DNA Marker Screenings in Fruit Tree Gene Banks

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Introduction
Maintenance of live plant collections is very expensive but necessary for many crops like the vegetatively propagated fruit trees. Fortunately, live collections are presently enjoying increased attention in connection with phenotyping to identify QTl for plant breeding purposes. Access to properly identified material is, however, needed for producing meaningful information BUT previous studies using simple sequence repeats (SSR) have shown that up to 20–40% of the accessions may be mislabeled in e.g. apple and pear gene banks (review in Nybom and Weising, 2010)

Cherries
Sweet cherries Prunus avium, diploid, and sour cherries P. cerasus, tetraploid, have long been cultivated in Europe. Both seed and vegetative propagation has been used in the past and cultivar discrimination is notoriously difficult, especially in older plant collections!

Materials and Methods
14 cultivars of sweet cherry (25 samples in total) and 9 cultivars of sour cherry (19 samples in total) from Balsgård and 6 other collections in Sweden, were analysed with 6 SSR primer pairs suggested by ECPGR (Clarke and Tobutt 2009).

Results
The investigated loci displayed 8–18 alleles each. Parentage could be verified in some cases where both parent and offspring cultivars were analysed. Most sour cherries clustered together but Nefris behaved like a diploid – mislabelled? Different samples of the same sour cherry cultivar were usually identical. Sweet cherries were, on the whole, more problematic and also more diverse. Only a maximum of 57% of the cherry trees included in this study appear to have been correctly labeled!

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References