

The Next Generation of Peanut Genomics

J. CLEVENGER*, Mars-Wrigley Confectionary, Center for Applied Genetic Technologies, Athens, GA 30602; S. A. JACKSON and W. KORANI, University of Georgia, Athens GA 30602; and P. OZIAS-AKINS, Department of Horticulture, The University of Georgia, Tifton, GA 31793-0748.

Peanut genomics now suffers from an embarrassment of riches. There are resources available for high throughput genotyping to suit almost any preference. There are two SNP arrays to choose from, an initial 58K chip and an improved 48K chip. There are computational pipelines that identify SNP polymorphisms from sequence data that have been validated with these arrays in numbers not seen in other polyploids. There are resources available to quickly map alien introgressions in interspecific populations to a high resolution with only low coverage sequence data. In 2018 alone two genetic maps were constructed from re-sequencing data with over 10,000 markers each, and hundreds of accessions were assayed for genetic diversity with millions of sequence-based markers. There is now no barrier for efficient genotyping for genetic experiments. The impetus is utilizing these resources effectively, designing experiments with these resources in mind more efficiently, and training the next generation of peanut scientists to think beyond genotyping as a limitation.