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Comparative Genome Mapping of the Rosaceae

A thesis presented in partial fulfillment of the requirements

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ABSTRACT

Comparative genome mapping uses genetic map and DNA sequence alignment to assess genome conservation between two or more organisms. This study makes use of the recent genome sequence availability of four Rosaceae genera, and the development of new, and the expansion of existing, linkage maps to: 1) explore overall genome synteny between apple and strawberry; 2) assess homology between, and the degree of ancestral genome rearrangement among, four genera; and 3) compare genome synteny with respect to the production of anthocyanins between raspberry and strawberry.

The inter-tribal comparison of the genomes of apple and diploid strawberry, conducted by adding 56 newly developed orthologous markers to existing linkage maps, identified 21 regions of genomic synteny between the linkage groups of apple and strawberry. In addition, this work identified two each of potential translocations, inversions and insertions, and provided a set of orthologous markers that will be useful for orienting and anchoring other Rosaceae genome sequences.

Orthologous- and other DNA sequence-based markers were used in the construction of new linkage maps for Rubus occidentalis 96395S1 and R. idaeus ‘Latham’. The sequences from which the Rubus markers were designed were compared with the draft genome sequences of Malus × domestica ‘Golden Delicious’, Fragaria vesca ‘Hawaii 4’, and Prunus persica ‘Lovell’ to identify regions of orthology. This first comparison of Rubus linkage maps with other members of the Rosaceae identified a nearly 1:1 homology between the linkage groups of Rubus and F. vesca, as well as family-wide conservation among some linkage groups.

The F₁ progeny of Rubus occidentalis 96395S1 × R. idaeus ‘Latham’ was used to conduct a quantitative trait locus (QTL) analysis to explore the presence of associations between genotype and the variation in concentrations of anthocyanins in the fruit. Seven associations of traits with markers designed from the sequences of transcription factors and anthocyanin biosynthetic pathway genes were identified, providing opportunities for further fine-scale mapping, as well as cloning and expression analyses. The comparison of QTL maps of Rubus and Fragaria × ananassa suggests that homologous genomic regions may be important in the expression of various fruit quality traits.
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Finally, I would like to dedicate this thesis to my parents, who instilled in me a sense of adventure and willingness to try new things. I miss you both.
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<tr>
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<th>Definition</th>
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<tbody>
<tr>
<td>A</td>
<td>Adenosine</td>
</tr>
<tr>
<td>a/a/p</td>
<td>Amygdalus/Armeniaca/Prunocerasus</td>
</tr>
<tr>
<td>ACY</td>
<td>Anthocyanins</td>
</tr>
<tr>
<td>AFLP</td>
<td>Amplified fragment length polymorphism</td>
</tr>
<tr>
<td>Amplicon</td>
<td>Amplified product of PCR</td>
</tr>
<tr>
<td>BLAST</td>
<td>Basic local alignment search tool</td>
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<tr>
<td>bp</td>
<td>Base pair</td>
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<tr>
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<td>Cytosine</td>
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<tr>
<td>c/l/p</td>
<td>Cerasus/Laurocerasus/Padua</td>
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<td>C3G</td>
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<td>C3XR</td>
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<td>Complementary DNA</td>
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<td>Contig</td>
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<td>COS</td>
<td>Conserved orthologous set</td>
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<td>Deoxyribonucleic acid</td>
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<td>Double stranded DNA</td>
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<td>FISH</td>
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<td>FV×FB</td>
<td>Fragaria vesca × F. bucharica</td>
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<td>HG</td>
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<tr>
<td>HPLC</td>
<td>High performance liquid chromatography</td>
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<tr>
<td>HRM</td>
<td>High-resolution melting</td>
</tr>
<tr>
<td>IM</td>
<td>Interval mapping</td>
</tr>
<tr>
<td>indel</td>
<td>Insertion or deletion</td>
</tr>
<tr>
<td>kb</td>
<td>Kilobase</td>
</tr>
<tr>
<td>K-S DMax</td>
<td>Kolmogorov-Smirnov Dmax test</td>
</tr>
<tr>
<td>LG</td>
<td>Linkage group</td>
</tr>
<tr>
<td>LOD</td>
<td>Logarithm of odds</td>
</tr>
<tr>
<td>M.9×R5</td>
<td>‘Malling 9’ × Robusta 5</td>
</tr>
<tr>
<td>Abbreviation</td>
<td>Description</td>
</tr>
<tr>
<td>--------------</td>
<td>-------------</td>
</tr>
<tr>
<td>MAB</td>
<td>Marker assisted breeding</td>
</tr>
<tr>
<td>Mb</td>
<td>Megabase</td>
</tr>
<tr>
<td>μg</td>
<td>Microgram</td>
</tr>
<tr>
<td>mL</td>
<td>Milliliter</td>
</tr>
<tr>
<td>MQM</td>
<td>Multiple-QTL model</td>
</tr>
<tr>
<td>mRNA</td>
<td>Messenger RNA</td>
</tr>
<tr>
<td>MS</td>
<td>Mass spectrometry</td>
</tr>
<tr>
<td>my</td>
<td>Million years</td>
</tr>
<tr>
<td>nm</td>
<td>Nanometers</td>
</tr>
<tr>
<td>P3R</td>
<td>Pelargonidin 3-O-rutinoside</td>
</tr>
<tr>
<td>PCR</td>
<td>Polymerase chain reaction</td>
</tr>
<tr>
<td>pg</td>
<td>Picogram</td>
</tr>
<tr>
<td>QTL</td>
<td>Quantitative trait locus</td>
</tr>
<tr>
<td>R gene</td>
<td>Resistance gene</td>
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<tr>
<td>RAPD</td>
<td>Random amplification of polymorphic DNA</td>
</tr>
<tr>
<td>Rf</td>
<td>Recombination frequency</td>
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<tr>
<td>RFLP</td>
<td>Restriction fragment length polymorphism</td>
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<td>RLG</td>
<td>Rubus linkage group</td>
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<tr>
<td>SCAR</td>
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<td>SD</td>
<td>Standard deviation</td>
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<tr>
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<td>Standard error</td>
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<tr>
<td>SEM</td>
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<td>SNP</td>
<td>Single nucleotide polymorphism</td>
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<tr>
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<td>T</td>
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<tr>
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<tr>
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<td>Unique gene</td>
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### LIST OF COMMONLY REFERRED TO ROSACEAE SPECIES

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