Identification of almond genomic regions in four 3-way interspecific hybrid progenies S6P10

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The challenge in rootstock breeding programs is the combination of abiotic stress tolerances in new interspecific hybrids including crosses combining almond, peach and plum genotypes in order to obtain rootstocks adapted to a wide range of soil conditions. Marker Assisted Introgression (MAI) can efficiently be used to identify almond regions in several progenies. We analyzed four 3-way interspecific hybrid progenies and their parental genotypes (two myrobalan plums 'P.2175' and 'P.2980', the almond-peach hybrids 'Garnem' and 'Felinem', 'Garfi' almond and 'Nemared' peach). Forty-eight polymorphic SSRs in the parental genotypes were screened along the eight linkage groups obtained from several Prunus reference maps. The UPGMA dendrogram generated using the genetic variability observed, classified the genotypes in five different clusters allowing us to differentiate the almond genomic regions from the peach and plum background in our progenies. The study of some candidates genes involved in drought stress tolerance in those regions will be accomplished as well as comparative genomic analysis once the almond genome will be available.