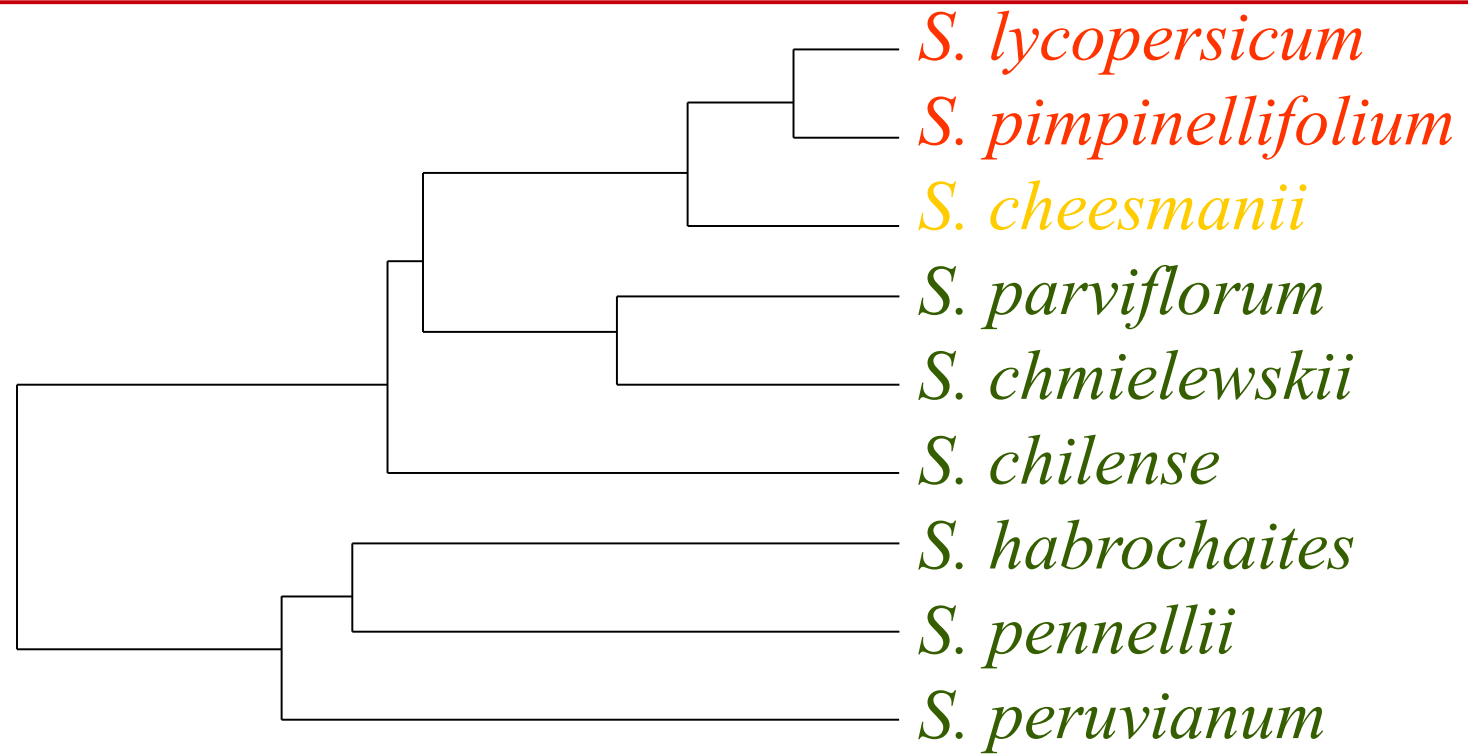


# TOMATO MAGIC



Laura Pascual

## Why developing a MAGIC population on tomato?



### TOMATO

- Autogamous species
- Low genetic diversity
- Great phenotypic diversity



# Why developing a MAGIC population on tomato?

## Available resources for QTL detection on Tomato

Low molecular diversity

Mapping populations (bi-parental):

Inter-specific RILs, ILs

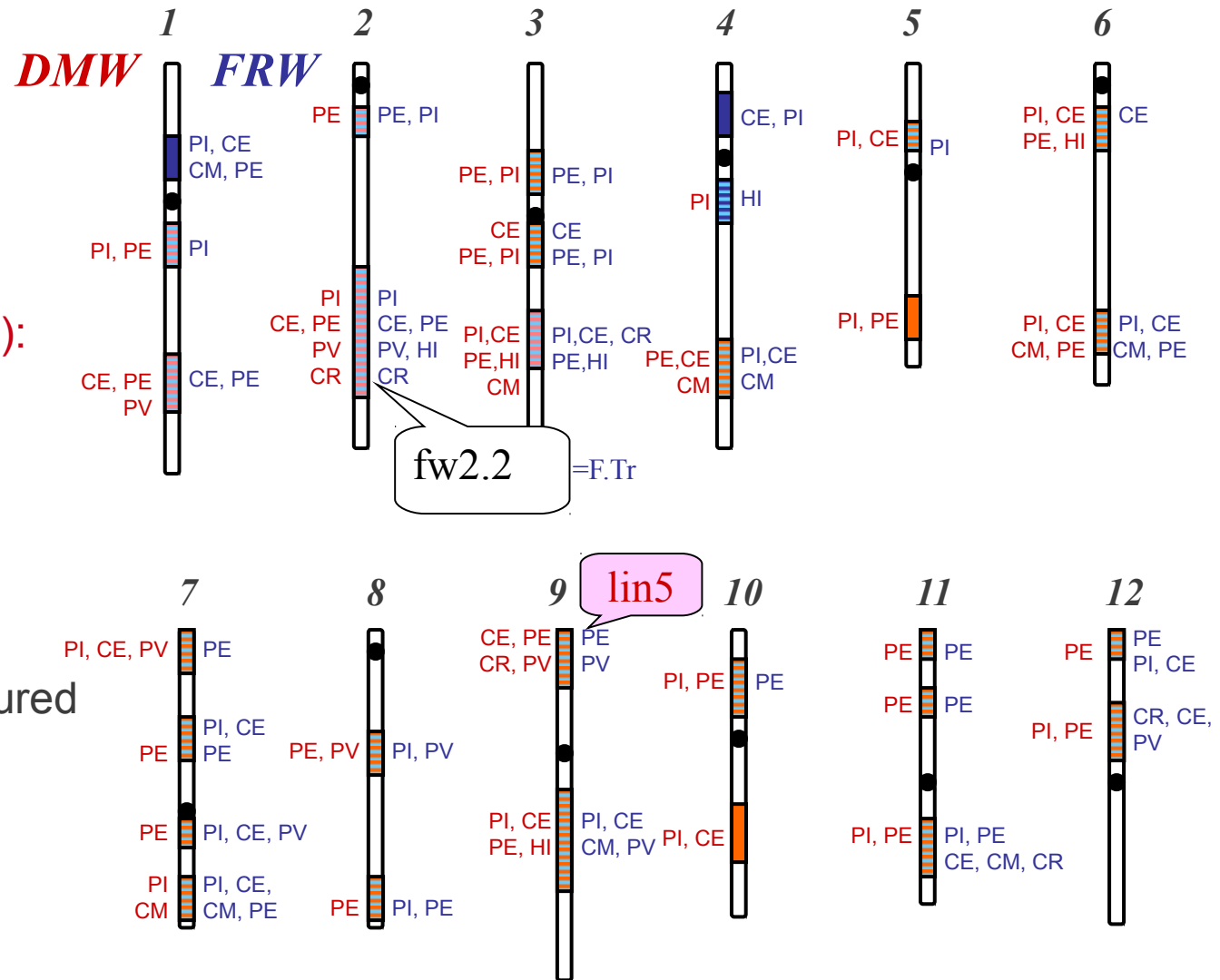
Intra-specific RIL

Association analysis:

Collections are genetically structured

High LD expected

Low values for MAF



Synthesis of 10 studies involving 7 species

# Why developing a MAGIC population on tomato?

Genome size: ~ 900Mb; 12 chromosomes

**Assembly** 760 Mb (84%) & 91 scaffold; chr0 (20Mb)

**Annotation** 35,000 genes                      30,800 identified by RNAseq  
90% homology x Ath



**Tomato chromosomes:** pericentric heterochromatin and distal euchromatin

**Original genome** : most of the DNA low copy nb

➔ Distribution of the genes heterogeneous with recombinations & genes in euchromatin

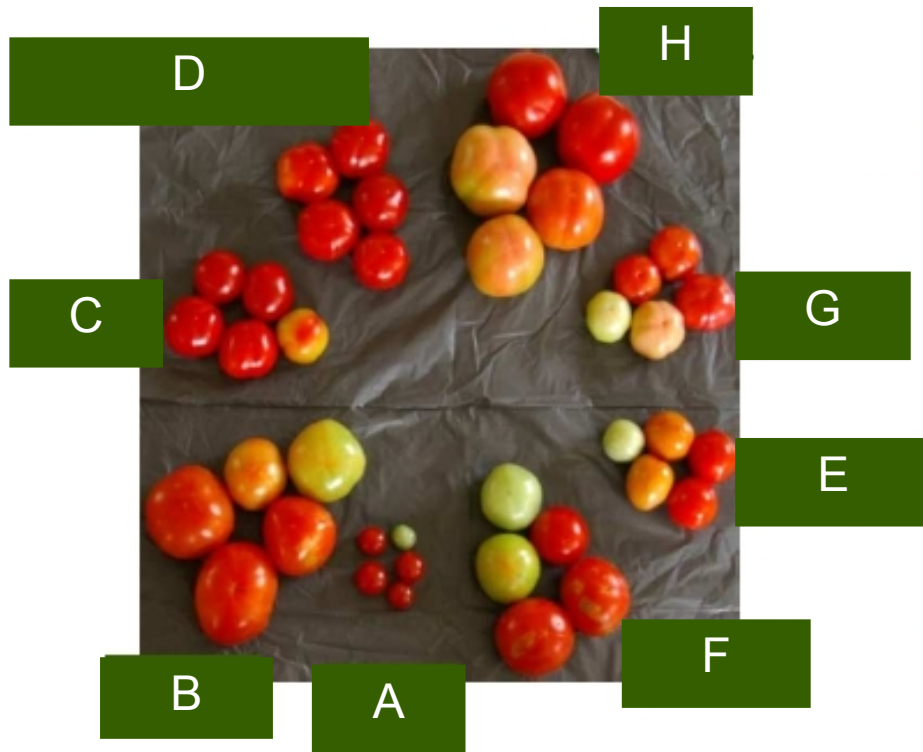
The Tomato Genome Consortium,  
*Nature*, may 2012  
14 countries 300 authors



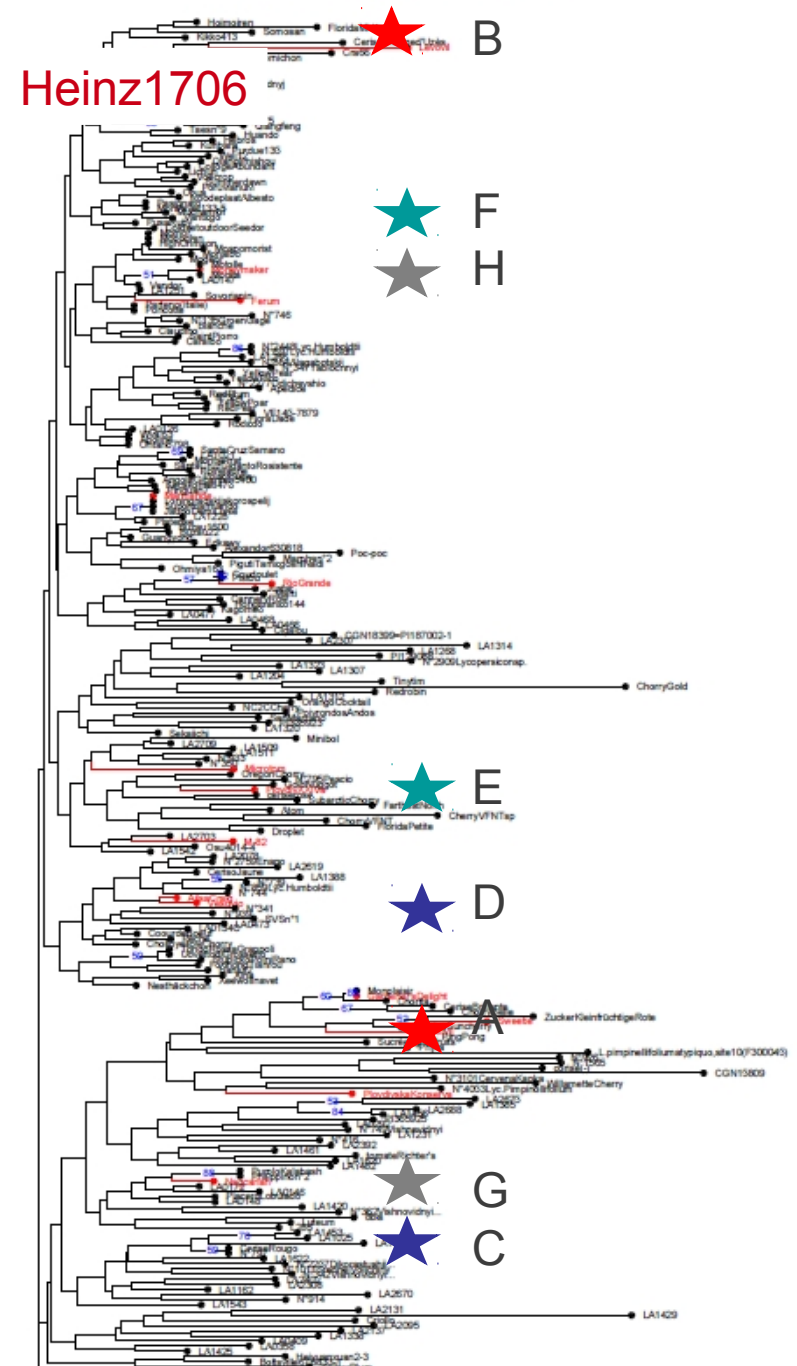
Heinz1706

# Population design – Founding individuals

8 divergent lines



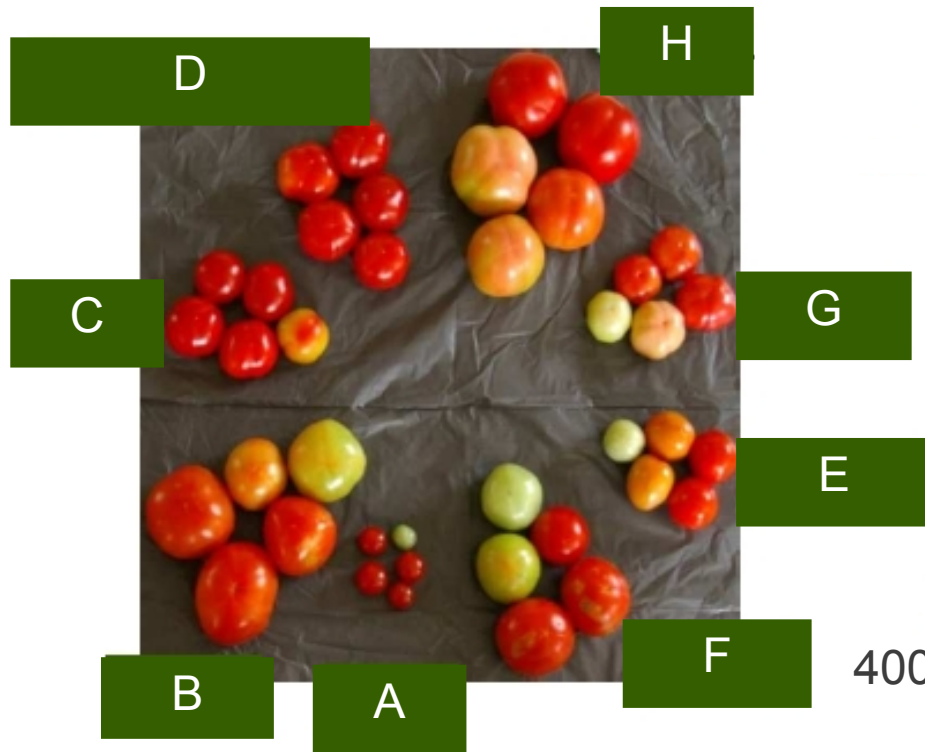
Subset from a 300 accession collection



NJ with 20 SSR markers (Ranc et al, 2008)

# Population design – Founding individuals

8 divergent lines



Fruit growth, plant vigor ...

32 metabolites (I & II)  
26 enzyme activities

400 protein spots variable

4000 genes differentially expressed

8 founders re-sequenced (GAII)

Development of specific SNPs for the MAGIC genotyping

12 Genotypes Sampling  
8 parental lines + 4 F1

Phenotype

Metabolome

Proteome

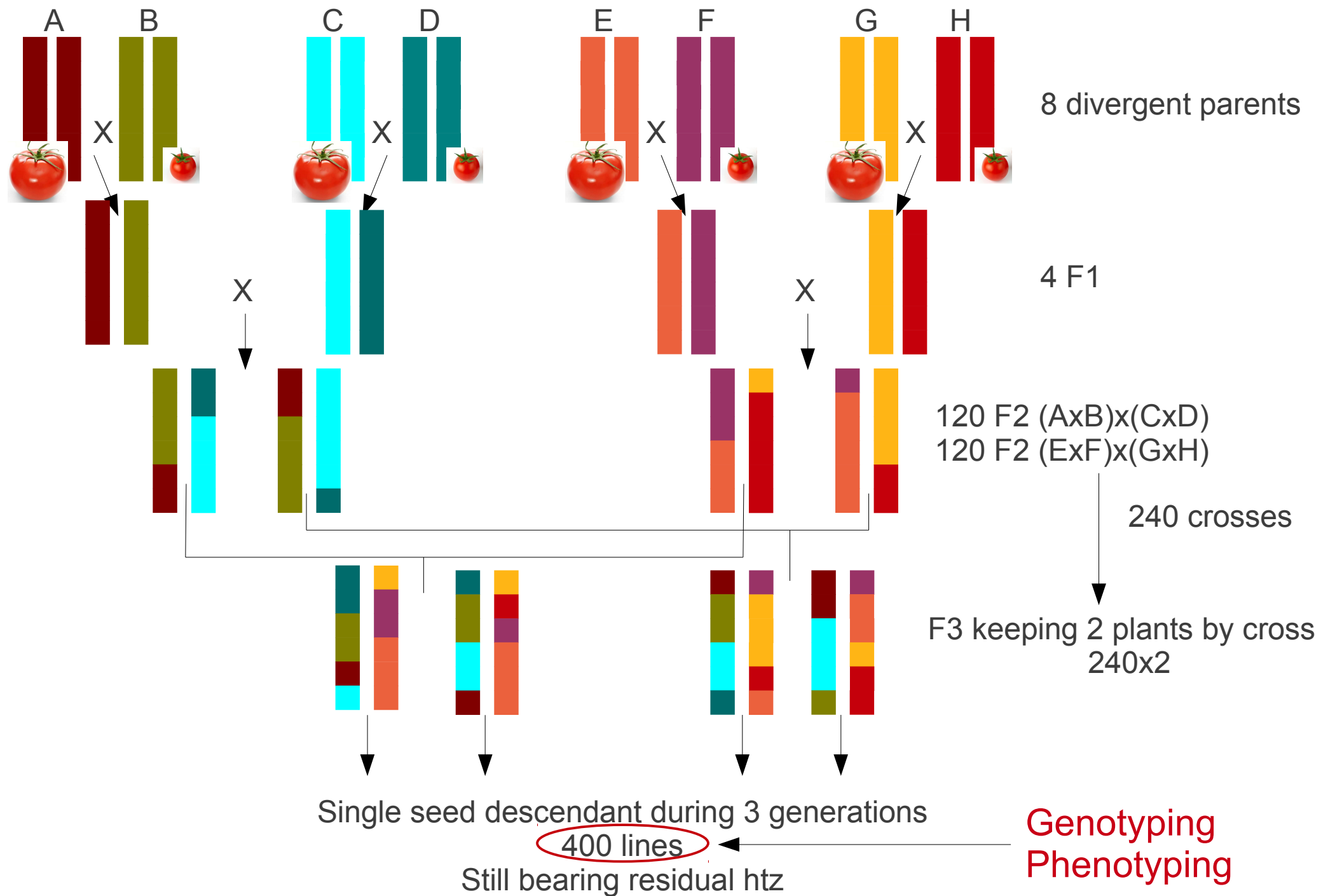
Transcriptome

Genome

Genetic distances of the 8 parental lines were far from each other

The 8 parental lines capture 96% of the molecular diversity

# Population design – Construction



## Phenotyping two different locations

| N° ligne | 10   |      | 8    |      | 6    |      | 4    |      | 2    |      |
|----------|------|------|------|------|------|------|------|------|------|------|
|          | bord | bord | bord | bord | bord | bord | bord | bord | Bord | Bord |
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| 80       |      |      |      |      |      |      |      |      |      |      |
| 81       |      |      |      |      |      |      |      |      |      |      |



Plant/leaves

Flower/flowering

Fruit

Fruit composition  
Enzymes /Metabolites

Gene expression (Fruit)

Seeds

## Results – Constructing a genetic map, based on the physical map

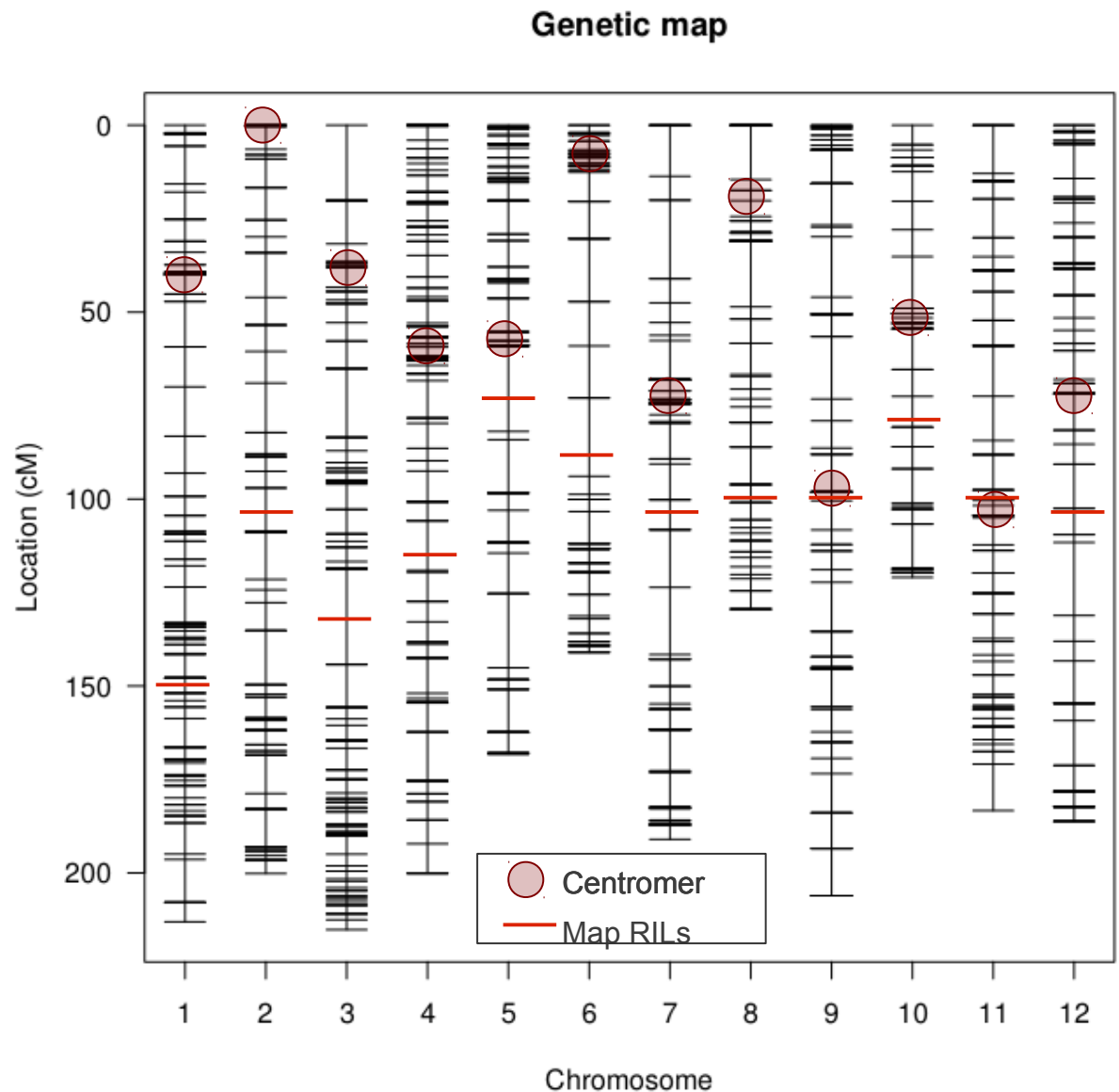
Map size on cM:

|      | MAGIC | Bi-parental RILs |
|------|-------|------------------|
| CH1  | 214   | 153              |
| CH2  | 200   | 105              |
| CH3  | 215   | 135              |
| CH4  | 200   | 118              |
| CH5  | 168   | 74               |
| CH6  | 141   | 90               |
| CH7  | 191   | 108              |
| CH8  | 129   | 98               |
| CH9  | 206   | 99               |
| CH10 | 120   | 84               |
| CH11 | 183   | 99               |
| CH12 | 186   | 108              |

Total length MAGIC: 2156 cM

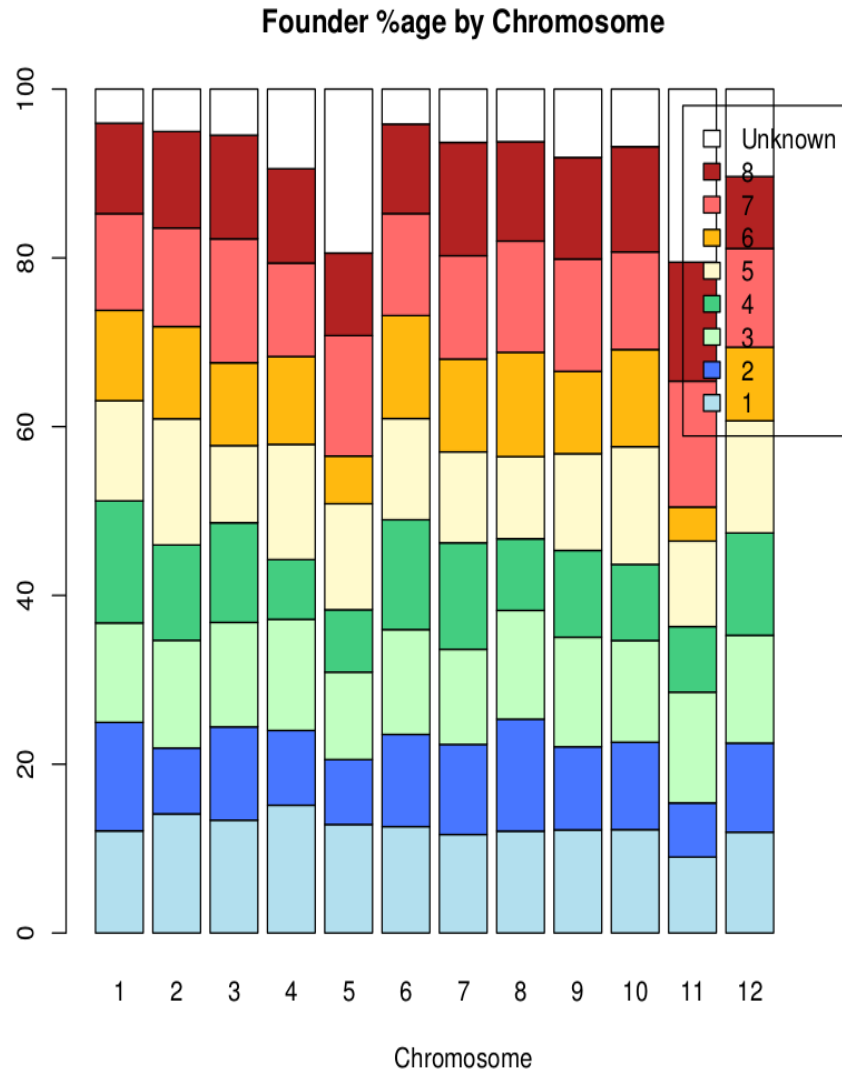
Total length bi-parental: 1271 cM

**Increase: 59%**



# Results - Detecting QTLs

## Predicting haplotypes

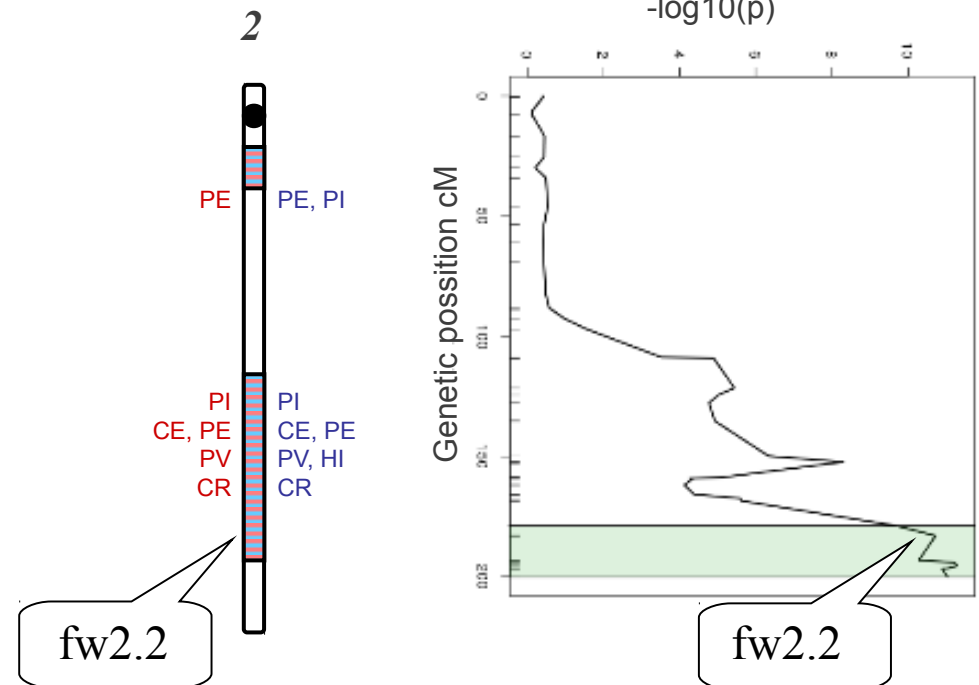


## Finding associations Detecting QTLs with IM

Fruit weight analysis

7 QTL detected in different chromosomes

5 located in regions of known QTLs



# Thanks

## INRA, UR GAFL, Avignon

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*ANR Magic TOM SNP  
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