# Building high-density peach linkage maps based on the ISPC 9K SNP chip for mapping mendelian traits and QTLs: benefits and drawbacks

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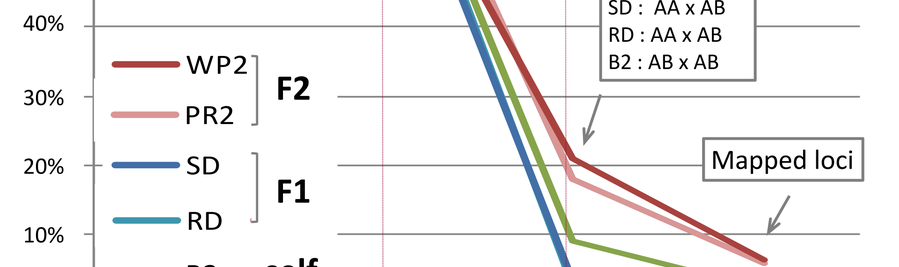
## Context

"FruitBreedomics" European project has been designed by an international consortium including scientists, stakeholders and breeding companies. One of its aims is to increase the efficiency of breeding programs in apple and peach by developing Marker Assisted Breeding (MAB) using novel genomic tools. In the frame of this project, six peach mapping populations (two intraspecific F2, two interspecific F1 derived from *P. davidiana*, one self pollinated derived from Bolinha and one advanced pseudo-backcross) segregating for mendelian traits and/or Quantitative Trait Loci (QTLs) for pest resistance and fruit quality were genotyped using an Infinium II Illumina bead-chip containing 8144 SNPs derived from the sequencing of the peach genome. Mapping results were contrasted depending on the population considered. Relevancy of using general medium-range SNP bead-chips for breeding purposes is discussed in this study.

| Parents | Pop. ID | Pop. type | Pop. size | Useful SNPs | Cross type |
|---|---|---|---|---|---|
| Pamir x Rubira® | $PR^2$ | F2 | 98 | AAxBB | intraspecific |
| Weeping Flower Peach x Pamir | $WP^2$ | F2 | 95 | AAxBB | intraspecific |
| Rubira® x *P. davidiana* | RD | F'1 | 68 | AAxAB | interspecific |
| Summergrand x *P. davidiana* | SD | F'1 | 97 | AAxAB | interspecific |
| Bolinha x Bolinha | $B^2$ | self | 112 | ABxAB | - |

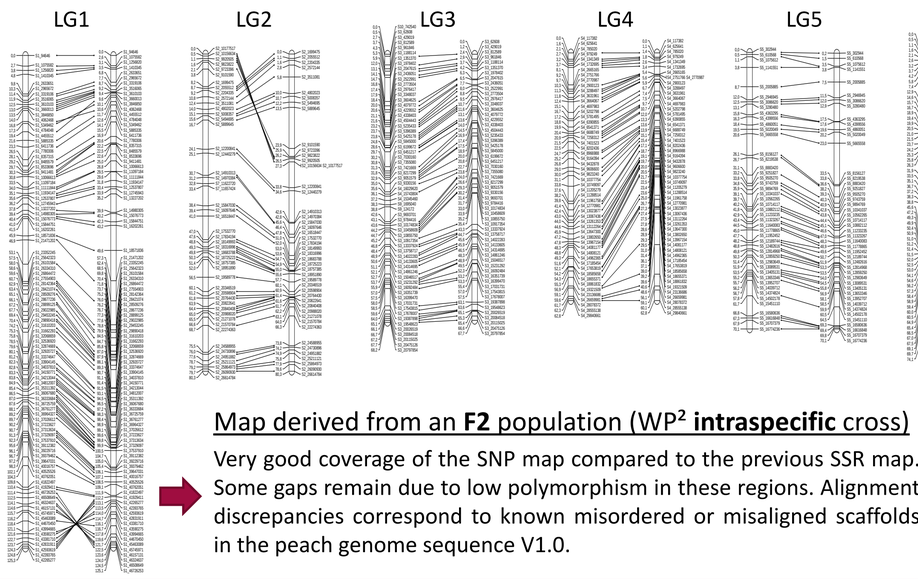
## Percentage of homo/heterozygous SNPs of parents




## SNPs losses at different stages of the mapping process

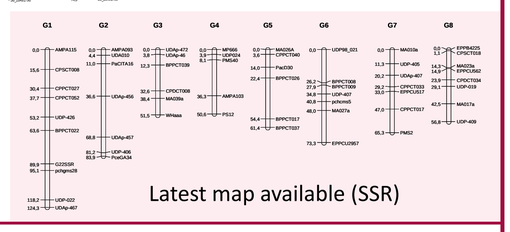



## Mapping results




Map derived from an **F2** population ($WP^2$ **intraspecific** cross)

Very good coverage of the SNP map compared to the previous SSR map. Some gaps remain due to low polymorphism in these regions. Alignment discrepancies correspond to known misordered or misaligned scaffolds in the peach genome sequence V1.0.



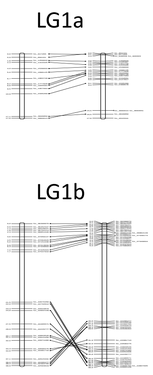

Latest map available (SSR)




Map derived from an **F1** population (SD **interspecific** cross)

Poor and uneven map coverage due to low transferability of many SNPs from peach to *P. davidiana* compared to SSRs. Quality of the SNP map lower than that obtained with SSRs markers despite a high general level of heterozygosity. observed in *P. davidiana*. Need for SNPs developed specifically from *P. davidiana* genome.


Latest map available (SSR)




Map derived from the **self-pollinated** population ($B^2$ cross)

Uneven distribution of SNPs over the Bolinha genome. Most of the linkage groups are missing due to low heterogenous heterozygosity rate in Bolinha which leads to a lack of segregating SNPs (LG2, LG4, LG5, LG7, LG8 not mapped). Inappropriate choice of the cross type (F1) for mapping.

## Conclusion

For each cross, the number of mapped SNPs is clearly below the number of SNPs initially present on the chip. This loss was caused by the filtering steps necessary to the selection of appropriate and reliable markers for genetic mapping. Approximately 20 to 30% poor quality (non-functional or aberrant) and 56 to 70% non-appropriate polymorphic SNPs were removed leading to **variable proportions of useful markers depending of the cross type**: on the one hand the SNP linkage maps derived from F2 populations display higher densities than the previous SSRs maps with an average distance of 1,5 and 1,3 cM respectively for $PR^2$ and $WP^2$ crosses. They perfectly align with the peach genome sequence v1.0 (IPGI). On the other hand, very few SNPs (<3%) turned out to be useful to map *P. davidiana* polymorphism. Linkage maps derived from F1 **interspecific crosses display low coverage** (almost identical to SSR map) **and heterogeneous distributions** with an average distance of 4,3 and 5,1 cM respectively for RD and SD crosses. This is due to the low rate of heterozygosity of *P.davidiana* for the SNPs included in the 9K SNP chip and demonstrates their **poor transferability** between species, even closely related. For Bolinha, low allelic variability of the SNPs coupled to low genome heterozygosity give similar results. In consequence, a good knowledge of the degree of heterozygosity of the selected cultivar is thus of first importance prior to using F1 crosses.

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