Comparative Mapping of *Prunus armeniaca, Prunus cerasifera* x *Prunus armeniaca* and *Prunus* Reference Map

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Abstract

Apricot and plum x apricot genetic linkage maps were constructed taking as a reference the almond 'Texas' x peach 'Earlygold' map (Joobeur et al., 1998; Aranzana et al., 2003) named 'T x E'. The apricot mapping population was an intra-specific cross between 'Polonais' and 'Stark Early Orange'. The plum x apricot mapping population (*P. ×dasycarpa*) was issued from an interspecific cross between Myrobalan plum (*Prunus cerasifera* Ehrh.) and apricot (*Prunus armeniaca* L.). The apricot parent (A3923) was a hybrid between 'Screara' and 'Stark Early Orange' (clone A669). These populations are part of breeding programs which aim at creating new genotypes combining several important traits: mainly fruit quality traits and disease resistance including sharka for apricot cultivars, graft compatibility, and pest and disease resistance for rootstocks. Apricot and Myrobalan maps were constructed by selecting a set of codominant markers on the 'T x E' map and by adding dominant markers. A total of 232 markers were distributed in the Myrobalan and apricot 'A3923' maps and 251 in the integrated apricot map ('P x S'). A set of common markers allowed anchoring of the 8 groups of the apricot maps ('P x S' and 'A3923') and 6 groups of the Myrobalan map to the homologous groups of the 'T x E' map and displayed a good colinearity. The remaining linkage group of the Myrobalan map was found to be composed of two linkage groups of the reference map.

INTRODUCTION

In this study, the apricot mapping population is part of a genetic program aiming to improve the knowledge on the genetics of major agronomic traits such as resistance to diseases including 'Plum pox virus' (sharka) and quality traits. The *P. ×dasycarpa* population was obtained within the framework of the apricot rootstock breeding program in order to combine favorable traits from both species: rootstock traits (adaptation to heavy soil and rooting ability from Myrobalan), graft compatibility with apricot scion and resistance to pest and disease (root-knot nematodes from both species and sharka from 'Stark Early Orange'). In Europe the virus of sharka is the most important virus affecting *Prunus* fruit crops, mainly apricot and European plum. The virus is spread by grafting on infected rootstocks and by aphids through the orchards in a non-persistent way. In *Prunus* species, sources of resistance were found in apricot, mainly carried by a few North-American cultivars including 'Stark Early Orange' (Martinez-Gomez et al., 2000) which is represented in both our mapping populations, either as a parent or grand parent. Consequently, the mapping of regions of the genome involved in the resistance to sharka is an important objective. The construction of genetic maps is quite recent in *Prunus* species. Peach was emphasized because of its economical importance but several genetic maps have been developed in other *Prunus* species: One of them (Joobeur et al., 1998; Aranzana et al., 2003) constructed in an almond 'Texas' x peach 'Earlygold' ('T x E') progeny is considered a reference for *Prunus* and we used it as a standard for both apricot and *P. cerasifera* maps. We selected codominant RFLPs and SSRs mapped on the 'T x E' map for constructing and anchoring the maps and used AFLPs to improve the markers density.

MATERIALS AND METHODS

Plant Material

The apricot mapping population comprised 142 individuals obtained from an intraspecific cross between the French cultivar 'Polonais' (A1352) and 'Stark Early Orange' (A1145) which is a North-American cultivar that segregates for resistance to sharka and *Agrobacterium tumefaciens*, and for some traits involved in fruit quality and architecture. The rootstock mapping population (*P. ×dasycarpa*) was produced from an interspecific cross between Myrobalan plum (*P. cerasifera* Ehrh.) P2980 and apricot (*P. armeniaca* L.) A3923. 'A3923' is a hybrid between 'Screara' (A804) and the clone 'A669' of 'Stark Early Orange'. This population of 106 hybrids segregates for resistance to *Meloidogyne* nematodes and sharka, graft compatibility, rooting ability and waterlogging tolerance.

Molecular Markers

Three types of markers were used for map construction: RFLPs for apricot, SSRs and AFLPs for both apricot and *P. ×dasycarpa*. Eighty-eight *Prunus* probes placed in the 'T x E' map were also mapped in the apricot population. A total of 90 *Prunus* SSR primer combinations were tested: 35 *Prunus* SSRs were mapped in apricot and 36 in *P. ×dasycarpa*. Eighty-eight AFLPs were mapped in apricot and 170 in *P. ×dasycarpa.*

Linkage Analysis and Map Construction

For each population, linkage analysis was performed using MAPMAKER/EXP 3.0 software (Lincoln et al., 1992) for the construction of each parental map following a double pseudo-testcross model of analysis (Grattapaglia et al., 1994). Marker distances were calculated using Kosambi function (Kosambi, 1944). Markers heterozygous in both parents were used as anchor loci for the alignment of the parental maps. Integrated maps were constructed using CarthaGene 0.5 software (Bouchez et al., 2002).

RESULTS AND DISCUSSION

In apricot, 141 markers were distributed in the 'Stark Early Orange' map and 110 in the 'Polonais' map defining a total length of 699 cM and 538 cM respectively. Thirty-nine loci were heterozygous in both parents allowing the alignment of the 8 homologous linkage groups of each map and the construction of the 'P x S' integrated map where the resulting length was 701 cM. One hundred and fifteen loci were common to the 'P x S' map and the 'T x E' reference map and allowed full alignment of all linkage groups. In the interspecific cross *P. ×dasycarpa*, 8 linkage groups were found in the maternal apricot (A3923) map, but only 7 in the paternal Myrobalan plum map. One hundred and twenty eight markers were distributed in the apricot 'A3923' map defining a total length of 1198 cM. Among them, 29 SSRs were placed on the 8 linkage groups corresponding to the 8 homologous linkage groups of the 'T x E' map. Ninety-seven markers covered the Myrobalan plum map defining a total length of 970 cM. Twenty-one SSRs were placed on 6 linkage groups corresponding to the 6 homologous groups of the 'T x E' map and the 'P x S' integrated map. Five SSRs were placed on the seventh linkage group that was found to be composed of the homologous linkage groups 3 and 5 of the 'T x E' map (see Fig. 1). A mapping artifact is unlikely since no marker on this group was deviating significantly from the expected segregation ratio for an F1 population ($P<0.1\%$) and the linkage between the markers was strong: a LOD threshold of 11.0 was necessary to split this group into the 2 'underlying' ones. This merging of linkage groups could therefore result from a reciprocal translocation as described by Jauregui et al. (2001).

Adding additional markers is needed for final confirmation of this hypothesis. Since all our apricot and Myrobalan plum maps could be aligned to the 'T x E' reference map, the same terminology for group numbering could be followed. An example is given in Fig. 2. The comparison of marker order supports the conclusions of the colinearity of the genomes and of their high conservation. This would allow the ready use of informa-

tion obtained in one progeny in another and would also allow the search for common portions of the genome carrying quantitative traits loci such resistance.

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Figures

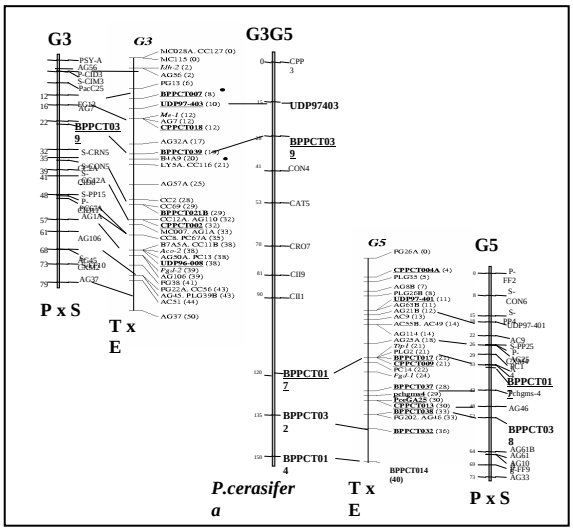

Fig. 1. Comparison of a linkage group of *P. cerasifera* with group 3 and 5 of the 'P x S' and 'T x E' maps. Markers common to the 'T x E' map and the 'P x S' and/or *P. cerasifera* map(s) are connected by a line. Markers common to the three maps are underlined.

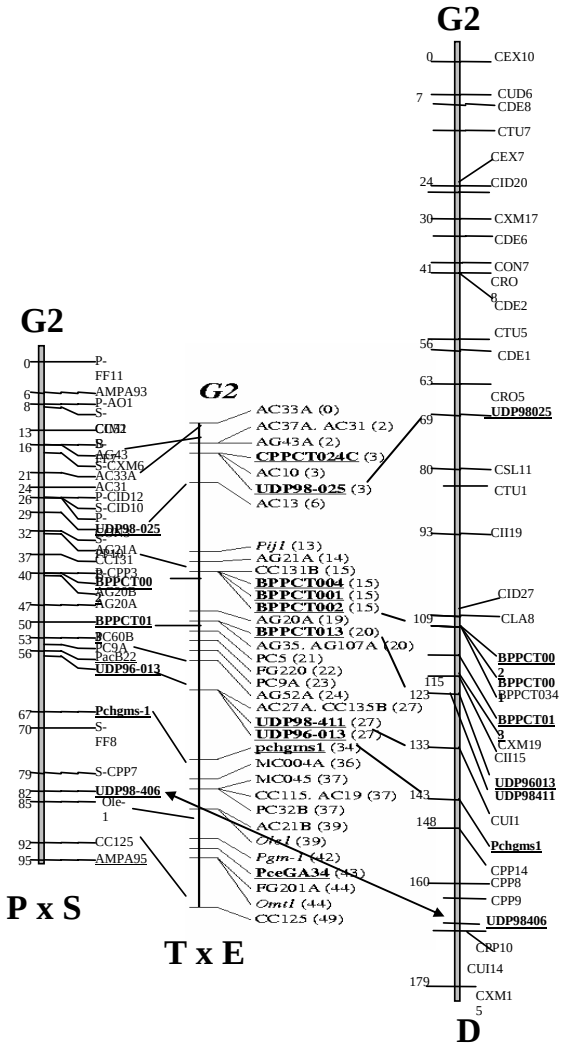

Fig. 2. Comparison of marker alignment in linkage group 2 of the 'Stark Early Orange' x 'Polonais' ('P x S'), *P.* ×*dasycarpa* ('D') and 'T x E' maps. Markers common to the 'T x E' and the apricot and/or the *P.* ×*dasycarpa* maps are connected by a line. Markers common to the three maps are underlined. The respective locations of UDP98-406 that is positioned in the 'P x S' and the 'D' maps, but not in the 'T x E' map, are linked by an arrow. In Fig. 1 and Fig. 2, the 'T x E' linkage groups are not to scale for legibility reasons.