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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

Organizing Committee

- Chair:** H. Thomas Stalker
- Co-Chairs:** David Bertioli
Richard Wilson
Farid Waliyar
Xinyou Zhang
- Secretary:** Soraya Leal-Bertioli
- Members:** Mark Burow, USA
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Local Arrangements Committee

- Chair:** Erica Davies
- Members:** Peggy Ozias-Akins
Shyam Tallury
Corley Holbrook
Noelle Barkley
Patrick Archer



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PROGRAM HIGHLIGHTS

Monday, November 10

14:00 – 18:00	Registration	Foyer
14:00 – 18:00	Poster set-up	Pre-function

Tuesday, November 11

07:00 – 08:00	Breakfast	Ballroom A
08:00 – 17:00	Registration	Foyer
09:00 – 10:00	Session I: Inauguration	Ballroom D & E
10:00 – 10:30	Tea/Coffee Break	Foyer
10:30 – 12:00	Session I (cont.)	Ballroom D & E
12:00 – 13:30	Lunch	Ballroom A
13:30 – 15:10	Session IIA: The Peanut Genome Project	Ballroom D & E
15:10 – 15:40	Tea/Coffee Break	Foyer
15:40 – 16:40	Session IIB: The Peanut Genome Project	Ballroom D & E
16:40 – 17:00	Group Picture	
17:00 – 18:00	Reception	Atrium
18:30 – 21:00	River Cruise and Dinner	Waterfront

Wednesday, November 12

07:00 – 08:00	Breakfast	Ballroom A
08:00 – 17:00	Registration	Foyer
08:00 – 9:50	Session III: Allelic Diversity & Germplasm Resources	Ballroom D & E
09:50 – 10:20	Tea/Coffee Break – Poster Viewing.....	Foyer/Pre-function
10:20 – 12:00	Session IV: Aflatoxin Elimination	Ballroom D & E
12:00 – 13:30	Lunch	Ballroom A
13:30 – 15:10	Session V: Genetic Trait Mapping & Gene Discovery ...	Ballroom D & E
15:10 – 15:40	Tea/Coffee Break – Poster Viewing.....	Foyer/Pre-function
15:45 – 18:00	Session VI: PeanutBase & Bioinformatic Resources	Ballroom D & E
18:00 – 19:30	Dinner (on your own)	
19:40 – 21:00	Trolley/Ghost Tour.....	Waterfront (staggered times with 30/group)

Thursday, November 13

07:00 – 08:00	Breakfast	Ballroom C
08:00 – 18:00	Registration	Foyer
08:00 – 10:10	Session VIIA: Crop Improvement	Ballroom D & E
10:10 – 10:40	Tea/Coffee Break – Poster Viewing.....	Foyer/Pre-function
10:40 – 12:00	Session VIIB: Crop Improvement	Ballroom D & E
12:00 – 13:30	Lunch	Ballroom C
13:30 – 15:30	Session VIII: The Path forward	Ballroom D & E
15:30 – 16:00	Tea/Coffee Break – Poster Viewing.....	Foyer/Pre-function
16:00 – 17:00	Session IX: Closing Ceremony	Ballroom D & E
17:00	Adjourn	
19:00 – 21:00	The Pirates' House (Dinner)	20 E. Broad Street
21:00 – 22:30	Moon River Brewery	21 W. Bay Street

Friday, November 14

Optional Tours

Coastal Georgia Botanical Gardens at the Historic Bamboo Farm
Savannah Trolley Tours
Museum Tours

TECHNICAL PROGRAM

Tuesday Morning, November 11

Session I: Inauguration

Chair: H. Thomas Stalker

- 9:00 **Welcome**Tom Stalker
Chair, AAGB-2014
- 9:10 **Video, President Jimmy Carter**Howard Valentine
*Executive Secretary
The Peanut Foundation*
- 9:25 **Importance of Agriculture in Georgia**Dean J. Scott Angle
*UGA College of Agriculture
& Environmental Sciences*
- 9:40 **Importance of Genomics to the International Community**David Hoisington
*International Director Peanut
& Mycotoxin Program*
- 9:55 **Announcements**Tom Stalker
- 10:00 **Break**
- 10:30 **Genomic selection in plants: Empirical results and implications for crop improvement**
ME Sorrels
Department of Plant Breeding & Genetics, Cornell University, Ithaca, NY
USA
- 11:15 **Genomic enhancement of maize for aflatoxin resistance**
M Warburton*, P Williams, G Windham, S Murray, W Xu, A Perkins,
J Tang & L Hawkins
*USDA ARS Corn Host Plant Resistance Research Unit, Mississippi
State, MS; USA
- 12:00 **Lunch**

Tuesday Afternoon, November 11

Session IIA: The Peanut Genome Project

Chairs: Xin Liu & Manish Pandey

- 13:30 **The genome architectures of *Arachis duranensis* and *A. ipaënsis* and their comparison to the component genomes of *A. hypogaea***
D Bertioli*, L Froenicke, X Liu, S Cannon, B Vidigal, D Gao, A Farmer, B Abernathy,
M Moretzsohn, ACG Araujo, P Ozias-Akins, S Bertioli, R Michelmore & SA Jackson
*UGA, Athens, GA, USA; University of Brasília, Brasília, Brazil
- 14:00 **Phenotyping *Arachis hypogaea* populations for development of genetic markers that can be used in MAS**
CC Holbrook*, P Ozias-Akins, Y Chu, T G Isleib, A Culbreath, T Brenneman, C Chen, J
Clevenger, C Chavarro, S Jackson, C Butts, M Lamb, T Sinclair, A Shekoofa, B
Tillman, M Burow, B Guo, Z Abdo & S Kim
*USDA-ARS; Tifton, GA, USA
- 14:20 **Assessing the BAC-to-BAC assembly strategy for the *A. hypogaea* genome**
X Liu*, G Huang, L Liang, S Cheng, X Xun
*BGI, China
- 14:40 **Update on the peanut genome and comparisons to other legumes**
SA Jackson*, D Gao, D Bertioli, S Bertioli, J P Clevenger, Y Chu, C Chavarro, A Iwata,
B Abernathy, S Cannon, L Froenicke, X Liu & P Ozias-Akins
*UGA, Athens, GA, USA
- 15:00 **Break**
- Session IIB: The Peanut Genome Project**
Chairs: Ran Hovav & Scott Jackson
- 15:40 **The *Arachis* transcriptome**
J Clevenger, Y Chu, D Bertioli, S Bertioli, B Scheffler, L Froenicke, R Hovav, B
Abernathy, S Jackson, C Holbrook & P Ozias-Akins*
*The University of Georgia, Tifton, USA
- 16:00 **Whole-transcriptome analysis of peanut tissues using next-generation sequencing: Toward an RNA-Seq atlas for NM Valencia C**
P Payton, K R Kottapalli*, P Puppala
*Texas Tech University, Lufkin, TX
- 16:20 **Transcriptome profiling of peanut developing seed with a focus on duplicate oil related pathways**
K Gupta, I Hedvat, P Ozias-Akins, J P Clevenger, R Hovav*
*Plant Science Institute, ARO, Bet-Dagan, Israel

Wednesday Morning, November 12

Session III: Allelic Diversity & Germplasm Resources

Chairs: Guillermo Seijo & Tom Stalker

- 8:10** **Arachis species and germplasm management**
HT Stalker
NC State University, Raleigh, NC, USA
- 8:30** **Roadmap of the USDA peanut germplasm collection: Past, present and future direction**
NA Barkley
USDA-ARS PGRCU, Griffin, GA, USA
- 8:50** **An overview on peanut germplasm collection, evaluation, and utilization in China**
H Jiang, X Ren, Y Chen, L Huang, X Zhou, Y Lei, L Yan, L Wan, B Liao*, H Upadhyaya & B Guo
*Oil Crops Research Institute -CAAS, Wuhan, Hubei, PR China
- 9:10** **Species, genomes and diversification in section Arachis**
G Seijo*, S Samoluk, L Chalup, M Grabiele and G Robledo.
Botanical Institute of the Northeast (IBONE, UNNE-CONICET). Corrientes, Argentina
- 9:30** **Characterization of Gregory x Arachis diogeni (GK 10602; PI276235) interspecific hybrid population**
SP Tallury*, R Srinivasan, P Chu, W Park & T Ranney
*Clemson University, PDREC, Florence, SC, USA

Session IV: Aflatoxin Elimination

Chairs: David Hoisington & Farid Waliyar

- 10:20** **Developing an in vitro method to assess aflatoxin biosynthesis suppression in Aspergillus flavus through RNAi technologies**
ER Palencia, RS Arias, V Sobolev & P Dang*
*USDA-ARS National Peanut Research Laboratory, Dawson, GA, USA
- 10:40** **Using RNAi technology against mycotoxin-producing Aspergillus and Fusarium species**
CL Niblett* & AM Bailey
*Venganza, Inc., St. Augustine, FL, USA
- 11:00** **Transgenic interventions for host-plant resistance for Aspergillus flavus infection and aflatoxin contamination in peanut**
P Bhatnagar-Mathur*, HK Sudini & KK Sharma
*ICRISAT, Patancheru, Hyderabad, India

- 11:20** **Combining genomic approaches to understand genetic control of aflatoxin contamination in peanut**
SN Nayak*, HK Sudini, G Agarwal, MK Pandey, HD Upadhyaya, P Janila, F Hamidou, H Desmae, P Ozias-Akins, B Guo & RK Varshney
*ICRISAT, Hyderabad, India
- 11:40** **Discussion**
- 12:00** **Lunch**

Wednesday Afternoon, November 12

Session V: Genetic Trait Mapping & Gene Discovery

Chairs: Boshou Liao & Peggy Ozias-Akins

- 13:30** **Progress on genetic linkage maps, traits/QTLs, and utilization in two recombinant inbred line populations of peanuts (Arachis hypogaea L.)**
B Guo*, P Khera, H Wang, A K. Culbreath, MK Pandey, RK Varshney, D Bertoli4, X Wang, B Liao, X Zhang & CC Holbrook
*USDA-ARS, Crop Protection and Management Research Unit, Tifton, GA, USA
- 13:50** **Prospects for a SNP chip in cultivated Peanut (Arachis hypogaea) utilizing the leaf transcriptome**
JP Clevenger*, C Chavarro, S Pearl, S Jackson & P Ozias-Akins
*University of Georgia, GA, USA
- 14:10** **The use of the diploid Arachis genomes to aid introgression of wild segments into peanut**
S Leal-Bertioli*, MM Moretzsohn, P Ozias-Akins, Y Chu, C Holbrook, C Ballen, C Chavarro, B Abernathy, AP Fávero, S Pearl, I Godoy, SA Jackson & DJ Bertoli
*Embrapa, Brasilia, Brazil; University of Georgia, Athens, GA, USA
- 14:30** **Interspecific resolutive mapping populations for marker/trait association in peanut**
D Fonceka*, H-A Tossim, I Faye, D Bertoli, S Leal-Bertioli, V Vadez, JC Glaszmann, B Courtois & JF Rami
*CIRAD UMR AGAP, CERAAS, Thiès, Senegal
- 14:50** **Research progress on peanut genetic trait mapping in China**
XY Z*, S.Y. Han1, BY Huang & XJ Wang
*Henan Academy of Agricultural Sciences, Zhengzhou 450002, PR China
- 15:10** **Break**

Session VI: PeanutBase & Bioinformatic Resources

Chairs: Steven Cannon & Jean-Marcel Ribaut

- 15:45 Using PeanutBase to explore the *Arachis* genomes and peanut genetic information.**
S Dash, EKS Cannon, S Kalberer, J Singh, D Bitragunta, L Ren, W Huang, N Weeks, J Dickerson, A Farmer, S Cannon*
*USDA-ARS, Ames, IA, USA
- 16:45 Integrated Breeding Platform: A novel set of tools and services to support breeding programs**
JM Ribaut
Generation Challenge Program, c/o CIMMYT, El Batan, Texcoco, Mexico
- 17:45 General Discussion on Software Options for Peanut**

Thursday Morning, November 13

Session VIIA: Crop Improvement

Chairs: Soraya Bertoli & Mark Burow

- 8:10 Challenges and Research Opportunities for Peanut Production and Pest Management in the USA**
DL Jordan*, WS Monfert & JE Woodard
*Department Crop Science, North Carolina State University, Raleigh, NC, USA
- 8:30 Peanut improvement for drought prone environments of Sub-Saharan Africa: Did we get good old agronomy right?**
V Vadez, O Halilou, F Hamidou, A Soltani, T Sinclair & F Waliyar*
*ICRISAT, Sahelian Center, BP, Niamey, Niger
- 8:50 Diseases of Peanut**
AK Culbreath*, TB Brenneman & IL Power
*The University of Georgia, Tifton, GA, USA
- 9:10 Considerations for marker-assisted selection in peanut**
MD Burow*, R Chopra, J Chagoya, CE Simpson, D Bertoli, Soraya Leal-Bertoli, CC Holbrook, HT Stalker, B Guo & R Varshney
*Texas A&M AgriLife Research, Lubbock, TX, USA
- 9:30 Changes in yield potential, grade, and seed weight among University of Florida advanced breeding lines and recently released cultivars**
BL Tillman
North Florida REC, University of Florida, Marianna, FL, USA
- 9:50 Towards deploying genomic selection for improving complex traits in peanut**
MK Pandey*, HD Upadhyaya, P Janila, A Rathore, P Khera, Y Hong, X Liang, B Guo & RK Varshney
* ICRISAT, Hyderabad, India
- 10:10 Break**

Session VIIB: Crop Improvement

Chairs: Jean-Marcel Ribaut & Noelle Barkley

- 10:40 Mapping quantitative trait loci for resistance to early leaf spot of groundnut**
E Tembo*, H Charlie, SMC Njoroge, AM Mweetwa, L Tembo, E Kaimoyo, ES Monyo, R Paliwal & DA Odeny
*University of Zambia, Lusaka, Zambia
- 11:00 Biological and genetic basis of peanut nodulation: More questions than answers**
J Wang*, L Tan, F Liu, Y Lopez, Z Peng & M Gallo
*University of Florida, Gainesville, FL, USA
- 11:20 *Botryosphaeria rhodina* as a biotic elicitor to enhance resveratrol biosynthesis during peanut seed germination**
RS Chen, YH Lai, JC Chang, CD Liu, C Chu, HF Ni & RYY Chiou*
*National Chiayi University, Chiayi, Taiwan
- 11:40 Discussion**
- 12:00 Lunch**

Thursday Afternoon, November 13

Session VIII: The Path Forward

Chairs: Rich Wilson & Victor Nwosu

- 13:30 Establishing Research Priorities to Meet Stakeholder Expectations**
Richard Wilson
- 13:45 What Does the Industry Expect From IPGI?**
George Birdsong
- 14:00 Interactive General Session Discussion & Strategic Planning Topics: Important problems that threaten global peanut supply & quality**
Up to Three Facilitated Breakout Groups
- 16:30 Tea/Coffee Break View Posters**
- 17:00 Reports from Breakout Groups**Breakout Facilitators
- 17:20 Awards & Recognition**Richard Wilson
- 17:30 Conference Wrap-up and Next Steps**Tom Stalker
- 17:45 Next Meeting & other Business**Howard Valentine

Session IX: Closing Ceremony

POSTER PRESENTATIONS

- 1. Drought tolerance mechanisms for responses to pre and post flowering drought stress of groundnut in a dryland ecology**
AA Adnan, JM Jibrin, SG Mohammed, HA Ajeigbe, BN Motagi & AS Shaibu
- 2. Impact of groundnut rosette disease on nutritive value and elemental composition of four varieties of peanut (*Arachis hypogaea*)**
AS Appiah, R Tegg, SK Offei & CR Wilson
- 3. Mapping of differentially expressed genes of *Arachis stenosperma* under *Meloidogyne arenaria* infection onto *Arachis duranensis* pseudomolecules**
C Ballen, S Leal-Bertioli, P Guimaraes, OB Silva-Júnior, ACM Brasileiro, SA Jackson & D Bertioli
- 4. Analysis of mutant populations for association of taxonomic and productivity traits with transposable element (TE) markers in peanut**
RS Bhat, Venkatesh, MV Kamble, AA Hake, BN Motagi, HL Nadaf, S Lingaraju, Suvendu Mondal, AM Badigannavar & MVC Gowda
- 5. Identification of SNPs for *Arachis hypogaea* L. genotypes using GBS and RNA-Seq based on the two diploid reference genomes**
C Chavarro, J Clevenger, S Pearl, Y Chu, B Abernathy, CC Holbrook, N Barkley, S Jackson, P Ozias-Akins
- 6. A study on influencing factors of seed dormancy in peanut (*Arachis hypogaea* L.)**
J Chen, L Jiang, CM Wang, XH Hu, HQ Zhai & JM Wan
- 7. Expression analysis of cDNAs fragment encoding ABA 8'-hydroxylase in peanut (*Arachis hypogaea* L.) dormant seeds**
J Chen, L Jiang, CM Wang, XH Hu, HQ Zhai & JM Wan
- 8. Transcriptome comparison of resistant and susceptible peanut (*Arachis hypogaea* L.) in response to *Ralstonia solanacearum***
Y Chen, H Jiang, L Huang, X Ren, X Zhou, Y Lei & B Liao
- 9. Cloning and functional analysis of fatty acid desaturase genes from peanut (*Arachis hypogaea* L.)**
X Chi, L Pan, N Chen, M Chen, T Wang, M Wang, Z Yang & S Yu
- 10. Transcript-based SNP map and QTL analysis of plant architecture and seed traits of F₂ lines developed from an interspecific cross of *Arachis duranensis* x *Arachis cardenasii***
R Chopra, CE Simpson, A Hillhouse, P Payton, J Sharma & MD Burow
- 11. A transcriptome map for geocarpic fruit development in *Arachis hypogaea***
J Clevenger, Y Chu, J Conner, B Abernathy, B Scheffler, S Jackson, CC Holbrook & P Ozias-Akins
- 12. Phenotyping the RIL population of Tifrunner × C76-16 for drought tolerance in peanuts**
P Dang, J Carter, R Sorensen, M Lamb, C Butts, CC Holbrook, TG Isleib, P Ozias-Akins, Y Chu & C Chen
- 13. PeanutBase: A community resource to help improve peanut varieties by integrating genetic, genomic, and trait information**
S Dash, EKS Cannon, S Kalberer, J Singh, D Bitragunta, L Ren, W Huang, N Weeks, J Dickerson, A Farmer, S Cannon
- 14. The potential role of oxidative stress in *Aspergillus flavus* survivability and aflatoxin biosynthesis**
JC Fountain, L Yang, P Khera, RC Kemerait, R D Lee, RK Varshney, BT Scully & B Guo
- 15. Selection for high oleate phenotype with foliar disease resistance from backcross population in groundnut (*Arachis hypogaea* L.)**
K Gangadhara, HL Nadaf & G Mukri
- 16. Molecular cloning and functional analysis of the Annexin gene family in peanut (*Arachis hypogaea* L.)**
M He, X Yang, S Cui, G Mu, M Hou, H Chen & L Liu
- 17. Cloning and expression analysis of four DELLA genes in peanut**
L Hou, J An, C Li, CX Wang, H Xia, CS Li, YX Zheng, YX Zhao & XJ Wang
- 18. Three high oleic groundnut varieties from SPRI**
M Huarong, H Xiaohui, C Fenggao, Y Weiqing, S Yunqing & C Jing
- 19. Genetic variability and marker detection for rust resistance in recombinant inbred lines and backcross inbred lines of groundnut (*Arachis hypogaea* L.)**
SA Jakkeral, HL Nadaf, MVC Gowda, RS Bhat, B Motagi, G Mukri, P Ganagshetty, A Talawar & B Archana
- 20. Backcross breeding in groundnut (*Arachis hypogaea* L.)**
SA Jakkeral, HL Nadaf, MVC Gowda, RS Bhat, B Motagi, G Mukri, P Ganagshetty, A Talawar & S Kolakar
- 21. Association of relative water content (RWC) and specific leaf weight (SLW) as indicators of drought tolerance in peanut (*Arachis hypogaea* L.)**
Jakkeral, SA, Savita, PV Kenchanagoudar, HL Nadaf & HD Upadhyaya
- 22. Quantitative trait locus analysis and construction of consensus genetic map for agronomic traits based on three F₂ populations**
H Jiang, L Huang, X Ren, Y Chen, X Zhou, Y Lei & B Liao
- 23. Marker assisted backcrossing (MABC) to improve oil quality in peanut**
P Janila, MK Padney, MT Variath, HD Upadhyaya, SS Manohar, Y Shasidhar, P Nagesh, M Sriswathi, K Pawan, T Radhakrishnan, N Manivannan, R Vasanthi, KL Dobariya, SK Bera, JB Misra, SN Nigam, & R Varshney

24. **Analysis of differentially expressed leaf proteins and their interaction in response to water stress in peanut**
R Katam, K Sakata, JN Mays, MS Silva & KS Naik
25. **Development/identification of new genetic sources for high oleic acid in groundnut (*Arachis hypogaea* L.)**
K Biradar, G Mukri & HL Nadaf
26. **QTL mapping and quantitative disease resistance to TSWV and leaf spots in a recombinant inbred line population SunOleic 97R and NC94022 of peanut (*Arachis hypogaea* L.)**
P Khera, H Wang, AK Culbreath, MK Pandey, RK Varshney, X Wang, B Liao, X Zhang, J Wang, CC Holbrook & B Guo
27. **Development of introgression lines and advanced backcross QTL analysis for disease resistance, oil quality, and yield component traits in peanut**
P Khera, MK Pandey, N Mallikarjuna, M Sriswathi, M Roorkiwal, P Janila, K Shilpa, H Sudini, B Guo & RK Varshney
28. **Identification of conjoint genomic regions for multiple traits using RIL populations through meta-QTL analysis in peanut**
P Khera, Y Shasidhar, MK Pandey, M Sriswathi, V Vadez, Y Hong, S Yu, X Liang, H Li, B Guo & RK Varshney
29. **Functional identification of the oleosin gene promoter in peanut (*Arachis hypogaea* L.)**
FZ Liu, YP Lu, XD Li, K Zhang & YS Wan
30. **Studies on genetic parameters in early generation recombinant Inbred Lines of the cross NRCG 12568 × NRCG 12326 for growth parameters, traits related to WUE, yield and yield attributing traits in groundnut (*Arachis hypogaea* L.)**
K Mallikarjun, DL Savithramma, Vijayabharathi & SV Madhu
31. **K 1341, a high yielding large seed Virginia bunch groundnut variety with multiple resistances for biotic and abiotic traits released for cultivation**
KSS Naik, AP Rajesh, K Vemana, DS Kumar, K Ramesh, NT Sankara & SM Basha
32. **Comprehensive association analysis for 50 agronomic traits in peanut using the 'reference set' comprising 300 genotypes from 48 countries of the semi-arid tropics of the world**
MK Pandey, HD Upadhyaya, A Rathore, V Vadez, MS Sheshshayee, M Sriswathi, M Govil, A Kumar, MVC Gowda, S Sharma, F Hamidou, VA Kumar, P Khera, RS Bhat, AW Khan, S Singh, H Li, E Monyo, HL Nadaf, G Mukri, SA Jackson, B Guo, X Liang & RK Varshney
33. **Molecular marker discovery and validation from peanut (*Arachis hypogaea* L.) transcript sequences**
Z Peng, M Gallo, D Rowland & J Wang
34. **Evaluation of groundnut genotypes for resistance to aflatoxin contamination**
M Ranganathswamy, ST Naik, BN Motagi & HK Sudini
35. **K 1501, a high yielding large seed Virginia bunch confectionary groundnut at agricultural research station, India**
KR Reddy, KSS Naik, RA Prasanna, K Vemana, KD Sampath, NT Sankara & K Ramesh
36. **Physiological response and yield of paclobutrazol treated peanut (*Arachis hypogaea* L.)**
KD Sampath, KSS Naik, AP Rajesh, K Vemana & K Ramesh
37. **Inheritance of SPAD chlorophyll meter reading and specific leaf area in two crosses of groundnut (*Arachis hypogaea* L.)**
DL Savithramma & A Vijayabharathi
38. **Utilization of wild *Arachis* species for peanut improvement**
S Sharma, HD Upadhyaya & RK Varshney
39. **DArT/DArTseq based genetic mapping for identification of genomic regions controlling oil content in peanut**
Y Shasidhar, MK Pandey, P Janila, MK Vishwakarma, SN Nigam, HD Upadhyaya & RK Varshney
40. **Association between root and physiological traits in response to post flowering drought stress in groundnut (*Arachis hypogaea* L.)**
P Srivalli & HL Nadaf
41. **Candidate SNP markers for high oleate content in peanut**
Y Tang, X Wang, Q Wu, Q Sun & C Wang
42. **Identifying SSR markers linked to TSWV resistance in peanut cultivar, Florida-EPTM'113'**
YC Tseng, B Tillman, & J Wang
43. **An international initiative to conduct comprehensive genome-wide association studies (GWAS) for an array of agronomic traits in peanut**
RK Varshney, L Froencike, MK Pandey, SN Nayak, HD Upadhyaya, A Rathore, B Liao, N Barkley, B Guo, MVC Gowda, CC Holbrook, TB Breneman, RS Bhat, C Chen, J Damicone, MD Burrow, T Isleib, L Dean, ML Wang, V Vadez, S Jackson & RW Michelmore
44. **In Vitro evaluation of biocontrol agents against stem rot (*Sclerotium rolfsii*) and dry root rot (*Rhizoctonia bataticola*) of peanut**
K Vemana, S Shabeer, CS Md Khureshee, JG Padma, S Shamseer, TS Narayana, A Rajesh, D Sampath Kumar, KSS Naik & R Katam

- 45. Construction of genetic linkage map and QTL analysis for yield and WUE related traits based on SSR markers for cultivated groundnut (*Arachis hypogaea* L.)**
A Vijayabharathi & DL Savithramma
- 46. DArT/DArTseq based genetic mapping for identification of genomic regions for different fatty acids which control oil quality in peanut**
MK Vishwakarma, P Janila, MK Pandey, Y Shasidhar, SN Nigam, HD Upadhyaya & RK Varshney
- 47. Proteome analysis of peanut gynophores and early swelling pods**
XJ Wang, CZ Zhao, SZ Zhao, L Hou, CS Li & H Xia
- 48. Development of SNP markers associated with resistance to Northern Root-knot nematode disease in cultivated peanut**
MQ Xu, SL Li, H Wang, YM Shi, Y Ren, L Ying, M Yuan, ZW Liu & GH He
- 49. Development of late leaf spot and rust tolerant genotypes from TMV 2 and JL 24 by marker assisted backcross breeding in groundnut**
SB Yeri, RM Kolekar, BN Motagi, HL Nadaf, S Lingaraju, MVC Gowda & RS Bhat
- 50. The developmental oil mobilization of the peanut seed transcriptome**
D Yin, Y Wang, X Zhang, W Zhang, H Li, D Cui & S Chen
- 51. Molecular characterization of five lines and three commercial varieties of peanut (*Arachis hypogaea* L.)**
AR Zacarias-Martínez, S Sánchez-Domínguez, MG Peña-Ortega
- 52. Screening for early maturing germplasm and attributing characteristics to identify associated SNPs in cultivated peanut**
XY Zhang, BY Huang, ZQ Sun, LJ Miao, FY Qi, L Shi, WZ Dong & FS Tang
- 53. Cloning, expression and evolutionary analysis of peanut HIR gene**
CZ Zhao, Y Liu, CS Li, C Li & XJ Wang
- 54. Molecular cloning, expression and evolution analysis of type II CHI gene from peanut (*Arachis hypogaea* L.)**
SZ Zhao, Y Liu, CZ Zhao, HS Guan, L Hou & XJ Wang
- 55. Genetic mapping and QTL analysis of agronomic traits in cultivated peanut (*Arachis hypogaea* L.)**
X Yang, J Zhou, S Cui, G Mu, M Hou, H Chen & L Liu
- 56. Identification of quantitative trait loci for important agronomic traits in cultivated peanut (*Arachis hypogaea* L.)**
LZ Li, FZ Liu, YS Wan & K Zhang
- 57. Selection of interspecific lines at the first backcross generation for the runner market in Brazil**
TMF Suassuna, ND Suassuna, SCM Leal-Bertioli, DJ Bertioli, MC Moretzsohn & EP Medeiros