

Statistical tools and software for the construction of integrated genetic linkage maps of outbreeding species using SNP markers with apple as a model

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Integrated genetic linkage maps have become an indispensable tool in genetics and genomics. For outbreeding species with SNP markers, the construction of integrated genetic linkage maps is complicated by the fact that in different populations markers may either be segregating according to one of three types of segregation or be non-segregating. Further complications arise from the presence of unequal rates of recombination and from segregation distortion. In this presentation we will give a detailed description of the steps that have been made to construct an integrated genetic linkage map of apple using SNP data from three populations. We will also describe the tools that have been used in the process, which include tools for ordering markers, tools for selecting representative markers that can be used to construct framework maps, and tools for checking the quality of genetic linkage maps of individual populations as well as integrated genetic linkage maps. The integrated linkage map of apple with a total length of 1278 cM contains 1199 SNP markers. We will present a comparison of the integrated map and the genetic linkage maps of the individual populations. The SNP positions on the integrated linkage map will also be compared with the corresponding physical positions of the Golden Delicious reference genome and will be used in following QTL discovery studies. This work has been performed in the framework of the projects EU-FruitBreedomics and USA-SCRI RosBREED.