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MECHANISMS AND CANDIDATE GENES FOR SEED AND FRUIT SET IN GRAPEVINE

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Fruit set is a key trait for yield determination of most crop species. In parthenocarpic genotypes fruit setting is achieved independently of pollination and fertilization. Besides offering a way to face pollen-limiting environmental conditions, parthenocarpy is also linked to fruit quality because it is a pre-requisite for seedlessness, which is highly appreciated by consumers. The control of fruit set and of seedlessness has thus become a major breeding objective in many fruit crops, including grapevine. Most cultivated seedless grapes exhibit the Sultanina-derived stenospermocarpy, where seed development aborts at an early stage after fertilization. In the last years substantial advances have been achieved in the comprehension of the molecular mechanisms underlying Sultanina's stenospermocarpy, whereas different sources of seedlessness have been much less investigated and exploited. With the aim of providing additional insights into the regulation of seed/fruit formation and develop testable candidate gene hypotheses, we explored the grapevine germplasm collections at FEM and CNR-IPSP searching for clones with contrasting seed content. In total, we identified nine variant pairs that differ only in those characteristics related to the presence of seeds while showing identical microsatellite marker profile. Here we report their phenotypic and molecular characterization, with special emphasis on Sangiovese and its seedless variant, for which we previously performed a comprehensive transcriptomic comparison. These accessions were evaluated in up to 5 years for fruit and seed set in control, self-pollinated and emasculated conditions. Our observations suggest that when pollination is not prevented stenospermocarpy may be responsible for the seedless phenotype of the Sangiovese somatic variant and is potentially driven by pollen and/or ovule defects. In the seek for structural variation each seedless mutant was compared to its seeded reference variety by using the GrapeReSeq_Illumina_20K_SNP_chip. None of the putative SNPs was validated by resequencing, proving they are near-isogenic lines. Conversely, RNA-Seq-based variant calling allowed the identification of some SNPs that were experimentally confirmed in the original and additional Sangiovese accessions. These polymorphisms are suitable to be tested as diagnostic markers in clone identification and as functional candidates for the seedless phenotype.