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Beyond QTL discovery to routine marker assisted breeding in sweet cherry

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Marker-assisted breeding (MAB) holds the promise of improving breeding efficiency, delivering superior new cultivars to industry with expenditure of fewer resources and in less time. However, there are few cases of routine implementation of MAB in tree fruit breeding. A gap exists between genomics research that identifies marker-trait associations and its practical application to aid breeding decisions. Sweet cherry lags behind in genomic and genetic resources unlike other Rosaceae fruit crops including apple, peach, strawberry and pear. More recently, a SNP genome scan including a 6K Infinium array was developed in sweet cherry. The SNPs were chosen to be evenly spaced over the genome, anchored to the peach whole genome sequence. The germplasm comprise 600 pedigree-linked individuals including the Crop Reference Set and the Breeding Pedigree Set representing founders, important breeding parents, advanced selections, and seedling populations. The pedigree structure of cultivated cherry spans only 5-6 generations with very few missing ancestors and low genetic diversity, facilitating our identity-by-descent approach to detect and characterize valuable QTLs for many fruit attributes. Many of these marker-locus-trait associations are described while only MAB for fruit size and self-fruit-fullness will be illustrated with utility for providing knowledge on fruit size genetic potential and self-(in) compatibility of prospective parents to aid crossing decisions, and as tools for culling seedlings predicted to have small fruit before field planting.

Biography

Nnadozie Oraguzie received his Ph.D. in plant breeding and genetics at Lincoln University, New Zealand and worked for a year as a Post-Doctoral researcher at Canterbury University, Christchurch, New Zealand, before joining Plant and Food Research (PFR) Institute, New Zealand as Research Scientist in 1998. At PFR, he was the Manager of the national pome fruit germplasm collection and an Objective Leader in the Pome fruit breeding consortium program. With the help of a fellowship from the Science and Technology Agency (STA) of Japan in 2001, he led an international collaboration including PFR, Hirosaki University and the National Institute of Tree Fruit Science, Morioka, Japan, that first linked an allele of the Md-ACS1 gene to fruit softening in apple. He was also the recipient of an Invitation Fellowship from the Japan Ministry of Science and Technology in 2006. He joined the faculty of Washington State University (WSU) in 2008 as Associate Professor. He has authored over 40 peer-reviewed journal publications and a book, and currently serves on the editorial board of two journals.

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