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ABSTRACT BOOK
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Mechanisms and candidate genes for seed and fruit set in grapevine

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Fruit setting and seedlessness underpin grapevine yield and quality, with the latter being especially appreciated by the table grape consumer. Consequently, their control is a major breeding objective. Most seedless cultivars exhibit the Sultanina-derived stenospermocarpy, for which substantial advances have been made in the comprehension of the underlying molecular mechanisms, 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, we explored the 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 genetic profile at several microsatellite loci. We report their phenotypic and molecular characterization, as well as multi-year observations on fruit and seed set upon different pollination treatments, with special emphasis on the Sangiovese/Corinto Nero pair. Our morphometric data suggest that stenospermocarpy is not restricted to Sultanina-derived cultivars. The seedless phenotype of the false Corinto Nero is potentially driven by pollen and/or embryo sac defects, as supported by microscopic analysis of gametophytes, by genotyping/ploidy analysis of seedlings derived from embryo rescue and by differential gene expression with respect to Sangiovese. Moreover, three genotypes, including Sangiovese/Corinto Nero, were unexpectedly found to develop fruits without pollen contribution and occasionally showed normal-like seeds. In the search for structural variation each seedless mutant was compared to its seeded reference variety by using the GrapeReSeq_Illumina_20K_SNP_chip and a RNA-Seq dataset. Identified polymorphisms are suitable to be tested as diagnostic markers in clone identification and as functional candidates for the seedless phenotype.

Keywords: berry, flower, reproductive development, seed, single-nucleotide polymorphism, somatic variation, transcriptome