Molecular/Cellular/Plant-Microbe Interactions

Exploring Genomic and Molecular Mechanisms of Host–Parasite Interactions for Crop Protection

The Peanut Genome Consortium and Peanut Genome Sequence: Creating a better future through global food security

B. GUO (1), X. Liu (2), P. Ozias-Akins (3), X. Zhang (4), B. Liao (5), R. K. Varshney (6), V. Nwosu (7), R. F. Wilson (8), H. T. Stalker (9)

(1) USDA ARS, Crop Protection and Management Research Unit, Tifton, GA, U.S.A.; (2) BGI-ShenZhen, Shenzhen, China; (3) University of Georgia, Tifton, GA, U.S.A.; (4) Henan Academy of Agricultural Sciences, Zhengzhou, China; (5) Oil Crops Research Institute, Chinese Academy of Agricultural Sciences, Wuhan, China; (6) International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India; (7) Plant Science Program, Global Chocolate Science & Technology, Mars Chocolate North America, Hackettstown, NJ, U.S.A.; (8) Oilseeds & Bioscience Consulting, Raleigh, NC, U.S.A.; (9) North Carolina State University, Raleigh, NC, U.S.A.

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The competitiveness of peanuts has been threatened by losses in productivity and quality. The U.S. Peanut Genome Initiative (PGI) was launched in 2004, and expanded to global in 2006 to address these issues beginning with marker development and genetic map improvement. Ultimately, the peanut genome sequencing project was launched in 2012 by Peanut Genome Consortium, a coalition of international scientists and stakeholders that guide and implement research in Peanut Genome Project (PGP) as an integral program of International Peanut Genome Initiative (IPGI). IPGI has over 135 members in 20 countries at 79 institutions and is a committed step by the world-wide peanut research community to meet the needs of the peanut industry. PGP goals are: 1) a high quality tetraploid reference genome sequence, 2) high throughput genome and transcriptome characterization of tetraploid and diploid, 3) phenotypic trait association with genetic haplotypes, 4) interactive bioinformatic resources. The outcome will enable molecular breeding for enhancing peanut genetic improvement. The large size (2.8 Gb) and allotetraploid nature of peanut genome are challenges for peanut assembly. Therefore an integrated approach has been deployed that complements whole genome sequencing with BAC x BAC, GWAS with Recombinant Inbred Lines, and emerging sequencing technologies to bring

the assembly together. SNP discovery also will contribute to a high-density genetic map for chromosome level assembly.