



Seminar



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Genomic approaches to study somatic variation as a source of cultivar innovation

Somatic variation is a natural source of diversity that has long been exploited to improve traditional grapevine wine cultivars and adapt them to changing environmental conditions and market demands. Somatic variation is also a source of novel traits such as grape color variation enabling cultivar innovation and diversification of products. To understand the mutational mechanisms generating somatic variation in grape color, we compared the Tempranillo Blanco white berry somatic variant with its black berry ancestor, Tempranillo Tinto. By whole-genome resequencing and structural variation analysis we identified that complex genome rearrangements involving three chromosomes and hemizygous deletion of 1.7% of the genome resulted in the loss of the grape color locus functional allele in Tempranillo Blanco. We showed that this complex genome reshuffling has additional consequences affecting production in Tempranillo Blanco. Similar structural variation analyses in Grenache grape color somatic variants identified more simple deletion events as the causal mutations. To assist future intra-varietal studies in Tempranillo, the third most widely grown wine cultivar in the world, we are now using long-read sequencing PacBio and Nanopore technologies to build a haplotype-resolved genome assembly and to annotate it. These genomic tools will be exploited to search for causal mutations in improved Tempranillo somatic variants identified in clonal selection programs.

Room 6302 – Palazzo della ricerca e della conoscenza
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