

Construction of a SNP marker saturated linkage map of 'Vic' x 'Cristobalina' in sweet cherry

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Abstract

The development of SNP arrays with thousands of markers along the whole genome has allowed the construction of saturated linkage maps. These maps are a powerful tool for genetic studies such as QTLs analysis. In this work, a saturated linkage map was developed from a sweet cherry F1 population of 161 individuals, derived from the intra-specific cross of the cultivars 'Vic' and 'Cristobalina' (VxC). The parental cultivars were selected because their large differences in relevant agronomical characters such as bloom and maturity date, fruit color and fruit size. 'Vic' is a bred self-incompatible cultivar, which presents large fruits of very dark skin color maturing late in the season and harvested without the pedicel. On the other side, 'Cristobalina' is a local self-compatible variety from the Mediterranean area of Spain that blooms and matures very early in the season, and its fruits are red and smaller in size. The parental and individual progeny genotypes were analyzed using the RosBREED whole genome cherry 6K Illumina Infinium® SNP array v1 and the corresponding genetic map was constructed using this data. The resulting genetic map comprises eight linkage groups and was compared to other saturated linkage maps in sweet cherry. This map will be used for further analysis of the genetics of sweet cherry relevant traits like flowering and harvest time, and fruit quality traits.