Coffea canephora

Coffea canephora group

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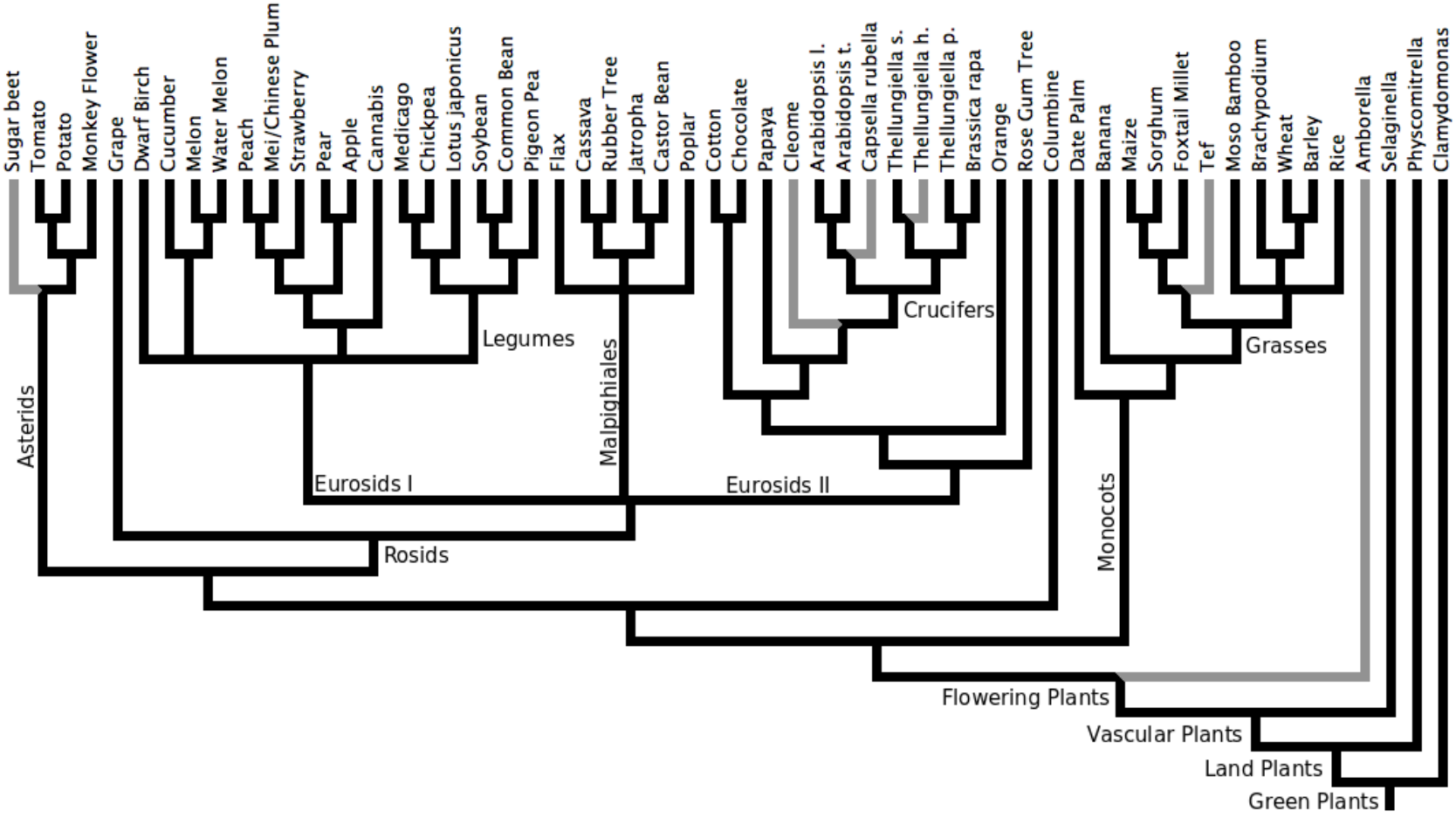
Кофе (сем. Маревые).
В промышленности используют два вида: *C. arabica* и *C. canephora* [http://en.wikipedia.org/wiki/Coffea]
Геном *C. canephora* недавно отсеквенирован: 11 пар хромосом, 710 Mbp.
[http://www.sciencemag.org/content/345/6201/1181.full].



Ближайший к кофе секвенированный геном — это либо помидор (*Solanum lycopersicum*), либо картофель (*S. tuberosum*). Проекты по секвенированию генома картофеля и томата живут здесь:
`http://www.sgn.cornell.edu/`.
+ классический модельный объект генетики растений *Arabidopsis thaliana*. Основной кладезь информации про этот геном здесь:
`http://www.arabidopsis.org/`.
Самая главная страница:
[`http://coffee-genome.org/download`]

5 предложенных белков

p01 >pdb|4G2M|A Hydroxycinnamoyltransferase
p02 >pdb|5MDH|A Malate Dehydrogenase
p03 >pdb|1WGP|A Ion Channel
p04 >pdb|2WVJ|A Thymidine Kinase
p05 >pdb|1U1H|A Methionine Synthase
...
p01: 33 потенциальных локуса
p02: 6 потенциальных локусов
p03: 23 потенциальных локуса
p04: 7 потенциальных локусов
p05: 1 потенциальный локус

Аннотация

Аннотация генов с помощью Augustus
Augustus по модели *Arabidopsis thaliana*:
chr1 – 3883 генов
Поиск по модели *Solanum lycopersicon*:
chr1 – 3575 генов.
====
Это одни и те же гены или нет?
intersectBed из bedtools

```
intersectBed -a \
./chr1_by_Arabidopsis_augustus.gff -b \
./chr1_by_tomato_Augustus.txt -r -f .9 \
>./chr1_intersectBed_r_f_90.gff
```

chr 1 – 2058 генов

Аннотация: тренировка Augustus

```
*****      Evaluation of gene prediction     *****

-----------------------------------------\
                 | sensitivity | specificity |
-----------------------------------------|
nucleotide level |       0.865 |       0.442 |
-----------------------------------------/

-----------------------------------------------------------------------------------------------------------
           |  #pred |  #anno |      |    FP = false pos. |    FN = false neg. |             |
           | total/ | total/ |   TP |--------------------|--------------------| sensitivity | specificity
           | unique | unique |      | part | ovlp | wrng | part | ovlp | wrng |             |
-----------------------------------------------------------------------------------------------------------
           |        |        |      |               1246 |                557 |             |
exon level |   2151 |   1462 |  905 | ------------------ | ------------------ |       0.619 |       0.421
           |   2151 |   1462 |      |  239 |   24 |  983 |  239 |   21 |  297 |             |
-----------------------------------------------------------------------------------------------------------

-------------------------------------------------------------------------\
transcript | #pred | #anno |   TP |   FP |   FN | sensitivity | specificity |
-------------------------------------------------------------------------|
gene level |   431 |   200 |   34 |  397 |  166 |        0.17 |      0.0789 |
-------------------------------------------------------------------------/

-----------------------------------------------------------------------\
            UTR | total pred | CDS bnd. corr. |   meanDiff | medianDiff |
-----------------------------------------------------------------------|
            TSS |         42 |              0 |         -1 |         -1 |
            TTS |         16 |              0 |         -1 |         -1 |
-----------------------------------------------------------------------|
            UTR | uniq. pred |    unique anno |      sens. |      spec. |
-----------------------------------------------------------------------|
                |  true positive = 1 bound. exact, 1 bound. <= 20bp off |
 UTR exon level |          0 |              0 |        nan |        nan |
```

Поиск повторов с помощью RepeatMasker на основе генома *Arabidopsis*

```
RepeatMasker -species arabidopsis -xsmall -gff ./chr1.fna
```

```
==================================================
file name: chr1.fna
sequences:             1
total length:   38193400 bp  (30728063 bp excl N/X-runs)
GC level:         36.14 %
bases masked:    1673760 bp ( 4.38 %)
==================================================
               number of      length   percentage
               elements*    occupied  of sequence
--------------------------------------------------
Retroelements         1027       921072 bp    2.41 %
   SINEs:                4          213 bp    0.00 %
   Penelope              0            0 bp    0.00 %
   LINEs:              164        66524 bp    0.17 %
    CRE/SLACS            0            0 bp    0.00 %
     L2/CR1/Rex          0            0 bp    0.00 %
     R1/LOA/Jockey       0            0 bp    0.00 %
     R2/R4/NeSL          0            0 bp    0.00 %
     RTE/Bov-B           0            0 bp    0.00 %
     L1/CIN4           164        66524 bp    0.17 %
   LTR elements:       859       854335 bp    2.24 %
     BEL/Pao             0            0 bp    0.00 %
     Ty1/Copia         380       386105 bp    1.01 %
     Gypsy/DIRS1       478       468183 bp    1.23 %
       Retroviral        0            0 bp    0.00 %
```

Поиск повторов с помощью RepeatMasker на основе генома *Arabidopsis* (continued)

```
RepeatMasker -species rice -no_is chr1.fna
```

```
DNA transposons          203         39568 bp    0.10 %
   hobo-Activator         94         18339 bp    0.05 %
   Tc1-IS630-Pogo         33          5832 bp    0.02 %
   En-Spm                  0             0 bp    0.00 %
   MuDR-IS905              0             0 bp    0.00 %
   PiggyBac                0             0 bp    0.00 %
   Tourist/Harbinger       3           477 bp    0.00 %
   Other (Mirage,          0             0 bp    0.00 %
    P-element, Transib)

Rolling-circles            0             0 bp    0.00 %

Unclassified:             71         18327 bp    0.05 %

Total interspersed repeats:       978967 bp    2.56 %


Small RNA:                12          1876 bp    0.00 %

Satellites:                0             0 bp    0.00 %
Simple repeats:        12222        536197 bp    1.40 %
Low complexity:         3011        157206 bp    0.41 %
==================================================

* most repeats fragmented by insertions or deletions
  have been counted as one element

The query species was assumed to be arabidopsis
```

Поиск повторов с помощью RepeatMasker на основе генома риса

```
==================================================
file name: chr1.fna * поиск по повторам из генома риса
sequences:             1
total length:   38193400 bp  (30728063 bp excl N/X-runs)
GC level:         36.14 %
bases masked:     713556 bp ( 1.87 %)
==================================================
               number of      length   percentage
               elements*    occupied  of sequence
--------------------------------------------------
SINEs:                17         1008 bp    0.00 %
      ALUs             0            0 bp    0.00 %
      MIRs             3          183 bp    0.00 %

LINEs:               105         6967 bp    0.02 %
      LINE1           10          449 bp    0.00 %
      LINE2           11          727 bp    0.00 %
      L3/CR1          60         4183 bp    0.01 %
```

Поиск повторов с помощью RepeatMasker на основе генома риса (continued)

```
LTR elements:          19          2445 bp    0.01 %
      ERVL              2           135 bp    0.00 %
      ERVL-MaLRs        0             0 bp    0.00 %
      ERV_classI        5           470 bp    0.00 %
      ERV_classII       1            54 bp    0.00 %

DNA elements:          29          1731 bp    0.00 %
     hAT-Charlie        4           165 bp    0.00 %
     TcMar-Tigger       6           380 bp    0.00 %

Unclassified:          24          2999 bp    0.01 %

Total interspersed repeats:      15150 bp    0.04 %


Small RNA:             77          6918 bp    0.02 %

Satellites:             0             0 bp    0.00 %
Simple repeats:     12270        535071 bp    1.40 %
Low complexity:      3016        157382 bp    0.41 %
==================================================

* most repeats fragmented by insertions or deletions
  have been counted as one element


The query species was assumed to be homo sapiens
RepeatMasker version open-4.0.5 , default mode

run with rmblastn version 2.2.27+
```

Поиск повторов с помощью RepeatMasker на основе генома кукурузы

```
RepeatMasker -species maize -no_is chr1.fna
```

```
==================================================
file name: chr1.fna
sequences:             1
total length:   38193400 bp  (30728063 bp excl N/X-runs)
GC level:         36.14 %
bases masked:    1632178 bp ( 4.27 %)
==================================================
               number of      length   percentage
               elements*    occupied  of sequence
--------------------------------------------------
Retroelements          841       849585 bp    2.22 %
   SINEs:                0            0 bp    0.00 %
   Penelope              0            0 bp    0.00 %
   LINEs:              111        32297 bp    0.08 %
    CRE/SLACS            0            0 bp    0.00 %
     L2/CR1/Rex          0            0 bp    0.00 %
     R1/LOA/Jockey       0            0 bp    0.00 %
     R2/R4/NeSL          0            0 bp    0.00 %
     RTE/Bov-B           0            0 bp    0.00 %
     L1/CIN4           111        32297 bp    0.08 %
   LTR elements:       730       817288 bp    2.14 %
     BEL/Pao             0            0 bp    0.00 %
     Ty1/Copia         296       328851 bp    0.86 %
     Gypsy/DIRS1       431       487305 bp    1.28 %
       Retroviral        0            0 bp    0.00 %
```

Поиск повторов с помощью RepeatMasker на основе генома кукурузы (continued)

```
DNA transposons          246         49637 bp    0.13 %
   hobo-Activator         77         16928 bp    0.04 %
   Tc1-IS630-Pogo         18          1956 bp    0.01 %
   En-Spm                  0             0 bp    0.00 %
   MuDR-IS905              0             0 bp    0.00 %
   PiggyBac                0             0 bp    0.00 %
   Tourist/Harbinger       1           226 bp    0.00 %
   Other (Mirage,          0             0 bp    0.00 %
    P-element, Transib)

Rolling-circles            0             0 bp    0.00 %

Unclassified:            143         48891 bp    0.13 %

Total interspersed repeats:       948113 bp    2.48 %


Small RNA:                12          1876 bp    0.00 %

Satellites:                0             0 bp    0.00 %
Simple repeats:        12125        527308 bp    1.38 %
Low complexity:         2993        155668 bp    0.41 %
==================================================

* most repeats fragmented by insertions or deletions
  have been counted as one element


The query species was assumed to be oryza sativa
RepeatMasker version open-4.0.5 , default mode
```

Поиск повторов с помощью RepeatMasker на основе генома *C. elegans*

```
RepeatMasker -species elegans -no_is chr1.fna
```

```
==================================================
file name: chr1.fna
sequences:             1
total length:   38193400 bp  (30728063 bp excl N/X-runs)
GC level:         36.14 %
bases masked:    1653432 bp ( 4.33 %)
==================================================
               number of      length   percentage
               elements*    occupied  of sequence
--------------------------------------------------
Retroelements         1029       869163 bp    2.28 %
   SINEs:                0            0 bp    0.00 %
   Penelope              0            0 bp    0.00 %
   LINEs:              145        22491 bp    0.06 %
    CRE/SLACS            0            0 bp    0.00 %
     L2/CR1/Rex          0            0 bp    0.00 %
     R1/LOA/Jockey       0            0 bp    0.00 %
     R2/R4/NeSL          0            0 bp    0.00 %
     RTE/Bov-B           0            0 bp    0.00 %
     L1/CIN4           145        22491 bp    0.06 %
   LTR elements:       884       846672 bp    2.22 %
     BEL/Pao             0            0 bp    0.00 %
     Ty1/Copia         349       361735 bp    0.95 %
     Gypsy/DIRS1       535       484937 bp    1.27 %
       Retroviral        0            0 bp    0.00 %
```

Поиск повторов с помощью RepeatMasker на основе генома *C. elegans* (continued)

```
DNA transposons          220         46689 bp    0.12 %
   hobo-Activator        131         28258 bp    0.07 %
   Tc1-IS630-Pogo          0             0 bp    0.00 %
   En-Spm                  0             0 bp    0.00 %
   MuDR-IS905              0             0 bp    0.00 %
   PiggyBac                0             0 bp    0.00 %
   Tourist/Harbinger      17           844 bp    0.00 %
   Other (Mirage,          0             0 bp    0.00 %
    P-element, Transib)

Rolling-circles            0             0 bp    0.00 %

Unclassified:             56         41852 bp    0.11 %

Total interspersed repeats:       957704 bp    2.51 %


Small RNA:                12          1876 bp    0.00 %

Satellites:                7           508 bp    0.00 %
Simple repeats:        12233        536270 bp    1.40 %
Low complexity:         3014        157560 bp    0.41 %
==================================================

* most repeats fragmented by insertions or deletions
  have been counted as one element

The query species was assumed to be zea
RepeatMasker version open-4.0.5 , default mode

run with rmblastn version 2.2.27+
```

Поиск повторов с помощью RepeatScout

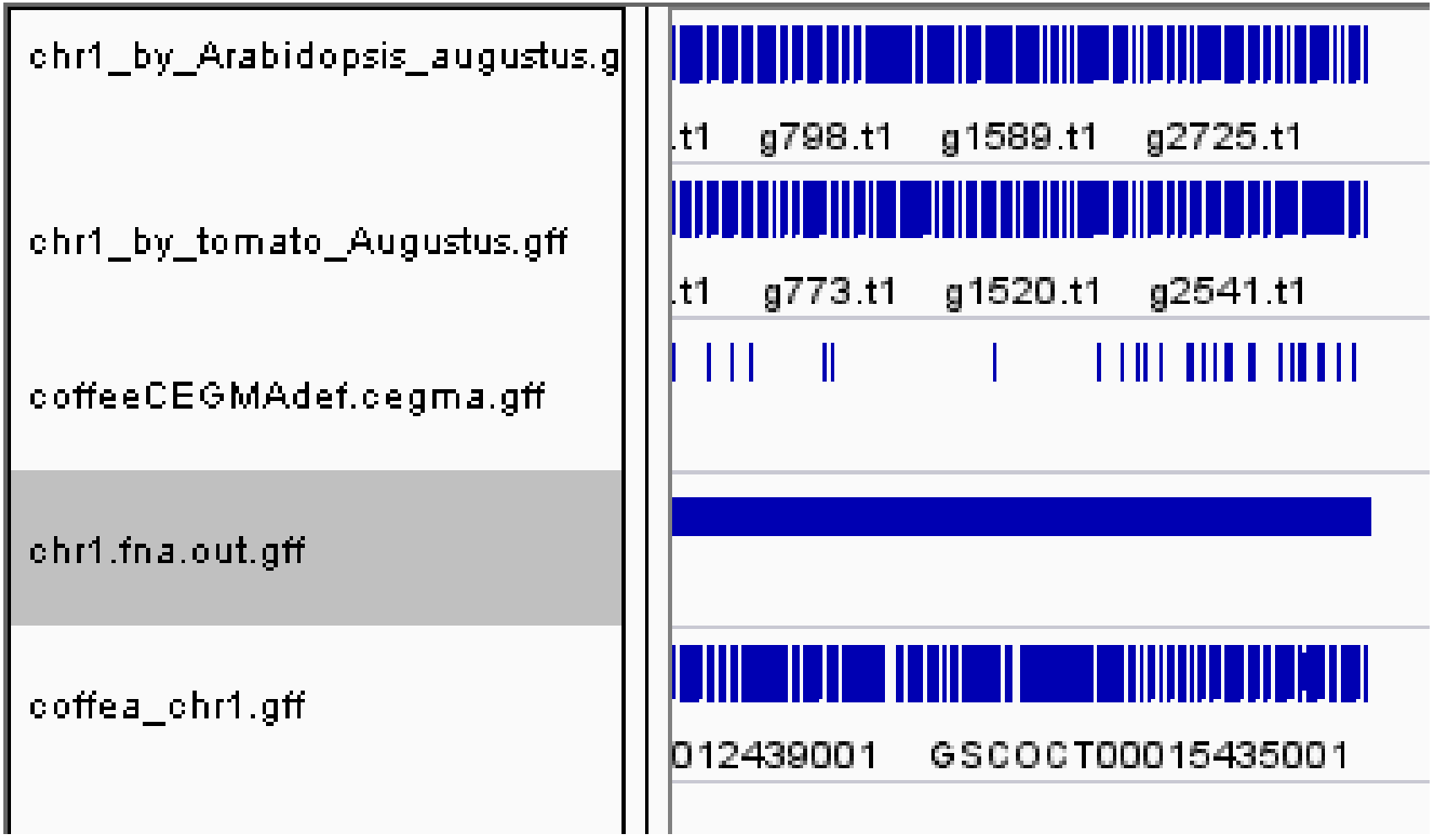
```
build_lmer_table -l 15 -sequence ./coffee_raw_data/chr1.fna \
-freq ./RepeatScout/chr1.lt -v

RepeatScout-1/RepeatScout -sequence ./coffee_raw_data/chr1.fna \
-output ./RepeatScout/chr1.rs -freq ./RepeatScout/chr1.lt -l 15


wc -l chr1.lt
1320654 chr1.lt


grep -c \> chr1.rs
2223
```

IGV


chr1_by_Arabidopsis_augustus.g
.t1 g798.t1 g1589.t1 g2725.t1
chr1_by_tomato_Augustus.gff
.t1 g773.t1 g1520.t1 g2541.t1
coffeeCEGMAdef.cegma.gff
chr1.fna.out.gff
coffea_chr1.gff
012439001 GSCOCT00015435001