IDENTIFICATION OF ALMOND GENOMIC REGIONS IN FOUR 3-WAY INTERSPECIFIC HYBRID PROGENIES

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Introduction

Rootstocks adapted to drought tolerance are highly demanded due to water shortage in Mediterranean areas. Currently, interspecific hybrids, almond x peach, 'Garfi' x 'Nemared' (GxN) which are resistant to root-knot nematodes of genus *Meloidogyne* spp., have a good performance in both conditions calcareous soils and replanting. However, these rootstocks show limitations to water shortage. Almond a crop species originated from arid regions is highly tolerant to water scarcity and has a good adaptation to a different range of water capability. Thus, the aim of this work was to identify the genes involved in drought tolerance of several plum x (almond x peach) progenies with several resistances to biotic and abiotic stresses within a rootstock breeding program.

Material & Methods

Four 3-way interspecific hybrid progenies obtained from crosses between two myrobalan plums 'P.2175' and 'P.2980' (*P. cerasifera* Ehrh) as female parentals, and the almond-peach (AxP) hybrids 'Garnem' and 'Felinem' [*P. amygdalus* Batsch, syn *P. dulcis* (Mill.) x P. *persica* (L.) Batsch] as male parentals were genotyped.

Forty-eight polymorphic SSRs along the parental genotypes were screened along the eight linkage groups obtained from several *Prunus* reference maps (Dirlewanger et al., 2004; Donoso, 2009; Howad et al., 2005).
Genetic similarity relationships among the individuals were calculated with NTSYSpc v2.1 software by UPGMA cluster analysis.

Results & Discussion

Individuals were classified in five different clusters depending on their genetic similarity (Fig.1). The almond 'Garfi' was the only genotype clustered at the group A. Cluster B grouped both peach 'Nemared' and the A x P hybrids 'Felinem' and 'Garnem'. The female parental myrobalan 'P.2175' appeared to belong to the cluster C, in which another individual was showed. The individuals whom female parental is the myrobalan 'P.2175' were classified in cluster D. The bigger genetic diversity of this cluster than the other clusters was remarkable (Fig.1). The female parental myrobalan 'P.2980' and its progeny were grouped at the cluster E. Furthermore, we could confirm the paternity of several individuals.

In addition, it was possible to identify the almond genome regions present along the eight linkage groups within our progenies and discriminate them from peach and plum genome regions (Fig. 2). It was observed more conserved areas in the five linkage groups (1.2.3.4.5) (Fig. 2, red rectangle) rather than in the other three (6, 7, 8). However, linkage groups 6, 7 and 8 presented a great number of crossovers (Fig.2). It is noteworthy that the locus screened in linkage group 7 with the *CPSCT004* SSR marker showed only almond alleles in the cluster D individuals (Fig.2, black rectangle).

Based on our results, we might be able to increase the efficiency on the identification of candidates genes involved in drought tolerance in these almond specific genomic regions.

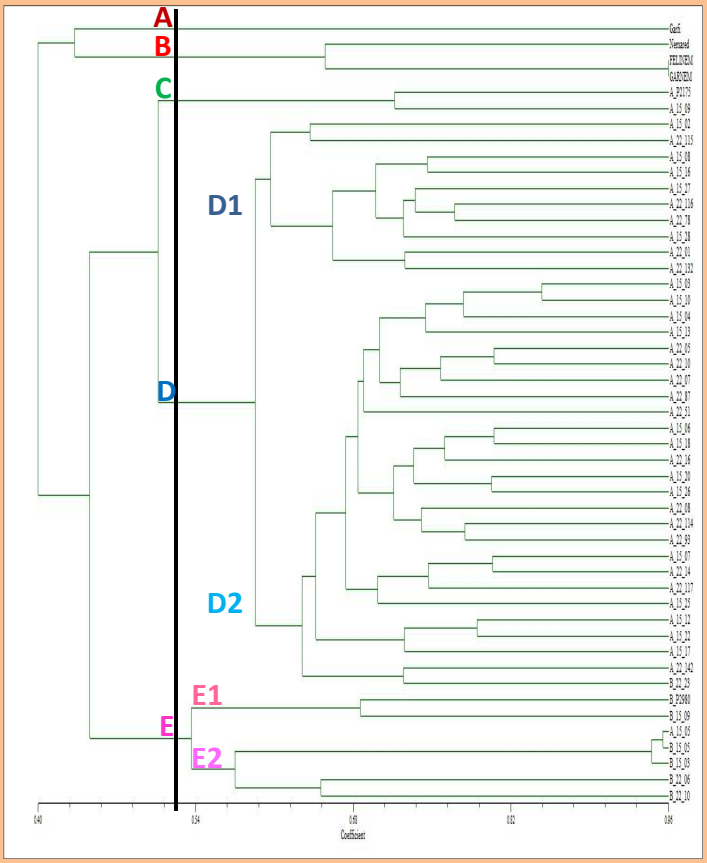

Fig 1. Dendrogram based on the diversity analysis of the six parentals and their four progenies based on UPGMA analysis after amplification with 48 SSRs.

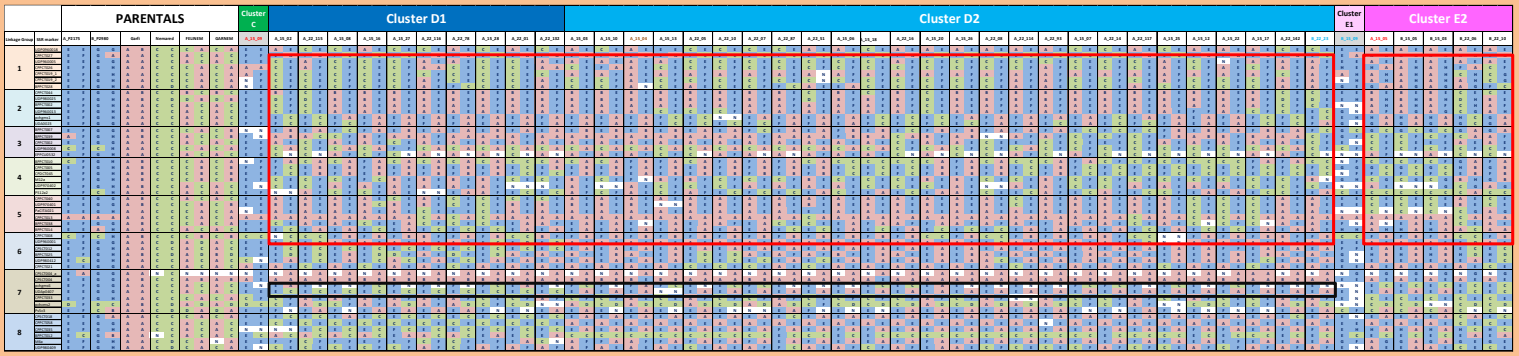

Fig 2. Graphical representation of the 6 parentals and their progenies identifying the almond, peach and plum regions along the eight LG. Plum genome is represented by blue colour. Peach genome is represented by green colour. Almond genome is represented by red colour. White colour represents no amplification. More conserved region was marked by red rectangle. Loci for CPSCT004 was marked by black rectangle.

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Donoso, J.M. 2009. Genética de la introgresión de genes del almendro (*Prunus dulcis* Mill.) en el melocotonero [*P. persica* (L) Batsch]: Desarrollo de una estrategia de selección de líneas casi isogénicas (NILs) con marcadores moleculares. Universidad Autónoma de Barcelona.
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