Introduction

Sicily has distinctive germplasm of diploid sweet cherry (P. avium) and tetraploid sour cherry (P. cerasus), cultivars as well as wild and/or escaped to the wild genotypes. Cherries are generally cultivated in the traditional way – often as isolated trees or in mixed orchards. They are also a frequent component of woodland and road margins. Many cultivars are disappearing as farmers stop growing them. The Department of Culture Arboree of Palermo University has started a programme to evaluate and conserve cherry genetic resources. This study is assessing the genetic diversity of Sicilian cherry accessions and determining their self-incompatibility genotypes, using a novel method developed at East Malling Research UK, based on multiplexing a simple Sequence Repeats primers with incompatibility (S) locus primers (Vaughan & Russell, 2004, Vaughan et al. submitted).

Materials and Methods

• 40 accessions of sweet cherry representing the majority of Sicilian cultivars, one indigenous wild sweet cherry and the international cultivar ‘Napoleon’.
• 25 accessions of sour cherry from the wild and farms (Fig. 1).
• Genomic DNA extracted from buds according to Doyle and Doyle (1997).
• 10 fluorescently labelled SSR primer pairs multiplexed in two PCRs – EMPa: 02, 06, 11, 14, EMPb: 04, 05, 15, 18 (East Malling); UP98-412 (Udine); and PceG34 (Michigan) – along with two primer pairs for the incompatibility (S) locus, amplifying across the first intron of the S-RNase gene and across the intron of the SFB gene.
• PCR product were sized using an ABI Prism 3100 running GENESCAN® and GENOTYPER® software.
• A UPGMA dendrogram was constructed using PAUP*.

Results

Sweet

• The number of alleles per SSR locus ranged from 4 to 11. The SSRs distinguished 33 Sicilian accessions; eight accessions fell into four non-distiguishable groups, indicating synonymy. Some accessions with same name but of different origin were distinguished (Fig. 2).
• ‘Napoleon’ did not separate from Sicilian accessions, but it was distinct from the ‘Napoleona’ accession groups from Sicily. The wild accession ‘Ciliegio Selvatico’ did not separate from the cultivars.
• Accessions were assigned to different incompatibility groups (Table 1). The most frequent groups were SS56, SS39, SS16 and SS616.
• Alleles S16 and S22 were frequent, though they generally occur in wild populations (De Cuypere et al. 2005), suggesting that some accessions may derive from cross-pollination between cultivated cherries and wild cherries (Fig. 3).

Sour

• The number of alleles per SSR locus ranged from 4 to 9.
• A low level of diversity was found among the 25 wild genotypes suggesting they may be derived from closely related seedlings or suckers.
• 24 genotypes showed the same incompatibility genotype S6, S13, SB, SD (according to the allele nomenclature adopted by Tobutt et al. 2004).
• One genotype was S10, S16, SB, SD, indicating it may be a Duke cherry.

Conclusion & Outlook

• The Multiplex method was useful for the analysis of incompatibility genotypes and molecular characterisation and could be useful for a world-wide comparison of cherry germplasm.
• Knowledge of the incompatibility genotypes could help farmers to choose appropriate pollinators to maximize production and breeders to design specific crosses.
• A larger number of sour cherry genotypes from across Sicily will be studied.

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