

## OMICS TOOLS DEVELOPMENT FOR PEAR-APPLE HYBRID IDENTIFICATION

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Hybrids between apple and pear provide a unique germplasm resource for genomic, transcriptomic and metabolic profiling studies and for breeding works focused on diseases resistance/susceptibility and fruits flavour and nutritional value. The similar chromosome number, genome size, and their recent divergence date, together with DNA-markers have shown that apple and pear genomes are highly co-linear. The main task of this project was to develop several-omics tools to enable fast and reliable identification of putative intergeneric hybrids. Using information derived from the recent apple and pear joint genome projects (Daccord *et al.*, 2017; Linsmith *et al.*, 2019) a comparative genomic approach was utilized. High Resolution Melting, single nucleotide polymorphism (SNP) analysis, simple sequence repeats (SSRs) and SNP-chip analysis were established and validated with the already identified apple-pear hybrid “Zwintschers Hybrid” (Fischer *et al.*, 2014). After successful validation, new putative hybrids obtained at UniBo were analyzed. In addition, this work described the genus-specific metabolite pattern found in these plants due to the assessment and quantification of arbutin and phloridzin content while only one or the other was present in pear and apple, respectively (Fischer *et al.*, 2014). The dihydrochalcone phloridzin (phloretin 2'-O-glucoside) is the major phenolic glucoside found in apple trees and contributes to the flavor, colour and health benefits of apple fruits and processed products (Li *et al.*, 2011). Arbutin, is a widely distributed compound in various higher plants such as leaves of bearberry and pear (Arend *et al.*, 2000; Ahmadian *et al.*, 2019) and, in the past, the presence of arbutin in pear has been correlated with the biochemical processes that operate as defence mechanisms against bacterial invasion. Finally, the DNA content of the UniBo samples was measured by Plant Cytometry Services (Plant Cytometry Services, Schijndel, the Netherlands). The markers analysis, carried out with new developed SNPs markers and with published SSRs markers (Liebhard *et al.*, 2002; Silfverberg-Dilworth *et al.*, 2006; Yamamoto *et al.*, 2001, 2002, 2007) and the analysis of the presence or absence of the genus-specific secondary metabolites, phloridzin for *Malus* and arbutin for *Pyrus*, demonstrated that ‘Abate’ x ‘Fuji’ hybrid are true full hybrids as found previously for the Zwintzscher’s Hybrid. Moreover, significant differences ( $p=0.0001$ ) in absolute DNA content of the *Malus*

and *Pyrus* genotypes, as well as for the putative hybrids were found by flow cytometry. In conclusion, this research demonstrated that SSR and SNP markers, the metabolomics analysis as well as DNA content can be useful tools to detect hybridity in progeny derived from crosses between apple and pear or *vice versa*. The true hybrids found with the methods used in this study can be used for breeding to introduce more traits of interest, such as flavour or texture in apple or pear.