



## Deciphering the genetic control of quantitative traits with magic

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## T028 - Laura Pascual-Bañuls

### *Deciphering the genetic control of quantitative traits with magic*

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Identification of the polymorphism controlling the variation of quantitative traits is still a challenge for plant geneticists. Traditionally, linkage mapping in bi-parental populations or association studies is used for quantitative trait locus (QTL) mapping. However, the results might be limited by the low variation between two parental lines, and by population structure in association studies. These limitations may be overcome by more complex experimental populations. To increase the number of recombinations the development of advanced intercross lines (AILs) was proposed. To increase the genetic variation analyzed, nested association mapping (NAM) populations were developed from a diverse set of parental lines that are crossed with a reference line. However, such populations do not allow the QTL analysis in different genetic backgrounds. To overcome this limitation AILs methodology was extended to multiple parent populations. Multi-parent advanced generation inter-cross (MAGIC) populations allow the screening of a wider genetic diversity by mixing the genomes of a greater number of parental lines and increase the precision of QTL mapping by including more rounds of informative meiosis. Following this assumption, a MAGIC population consisting in 1000 progenies developed from 8 founder lines should be able to map QTLs with a sub-centimorgan resolution.

In this study, we present the construction of the first tomato MAGIC population. The population (397 lines) was obtained by crossing 8 tomato lines, selected to include a wide range of genetic diversity of the species. These eight founder lines have been deeply characterized following a systems biology approach (Pascual *et al.* 2013) and their whole genomes were resequenced allowing the identification of more than 4 millions SNPs (Causse *et al.* 2013). Polymorphism information was employed to select a subset of 1486 markers specially designed to analyse the MAGIC population. The selected markers were employed to develop the first intra-specific saturated map in tomato. The linkage map covered 2156 cM, and showed an 87% increase in recombination frequencies compared to bi-parental populations. The map allowed the prediction of the haplotype origin for an average of 89% of the MAGIC line genomes. The MAGIC population was characterized under greenhouse conditions and QTLs related with fruit quality traits were detected. We demonstrated the power and precision of the MAGIC population for QTL mapping on fruit weight. We then highlighted the power of such population when coupled with whole genome sequencing to restrict the number of putative causal polymorphisms underlying the QTLs and conduct positional cloning. A strategy to fine map QTLs and identify the causal polymorphisms is proposed. In conclusion, we have established a population of genetically diverse lines that could be



analyzed for any quantitative trait under different environments, providing a fine resource to analyze the basis of phenotypic plasticity.

### References

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