Coffea canephora

Coffea canephora group

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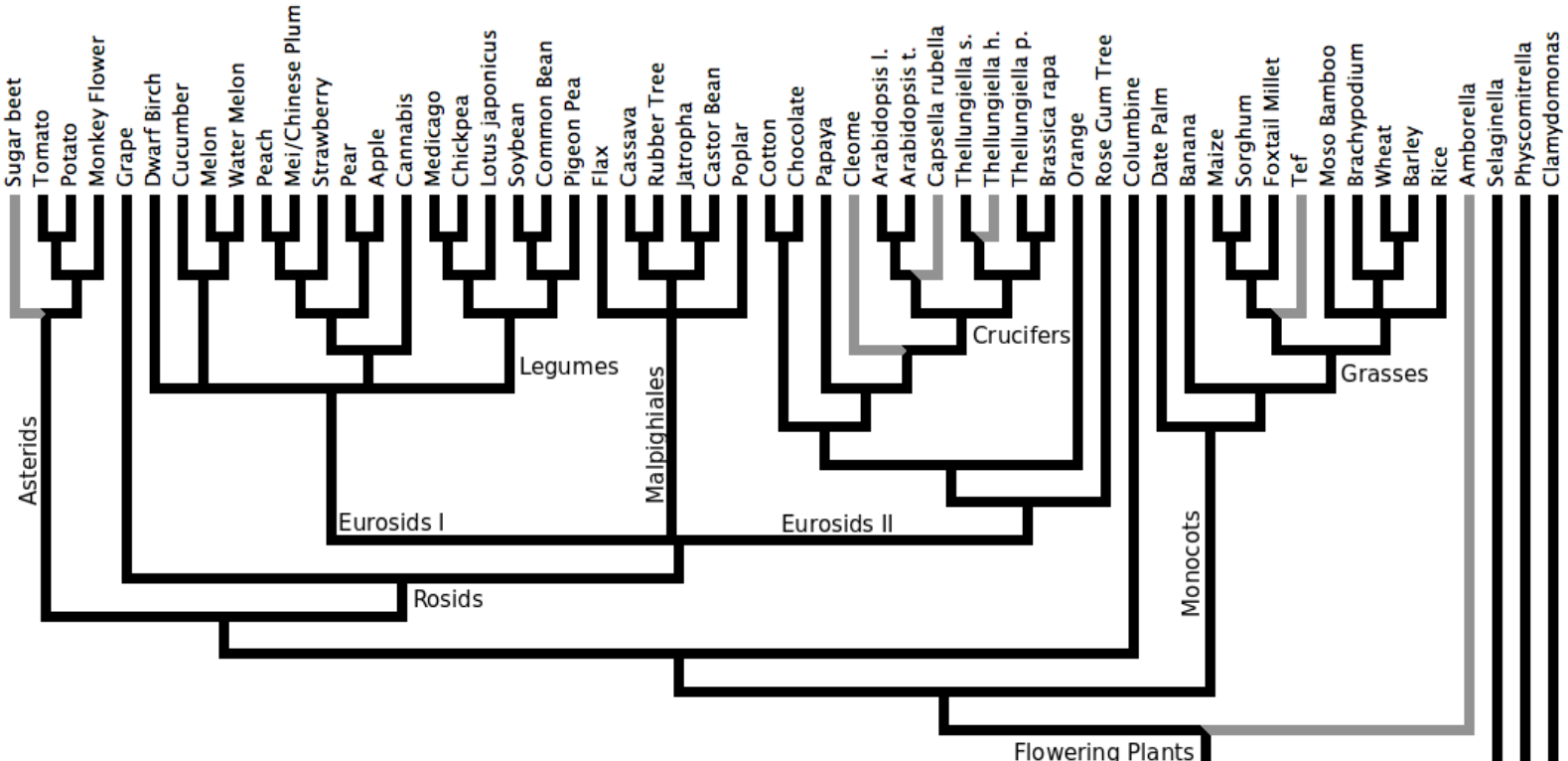
Кофе (сем. Маревые).
В промышленности используют два вида: *C. arabica* и *C. canephora* [http://en.wikipedia.org/wiki/Coffea]
Геном *C. canephora* недавно отсеквенирован: 11 пар хромосом, 710 Mbp. [http://www.sciencemag.org/content/345/6201/1181.full].



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

CEGMA: подготовка генов для Augustus


```
cegma -g pseudomolecules.fa -o coffeeCEGMAdef
```

```
#      Statistics of the completeness of the genome based on 248 CEGs      #

              #Prots  %Completeness  -  #Total  Average  %Ortho

  Complete      225       90.73      -   371     1.65     39.56

   Group 1       58       87.88      -    83     1.43     27.59
   Group 2       49       87.50      -    80     1.63     38.78
   Group 3       54       88.52      -    90     1.67     38.89
   Group 4       64       98.46      -   118     1.84     51.56

   Partial      240       96.77      -   452     1.88     49.17

   Group 1       63       95.45      -   102     1.62     38.10
   Group 2       54       96.43      -    94     1.74     42.59
   Group 3       59       96.72      -   115     1.95     54.24
   Group 4       64       98.46      -   141     2.20     60.94

#    These results are based on the set of genes selected by Genis Parra   #

#    Key:                                                                  #
#    Prots = number of 248 ultra-conserved CEGs present in genome          #
#    %Completeness = percentage of 248 ultra-conserved CEGs present        #
#    Total = total number of CEGs present including putative orthologs     #
#    Average = average number of orthologs per CEG                         #
#    %Ortho = percentage of detected CEGS that have more than 1 ortholog   #
```

Аннотация: обучение 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 | sp
           | unique | unique |      | part | ovlp | wrng | part | ovlp | wrng |             |
-------------------------------------------------------------------------------------------------
           |        |        |      |               1246 |                557 |             |
exon level |   2151 |   1462 |  905 | ------------------ | ------------------ |       0.619 |
           |   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. |
```

Сравнение наших результатов с официальной аннотацией


```
intersectBed -a coffea_canephora.chr1.gff3 \
-b chr1_by_coffee.gff -wa -u
>chr1_official_to_our_model_report_off_once.gff

grep -c gene chr1_official_to_our_model_report_off_once.gf
3780

grep -c gene coffea_canephora.chr1.gff3
11208

grep -c gene chr1_by_coffee.gff
39816
```

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 RepeatScout


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

RepeatScout-1/RepeatScout -sequence ./coffee_raw_data/chr1
-output ./RepeatScout/chr1.rs -freq ./RepeatScout/chr1.lt
```

```
wc -l chr1.lt
1320654 chr1.lt
```

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

Поиск повторов с помощью RepeatMasker на основе данных RepeatScout


```
==================================================
file name: chr1.fna
sequences:             1
total length:   38193400 bp  (30728063 bp excl N/X-runs)
GC level:         36.14 %
bases masked:   11761995 bp ( 30.80 %)
==================================================
               number of      length   percentage
               elements*    occupied  of sequence
--------------------------------------------------
....

Unclassified:     41342     12121768 bp   31.74 %

Total interspersed repeats: 12121768 bp   31.74 %


Small RNA:            0            0 bp    0.00 %

Satellites:           0            0 bp    0.00 %
Simple repeats:   11017       449018 bp    1.18 %
Low complexity:       0            0 bp    0.00 %
==================================================

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

Анализ семейств генов


```
cat <3 genomes> => kClust =>
kclust_out_for_cafe.py => CAFE3.0
```

```
load -i cafe_input.out
tree (>AT:5,(>Cc:1,>So:2):3)
lambda -s
lambda -l 0.17
report resultsfile
```