COTTON SNP 63K ARRAY - RESULTS AND FUTURE DIRECTIONS

A. M. Hulse
D. M. Stelly
F. Wang
X. Zheng
S. Hague
A. E. Pepper
Texas A&M University
College Station, TX
H. Ashrafi
A. Van Deynze
University of California-Davis
Davis, CA
M. A. Gore
Cornell University
Ithaca, NY
D. D. Fang
M. S. Islam
USDA-ARS
Cotton Fiber Bioscience Research Unit
New Orleans, LA
J. N. Jenkins
USDA-ARS
Starkville, MS
J. A. Poland
USDA-ARS Kansas State University
Manhattan, KS
J.-M. Lacape
M. Claverie
M. Giband
CIRAD
I. W. Wilson
Q. Zhu
D. J. Llewellyn
J. M. Taylor
A. Spriggs
CSIRO Plant Industry
S. V. Sawant
K. M.Rai
S. K. Singh
A. Bhardwaj
S. K. Bag
CSIR-National Botanical Research Institute
Don C. Jones
Cotton Incorporated
Cary, NC
J. A. Udall
R. L. Byers
D. B. Harker
S. M. Yourstone
Brigham Young University
Provo, Utah
R. Buyyarapu
Dow AgroSciences

J. J. Burke
M. Ulloa
USDA-ARS, SPA
Lubbock, TX
M. W. Ganal
J. Lemm
TraitGenetics GmbH
L. L. Hinze
R. G. Percy
J. Frelichowski
S. S. Wang
USDA-ARS-SPARC
College Station, TX
Jodi A. Scheffler
USDA-ARS
Stoneville, MS
C. T. Lawley
Illumina

Abstract

The CottonSNP63K will be a resource that will be used globally by public and private breeders, geneticists, and other researchers to enhance cotton genetic analysis, breeding, genome sequence assembly and many other uses. To assist the cotton community, a cluster file has been developed and resulted in 45,104 putative intra-specific SNP markers and 17,954 putative inter-specific putative SNP markers in the fixed content which will allow for automated genotyping. We report on the findings using the developed cluster file including high-density linkage maps and utilization possibilities for future analyses.