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# A MAGIC Population to decipher the genetic control of quantitative traits in tomato

Laura Pascual (1), Mathilde Causse (1), Jiaxin Xu (1,2), Christopher Sauvage (1), Guillaume Bauchet (1), Nelly Desplat (1), Jean-Paul Bouchet (1), Aurore Desgroux (1), Dominique Brunel (3), Marie-Christine Lepaslier (3)

(1) INRA, UR1052, GAFL, BP94,F-84143 Montfavet, France (mathilde.causse@avignon.inra.fr)

(2) Northwest A&F University, College Horticulture, Yang Ling, Shaanxin, 712100, P.R.China

(3) INRA, EPGV, Centre de Génotypage, Evry, France

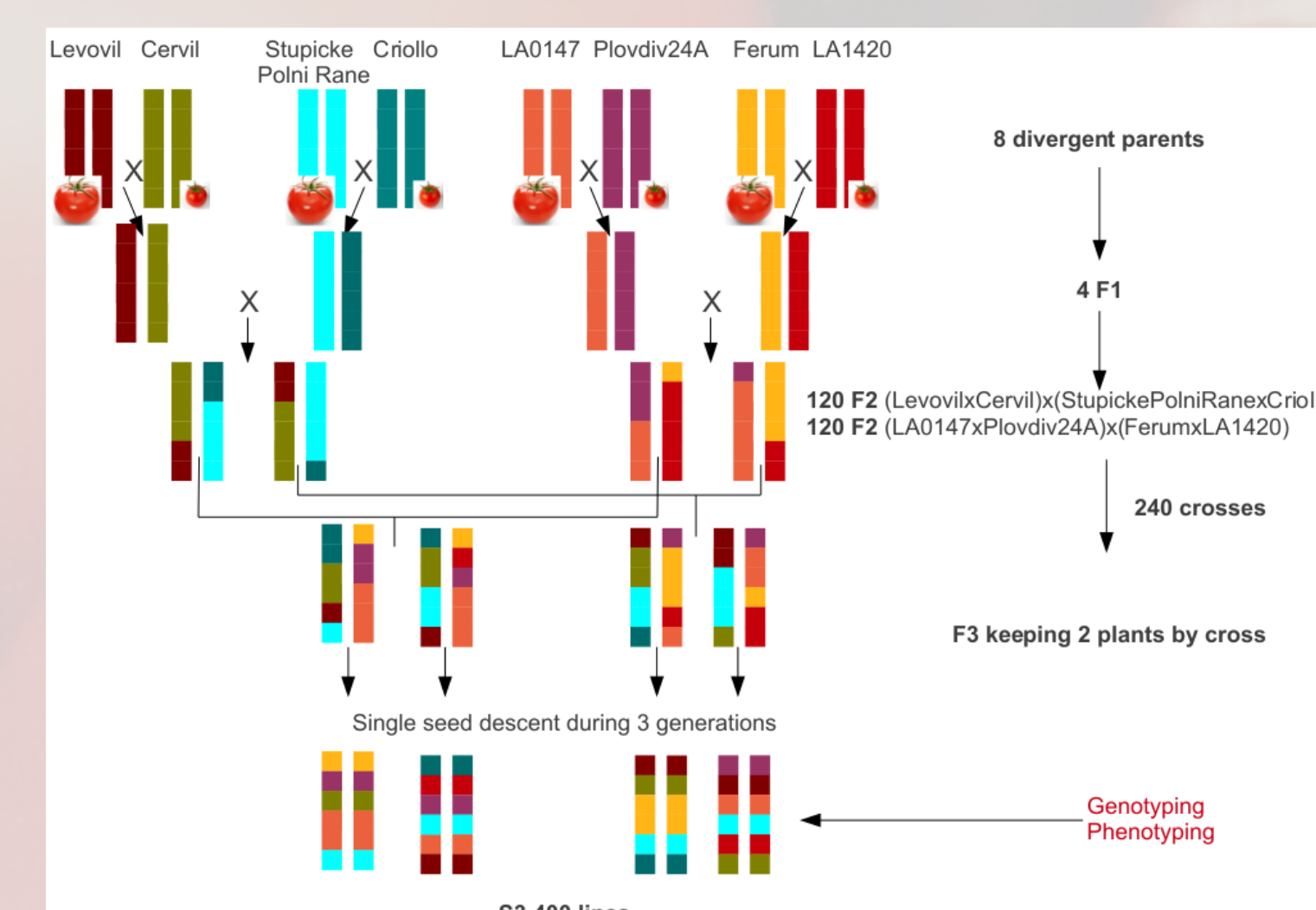
## Introduction

Identifying the genes controlling the variation of quantitative traits is a key goal for breeders. Genetic variations underlying **quantitative traits** (QTL) have been mapped by traditional linkage mapping, however this is limited to the analysis of traits differing between two lines. Thanks to the increase in molecular markers, **genome-wide association** studies (GWAs) were then proposed, nevertheless, the results might be limited by linkage disequilibrium. In contrast, analysis of **multi allelic advanced generation intercross** (MAGIC) populations allow a wide range of variability to be analyzed and avoids dealing with population structure.

We have constructed a MAGIC population by crossing 8 tomato lines, representing a wide range of genetic diversity within the species. A set of 1536 SNPs markers was selected to genotype the MAGIC population and used to construct a linkage map. The power and precision to detect QTLs controlling quantitative characters was tested.

## Materials and methods

A MAGIC population was developed from four *Solanum lycopersicum* lines (**Levovil**, **Stupicke Polni Rane**, **LA0147**, **Ferum**) and four cherry type tomato (*S. l. var cerasiforme*) lines (**Cervil**, **Criollo**, **Plovdiv 24A**, **LA1420**), cross scheme detailed down. The population, formed by 400 lines, was phenotyped at two different locations in the South of France. Plant, flower and fruit characteristics were scored. Fine metabolite and enzyme profilings were carried out for a subset of 130 lines. The 8 founders lines were re-sequenced and

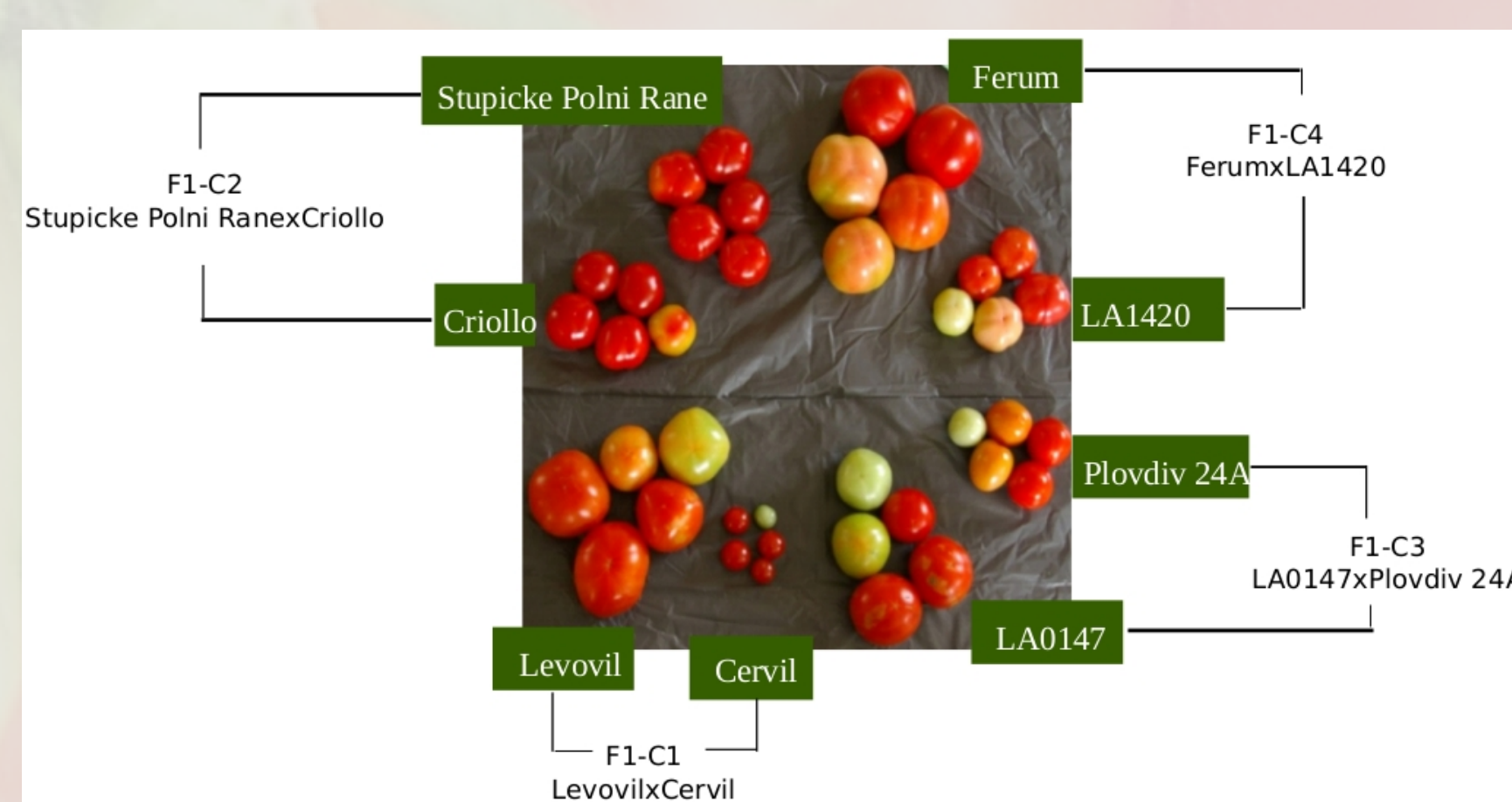


mapped against the tomato reference genome (TGC, 2012). We detected 4 millions of SNPs (Causse et al, In press). All the population was then genotyped with a subset of 1582 SNPs. Markers were selected, taking into account; SNPs quality, distance to genes, profiles in the founders for successive SNPs, genetic and physical distance. Genetic map construction and QTL analysis was performed with mpMap (Huang & George, 2011). GWAs tests were performed with TASSEL (Bradbury et al, 2007).

## Results : Analysis of Multi-allelic Advance Generation Inter-cross

### Increasing diversity

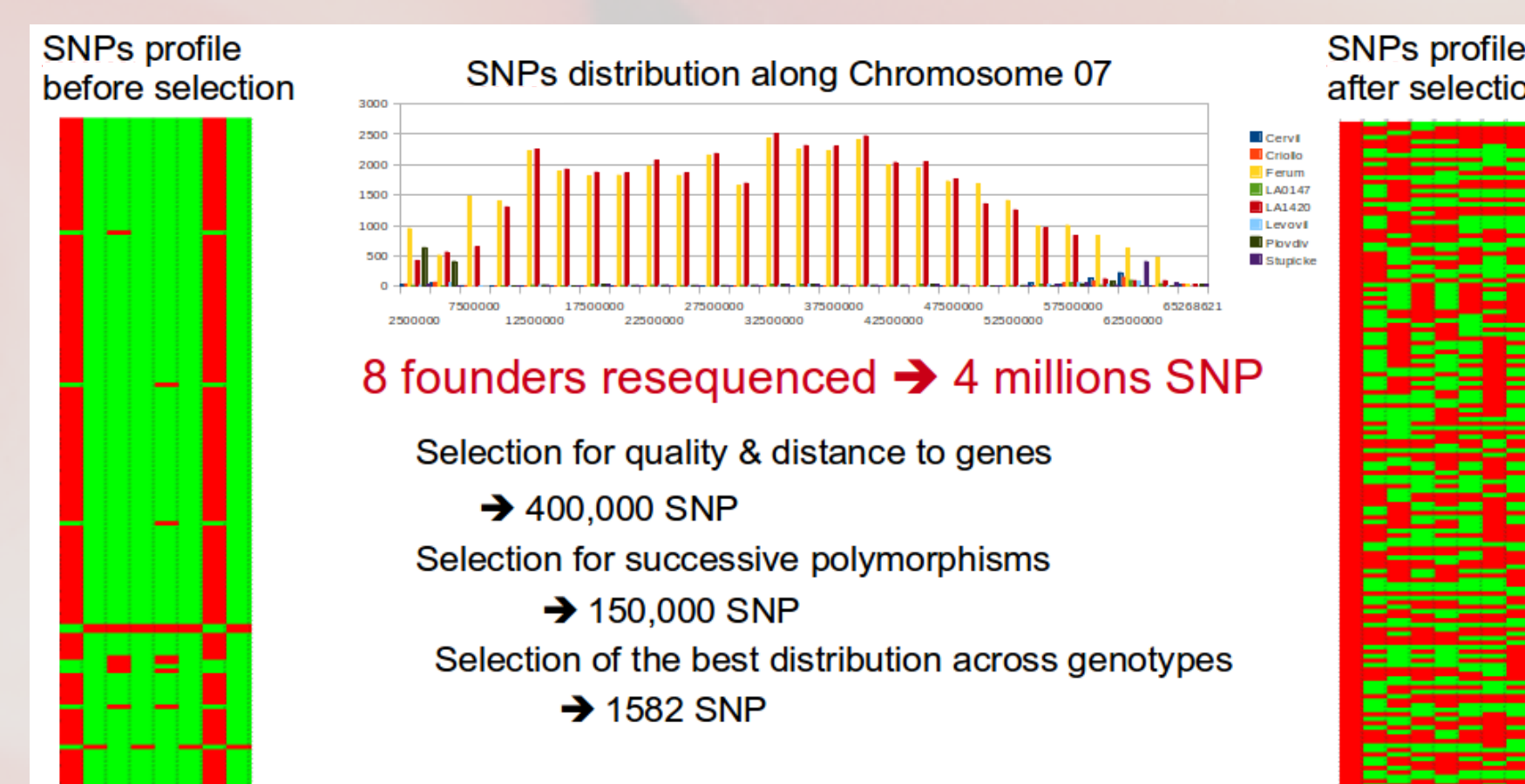
#### Founders lines diversity



#### MAGIC population diversity

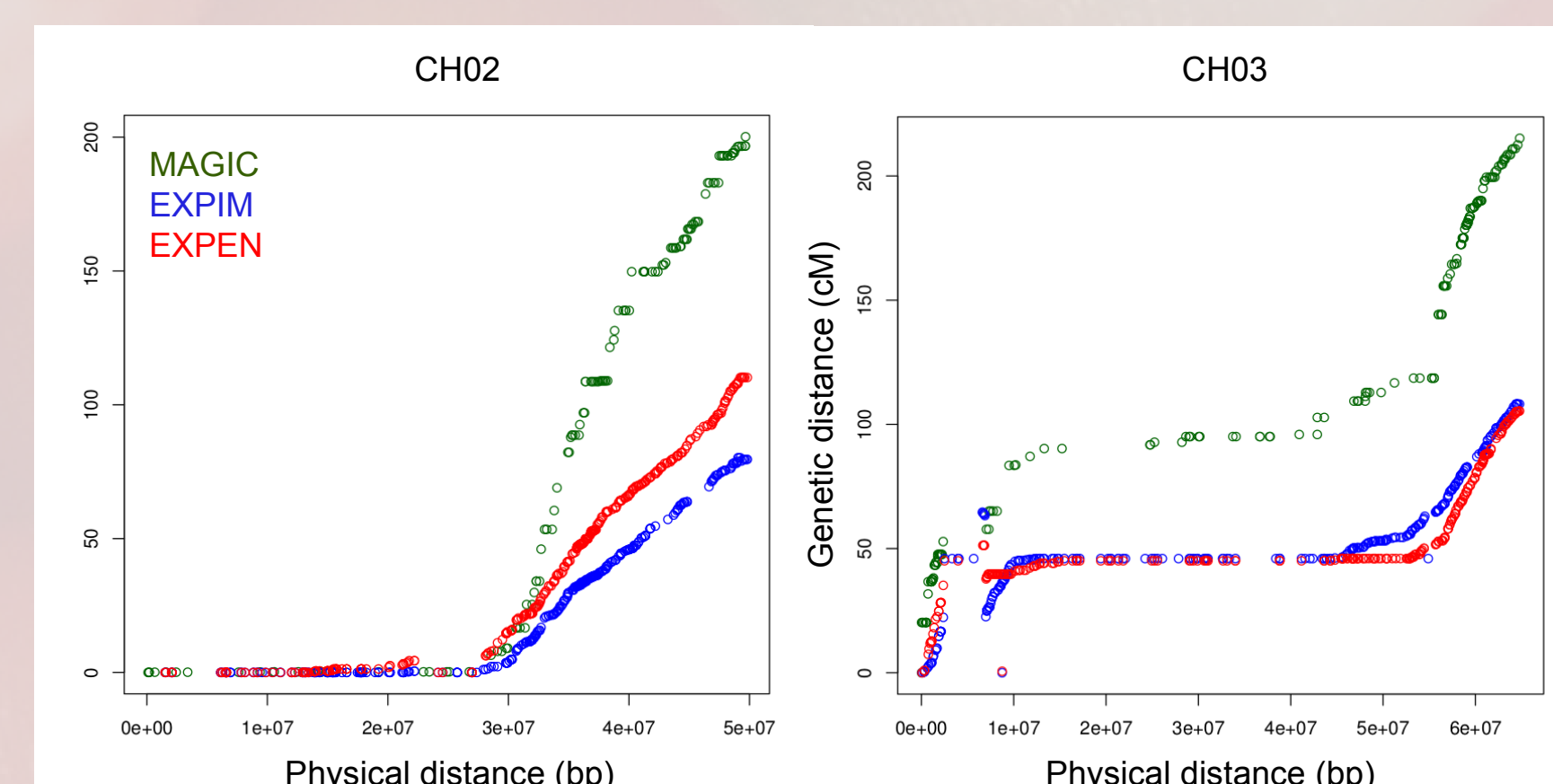


### SNPs detection and filtering



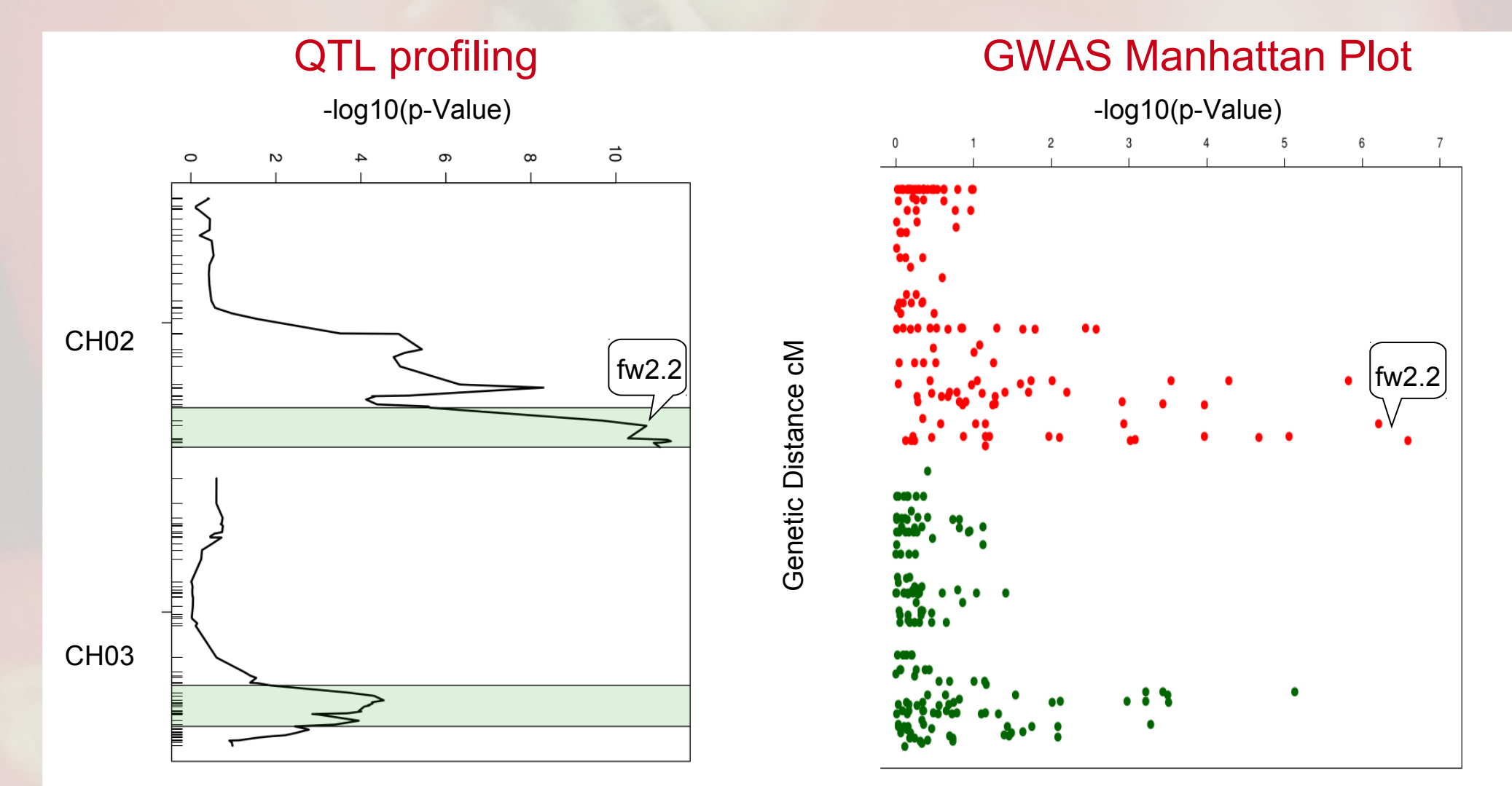
### Increasing recombination

Comparation between the MAGIC genetic map, with bi-parental populations maps (Sim et al, 2012). Recombination increases **60%**.

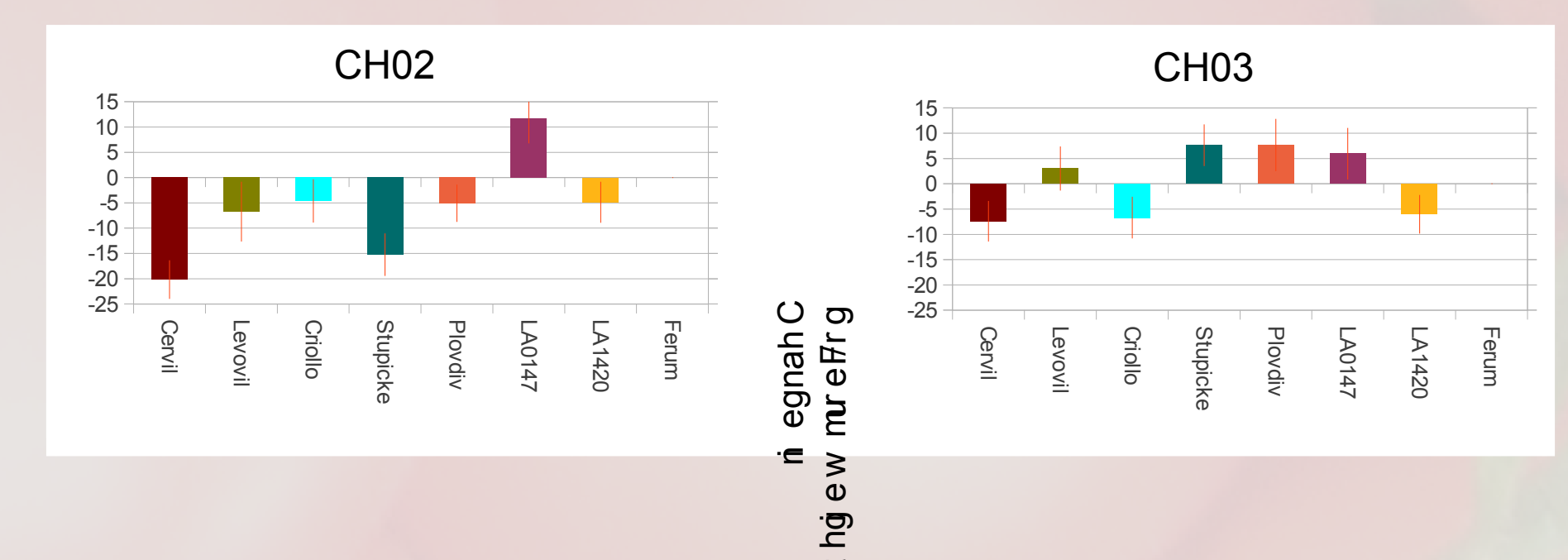


### Power to map quantitative characters

Mapping **fruit weight** control. Based on the QTL profiling with mpMap we detected **6 QTLs**, for five of them our position co-localized with already detected QTLs. For kown genes like fw2.2 we are less than **1Mb from the gene**. GWAs gives associations at similar locations.



### Different QTLs = Different effects



## Conclusion

The MAGIC population shows greater phenotypic diversity than the founders lines, including new phenotypes. This diversity can directly be introduced on breeding programs.

When compared to bi-parental populations, MAGIC populations present around the 60% of increase in recombination events.

Six different QTLs related with fruit weight were detected, showing the great power of MAGIC panels to map complex quantitative characteres. This is coupled with a great precession, QTLs co-localize with already cloned genes.

This approach allowed us to estimate the different founder line alleles on the quantitative character. This differences allow the dessign of new combinations of alleles to tune the final phenotypes in breeding programs.

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