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Comparative Genome Mapping In Rosaceae Using COS Markers

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Plant-derived single-copy conserved orthologous set (COS) markers reduce the difficulties of distinguishing orthology from paralogy as found in multigene families. Therefore, they are markers of choice for comparative genome mapping in plants. We tested a set of COS markers derived from Rosaceae EST to develop an understanding of genome evolution in this large and complex family. The 627 COS markers were mapped on the Prunus reference mapping population 'Texas' x 'Earlygold' (TxE) and then tested in apple using two different strategies:

1/ The COS PCR primers were screened for polymorphisms using the high-resolution melting (HRM) technique over the apple bin mapping population 'Malling 9' x 'Robusta 5'. The results from this initial screen revealed difficulties arising from the ancient polyploidy state of apple.

2/ The Rosaceae COS were aligned in silico with the apple reference genome of 'Golden Delicious'. This approach revealed 502 common markers in nineteen areas of homology between the Prunus and apple genomes. Of the 627 markers aligned, 220 had multiple sequence alignments, highlighting regions duplicated because of apple's ancient polyploidy.

The in silico results are being used to design COS markers specific for apple that can also be used for comparative mapping with other members of the Pyrinae (e.g. pear).

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