traits that could be used for species identification. By integrating population genetic and phylogenetic analyses we are able to more completely describe the historical relationships and diversity within these important crop wild relatives.

The USDA-ARS national plant germplasm system malus collection: diversity of cultivars and wild species

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The USDA-ARS National Plant Germplasm System (NPGS) Plant Genetic Resources Unit (PGRU) apple collection in Geneva, NY conserves over 2500 trees as grafted clones. We have compared the genotypes of 1131 diploid Malus × domestica Borkh. cultivars to a total of 1910 wild and domesticated samples representing 41 taxonomic designations in the NPGS collection to identify those that are genetically identical based on nine simple sequence repeat (SSR) loci. A total of 238 M. × domestica and 10 samples of other taxonomic groups shared a genotype with at least one other M. × domestica individual. We identified examples of genotypes for cultivars that matched genotypes of known rootstocks, and indicated that these accessions may not accurately represent the indicated named clones. Twenty three sport families, comprised of 104 individuals, were identified that could not be differentiated using the nine SSR loci. SSR markers as well as phenotypic traits were used to compare the di versity of the currently designated core collection to that of the entire diploid grafted collection. We have identified a set of individuals that augment the diversity of the existing core collection, thus capturing more than 95% of the allelic and phenotypic diversity. We have also identified sets of 100 individuals that also capture the desired diversity within the collection. Five of the selected markers (CH01h01, CH02d08, CH01f02, G12, GD147) overlap with sets of markers that have been used to fingerprint European apple collections, thus making it possible to compare and coordinate collection inventories on a world-wide scale.

A targeted metabolomics method for the rapid quantification of multiple classes of phenolics in the fruits of Rosaceae

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In recent years, the interest in phenolic compounds has been increasing due to compelling evidences of their beneficial health properties and to their impact on food

quality. The complexity and remarkable diversity of phenolics has challenged the analytical performances of separation and detection methods in terms of resolving power, selectivity and sensitivity for the identification and quantification of these compounds in different matrices. Targeted metabolomics is a strategy based on the use of predefined metabolite-specific signals, such as MRM transitions, that can be used to accurately determine the concentrations of a wide range of known metabolites.
We developed a rapid and versatile UPLC-MS/MS based method for the quantification of >150 phenolics, such as benzoates, phenylpropanoids, coumarins, stilbenes, dihydrochalcones and flavonoids in fruits. Compounds commonly occurring in plants were included in the method together with metabolites specific of a single species or family. Reverse-phase chromatography was optimised to achieve separation of the compounds over 15 min, reducing possible ion suppression effects and resolving many isomeric compounds. The optimal fragmentation conditions for each analyte were studied and MRM transitions were selected for accurate quantification. The effectiveness of the method was validated by studying the limits of detection and quantification, the linearity ranges of the instrumental response and the repeatability of the analysis.
The method was successfully applied and validated for the analysis of apples, cherries, raspberries, strawberries, as well as grape, wine and green tea, and was shown to represent a valuable tool for the quantitative evaluation of the chemical phenotype, measuring the presence, amount and natural variance in phenolics composition of these fruits.

Overexpression of a peach *Cbf*-transcription factor gene in apple regulates both dormancy and freezing tolerance in apple: lab and field studies

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Economic production of fruit trees in a temperate climate is dependent upon seasonal changes in cold acclimation and dormancy. Evidence indicates that these processes will be greatly affected by climate change (higher atmospheric carbon dioxide and temperatures). This problem may also be exacerbated by erratic weather patterns. Weather events in the USA in the spring of 2012, resulting in devastating losses to fruit crops, are an example of the potential danger. Wisniewski, et al. (2010. Planta 233: 971-983) previously demonstrated that a transgenic 'M.26' apple line (T166) overexpressing a peach CBF gene increased the freezing tolerance and induced earlier dormancy (Wisniewski, et al. 2010. Planta 233: 971-983). Since that study, the field performance of T166, has been monitored in comparison to wt ('M.26'), and apple lines in which expression of a native CBF has been suppressed (CBF-Si). Self-rooted trees were planted on October 7, 2010 and several phenotypic c haracteristics monitored. The T166 line exhibited an immediate response to cool temperatures and short photoperiod. Trees exhibited a large increase in anthocyanins in their leaves followed by rapid senescence. By November 4, 2010, T166 trees had lost all their leaves while wt, and CBF-Si trees still had green leaves. In spring of 2011, the CBF-Si line was the first to break bud, prior to