



20/20 Seeing Your Professional Future Coming to Focus at 2 -6 PM

Identification of Fruit Quality Associated Loci in Tomato (*Solanum lycopersicum*) Using Genome-Wide Association Mapping

Abstract

Tomato fruit quality is directly related to marketability and consumer appeal. Unfortunately, consumers are increasingly discontent with the flavor and quality of the product they are purchasing and requesting tomatoes with improved flavor, aroma, texture, and appearance. Traditionally, the selection for fruit quality traits in breeding programs has been done using conventional phenotyping approaches, in which large populations need to be screened for several breeding cycles. Although this approach has resulted in the release of high quality-high yielding cultivars, it is very time-consuming, delaying cultivar release. An alternative approach to improve breeding efficiency involves the use of modern molecular breeding techniques for population management. In this study, a diverse panel of 305 tomato genotypes, including 284 tomato breeding lines developed by Texas A&M tomato breeding programs were evaluated to identify loci associated with fruit quality. Phenotyping was carried out for color parameters, soluble solid content, titrable acidity, firmness and fruit weight over two years in field trials. Genotyping was conducted through low coverage whole-genome sequencing (SkimGBS) and genome-wide association study (GWAS) was performed with a total of 10,236 SNPs identified. Our study revealed wide variations in fruit phenotypes in all the tested traits. We identified a total of 1,836 significant SNP associations distributed on all 12 chromosomes for the seven fruit quality traits measured. Among them, 138 SNPs showed- significant associations with multiple traits, indicating pleiotropic effects. Upon validation, identified SNPs associated with fruit quality will be highly valuable for the implementation of fruit quality molecular breeding in tomato.

authors

Devi R. Kandel

Texas A & M AgriLife Research and Extension Center

[Henry O. Awika](#)

Texas A&M AgriLife Research

[Renesh Bedre](#)

Texas A&M AgriLife Research

[Kranthi Mandadi](#)

Texas A&M AgriLife Research

[Kevin Crosby](#)

Texas A&M University

[Carlos A. Avila](#)

Texas A&M AgriLife Research

View Related

[Vegetable Breeding 2](#)



[Oral Sessions](#)



Similar

[Identifying Candidate Genes for Tomato Flavor Volatiles By RNA-Seq with Multiple Reference Genomes](#)

Gurleen Kaur, Denise M. Tieman, Marcio Resende and Harry J. Klee, University of Florida

[Vitamin C Content in Spinach Germplasm: Phenotypic Diversity and Genome-Wide Association Mapping](#)

Dario D Rueda Kunz¹, Henry O. Awika² and Carlos A. Avila², (1)Texas A&M University, (2)Texas A&M AgriLife Research

[Genome-Wide Association of Leaf Spot \(*Stemphylium vesicarium*\) Resistance in USDA Spinach Germplasm](#)

Gehendra Bhattarai, Bo Liu, Ainong Shi, Chunda Feng and James C. Correll, University of Arkansas

[A Genomics Approach Towards Understanding Fruit Size Regulation in Apple](#)

Khalil Jahed¹, Peter M. Hirst² and Michael Gribskov¹, (1)Purdue University, (2)625 Agriculture Mall

Screening Tomato Breeding Lines for Bacterial Wilt Resistance in NC

Dilip R. Panthee, Ann Piotrowski and Frank J. Louws, North Carolina State University
