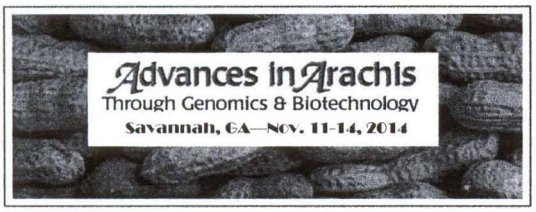

MEETING SPONSORS

THE PEANUT FOUNDATION

The Peanut Foundation

American Peanut Council

American Peanut Council

The Perfectly POWERFUL Peanut

National Peanut Board

Feed the Future Peanut & Mycotoxin Innovation Lab

Peanut & Mycotoxin Innovation Lab

MARS incorporated

Mars Chocolate

Georgia Peanut Commission
Working for farmers since 1961

Georgia Peanut Commission

and

U.S. Peanut State Grower Associations

AAGB-2014

Advances in Arachis
Through Genomics & Biotechnology

7th International Conference of the Peanut Research Community

November 11 – 14, 2014

Savannah Marriott Riverfront
Savannah, Georgia 31401 USA

Organized by

The Peanut Foundation

Peanut Mycotoxin and Innovative Programs, UGA/USAID

novel SSRs with primer sequences were developed after removing the sequences potentially containing known SSRs. Out of the 6,455 SSRs, 380 representing various SSR types were selected for PCR validation. The amplification rate was 89.2%. Twenty-two (6.5%) SSRs were polymorphic between at least one pair of four genotypes: Tifrunner, NC3033, Georgia Green, and C7616. SSRs with a 'AT/TA' motif have the highest polymorphism. By aligning the reads to assembled contigs, 11,902 SNPs and 2,949 INDELs were detected. To validate the SNPs, Sanger sequencing of PCR products targeting 110 SNPs was conducted. Sequence comparisons of the PCR products from four different genotypes revealed 13 true SNPs between tetraploid genotypes and 193 homoeologous SNPs, which were the SNPs between A and B genomes within genotypes. The results of this study enrich the peanut molecular marker tool box by providing over 6000 novel SSR markers covering the whole peanut genome and by providing the credentials for true peanut SNP marker development.

*wangjp@ufl.edu

Evaluation of groundnut genotypes for resistance to aflatoxin contamination

M. RANGANATHSWAMY[1], S.T. NAIK[1], B.N. MOTAGI[2]* & H.K. SUDINI[3]

[1]Department of Plant Pathology, University of Agricultural Sciences, Dharwad, Karnataka, India; [2]ICRISAT, Kano, Nigeria; [3]ICRISAT, Patancheru, Telangana, India

Groundnut (*Arachis hypogaea* L.) is one of the premier oilseed crops of the world with export potential. Aflatoxin contamination of groundnut caused by *Aspergillus flavus* is a widespread serious problem in most groundnut-producing countries where the crop is grown under rain-fed conditions which adversely affects health of consumers of groundnut and its products. The marketability of contaminated produce, particularly in international trade is diminished to nil due to stringent standards of permissible limits on aflatoxin contamination set by the importing countries. Alleviation of aflatoxin contamination through genetic manipulation has been attempted in many groundnut producing countries. Breeding resistant cultivars is possible only when there are sources with stable, high levels of resistance to different mechanisms are available. Therefore, efforts to identify resistant genotypes would make other measures more effective. In the present investigation 10 cultivars, 34 germplasm accessions and 25 advanced breeding lines were screened by following spore spray and pin prick method. In spore spray method, six genotypes showed moderately resistant reaction (ICG-1122, ICG-2857, ICG-3336, ICG-7633, ICG-14985 and ICGV-02266), twenty one showed susceptible reaction and 42 showed highly susceptible reaction. While in pin prick method, only ICGV-02266 showed moderate resistant reaction and the remaining genotypes (68) showed a highly susceptible reaction. ICGV-02266 recorded moderate degree of resistance in both the methods of screening and showed both seed coat and cotyledon resistance, indicating the scope for its utility in aflatoxin resistance breeding in groundnut.

*b.n.motagi@cgiar.org