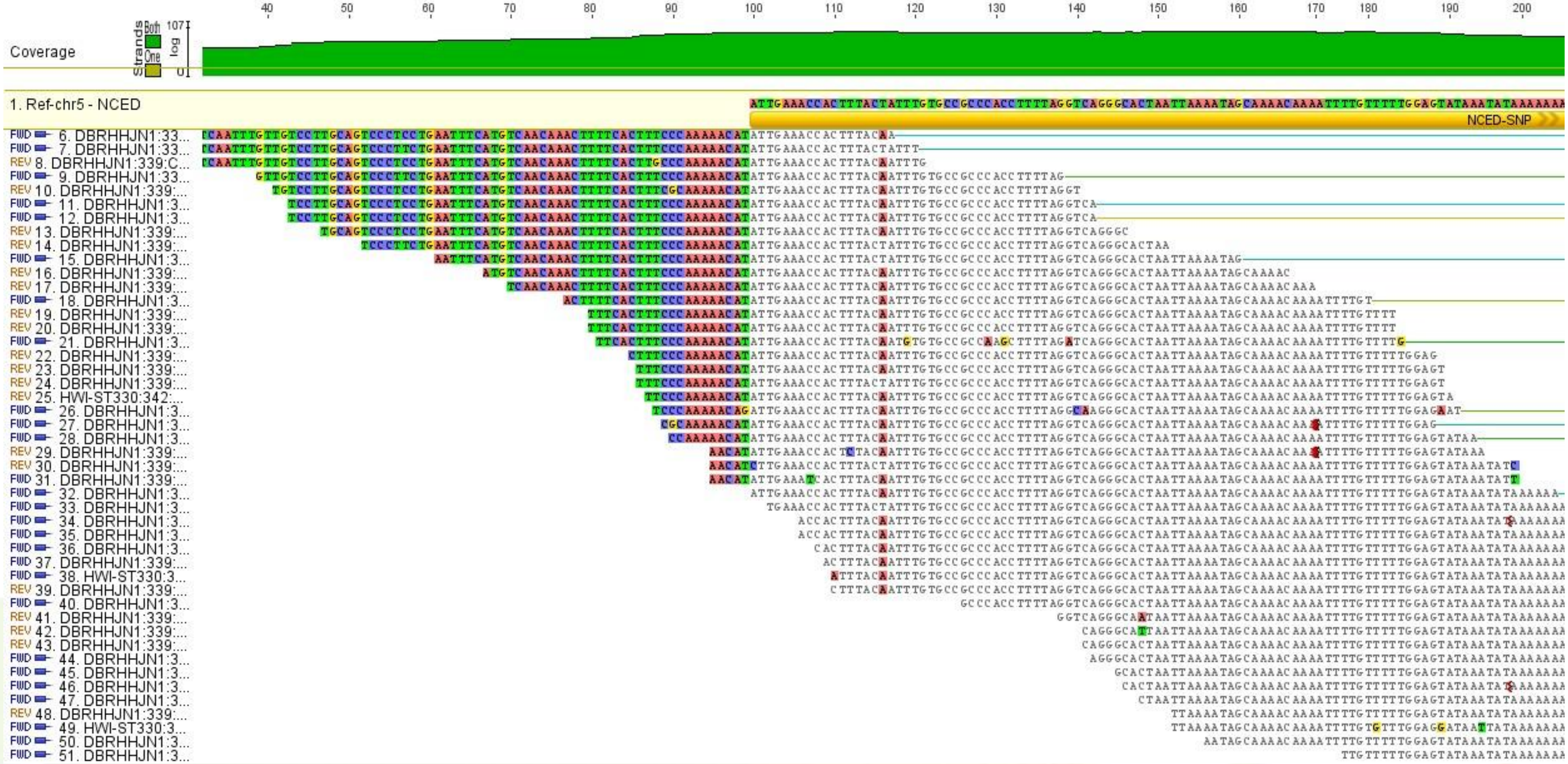
Identificação de SNPs



Selected base 4,602 in 840 sequences.

```
Length: 1
Sequences: 323
Identical Sites: 0 (0.0%)
Pairwise % Identity: 72.7%
Confidence Mean: 33.9
Expected Errors: 0.62
At least Q20: 95.7%
At least Q30: 75.8%
At least Q40: 31.1%

Coverage of base: 322
  Mean: -      Std Dev: -
  Minimum: -    Maximum: -
  Forward: 113   Reverse: 209
  Ref-Seq: 100%

Ungapped lengths of 322 reads:
  Mean: 431.4      Std Dev: 137.2
  Minimum: 100    Maximum: 800

      Freq   % of non-gaps
A:    50     15.6%
C:    0       0.0%
G:    271    84.4%
T:    0       0.0%

GC:   271    83.9%
-:    2       0.6% (of any)
```

Alinhamento

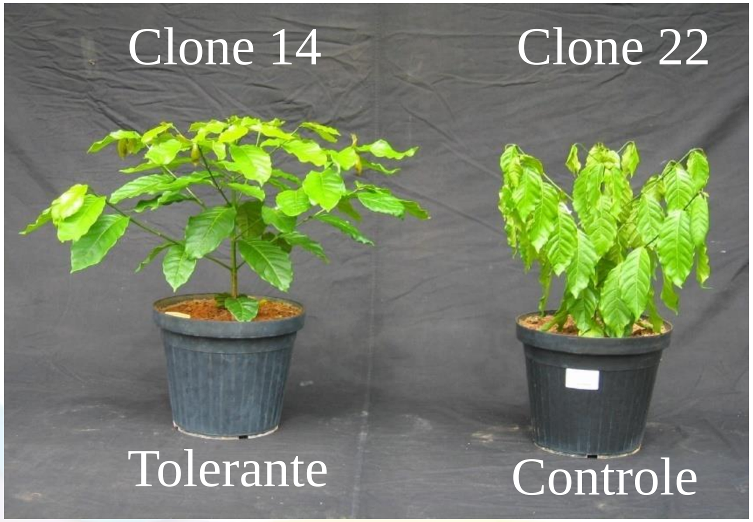


Estado da Arte

Material Vegetal	Seleção dos indivíduos (1300) Extração de DNA	✓
Fenotipagem	Avaliações fisiológicas (Ψam) Avaliações de Campo (Produção) Avaliações de laboratório (Parâmetros morfológicos e bioquímicos)	✓
Genotipagem	Mapeamento das sequencias (Grupos de diversidade, parentais) Mineração de SNPs Genotipagem	✓ ✓ X
Estudos de Associação	Análises Estatísticas	X

Re-sequenciamento

Tolerância à Seca e Nematóides



Nematóides

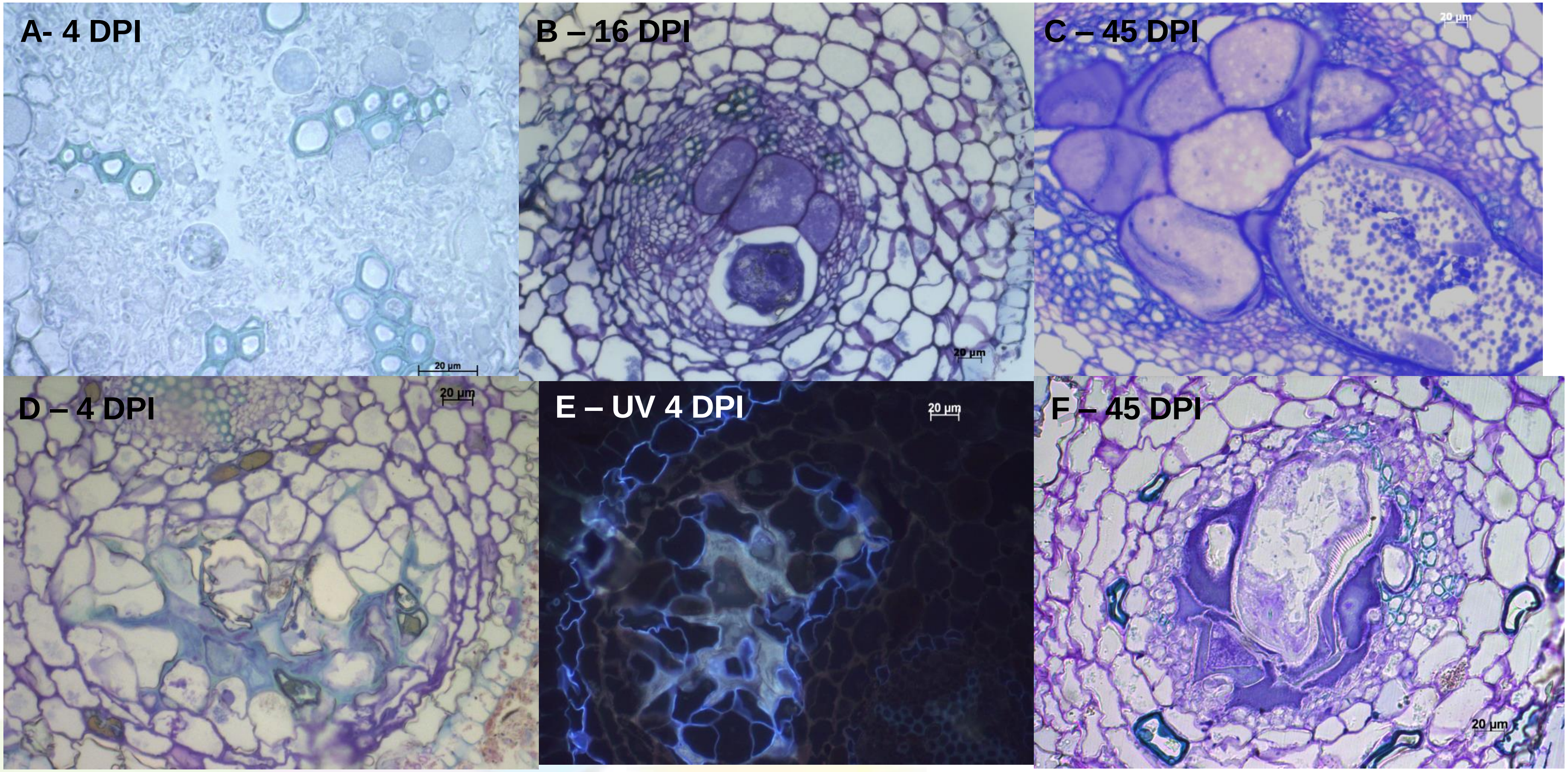


Fig. **A-C** clone 22, *Meloidogyne paranaensis* infection; **D-E** Incompatible reaction of *M. paranaensis* with clone 14 showing HR (D-E) e Cell-death (F) **Lima et al.2012**

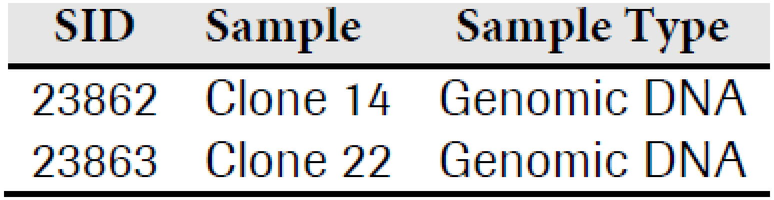
Re-sequenciamento

Clones 22 e 14

Genome Sequencer FLX+

Roche

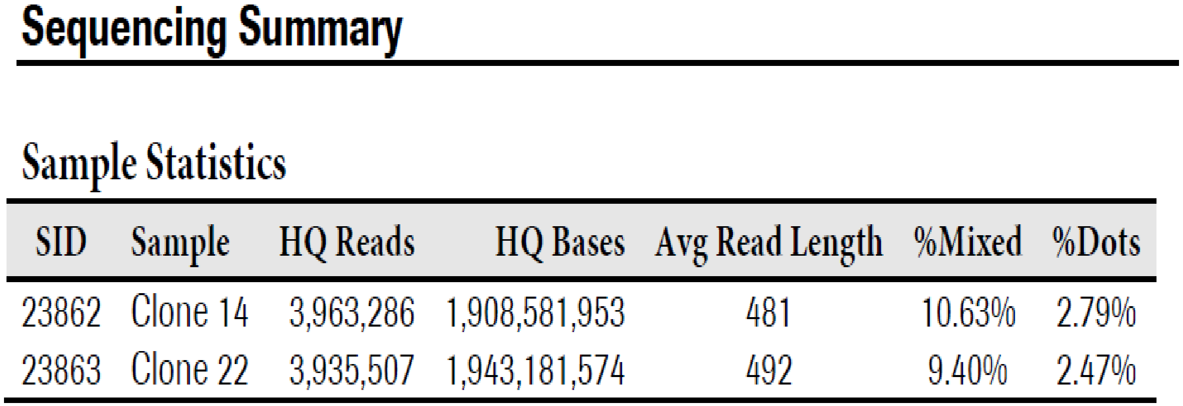
Whole genome sequencing



SID	Sample	Sample Type
23862	Clone 14	Genomic DNA
23863	Clone 22	Genomic DNA

6 runs

3 runs/library

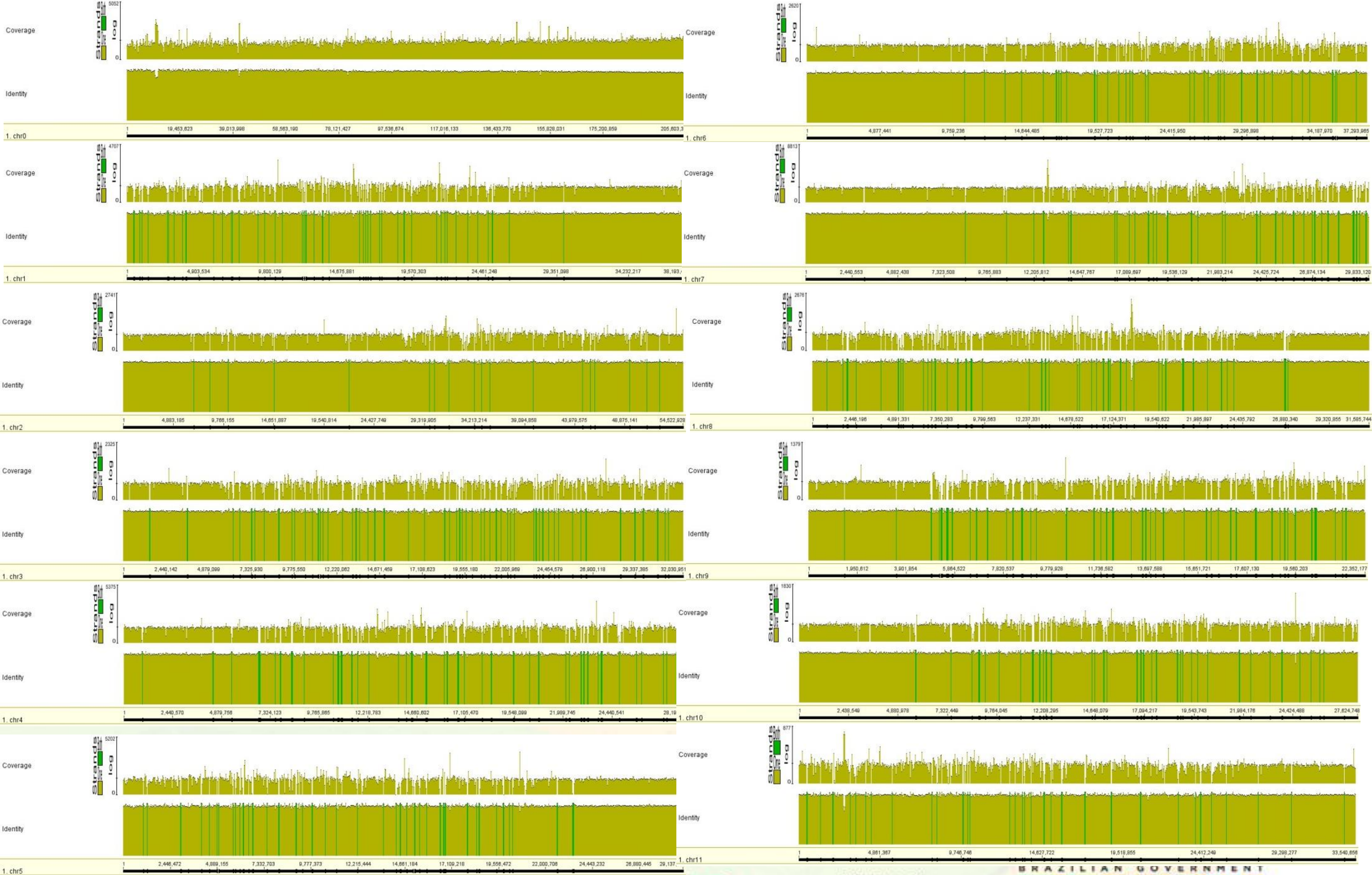


Sequencing Summary

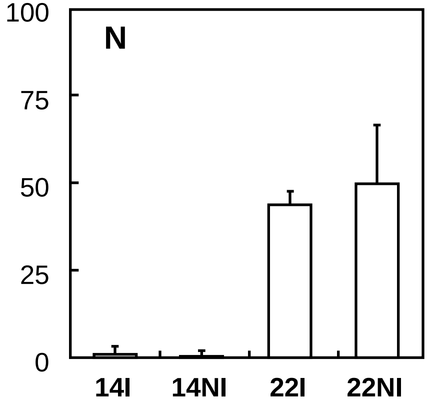
Sample Statistics

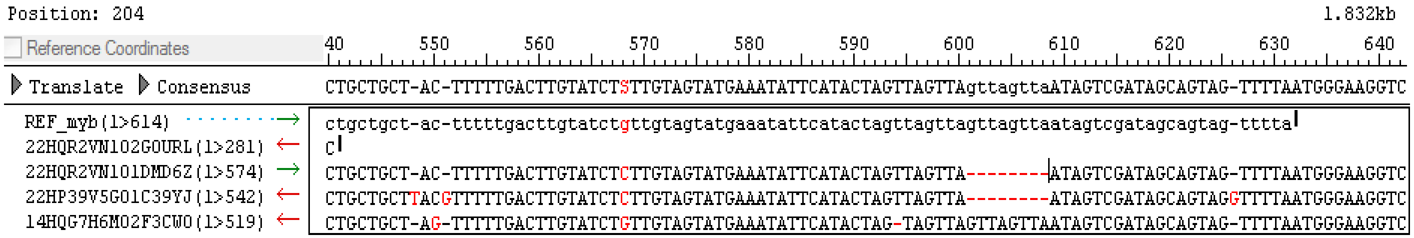
SID	Sample	HQ Reads	HQ Bases	Avg Read Length	%Mixed	%Dots
23862	Clone 14	3,963,286	1,908,581,953	481	10.63%	2.79%
23863	Clone 22	3,935,507	1,943,181,574	492	9.40%	2.47%

Re-sequenciamento

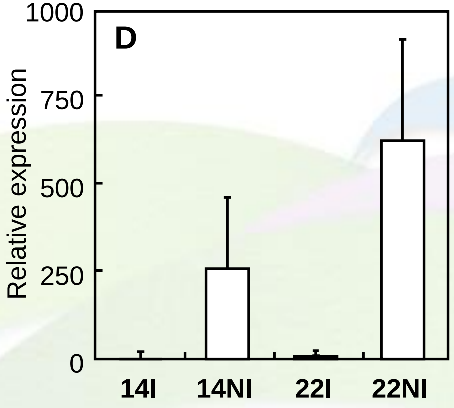


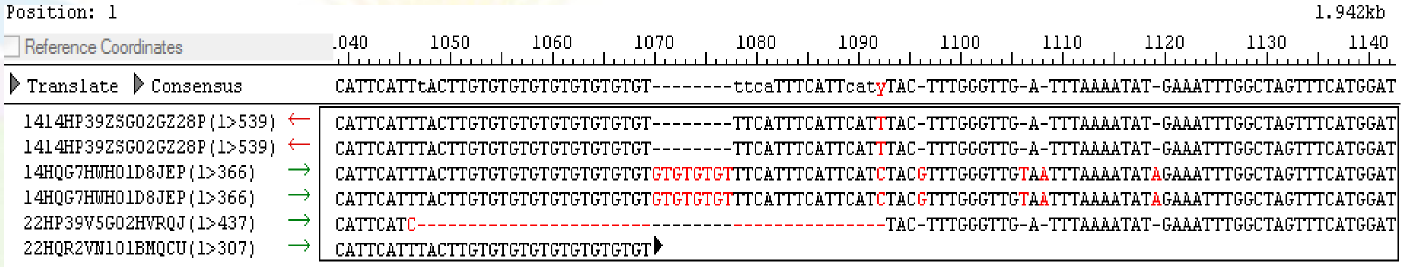
Re-sequenciamento





```
Position: 204                                                                                                  1.832kb
                     40        550        560        570        580        590        600        610        620        630        640
Consensus            CTGCTGCT-AC-TTTTTGACTTGTATCTSTTGTAGTATGAAATATTCATACTAGTTAGTTAgttagttaATAGTCGATAGCAGTAG-TTTTAATGGGAAGGTC
REF_myb(1>614)       ctgctgct-ac-tttttgacttgtatctgttgtagtatgaaatattcatactagttagttagttagttaatagtcgatagcagtag-tttta
22HQR2VN102G0URL(1>281)  C
22HQR2VN101DMD6Z(1>574)  CTGCTGCT-AC-TTTTTGACTTGTATCTCTTGTAGTATGAAATATTCATACTAGTTAGTTA--------ATAGTCGATAGCAGTAG-TTTTAATGGGAAGGTC
22HP39V5G01C39YJ(1>542)  CTGCTGCTTACGTTTTTGACTTGTATCTCTTGTAGTATGAAATATTCATACTAGTTAGTTA--------ATAGTCGATAGCAGTAGGTTTTAATGGGAAGGTC
14HQG7H6M02F3CW0(1>519)  CTGCTGCT-AG-TTTTTGACTTGTATCTGTTGTAGTATGAAATATTCATACTAG-TAGTTAGTTAGTTAATAGTCGATAGCAGTAG-TTTTAATGGGAAGGTC
```





```
Position: 1                                                                                                    1.942kb
                       .040       1050       1060       1070       1080       1090       1100       1110       1120       1130       1140
Consensus              CATTCATTtACTTGTGTGTGTGTGTGTGTGT--------ttcaTTTCATTcatyTAC-TTTGGGTTG-A-TTTAAAATAT-GAAATTTGGCTAGTTTCATGGAT
1414HP39ZSG02GZ28P(1>539)  CATTCATTTACTTGTGTGTGTGTGTGTGTGT--------TTCATTTCATTCATTTAC-TTTGGGTTG-A-TTTAAAATAT-GAAATTTGGCTAGTTTCATGGAT
1414HP39ZSG02GZ28P(1>539)  CATTCATTTACTTGTGTGTGTGTGTGTGTGT--------TTCATTTCATTCATTTAC-TTTGGGTTG-A-TTTAAAATAT-GAAATTTGGCTAGTTTCATGGAT
14HQG7HWH01D8JEP(1>366)    CATTCATTTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTTTCATTTCATTCATCTACGTTTGGGTTGTAATTTAAAATATAGAAATTTGGCTAGTTTCATGGAT
14HQG7HWH01D8JEP(1>366)    CATTCATTTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTTTCATTTCATTCATCTACGTTTGGGTTGTAATTTAAAATATAGAAATTTGGCTAGTTTCATGGAT
22HP39V5G02HVRQJ(1>437)    CATTCATC----------------------------------------------TAC-TTTGGGTTG-A-TTTAAAATAT-GAAATTTGGCTAGTTTCATGGAT
22HQR2VN101BMQCU(1>307)    CATTCATTTACTTGTGTGTGTGTGTGTGTGT
```

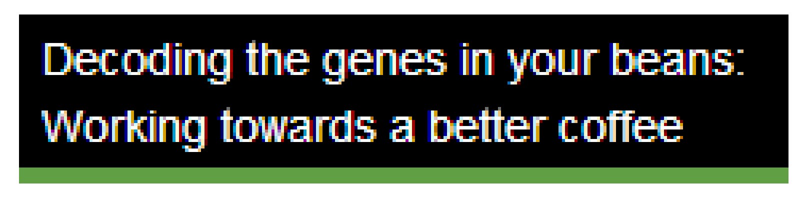
Coffee Genomics (*C. arabica*)

🇫🇷 **Dominique Crouzilat (Nestlé), Alexandre de Kochko and Romain Guyot (IRD), Pierre Marraccini**

🇺🇸 **Lukas Mueller and Susan Strickler (BTI),**

Ray Ming (UIUC)

🇧🇷 **Alan C. Andrade, Luis F. P. Pereira (Embrapa) and Douglas S. Domingues (IAPAR)**



Decoding the genes in your beans:
Working towards a better coffee

http://bti.cornell.edu/decoding-the-genes-in-your-beans-working-towards-a-better-coffee/

Embrapa
Ministry of
Agriculture, Livestock
and Food Supply
BRAZILIAN GOVERNMENT
BRASIL

Resumo

- Existe potencial para cultivo de *C. canephora* em altitudes elevadas.
- Plantas perenes como o café serão as mais beneficiadas com programas de seleção genômica (Custo de testes de campo/seleção precoce!)
- A plataforma de genotipagem beneficiará outros programas de *C. canephora* (DNA Chip).
- Os dados obtidos, já nos permite desenvolver métodos moleculares eficientes e de baixo custo, para proteção de cultivares em *C. canephora*.

Colaboradores: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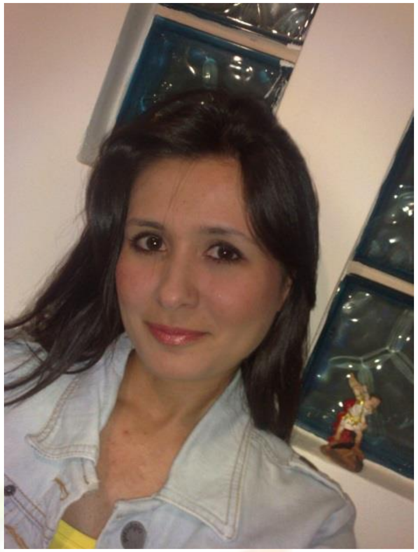
HDR / AGAP-EGV


D. THIS
Montpellier Supagro

Equipe do LGM



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Pesquisa Café

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Obrigado!