

## SNP discovery in olive tree

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### Abstract

The olive tree (*Olea europaea* L.) is an important oil crop that has been traditionally cultivated throughout the Mediterranean basin. Its cultivation has spread to North and South America and to Australia. The current consideration of olive oil as a healthy source of fats has led to its incorporation into the diet in many countries, besides the ones on the Mediterranean region. Olive oil varietal composition is an important quality parameter. With the aim of developing variety-specific PCR-based molecular markers in olive tree amenable to high-throughput detection systems, we have explored the levels of single nucleotide polymorphisms (SNPs) present within sequence characterized amplified regions (SCAR) markers. So far, eight SCAR loci in eight olive tree varieties and three wild olive trees have been sequenced, yielding an average of 5.5 SNPs per loci (2.75 SNPs per loci among cultivated varieties). These numbers correspond to one SNP every 82.5 bp (one SNP per 16 bp for cultivated varieties). All polymorphic loci with the exception of a retrotransposon-like sequence contained SNPs among varieties. The retrotransposon-like sequence contained no SNPs differentiating the cultivated varieties from the wild olive trees, confirming the phylogenetic value of such sequence and its use as internal amplification control. In total, C → T transitions, 14 A → G transitions, one G → T transition, 5 A → C transversions, A → T transversions and one G → C transversion were found. SCAR markers have therefore proven useful targets for SNP development in olive tree.

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### References

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