MOLECULAR CHARACTERIZATION OF CURRANT (RIBES SPP.) ACCESSIONS USING SNP AND SSR MARKERS

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Ribes species belong to the Saxifragaceae genus, which is taxonomically fairly isolated, and the most commercially important species, especially in Northern European countries, are the red currant (R. rubrum L.) mainly used for fresh consumption and blackcurrant (R. nigrum L.), used for processing. Currants have known a slight production increase in the last years for their health biocomponents, highly concentrated both in fresh and in processed products.

In Italy, a small germplasm collection is present at IASMA, and the plant material includes contributions from R. rubrum L., R. sativum Syme, R. petraeum Wulf., R. multiflorum, R. longeracemosum L., R. grossularia L., R. sanguineum Pursh., R. nigrum L. and R. dikuscha Blue.

Single Nucleotide Polymorphisms (SNPs) are the most abundant type of DNA sequence polymorphism and can be theoretically found within every genomic sequence. Thanks to their high availability and stability, also compared to Simple Sequence Repeats (SSRs), they can be used as molecular markers for many purposes, such as cultivar identification and evaluation of genetic diversity.

The aim of this work is represented by the development of informative molecular markers for characterizing the germplasm collection of these Ribes species, that have been phenotyped for six consecutive production season in order to obtain a large informative picture of the cultivars and selections, concerning flowering, fruiting, horticultural traits, biotic and abiotic resistances, and health compounds.

New SNP markers were detected by re-sequencing several loci amplified from a selection of Ribes accessions. Primers based on Expressed Sequence Tags having homology to known genes involved in fruit development were applied and a SNaPshot assays is now being developed for the SNP genotyping.

In order to investigate the genetic relationships among Ribes varieties a set of genomic and ESTs derived SSR marker was also tested.