

Identification of *Pyrus* single nucleotide polymorphisms (SNPs) and evaluation for genetic mapping in european pear and inter-specific *Pyrus* hybrids

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Genomic resources are becoming increasingly available for Rosaceae crops, including pears. We have used next generation sequencing (NGS) technologies to identify single nucleotide polymorphism (SNP) markers from three European pear (*Pyrus communis* L.) cultivars to develop a set of high throughput markers useful for large-scale genotyping in the genus *Pyrus*. A set of 1096 pear SNPs was chosen and combined with 7867 apple SNPs in an Infinium II® array (Illumina). The 9K Infinium II array was evaluated using a segregating population of European pear parents ('Old Home' x 'Louise Bon Jersey') and three inter-specific families derived from Asian (*P. pyrifolia* and *P. x bretschneiderii*) and European pear. In total, 806 polymorphic pear markers were used for the construction of the first SNP-based genetic maps for pear. In addition, 785 SNP markers derived from apple (10% of the total apple SNPs included in the array) were polymorphic, including markers with null alleles. The study is first to assess SNP transferability across the genera *Malus* and *Pyrus*. The construction of high density SNP-based and gene-based genetic maps represents an important step in the process of identifying chromosomal regions associated with horticultural characters, such as pest and disease resistance, fruit yield and quality.