

PhD School on Agriculture, Environment and Bioenergy

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(XXXVII cycle, 2021-24)

Project draft

1. Field of interest

AGR03/AGR07

2. Project title

Genome-wide diversity and recombination landscape in peach

3. Tutor (membro del Collegio dei Docenti)

Marco Cirilli

Eventually: co-tutor/s

Laura Rossini

4. Relevance of the topic and state of the art:

Plant breeders rely on natural recombination of genetic information occurring during crossing-overs (COs) to generate novel and favorable combinations of alleles. The frequency and distribution of COs events is tightly regulated at the chromosomal level and affect the ability of breeders to reintroduce genetic variance at sites of selective sweeps and/or incorporation of novel genetic variants without simultaneously introgress large segments from a donor chromosome (**linkage drag**). In peach, the low COs frequency and limitations in obtaining and evaluating large populations over many years is an important constraints for varietal improvement. Understanding early patterns of segregation and recombination following hybridization is important for predicting phenotypic outcomes in progenies, and the degree to which linkage will lead to trait correlations.

5. Layout of the project (draft)

5.1. Materials & Methods:

1. Genotyping and construction of genetic linkage maps: dataset of genotypic data from several bi-parental F₁ and F₂ populations and a large collection of accessions from MAS.PES breeding programme; available maps and genotypic data from abundant literature.
2. Identification of Cross-Over Intervals, estimation of recombination events and recombination rate (linear or mixed model for CO density)
3. Identification of intragenic and intergenic recombination events
4. Association analyses between recombination event and genetic and phenotypic variation; permutation testing for genomic feature associations (DNA methylation, historical recombination, GC content, etc.)
5. Identification of the relationships between recombination and gene expression variation
6. Linkage disequilibrium-based recombination hotspots detection

5.2. Schedule and major steps (3 years):

Year 1. Collection of genotyping data for the construction of genetic linkage maps (SNPchip array, whole-genome-resequencing); identification of cross-over intervals, recombination rate (develop linear or mixed model); in silico and laboratory analyses.

Year 2. Performing bioinformatics analysis for the identification of intragenic and intergenic recombination events; association analyses between recombination event and genetic and phenotypic variation; permutation testing for genomic feature associations (DNA methylation, historical recombination, GC content, etc.); identification of the relationships between recombination and gene expression variation; linkage disequilibrium-based recombination hotspots detection.

Year 3. PhD thesis writing

6. Available funds

FREECLIMB, VALTIFRU

7. Literature

Salomé, P., Bomblies, K., Fitz, J. *et al.* The recombination landscape in *Arabidopsis thaliana* F₂ populations. *Heredity* **108**, 447–455 (2012).

Wijnker, E., James, G.V., Ding, J., Becker, F., Klasen, J.R., Rawat, V., Rowan, B.A., de Jong, D.F., de Snoo, C.B., Zapata, L. et al. (2013) The genomic landscape of meiotic crossovers and gene conversions in *Arabidopsis thaliana*. *Elife*, 2.

Gion JM, Hudson CJ, Lesur I, Vaillancourt RE, Potts BM, Freeman JS. Genome-wide variation in recombination rate in Eucalyptus. *BMC Genomics*. 2016;17:590.

Pan, Q.C., Li, L., Yang, X.H., Tong, H., Xu, S.T., Li, Z.G., Li, W.Y., Muehlbauer, G.J., Li, J.S. and Yan, J.B. (2016) Genome-wide recombination dynamics are associated with phenotypic variation in maize. *New Phytol*, 210, 1083-1094.

Wall JD, Stevison LS. Detecting Recombination Hotspots from Patterns of Linkage Disequilibrium. *G3 (Bethesda)*. 2016;6(8):2265-2271.