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Title	<b>Genetic characterization of almond (<i>Prunus dulcis</i>) cultivars and natural resources</b>	
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<b>Abstract</b>		
<p>Almond (<i>Prunus dulcis</i>) is thought to have originated in central Asia and disseminated to Europe and America. This study was carried out to evaluate the genetic variability of almond cultivars, landraces and natural resources available for breeding in several countries from Kyrgyzstan to California. The analysis focused on the allelic variants of 13 SSR loci and the S-RNase gene. Almond was characterized by considerable genetic diversity (reflected by the average number of alleles, Shannon index, observed heterozygosity) in all geographic regions. The genetic constitution of almond germplasm seemed to be quite different according to their region of origin. Almond cultivars carried some <i>P. webbii</i>, <i>P. orientalis</i> and <i>P. arabica</i> S-RNase alleles indicating multiple introgression events. A considerable erosion of the genetic variability was attributed to the founder effect in a geographically isolated territory and also the occurrence of self-compatibility. However, self-compatibility is a relatively new trait in almond (spanning only some decades) compared to apricot and hence it has not been enough time for inducing major genetic erosion. Almond germplasm is currently in a stage where apricot has been thousands of years before. The history of apricot should be instructive for almond breeding to manage genetic resources of cultivated almonds. The correspondences between the genetic diversity and mating strategy highlight how powerful effects of the self-(in)compatibility system has in shaping the genetic basis of a fruit tree species.</p>		