

Present and future of marker-assisted breeding in sweet and sour cherry

José Quero-García^{1*}, José Antonio Campoy¹, Teresa Barrenenche¹, Loïck Le Dantec¹, Bénédicte Wenden¹, Mathieu Fouché¹, Elisabeth Dirlewanger¹, Herman Silva², Lichun Cai³ and Amy Iezzoni³

¹NRA Bordeaux-Aquitaine, 71 avenue Edouard Bourlaux CS 20032, Villenave d'Ornon, France

²Laboratorio de Genómica Funcional, y Bioinformática, Facultad de Ciencias Agronomicas, Santiago de Chile, Chile

³Department of Horticulture, Michigan State University, East Lansing Michigan 48824, United States of America

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Abstract

In the last decade, with the advent of next-generation sequencing technologies, numerous molecular markers have become available for genetic studies in sweet and sour cherries. Thanks to these tools, saturated linkage maps have been built in several countries allowing the detection of numerous Quantitative Trait Loci (QTLs). Hence, marker-assisted selection (MAS) has now become a reality for these crops. Given that sweet cherry is a species with a long period of juvenility and that large areas are needed to evaluate thousands of new hybrids, MAS will allow breeders to make decisions efficiently based on DNA information, such as which parents to choose, what crosses to make, and which hybrids to plant so that only those hybrids with favorable allelic combinations for the most critical agronomic traits are advanced. Nevertheless, the majority of these traits are complex, multi-genic and for some of them highly influenced by the environmental conditions. In this study, a synthesis of the main QTLs detected on sweet and sour cherry progenies from INRA Bordeaux and Michigan State University is presented for the following traits: self-fertility, bloom date and its components chilling and heat requirements, maturity period, productivity, fruit weight and firmness, fruit color, fruit acidity and sugar content, and tolerance to rain-induced fruit cracking. MAS has already been implemented for self-fertility, and fruit color in both sweet and sour cherry and fruit weight in sweet cherry and cherry leaf spot resistance in sour cherry. In some cases, the co-localization of QTLs and promising candidate genes (CGs) has been demonstrated. Perspectives dealing with fine mapping approaches, study of QTL x E interactions and QTL and/or CG validation through association genetics will be summarized. The full sweet cherry genome sequence of cultivar 'Regina' will soon be available, and will represent an invaluable tool for the whole cherry community of geneticists and breeders.