# Construction and Comparative Analyses of Highly Dense Linkage Maps of Two Sweet Cherry Intra-Specific Progenies of Commercial Cultivars

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Despite the agronomical importance and high synteny with other Prunus species, breeding improvements for cherry have been slow compared to other temperate fruits, such as apple or peach. However, the recent release of the peach genome v1.0 by the International Peach Genome Initiative and the sequencing of cherry accessions to identify Single Nucleotide Polymorphisms (SNPs) provide an excellent basis for the advancement of cherry genetic and genomic studies. The availability of dense genetic linkage maps in phenotyped segregating progenies would be a valuable tool for breeders and geneticists. Using two sweet cherry (Prunus avium L.) intra-specific progenies derived from crosses between 'Black Tartarian' × 'Kordia' (BT×K) and 'Regina' × 'Lapins'(R×L), high-density genetic maps of the four parental lines and the two segregating populations were constructed. For BT×K and R×L, 89 and 121 F1 plants were used for linkage mapping, respectively. A total of 5,696 SNP markers were tested in each