

## Development of gene-based markers for linkage map construction in sweet cherry (*Prunus avium* L.)

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Sweet cherry (*Prunus avium*) is one of the economically important fruit trees within the *Prunus* genus in the *Rosaceae* family. The long vegetative development, space requirement and the gametophytic self-incompatibility system make this species not amenable for rapid improvements through traditional breeding. The aim of this project is to develop a genetic map using gene-based markers for future marker assisted selection (MAS). Once markers linked to traits of interest are identified, plant selections can be made at the seedling stage as opposed to the mature tree stage. Our strategy focuses on identifying single nucleotide polymorphisms (SNPs) and insertions/deletions (InDels) in predicted introns using resources available in public databases. We were able to amplify and sequence PCR products from 80 primer pairs in the two cherry parents of our mapping population. Of this group, 48 harbored the predicted intron. Thirty seven percent (24) showed at least one SNP and/or InDel in either one or both parents and this information was used to map these markers in the sweet cherry population. With this approach, we plan to develop additional gene-based markers for sweet cherry and other *Rosaceae* species. From a total of 91,000 *Prunus* ESTs, 4,852 putative Conserved Orthologous EST Sequences (COS) were pre-selected after BLAST search against *Arabidopsis* single copy genes resulting in 1,374 *Prunus*-*Arabidopsis* COS. The developed COS markers will be an important resource to identify fruit quality QTLs in sweet cherry. Moreover, a COS markers-based linkage map will provide ample opportunities for genome comparative analysis within the *Rosaceae* family.