AAGB 2019
OCTOBER 21-25
JINAN CHINA

国际花生科学与技术大会

The 11th International Conference of the Peanut Research Community on

Advances in Arachis through Genomics and Biotechnology

PROGRAM BOOK & ABSTRACTS

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国际花生科学与技术大会

The 11th International Conference of the Peanut Research Community on

Advances in Arachis through Genomics and Biotechnology

主办单位

山东省农业科学院 Shandong Academy of Agricultural Sciences

THE PEANUT FOUNDATION

协办单位

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Welcome to the 11th International Conference of the Peanut Research Community on *Advances in Arachis through Genomics and Biotechnology* (AAGB-2019) conference. Please pay attention to the following instructions from the committee.

Please wear your name tags while attending the various activities of the conference. Please turn your mobile phones to mute or off during the conference.

During the opening ceremony, simultaneous translation service between Chinese and English will be provided for each seat. Please put on the earphone and select the language of your preference. At the end of the meeting, please put the earphone back to your seat.

The bags handed out by the conference staff contain conference materials, stationery and breakfast/lunch/dinner tickets, etc.

Breakfast starts at 7 am. Meal tickets should be presented to servers at each meal. Please bring your meal tickets and dine at the designated restaurant.

During the meeting, please abide by the laws and regulations of the People's Republic of China.

Contacts of Local Organizing Committee(Main Building Room 1001, 1002):

Zhongxue FAN	**+86-13335146825**
Han XIA	**+86-15953182519**
Yuxia GU	**+86-15966055587**
Chuanzhi ZHAO	**+86-15966671002**
Lei HOU	**+86-18660176192**
Zhen YANG	**+86-18153270927**
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We wish everyone enjoys the conference and your visit to China!

Introduction of AAGB-2019

Since the first International Peanut Conference held in Guangzhou, China in 2006, the international peanut research community has worked through the International Peanut Genome Initiative (IPGI) to integrate genetics, genomics and biotechnological approaches into the process of developing effective, environmentally friendly solutions that mitigate economic risks of peanut production. The IPGI has facilitated and improved collaboration between international scientists and stakeholders through a series of international conferences on *Advances in Arachis through Genomics and Biotechnology* (AAGB), which provide a forum to develop, implement, and report results of scientific research toward strategic plans that ultimately lead to more productive varieties and products of more exceptional quality. The international peanut community through IPGI has come a long way, from lack of availability of molecular markers to the completion and releases of high-quality genome sequences of diploid and cultivated peanuts. However, there remains a long way to go for genomics-assisted breeding as routine implementation. Nevertheless, the stage is now set to harvest the fruits of genomics research for peanut genetic improvement, cultivation, and production. This will contribute to the entire peanut community, and global food safety and security in general to fight malnutrition.

The 11th International Conference of the Peanut Research Community on *Advances in Arachis through Genomics and Biotechnology* (AAGB-2019) will be convened October 21-25, 2019 in Ji'nan, China. The venue will be the Nanjiao Hotel and Resort, which is located just south of the City Center near the Thousand-Buddha Mountain and Quancheng Park. Jinan, the Capital City of Shandong Province, also called as the Spring-Water City. Shandong Province is one of the top peanut producing regions in China with an average annual peanut growing area of 800,000 hectares.

AAGB-2019 will be a forum to foster scientific exchange between members of the international peanut research community through oral and poster presentations, and also to discuss the future of the international peanut conference after the completion of peanut genome sequencing project. In addition, the organizing committee would also like to recognize the leaderships and the "real heroes" who have been working tirelessly behind the scenes from the start to the finish, making this IPGI and peanut genome sequencing project a reality and a success story.

Sponsor	Shandong Academy of Agricultural Science (SAAS), The Peanut Foundation
Organizers	Biotechnology Research Center (BRC), SAAS Shandong Peanut Research Institute (SPRI), SAAS
Co-Organizers	Shandong Luhua Group Co., LTD, Jinsheng Group, Stanley Agriculture Group Co., LTD, Shandong Seed Industry Group Co., LTD

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The 11th International Conference of the Peanut Research Community on *Advances in Arachis through Genomics and Biotechnology*
(AAGB-2019)
October 21-25, 2019
Jinan, China

Schedule of Program

Monday, October 21, 2019	
All Day	**Registration and Hotel Check-In**
14:00 - 17:00	**Poster Set-up**
18:00 - 21:00	**Dinner**

Tuesday, October 22, 2019	
Session I: Inauguration & Celebration	
8:30 - 9:20	**Inauguration** **Chairperson: Shubo Wan,** President, SAAS **Official address** Shandong Provincial Leader Ministry of Agricultural and Rural Affairs of the P.R.C. leader Ministry of Sciences and Technology of the P.R.C. leader National Peanut Board of USA leader Shandong Academy of Ag. Sci. Leader
9:20 - 9:40	**Celebration** **Chairperson: Steve Brown**, Executive Director, PRF **Path to Success: Celebration, Recognition, Winning** **Baozhu Guo,** USDA-ARS **Howard Valentine**, Executive Director, Peanut Foundation (retired)
9:40 - 10:20	**Group Picture** **Tea/Coffee Break**

Session II: Keynote Address **(Celebration, Recognition, Winning)** **Chairpersons: Boshou Liao & Tom Stalker**	
10:20 - 10:50	Current situation and prospect of high yield and effiency of peanut cultivation technology in China **Shubo Wan** Shandong Academy of Agricultural Sciences, China
10:50 - 11:20	Genomics applications in post-genome sequence era in groundnut: a way forward **Rajeev Varshney** ICRISAT, India
11:20 - 11:50	The future is now for accelerated peanut improvement **Josh Clevenger** Mars & Wrigley, USA
12:00 - 13:30	**Lunch**
Session III: Peanut Genomics **Chairpersons: Baozhu Guo & Josh Clevenger**	
14:00 - 14:30	The *Arachis hypogaea* genome provides insight into the polyploid origin and differential A and B subgenome evolution **Weijian Zhuang** Fujian Agriculture and Forestry University, China
14:30 - 15:00	The neotetraploid peanut IpaDur1 provides a model for genetic and genomic studies and increases crop diversity **Soraya Leal-Bertioli** University of Georgia, USA
15:00 - 15:30	The genomes of cultivated peanut and its suspected wild progenitors **Xiaoping Chen** Guangdong Academy of Agricultural Sciences, China
15:30 - 16:00	Optimizing effective genomic selection strategy for achieving higher genetic gains in groundnut **Manish Pandey** ICRISAT, India
16:00 - 16:20	**Coffee and Tea Break**

Session IV: Genetic Trait Mapping & Gene Discovery I **Chairpersons: Weijian Zhuang & David Bertioli**	
16:20-16:40	Solving the leaf spot problem in peanut **Thomas Stalker** North Carolina State University, USA
16:40-17:00	Understanding the molecular basis of disease resistance of *Arachis glabrata* through transcriptome and genome sequencing **Xingjun Wang** Biotechnology Research Center, SAAS, China
17:00-17:20	Segmental subgenome exchange is captured in the nascent synthetic allotetraploid [*A. ipaensis* x *A. correntina*] 4x and its derivatives **Ye Chu** University of Georgia, USA
17:20-17:40	Fine mapping towards identifying major QTLs and candidate resistance genes for TSWV on chromosome A01 of peanut **Chuanzhi Zhao** University of Georgia, USA and Biotechnology Research Center, SAAS, China
17:40-18:00	The positional cloning of Bunch1 gene that controls branching habit in peanut **Ran Hovav** Plant Sciences Institute, ARO, Bet-Dagan, Israel
18:00 – 18:20	Increasing power to dissect morphological and disease resistance traits in peanut using multi-parental mapping populations **Baozhu Guo** USDA-ARS Crop Protection and Management Unit, USA
19:00-21:00	**Open Ceremony Dinner** Blue Hall

Wednesday, October 23, 2019	
Session V: Plenary Lecture **Chairperson: Victor Nwosu**	
8:00 - 8:40	The origin and evolution of peanut inform new pathways to genetic diversity and sustainability **David Bertioli** Professor and GRA (Georgia Research Alliance) Distinguished Investigator University of Georgia, USA
Session VI: Genetic Trait Mapping & Gene Discovery II **Chairpersons: Xingjun Wang & Peggy Ozias-Akins**	
8:40 - 9:00	Marker assisted breeding to develop peanut cultivars with resistance to late leaf spot **Corley Holbrook** USDA-ARS Crop Breeding and Genetics Research Unit, USA
9:00 - 9:20	Genome of an allotetraploid wild peanut *Arachis monticola*: a de novo assembly **Dongmei Yin** Henen Agriculture University, China
9:20 - 9:40	Identification of QTL with resistance to Northern root-knot nematode in peanut **Mei Yuan** Shandong Peanut Research Institute, China
9:40 - 10:00	Identification of AhNPR-A04 as a leaf spot disease related gene in peanut through MutMap combined with BSR approach **Suoyi Han** Henan Academy of Agricultural Sciences, China
10:00 - 10:20	**Coffee and Tea Break**
Session VII: Germplasm Diversity & Utilization **Chairpersons: Rajeev Varshney & Chuanzhi Zhao**	
10:20 - 10:40	Genetic diversity of historical and contemporary African germplasm lines **Peggy Ozias-Akins** University of Georgia, USA
10:40 - 11:00	Genomic analysis identifies genomic variation and history of peanut breeding

	Zheng Zheng Henan Academy of Agricultural Sciences, China
11:00 - 11:20	Mobilizing genetic diversity for strengthening peanut breeding programs in Africa **Daniel Fonceka** National Agricultural Research Center, Senegal
11:20 - 11:40	Understanding the genetic and molecular mechanisms for resistance to aflatoxin contamination in groundnut **Rajeev K. Varshney** ICRISAT, India
11:40 - 12:00	Twelve complete chloroplast genomes of wild peanuts: great genetic resources and a better understanding of Arachis phylogeny **Shihua Shan** Shandong Peanut Research Institute, China
12:00 - 13:30	**Lunch**
Session VIII: Crop Improvement I **Chairpersons: Manish Pandey & Han Xia**	
14:00 - 14:20	Integrating resistance to major soil-borne diseases in peanut through conventional and genomic approaches **Boshou Liao** Chinese Academy of Agricultural Sciences, Oil Crop Research Institute, China
14:20 - 14:40	Identification of abiotic stress tolerant germplasms and functional analysis of related genes in peanut **Xiaoyuan Chi** Shandong Peanut Research Institute, China
14:40 - 15:00	Genetic dissection of growth-habit related traits in cultivated peanut **Lifeng Liu** Hebei Agricultural University, China
15:00 - 15:20	QTL identification for seed weight and size based on a high-density SLAF-seq genetic map in peanut **Jing Chen** Shandong Peanut Research Institute, China
15:20 - 15:40	GWAS and co-expression network reveal Ionomic variation in cultivated peanut **Charles Chen**

	Auburn University, USA
15:40 - 16:00	Translation initiation factor eIF4E and eIFiso4E are both required for peanut stripe virus infection in peanut **Yucheng Chi** Shandong Peanut Research Institute, China
16:00 - 16:20	**Coffee and Tea Break**
Session IX: Crop Improvement II **Chairpersons: Charlers Chen & Shihua Shan**	
16:20 - 16:40	Screening of genomic selection training population for ahFAD2A and ahFAD2B mutant alleles responsible for high oleic trait in peanut **Sunil Chaudhari** ICRISAT, India
16:40 - 17:00	Comparative analysis of lipidomes and transcriptomes reveals molecular mechanism of cold tolerance in peanut **Haiqiu Yu** Shenyang Agricultural University, China
17:00 - 17:20	Evaluation of *A. ipaënsis* x *A. correntina* wild-peanut derived materials for resistance to fall armyworm **Chandler Levisnon** University of Georgia, USA
17:20 - 17:40	Chromosome correspondence between karyotype and genome sequence map of *Arachis duranensis* **Pei Du** Henan Academy of Agricultural Sciences, China
17:40 - 18:00	The molecular and ecological mechanism of improving iron nutrition in peanuts intercropped with maize in calcareous soil **Yuanmei Zuo** China Agricultural University, China
18:30 - 21:00	**Dinner**

Thursday, October 24, 2019	
Session IX: Biotic & Abiotic Stresses **Chairpersons: Ran Hovav & Xinguo Li**	
8:00 - 8:20	Comparative transcriptome analysis identified key genes for seed germination in response to Zn fertilizers in peanuts **Weichang Yu** Shenzhen University, China
8:20 - 8:40	Identification of metabolites and transcripts involved in salt stress and recovery in peanut **Guowei Li** Biotechnology Research Center, SAAS, China
8:40 - 9:00	Virus induced gene silencing of *AhABI4s* enhance salt tolerance of peanut seedling via regulation of ion homeostasis **Lu Luo** Shandong Agricultural University, China
9:00 - 9:20	Stress-related transcriptional signaling and its roles in aflatoxin production and stress tolerance in *Aspergillus flavus* **Jake Fountain** University of Georgia, USA
9:20 - 9:40	Identification and molecular mechanism dissection of drought resistance in peanut **Xiurong Zhang** Shandong Agricultural University, China
9:40 - 10:00	Two adjacent genomic regions on chromosome B02 control genetic resistance to bacterial wilt in peanut **Huaiyong Luo** Chinese Academy of Agricultural Sciences, Oil Crop Research Institute, China
10:00 - 10:20	**Coffee and Tea Break**
Session X: Crop Production & Cultivation **Chairpersons: Zheng Zheng & Jake Fountain**	
10:20 - 10:40	Progress in peanut photosynthesis under abiotic stress **Xinguo Li** Biotechnology Research Center, SAAS, China
10:40 - 11:00	Farmer's perceived constraints to groundnut production, and

	their variety choice and preferred traits in eastern Ethiopia: implications for drought tolerance breeding **Seltene Abady** University of KwaZulu-Natal, African Centre for Crop Improvement, South Africa
11:00 - 11:20	Decreasing content of very long chain fatty acids in peanut **Dongxin Huai** Chinese Academy of Agricultural Sciences, Oil Crop Research Institute, China
11:20 - 11:40	Research on diversity of rhizosphere microorganism in peanut-maize intercropping system **Xiaozhu Chen** Jilin Academy of Agricultural Sciences, China
11:40 - 12:00	RNA-Seq to dissect candidate genes associated with groundnut stem-rot disease interaction **Radhakrishnan Thankappan** ICAR-Directorate of Groundnut Research,India.
12:00 - 13:30	**Lunch**
Session XI: The Path Forward **AAGB and International Peanut Community** **Chairperson: Tom Stalker & Steve Brown**	
14:00 - 15:30	**Closing Remarks** **Wan Shubo**, President, SAAS
15:30 - 18:00	**Free time**
18:00 - 21:00	**Dinner**

Friday, October 25, 2019
Departure

Abstracts for AAGB-2019

1. Peanut Genomics

1.1 The genomes of cultivated peanut and its suspected wild progenitors .....Xiaoping Chen, Qing Lu, Hao Liu, *et al.* (1)

1.2 DNA shuffling between subgenomes of Arachis induced allotetraploids .....ACG Araujo*, EFMB Nascimento, SMC Leal-Bertioli, *et al.* (2)

1.3 The origin and evolution of peanut inform new pathways to genetic diversity and sustainability .....David Bertioli (3)

1.4 Genome of an allotetraploid wild peanut Arachis monticola: a de novo assembly .....Dongmei Yin*, Xingli Ma, Wanke Zhang, *et al.* (4)

1.5 Twelve complete chloroplast genomes of wild peanuts: great genetic resources and a better understanding of *Arachis* phylogeny .....Juan Wang#*, Yuan Li#, Chunjuan Li, *et al.* (5)

1.6 Functional characterization of full-length transcriptome dataset of peanut during seed germination .....Shengzhong Zhang, Xiaohui Hu, Huarong Miao, *et al.* (6)

1.7 Chromosome correspondence between karyotype and genome sequence map of *Arachis duranensis* .....Pei Du, Liuyang Fu, Siyu Wang, *et al.* (7)

1.8 Segmental subgenome exchange is captured in the nascent synthetic allotetraploid [*A. ipaensis* x *A. correntina*]4x and its derivatives.....Ye Chu, David Bertioli, Scott Jackson, *et al.* (8)

1.9 Genome-wide identification of circular RNAs in peanut (*Arachis hypogaea* L.).....XG Zhang, XL Ma, LL Ning, *et al.* (9)

1.10 Understanding the molecular basis of disease resistance of *Arachis glabrata* through transcriptome and genome sequencing.....Xingjun Wang*, Chuanzhi Zhao, Liangqiong He, *et al.* (10)

1.11 Genomic analysis identifies genomic variation and history of peanut breeding .....Zheng Zheng#, Ziqi Sun#, Yuanjin Fang#, *et al.* (11)

1.12 Genomics applications in post-genome sequence era in groundnut: a way forward .....Rajeev K Varshney*(12)

1.13 The *Arachis hypogaea* genome provides insight into the polyploid origin and differential A and B subgenome evolution .....Weijian Zhuang*, Hua Chen, Chong Zhang, *et al.* (13)

2. Marker development, QTL Mapping and Gene Discovery

2.1 QTLs mapping and marker analysis for pod size and yield-related Traits in peanut (*Arachis hypogaea* L.).....Hui Yang, Yingjie Li, Jiaqi Liu, *et al.* (14)

2.2 Genome-wide identification of microsatellite markers from cultivated peanut (*Arachis hypogaea* L.).....Qing Lu#, Yanbin Hong#, Shaoxiong Li, *et al.* (15)

2.3 Identifying loci control growth habit-related traits using bulked segregant analysis and genome-wide association study in peanut.....L Li, X-L Yang, S-L Cui, *et al.* (16)

2.4 Characterization and allelic polymorphism of glycerol-3-phosphate acyltransferase 9 (AhGPAT9) genes in peanut (Arachis hypogaea L.)..... Yuying Lv, Xiongrong Zhang, Lu Luo, *et al.* (17)

2.5 Association analysis of leaf SPAD value and SSR markers in peanut .....Suqing Zhu, Xiurong Zhang, Kun Zhang, *et al.* (18)

2.6 QTL mapping of seed size in peanut (*Arachis hypogaea* L.).....C Zhang, H Chen, QZ Liu, *et al.* (19)

2.7 Genome wide identification and expression of germin-like protein family in peanut .....T Wang, LJ Pan, M Wang, *et al.* (20)

2.8 High density genetic linkage map construction and QTL mapping for pod size related traits in peanut (*Arachis hypogaea* L.).....H Chen, Q Yang, C Zhang, *et al.* (21)

2.9 Mapping of quantitative trait loci for Aspergillus flavus resistance in peanut .....SAKhan, H Chen, C Zhang, *et al.* (22)

2.10 Overexpression of a peanut ERECTA-like gene positively regulates responses to *Ralstonia solanacearum* infection in tobacco and peanut .....G Mamadou, N Ali, C Zhang, *et al.* (23)

2.11 QTL identification for seed weight and size based on a high-density SLAF-seq genetic map in peanut (*Arachis hypogaea* L.).....Shengzhong Zhang, Xiaohui Hu, Huarong Miao, *et al.* (24)

2.12 QTL mapping for pod and seed traits using RIL population derived from Huayu 28 and P76 (*Arachis hypogaea* L.).....Xiaohui Hu, Shengzhong Zhang, Huarong Miao, *et al.* (25)

2.13 Linkage disequilibrium analysis in Togo groundnut germplasm and implications in marker-trait association.....Essohouna Modom Banla*, Daniel Kwadjo Dzidzienyo, Samuel Kwame Offei, *et al.* (26)

2.14 Fine mapping towards identifying major QTLs and candidate resistance genes for TSWV on Chromosome A01 of Peanut .....Chuanzhi Zhao, Hui Wang, Yaduru Shasidhar, *et al.* (27)

2.15 GWAS and co-expression network reveal ionomic variation in cultivated peanut .....Hui Zhang, Ming Li Wang, Rob Schaefer, *et al.* (28)

2.16 The positional cloning of Bunch1 gene that controls branching habit in peanut .....S. Kunta, G. Kayam, Y. Levy, *et al.* (29)

2.17 Cloning and expression analysis of oil biosynthesis related gene AhGL2 in peanut (*Arachis hypogaea* L.)..... .....YJ Liu, SL Chen*, J Wang, *et al.* (30)

2.18 Increasing power to dissect morphological and disease resistance traits in peanut using nested association mapping populations .....B. Guo*, S. Gangurde, M.K. Pandey, *et al.* (31)

2.19 Identification of quantitative trait loci for surrogate traits of water use efficiency, pod yield and yield related traits in groundnut (*Arachis hypogaea* L.) under different water regimes .....D. L. Savithramma, Savita S. K, Bharath Kumar P. Jambagi,(32)

2.20 Developing a high-density molecular map of the A-Genome species *Arachis duranensis* .....E Nagy, Y Guo, S Khanal, et al.(33)

2.21 Characterization of the AhLea-3 and the enhanced salt tolerance in transgenic peanut plants .....Lixian Qiao, Pingping Jiang, Mingyang Yu, *et al.* (34)

2.22 Cloning, genetic transformation and salt tolerance validation of AhWRKY75 gene from *Arachis hypogaea* L. .....Hong Zhu, Yue Guo, Yanan Jiang, *et al.* (35)

2.23 Virus induced gene silencing of AhABI4s enhance salt tolerance of peanut seedling via regulation of ion homeostasis.....Lu Luo, Qian Wan, Kun Zhang, *et al.* (36)

2.24 Genome-wide identification and characterization of NF-Y gene family in peanut (*Arachis hypogaea* L.)..... .....Qian Wan, Lu Luo, Xiurong Zhang, *et al.* (37)

2.25 Marker assisted breeding to develop peanut cultivars with resistance to late leafspot .....C.C. Holbrook*, Y. Chu, S. Lamon, *et al.* (38)

2.26 Expression analysis of AhMITE1-associated genes among the diverse genotypes of peanut (*Arachis hypogaea* L.).....RS Bhat*, R Choudhari & K Shirasawa(39)
2.27 Genome-wide identification and expression analysis of expansin family genes in *Arachis duranensis* and *A. ipaensis*.....Chuanzhi Zhao*, Ming li, Ximeng Zhou, *et al.* (40)
2.28 Whole-genome resequencing-based BSA-seq identified AhTc1 gene encoding a R2R3-MYB transcription factor controlling peanut purple testa color.....Chuanzhi Zhao, Yuhan Zhao, Junjie Ma, *et al.* (41)
2.29 Genome-wide identification of microsatellite markers through scanning and comparing the tetraploid and diploid peanut genomes.....Junjie Ma, Yuhan Zhao, Hua Chen, *et al.* (42)
2.30 Identification of AhNPR-A04 as a leaf spot disease related gene in peanut through MutMap combined with BSR approach.....Suoyi Han§, Chuanzhi Zhao§, Lei Shi, *et al.* (43)
2.31 Rapid phenotyping and genotyping tools improving selection for resistance to web blotch (*Didymella arachidicola*)in peanuts (*Arachis hypogaea* L.) .....S Wood*, G Wright, M Dieters, *et al.* (44)
2.32 Comparative transcriptome analysis of anthocyanin synthesis in black and pink peanut testa (*Arachis hypogaea* L.).....Lin Zhu, Chaunzhi Zhao, Ke Li, *et al.* (45)
2.33 Genome-wide analysis of *WRI1* gene family and their expression profiles in peanut .....JB Sun#, SH Shi, FL Li, *et al.* (46)
2.34 Decreasing content of very long chain fatty acids in peanut .....D Huai, X Xue, J Li, *et al.* (47)
2.35 Genome-wide association studies of production and quality traits in cultivated peanut (*Arachis hypogaea* L.) .....Xiaojing Zhou, Jiaojiao Zhao, Haiwen Chen, *et al.* (48)
2.36 Genome-wide expression quantitative trait loci analysis in a recombinant inbred line population for trait dissection in peanut.....Li Huang, Xia Liu, Manish K Pandey, *et al.* (49)
2.37 Identification of QTLs associated with shelling percentage in cultivated peanut .....YN Chen, WT Li, L Huang, *et al.* (50)
2.38 High-resolution mapping of a major and consensus quantitative trait locus for oil content to a ~0.8 Mb region on chromosome A08 in peanut (*Arachis hypogaea* L.).....Nian Liu, Jianbin Guo, Xiaojing Zhou, *et al.* (51)
2.39 High density genetic mapping and whole genome re-sequencing identified genomic regions and candidate genes for seed weight in groundnut.....Sunil S. Gangurde, Murali T. Variath, Aamir W Khan, *et al.* (52)
2.40 RNA-Seq to dissect candidate genes associated with groundnut stem-rot disease interaction.....Tejas C. Bosamia, Suhail Ahmad, Gyan P. Mishra, *et al.* (53)

3. Germplasm Resources Identification, Creation and Utilization

3.1 Groundnut rosette disease donors identified in Uganda.....Okello D. K*, Ochuga, S.E., Owiny, R., *et al.* (54)
3.2 Evaluation of *A. ipaënsis x A. correntina* wild-peanut derived materials for resistance to fall armyworm .....CM Levinson, Y Chu, X Ni , *et al.* (55)
3.3 Mobilizing genetic diversity for strengthening peanut breeding programs in Africa .....D Fonceka*, A Sambou, T Hodo-Abalo, *et al.* (56)
3.4 Identification and characterization of high oleic acid peanut mutant tolerance to imidazolinone herbicide.....SL Chen, YR Li, J Wang, *et al.* (57)
3.5 Gene action and prediction of genotypes performance for late leaf spot resistance and yield related traits improvement in groundnut.....Essohouna Modom Banla, Daniel Kwadjo Dzidzienyo, Samuel Kwame Offei, *et al.* (58)

3.6 Molecular and phenotypic diversity of groundnut cultivars from Togo.....Essohouna Modom Banla, Daniel Kwadjo Dzidzienyo, Mouhamadou Moussa Diangar, *et al.* (59)

3.7 Genetic diversity of historical and contemporary African germplasm lines .....Peggy Ozias-Akins*, Ye Chu, Josh Clevenger, *et al.* (60)

3.8 Screening of drought tolerant recombinant inbred lines derived from the cross NRCG 12568 × NRCG 12326 in groundnut using different statistical procedures.....Bharath Kumar P Jambagi and D. L. (61)

3.9 Useful Traits in the US Peanut Germplasm Collection .....S.P. Tallury*, B. D. Tonnis , M. L. Wang, *et al.* (62)

3.10 Evaluation of the Argentine peanut core collection using a molecular marker associated with resistance to Sclerotinia minor Jagger.....K.D. CHAMBERLIN*, Baldessari, J., Moreno, *et al.* (63)

3.11 The neotetraploid peanut IpaDur1 provides a model for genetic and genomic studies and increases crop diversity .....Leal-Bertioli, S.C.M.*, Suassuna, T.F., Araújo A.C.G., *et al.* (64)

3.12 Screening of genomic selection training population for ahFAD2A and ahFAD2B mutant alleles responsible for high oleic trait in peanut (*Arachis hypogaea* L.).....Sunil Chaudhari, D Khare, Sudam C Patil, *et al.* (65)

3.13 Comparative lipidomic analysis of high oleate and normal oleate peanut .....D Huai, X Xue, J Li, *et al.* (66)

4. Traits Improvement and Breeding

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1.1 The genomes of cultivated peanut and its suspected wild progenitors

Xiaoping Chen[1*], Qing Lu[1], Hao Liu[1], Yanbin Hong[1], Shaoxiong Li[1], Jianan Zhang[6], Haofa Lan[6], Shanlin Yu[2], Zhongjian Liu[3], Andrew H. Paterson[4], Rajeev Varshney[5], Xuanqiang Liang[1]

[1]South China Peanut Sub-center of National Center of Oilseed Crops Improvement, Guangdong Key Laboratory for Crops Genetic Improvement, Crops Research Institute, Guangdong Academy of Agricultural Sciences (GAAS), Guangzhou, China.
[2]Shandong Peanut Research Institute, Shandong Academy of Agricultural Sciences, Qingdao, China.
[3]Key Laboratory of National Forestry and Grassland Administration for Orchid Conservation and Utilization at College of Landscape Architecture, Fujian Agriculture and Forestry University, Fuzhou 350002, China; Fujian Colleges and Universities Engineering Research Institute of Conservation and Utilization of Natural Bioresources, College of Forestry, Fujian Agriculture and Forestry University, Fuzhou 350002, China.
[4]Plant Genome Mapping Laboratory, University of Georgia, Athens, USA.
[5]Center of Excellence in Genomics & Systems Biology, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India.
[6]MolBreeding Biotechnology Co., Ltd., Shijiazhuang, China.

***Author for correspondence: chenxiaoping@gdaas.cn**

Cultivated peanut (*Arachis hypogaea*), originated from South America and planted in Asia, Africa, and America, is one of most important oil crops. It was proposed to be the result of hybridization between two wild diploids, *Arachis duranensis* and *Arachis ipaensis*. To date, we have published the genomes of cultivated peanut and its two diploid progenitors. Sequencing of these genomes provided insights into multiple collections of biological issues, including genome evolution, geocarpy, oil improvement, allergens and biological nitrogen fixation. Genome evolutionary analysis showed that the *A. hypogaea* subgenomes have evolved asymmetrically, with the B subgenome resembling the ancestral state and the A subgenome undergoing more gene disruption, loss, conversion and transposable element proliferation, and having reduced gene expression during seed development despite lacking genome-wide expression dominance. *A. duranensis* might not be the single/direct A-genome donor as previously expected, or that multiple hybridizations of *A. ipaensis* with several varieties of *A. duranensis* contributed to the formation of the allotetraploid. Genomic and transcriptomic analyses identified more than 2500 oil metabolism-related genes and revealed that most of them show altered expression early in seed development while their expression ceases during desiccation, presenting a comprehensive map of peanut lipid biosynthesis. Analysis of geocarpy, a prominent feature in the *Arachis* genus, revealed that FAR1TF families were expanded in *A. hypogaea* and its wild progenitors. These genomes provide an important source of candidate genes for subterranean fructification, oil biosynthesis, allergens and biological nitrogen fixation, and will substantially advance global peanut improvement in future.

1.2 DNA shuffling between subgenomes of Arachis induced allotetraploids

ACG Araujo[1*], EFMB Nascimento[1,2], SMC Leal-Bertioli[3], PM Guimarães[1], J Chu[3], POzias-Akins[3], MC Moretzsohn[1] & DJ Bertioli[3]

[1]Embrapa Genetic Resources and Biotechnology, PqEB W5 Norte Final, CP 02372, CEP 70.770-917, Brasília, DF, Brazil.
[2]University of Brasilia, Institute of Biological Sciences, Campus Darcy Ribeiro, CEP 70.910-900, Brasília, DF, Brazil.
[3]University of Georgia, Georgia, USA.

***Author for correspondence: ana-claudia.guerra@embrapa.br**

The reduced genetic diversity in cultivated peanut, *Arachis hypogaea*, can be explained by the single origin and sexual isolation from its diploid wild relatives. Recently, tetrasomic segmental recombinations in *A. hypogaea* between A and B subgenomes, each coming from ancestral wild diploid species, *A. duranensis* and *A. ipaensis*, has been detected. Confirmation of evident genetic shift between homeologous chromosomes was obtained with the sequencing of the genome of peanut, at least partially genome justifying, its diversity. Here, cytogenetic and genotyping (SNPs) analysis of two induced allotetraploids, IpaDur1 and IpaDur2 obtained from the cross between the same species that originated peanut, confirmed the genetic swap between the chromosomes. Besides being recurrent, DNA swap was detected in all generations studied. By double GISH, using whole genome of each parental species as probes, amosaic pattern of hybridization was observed, indicating genome recombination. Moreover, we identified interchange of specific SNPs for A and B genomes between the chromosomes, drifting mostly towards B subgenome. This DNA flow may explain some of the genome remodeling observed cytogenetically. DNA shuffling between the subgenomes in the *Arachis* hybrids has a significant effect immediately after hybridization, together with changes in other elements. This structure remained basically the same along further generations studied.

1.3 The origin and evolution of peanut inform new pathways to genetic diversity and sustainability

David Bertioli

Institute of Plant Breeding, Genetics and Genomics, University of Georgia, USA

Author for correspondence: bertioli@uga.edu

The sequencing of complete genomes of cultivated peanut (*Arachis hypogaea*) and its two ancestral species (*A. duranensis* and *A. ipaënsis*) gives unprecedented tools to understand the origin, evolution and genetics of cultivated peanut. The extraordinarily high DNA identity of the *A. ipaënsis* genome and the B subgenome of cultivated peanut indicate a polyploidy of less than 10,000 years ago. This very recent, genetically-narrow origin, could, in principle, have reduced the variability on which human selection could act. However, after polyploidy the peanut genome generated diversity, through mobile-element activity, deletions and, most notably, by the flow of genetic information between corresponding ancestral chromosomes (that is, homeologous recombination, which generates genetic diversity orders of magnitude faster than mutation). Lineages of new tetraploid hybrids between the ancestral species rapidly generate phenotypic diversity, demonstrating how these peculiar segmental allotetraploid genetic mechanisms would have favored the domestication of the polyploid *A. hypogaea* over other diploid *Arachis* species cultivated by humans.

Homeologous recombination generates genetic diversity, but it is a diversity based on variation in allele dosage: the actual number of alleles available to breeders remains limited by the recent polyploidy and genetic bottle-neck. This limits the genetic improvement that can be made using peanut germplasm of pure pedigree. Fortunately, new advances in knowledge of the origin of peanut, and the relationships of the wild and domesticated species has allowed the design of efficient new crossing schemes for the incorporation of wild alleles into the peanut crop. Furthermore, the genome sequences have provided common references and tools for genotyping which increase the speed and ease with which introgressions can be identified and tracked. This enables the identification of new high-value wild species chromosome segments, and the implementation of much more efficient marker-assisted breeding. New wild-derived traits that have already become available to the peanut crop include resistances to root-knot nematode, late leaf spot and rust. Peanut breeding has entered a new phase, of faster introduction and stacking of traits, and of greater gains in productivity and sustainability.

1.4 Genome of an allotetraploid wild peanut *Arachis monticola*: a de novo assembly

Dongmei Yin[1*], Xingli Ma[1], Wanke Zhang[2], Kunkun Zhao[1], Xingguo Zhang[1]and Jinsong Zhang[2]

[1] College of Agronomy, Henan Agricultural University, Zhengzhou 450002, China
[2] State Key Lab of Plant Genomics, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing 100101, China

***Author for correspondence: yindm@126.com**

Arachis monticola (2n = 4x = 40) is the only allotetraploid wild peanut within the *Arachis* genus, with an AABB-type genome of ~2.7 Gb in size. The AA-type subgenome is derived from diploid wild peanut *Arachis duranensis*, and the BB-type subgenome is derived from diploid wild peanut *Arachis ipaensis*. *A.monticola* is regarded either as the direct progenitor of the cultivated peanut or as an introgressive derivative between the cultivated peanut and wild species. The large polyploidy genome structure and enormous nearly identical regions of the genome make the assembly of chromosomal pseudomolecules very challenging. Here we report the first reference quality assembly of the *A. monticola* genome, using a series of advanced technologies. The final whole genome of *A. monticola* is ~2.62 Gb and has a contig N50 and scaffold N50 of 106.66 Kb and 124.92 Mb, respectively. The majority (91.83%) of the assembled sequence was anchored onto the 20 pseudo-chromosomes, and 96.07% of assemblies were accurately separated into AA- and BB-subgenomes. We demonstrated efficiency of the current state of the strategy for de novo assembly of the highly complex allotetraploid species based on whole-genome shotgun sequencing, single molecule real-time sequencing, high-throughput chromosome conformation capture technology, and BioNano optical genome maps.

Reconstruction of peanut genomes demonstrated a monophyletic origin of allotetraploid peanut subgenomes. The tetraploids underwent asymmetric subgenome evolution, including homoeologous exchanges, homoeolog expression bias, gene family expansion, and structural variation (SV), leading to subgenome functional divergence during peanut domestication. These genomic resources are uniquely valuable for studying polyploid genome evolution, crop domestication, and genome-assisted improvement of peanut production.

1.5 Twelve complete chloroplast genomes of wild peanuts: great genetic resources and a better understanding of *Arachis* phylogeny

Juan Wang[1#*], Yuan Li[2#], Chunjuan Li[1], Caixia Yan[1], Xiaobo Zhao[1], Cuiling Yuan[1], Quanxi Sun[1], Chengren Shi[1], Ronghua Tang[3], Shihua Shan[1*]

[1] Shandong Peanut Research Institute, Qingdao, China
[2] Computational Biology and Biological Physics, Astronomy and Theoretical Physics, Lund University, Lund, Sweden
[3] Guangxi Academy of Agricultural Sciences, Guangxi, China
[#] These authors contributed equally to this work

***Author for correspondence: shihshan@sina.com**

The cultivated peanut (*Arachis hypogaea*) is one of the most important oilseed crops worldwide, however, its improvement is restricted by its narrow genetic base. The highly variable wild peanut species, especially within Sect. *Arachis*, may serve as a rich genetic source of favorable alleles to peanut improvement; Sect. *Arachis* is the biggest taxonomic section within genus *Arachis* and its members also include the cultivated peanut. In order to make good use of these wild resources, the genetic bases and the relationships of the *Arachis* species need to be better understood.

Here, in this study, we have sequenced and assembled twelve *Arachis* complete chloroplast (cp) genomes (eleven from Sect. *Arachis*). These cp genome sequences enriched the published Arachis cp genome data. From the twelve acquired cp genomes, substantial genetic variation (1,368 SNPs, 311 InDels) has been identified, which, together with 69 SSR loci that have been identified from the same data set, will provide powerful tools for future explorations. Phylogenetic analyses in our study have grouped the Sect. *Arachis*species into two major lineages (I & II), this result together with reports from many earlier studies show that lineage II is dominated by AA genome species that are mostly perennial, while lineage I includes species that have more diverse genome types and are mostly annual/biennial. Moreover, the cultivated peanuts and *A. monticola* are nested within the AA genome species-dominated lineage. This result together with the maternal inheritance of chloroplast indicates a maternal origin of the two tetraploid species from an AA genome species. In summary, we have acquired sequences of twelve complete *Arachis* cp genomes, which have not only helped us better understand how the cultivated peanut and its close wild relatives are related, but also provided us with rich genetic resources that may hold great potentials for future peanut breeding.

1.6 Functional characterization of full-length transcriptome dataset of peanut during seed germination

Shengzhong Zhang[1†], Xiaohui Hu[1†], Huarong Miao[1†], Fenggao Cui[1], Yi Shen[2], Jiancheng Zhang[1], Weiqiang Yang[1*], & Jing Chen[1 *]

[1] Shandong Peanut Research Institute, Qingdao, 266100 P.R. China;
[2] Institute of Industrial Crops, Jiangsu Academy of Agricultural Sciences, Nanjing, 210014, P.R. China
[†] Equal contributors.

***Author for correspondence: mianbaohua2008@126.com**

Peanut (*Arachis hypogaea* L.) is one of the most important oil and cash crops in the world. Considerable yield loss and quality degradation occurs frequently each year due to improper germination. To improve peanut seed germination, a comprehensive full-length transcriptome dataset was generated by PacBio (Pacific Bioscience) single molecule real-time (SMRT) sequencing using one mixed RNA sample during *A. hypogaea* seed germination. The sequencing result showed 499,575 polymerase reads, 6,405,104 subreads and 338,584 reads of insert (ROIs) with a mean length of 2,223bp. A total of 47,697 unigenes were identified, of which 43,930 had functional annotations, and 16,927 generated alternative splicing (AS) sequences. In addition, 112,407 coding DNA sequences (CDS) were predicted with Angle classifier. Moreover, we found 16,701 simple sequence repeats (SSR) markers using the extensive dataset. Our results provide public data for research on population genetic features and functional variations in *A. hypogaea* germination.

1.7 Chromosome correspondence between karyotype and genome sequence map of *Arachis duranensis*

Pei Du[1], Liuyang Fu[1, 2], Siyu Wang[1, 2], Bingyan Huang[1], Wenzhao Dong[1], Xinyou Zhang[1*]

[1] Industrial Crops Research Institute, Henan Academy of Agricultural Sciences/ Key Laboratory of Oil Crops in Huang-Huai-Hai Plains, Ministry of Agriculture/ Henan Provincial Key Laboratory for Oil Crops Improvement, Zhengzhou 450002, Henan, China.
[2] School of Life Sciences, Zhengzhou University, Zhengzhou 450001, Henan, China.

***Author for correspondence: haasz@126.com**

Distinguishing chromosomes and chromosome aberrations and establishing correspondence between karyotype and genome sequence map of peanut are essential to better understand the genetics of important traits. However, the smaller sizes of their chromosomes and insufficient cytological markers have made chromosome identification quite difficult. Moreover, the peanut genome sequence map does not correspond to its actual chromosomes. To solve these problems, we firstly developed high-resolution karyotypes of 16 *Arachis* species, two interspecific F1 hybrids, and one radiation-induced M1 plant by fluorescence in situ hybridization (FISH) using single stranded oligonucleotides (SSONs) derived from repetitive sequences, 45S and 5S rDNAs, and genomic *in situ* hybridization (GISH) using total genomic DNA of *A. duranensis* and *A. ipaënsis* as probes. Genomes, chromosomes, and aberrations were clearly identifiable in the established karyotypes. All cultivars in our study had similar karyotypes, whereas the wild species exhibited various chromosomal variations, indicated that the development of repetitive and single-copy SSON probes for FISH and GISH provides useful tools for the differentiation of chromosomes and identification of structural chromosomal rearrangement. Secondly, ten chromosome-specific SSON libraries were developed based on the single-copy sequence of chromosome A01-A10 of *A. duranensis*. In combination with repetitive SSONs and rDNA FISH, we established the correspondence between karyotype and genome sequence map of *A. duranensis* for the first time. The results would benefit genome selection and gene mining for peanut improvement.

1.8 Segmental subgenome exchange is captured in the nascent synthetic allotetraploid [*A. ipaensis* x *A. correntina*]4x and its derivatives

Ye Chu[1], David Bertioli[2,3,4], Scott Jackson[2,3,4], Peggy Ozias-Akins[1,3*]

[1]Horticulture Department, University of Georgia, Tifton, GA, USA;
[2]Center for Applied Genetic Technologies, University of Georgia, Athens, GA, USA.
[3]Institute of Plant Breeding, Genetics and Genomics, University of Georgia, Athens, GA, USA.
[4]Department of Crop and Soil Science, University of Georgia, Athens, GA, USA

***Author for correspondence: pozias@uga.edu**

Wild introgression from diploid species provides the opportunity to broaden the gene pool of cultivated peanut for disease resistance and quality improvement. However, the genome stability and recombination of newly synthesized allotetraploids is not well characterized. A new interspecific hybrid *A. ipaensis* x *A. correntina* was made and produced fertile progenies after chromosome doubling via colchicine treatment. Selfed progenies of the new allotetraploid and F_1 hybrids from the [*A. ipaensis* x *A. correntina*]4x and *A. hypogaea* crosses were genotyped by the Axiom_Arachis2 SNP array. Gene conversion was observed in 104 markers out of 7,462 markers in the polyhigh resolution marker category. Segmental replacement between the *A. ipaensis* and *A. correntina* subgenomes was observed in the S_0 generation and segregation of the segmental replacement among the S_1 progenies followed Mendelian laws of inheritance. New events of segmental replacement were found in the S_1 generation. The genomic region with segmental replacement was found to segregate in the F_1 hybrids between the [*A. ipaensis* x *A. correntina*]4x and *A. hypogaea*. New events of segmental replacement were found in the F_1 hybrids as well as the S_1 progenies. The observation of gene conversion and segmental subgenome exchanges suggested genome instability in the newly synthesized allotetraploids. From the breeding perspective, this phenomenon could be a double-edged sword since introgressing desirable traits needs to be further confirmed as generations are advanced. On the other hand, new combinations of target traits may arise in the same series of genetic materials.

1.9 Genome-wide identification of circular RNAs in peanut (*Arachis hypogaea* L.)

XG Zhang, XL Ma, LL Ning, ZF Li, K Zhao, K Li, JL He, DM Yin*

College of Agronomy, Henan Agricultural University, Zhengzhou, Henan, 450002

***Author for correspondence: yindm@126.com**

Circular RNAs (circRNAs), a class of widely expressed endogenous regulatory RNAs, are involved in diverse physiological and developmental processes in eukaryotic cells. However, there have been no related studies on the number of circRNAs and their overall characteristics in peanut, which is one of the most important edible oil seed crops in the world. We performed a genome-wide identification of circRNAs using ribosomal-depleted RNA-sequencing from the seeds of two peanut eighth-generation recombinant inbred lines (RIL8): 'Hua 8106' (a medium-pod variety) and 'Hua 8107' (a super-pod variety), at 15 and 35 days after flowering (DAF), respectively. A total of 347 circRNA candidates were detected by two computational pipelines: CIRCexplorer and CIRI, with at least two supporting junction reads. All these circRNAs were generated from exons of annotated genes, and widespread on the 20 chromosomes. The expression profiles revealed that circRNAs were differentially expressed between two stages and between two lines. GO enrichment analysis of the host genes produced differentially-expressed circRNAs suggested that circRNAs are involved in seed development and regulation of seed size. 15 circRNAs were experimentally analyzed by qRT-PCR, and six circRNAs were resistant to digestion with RNase R exonuclease, and the back-splicing sites were further validated by Sanger DNA sequencing. We present the first systematical investigation of the genomic characteristics and expression profiles of circRNAs in peanut. The results revealed that circRNAs are abundant and widespread in peanut, and the differentially-expressed circRNAs between two lines suggested that they might play regulatory roles in peanut seeds development.

1.10Understanding the molecular basis of disease resistance of *Arachis glabrata* through transcriptome and genome sequencing

Xingjun Wang[1*], Chuanzhi Zhao[1], Liangqiong He[2], Ronghua Tang[2], Han Xia[1], Shuzhen Zhao[1], Lei Hou[1], Guanghui Li[1]

[1]Biotechnology Research Center, Shandong Academy of Agricultural Sciences; Shandong Provincial Key Laboratory of Crop Genetic Improvement, Ecology and Physiology, Jinan 250100, PR China
[2]Cash Crop Research Institute, Guangxi Academy of Agricultural Sciences, 530007 Nanning, China

***Author for correspondence: xingjunw@hotmail.com**

Wild type peanuts exhibit high level of resistance to a number of diseases that seriously affect cultivated varieties. Previous studies demonstrated that *A. glabrata* exhibited immune or high resistance to several diseases, including nematodes, rust, bacterial wilt, leaf spot and virus disease. It is a good source for identification of disease resistant genes. To understand the molecular mechanisms and identify disease resistant genes, we carried out transcriptome analysis, miRNA identification and whole genome sequencing of *A. glabrata.* The results provided a whole picture of the transcriptome and identified a large number of genes and miRNAs that may be involved in its disease resistance. The genome survey results indicated that *A. glabrata* is a tetraploid species with the genome size of 2.26 Gb. Totally, 721.66 Gb sequences were generated, and after assembly a total contig length of 3.69 Gb was obtained with the N50=472.44 Kb. The length of the assembled 40 chromosomes ranged from 50 Mb to 113 Mb. The mapping rate of the sequencing reads is 99.2% and the coverage of the genome is 99.25%. The genome of *A. glabrata* was closer to *A. ipaensis* (72.52% similarity) than that to *A. duranensis* (69.51% similarity). Disease resistant gene families including NBS-LRR and LOX were compared with the species in *Arachis* section. The completed genome of *A. glabrata* and the comparative genomic results could greatly promote the understanding of the disease resistance mechanism and the utilization of this species in the future genetic improvement of cultivated peanut.

1.11 Genomic analysis identifies genomic variation and history of peanut breeding

Zheng Zheng#, Ziqi Sun#, Yuanjin Fang#, Feiyan Qi#, Ke Lin#, Hua Liu, Zhongxin Zhang, Wenzhao Dong, Fengshuo Tang, Haiyan Hu, Bingyan Huang and Xinyou Zhang*

Industrial Crops Research Institute, Henan Academy of Agricultural Sciences / Key Laboratory of Oil Crops in Huanghuaihai Plains, Ministry of Agriculture / Henan Provincial Key Laboratory for Genetic Improvement of Oil Crops, Zhengzhou, 450002, China

***Authors for correspondence: haasz@126.com**

The polyploidization of *A. hypogaea* was estimated to ~3,500-4,500 years ago, since then, no evidence of natural introgression from wild species were reported due to sterility barriers and ploidy differences which resulted the isolation of cultivated peanut from other *Arachis* species. Therefore, in the cultivated peanuts, narrow genetic diversity and low genomic polymorphism with lack of variation at molecular level were widely recognized. On the other hand, morphological characters were observed in the cultivated peanuts. Based on these characteristic features, peanuts were classified into two subspecies (subsp. *hypogaea* and subsp. *fastigiata*), which were further divided to six botanical groups on the basis of different growth habits, seeds/pods morphology and inflorescence characteristics. These morphological differences resulted diversification in peanuts is considered mainly caused by intensive selection pressure during cultivation. However, the population structure of genetic variation between subspecies and botanical groups besides sweeps of selection during domestication and improvement by plant breeding activities in peanuts remain largely elusive. Recently, the International Peanut Genome Initiative (IPGI) as well as two other independent groups announced finishing assembly of the cultivated peanut genome sequences makes it possible to explore the genetic basis of diversity and domestication of peanuts via population genomics. To understand genome diversity and evolution in cultivated peanuts, we re-sequenced a population comprised worldwide cultivated peanut accessions. In addition, we identified loci associated with several important agronomical traits for peanut breeding by conducting a genome-wide association study (GWAS).

1.12 Genomics applications in post-genome sequence era in groundnut: a way forward

Rajeev K Varshney*

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India

***Author for correspondence: r.k.varshney@cgiar.org**

International groundnut research community has made tremendous progress during the last one decade but mainly during the last five years. This includes high quality reference genomes for diploid progenitors and cultivated tetraploid groundnut as well as other important genomic resources such as gene expression atlas and high density genotyping arrays. It is high time now for the groundnut community to plan and adopt effective strategies for deploying genome information for achieving higher genetic gains in breeding programs and develop better varieties with high resilience and excellent quality in faster way. The groundnut community needs to sequence diverse germplasm collection and if possible then entire germplasm collections at international level for identifying all possible haplotypes. Multi-location precision phenotyping of such germplasm collection can be used for high-resolution genome-wide association studies for identifying genes/ haplotypes associated with traits of interest. Similarly sequencing-based trait mapping approaches can be used with bi-parental as well as multi-parental populations for identifying diagnostic markers for breeding traits. While marker-assisted selection/ marker-assisted backcrossing approaches has been used to develop better varieties, marker-use should be started from the parental selection and should be continued at different steps in the breeding programs. Time has come now to bring paradigm shift from single to few loci-based selection to haplotype- based selection or genomic selection to select the lines for the next generation. Breeding programs need to make more crosses and larger populations that can be subjected to low-cost genotyping based early generation selection to enhance selection intensity in the breeding programs. Speed breeding is a new approach that can be integrated in the breeding program to have 4-6 generations per year. Advanced/fixed lines need to be tested in target populations of environment for selecting the best lines for nominations for release as commercial varieties. Once the better varieties are developed, it is important to take them to farmers field and this can be achieved by speeding up varietal replacement rate. Subsequently suitable agronomic package should be used for harnessing the full potential of genetics inside the better varieties. These approaches will be presented with some examples coming out from the collaborative efforts of ICRISAT and its partners.

1.13 The *Arachis hypogaea* genome provides insight into the polyploid origin and differential A and B subgenome evolution

Weijian Zhuang[1]*, Hua Chen[1], Chong Zhang[1], Rajeev K. Varshney[2*], Xiyin Wang[3*], Meng Yang[4], Qiang Yang[1], Yue Deng[1], Dongyang Xie[1] and Tiecheng Cai[1]

[1]Fujian Provincial Key Laboratory of Plant Molecular and Cell Biology, Oil Crops Research Institute, Fujian Agriculture and Forestry University, Fuzhou, Fujian, China.
[2] Center of Excellence in Genomics & Systems Biology, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India. China.
[3] North China University of Science and Technology.
[4] Grandomics Biosciences Co., Ltd, Wuhan, Hubei, China.

*** Author for correspondence: weijianz1@163.com**

Arachis hypogaea (peanut or groundnut) is a globally important crop of oil and protein. The most exciting events this year were the completion of genomes sequencing which provides a landmark for peanut research. Differential evolution of A and B subgenome was found based on the Shitouqi genome. B subgenome showed more gene expansion (12.46% versus 0.88%) than A subgenome after tetroploidization. A total of 30,596 non-redundant peanut genes were identified including 24,208 homeologs pairs genes which demonstrated widespread differential expression with dominant expression much more frequent among B homeologs. The B subgenome is more similar to *A. ipaensis* with more anchored contigs (55.49% of assemblies) and shared more (38,417) colinear genes. More A subgenome genes (58.7% of 629) were converted by their B subgenome counterparts. Congruently, peanut A subgenomes underwent more unbalanced structural rearrangements after polyploidy and its LTR transposable elements expanded only after tetraploidization, but B subgenome mainly derived from *A. ipaensis*. The results not only explain the prevalence of dysfunctional expression or loss of A subgenome homeologs but also deny the sequenced *A. duranensis* was the A subgenome progenitor. Besides, origin of polyploidy was also determined definitely.

2.1 QTLs mapping and marker analysis for pod size and yield-related Traits in peanut (*Arachis hypogaea* L.)

Hui Yang†, Yingjie Li†, Jiaqi Liu, Yuying Lv, Kun Zhang, Fengzhen Liu*, Yongshan Wan*

State Key Laboratory of Crop Biology, Shandong Key Laboratory of Crop Biology, College of Agronomy, Shandong Agricultural University, Tai'an, 271018 Shandong, China.

† Hui Yang and Yingjie Li contributed equally to this work.

***Author for correspondence: liufz@sdau.edu.cn; yswan@sdau.edu.cn**

Peanut *(Arachis hypogaea* L.) is an important oil crop in the world. The objective of this study was to identify main effect quantitative trait loci (QTLs) associated with peanut yield-related pod traits, and explore the genetic mechanism of pod traits. A recombinant inbred line (RIL) population with 151 lines derived from two cultivated peanut (79266 × D893) was developed to map QTLs for single pod weight (SPW), pod length (PL), pod width (PW), pod shell thickness (PST) and shelling percentage (SP) by both unconditional and conditional QTL analyses in 5 planting environments and the best linear unbiased predictions (BLUPs) dataset. Using an available simple sequence repeat genetic linkage map, 30 putative unconditional QTLs for pod traits were detected on chromosomes A03, A05, A06, A08, A09, B03, B04, B07 and B09, and ten of them were detected in at least two environments. Six of these ten stable QTLs *(qPWA08.1, qPWA08.2, qPSTA08.2, qPSTA08.3, qSPA08.1, qSPA08.2*) were located between markers GM2289 and Seq2G03 in the chromosome A08, and explained 11.28–28.05% of the phenotypic variance in different environments. In addition, *qPWA08.1*and *qPSTA08.2* were detected between markers ARS120 and GM1901 in BLUP dataset. Moreover, conditional QTL mapping found that PST had strong influences on PW and SP. This study confirmed target regions for fine-mapping and marker-assisted selection in peanut high-yielding breeding programs, and PST may be an important factor affecting pod size and yield.

2.2 Genome-wide identification of microsatellite markers from cultivated peanut (*Arachis hypogaea* L.)

Qing Lu[1#], Yanbin Hong[1#], Shaoxiong Li[1], Hao Liu[1], Haifen Li[1], Jianan Zhang[4], Haofa Lan[4], Haiyan Liu[1], Xingyu Li[1], Shijie Wen[1], Guiyuan Zhou[1], Rajeev K. Varshney[3], Huifang Jiang[2], Xiaoping Chen[1 *], Xuanqiang Liang[1 *]

[1]Crops Research Institute, Guangdong Academy of Agricultural Sciences, South China Peanut Sub-Center of National Center of Oilseed Crops Improvement, Guangdong Provincial Key Laboratory for Crop Genetic Improvement, Guangzhou 510640, China.
[2]Key Laboratory of Biology and Genetic Improvement of Oil Crops, Ministry of Agriculture, Oil Crops Research Institute of the Chinese Academy of Agricultural Sciences, Wuhan430062, China.
[3]Center of Excellence in Genomics & Systems Biology, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India.
[4]Mol Breeding Biotechnology Co., Ltd., Shijiazhuang, China.

***Author for correspondence: chenxiaoping@gdaas.cn; liangxuanqiang@gdaas.cn**

Microsatellites, or simple sequence repeats (SSRs), represent DNA variations widely distributed across the genome and can be used to develop SSR markers. Cultivated peanut is an allotetraploid plant species. Sequencing of cultivated peanut genome allowed us to develop genomic markers and construct a high-density physical map. Here, a total of 8,329,496 SSRs were identified, including 3,772,653, 4,414,961, and 141,882 SSRs that were distributed in subgenome A, B, and nine scaffolds, respectively. Based on the flanking sequences of these SSRs, a total of 973,984 newly developed SSR markers were developed in subgenome A (462,267), B (489,394), and nine scaffolds (22,323), with an average density of 392.45 markers per Mb. in silico PCR evaluation showed that an average of 88.32% of the SSR markers generated only one in silico-specific product in two tetraploid A. hypogaea varieties. A total of 39,599 common SSR markers were identified among two A. hypogaea varieties and their two progenitors. Amplification effectiveness of 44.15% was observed by real PCR validation. Moreover, a total of 1,276 public SSR loci were integrated with the newly developed SSR markers. Our research provides reliable marker resources for trait genetic analyses and molecular breeding in cultivated peanut.

2.3 Identifying loci control growth habit-related traits using bulked segregant analysis and genome-wide association study in peanut

L Li[1,2], X-L Yang[1,2], S-L Cui[1], H-Zhang[2], J Bagwell[2], G-J Mu[1], M-Y Hou[1], L-F Liu[1*] and C-Y. Chen[2*]

[1]North China Key Laboratory for Crop Germplasm Resources of Education Ministry, College of Agronomy, Hebei Agricultural University, Baoding, China,
[2]Department of Crop, Soil and Environmental Sciences, Auburn University, Auburn, AL, USA

***Author for correspondence: liulifeng@hebau.edu.cn; cyc0002@auburn.edu**

Peanut growth habit affects the adaptability, planting patterns, mechanized harvesting, disease resistance, and yield. To understand the genetic architecture of peanut growth habit, it was decomposed into five related traits, including lateral branch angle (LBA), main stem height (MSH), lateral branch height (LBL), extent radius (ER), and the index of plant type (IOPT). To map the quantitative trait loci (QTL) associated with peanut growth habit-related traits, we combined the genome-wide association analysis (GWAS) and bulked segregant analysis sequencing (BSA-seq) methods. GWAS was performed with 17,223 single nucleotide polymorphisms (SNPs) in 103 U.S. mini core collection genotyped using an Affymetrix version 2.0 SNP array. A total of 12,342 high-quality polymorphic SNPs, and 91 suggestive and significant SNPs associated with five growth habit-related traits were identified and these SNPs were distributed among 15 chromosomes. These SNPs were associated with 573 candidate genes, which play important roles in biological processes, hormone signaling, growth, and development. BSA-seq conducted with a specific length amplified fragment sequencing (SLAF-seq) method to find association with LBA. A 4.08 Mb genomic region on B05 was identified for LBA. Based on LD decay distance, we narrowed down and confirmed the region in 160 kb on B05 (144,193,467-144,513,467). Four candidate genes in this region were involved in plant growth. These results of SNPs and candidate genes should be useful in marker- assisted selection for peanut growth habits.

2.4 Characterization and allelic polymorphism of glycerol-3-phosphate acyltransferase 9 (*AhGPAT9*) genes in peanut (*Arachis hypogaea* L.)

Yuying Lv[1 †], Xiongrong Zhang[1 †], Lu Luo[1], Hui Yang[1], Kun Zhang[1], Yongshan Wan[1] Fengzhen Liu[1*], Pinghua Li[*].

[1] State Key Laboratory of Crop Biology, Shandong Key Laboratory of Crop Biology, College of Agronomy, Shandong Agricultural University, Tai'an, 271018 Shandong, China.
[†] Yuying Lv and Xiongrong Zhang contributed equally to this work.

***Author for correspondence: liufz@sdau.edu.cn; pinghuali@sdau.edu.cn**

Glycerol-3-phosphate acyltransferase (GPATs) are involved in the biosynthesis of glycerolipid in plants. GPAT9, located in the ER, has sn-1 activity and may be involved in the synthesis of stored lipids. Since peanut is an allotetraploid species (2n=4x=40, AABB), two GPAT9 genes (*AhGPAT9A* and *AhGPAT9B*) were obtained from A- and B- genome in peanut cultivar Fenghua2, which were 5537 bp and 5516 bp in length, respectively. The two genes both contained 13 exons and 12 introns and shared a similarity of 95.65% with 165 site differences, including substitutions, deletions and insertions. Expression analysis in different tissues showed that the seeds had the highest transcript accumulation. Allelic polymorphisms of *AhGPAT9* in 171 peanut germplasm were analyzed and a total of 118 polymorphic sites were identified in *AhGPAT9A*, forming 64 haplotypes (a1 to a64), and 94 polymorphic sites were detected in *AhGPAT9B*, forming 75 haplotypes (b1 to b75). Amino acid sequences analysis showed 64 *AhGPAT9A* haplotypes produced 12 protein types, named as AP1 to AP12, and proteins of 157 peanut accessions were identical to AP1. The 75 *AhGPAT9B* haplotypes produced seven protein types, named as BP1 to BP7, and proteins of 165 peanut accessions were identical to BP1. AP1 and BP1 were taken as the wild type. AP7, BP5 and BP6 lacked both binding sites for substrates G3P and enzyme catalytic centers, and displayed significantly different protein spatial structure. The results will provide valuable information for further understanding and utilization of AhGPAT9 genes in peanut.

2.5 Association analysis of leaf SPAD value and SSR markers in peanut

Suqing Zhu [1,2], Xiurong Zhang [1,2], Kun Zhang [1,2], Qingfang Sun [1,2], Yongshan Wan [1,2*], and Fengzhen Liu[1,2*]

[1] State Key Laboratory of Crop Biology, Shandong Key Laboratory of Crop Biology, Shandong Agricultural University, Tai'an 271018, China;
[2] College of agronomy, Shandong Agricultural University, Tai'an 271018, China

***Author for correspondence: yswan@sdau.edu.cn; liufz@sdau.edu.cn**

Leaf SPAD value can reflect chlorophyll content in crop leaves. In this study, we identified SPAD value of a total of 268 peanut lines and conducted association analysis with 391 polymorphic SSR markers. In total, 2 044 alleles were tested, and the number of alleles per marker ranged from 2 to 15, with an average of 5.228 alleles per locus. The associated location of leaf SPAD value was performed in TASSEL v2.1 using GLM (Simple and Q model) and MLM (K and Q+K model) option. Model comparisons showed Q+K was the most suitable model for association analysis. A total of 28 markers were detected to be significantly associated with SPAD ($p<0.01$) in two years, 15 of which were detected with remarkably significant difference ($p<0.001$). Among these markers, 6 were repeatedly found at significant level in two years, 4 of which were detected at remarkably significant level. A total of 18 alleles were examined by the 4 significantly associated markers, containing 5 key positive alleles, such as *AhTE1030-A285*, *AhTE0633-A394*, *AHGS1280-A289*, *AHGS-1952-A233* and *AHGS1952-A239*, and typical positive allele carriers, including Hua17, Ji0212-4, 98 D080-2 and Qianye55 were also identified. In addition, there were three main negative alleles (*AhTE0633-A286*, *AHGS1280-A339*, *AHGS1952-A250*) and typical negative allele carriers (Funingduoli, AH31613). These alleles and germplasm resources could provide reference for marker-assisted selection for peanut improvement.

2.6 QTL mapping of seed size in peanut (*Arachis hypogaea* L.)

C Zhang[1,2], H Chen[1,2], QZ Liu[1,2], TC Cai[1,2], Y Deng[1,2], YT Chen[1,2], WP Xie[1,2], K Chen[1,2], SS Zhao[1,2], WT Chu[1,2], SAKhan, RK. Varshney[3], WJ Zhuang[1,2*]

[1]Fujian Provincial Key Laboratory of Plant Molecule and Cell Biology, Oil Crop Research institute,
[2]State key laboratory of ecological pest control for Fujian and Taiwan crops, Fujian Agriculture and Forestry University, Fuzhou, Fujian 350002, China.
[3]Center of Excellence in Genomics & Systems Biology, ICRISAT, Hyderabad, India,502324.

***Author for correspondence: weijianz1@163.com**

Peanut (*Arachis hypogaea* L.) is an important oil and food crop worldwide,but the QTLs and the underlining mechanism of important agronomic traits such as seed size is mostly unclear. In this study, 267 recombinant inbred lines (RIL)chosen from a big RIL population were sequenced by SLAF-seq techniques for genotyping and SNP linkage map construction. Bulked Segregant Analysis (BSA) of seed size was also performed. An ultra-dense genetic linkage map was made which contained 7,929 SNPs in 20 linkage groups, covering 3,441.02 cM with an average distance of 0.56 cM between markers. Three kernel traits including seed length, seed width and 100-seed weight were phenotyped in well-designed trials in 2016 and 2017, respectively. A total of 18 QTLs located at 7 linkage groups were detected in two years. Combining two-year's mapping results, three QTLs can be repeatedly detected, which explained 9.68-11.14% of phenotypic variation and all located on A07 linkage group. Based on the 100-seed weigh, 54 extreme large and 54 extreme small seeds of RIL progenies were selected to construct two 54 + 54 extremely mixed pools for BSA. After sequencing, a total of 453,721 SNPs, and 81,118 InDels were obtained. Five related regions were detected with one the same with the mapped QTL as above and the related regions covered 1.75Mb, contain 23 genes. Several candidate genes were used for further characterization of the function for disclosing the mechanism of peanut seed size.

2.7 Genome wide identification and expression of germin-like protein family in peanut

T Wang, LJ Pan, M Wang, N Chen,MN Chen, Z Yang*, XY Chi*

Key Laboratory of Peanut Biology and Genetic Improvement, Ministry of Agriculture, P.R. China, Shandong Peanut Research Institute, Qingdao 266100, China

***Author for correspondence: chixy2019@163.com**

The germin-like protein (GLP) family genes, an important class of plant-ubiquitous proteins characterized by the cupin domain, play important rolesin plants. Available genome sequences of peanut have promoted the identification GLP family genes. We identified 52 GLP genes in peanut genomes. The results of domain analysis indicated that the GLP regions contained a highly conserved cupin motif. The results of structural and phylogenetic analysis revealed that 52 peanut GLP proteins are classified into three subfamilies. Twenty peanut GLP protein genes with 2-3 exons belong to Subfamily I. Eleven peanut GLP protein genes with 1-6 exons are distributed to Subfamily II. And there was no intron in Subfamily III which contains 21 genes, except *AhGL3-1a* with only one intron. This result indicates that there is a certain relationship between gene structure and phylogenetic evolution. Chromosome mapping analysis showed that peanut GLP genes were distributed with different densities on 17 chromosomes. The largest number of peanut GLP genes were found on chromosomes A06 (9 genes), followed by chromosome B06 (7 genes). However, there is only one gene located on chromosomes A04/05/10 and B01/04. Transcription analysis revealed that peanut GLP genes of subfamily I showed significantly high expression in seed. And there is predominant expression of subfamily III GLP genes in leaves, roots and aerial gynophore tips. These results will facilitate functional analysis and utilization of GLP genes in peanut.

2.8 High density genetic linkage map construction and QTL mapping for pod size related traits in peanut (*Arachis hypogaea* L.)

H Chen[1,2], Q Yang[1,2], C Zhang[1,2], QZ Liu[1,2], WP Xie[1,2], SS Zhao[1,2], K Chen[1,2], TC Cai[1,2], WT Chu[1,2], YT Chen[1,2], WJ Zhuang[1,2*]

[1]Fujian Provincial Key Laboratory of Plant Molecule and Cell Biology, Oil Crop Research institute,
[2]State key laboratory of ecological pest control for Fujian and Taiwan crops, Fujian Agriculture and Forestry University, Fuzhou, Fujian 350002, China.

***Author for correspondence: weijianz1@163.com**

Peanut is an important oil and economic crop. Pod size directly affects peanut yields. Identifying peanut pod QTLs and further exploring specific molecular markers and functional genes are the basis for peanut high-yield molecular breeding. In this study, a F10 recombinant inbred line (RIL) population of 945 lines was developed from a cross between Yueyou92×Xinhuixiaoli and 267 RILs were randomly chosen and sequenced by SLAF-seq techniques for pod genotyping and SNP linkage map construction. A total of 2,754,581 SLAF tags with 314-464 bp were obtained by Illumian high-throughput sequencing. Among them 8,019 SNP tags were used for constructing a genetic linkage map, covering 20 linkage groups and containing 7,929 SNP markers. The total map distance is 3441.02cM, and the integrity of average distance is 0.5 cM. A total of 25 QTLs were detected for pod traits, with 8, 4, 3 and 10 QTLs for pod length, pod width, pod thickness and 100-pods weight, respectively. Among these QTLs, we paid close attention to 11 intervals including pod length QTLs with 12.51% and 19.45% phenotypic variation on linkage group B04 and B07, pod width QTLs 11.98-20.30% phenotypic variation on linkage group A07, B02 and B09, 100-pods weight QTLs 10.44-19.31% phenotypic variation on chromosome A07、B02、A10and B04 and pod thickness QTLs 11.61% phenotypic variation on chromosome B03. Several candidate genes on A07 and B02 were cloned for functional characterization. This study provided the foundation for fine mapping of peanut pod size and high-yield molecular breeding.

2.9 Mapping of quantitative trait loci for Aspergillus flavus resistance in peanut

SAKhan[1,2], H Chen[1,2], C Zhang[1,2], Y Deng[1,2], Q Yang[1,2], TC Cai[1,2], QZ Liu[1,2], K Chen[1,2], SS Zhao[1,2], WT Chu[1,2], YT Chen[1,2], WP Xie[1,2], RK Varshney[3*], WJ Zhuang[1,2*]

[1]Fujian Provincial Key Laboratory of Plant Molecule and Cell Biology, Oil Crop Research institute,
[2]State key laboratory of ecological pest control for Fujian and Taiwan crops, Fujian Agriculture and Forestry University, Fuzhou, Fujian 350002, China.
[3]Center of Excellence in Genomics & Systems Biology, ICRISAT, Hyderabad, India, 502324.

***Author for correspondence: weijianz1@163.com**

Peanut (*Arachis hypogaea* L.) is grown worldwide for its protein and oil. However, the production and quality of peanut are greatly threatened by aflatoxins (AFs) contamination, produced mainly by *Aspergillus flavus* and *Aspergillus parasiticus*. Many biological control agents have been applied to solve this intricate problem, but stable resistant cultivars development is the best option. Here we characterized ~1300 recombinant inbred lines (RILs), obtained from two highly contrasting parents against A. flavus infection. Based on infection index 210 RILs were found resistance consistently under multiple seasons by in vitro inoculation. Using SLAF-seq technology, 790,026 high-quality SLAFs were obtained, of which 56,011 were polymorphic. Using 19,064 high-quality polymorphic SLAFs a high-density genetic map was constructed, consisted of 5,022 SNPs covering 20 linkage groups spanning 2,231.25 cM with an average adjacent marker distance of 0.44 cM. Using the mean phenotypic data and the genotypic data generated via SLAF-seq, two resistant QTLs, qRAF-3-1 and qRAF-14-1, were mapped on linkage groups (LGs) A03 and B04, respectively. qRAF-3-1 was mapped within 0.38 cM with more than 19 % phenotypic variation explained. In comparison with the reference genome, qRAF-3-1 and qRAF-14-1 were located within a physical distance of 1.45 Mb and 2.22 Mb, harboring 67 and 137 genes, respectively. Using microarray gene expression study, most genes including, pentatricopeptide repeat-containing-like protein, WRKY transcription factor, RPP13-like protein 1 and lipoxygenase responded to *A. flavus* challenge. This study will provide great assistance in fine mapping of genes resistance to *A. flavus* in peanut.

2.10 Overexpression of a peanut ERECTA-like gene positively regulates responses to *Ralstonia solanacearum* infection in tobacco and peanut

G Mamadou[1], N Ali[1,2], C Zhang[1,2], H Chen[1,2], SA Khan[1], R Zhuang[1], Q Yang[1,2], TC Cai[1,2], K Chen[1,2], WJ Zhuang[1,2*]

[1]Fujian Provincial Key Laboratory of Plant Molecule and Cell Biology, Oil Crop Research institute;
[2]State key laboratory of ecological pest control for Fujian and Taiwan crops, Fujian Agriculture and Forestry University, Fuzhou, Fujian 350002, China.

***Author for correspondence: weijianz1@163.com**

Bacterial wilt caused by *Ralstonia solanacearum* is a disease which leads to severe damages to peanut and no effective chemical control method had been developed. *ERECTA* is one of the genes in the LRR receptor kinase family which participate in the development and immunity in Arabidopsis. In our present work, a candidate gene *ERECTA-like* was cloned which was upregulated in resistant peanut cultivar Yueyou 92 after inoculated by *R. solanacearum*. The full-length cDNA of *AhERECTA* was 2919 bp encoded 997 amino acids. BLASTX results showed that *AhERECTA* contained 12 LRR and a kinase domain. Confocal microscopy revealed *AhERECTA* is located in the cell membrane, cytoplasm and nucleus. It induced hypersensitive response by transient over expression of *AhERECTA* in *Nicotiana benthamiana*. We generated *AhERECTA* transgenic tobacco plants via the leaf disc method. Transgenic tobacco lines challenged with *R. solanacearum* strain under greenhouse condition appeared improved resistance to R. solanacearum. We also developed transgenic peanut using pollen tube passage transformation and generate transgenic peanut plants, which was confirmed by both PCR and RT-PCR. After inoculated by R. solanacearum, transgenic T_1 show improved resistance in peanut. Bacterial wilt resistance was recorded after visualizing the symptoms for 21 days post inoculation. Therefore, our results reveal that *AhERECTA* may participate in the defense response to *R. solanacearum* in tobacco and peanut. However, its function relating to growth and development is needed for further evaluation.

2.11 QTL identification for seed weight and size based on a high-density SLAF-seq genetic map in peanut (*Arachis hypogaea* L.)

Shengzhong Zhang[1†], Xiaohui Hu[1†], Huarong Miao[1†], Ye Chu[2], Fenggao Cui[1], Weiqiang Yang[1], Chunming Wang[3], Yi Shen[4], Tingting Xu[1], Libo Zhao[5], Jiancheng Zhang[1], Jing Chen[1]*

[1] Shandong Peanut Research Institute, Qingdao, 266100, P. R. China
[2] Department of Horticulture, University of Georgia Tifton Campus, Tifton, GA 31793 United States
[3] State Key Laboratory for Crop Genetics and Germplasm Enhancement, Jiangsu Plant Gene Engineering Research Center, Nanjing Agricultural University, Nanjing 210095, P. R. China
[4] Institute of Industrial Crops, Jiangsu Academy of Agricultural Sciences, Nanjing, 210014, P. R. China
[5] Qingdao Agricultural Radio and Television School, Qingdao, 266071, P. R. China
[†]Equal contributors

***Author for correspondence: mianbaohua2008@126.com**

Genetic markers for yield and yield components in peanut are limited due to poor knowledge of genomic regions conditioning yield and its related traits. Specific locus amplified fragment sequencing (SLAF-seq) is a powerful tool for high density genetic map (HDGM) construction and quantitative trait loci (QTLs) mapping. In the present study, recombinant inbred lines (RIL) were advanced from a cross between a cultivar 'Huayu36' and a germplasm '6-13' with contrasting seed weight, size and shape. A HDGM was constructed with 3,866 loci consisting of SLAF-seq and simple sequence repeat (SSR) markers distributed on 20 linkage groups covering a total map distance of 1,266.87cM. Phenotypic data of four seed related traits were obtained in four environments, which mostly displayed normal distribution with varied levels of correlation. A total of 27 QTLs for 100 seed weight (100SW), seed length (SL), seed width (SW) and length to width ratio (L/W) were identified on 8 chromosomes, with LOD values of 3.16-31.55 and explaining phenotypic variance (PVE) from 0.74% to 83.23%. Gene content within these two stable QTL regions on chromosomes 2 and 16 provided valuable information for further functional analysis of yield component traits.

Keywords: Peanut, SLAF-seq, High density genetic map, QTL, Seed weight, Seed size

2.12 QTL mapping for pod and seed traits using RIL population derived from Huayu 28 and P76 (*Arachis hypogaea* L.)

Xiaohui Hu[1†], Shengzhong Zhang[1†], Huarong Miao[1†], Fenggao Cui[1], Weiqiang Yang[1], Libo Zhao[2], Jiancheng Zhang[1], Jing Chen[1*]

[1] Shandong Peanut Research Institute, Qingdao, 266100, P. R. China
[2] Qingdao Agricultural Radio and Television School, Qingdao, 266071, P. R. China
[†]Equal contributors

[*] **Author for correspondence: mianbaohua2008@126.com**

Based on RIL population from Huayu 28 and P76, a high density genetic map (SLAF) was constructed. In this study, pod and seed weight, seed size was collected in 2-3 environments. QTL mapping were conducted with the QTL IciMapping and rQTL. A total of 5 QTLs for 100 pod weight, 10 for 100 seed weight, 7 for seed length, 5 for seed width, and 8 for seed length to width ratio were identified by the QTL IciMapping software. Based on rQTL, 3 QTLs for 100 pod weight, 4 for 100 seed weight, 6 for seed length, 4 for seed width and 7 for seed length to width ratio were identified. Comparative analysis of all QTLs revealed QTL clusters, located on chromosome 2,7,9 and 19. Six and five QTLs for seed size traits were detected near 39 cM and in 90.46-111.07 cM on 2 chromosomes, and showed negative additive effect. This indicated that the increasing alleles were from P76. The QTL region (0-7cM) for seed length, seed length to width ratio, 100 pod weight and 100 seed weight was identified on 7 chromosomes, with the Huayu 28 allele increasing these trait values. QTLs for seed length, seed width and seed length to width ratio were detected in 9.22-19.64cM on 9 chromosomes, and all these QTL displayed positive additive effect indicating Huayu 28 allele increasing these trait values. The QTL region (near 61 cM on 19 chromosomes) for seed length, seed width and seed length to width ratio was identified with negative additive effect indicating P76 alleles increasing these traits.

Keywords: Peanut, SLAF-seq, High density genetic map, QTL, Pod, Seed

2.13 Linkage disequilibrium analysis in Togo groundnut germplasm and implications in marker-trait association

Essohouna Modom Banla[1*], Daniel Kwadjo Dzidzienyo[2], Samuel Kwame Offei[2], Pangirayi Tongoona[2] and Haile Desmae[3]

[1]Togolese Research institute of Agriculture (ITRA), Lomé, Togo;
[2]West Africa Centre for Crop Improvement (WACCI)-University of Ghana (UG), Accra, Ghana;
[3]International Crops Research Institute for the Semi-Arid tropic (ICRISAT-WCA), Bamako, Mali

***Author for correspondence: ebanla@wacci.ug.edu.gh**

The success of implementation of a large number of breeding methodologies used in genetics nowadays such as genome-wide association studies (GWAS), marker-assisted selection (MAS), quantitative trait loci (QTL) mapping is dependent on the linkage disequilibrium (LD) level between markers in the population. Thus, the objectives of this study were to determine the LD level in the germplasm collection and identify candidate genomic regions associated with LLS and yield-related traits. The LD in Togo groundnut collection was found to be high (0.36). Mean r2 ranged from 0.058 to 0.99 with the genomic distance between loci ranging from 0 to 148 Mb for intrachromosomal linkage disequilibrium. The interchromosomal LD was found to be significant at p = 0.01 with a certain number of loci located on different chromosomes exhibiting r2 above 0.1. Association study revealed that out of 31 agro-morphological traits analyzed, significant associations between SNPs and agronomic traits of interest ($p \leq 10\text{-}7$) were established for nine traits. Chromosomes A02, A03, A05 and B10 were significantly associated with LLS resistance with r2 ranging from 0.50 to 0.57. Hundred seed weight, pod width, pod length, seed length, seed width, growth habit and pod reticulation were also associated with various genomic regions. However, likely due to the high LD, significant association seems to cover the whole individual linkage group.

2.14 Fine mapping towards identifying major QTLs and candidate resistance genes for TSWV on Chromosome A01 of Peanut

Chuanzhi Zhao[1,2,3], Hui Wang[1,3], Yaduru Shasidhar[1,3], Jake C. Fountain[1,3], Xingjun Wang[2], Baozhu Guo[1,3*]

[1]USDA-ARS, Crop Protection and Management Research Unit, Tifton, GA 31793, USA, [2]Shandong Academy of Agricultural Sciences, Biotechnology Research Center, Jinan 250100, China,
[3]University of Georgia, Department of Plant Pathology, Tifton, GA, USA.

***Author for correspondence: baozhu.guo@usda.gov**

Tomato spotted wilt virus (TSWV) causes severe yield losses and management strategies are limited. Therefore, it is important to understand the genetics of host resistance and to identify the markers/genes for breeding resistant peanut cultivars. Several QTLs linked to TSWV resistance have been identified from the resistant cultivar NC94022 on chromosome A01. These QTLs explained phenotypic variation (PVE) ranging from 22.7% to 35.8%. However, most of these QTLs were identified using SSR markers and their physical locations were uncertain. To begin fine mapping these QTLs for candidate resistance gene identification, we summarized all reported QTLs and mapped them onto the peanut genome, and found they were localized to the upper arm of chromosome A01. We also used peanut Axiom_Arachis 58 K SNP array to genotype 143 recombinant inbred lines (RILs) from the SunOleic 97R x NC94022 population, and 1,741 polymorphic SNPs were identified. A SNP-based genetic linkage map was constructed which spanned distance of 3,378.85 cM with 1,009 markers/loci. We further identified six polymorphic SSRs from 38 newly developed SSRs in the first 12 Mb of A01. Using these SSRs, the genetic linkage map was improved, resulting in identifying a major QTL with a higher PVE of 42.93% across four years of phenotypic evaluations. Finally, we narrowed down the potential candidate genes to a region from 9.4-9.8 Mb on A01 which contains an NBS-LRR gene and a cluster of six chitinase genes. In summary, this major QTL for TSWV resistance has been improved to 43% PVE and spans 400 kb on the upper arm of A01, and may contain candidate R-gene(s) for further map-based cloning.

2.15 GWAS and co-expression network reveal ionomic variation in cultivated peanut

Hui Zhang[1], Ming Li Wang[2], Rob Schaefer[3], Phat Dang[4], Tao Jiang[1], & Charles Chen[1*]

[1]Department of Crop, Soil, and Environmental Sciences, Auburn University, Auburn, AL 36849, USA.
[2]USDA-ARS Plant Genetic Resources Conservation, Griffin, GA 30223, USA.
[3]Equine Genetics and Genomics Lab, University of Minnesota, Minneapolis MN 55455, USA.
[4]USDA-ARS National Peanut Research Laboratory, Dawson, GA 39842, USA.

***Author for correspondence: cyc0002@auburn.edu**

Peanut is an important legume providing products with nutrient dense including mineral nutrition. However, the genetic basis underlying the variations in the mineral composition in peanut is still unknown. A genome-wide association studies (GWAS) of the concentrations of 13 mineral elements combine with co-expression network were performed using a diverse panel of 120 genotypes mainly selected from the U.S. peanut mini core collection grown in two years to study genetic variation in peanut ionome. A total of 36 significant quantitative trait loci (QTLs) associated with 5 elemental concentrations were identified with phenotypic variation explained (PVE) from 18.35% to 27.56%, in which 24 QTLs are for boron (B), 2 QTLs for copper (Cu), 6 QTLs for sodium (Na), 3 QTLs for sulfur (S), and 1 QTL for zinc (Zn). A total of 110 non-redundant candidate causal genes identified were significantly associated with elements accumulation, which include one high-priority overlap (HPO) candidate gene arahy. KQD4NT, an important elemental/metal transporter gene located on LGB04 with position 5,413,913-5,417,353.

2.16 The positional cloning of Bunch1 gene that controls branching habit in peanut

S. Kunta, G. Kayam, Y. Levy, I. Hedvat & R. Hovav*

Department of Field Crops, Plant Sciences Institute, ARO, Bet-Dagan, Israel.

***Author for correspondence: ranh@agri.gov.il**

Branching habit (BH) is an important descriptive and agronomic character of peanut. Yet, the genetic mechanisms that control BH are not clear. We reported previously that in our Virginia-type background the spreading/bunch trait is controlled by a single gene, termed Bunch1. By using SNP-array and a RIL population, Bunch1 was initially located in ~640kb genomic segment at chromosome B5. Here, we used a map-based approach to further reduce this genomic segment. Nearly 2000 plants segregating for BH were grown in the field. KASP™ genotyping assay was performed with two spanning SNPs. A total of ~30 recombinants were found informative. Targeting additional SNPs inside the region enabled the narrowing down of the segment to 14.7kb. This segment contained only two gene models, MADS-box transcription factor 17-like (MADS) and pfkB-like carbohydrate kinase protein (pfkB), both were not reported previously to associate with BH in plants. Further analyses showed that pfkB is not expressed in vegetative tissues, or includes informative SNPs between Tifrunner, Shitouki, A- or B-genomes. However, MADS showed high expression levels in shoot tips and had significant polymorphic changes between the genomes. Furthermore, sequence alignment between the two parental lines, Hanoch (spread) and Harari (bunch), found a splice site mutation in the MADS gene in Harari. Therefore MADS is the preferred candidate to encode Bunch1. Additional analyses are currently being done to prove the role of MADS in controlling BH. This study demonstrates the utilization of the latest advances in Arachis genomics for trait cloning, even in the low polymeric background of cultivated peanut.

2.17 Cloning and expression analysis of oil biosynthesis related gene AhGL2 in peanut (*Arachis hypogaea* L.)

YJ Liu, SL Chen*, J Wang, ZSh Cheng, YH Song, YR Li*

Hebei Academy of Agriculture and Forestry Sciences, Hebei Provincial Laboratory of Crop Genetics and Breeding, Cereal and Oil Crops Institute, Shijiazhuang, CN 050035

***Author for correspondence: chsl99@163.com; liyrl@163.com**

Peanut (*Arachis hypogaea* L.) seed oil is one of the major resources of the edible oil for human consumption. However, the regulatory genes involved in oil accumulation are largely unclear. GL2 gene is a positive regulator of seed oil accumulation and belongs to the class IV homeodomain-leucine zipper (HD-ZIP) gene family. In this study, we isolated two full-length coding sequences (CDS), AhGL2-12 and AhGL2-19, from wild peanut A. duranensis by homology-based cloning. Real-time fluorescence quantitative PCR analysis indicated that AhGL2-12 and AhGL2-19 genes were expressed in all peanut organs examined, but their mRNA expression levels were quite different between high-oil and low-oil peanut varieties. In high-oil variety Jihua 20, AhGL2-12 and AhGL2-19 expression were examined in different organs, and relatively higher expression levels were observed in seeds at developmental stages than root, leaf, stem, fruit-needle, and flower. Whereas the results of Jihuatian 1 with low oil content were just the reverse. Therefore, the findings obtained in this study provide the basis for future investigation of AhGL2 genes in terms of the regulatory mechanism for oil accumulation in peanut seed. Furthermore, these novel genes may facilitate improvements in oil production in peanut through genetic manipulation of the GL2 genes.

2.18 Increasing power to dissect morphological and disease resistance traits in peanut using nested association mapping populations

B. Guo[1*], S. Gangurde[2], M.K. Pandey[2], R.K. Varshney[2], H. Wang, S. Yaduru, C. Zhao, A. Culbreath, Y. Chu, P OZIAS-AKINS, T.G. Isleib, C. Holbrook

[1] USDA-ARS, Crop Protection and Management Research Unit, Tifton, GA 31793;
[2] Center of Excellence in Genomics & Systems Biology, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad-502324, India;
[3] Department of Plant Pathology, University of Georgia, Tifton, GA 31793;
[4] Horticulture Department, University of Georgia, Tifton, GA 31793;
[5] Department of Crop Science, North Carolina State University, Raleigh, NC 27695;

***Author for correspondence: baozhu.guo@usda.gov**

Quantitative trait locus (QTL) mapping studies have been used in peanut for the genetic dissection of complex traits, mainly in biparental populations. The U.S. peanut community has developed two nested association mapping (NAM) populations with two common parents (Tifrunner and Florida-07) and eight diverse, unique parents, resulting in 16 bioparental recombinant inbred line (RIL) families to maximize genetic diversity while meeting practical breeding objectives. Here, we used a subset of Set A (2 x 4) of these two peanut NAM populations, NAM_Tifrunner (581 RILs) and NAM_Florida-07 (496 RILs) to demonstrate utility and power of this approach for dissecting complex traits including: morphology (main stem height, plant size, leaf length and width), pod-size (100-pod weight and 100 seed-weight), and disease-resistance (Tomato spotted wilt virus, early and late leaf spots) traits. Following genotyping using the 58K Axiom_ Arachis SNP array, two high-density linkage maps with 3,341 loci (NAM_Tifrunner) and 2,668 loci (NAM_Florida-07) were developed. Compared with biparental populations, these maps showed much greater marker density and QTL mapping resolution and detection, clearly demonstrating the power of this approach for QTL discovery. Furthermore, we compared joint-QTL mapping to genome-wide association mapping (GWAS) and found several of these QTLs and their respective associated SNP markers were consistently identified with the NAM populations. These QTLs and QTNs mapped to known physical locations in the peanut genome provide candidate regions for further exploration to identify putative genes regulating these important traits. Therefore, multiple-parental populations like NAM and MAGIC (Multiple-parental Advanced Generation Inter-Cross) increase genetic diversity gene-pool with more recombination exchange events, which will lead to higher resolution of genetic maps and detection of trait-associated markers.

2.19 Identification of quantitative trait loci for surrogate traits of water use efficiency, pod yield and yield related traits in groundnut (*Arachis hypogaea* L.) under different water regimes

D. L. Savithramma[1], Savita S. K[2], Bharath Kumar P. Jambagi[2]

[1]Dean of Post Graduate Studies (PGs), University of Agricultural Sciences, GKVK, Bengaluru-560065.
[2]Ph.D Scholar, Department of Genetics and Plant Breeding, University of Agricultural Sciences (UAS), GKVK, Bengaluru-560065.

***Author for correspondence: nesarns@gmail.com**

Drought is the greatest impact on yield losses in groundnut. Pod yield under moisture stress is a highly complex trait with large influence even for minor fluctuations in environmental conditions. Genomics assisted breeding holds great promise for improving such complex traits more efficiently in less time, but requires markers associated with the trait of interest. In this context, a recombinant inbred line mapping population derived from GKVK 4 × NRCG 12473 was used to identify markers associated with quantitative trait loci (QTLs) for surrogate traits of water use efficiency (WUE), yield and yield related traits under well-watered (WW) and water stress (WS) conditions. Genotypic and phenotypic data (F7WW, F8WW, F8WS and pooled mean of F7 and F8WW) were integrated to identify the genomic regions/ QTL controlling traits related to WUE and pod yield and yield related parameters using Inclusive Composite Interval Mapping. Linkage map analysis of the 164 marker loci resulted in the mapping of 105 marker loci on 22 linkage groups (LGs) and total map distance of 763.1 cM was developed. QTL analysis detected a total of four main effect QTL (M-QTL) for SCMR and two QTL for SLA with 8.64 and 11.35% phenotypic variation explained (PVE) and a total of 44 M-QTLs were obtained for pod yield and yield related parameters with PVE % upto 43.74 %. A total of 56 significant epistatic-QTL (E-QTL) interactions were detected with PVE % upto 29.70 %. M-QTL and E-QTL interaction explained a fairly large magnitude of PVE % for traits related to WUE, pod yield and its attributing parameters. Identified linked markers/QTLs have to be validated for their potential use in marker assisted breeding for high WUE.

2.20 Developing a high-density molecular map of the A-Genome species *Arachis duranensis*

E Nagy[1], Y Guo[1], S Khanal[1], C Taylor[1], S Knapp[2], P Ozias-Akins[3], HT Stalker[4*] & N Nielsen[4].

[1]Institute of Plant Breeding, Genetics, and Genomics, University of Georgia, Athens, GA 30602.
[2]Monsanto Inc., Woodland, CA 95696.
[3]Department of Horticulture, The University of Georgia Tifton Campus, Tifton, GA 31793-0748.
[4]Department of Crop Science, North Carolina State University, Raleigh, NC 27695-7629.

***Author for correspondence: tom_stalker@ncsu.edu**

Although markers have been mapped into linkage groups of both wild and cultivated peanut since the early 1990's, the maps have been extremely low density. To overcome difficulties associated with molecular polymorphism, Expressed Sequence Tag libraries were created to facilitate identifying Simple Sequence Repeats (SSR) and Single Nucleotide Polymorphism (SNP) markers in peanut. *Arachis duranensis* was used for genetic mapping experiments with the goal of utilizing the data for fine-mapping in the cultivated species. The objectives of this research were to first identify a large number of SSRs and SNPs in peanut and then to map polymorphic markers into linkage groups. Two *A. duranensis* accessions 15039 were used. Normalized cDNA was produced from leaf and root tissues of both accessions from which 22,356 and 21,487 long-read ESTs from leaves and roots, respectively, were produced for PI 475887 using the Sanger technology. Short-read ESTs also were produced from leaves (212,938 and 296,242 for PI 475887 and Grif. 15039, respectively) and roots (266,575 and 235,245 for PI 475887 and Grif. 15039, respectively). In addition, 2,134 SSR markers developed from an A. hypogaea EST database were evaluated for polymorphism in the two diploid accessions. 2,319 markers were mapped into 10 linkage groups, including 971 SSRs, 221 single-stranded DNA conformation polymorphism (SSCP) markers, and 1,127 SNPs. This represents the first high-density map for a peanut species. The linkages identified in this study will be an invaluable resource for sorting the A and B genomes and linkage relationships in the cultivated

2.21 Characterization of the AhLea-3 and the enhanced salt tolerance in transgenic peanut plants

Lixian Qiao, Pingping Jiang, Mingyang Yu, Yanyan Tang, Hong Zhu, Jiongming Sui, Jingshan Wang*

College of Agronomy, Qingdao Agricultural University / Peanut Industry Cooperative Innovation Center / Dry-land Farming Technology Lab, Qingdao 266109, Shandong, China

***Author for correspondence: jswang319@126.com**

Lea-3 from *Arachis hypogaea* L. (AhLea-3) was considered to be related to the salt resistance according to the result of transcriptome profiling and digital gene expression analysis and further qRT-PCR validation. AhLea-3 was isolated from the peanut salt-resistance mutant M34 with cDNA as template. AhLea-3 contained one introns and two extrons, the full length cDNA sequence contained 303 bp that coded for a 100-amino acid protein with a calculated molecular weight of 10.8 kDa. AhLea-3 was ligated to pCAMBIA1301 to obtain the over-expressing vector pCAMBIA1301- AhLea-3, which was then transferred to peanut variety Huayu23 by infecting the pollen tube with recombinatant Agrobacterium Strain GV3101 containing pCAMBIA1301-AhLea-3. The positive transgenic plants were screened by PCR amplification with 35S primer sequence. The expression level was determined to be over 10 times in transgenic plants than that in non-transgenic plants by qRT-PCR analysis. The transgenic plants showed weaker leaf wilting, higher enzymatic activity of SOD, POD, CAT and lower MDA content than non-transgenic plants, 5 days after they were irrigated by 250mM NaCl. Transgenic plants had higher net photosynthetic rate, stomatal conductance, transpiration rate, and lower intercellular CO_2 concentration than the non-transgenic plants after the salt stress treatment by 250 mM NaCl. These results suggested that over expression of AhLea-3 improved the salt tolerance of transgenic peanut plants.

Key words: peanut, Lea-3, salt resistance, transformation, pollen tube infection

2.22 Cloning, genetic transformation and salt tolerance validation of AhWRKY75 gene from *Arachis hypogaea* L.

Hong Zhu, Yue Guo, Yanan Jiang, Wenjie Zhou, Yanyan Tang, Jiongming Sui, Jingshan Wang, Lixian Qiao*

College of Agronomy, Qingdao Agricultural University/Peanut Industry Cooperative Innovation Center / Dry-land Farming Technology Lab, Qingdao 266109, Shandong, China

***Author for correspondence: lxqiao73@163.com**

Peanut is one of the most important economical oilseed crop whose production is threatened by various abiotic and biotic stress. Therefore, investigating the molecular mechanism of salt tolerance will provide important information for the improvement of salt tolerance in this crop. WRKY, is one of the largest transcriptional factor (TF) family specific in plants involving in growth and development, defense regulation and stress response. In this study, we cloned a novel WRKY transcription factor gene belonging to WRKY IIc subfamily, named AhWRKY75, from the salt-tolerant mutant M34 which originated from mutagenic progenies of peanut variety 'Huayu20'. The expression of AhWRKY75 in M34 was induced by NaCl stress treatment. The AhWRKY75-overexpressing vector was transformed into peanuts through pollen tube infection method, which showed that the transgenic peanuts grew better than wild type under salt stress treatment. After salt treatment, several genes related to reactive oxygen species (ROS) scavenging system were up-regulated and the activity of superoxide dismutase (SOD), peroxidase (POD) and catalase (CAT) in transgenic lines were significantly higher than that in non-transgenic control plants, and the superoxide anion content of the transgenic lines was significantly lower than control plants. Meanwhile the net photosynthetic rate (Pn), stomatal conductance (GS) and transpiration rate (Tr) of transgenic lines were significantly higher and the intercellular CO2 concentration (Ci) of transgenic plants were significantly lower than those of control plants. These results demonstrated that the AhWRKY75 gene conferred salt tolerance in transgenic peanut lines through improving the ability of ROS scavenging system and the efficiency of phoyosynthesis under stress treatment. This study provides a novel WRKY gene for enhancing the tolerance of peanut and other plants to abiotic stresses.

Key words: peanut (*Arachis hypogaea* L.), genetic transformation, AhWRKY75, salt tolerance, ROS

2.23 Virus induced gene silencing of AhABI4s enhance salt tolerance of peanut seedling via regulation of ion homeostasis

Lu Luo[1,3†], Qian Wan[1†], Kun Zhang[1], Xiurong Zhang[1], Ruijie Guo[1], Cai Wang[1], Chengchao Zheng[2], Fengzhen Liu[1*], Yongshan Wan[1*].

[1] State Key Laboratory of Crop Biology, Shandong Key Laboratory of Crop Biology, College of Agronomy, Shandong Agricultural University, Tai'an, 271018 Shandong, China.
[2] State Key Laboratory of Crop Biology, Shandong Key Laboratory of Crop Biology, College of Life Sciences, Shandong Agricultural University, Tai'an, 271018 Shandong, China.
[3] College of Life Sciences, Shandong University, Qingdao, 266237, Shandong, China.

[†] Lu Luo and Qian Wan contributed equally to this work.

***Author for correspondence: liufz@sdau.edu.cn; yswan@sdau.edu.cn**

Soil salinity is one of the major factors that limits area of cultivable land and yield potential of crops. Considered as a moderately salt sensitive economically-important crop, biological processes involved in salt stress response in peanut remain elusive. Publishing of the genomic sequence of cultivar peanut represent a new opportunity for further research. ABA INSENSITIVE 4 (ABI4) is an evolutionary conserved transcription factor. Mutation of ABI4 in Arabidopsis enhanced salt tolerance of seedlings significantly by targeting and down-regulating of HKT1;1. However, few achievements were reported in other aspects. In this study, AhABI4s in peanut were first cloned and silenced via virus-induced gene silencing method. Phenotype analysis showed that down-regulation of AhABI4s enhanced salt tolerance of peanut significantly. According to proteome and phosphoproteome analysis, expression of 1,900 proteins and 2,620 phosphorylation sites were predicted to be affected by silencing of AhABI4s under salt stress. Proteins with ion transporting activity were enriched by GO analysis. Further analysis showed that, 31 proteins may participate in homeostasis maintain of Na+, K+, Ca2+, H+ and Cl- in plant cells. Combined transcriptome and proteome analysis indicated that 63 genes may regulated by AhABI4s directly and 7 of them, ABI5-like5, RABA1f, SCAMP3, PK, RP-S26e, HSP70, cysteine proteinase inhibitor, were able to interact with the predicted ion transporters. Silencing of AhABI4s altered down-stream protein-protein interaction network to regulate expression/phosphorylation level of ion transporters, and finally influence homeostasis under salt stress. This work provides novel insights for salt.

2.24 Genome-wide identification and characterization of NF-Y gene family in peanut (*Arachis hypogaea* L.)

Qian Wan[1, 2†], Lu Luo[1, 2†], Xiurong Zhang[1, 3], Yuying Lv[1, 2], Suqing Zhu[1, 2], Lingrang Kong[1, 2], Yongshan Wan[1, 2], Fengzhen Liu[1, 2*], Kun Zhang[1, 2*]

[1] State key Laboratory of Crop Biology, Shandong key Laboratory of Crop Biology, Shandong Agricultural University, Tai'an 271018, China.
[2] College of Agronomy, Shandong Agricultural University, Tai'an 271018, China.
[3] College of Life Science, Shandong Agricultural University, Tai'an 271018, China.

[†] Qian Wan and Lu Luo contributed equally to this work.

***Author for correspondence: liufz@sdau.edu.cn; kunzh@sdau.edu.cn**

Nuclear factor Y (NF-Y) gene family consists of NF-YA, NF-YB and NF-YC subfamilies. Many members of NF-Y family have been involved in plant development processes, phytohormone signaling and tolerance to stresses in Arabidopsis and other plant species. However, little attention has been given in peanut. In this study, a total number of 33 AhNF-Y genes (AhNF-Ys) were identified and distributed on 16 chromosomes. A phylogenetic analysis indicated that NF-Y genes possessed highly conservation in different plants. Gene duplication analyze indicated that only segmental duplication was detected. The abiotic stress-related regulatory elements analysis showed that AhNF-Ys, except for AhNF-YB6, contained at least one abiotic stress response element. With RNA-seq data, the tissue/organ-specific expression and differential expression profiling under salt stress were analyzed, indicating that six selected AhNF-Y gene may play potential roles in the regulation of salt stress response. qRT-PCR results suggested that these AhNF-Y genes also responded to ABA (Abscisic Acid), SA (Salicylic acid) and osmotic stresses. These results may contribute to functional characterization of AhNF-Y genes in further research.

2.25 Marker assisted breeding to develop peanut cultivars with resistance to late leafspot

C.C. Holbrook[1*], Y. Chu[2], S. Lamon[3], A.K. Culbreath[5], D. Bertioli[3,4], S. C. M. Leal-Bertioli[5], I.J Godoy[6], and P. OZIAS-AKINS[2,4].

[1]United States Department of Agriculture-Agricultural Research Service, Tifton, GA 31793-0748.
[2]Department of Horticulture, University of Georgia, Tifton, GA, USA.
[3]Department of Crop & Soil Sciences, The University of Georgia, Tifton GA 31793-0748 and Athens GA 30605. The University of Georgia, Tifton, GA 31793-0748.
[4]Institute of Plant Breeding, Genetics & Genomics, University of Georgia, Tifton, GA 31793.
[5]Department of Plant Pathology, The University of Georgia, Tifton, GA 31793, and Athens, GA 31793.
[6]Instituto Agronomico (IAC), Campinas, SP, Brazil.

***Author for correspondence: Corley.holbrook@usda.gov**

Late Leaf Spot (LLS) disease caused by Cercosporidium personatum (Berk. & M.A. Curtis) Deighton is one of the most cost diseases of U.S. grown peanut (Arachis hypogaea L.). IAC 322 is a breeding line that contains three introgressed chromosome segments from a wild species that provides a very high level of resistance to LLS. Although this line has excellent resistance to leaf spot, it does not have acceptable agronomic performance in Georgia. Genetic markers are available for these genomic regions, so marker assisted selection (MAS) to combine resistance with acceptable agronomic performance is feasible. The goal of this research was to identify the genomic regions or combinations of genomic regions that provide the highest level of resistance. 'TifNV-High O/L' was crossed with IAC 322, and 400 resulting F2 progeny were genotyped. Individuals with single introgressed regions, individuals with all pairwise combinations, and individual with all three introgressions were identified. This material was then advanced to the F5 generation. In 2018 we planted this material in replicated field studies at two locations. No fungicide sprays were used for leaf spot control. Results indicated that major genes for resistance are contained on the introgressions from the bottom of chromosome A03 and the top of chromosome A02. The third introgressed region was from the bottom of chromosome A02 and did not add significantly to the levels of resistance to LLS. These results can be used to improve the efficiency and effectiveness of MAS to develop leaf spot resistant cultivars.

2.26 Expression analysis of AhMITE1-associated genes among the diverse genotypes of peanut (*Arachis hypogaea* L.)

RS Bhat[1]*, R Choudhari[1] & K Shirasawa[2]

[1]Department of Biotechnology, University of Agricultural Sciences, Dharwad 580 005, India
[2]Department of Frontier Research, Kazusa DNA Research Institute, Chiba 292-0818, Japan

***Author for correspondence: bhatrs@uasd.in**

Arachis hypogaea miniature inverted-repeat transposable element (AhMITE1) is a non-autonomous element of MITE DNA transposon (class II) system. With the genome-wide distribution and the transpositional preference to the genic regions, AhMITE1 is active under genetic instability, mutagenesis, hybridization, in vitro culture etc., thereby playing an important role in genome rearrangements and evolution. An effort was made in this study to compare the expression levels of the genes associated with AhMITE1 among the 11 diverse genotypes of peanut. The site of insertion of AhMITE1 among the 19 trait-specific genes was identified. It ranged from gene body (UTRs, exon and intron) to 1 kb upstream and downstream regions. The genotypes showed polymorphism for the AhMITE1 insertion at these 19 genes. Expression levels of these 19 genes varied among the genotypes. Of the 19 genes, 11 showed significant differential expression between TMV 2 and its EMS-derived mutant TMV 2-NLM, which carried alternate alleles for AhMITE1 insertion. In general, the genes with AhMITE1 insertion either in the gene body or regulatory regions showed higher expression, indicating the importance of AhMITE1 in genome expression.

2.27 Genome-wide identification and expression analysis of expansin family genes in *Arachis duranensis* and *A. ipaensis*

Chuanzhi Zhao[1,3*], Ming li[1,2], Ximeng Zhou[1,3], Han Xia[1,2], Jingjing Qiu[1,3], Ye Zhang[1,4], Yuhan Zhao[1,3], Lin Zhu[1,3], Junjie Ma[1], Changsheng Li[1,3], Aiqin Li[1,3], Changle Ma[1,3], Xingjun Wang[1,3*]

[1]Biotechnology Research Center, Shandong Academy of Agricultural Sciences, PR China,
[2]Key Laboratory of Biochemistry and Molecular Biology in University of Shandong Province, Biological and Agricultural College, Weifang University, Weifang 261061, PR China.
[3]College of Life Sciences, Shandong Normal University, Jinan 250014, PR China.
[4]Institute of Vegetables and Flowers, Shandong Academy of Agricultural Sciences and Shandong Key Laboratory of Greenhouse Vegetable Biology and Shandong Branch of National Vegetable Improvement Center, Jinan 250100, PR China

***Author for correspondence: xingjunw@hotmail.com; chuanzhiz@126.com**

Expansins are plant cell wall loosening proteins which play important roles during plant development and adaptation to stresses. Here, using the released genome sequence of ancestral species of peanut Arachis duranensis and A. ipaensis, genome-wide expansins identification was performed. A total of eighty-four expansin genes were identified and the classification, chromosomal localization and phylogenetic relationships of these expansin genes were clarified. Paraffin section revealed that the number and size of sclerenchyma cells varied between the leaves from main stem and lateral branches in peanut. Transcriptome analysis further proved that the expression of AdEXLB4, AdEXPA9, AiEXLB4 and AiEXPA9 was up-regulated in the main stem leaves, implying that these genes might be the potential genes regulating the development of leaves of main stem and lateral branch. In addition, we also found that the expression of five expansins was significantly up-regulated in response to root-knot nematode. Moreover, the expression of AdEXLB8 and AdEXPA1 was up-regulated in response to drought, suggesting that these genes might be related with the resistance of peanut. In conclusion, a comprehensive analysis of expansin genes was performed, which provided valuable information to better understand the functions of expansin genes in peanut development and response to biotic and abiotic stresses.

2.28 Whole-genome resequencing-based BSA-seq identified AhTc1 gene encoding a R2R3-MYB transcription factor controlling peanut purple testa color

Chuanzhi Zhao[1,2,6,7*], Yuhan Zhao[1,2], Junjie Ma[1,3], Ming li[1], Li Deng[4], Guanghui Li[1], Han Xia[1,2], Shuzhen Zhao[1,2], Lei Hou[1], Pengcheng Li[1,2], Changle Ma[2], Mei Yuan[5], Li Ren[4], Jianzhong Gu[4], Baozhu Guo[6,7], Xingjun Wang[1,2,3*]

[1] Biotechnology Research Center, Shandong Academy of Agricultural Sciences, PR China,
[2] Shandong Normal University, Jinan 250014, PR China,
[3] Shandong University, Jinan 250100, PR China,
[4] Kaifeng Academy of Agriculture and Forestry, PR China,
[5] Shandong Peanut Research Institute, P.R. China,
[6] Crop Protection and Management Research Unit, USDA-Agricultural Research Service, USA
[7] Department of Plant Pathology, University of Georgia, USA

***Author for correspondence: xingjunw@hotmail.com; chuanzhiz@126.com**

The common testa colors of peanut varieties are pink or red. But the peanut varieties with dark purple testa have been focused in recent years due to the potential high levels of anthocyanin, an added nutritional value of antioxidant. However, the genetic mechanism regulating testa color of peanut is unknown. In this study, we found that the purple testa was decided by the female parent and controlled by a single major gene named AhTc1. To identify the candidate gene controlling peanut purple testa, whole-genome resequencing-based approach (BSA-seq) was applied, and a total of 260.9 Gb data was generated from the parental and bulked lines. SNP index analysis indicated that AhTc1 located in a 4.7 Mb region in chromosome A10, which was confirmed by Bulked Segregant RNA sequencing (BSR) analysis in three segregation populations derived from the crosses between pink and purple testa varieties. Allele-specific markers were developed and demonstrated that the marker pTesta1089 was closely linked with purple testa. Further, AhTc1 encoding a R2R3-MYB gene was positional cloned. The expression of AhTc1 was significantly up-regulated in the purple testa parent YH29. Overexpression of AhTc1 in transgenic tobacco plants led to purple color of leaves, flowers, pods and seeds. In conclusion, AhTc1, encoding a R2R3-MYB transcription factor and conferring peanut purple testa, was identified, which will be useful for peanut molecular breeding selection for cultivars with purple testa color for potential increased nutritional value to consumers.

2.29 Genome-wide identification of microsatellite markers through scanning and comparing the tetraploid and diploid peanut genomes

Junjie Ma[1,2], Yuhan Zhao[1,3], Hua Chen[4], Lin Zhu[1,3], Ximeng Zhou[1,3], Han Xia[1,3], Lei Hou[1], Guanghui Li[1], Weijian Zhuang[4], Xingjun Wang[1,2,3*], Chuanzhi Zhao[1,3*]

[1] Biotechnology Research Center, Shandong Academy of Agricultural Sciences, PR China,
[2] College of Life Sciences, Shandong University, Qingdao 266237, PR China.
[3] College of Life Sciences, Shandong Normal University, Jinan 250014, PR China.
[4] Fujian Provincial Key Laboratory of Plant Molecular and Cell Biology, Oil Crops Research Institute, State Key Laboratory of Ecological Pest Control for Fujian and Taiwan Crops, Fujian Agriculture and Forestry University, Fuzhou, China

***Author for correspondence: xingjunw@hotmail.com; chuanzhiz@126.com**

Cultivated peanut (*Arachis hypogaea* L) represents one of the most important oil crops in the world. Although effort has been conducted to characterize the microsatellites (or SSRs) in peanut, the quantity and quality of SSRs are still been limited, due in part to the lack of genome sequences. In the present study, genome-wide SSR characterization and marker development were performed using the recently sequenced cultivated peanut species, Tifrunner. In total, 512,900 SSRs were identified from 2,556.9 Mb genomic sequences. According to the flanking sequences of the identified SSRs, 7,757 filtered primer pairs (markers) were designed, and further evaluated in the assembled genomic sequences of the tetraploid Arachis species, Tifrunner and Shitouqi, and diploid ancestral species, *A. duranensis* and *A. ipaensis*. In silico PCR analysis showed that these SSRs had high amplification efficiency and polymorphism in the wild type and cultivated peanuts. Notably, nearly 60% of theses markers were single-locus SSRs in tetraploid species, indicating they are more specific in distinguishing the alleles of A and B sub-genomes of peanut. In addition, two markers closely related with the purple testa and twenty-seven SSR markers near to FAD2 genes were identified, which could be used for breeding the purple testa and high-oleic peanut varieties, respectively. Moreover, the potential application of these SSR markers in utility of wild Arachis was discussed. Taken together, these results suggested that these SSR markers developed will be useful for diversity analysis, gene mapping and functional genomics studies in peanut.

2.30 Identification of AhNPR-A04 as a leaf spot disease related gene in peanut through MutMap combined with BSR approach

Suoyi Han[1§], Chuanzhi Zhao[2,3§], Lei Shi[1], Huayang Zhang[1],Yuanjin Fang[1],Han Xia[2,3], Hua Liu[1],Shuzhen Zhao[2,3], Lijuan Miao[1],Lei Hou[2,3], Zhongxin Zhang[1],Jing Xu[1], Yuhan Zhao[3], Changle Ma[3], Zheng Zheng[1], Yifei Du[1], Bingyan Huang[1], Wenzhao Dong[1], Fengshou Tang[1], Xinyou Zhang[1*], Xingjun Wang[2,3*]

[1]Industrial Crops Research Institute, Henan Academy of Agricultural Sciences, Zhengzhou 450002, P.R. China.
[2]Biotechnology Research Center, Shandong Academy of Agricultural Sciences, Jinan 250100, PR China.
[3]College of Life Sciences, Shandong Normal University, Jinan 250014, PR China.
[§]Suoyi Han and Chuanzhi Zhao contributed equally to this paper.

***Author for correspondence: xingjunw@hotmail.com; haasz@sohu.com**

Leaf spot (LS) diseases are the main diseases causing yield decrease and increasing chemical spray for peanut production. However, we know little about the molecular mechanisms for peanut in response to LS. Yuanza 9102 is a dominant peanut variety in Henan province of China, and with high resistance to LS. M14, an EMS induced mutant from Yuanza9102, is high susceptible to LS. Using MutMap together with BSR (Bulked Segregation Analysis), AhNPR-A04 was identified as a candidate gene involved in LS resistance in peanut. A G-to-A mutation in the 4th exon of AhNPR-A04 caused a transition from Gly to Arg within the C-terminal transactivation domain, leading to significant changes in gene expression in response to LS and salicylic acid (SA) treatment. Our data suggested that mutantion of AhNPR-A04 did not affect the induction of PR gene by SA. Instead, the mutation resulted in up-regulation of some PR genes including pathogenesis-related thaumatin protein and chitinase family proteins coding genes. The further study on AhNPR genes will be valuable for understanding the molecular mechanism of LS resistance in peanut. In addition, this is the first report on identification of disease response gene from peanut using positional cloning strategy, suggesting that combination of MutMap and BSR was an effective way for gene identification from peanut mutants.

2.31 Rapid phenotyping and genotyping tools improving selection for resistance to web blotch (*Didymella arachidicola*) in peanuts (*Arachis hypogaea* L.)

S Wood[1*], G Wright[2], M Dieters[3], M Pandey[4], G Ash[1]

[1] Centre for Crop Health, University of Southern Queensland, Toowoomba, QLD, Australia.
[2] Peanut Company of Australia, Kingaroy, Australia.
[3] School of Agriculture and Food Sciences, University of Queensland, Brisbane, Australia.
[4] International Crops Research Institute for the Semi-arid Tropics, Patancheru, India.

***Author for correspondence: shona.wood@usq.edu.au**

The fungal foliar leaf pathogen, web blotch (*Didymella arachidicola*), is found in most peanut producing regions around the world, and is capable of inducing premature defoliation and yield reductions of up to 50%. There is a lack of molecular knowledge of the pathogen itself as well as peanut's genetic mechanisms of resistance. A barrier to identifying genetic resistance in Australian peanuts is that disease epidemics in the field occur intermittently making field screenings for resistance difficult. The first step in identifying genetic resistance was to develop a rapid and reliable glasshouse screening method capable of distinguishing between resistant and susceptible genotypes. A recombinant inbred line (RIL) population derived from a cross of a resistant (Sutherland) and susceptible type (Middleton) was phenotyped under field and glasshouse conditions, and then genotyped using the 58K Axiom_Arachis SNP array. The aim of this study was to identify quantitative trait locus (QTLs) controlling D. arachidicola resistance. To identify genetic diversity within the pathogen over 200 isolates were collected from the South Burnett in Australia in the 2018/19 growing season. Loci investigated for genetic diversity are the nuclear ribosomal internal transcribed spacers (ITS), partial 28S ribosomal RNA gene (LSU), partial beta-tubulin gene (b-tub), and the partial RNA polymerase II second largest subunit (RPB2). So far no diversity has been identified within the Australian populations. Outcomes from this research will include development of molecular markers to assist in early generation selection for web blotch resistance to assist breeders with more efficient selection methods.

2.32 Comparative transcriptome analysis of anthocyanin synthesis in black and pink peanut testa (*Arachis hypogaea* L.)

Lin Zhu[1,2], Chaunzhi Zhao[1], Ke Li[1], Caili Shang[1,2], Lei Hou[1], Shuzhen Zhao[1], Shoujin Fan[2], Jing Shi[2], Han Xia [1,2*], Xingjun Wang [1,2*]

[1]Biotechnology Research Center, Shandong Academy Agricultural Sciences, Ji'nan, China;
[2]College of Life Sciences, Shandong normal University, Ji'nan, China.

***Author for correspondence: coldxia@126.com, xingjunw@hotmail.com.**

In recent years, black testa peanut (*Arachis hypogaea* L.) has been favored because of its nutritional value and health function. To explore the genetic basis of peanut testa color, high-throughput sequencing technology was used to sequence the transcriptome of black testa peanut 'ZH9' and pink testa peanut 'ZH8'. Over 18 million high-quality reads were assembled into 49,404-52,578 unigenes for these two cultivars using a combined assembly strategy. Totally, 4,122 differentially expressed genes (DEGs) were identified between ZH8 and ZH9, among which 1317 (32%) were up-regulated and 2805 (68%) were down-regulated. KEGG analysis showed that the pathways of anthocyanin biosynthesis, isoflavonoid biosynthesis, flavone and flavonol biosynthesis and phenylpropanoid biosynthesis were in the top 20 differentially expressed genes enriched pathways. Further analysis showed that the formation of the black color of ZH9 testa was mainly due to the reduction of lignin biosynthesis. And more substrate flow to anthocyanin biosynthesis. The up-regulation of all unigenes associated with DFR, a key enzyme determining flavonoid synthesis or anthocyanin synthesis in flavonoid metabolic pathway, is also a strategy for increasing dihydroflavonol, a substrate for anthocyanin and flavonol biosynthesis. In addition, we identified three up-regulated R2R3MYB transcription factors associated with anthocyanin biosynthesis in ZH9. Finally, we verified the expressions of 15 unigenes that encode key enzymes and transcription factors by quantitative real-time PCR (qRT-PCR).

2.33 Genome-wide analysis of *WRI1* gene family and their expression profiles in peanut

Jinbo Sun[1,2#], Suhua Shi[1,2], Fengli Li[1,3], Li Yang[1,2], Guanghui Li[1], Aiqin Li[1], Xingjun Wang[1,2,3*] and Shuzhen Zhao[1,2*].

[1]Biotechnology Research Center, Shandong Academy of Agricultural Sciences; Shandong Provincial Key Laboratory of Crop Genetic Improvement, Ecology and Physiology, Jinan 250100, PR China.
[2] Life Science College, Shandong Normal University, Jinan 250014, PR China.
[3] Life Science College, Shandong University, Jinan 250100, PR China.

***Author for correspondence:Xingjunw@hotmail.com; zhaoshuzhen51@126.com**

Peanut (*Arachis hypogaea* L.) is an importance crop worldwide due to its high contents of oil and protein. The WRINKLED1 (WRI1) transcription factor is vital for the transcriptional control of plant oil biosynthetic pathways. However, Genome-wide systematic investigation and analyses of the WRI1 gene family in peanut are lacking in spite of the availability of the peanut genome sequence. In this study,20 WRI1 transcription factors were identified from the reference genome of wild-type diploid peanut and cultivated tetraploid peanut. The results showed that the 20 WRI1 were all hydrophilic proteins, located in the nucleus, except for Aradu.M2I8I.1 and Araip.RB7C2.1. The secondary structure was mainly composed of random curl and followed by α-helix. The structures of 20 WRI1 genes contained 5-8 introns. Phylogenetic analysis showed that peanut WRI1 genes had a close relationship with WRI1 members of other species. Transcriptome data indicated that WRI1 expression was higher in seeds than other tissues, and qRT-PCR results further showed that WRI1 expression gradually increased with the level of seed maturity. This genome-wide identification, characterization and expression analysis of WRI1 genes in peanut genomes provides insights into the function of WRI1 genes during seed development.

2.34 Decreasing content of very long chain fatty acids in peanut

D Huai[1], X Xue[1], J Li[1], L Yan[1], Y Chen[1], X Wang[1], Y Kang[1], Z Wang[1], N Liu[1], H Jiang[1], Y Lei[1] & B Liao[1]*.

[1] Key Laboratory of Biology and Genetic Improvement of Oil Crops, Ministry of Agriculture and Rural Affairs, Oil Crops Research Institute of Chinese Academy of Agricultural Sciences, Wuhan, China

***Author for correspondence: lboshou@hotmail.com**

Peanut (*Arachis hypogaea* L.) is an important oilseed crop worldwide. Fatty acid composition is the main factor determining the nutritional value and utilization purpose of vegetable oil. Compared to common edible vegetable oils, peanut oil contains higher content of saturated fatty acid (SFA) (18%-23%), approximately half of which were very long chain fatty acids (VLCFAs). Even in high oleate (HO) peanut, high content of VLCFA (totally up to 8%) is still the main defect, because most of them are SFAs which more prone to promote atherogenesis and increase inflammation in adipose tissue. To decrease the VLCFA content, we crossed a peanut germplasm line C-140 with low content of VLCFA (<5%) with a HO cultivar Jihua 16 (7%-8%), and a population consisting 220 recombinant inbred lines (RILs) was developed. From the progenies, thirteen lines with high oleic acid content (>80%) and low VLCFA content (<5%) were obtained, the total SFA contents of which were reduced to nearly 10%. To identify the genomic regions for controlling VLCFA content, QTL-seq was applied. A total of 257.21 Gb was generated from the parental and bulked lines. SNP index analysis revealed that only one candidate genomic region on chromosome B04 was associated with regulation of VLCFA content. This study was the first step toward understanding of the biosynthesis of VLCFA in peanut, and supplied valuable information for improving quality of peanut.

2.35 Genome-wide association studies of production and quality traits in cultivated peanut (*Arachis hypogaea* L.)

Xiaojing Zhou, Jiaojiao Zhao, Haiwen Chen, Zhihui Wang,Xiaoping Ren, Li Huang, Huaiyong Luo, Yuning Chen,Nian Liu,Weigang Chen, Xiaomeng Xue, Yong Lei, Boshou Liao, Liying Yan, Huifang Jiang*

Oil Crops Research Institute of the Chinese Academy of Agricultural Sciences, Key Laboratory of Biology and Genetic Improvement of Oil Crops,Ministry of Agriculture,Wuhan, 430062, China

***Author for correspondence:peanutlab@oilcrops.cn**

Cultivated peanut (*Arachis hypogaea* L.), is an excellent important oilseed crop worldwide, but the genetic basis of the yield and quality is unclear. Here we have identified 105,768 single nucleotide polymorphisms (SNPs) of the genomic variation by sequencing 250 diverse peanut varieties of Chinese peanut mini-core collection. We performed genome-wide association studies (GWAS) for 20 traits in four environments and identify 36~98 associated loci. Of these, 49 alleles were repeatedly detected in at least two environments, and 27 alleles were commonly detected to be associated with multiple traits. Examination of the major and repeated loci identifies 90 putative candidate genes, including genes related to fatty acid biosynthesis and yield. Notably, the previously uncharacterized loci on chromosome A06 and A02 was simultaneously and repeatedly associated with seven pod and seed related traits in multiple environments with major phenotypic variance (19.4-36.27% for A06; 17.83-29.55 for A02). One putative candidate genes on chromosome A06 related to cell cycle in the candidate genomic region had amino acid change in the coding region. The allele-specific markers were developed and demonstrated that the marker was closely linked with pod/seed related traits in diverse varieties. This study provides a fundamental resource for peanut genetics research and breeding.

2.36 Genome-wide expression quantitative trait loci analysis in a recombinant inbred line population for trait dissection in peanut

Li Huang[1,2], Xia Liu[3], Manish K Pandey[4], Xiaoping Ren[1], Haiwen Chen[1], Xiaomeng Xue[1], Nian Liu[1], Dongxin Huai[1], Yuning Chen[1], Xiaojing Zhou[1], Huaiyong Luo[1], Weigang Chen[1], Yong Lei[1], Kede Liu[2], Yingjie Xiao[2], Rajeev K Varshney[4], Boshou Liao[1], Huifang Jiang[1]*.

[1]Key Laboratory of Biology and Genetic Improvement of Oil Crops, Ministry of Agriculture, Oil Crops Research Institute of the Chinese Academy of Agricultural Sciences, Wuhan 430062, China.
[2]National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan 430070, China.
[3]Novogene Bioinformatics Technology Co., Ltd, Beijing 100083, China.
[4]Center of Excellence in Genomics & Systems Biology, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad 502324, India.

***Author for correspondence: peanutlab@oilcrops.cn**

The transcriptome connects genome to the gene function and ultimate phenome in biology. So far transcriptomic approach was not used in peanut for performing trait mapping in bi-parental populations. In this research, we sequenced the whole-transcriptome in immature seeds in a peanut recombinant inbred line (RIL) population and explored thoroughly the landscape of transcriptomic variations and its genetic basis. The comprehensive analysis identified total 49,691 genes in RIL population, of which 92 genes followed a paramutation-like expression pattern. Expression quantitative trait loci (eQTL) analysis identified 1,207 local eQTLs and 15,837 distant eQTLs contributing to the whole-genome transcriptomic variation in peanut. There were 94 eQTL hotspot regions detected across the genome with the dominance of distant eQTL. By integrating transcriptomic profile and annotation analyses, we unveiled a putative candidate gene and developed a linked marker InDel02 underlying a major QTL responsible for purple testa color in peanut. Our result provided a first understanding of genetic basis of whole transcriptomic variation in peanut and illustrates the potential of the transcriptome-aid approach in dissecting important traits in non-model plants.

2.37 Identification of QTLs associated with shelling percentage in cultivated peanut

YN Chen, WT Li, L Huang, HY Luo, JB Guo, XJ Zhou, LY Yan, N Liu, WG Chen, LY Yan ,Y Lei, BS Liao, DX Huai, HF Jiang*

Oil Crop Research Institute of Chinese Academy of Agricultural Sciences, Wuhan 430062, Hubei, China

***Author for correspondence: peanutlab@oilcrops.cn**

Shelling percentage (SP) is a major objective in peanut breeding. In this study, a mapping population (derived from Xuhua 13 × Zhonghua 6) consisting of 187 recombinant inbred lines (RILs) was used to map QTLs controlling SP. Even the parents showed little difference in SP with the value of 75.96 % and 76.63 %, the RILs showed wider variance of SP ranged from 59.89% to 82.44% across four environments. The unconditional QTL analysis detected 9 QTLs with 4.58%-28.47% phenotypic variation explained (PVE) on chromosomes A07, A08, A09 and B05. QTLs *qSPA07.1*, *qSPA07.2*, *qSPA07.3* and *qSPA09.1* were identified as major and stable QTLs with more than 10% PVE across four environments. Conditional QTL analysis further indicated that SP controlled by *qSPA07.1*, *qSPA07.2* and *qSPA07.3* was affected by pod length (PL), pod width (PW) and hundred-pod weight (100PW), while *qSPA09.1* could be detected both by conditional and unconditional analysis. The potential utilization of QTLs for SP improvement in peanut breeding was also evaluated. The present findings preliminarily shed light on the genetic basis of SP. The major QTL *qSPA09.1* for SP could be used as candidate for further positional cloning.

2.38 High-resolution mapping of a major and consensus quantitative trait locus for oil content to a ~0.8 Mb region on chromosome A08 in peanut (*Arachis hypogaea* L.)

Nian Liu, Jianbin Guo, Xiaojing Zhou, Bei Wu, Li Huang, Huaiyong Luo, Yuning Chen, Weigang Chen, Yong Lei, Yi Huang, Boshou Liao, Huifang Jiang*

Key Laboratory of Biology and Genetic Improvement of Oil Crops, Ministry of Agriculture, Oil Crops Research Institute of the Chinese Academy of Agricultural Sciences, Wuhan 430062, P.R. China.

***Author for correspondence: peanutlab@oilcrops.cn**

Enhancing oil content is an important breeding objective in peanut. High-resolution mapping of quantitative trait loci (QTLs) with linked markers could facilitate marker-assisted selection (MAS) in breeding for target traits. In the present study, a recombined inbred line (RIL) population (Xuhua 13 × Zhonghua 6) was used to construct a genetic map based on double-digest restriction-site associated DNA sequencing (ddRAD-seq). The resulting high-density genetic map (HDGM) contained 2595 loci, and spanned a length of 2465.62 cM, with an average distance of 0.95 cM/locus. Seven QTLs for oil content were identified on five linkage groups (LGs), including the major and stable QTL qOCA08.1 on chromosome A08 with 10.14-27.19% phenotypic variation explained (PVE). The physical interval of qOCA08.1 was further delimited to ~ 0.8 Mb genomic region where two genes affecting oil synthesis had been annotated. The marker SNPOCA08 was developed targeting the SNP loci associated with oil content and validated in peanut cultivars with diverse oil contents. The major and stable QTL identified in the present study could be further dissected for gene discovery. Furthermore, the tightly linked marker for oil content would be useful in marker-assisted breeding in peanut.

2.39 High density genetic mapping and whole genome re-sequencing identified genomic regions and candidate genes for seed weight in groundnut

Sunil S. Gangurde, Murali T. Variath, Aamir W Khan, Surendra S. Manohar, Rajeev K. Varshney, Pasupuleti Janila*, Manish K. Pandey*

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India

***Author for correspondence: m.pandey@cgiar.org; p.janila@cgiar.org**

Groundnut oil seed ranks fourth in the world's total oil seed production after soybeans, rapeseed, and sunflower. Big seed size attracts consumer's attention and fetches high market price. The main objective of this research was to study the genetic control of hundred seed weight (HSW) in groundnut and to identify the genes responsible for big seeds. In this context, a RIL population (Chico × ICGV 02251) was developed and phenotyped for two seasons for HSW and genotyped using 58K SNP array. A high density genetic map was constructed with 4199 SNP loci spanning a distance of 2708 cM. QTL analysis using phenotypic data and genotypic data identified 16 main effect QTLs for HSW. *BIG SEED* locus and *spermidine synthase* genes were identified in QTL region on chromosome B09 and A09. Whole genome re-sequencing (WGS) was performed for high HSW parent ICGV 02251 (28.44 GB), high seed weight bulk (32.61 GB) and low seed weight bulk (31.43 GB). The QTL-Seq analysis identified a QTL region on B09 delimited to 930 Kb on chromosome B09 harboring 30 non-synonymous SNPs with Δ-SNP index -1. Our findings showed that BIG SEED and spermidine synthase are negative regulators of high seed weight as presence of these genes showed reduction in seed size of extreme RILs. Additionally, the QTL-Seq also identified the associated genomic regions on chromosomes B06 and B08 harboring genes such as zinc finger proteins, ethylene responsive factors, MYB transcription factors. Further, the markers will be developed for HSW for improving the seed weight in groundnut.

2.40 RNA-Seq to dissect candidate genes associated with groundnut stem-rot disease interaction

Tejas C. Bosamia[1], Suhail Ahmad[1], Gyan P. Mishra[1,2], Sneha M Dodia[1], Binal Joshi[1], Polavakkalipalayam P Thirumalaisamy[1], Narendra Kumar[1], Arulthambi L. Rathnakumar[1], Jentilal R. Dobaria[1], Chandramohan Sangh[1], Abhay Kumar[1,3], Radhakrishnan Thankappan[1*]

[1]ICAR-Directorate of Groundnut Research (ICAR-DGR), Junagadh, 362001, India.
[2]Indian Agricultural Research Institute (IARI), New Delhi, 110012, India.
[3]ICAR-National Research Centre on Litchi, Muzaffarpur, 842002, India.

***Author for correspondence: radhakrishnan.nrcg@gmail.com**

Stem rot, caused by *Sclerotium rolfsii,* cause yield loss up to 40%, especially under irrigated conditions. We have RNA-Seq approach to reveal the complex host-pathogen interaction. The illumina 2500 transcriptome sequencing of resistant (NRCG-CS85) and susceptible (TG37A) genotypes under control and infected conditions have been performed and ~290 million reads have been generated. 251 million (92.22%) high-quality reads were aligned to wild progenitors of peanut the *Arachis duranensis* and *A. ipaensis* genomes. Among the total differential expressed genes (DEGs), 48.6% of genes are commonly regulated, while 21.8% and 29.6% as uniquely regulated from *A. duranensis* and *A. ipaensis* genomes, respectively. Several DEGs were annotated as receptor-like kinases, transcription factors (TFs) like WRKY, Zinc finger protein and C2-H2 zinc finger and jasmonic acid (JA) pathway enzymes showed higher expression upon infection in resistant genotype. Our results revealed the perception of the pathogen by receptor-like kinases playing a very important role in the downstream resistance mechanism and activation of JA mediated defence pathway. The transcripts of WRKY transcription factor, zinc finger protein, lipoxygenase, terpene synthase, CAP superfamily protein (PR-1), and endochitinases genes were highly up-regulated upon pathogen infection and play a crucial role in imparting the stem-rot resistance. Higher expression of WRKY transcripts upon pathogen perception might have induced the systemic acquired resistance. The quantitative real-time PCR of 13 transcripts was also carried out. The study suggested PAMP- triggered immunity as a probable resistance mechanism, while JA derived resistance pathway as a possible defence mechanism in the peanut.

3.1 Groundnut rosette disease donors identified in Uganda

Okello D. K[1*], Ochuga, S.E., Owiny, R[1]., Ugen, M. A[1]., Achola, E[2], Odong, T. L[2]., Okori, P[3]., and Deom, C.M[4]

[1]National Semi-Arid Research Resources Institute (NaSARRI), P. O Private Bag Soroti, Uganda.
[2]Makerere University, P. O. Box, 7062, Kampala, Uganda
[3]ICRISAT Malawi, Chitedze Research Station, P. O. Box 1096. Lilongwe Malawi
[4]Department of Pathology at the University of Georgia, Miller Plant Sciences Building, Athens 30602.

***Author for correspondence: kod143@gmail.com**

Groundnut rosette disease (GRD), first reported in 1907 from Tanzania, is the most devastating disease of groundnut in sub-Saharan Africa including its offshore islands where it is endemic and responsible for annual groundnut yield loss worth over US$150 million. It is caused by a complex of three agents: Groundnut rosette assistor virus (GRAV), Groundnut rosette virus (GRV), and the satellite RNA (sat-RNA) of GRV.

Varieties resistant to GRD provide the most economical and practical solution to control GRD in the field, and thus, substantial efforts have been made to identify durable GRD resistant sources. Since the identification of resistance to GRD in West Africa germplasm breeding for host plant resistance by ICRISAT and partners have largely been using few donor parents with good agronomic attributes thereby narrowing germplasm base in the process. It is important for groundnut breeders to have access to a diverse GRD donor sources in developing improved varieties.

This study identified two additional GRD donors (ICGV-SM 91707 and ICGV-SM 89751) and validated their donor potential using a common GRD susceptible recurrent parent CG7. Pedigree and single seed descent were used to advance selected plants towards uniformity. Nine advanced lines each were selected both for GRD and Late leaf spot resistances (1-3 rating), high yield, soft shell, confectionery grade seeds, attractive plain tan and red seedcoat phenotypes, stay green and drought tolerance. They are in National performance trials for identification of superior wide adapted lines for possible release as varieties and breeding lines.

Key words: Peanut, Groundnut rosette disease, donor, sub-Saharan Africa

3.2 Evaluation of *A. ipaënsis* x *A. correntina* wild-peanut derived materials for resistance to fall armyworm

CM Levinson[1], Y Chu[1], X Ni[2] & P Ozias-Akins[1]

[1]Department of Horticulture and Institute of Plant Breeding, Genetics & Genomics, University of Georgia, Tifton, GA 31793.
[2]USDA-ARS, Crop Genetics and Breeding Research Unit,Tifton, GA, 31793.

***Author for correspondence: chandler.maddox@uga.edu**

Fall armyworm (FAW), Spodoptera frugiperda, is an economically devastating, emerging pest in Sub-Saharan Africa. FAW has rapidly spread throughout Africa after it was first reported there in 2016. This pest feeds on more than 80 plant species, including maize, peanut, and sorghum, and it threatens the food security of millions of people in Sub-Saharan Africa who rely on these crops. An integrated pest management strategy including resistant crops is needed to control FAW, since FAW populations developing insecticide resistance have been reported. For cultivated peanut, breeding host plant resistance to FAW is limited by the narrow genetic base of this species. Lynch et al. (1981) identified the wild peanut relative Arachis correntina as a donor source of FAW resistance. In this study, we tested diploid A. correntina accession 9530 and accession 9548, synthetic tetraploids [*A. ipaënsis* KG37006 x *A. correntina* 9530]4x, and F2 plants [*A. hypogaea* x (*A. ipaënsis* KG30076 x *A. correntina* 9530)4x] for FAW resistance to identify priority materials for our breeding program. Replicated thrice (n = 300), 10 FAW larvae were reared on the listed materials and an A. hypogaea susceptible control. We measured survival rate, 7- and 14-day larvae weight, days taken to develop from first-instar to pupa, and moth hatch rate. We identified all synthetic tetraploids and two of the three F2 plants as sources of FAW resistance for our breeding program. This resistance was donated from the *A. ipaënsis* source, not *A. correntina*, as expected.

3.3 Mobilizing genetic diversity for strengthening peanut breeding programs in Africa

D Fonceka[1,2*], A Sambou[1], T Hodo-Abalo[1], D Okello[3], JF Rami[2], S Leal-Bertioli[4], D Bertioli[5], P Ozias-Akins[6].

[1]Centre d'Etude Régional pour l'Amélioration de l'Adaptation à la Sécheresse (CERAAS), BP3320 Thiès, Senegal.
[2]CIRAD UMR AGAP, TA A-108/03 Avenue d'Agropolis, Montpellier Cedex 5, France.
[3]National Semi-Arid Resources Research Institute (NaSARRI), P.O Box 56, Soroti, Uganda.
[4]University of Georgia – Department of Plant Pathology / CAGT. 111 Riverbend Road, Athens, GA.
[5]University of Georgia - Crop & Soil Sciences Department/CAGT. 111 Riverbend Road, Athens, GA.
[6]Department of Horticulture, The University of Georgia Tifton Campus, Tifton, GA.

***Author for correspondence: daniel.fonceka@cirad.fr**

The aim of breeding is to combine as much as possible desirable alleles for traits of interest in order to produce new varieties that meet the needs of end-users. Thus, genetic diversity is the foundation of any breeding program. Peanut genetic diversity is low and breeding programs have until recently exploited a limited portion of the existing diversity. In an international effort involving several NARS in Africa, UGA, ICRISAT and CIRAD, a two-pronged strategy is being implemented for increasing diversity used by breeders. On one side, synthetic allotetraploids that combines A and B genomes of diverse wild diploid species are developed and used for moving genes from the wild species to the cultivated species. Wild alleles conferring resistance to diseases and yield have been mapped, and are currently being deployed in elite cultivars. On the other side, hundreds of accessions hold by NARS breeders and thousands of US germplasms, including African germplasm maintained at USDA, have been assembled and genotyped using the V2 Axiom-Arachis. A core set of lines will be defined from the genotyping work and phenotyped in eight countries in West and East Africa. It will provide comprehensive analysis of the diversity used by breeders, offer opportunity to breeders to accessing wider genetic variation, offer the opportunity to map genes of interest via association studies.

3.4 Identification and characterization of high oleic acid peanut mutant tolerance to imidazolinone herbicide

SL Chen*, YR Li, J Wang, ZS Cheng, YH Song & YJ Liu.

Hebei Provincial Laboratory of Crop Genetics and Breeding, Cereal and Oil Crops Institute, Hebei Academy of Agricultural and Forestry Science, China, Shijiazhuang 050031.

***Author for correspondence: CHSL99@163.com**

Weed management is essential for peanut production. New sources of tolerance to herbicides are needed for peanut so that applied herbicides can be rotated or combined to prevent the evolution of resistant weeds. There is little information on the molecular mechanisms involved in herbicide tolerance in peanut germplasm. In our study, a single dose screening test was used to identify the sensitivity to imazethapyr in 21 peanut lines. All lines showed significantly different levels of imazethapyr tolerance at ten times the recommended field-use rates. The results indicated that JiC814T was unaffected significantly in plant height and biomass. The inhibition ratio of plant height, fresh weight and dry weight from JiC814T are under 42.7%-74.6%, 30.1%-62.7%, and 41.8%-81.6% comparing to the other 20 lines. Moreover, JiC814T is a novel high oleic acid line with 84.55% oleic acid content, which was screened and isolated from collection of peanut germplasm. Imidazolinone herbicides targeted acetolactate synthase (ALS) genes (AhALS1 and AhALS2), which were isolated from the A and B subgenomes of JiC814T and 20 susceptive lines by homologous strategy. We found that all lines possess identical and sensitive ALS sequences, although AhALS1 has an alanine rather than a serine residue at position 653. We did not observe any sequence polymorphism between the AhALS genes in the resistance or sensitivity lines to the imazethapyr herbicide. This result indicated that the ALS gene per se is not directly responsible for the imidazolinone herbicide tolerance observed in our peanut resources. Our discovery of this peanut germplasm made possible for further study of the novel herbicide-tolerant peanut genes and varieties.

3.5 Gene action and prediction of genotypes performance for late leaf spot resistance and yield related traits improvement in groundnut

Essohouna Modom Banla[1*], Daniel Kwadjo Dzidzienyo[2], Samuel Kwame Offei[2], Pangirayi Tongoona[2] and Haile Desmae[3]

[1]Togolese Research institute of Agriculture (ITRA), Lomé, Togo;
[2]West Africa Centre for Crop Improvement (WACCI)-University of Ghana (UG), Accra, Ghana;
[3]International Crops Research Institute for the Semi-Arid tropic (ICRISAT-WCA), Bamako, Mali

***Author for correspondence: ebanla@wacci.ug.edu.gh**

Nature of gene action involved in the expression of a trait, is one of the considerations among others that the breeder must look at when starting a breeding program. In addition, identification of best performing lines to use in future crosses is a prerequisite in starting improved genotypes development. The objectives of the present study were to determine the type of gene action conditioning late leaf spot (LLS) resistance and yield-related traits and identify parents with a good combining ability to initiate groundnut breeding program in Togo. Genetic mechanism analysis for LLS using sixteen F_2 progenies from full factorial design crosses (8 parents) indicated additive gene and maternal effects for LLS resistance with 48,3 % and 3.86 % of the phenotypic variance explained, respectively. Non-additive genetic variance was close to zero for LLS resistance. In contrast to LLS resistance, non-additive gene effects played a greater role than additive effects for pod weight per plant (21.79 % phenotypic variance explained). For the other yield-related traits, additive genetic variance was more important than the other variance components. Lines43AH and ICG 7878 with the highest general combining ability could be considered as the best parents for LLS resistant lines development. For yield improvement lines 12CS_22 and 12CS_36 from Senegal appeared to be the best parents.

3.6 Molecular and phenotypic diversity of groundnut cultivars from Togo

Essohouna Modom Banla[1*], Daniel Kwadjo Dzidzienyo[2], Mouhamadou Moussa Diangar[3], IfieElohor Beatrice[2], Samuel Kwame Offei[2], Pangirayi Tongoona[2] and Haile Desmae[4]

[1]Togolese Research institute of Agriculture (ITRA), Lomé, Togo;
[2]West Africa Centre for Crop Improvement (WACCI)-University of Ghana (UG), Accra, Ghana;
[3]Centre d'Etude Regional pour l'Amelioration de l'Adaptation a la Secheresse (CERAAS);
[4]International Crops Research Institute for the Semi-Arid tropic (ICRISAT-WCA), Bamako, Mali

***Author for correspondence: ebanla@wacci.ug.edu.gh**

Morphological and molecular diversity analyses are very useful in identifying potential parent genotypes in breeding program as genes discovered in diverse germplasm resources can be introgressed into farmers' preferred varieties for the improvement of traits of interest. In the present study, diversity assessment of 94 lines from Togo, Senegal and ICRISAT, underscored quantitative traits such as hundred seed weight, days to maturity, and Late leaf spot incidence, as the main traits contributing to the divergence based on principal component analysis. The most diverse qualitative traits based on Simpson index were primary seed colour (0.75), stem pigmentation (0.60), and growth habit (0.59). Correlation analysis and path analysis showed that the number of pods per plant was the main yield-related trait positively affecting yield (PC=0.84; p=0.01). Overall, SNP markers revealed high genetic variability in the genotypes and the percentage of heterozygous genotypes varied from 0 to 50% for all loci. AMOVA revealed that only 1.1% of the total molecular variance accounted for geographical contribution to the diversity. Cluster analysis delineated three clusters harbouring useful alleles and interesting phenotypic features such as late leaf spot resistance, a high number of pods per plant and early maturity. Structure co-analysis of phenotypic and SNP data showed that differences observed at the phenotypic level are underlined by genotypic differences. The phenotypic and genotypic diversity revealed appreciable diversity that could be exploited for the identification of parents with preferred traits for use in the breeding program in Togo.

3.7 Genetic diversity of historical and contemporary African germplasm lines

Peggy Ozias-Akins[1,2*], Ye Chu[1], Josh Clevenger[3], Jean-Francois Rami[4], Shyam Tallury[5], David Okello[6], and Daniel Fonceka[7]

[1]Horticulture Department, University of Georgia, Tifton, GA, USA;
[2]Institute of Plant Breeding, Genetics and Genomics, University of Georgia, Athens, GA, USA; [3]Mars-Wrigley Confectionery, USA;
[4]CIRAD, Montpellier, France;
[5]USDA-ARS-PGRCU, Griffin, GA, USA;
[6]NaSARRI, Sotori, Uganda;
[7]ISRA-CERAAS, Thies, Senegal

***Author for correspondence: pozias@uga.edu**

Peanut yield in Africa ranks the lowest in the world. Improving yield potential of adapted peanut cultivars in Africa would benefit from a coordinated breeding strategy to pyramid desirable traits for resistance to biotic and abiotic stresses. However, there has been insufficient genetic and phenotypic characterization of African peanut lines to guide breeders in parental selection. In order to more comprehensively explore genetic resources adapted to Africa, a historical pool consisting of ~2,800 US germplasm lines collected from Africa starting in the 1940s and a contemporary pool comprising 1,050 cultivars and germplasm lines contributed by current African peanut breeding programs were curated. Single plant advancement of the historical pool was performed in Georgia, USA and the contemporary pool was advanced in Senegal, Africa. Progenies from each plant were saved for seed increase and distribution for phenotyping. DNA from the same plant of each line was genotyped by the Axiom_Arachis2 SNP array. These SNP data were used to explore evolutionary relationships of the two sets of African germplasm collections. Lines representative of each clade were selected to comprise a set of a few hundred lines manageable for an extensive phenotyping effort. Genotyping and phenotyping data collected from the African adapted lines will become a useful resource for African breeding programs to improve locally adapted cultivars.

3.8 Screening of drought tolerant recombinant inbred lines derived from the cross NRCG 12568 × NRCG 12326 in groundnut using different statistical procedures

Bharath Kumar P Jambagi[1*] and D. L. Savithramma[2]

[1] Department of Genetics and Plant Breeding, University of Agricultural Sciences (UAS), GKVK, Bengaluru-560065.
[2] University of Agricultural Sciences, GKVK, Bengaluru-560065.

***Author for correspondence: bharathjambagi@gmail.com**

In order to study the response to drought stress in groundnut, a mapping population of 147 recombinant inbred lines (RILs) resulting from the cross of NRCG 12568 × NRCG 12326 were evaluated under four water regimes viz., well-watered (WW), water stress-I (WS-I) - withholding irrigation from 30-45 DAS (flowering and peg initiation stage), water stress-II (WS-II) -withholding irrigation from 45-65 DAS (peg penetration and pod development stage), water stress-III (WS-III) -withholding irrigation from 65-85 DAS (pod development stage) for drought tolerance at UAS, Bengaluru, India during summer 2017 and 2018 in augmented design along with parents and checks. The drought tolerance was quantified by 15 drought tolerant indices for effective discrimination and selection of moisture stress tolerant RILs. Based on the criteria of both correlation and discriminating ability of the indices, only four indices namely stress tolerant index (STI), mean productivity (MP), harmonic mean productivity (HMP) and geometric mean productivity (GMP) showed highly significant and positive correlation with pod yield under well-watered and water stress conditions. Therefore, these indices aid successfully as selection criteria for screening of genotypes for performance under various soil moisture levels. Principal component analysis indicated that first and second components justified 91.98%, 92.19% and 89.23% of variations among drought tolerance criteria in WS-I, WS-II and WS-III respectively. The results of PCA were interpreted through biplot analysis and revealed STI, GMP, MP, K1STI, ATI (abiotic tolerant index) and HMP are effective for identifying drought tolerant genotypes with high pod yield. Based on rank sum method, involving the four indices distinguished RIL -145 and RIL-25 in WS-I, RIL-126, RIL-249 and RIL-133 genotypes in WS-II whereas, in WS-III conditions RIL-133, RIL-541 and RIL-126 were the most drought tolerant RILs. In consideration with all different statistical procedures for screening drought tolerant lines; among all genotypes, RIL-126 and RIL-133 were identified as the genotype with high and stable yield under moisture stress conditions in comparison of standard check GKVK 5. The identified lines can be evaluated in varied rainfed environments to exploit their drought tolerance and yield potentials. The validated lines can be utilized as peanut cultivars for rainfed or drought prone environments under changing climate.

3.9 Useful Traits in the US Peanut Germplasm Collection

S. P. Tallury [1*], B. D. Tonnis [1], M. L. Wang [1], M. B. Mobley [2] and M. L. Harrison [1]

[1] USDA-ARS, PGRCU, Griffin, GA 30223, USA.
[2] Univ. of Georgia-Griffin, GA 30223, USA.

***Author for correspondence: Shyam.Tallury@usda.gov**

The United States peanut germplasm collection is maintained by the USDA-ARS managed National Plant Germplasm System (NPGS) at the Plant Genetic Resources Conservation Unit (PGRCU) in Griffin, Georgia. Currently, there are 9275 accessions of Arachis hypogaea and 558 accessions of wild Arachis species in the collection. Of this, 94 % of *A. hypogaea* and 87 % of wild Arachis species are available for distribution.The germplasm collection is invaluable for researchers to improve *A. hypogaea* forcommercial use. It has been well curated to maintain original genetic diversity with high levels of seed viability. Over many years and locations, the collection has been well characterized for several useful traits for peanut cultivar development. A summary of the characterization data suggested that there are about 702 early maturing (<125 days) accessions, 856 accessions which are immune or highly resistant to the leafspots and 1009 accessions with field tolerance to TSWV. The 100 seed weight among the *A. hypogaea* accessions ranged from 22 g to 160 g (mean 50 g) and total seed oil varied from 37 % to 59 % with a mean of 49 %. Fatty acid profiles indicated three new high oleic acid mutants. Many of these traits are of economic value for peanut industry. Accessions containing some of the above useful traits can be used as parental materials to develop new peanut cultivars or improve the existing ones.

3.10 Evaluation of the Argentine peanut core collection using a molecular marker associated with resistance to Sclerotinia minor Jagger

K.D. Chamberlin*, Baldessari, J., Moreno, M.V. and Mamani, E.M.C.

USDA-ARS, Wheat, Peanut and other Field Crops Research Unit, 1301 N. Western, Stillwater, OK, USA, 74075; 2 INTA, Ruta Nac. 9, Km. 636, (5988) Manfredi, Argentina.

***Author for correspondence: chamberlin@ars.usda.gov**

Sclerotinia minor Jagger (S. minor), the causal agent of Sclerotinia blight, Sclerotinia blight was first observed on peanut in Argentina in 1922 and by 1960 reports of S. minor causing root and pod rot on peanut were published. Sclerotinia blight is now present in most peanut producing countries of the world. Host plant resistance would provide the most effective solution to managing Sclerotinia blight, limited sources of resistance to the disease are available for use in breeding programs. This objective of this study was to characterize the Argentine peanut core collection with a molecular marker associated with Sclerotinia blight resistance. A total of 194 different genotypes were analyzed using the marker, including154 core collection accessions and various cultivars and resistant and susceptible controls of which 25 had been extensively phenotyped for resistance. Marker scoring among the phenotyped entries agreed with demonstrated resistance or susceptibility at a rate of 82%. Marker scoring was used to predict the reaction of the un-phenotyped entries to infection by S. minor. These results can be used to identify potentially resistant entries and improve the efficiency of phenotypic evaluation of the Argentine peanut core collection for resistance to Sclerotinia blight.

3.11 The neotetraploid peanut IpaDur1 provides a model for genetic and genomic studies and increases crop diversity

Leal-Bertioli, S.C.M. [1]*, Suassuna, T.F.[2], Araújo A.C.G.[3], Custódio, A.[3], Shin J.-H.[1,4], Chavarro, M.C.[1], Fonceka, D.[5], Moretzsohn, M.C.[3] & Bertioli, D.J[6]

[1]Institute of Plant Breeding, Genetics, and Genomics, Department of Plant Pathology, University of Georgia, Athens, GA 30602
[2]Embrapa Rice and Beans, Goiania, Goias, Brazil.
[3]Embrapa Genetic Resources and Biotechnology, Brasilia, Brazil.
[4]Corporate R&D, LG Chem, Seoul, Republic of Korea.
[5]Centre d'Etude Régional pour l'Amélioration de l'Adaptation à la Sécheresse (CERAAS), BP3320 Thiès, Senegal.
[6]Institute of Plant Breeding, Genetics, and Genomics, Department of Crop and Soil Science, University of Georgia, Athens, GA 30602.

***Author for correspondence: sbertioli@uga.edu**

The genetic bottleneck of polyploid formation can be mitigated by multiple origins, gene flow, and recombination among different lineages. In crop plants with limited origins, efforts to increase genetic diversity have limitations. Here we used lineage recombination to increase genetic diversity in peanut, an allotetraploid of single origin, by crossing with a neotetraploid and selecting improved lines. The new genotype is an attempt to synthesize peanut, using the wild progenitors, *A. ipaensis* and *A. duranensis*. Single backcross progeny from cultivated peanut x wild species-derived allotetraploid cross were studied over successive generations. Using genetic assumptions that encompass segmental allotetraploidy, single nucleotide polymorphisms and whole genome sequence data were used to infer genome structures. Selected lines, despite a high proportion of wild alleles, are agronomically adapted, productive, and with improved disease resistances. Wild alleles mostly substituted homologous segments of the peanut genome, but interesting deviations were observed. Furthermore, some subgenome regions historically lost in cultivated peanut were "recovered" by wild chromosome segments. These processes resulted in lines with new genome structure variations. Genetic diversity was introduced by wild allele introgression, and by introducing new genome structure variations. These results highlight the special possibilities of segmental allotetraploidy to increase genetic diversity in peanut, mirroring what occurs in natural allopolyploids with multiple origins. The proximity of the genome of the two neotetraploid parental species with peanut subgenomes provided an excellent model for genetic, genomic and expression studies and the production of new cultivars.

3.12 Screening of genomic selection training population for ahFAD2A and ahFAD2B mutant alleles responsible for high oleic trait in peanut (*Arachis hypogaea* L.)

Sunil Chaudhari[1], D Khare[2], Sudam C Patil[3], S Sundravadana[4], Murali T Variath[1], Dyaneshwer B Deshmukh[1], Manish K Pandey[1], Surendra S Manohar[1] and P Janila[1*]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad, Telangana, India
[2]Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Jabalpur, India
[3]Regional Oilseeds Research Station, Mahatma Phule Krishi Vidyapeeth (MPKV), Jalgaon, Maharashtra, India
[4]Coconut Research Station, Tamil Nadu Agricultural University (TNAU), Aliyarnagar, Tamil Nadu, India

***Author for correspondence: p.janila@cgiar.org**

Desirable modification of fatty acid profile of vegetable oils is one of the major breeding goals in different oilseed crops. A set of 336 diverse peanut genotypes of genomic selection training population (GSTP) originating from 21 countries were screened for ahFAD2A and ahFAD2B mutant alleles responsible for high oleic trait in peanut. Allele-specific markers were used to detect both the mutant alleles and their wild types. The field evaluation of GSTP was done across four different environments in alpha lattice design during 2015-16. The high-throughput phenotyping for oil, protein and fatty acid profile across the environments was done using Near-Infrared Reflectance Spectroscopy (NIRS). The results revealed 87 (25.6%) genotypes with 1-bp substitution mutation in ahFAD2A gene on A genome while only a single known genotype "SunOleic 95R" had mutation in both alleles along with high oleic acid content (>75%) across the environments. The frequency of ahFAD2A mutant alleles was higher in var hypogaea Virginia runner type (36.4%), followed by var vulgaris (28.9%) whereas genotypes of var peruviana, var fastigiata (Valencia), var aequatoriana and var hirsute had wild type alleles on both the genomes. There was no significant effect of a single mutant allele (ahFAD2A) reported on fatty acid profile in peanut. However, the presence of both the mutant alleles resulted in expression of high oleic trait irrespective of locations.

3.13 Comparative lipidomic analysis of high oleate and normal oleate peanut

D Huai[1], X Xue[1], J Li[1], L Yan[1], Y Chen[1], X Wang[1], Y Kang[1], Z Wang[1], N Liu[1], H Jiang[1], Y Lei[1]*& B Liao[1]*

[1] Key Laboratory of Biology and Genetic Improvement of Oil Crops, Ministry of Agriculture and Rural Affairs, Oil Crops Research Institute of Chinese Academy of Agricultural Sciences, Wuhan, China

***Author for correspondence: lboshou@hotmail.com; leiyong@caas.cn**

High oleate (HO) peanut with enhanced nutritive value and prolonged shelf-life has been increasingly favored by peanut customers and processing enterprises. Due to the mutations in *fatty acid desaturase 2* (*fad2*) genes, the oleic acid content is significantly increased, while the linoleic acid and palmitic acid contents are significantly decreased in triacylglycerols (TAGs) of HO peanut. However, the changes of other lipids are still unknown. In this study, liquid chromatography-mass spectrometry (LC-MS) was used to characterize the free fatty acids, glycerolipids, phospholipids, sphingolipids and glycolipids in HO and normal oleate (NO) peanuts at developing stages. A total of 428 species of lipids were identified in both HO and NO peanuts. With the development of seeds, the number of lipids decreased. Comparing with NO peanut, less species of TAG, diacylglycerol (DAG), monogalactosyl diacylglycerol (MGDG) and digalactosyl diacylglycerol (DGDG) were characterized in HO peanut. The relative abundances of phosphatidylcholine (PC), phosphatidylethanolamine (PE), phosphatidylinositol (PI), sphingomyelin, MGDG, DGDG, DAG and TAG species with oleic acid were detected in HO peanut. Conversely, the content of those lipid species with linoleic acid or linolenic acid were significantly decreased in HO peanut. These findings improved understanding of both HO and NO peanut lipid metabolism, and provided theoretical foundation for further researches of HO peanut.

4.1 Breeding of a new peanut variety Huayu 6801 with high oil content

Yanmao Shi, Mei Yuan*, Yan Ren, Shuangling Li, Liang Yin, Lijun Wu, Hongjun Zhao*.

Shandong Peanut Research Institute Key Laboratory of Peanut Biology and Genetics Breeding, Ministry of Agriculture, Qingdao 266100, China

***Author for correspondence: yuanbeauty@126.com; 13964190239@139.com**

Huayu 6801 was bred from the cross of Luhua 8 × D089. The variety is characterized with high oil content of 58.58 %, high yield, medium maturity, wide adaptability, drought and lodging resistance. In regional test of peanut varieties in Sichuan province, in 2014 and 2015, the average pods yield and average seeds yield were 4635.5 kg/hm^2 and 3591.8 kg/hm^2, respectively, which were 5.36 % and 8.66 % higher than those of the control (Tianfu 14). In national regional test of small-seeded peanut varieties in northern China, the average yield of pods and seeds was 4553.8 kg/hm^2 and 3336.2 kg/hm^2, respectively, which were 12.0 % and 13.07 % higher than those of the control (Huayu 20), respectively. Huayu 6801 was approved by Sichuan Crop Variety Approval Committee in 2017.

4.2 Advances in peanut breeding for resistance tolateleaf spot

Lijun Wu[1], Shuangling Li[1], Suoyi Han[2], Han Xia[3], Yucheng Chi[1], Yan Ren[1], Yanmao Shi[1], Liang Yin[1], Xingjun Wang[3]* & Mei Yuan[1]*

[1]Shandong Peanut Research Institute/Shandong Provincial Key Laboratory of Peanut/Key Laboratory of Peanut Biology and Genetic Improvement, Ministry of Agriculture, Qingdao 266100, China.
[2]Industrial Crops Research Institute, Henan Academy of Agricultural Sciences,Zhengzhou 450002, China.
[3]Biotechnology Research Center, Shandong Academy of Agricultural Sciences, Jinan 250100, China.

***Author for correspondence: yuanbeauty@126.com.**

Late leaf spot (LLS) disease is one of the most important leaf diseases in peanut (*Arachis hypogaea* L.), which could cause substantial yield losses and reduce the fodder and seed quality. Application of resistant varieties is one of the most economical and effective methods for controlling this disease. In this paper, the damage and control ways of LLS in peanut were summarized, the recent research progress on identification of resistance germplasms resources (Including screening of wild germplasms resources and selection & creation of cultivated germplasms), QTLs and molecular markers, resistance inheritance and breeding of LLS resistant varieties were reviewed. Faced with the problems in the cultivation of peanut varieties resistant to LLS, the following suggestions were put forward: (1) Combined with the research results of whole genome sequencing of cultivated and wild peanuts, the key genes of resistance to LLS should be identified and the molecular mechanism should be further studied through comparative genomics; (2) Fully exploring the genetic diversity of peanut germplasms resisted to LLS, combining conventional breeding with molecular marker-assisted selection, aggregating multiple resistance genes and carrying out the cultivation of new varieties of multi-resistant high-quality peanut; (3) Through genetic engineering, interspecific hybrid artificial tetraploid synthesis and other approaches, LLS resistance genes from wild resources will be gradually infiltrated into cultivated species and a large number of cultivation of wild infiltration system will be created. All these will provide technical support for the efficient and smooth development of the genetic breeding of peanut LLS disease, so as to guarantee the sustainable development of peanut industry.

4.3 Breeding of peanut varieties with high oil content by in vitro mutagenesis and screening

Jingshan Wang, Mingxia Zhao, Lixian Qiao, Jiongming Sui, Xia Wang, Guan Li, Shanlin Yu*

College of Agronomy, Qingdao Agricultural University, Dry-land Farming Technology Laboratory, Qingdao 266109, China

***Author for correspondence: yshanlin1956@163.com**

A practical and reliable method for creating new peanut varieties with high oil content was established using in vitro mutagenesis and directional selection of high oil content. Our previous studies found that osmotic pressure (OP) of leaves of peanut plants subjected to drought stress was significantly negatively correlated with oil content of the kernels. Using embryonic leaflets of peanut cultivar Huayu 20 as explant and pingyangmycin (PYM) as the mutagen and hydroxyproline (HYP) as OP regulator, 15 hydroxyproline (HYP)-tolerant regenerated plants with an increase of OP from 77.0 mmol/kg to 85.5 mmol/kg in medium were obtained. The offsprings of each regenerated plant were selected with oil content over 55% compared to 49.5% for Huayu 20. Three varieties named Yuhua 4, Yuhua 9 and Yuhua 16 which have the significant characteristics of high yield and high oil content were released from the offsprings of the HYP-tolerant regenerated plants. Their oil content reached 57.68%, 61.05%, 58.94%, respectively. The results indicate in vitro mutagenesis with PYM following a screening in HYP-supplemented media is an effective method for obtaining high-oil peanut variants. Three new peanut cultivars with high yield and high oil content were obtained. Our study paves the way for further increase in oil content of peanuts and provides materials to further study genes associated with high oil content.

4.4 Transcriptome profiling provides insights into molecular mechanism in peanut semi-dwarf mutant (*Arachis hypogaea* L.)

Fengdan Guo[1,2#], Junjie Ma[2,3#], Suhua Shi[1,2], Jinbo Sun[1,2], Guanghui Li[2], Chuanzhi Zhao[2], Han Xia[2], Shuzhen Zhao[2], Xingjun Wang[2*], Lei Hou[2*]

[1] College of Life Science, Shandong Normal University, Jinan, PR China
[2] Biotechnology Research Center, Shandong Academy of Agricultural Sciences; Shandong Provincial Key Laboratory of Crop Genetic Improvement, Ecology and Physiology, Jinan, PR China,
[3] Life Science College of Shandong University, Jinan 250100, People's Republic of China

*** Author for correspondence: xingjunw@hotmail.com; houlei9042@163.com**

Plant height is the major agronomic trait and closely correlated to crop yield. Plant height development is an important area of plant developmental biology and numerous studies about its molecular genetic basis had been conducted on model plants and crops. However, little is known on the molecular mechanisms of peanut plant height. In this study, a semi-dwarf peanut mutant was identified from Co^{60} gama ray induced mutant population and designated as semi-dwarf mutant 2 (*sdm2*). The height of *sdm2* was only 59.3% of its wild line Fenghua 1 (FH1) at the mature stage. Both the internode number and internode length of *sdm2* were less than those of FH1. Gene expression profiles of stems and leaves from both *sdm2* and FH1 were analyzed using high throughput RNA sequencing. The identified differentially expressed genes (DEGs) were involved in hormone biosynthesis and signaling pathways, cell wall synthetic and metabolic pathways. BR, GA and IAA biosynthesis and signal transduction pathways were significantly enriched. The expression of several genes in both BR biosynthesis and signaling were found to be significantly down-regulated in stems and leaves of *sdm2* as compared to FH1. Many transcription factor genes were identified as DEGs. These results provide useful information for uncovering the molecular mechanism regulating peanut stem height. It could facilitate identification of causal genes for breeding advanced peanut varieties with semi-dwarf phenotype.

4.5 Development of peanut runner cultivars for the main agricultural areas in Brazil

T. M. F. Suassuna*, N. D. Suassuna, J. Heuert

Embrapa Algodão, Campina Grande, PB, Brazil

***Author for correspondence: tais.suassuna@embrapa.br**

Peanut (*Arachis hypogaea* L.) production and commercialization in Brazil is concentrated in the Southeast region. However, other annual crops are cultivated in the South and Central regions with high yields, a remarkable combination of management and cultivar development for the Brazilian agribusiness. The Breeding Program for Runner market-type at Embrapa started in 2010. Since then, three high oleic acid cultivars were released in 2017: BRS 421, BRS 423 and BRS 425. These cultivars were evaluated in the main crop growing areas in Brazil in 2015/2016, 2016/2017, and 2017/2018, resulting in a total of 20 field trials. Mixed model analysis via REML/BLUP was used to obtain the HMPRGV (harmonic means relative to the predicted performance of genotypic values) for yield. BRS 423 (5084 $kg.ha^{-1}$), BRS 425 (4987 $kg.ha^{-1}$) and BRS 421 (4813 $kg.ha^{-1}$) exceed all the checks, with an accuracy of 0.82 and CV of 17.7. BRS 421 is indicated for high performing conditions, specially regard to disease management; BRS 425 can be cultivated when disease management is not efficient, like late season planting, and; BRS 421 has the largest seed size (84 g per 100 g) and good performance in a broad range of environments.

4.6 Optimizing effective genomic selection strategy for achieving higher genetic gains in groundnut

Manish K Pandey[1*], Diego Jarquin[2], Sunil Chaudhari[1], Irene Breider[3], Pasupuleti Janila[1], Jose Cossa[2], Ramesh Bhat[4], Thankappan Radhakrishnan[5], John Hickey[3], Rajeev K Varshney[1*]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]International Maize and Wheat Improvement Center (CIMMYT), Mexico, Mexico
[3]The Roslin Institute, The University of Edinburgh, Scotland, UK
[4]University of Agricultural Sciences (UAS)-Dharwad, Dharwad, India
[5]ICAR-Directorate of Groundnut Research (DGR), Junagadh, India

***Authors for correspondence: m.pandey@cgiar.org; r.k.varshney@cgiar.org**

Groundnut has entered in post-genome sequencing era and has now ample genomic resources for deploying genomic selection (GS) breeding. GS has emerged as the most promising, efficient and cost-effective breeding approach which capture both small- and large-effect genetic factors and therefore, promises to achieve higher genetic gains in less time with the help of genetic markers to improve complex traits such as yield and oil content. In this context, a training population was constituted with 340 elite lines followed by their genotyping with 58K "Axiom_Arachis" SNP array and phenotyping for key agronomic traits at three locations in India. Four GS models (two main-effect models, one naïve interaction model and one naïve and informed interaction model) were tested using three different random cross-validation (CV) schemes (CV1, CV2 and CV0). Prediction accuracy estimated by four models indicated clear advantage of the inclusion of marker information which was reflected in better prediction accuracy achieved from models L+E+G, informed interaction (L+E+G+GE) and Naïve and informed interaction as compared to L+E model. Assessment of comparative prediction accuracy for different genomic selection models to perform selection for untested genotypes, and unobserved and unevaluated environments provided greater insights on potential application of GS breeding in groundnut. Further work is in progress on 4-part breeding strategy simulation using phenotypic selection and getting insight in the effect of different compositions of training populations for genomic selection in a breeding program using introgression.

4.7 The Future is now for accelerated peanut improvement

J Clevenger

International Peanut Genome Initiative.

Author for correspondence: josh.clevenger@effem.com

A review of peanut literature in the past decade uncovers a prevalent message: "peanut genomics resources has lagged behind other crops." This sentiment is no longer true. In fact, now it is more accurate to say, "peanut genomics resources have sprinted ahead of other crops." This is due in large part to the strong international collaborations that have led to tetraploid reference genomes, high throughput genotyping arrays, agronomically elite interspecific varieties, and developed markers associated with high value traits. The author list of the publications outlining these advancements are full of the names of talented graduate students who were not willing to accept the current status of peanut genomics. Now, imagine nascent scientists being asked to approach the next set of challenges peanut faces, with every tool they need in their arsenal. Mapping key traits now will accompany parental-specific reference-quality genomes, allowing high resolution analysis of structural variation. Marker development will happen in half the time. The goals of PhD projects will no longer be mapping QTL but identifying genes that will have a real impact on feeding the world. In this new present, the young scientists must keep dreaming big and push for real change, more progress, and creative innovation. It is right to celebrate the accomplishments of the near past, but the real excitement should be about the present.

4.8 Genome-wide association study of aflatoxin accumulation resistance in a Chinese peanut mini-mini core collection

BL Yu[1], XJ Zhou[1], DX Huai[1], L Huang[1], YP Kang[1], Hari Sudini[2], XP Ren[1], YN Chen[1], HY Luo[1], N Liu[1], WG Chen[1], Y Lei[1], LY Yan[1], BS Liao[1], HF Jiang[1]*

[1]Oil Crops Research Institute of Chinese Academy of Agricultural Sciences, Wuhan, 430062, China.

[2] International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad 502324, India

***Author for correspondence: peanutlab@oilcrops.cn**

Aflatoxin contamination is a giant risk for peanut industry worldwide. Aflatoxin B_1 (AFB_1) and aflatoxin B_2 (AFB_2) are the most common aflatoxins produced by *Aspergillus flavus* with high carcinogenicity and teratogenicity. Identification of DNA markers associated with resistance genes for aflatoxin accumulation will offer breeders efficient tools to develop resistant cultivars in crops including peanut. In this study, seeds of 99 accessions of the Chinese peanut mini-mini core collection were used for aflatoxin accumulation resistance by kernel inoculation assay under laboratory conditions. As a result, two relatively resistant accessions were identified, with their aflatoxin content being 8.41% and 22.52% of the susceptible control respectively. The 99 accessions were genotyped by restriction site associated DNA sequencing (RAD-Seq) and 36,085 high quality genome-wide SNP markers were identified for genome-wide association study (GWAS). A total of 60 SNP markers associated with aflatoxin accumulation were detected across three environments, which explained 16.87 % - 31.70% of phenotypic variation. The aflatoxin content of the accessions with "GG" of either SNP19994 or SNP02686 was significantly lower than that with "AA". Besides, genes coding WRKY transcript factor and proteins with leucine-rich repeat domain, which were reported responsible for disease resistance in plants, were identified in the candidate region of peak SNP marker SNP19994. These results improved our understanding of the genetic mechanism of aflatoxin accumulation resistance. The resistant peanut accessions and molecular markers identified in this study will play a significant role in aflatoxin resistance breeding.

5.1 Solving the leaf spot problem in peanut

H. T. Stalker[1*], S.C.M. Leal-Bertioli[2], and D.J. Bertioli[3]

[1] Department of Crop and Soil Sciences, NC State University, Raleigh, NC 27695, USA;
[2] Department of Plant Pathology, The University of Georgia, Athens, GA 30621, USA;
[3] Department of Crop and Soil Science, the University of Georgia, Athens, GA 30621, USA.

***Author for correspondence: tom_stalker@ncsu.edu**

Leaf spot is a severe global problem and efforts to develop resistant cultivars have had varying levels of success for disease suppression. However, leaf spot continues to persist at epidemic proportions. So why hasn't it been eradicated? First is the problem of pathogen identification or reporting. The term "leaf spot" is widely used for the diseases early leaf spot (*Passalora arachidicola* syn. *Cersospora arachidicola*) or late leaf spot (*Northopassalora personata* syn. *Cercosporidium personatum*), which must be clearly defined. Although both can be present in a field, one or the other usually predominates. Because the frequency of either pathogen can vary over time, cultivars developed for one pathogen may later be devastated by the other. Secondly, although the two pathogens cause similar plant damage, good evidence exists indicating that different genes condition resistance. Resistance has several components (sporulation, lesion size, number of lesions/leaf, latent period, incubation period and defoliation), but most reports of "resistance" are field ratings on a numerical scale, which only indicates percent defoliation. Third, sources of resistance to either pathogen have been limited to several moderately "resistant" land races or more recently, introgression lines derived from the wild species *Arachis cardenasii*. Molecular markers are available for the *A. cardenasii* segments conferring late and possibly early leaf spot resistances, but not for cultivated land races. However, traditional field selection has combined the two sources and partially solved the early leaf spot problem and progress is being made for late leaf spot. Finally, new sources of resistance to both pathogens have only recently been identified in *A. diogoi* and *A. stenosperma* introgression lines. Molecular marker associations for both pathogens have been tentatively identified. For the first time, genetic materials are available from multiple sources for both pathogens so that segments conferring resistance can be pyramided into a single genotype. A long-term solution to leaf spot disease suppression will require positive/precise identification of early and late leaf spot diseases, and developing cultivars with at least three of the above sources of resistance and combining both resistances into cultivars.

5.2 Comparative transcriptome analysis identified key genes for seed germination in response to Zn fertilizers in peanuts

Chao Luo, Mingnan Qu, Kaijia Zheng,Xuan Peng,Mingxu Li,Haoyang Yin,Weichang Yu*

College of Life Sciences, Guangdong Provincial Key Laboratory for Plant Epigenetics, Shenzhen University, Shenzhen, 518060, China.

***Author for correspondence: wyu@szu.edu.cn**

Micronutrients including Zinc participate in various biological process. Priming seeds with Zn was intensively applied in agricultural practices to out-compete weeds, while molecular mechanisms especially in peanuts during this process remain to be addressed. In this study, We found micronutrient Zinc fertilizer played significant positive effects on peanut germination and root elongation when seeds of Luhua 11 were treated with both 5 mM zinc sulphate heptahydrate ($ZnSO_4.7H_2O$) and zinc chloride ($ZnCl_2$). Meanwhile we conducted a genome-wide transcripts analysis on peanuts seeds priming with different Zinc, to identify differentially expressed genes (DEGs) and biological pathways. After qPCR validation, we found that 14 genes were significantly up-regulated by Zinc treatments relative to the control, involving Zinc binding, signal transduction, cell membrane biosynthesis, ion/carbohydrate transport and amino acids metabolism. We found two stress responsive genes, HSP20 and GOLS, were down-regulated.

5.3 Evaluation of drought resistance of peanut cultivars at seedling stage using tissue culture method

Yan Ren[1], Xiao Cui[2], Shuangling Li[1], Lei Li[2], Lijun Wu[1], Yanmao Shi [1], Liang Yin[1], Mei Yuan[1]*.

[1]Shandong Peanut Research Institute/ Key Laboratory of Peanut Biology and Genetic Breeding, Ministry of Agriculture, Qingdao 266100, China.
[2] Qingdao Academy of Agricultural Sciences, Qingdao 266100, China.

***Author for correspondence: yuanbeauty@126.com**

In order to evaluate drought resistance of peanut varieties (advanced breeding lines) at seedling stage, polyethylene glycol (PEG)-6000 was added to the MS_0 medium to simulate water stress. The rooting characteristics of main stems from12 peanut cultivars at different concentrations of PEG-6000 were measured. The subordinate function value method was used to evaluate drought resistance of peanut. The results showed that 45 g/L of PEG-6000 was suitable to evaluate drought resistance of peanut varieties. According to the subordinate function value, Huayu 16 showed high drought-resistance, followed by Huayu 19 and H1816 (moderate drought-resistance varieties). C70532, Huayu 46, Huayu 9812, NP13, H2833 and Fenghua 1 were weak drought-resistance varieties. Huayu 45, Huayu 53 and Huayu 25 were non-drought-resistance varieties.

5.4 Study on relationship of kernel phosphorus concentration with the yield and phosphorus utilization efficiency in 272 peanut (*Arachis hypogaea* L.) lines

Suqing Zhu[1,2], Xiurong Zhang[1,2], Fengzhen Liu[1,2*], Lu Luo[1,2], Ying Fang[1,2], Yongshan Wan[1,2*] and Kun Zhang[1,2]

[1]State Key Laboratory of Crop Biology, Shandong Key Laboratory of Crop Biology, Shandong Agricultural University, Tai'an 271018, China;
[2]College of agronomy, Shandong Agricultural University, Tai'an 271018, China

***Author for correspondence: yswan@sdau.edu.cn; liufz@sdau.edu.cn**

Phosphorus (P) is essential for plant growth and yield production, and P uptake and utilization efficiency among peanut varieties had extensive variation. However, few researches focused on relationship of vegetative P concentration (VPC) and kernel P concentration (KPC) with the yield (KDM) and P utilization efficiency (PUEk). In our study, 272 peanut lines were planted at two P fertilization levels to investigate the effects of P on different traits. Under the two P levels, significant differences were detected in many traits among peanut genotypes. Correlation analysis indicated that P accumulation had positive effect on vegetation growth, but it was negatively correlated with KDM and PUEk. VPC, KPC, KDM, and PUEk were considered to be key traits for genotype screening. A total of 32 peanut genotypes with high KDM and PUEk but low VPC and KPC were selected. The results provided a new method for evaluating P use efficiency in peanut. These elite lines will have great potential in application. They are also excellent germplasm resources to reveal the molecular mechanism of high P use efficiency in peanut. In addition, because of showing a same change trend, KPC is a representative indicator of genotype screening at the same yield level in peanut. It is simpler and more stable than VPC.

5.5 Farmer's perceived constraints to groundnut production, and their variety choice and preferred traits in eastern Ethiopia: implications for drought tolerance breeding

Seltene Abady[1,2,3*], Hussein Shimelis[1] and Pasupuleti Janila[3]

[1]University of KwaZulu-Natal, School of Agricultural, Earth and Environmental Sciences, African Centre for Crop Improvement (ACCI), Pietermaritzburg, South Africa;
[2]Haramaya University, School of Plant Sciences, P.O.Box: 138 Dire Dawa, Ethiopia;
[3]International Crops Research Institute for Semi-Arid Tropics (ICRISAT), Patancheru India.

***Author for correspondence: selteabady@yahoo.com**

Groundnut (*Arachis hypogaea* L.) is an important food and cash crop globally. The eastern region of Ethiopia is known for its groundnut production despite the low productivity attributable to diverse biotic and abiotic stresses and socioeconomic constraints. The objective of this study was to assess farmers' perceived production constraints, variety choice, and preferred traits of groundnut in eastern Ethiopia to guide future groundnut variety development. Participatory rural appraisal studies were conducted in two major groundnut-producing districts (Babile and Fedis) in eastern Ethiopia. Data were collected through a semi-structured questionnaire, transect walks, and focus group discussions. All respondent farmers widely cultivated local or obsolete, introduced varieties because of a lack of seed of modern groundnut cultivars. Ninety percent of respondents reported drought stress, mainly occurring during the flowering stage, as the leading constraint to groundnut production. Other groundnut production constraints included poor soil fertility (reported by 88% of respondents), lack of access to improved seed (67%), pre-harvest diseases (59.5%), use of low yielding varieties (52.5%), inadequate access to extension services (41.5%), limited access to credit (21.5%), and limited availability of improved varieties (18.5). Farmer-preferred traits included high shelled yield (reported by 27.67% of respondents), early maturity (16.84%), drought tolerance (13.67%), market value (11.17%), good seed quality (10%), adaptability to local growing conditions (5.8%), and resistance to diseases (5.17%). Therefore, the aforementioned production constraints and farmer-preferred traits are key drivers that need to be integrated into groundnut breeding and variety release programs in eastern Ethiopia.

5.6 Isolation and identification of *Bacillus Sinensis* ZHX-10 and analysis of its biological control effect

Xia Zhang, Manlin Xu, Zhiqing Guo, Jing Yu, Yucheng Chi*

Shandong Peanut Research Institute, Qingdao 266100, China

***Author for correspondence: 87626681@163.com**

In order to screen the resources of bio-control bacteria strains for the control of southern stem rot caused by *Sclerotium rolfsii* Sacc., a bacteriaZHX-10 was isolated from peanut field with serious soil-borne diseases. The strain ZHX-10 was identified based on morphological characteristics, physiological, biochemical characteristics and 16S rDNA sequence analysis. The antifungal spectrum of strain ZHX-10 was determined by the dural culture method, and the inhibitory effects of bacterial suspension, volatile gases, fermentation broth from strain ZHX-10 against *Sclerotium rolfsii* Sacc. were preliminarily determined. The results showed that ZHX-10 was *Bacillus siamensis*, which could inhibit all the eight pathogenic fungi tested. The bacterial suspension, volatile gases and fermentation broth of ZHX-10 had extremely high inhibitory effect on Sclerotium rolfsii Sacc.. At the same time, the volatile gas produced by the suspension of ZHX-10 had significant resistance to *Sclerotium rolfsii* Sacc. in vitro. It indicted that strain ZHX-10 had high research value and potentials for biological control of *Sclerotium rolfsii* Sacc.

Keywords: *Sclerotium rolfsii* Sacc.; ZHX-10; *Bacilus siamensis*; Inhibitory effects; Biological control.

5.7 Mechanism of potassium deficiency regulating peanut root system architecture through miRNAs

Qian Li[1†], Lijie Li[1†], Kyle Davis[2], Zhiyong Zhang[1*], Baohong Zhang[2]

[1] Henan Collaborative Innovation Center of Modern Biological Breeding and Henan Key Laboratory for Molecular Ecology and Germplasm Innovation of Cotton and Wheat, Henan Institute of Science and Technology, Xinxiang, Henan 453003, China.
[2] Department of Biology, East Carolina University, Greenville, NC 27858, US.

***Author for correspondence: z_zy123@163.com**

Potassium (K) is fundamental for plant growth and development. In present study, growth chamber experiments were conducted using peanut cultivar YZ9102 to record the effects of K deficiency on plant growth, root respiration characteristics, root vitality, root architecture, microRNA expression (miRNA, e.g miR160, miR164, miR165, and miR393) and the expression of their target genes (e.g AFB3 andNAC4). The result showed that K deficiency resulted in significant reduction in plant growth, as indicated by the significantly decreased dry weight of shoot and root on both the 4th and 8th day under K deficiency conditions. Potassium deficiency decreased root vitality on the 4th day and weakened root respiration, as indicated by the reduced O_2 consuming rate on both the 4th and 8th day under K deficiency conditions. The total root length was significantly deceased, which may be associated with the up regulation of miR160, while the primary root length was significantly increased on the 8th day, which may be associated with the down-regulation of miR165, under K deficiency conditions. In addition, K deficiency induced lateral root formation as indicated by the increased branch root number and branch root zone length on the 8th day under K deficiency conditions, which may be associated with the up regulation of miR164, and the down-regulation of miR393 and NAC4.
Keywords: Peanut (*Arachis hypogaea* L.); low-potassium stress; root system architecture; miRNA

5.8 Expression of peanut iso-Arah3 responding to drought stress and infection of *Aspergillus flavus*

T Wang, MN Chen, SL Yu, N Chen, LJ Pan, M Wang, XY Chi*

Key Laboratory of Peanut Biology and Genetic Improvement, Ministry of Agriculture, P.R. China, Shandong Peanut Research Institute, Qingdao 266100,China

***Author for correspondence: chixy2019@163.com**

A. flavus infection of peanut seeds and subsequent contamination of aflatoxin, especially under drought condition is a serious food safety issue. Our previous proteomic study showed that isogenous allergen 3 (iso-Arah3) was induced by drought and *A. flavus* infection. In order to better understand iso-Arah3 regulation and function during drought tolerance and *A. flavus* infection, this study examined the expression of iso-Arah3 at transcript level using real time RT-PCR and Western blot. There were significantly more proteins in matured seed, and young pod and leaf during drought treatment and *A. flavus* infection. iso-Arah3 gene expression was also upregulated in matured seed but in young pod and leaf the gene expression was down regulated, In addition, sub-cellular localization analysis showed that transient expression of iso-Arah3 occurred in cytoplasm and plasma membrane. Also, the over-expression of iso-Arah3 in Arabidopsis enhanced tolerance to drought (PEG2000, 20%) compared to wild type and control line. The antibacterial peptide in trypsin inhibitor domain of iso-Arah3 showed more in vitro inhibition to *A. flavus* than the full-length of refolded iso-Arah3 fusion protein. This result indicates that iso-Arah3 expression is tissue-specific but protein accumulation is non tissue-specific. These results suggest that expression and translation of iso-Arah3 core functional domain could play important roles in responding to drought stress and *A. flavus* infection.

5.9 Pathogen of peanut pod rot: *Pythium myriotylum* only infected the peanut pod but not the peanut root

Jing Yu, Manlin Xu, Xia Zhang, Zhiqing Guo, Juxiang Wu, Yucheng Chi*

Shandong Peanut Research Institute, Qingdao, Shandong, China

***Author for correspondence: 87626681@163.com;**

Peanut is a globally important crop for food and oil production. In recent year, pod rot symptoms showed increased in China. The pathogen was identified as *P. myriotylum* based on molecular analysis and morphological characteristics. Interestingly, in previous field investigations, we found that *P. myriotylum* only infected peanut pods, causing pod rot, and the roots were free of any disease spots. Later, we verified this phenomenon through indoor pot culture inoculation test and got the same conclusion. qRT- PCR was used to determine the biomass of *P. myriotylum* in peanut pods and roots, the results show that the mass - forming hyphae were concentrated in peanut pod and almost absent in peanut root. In order to further prove the tissue specificity of *P. myriotylum* infection, we conducted transcriptome sequencing and found that the mass - reads were concentrated in peanut pod samples and almost absent in peanut root samples. The number of differentially expressed genes in peanut pod samples (compared with no infected pods samples) was 5722 but in peanut root samples was only 52. The above evidences indicate that *P. myriotylum* only infects peanut pod, but not peanut root.

5.10 *Aspergillus flavus* and aflatoxins contamination investigation in Shandong peanut production area soil and peanut pods

Zhiqing Guo[1], Juxiang Wu[1], Xia Zhang[1], Manlin Xu, Jing Yu[1], Dianxu Chen[1], zhimeng Zhang[1], Xinguo Li[2], Jianlei Yu[3], Tongjin Liu[3], Yucheng Chi[1*], Shubo Wan [4*]

[1]Shandong Peanut Research Institute, Qingdao 266100, China;
[2]Biotechnology Research Center, Shandong Academy of Agricultural Sciences, Jinan 250100 China;
[3]Institute of Plant Protection, Shandong Academy of Agricultural Sciences, Jinan, 250100;
[4]Shandong Academy of Agricultural Sciences, Jinan, 250100

***Author for correspondence: 87626681@163.com; wanshubo2016@163.com**

In order to determine the contamination of *Aspergillus flavus* and aflatoxins in the soil and harvested peanut pods, we collected the soil samples and peanut pods from main peanut production area of Shandong province as following: Yantai, Qingdao, Linyi, Taian, Zaozhuang and Heze. The *A. flavus* contamination sample percentages of the soil, peanut pod and peanut seed were calculated and the content of aflatoxin in peanut seeds was quantified. The results illustrated that 3.33-33.33% soil samples from different area were contaminated by *A. flavus* while 10.89-27.78%, 3.11-11.56% of the peanut pods and peanut seeds were contaminated, respectively. The content of aflatoxin in peanut seeds was 5.01-26.80 ppb. According to the data analyzed by SPSS, we found that there was strong correlation (r=0.896) between aflatoxin content from peanut seeds and percentages of *A. flavus* from soil samples while medium strong correlation (r=0.575; r=0.427) existed between aflatoxin content in peanut seeds and infection percentages of *A. flavus* from peanut pods and seeds samples, respectively. Our research will provide base for the biological control of *A. flavus* and aflatoxins contamination management to enhance the quality and safety of the crop products.

Key words: Peanut; Aspergillus flavus; aflatoxins; Shandong production area.

5.11 Studies on Transcriptomics of Peanut Induced by *Phoma arachidicola*

Jing Yu[1], Manlin Xu[1], Xia Zhang[1], Zhiqing Guo[1], Juxiang Wu[1], Dianxu Chen[1], Zhimeng Zhang[1], Xinguo Li[2], Yucheng Chi[1*], Shubo Wan[3*]

[1] Shandong Peanut Research Institute, Qingdao, Shandong, China
[2] Biotechnology Research Center, Shandong Academy of Agricultural Sciences, Jinan, Shandong, China
[3]Shandong Academy of Agricultural Sciences/Shandong Provincial Key Laboratory of Crop Genetic Improvement, Ecology and Physiology, Jinan, Shandong, China

***Author for correspondence: 87626681@163.com; wanshubo2016@163.com**

Using RNA-Seq technology, we performed high-throughput sequencing of peanut transcriptomes 7, 14, 27 days after inoculation (DPI) with *Phoma arachidicola*. The differentially expressed genes of peanut under the induction of *P. arachidicola* were analyzed. It was found that the number of differentially expressed genes increased with the infection process and reached a maximum at 14 days. The GO functional annotation analysis was performed on the differentially expressed genes. The biological process is significantly enriched in cellular processes, metabolic processes, single organism processes, cellular component composition and biosynthesis, and stimuli response; Significant enrichment in cellular components, organelles, macromolecular complexes, membranes, etc. Peanuts undergo a variety of biological processes during *P. arachidicola* infecting the leaves. Pathway enrichment analysis of differentially expressed genes, only one process of ribosomes is significantly enriched after 7 DPI. After 14 DPI, the circadian rhythm and tryptophan metabolism of the plant was significantly enriched. With the infection of *P. arachidicola*, plants responded to defenses by mobilizing multiple metabolic processes. In the early stage, there were changes in components such as ribosomal proteins and ribosomal RNA. The mid-term tryptophan pathway is involved in the synthesis of secondary metabolites, and it inhibits pathogenic bacteria by synthesizing small molecule active substances. The participation of metabolic pathways such as secondary metabolic biosynthesis, phenylpropanoid biosynthesis, flavonoid biosynthesis, cytochrome P450, phenylalanine metabolism, and glutathione metabolism in the later period indicated that the plant's defense response was activated.

Keywords: Peanut; web blotch; *Phoma arachidicola*; transcriptome analysis; metabolic pathways;

5.12 Identification of abiotic stress tolerant germplasms and functional analysis of related genes in peanut (*Arachis hypogaea* L.)

Xiaoyuan Chi[1], Na Chen[1], Lijuan Pan[1], Mingna Chen[1], Tong Wang[1], Mian Wang[1], Zhen Yang[1], Shanlin Yu[1]*

[1]Laboratory of Genetics and Breeding, Shandong Peanut Research Institute, Qingdao, China.

***Author for correspondence: shanlinyu1956@163.com**

Peanut (*Arachis hypogaea* L.) is one of the most important oil crops in China and the production ranks first in the world. The main goal of peanut breeding is to cultivate high-yield, high-quality, multi-resistant peanut varieties. Our research group owned more than 600 peanut germplasms and 1500 mutants in. We have released 26 new peanut varieties. We screened genes regulated by cold and salt stress in peanut using microarray profiling. In total, 1478 up-regulated and 1510 down-regulated genes were identified in leaves of peanut subjected to cold stress, and 4828 up-regulated and 3752 down-regulated genes were identified in peanut roots subjected to salt stress. According to the microarray results, we selected 6 AP2/ERF and 8 MYB transcription factor genes for function verification. Up to present, our results showed that *AhERF6* and *AhMYB6* could enhance the tolerance of plants to cold and salt stresses in transgenic Arabidopsis.

5.13 Translation initiation factor eIF4E and eIFiso4E are both required for peanut stripe virus infection in Peanut (*Arachis hypogaea* L.)

ML Xu[1,2], HF Xie[1], JX Wu[1], LH Xie[2], JG Yang[3*], YC Chi[1*]

[1] Shandong Peanut Research Institute, Qingdao, 266100
[2] Fujian Agriculture and Forestry University, Fuzhou, 350002
[3] Open Project Program of Key Laboratory of Tobacco Pest Monitoring Controlling & Integrated Management, Tobacco Research Institute of Chinese Academy of Agricultural Sciences, Qingdao, 266100

***Author for correspondence: 87626681@163.com**

Peanut stripe virus (PStV) belongs to the genus Potyvirus and is the most important viral pathogen of cultivated peanut (*Arachis hypogaea* L.). The eukaryotic translation initiation factor, eIF4E, and its isoform, eIF (iso) 4E, play key roles during virus infection in plants, particularly Potyvirus. In the present study, we cloned the eIF4E and eIF (iso) 4E homologs in peanut and named these as PeaeIF4E and PeaeIF(iso)4E, respectively. Quantitative real-time PCR (qRT-PCR) analysis showed that these two genes were expressed during all growth periods and in all peanut organs, but were especially abundant in young leaves and roots. These also had similar expression levels. Yeast two-hybrid (Y2H) analysis showed that PStV multifunctional helper component proteinase (HC-Pro) and viral protein genome-linked (VPg) both interacted with PeaeIF4E and PeaeIF (iso) 4E. Bimolecular fluorescence complementation (BiFC) assay showed that there was an interaction between HC-Pro and PeaeIF4E/PeaeIF (iso) 4E in the cytoplasm and between VPg and PeaeIF4E/PeaeIF (iso)4E in the nucleus. Silencing either PeaeIF4E or PeaeIF (iso) 4E using a virus-induced gene silencing (VIGS) system did not significantly affect PStV accumulation. However, silencing both PeaeIF4E and PeaeIF (iso) 4E genes significantly weakened PStV accumulation. The findings of the present study suggest that PeaeIF4E and PeaeIF(iso)4E play important roles in the PStV infection cycle and may potentially contribute to PStV resistance.

5.14 Stress-related transcriptional signaling and its roles in aflatoxin production and stress tolerance in *Aspergillus flavus*

JC Fountain[1,2*], JP Clevenger[3,4], J Vaughn[5], RC Callahan[5], D Starr[3], AK Pandey[6], SN Nayak[6], P Bajaj[6], V Kumar[6], A Chitikineni[6], RC Kemerait[2], MK Pandey[6], RK Varshney[6] & B Guo[1]

[1]USDA-ARS, Crop Protection and Management Research Unit, Tifton, GA 31793

[2]Department of Plant Pathology, University of Georgia, Tifton, GA 31793
[3]Legume Research, Mars Incorporated, Athens, GA, 30605
[4]Institute of Plant Breeding, Genetics, & Genomics, University of Georgia, Athens, GA, 30605.
[5]USDA-ARS Genomics and Bioinformatics Research Unit, Stoneville, MS, 38776
[6]Center of Excellence in Genomics & Systems Biology, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, Telangana 502324, India

***Author for correspondence: baozhu.guo@usda.gov**

Signaling regulating aflatoxin production in *Aspergillus flavus* and other aflatoxigenic fungi is a research focus due to its potential utility in mitigating aflatoxin contamination. Mimicking stress experienced under drought and when encountering host defenses, conidia of diverse isolates of *A. flavus* were exposed in varying levels of H_2O_2 stress in aflatoxin conducive and non-conducive media and resultant mycelia were sampled for transcriptomic analyses. Select highly and moderately toxigenic isolates were used for a follow-up experiment where established mycelia at 48 hours post inoculation (HPI) were exposed to H_2O_2 stress over time. Comparing between conducive and non-conducive media indicated a significant effect of carbon source on stress responses and the expression of several secondary metabolite gene clusters including those for aflatoxin, aflatrem, aflavarin, cyclopiazonic acid, and kojic acid. It is hypothesized that this is due to limitations in non-conducive medium on the availability of glycolytic intermediates and acetyl-CoA used in the production of polyketide mycotoxins. Differential expression profiles among atoxigenic isolates were also found to correlate with known biocontrol efficacy suggesting the use of this method in the identification and characterization of potential biocontrol isolates. Examining stress responses in both experiments also revealed a significant role for MAP kinase signaling cascades. The expression and potential roles of downstream targets of these pathways, such as bZIP transcription factors, in aflatoxin regulation and stress tolerance will also be discussed.

5.15 Identification of metabolites and transcripts involved in salt stress and recovery in peanut

Guowei Li*, Feng Cui, Yiyang Liu, Rongchong Li and Shubo Wan

Biotechnology Research Center, Shandong Academy of Agricultural Sciences, Jinan, Shandong, China

***Author for correspondence: ligw_saas@163.com**

Peanut is considered as a moderately salt-sensitive species and soil salinity is a limiting factor for peanut cultivation. To gain comprehensive insights into the response of peanut to salt stress, the plant physiological parameters including photosynthesis, transpiration and relative electrolyte leakage of leaf etc. were characterized. And further the metabolome and transcriptome were analyzed by GC/MS and RNA-seq method, respectively. RECs were higher when plants were subjected to salt stress. However, in contrast to expectations, RECs were even higher when plants were transferred from salt stress to standard conditions (recovery). Totally 391 metabolites were identified in shoots and roots. Ninety-two metabolites varied in response to salt and 42 metabolites responded to recovery specifically. Transcriptomics data showed that 372 transcripts in shoots and 1,386 in roots responded specifically to recovery, but not salt stress. A representative inferred network was built based on the plant physiological, metabolite and transcript variables. Data suggested that H^+-ATPase and aquaporin family played roles in salt stress and the inference was confirmed by using overexpressing lines. This study provides valuable information on peanut response to salt stress and recovery and may inspire further study to improve salt tolerance in peanut germplasm innovation.

5.16 Comparative analysis of lipidomes and transcriptomes reveals molecular mechanism of cold tolerance in peanut

He Zhang, Chunji Jiang, Jiale Dong, Xinhua Zhao, Jing Wang, Xiaoguang Wang, Shuli Zhao, Xibo Liu, Chao Zhong, Haiqiu Yu*

Peanut Research Institute, College of Agronomy, Shenyang Agricultural University, Shenyang, China, 110161.

***Author for correspondence: yuhaiqiu@syau.edu.cn**

Cold stress has become a major constraint for geographical distribution and growth of peanut in Northeast China. Biomembrane is the barrier that protects cells from injury as well as the primary place for sensing cold signals. To elucidate the molecular regulation mechanism of membrane lipid metabolism in peanut cold tolerance, comparative analysis of lipidomes and transcriptomes in cold tolerant and cold sensitive varieties was taken. Membrane lipidomic data analysis revealed that the cold tolerance of peanut can be improved through membrane lipid remodeling under cold stress. For example, the significant increase in phosphatidic acid and decrease in phosphatidylcholine, phosphatidylethanolamine and phosphatidylinositol. Comparative transcriptomics revealed 14 pathways related to lipid metabolism were involved in cold tolerance response, and in which most of the differentially expressed genes were up regulated. The combined analysis of transcriptional group and lipid group showed that phosphatidic acid can be accumulated in four ways to enhance cold tolerance, including the activity of glycerol-3-phosphate acyltransferase was up regulated in the de novo biosynthesis of phospholipids, enhanced hydrolysis of phosphatidylcholine by phospholipase D resulted from the increase of phospholipase D activity, the phosphorylation of diacylglycerol was promoted because of the enhanced activity of diacylglycerol kinase, and the inhibition of phosphatidic acid phosphatase activity by diacylglycerol. These molecular systems underlying cold response could build a foundation for promoting the genetic improvement of peanut cold tolerance.

5.17 Long-term continuously monocropped peanut significantl changed the abundance and composition of soil fungal communities

Mingna Chen[1,2], ShanLin Yu[1], Mian Wang[1], LiJuan Pan[1], Na Chen[1], Tong Wang[1], Binghai Du[2*], Xiaoyuan Chi[1*]

[1]Shandong Peanut research institute, Qingdao, China
[2]College of Life Sciences, Shandong Key Laboratory of Agricultural Microbiology, National Engineering Laboratory for Efficient Utilization of Soil and Fertilizer Resources, Shandong Agricultural University, Taian, China

***Author for correspondence: chixy2019@163.com**

Soil microbial diversity and abundance is critical to sustaining soil health, but soil microorganism responses to long-term peanut monocropping have not been determined. This study used previously constructed gradient continuous monocropping plots and selected four varieties with different monocropping responses. The feedback responses of their root soil fungal communities to short-term and long-term continuous monocropping were tracked using high-throughput sequencing techniques. The results showed that monocropping over the long-term could lead to remarkable changes in fungal abundance and composition, and a general loss in diversity. The analyses indicated that soil samples from 1 and 2 year monocropped plots were grouped into one class, and samples from the 11 and 12 year plots were grouped into another. Genus Talaromyces was most common in our libraries, the two most abundant Talaromyces species, Talaromyces flavus and Talaromyces purpureogenus, generally decreased in the long-term monocropped plots. The genus Fusarium was relatively abundant. The most abundant species, Fusarium solani, generally increased in the long-term monocropped plots for all varieties, and Fusarium oxysporum abundance increased in the 2-year libraries, but did not obviously vary in the long-term monocropped plots. The increase in pathogen abundances and the decrease in beneficial fungi abundances seem to be the main cause for the yield decline and poor growth of long-term monocultured peanut. Simplification of fungal community diversity could also contribute to peanut soil sickness under long-term monocropping. Additionally, the different responses of peanut varieties to monocropping may also be related to their microbial community structure variation.

5.18 Transcriptome analysis reveals salt-stress-regulated biological processes and key pathways in roots of peanut (*Arachis hypogaea* L.)

Na Chen[1†], Maowen Su[2†], Xiaoyuan Chi[1], Zhimeng Zhang[1], Lijuan Pan[1], Mian Wang[1], Mingna Chen[1], Zhen Yang[1], Tong Wang[1], Shanlin Yu[1*]

[1]Shandong Peanut Research Institute, Qingdao, 266100, P R China
[2]Qingdao Entry-Exit Inspection and Quarantine Bureau, Qingdao, 266001, P R China

***Author for correspondence: yshanlin1956@163.com**

The cultivated peanut is important oil crop and salt stress seriously influences its development and yield. Tolerant varieties produced using transgenic techniques can effectively increase peanut plantation area and enhance its yields. However, little is known about how gene expression is regulated by salt stress in peanut. In this study, we screened genes regulated by salt stress in peanut roots using microarray technique. In total, 4828 up-regulated and 3752 down-regulated probe sets were successfully identified in peanut roots subjected to 3 h and 48 h of salt stress. Data analysis revealed that different response groups existed between the up and down-regulated probe sets. The main up-regulated biological processes involved in salt stress responses included transcription regulation, stress response, and metabolism and biosynthetic processes. The main down-regulated biological processes included transport processes, photosynthesis and development. The Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis indicated that metabolic pathway, biosynthesis of unsaturated fatty acids and plant-pathogen interaction, were mainly up-regulated in peanut under salt stress. However, photosynthesis and phenylalanine metabolism were mainly down-regulated during salt stress. The function of some probe sets in salt stress regulation was not clarified (e.g. protein functioning in cell cycle regulation and xylem development). Many of the genes we identified lacked functional annotations and their roles in response to salt stress are yet to be elucidated. These results identified some candidate genes as potential markers and showed an overview of the transcription map, which may yield some useful insights into salt-mediated signal transduction pathways in peanut.

5.19 Transcriptomics and miRNAs analysis of peanut (*Arachis hypogaea* L.) response to pod rot pathogeninfection

Mian Wang[1], Zhen Yang[1], Lijuan Pan[1], Tong Wang[1], Na Chen[1], Mingna Chen[1,2], Shanlin Yu[1], Xiaoyuan Chi[1*]

[1] Shandong Peanut Research Institute, Qingdao, 266100, PR China
[2] State Key Laboratory of Crop Biology, College of Life Science, Shandong Agricultural University, Taian, Shandong, 271018, PR China

***Author for correspondence: chixy2019@163.com**

Peanut pod rot has become a major disease in peanut production, posing a serious threat to the yield and quality of peanut. Researches on peanut pod rot mainly focus on the known pathogenic fungi, whereas there are few reports on the mechanism of peanut responding to pod rot. In this study, the seeds of peanuts before and after being infected by pod rot disease were taken as samples and the expression profile of the related genes and miRNAs were constructed. A total of 60,756 Unigene was obtained through transcriptome sequencing, among which are a total of 14,482 DEGs including 10,147 up-regulated genes and 4,334 down-regulated genes. A total of 334 miRNAs including 27 up-regulated and 97 down-regulated miRNA stressed by pod rot were detected through small RNA sequencing. The expression trends of the randomly selected 21 genes and 15 miRNAs analyzed by qRT-PCR were consistent with the prediction of transcriptome, which indicated that the sequencing results were reliable. Target gene prediction was conducted on miRNA and 1,998 target genes and 2,646 target sites were predicted in 303 miRNAs, Whereas 152 target genes were predicted in 119 differentially expressed miRNAs. The correlation analysis between transcriptome and miRNAs sequencing revealed that 14 target genes regulated by 10 miRNAs in transcriptome sequencing results. These analyses indicate that there are a large number of DEGs and miRNAs in the process of peanut responding to pod rot, and it is speculated that the disease-resistant process is the result of the combined action by multiple genes and miRNAs.

5.20 De novo full-length transcriptome analysis of *Arachis glabrata* provides insight into gene expression dynamics in response to biotic and abiotic stresses

Chuanzhi Zhao[1*], Liangqiong He[2], Ximeng Zhou[3], Han Xia[1,3], Yun Geng[1], Lei Hou[1], Pengcheng Li[1,2], Guanghui Li[1], Shuzhen Zhao[1,2], Changle Ma[3], Ronghua Tang[2], Xingjun Wang[1, 3*]

[1] Biotechnology Research Center, Shandong Academy of Agricultural Sciences, 250100, Jinan, PR China,
[2] Cash Crop Research Institute, Guangxi Academy of Agricultural Sciences, 530007 Nanning, China,
[3] Shandong Normal University, Jinan 250014, PR China

***Author for correspondence: xingjunw@hotmail.com; chuanzhiz@126.com**

Arachis glabrata represents one of the most adaptable wild Arachis species and is a valuable resource for improving disease resistance of cultivated peanut. However, the genome and transcriptome information for *A. glabrata* is lacking. We therefore used PacBio single-molecule long-read sequencing combined with BGISEQ-500 RNA-seq to study the transcriptome and gene expression dynamics of *A. glabrata*. In total, 712,736 reads of inserts (ROIs) were obtained from a pooled RNA library derived from root, stem, leaf, flower, peg and pod, resulting in 109,747 unique transcripts. Notably, more than 90,566 transcripts (85.52%) contained the complete coding sequence (CDS). By comparing with the reference genome sequences of cultivated peanut Tifrunner, a total of 54,847 alternative splicing events and 35,731 polyadenylation sites were identified. RNA-seq revealed that 1,229, 1,039, 1,671, 3,923, 1,521 and 1,799 transcripts expressed specifically in root, stem, leave, flower, peg and pod, respectively. Thousands of differential expressed transcripts in response to drought, salt and cold including 7,373 transcripts was significantly changed in response to all three kinds of abiotic stresses. In addition, the expression of 8,807 and 14,353 transcripts was up-regulated and down-regulated after infection with leaf spot disease, respectively. KEGG analysis showed that the pathways related with metabolism of sphingolipids, cutin and wax, plant-pathogen interaction and MAPK signaling pathway were enriched in response to pathogen. Further analysis found that 124 NBS-LRR genes was significant changed after infection with leaf spot disease. Furthermore, we identified thirty polyphenol oxidase encoding genes, which have been reported to be associated with the quality of forage of *A. glabrata.* In conclusion, this is the first report of large-scale transcriptome study of *A. glabrata* which facilitating for genetic study, gene cloning, utility and further genome sequencing of *A. glabrata.*

5.21 Understanding the genetic and molecular mechanisms for resistance to aflatoxin contamination in groundnut

Rajeev K Varshney[1]*, Hari K Sudini[1], Manish K Pandey[1], Spurthi Nayak[2], Pooja Soni[1], Arun K Pandey[1], Rakesh Kumar[1], Annapurna Chitikineni[1], Sarita Pandey[1], Jake Fountain[3,4], Prasad Bajaj[1], Weijian Zhuang[5], Baozhu Guo[3], Boshou Liao[6]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]University of Agricultural Sciences (UAS)-Dharwad, Dharwad, India
[3]Crop Protection and Management Research Unit, United State Department of Agriculture – Agricultural Research Service (UASDA-ARS), Tifton, USA
[4]Department of Plant Pathology, University of Georgia (UGA), Tifton, USA
[5]Institute of Oil Crops, Fujian Agriculture and Forestry University (FAFU), Fuzhou, China
[6]Oil Crops Research Institute (OCRI) of Chinese Academy of Agricultural Sciences (CAAS), Wuhan, China

***Author for correspondence: r.k.varshney@cgiar.org**

Aflatoxin, a "hidden poison" due to its slow and adverse effect on various biological pathways in humans, is a major food safety concern across globe which adversely impact the global groundnut trade and commerce. A combination of genetic resistance for *in vitro* seed colonization (IVSC), pre-harvest aflatoxin contamination (PAC) and aflatoxin production (AP) together with pre- and post-harvest management may provide a sustainable solution to aflatoxin contamination. In this context, we have performed transcriptomic analyses and genome-wide association study (GWAS) in diverse panel as well as multi-parent advanced generation intercross (MAGIC) populations. The transcriptome analyses have identified several important candidate genes and their involvement in pathways for three types of resistance mechanisms for aflatoxin contamination. The plant defense response to resistance seems to be a multifaceted endeavor that includes the recognition of a pathogen, the activation of a number of genes that lead to changes in the plant cell wall, changes in ion flux across the plasma membrane, formation of reactive oxygen species (ROS), production of phytoalexins, PR related proteins that induce resistance against pathogen attack. The GWAS analysis in diverse collection identified associated genomic regions on chromosome 12 for resistance to *A. flavus* infection and chromosomes 7, 9, 14, 15 and 18 for resistance to aflatoxin contamination. Also the genetic analysis is in progress using MAGIC population. The above efforts are likely to improve understanding of molecular mechanisms and identify associated genomic regions/ candidate genes for aflatoxin contamination which in turn would help accelerating breeding of aflatoxin contamination resistant groundnut varieties.

5.22 Identification and molecular mechanism dissection of drought resistance in peanut (*Arachis hypogaea* L.)

Xiurong Zhang, Suqing Zhu, Lu Luo, Kun Zhang, Yongshan Wan* and Fengzhen Liu*

State Key Laboratory of Crop Biology, Shandong Key Laboratory of Crop Biology, Shandong Agricultural University, Tai'an 271018, China.

***Author for correspondence: yswan@sdau.edu.cn; liufz@sdau.edu.cn**

Peanut is an important oilseed crop, but drought stress is the primary limiting factor affecting yield and quality. In our study, the drought resistance including drought resistance coefficient (DC) and drought resistance index (DI) of peanut germplasm resources was identified and evaluated under natural drought stress. A total of 32 drought-resistant traits which were significantly correlated with drought resistance were investigated, including agronomic, leaf and root morphological characters, osmotic regulation and antioxidant ability, and 10 key traits and their selection criteria were subsequently developed. An association panel comprised of 268 accessions was constructed, and the genotypic database was established by 391 classical SSR and 17000 SNP markers. Through association analysis, 22 SSR were found to be associated with drought resistance and drought-resistant traits, and 27 SNP were related to leaf morphology and structure. The dominant drought resistance characters and utilization ways of each germplasm were analyzed based on traits performance and allelic variation information. Meanwhile, the drought resistance mechanism was analyzed for breeding varieties including Shanhua7, Shanhua9, Shanhua11, Shanhua13, Shanhua8 and Shanhua12, among which Shanhua9 aggregated elite traits related to root and leaf morphology accompanied by 15 excellent alleles derived from related markers from its parents, ranking the first place in planting area in China. The results provided reference information for the utilization of drought resistant germplasm and dissection of drought resistance mechanism, providing valuable clues for marker assisted selection (MAS) in improving breeding efficiency for drought resistance.

5.23 Identification of shell resistance to infection of *Aspergillus flavus* in peanut (*Arachis hypogaea* L.)

YB Ding, XK Qiu, YP Kang, L Huang, XP Ren, YN Chen, HY Luo, N Liu, WG Chen, DX Huai, LY Yan, Y Lei,HF Jiang*, BS Liao*

Oil Crops Research Institute of Chinese Academy of Agricultural Sciences, Wuhan, 430062, China

***Author for correspondence: lboshou@hotmail.com**

Aflatoxin contamination has been a serious factor affecting food safety and industry development of peanut. The pod shell is the preliminary physical protection mechanism of peanut seeds against infection of fugus, but little research has been made on shell resistance. In this research, we developed a reliable method for evaluating the shell resistance to infection of *Aspergillus flavus* by comparing reaction to pod inoculation of different peanut varieties under laboratory conditions. The degree of infection of shell by *A.flavus* was divided into 1 to 9 scales. The optimal combination of an inoculum concentration as 2×10^6 spores per milliliter and incubation for 7 days after inoculation was determined by comparing several combinations of inoculum concentration and incubation period. Shell resistance of 99 accessions of the Chinese peanut mini-mini core collection during 2016 to 2018 was evaluated using the techniques developed. Several accessions including XH-13 were repeatedly found as relatively resistant with their average infection index less than 0.5. Further research efforts for investigating mechanism of the shell resistance are underway.

5.24 Integrating resistances to the major soil-borne diseases in peanut through conventional and genomic approaches

Boshou Liao[1*], Yong Lei[1], Liying Yan[1], Hari Sudini[2], Yingbin Ding[1], Xike Qiu[1], Bolun Yu[1], Li Huang[1], Yunning Chen[1], Huaiyong Luo[1], Manish K. Pandey[2], Xiaojing Zhou[1], Rajeev K. Varshney[2], Huifang Jiang[1]

[1] Oil Crops Research Institute (OCRI) of the Chinese Academy of Agricultural Sciences (CAAS), Wuhan, 430062, China
[2] International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad 502324, India

***Author for correspondence: Boshou Liao, lboshou@hotmail.com**

Concurrent occurrence of several important soil-borne diseases is becoming more and more frequent and devastating to yield and food safety of peanut in many regions. As most soil-borne diseases including bacterial wilt, pod rot, stem rot, and pre-harvest infection by *Aspergillus* spp are very difficult to control in field, breeding and planting peanut varieties with desirable multiple resistance is the most effective control approach. At OCRI-CAAS, improved peanut varieties including Zhonghua 6 with resistance to bacterial wilt, pod rot and aflatoxin production have been developed. More recently, elite germplasm accessions with desirable shell resistance to *Aspergillus* infection were identified. Progress has also been made on developing artificial inoculation techniques for white mold of peanut and identifying resistant germplasm lines. Molecular markers for resistance to bacterial wilt and aflatoxin have been identified. More research efforts are underway for identifying more reliable markers especially for resistance to pod rot and white mold in order to facilitate marker-assisted breeding. In terms of the peanut producing regions in central and south China, more breeding efforts are needed to integrate the resistance to bacterial wilt, pod rot, white mold, and three mechanisms to aflatoxin contamination (shell and testa resistance to *Aspergillus* infection and resistance to aflatoxin production in seed) into the high yielding and high oleate peanut genotypes.

5.25 Two adjacent genomic regions on chromosome B02 control genetic resistance against bacterial wilt in peanut

Huaiyong Luo[1], Manish K. Pandey[2], Ye Zhi[3], Huan Zhang[1], Siliang Xu[1], Jianbin Guo[1], Bei Wu[1], Haiwen Chen[1], Xiaoping Ren[1], Xiaojing Zhou[1], Yuning Chen[1], Weigang Chen[1], Li Huang[1], Nian Liu[1], Hari K. Sudini[2], Rajeev K. Varshney[2], Yong Lei[1], Boshou Liao[1*], Huifang Jiang[1*]

[1]Oil Crops Research Institute (OCRI) of Chinese Academy of Agricultural Sciences (CAAS), Wuhan 430062, China;
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad 502324, India;
[3]Angel Yeast Co., Ltd, Yichang, Hubei 443003, China

***Author for correspondence: Huifang Jiang, peanutlab@oilcrops.cn**

Bacterial wilt is one of the most devastating plant diseases and attacks more than 450 plant species including peanut. Utilization of genetic resistance is the most economic and effective approach to control bacterial wilt in peanut. However, the genetic study of bacterial wilt resistance (BWR) in peanut is still quite limited. In this context, we deployed linkage mapping as well as sequencing-based mapping approach for discovery of genomic regions and candidate genes for BWR in a recombination inbred line (RIL) population (268 progenies) of peanut. The linkage map-based quantitative trait locus (QTL) mapping identified a stable QTL (*qBWRB02.1*) on chromosome B02 with 37.79%-78.86% phenotypic variation explained (PVE) across five environments. The sequencing-based mapping approach, QTL-seq, facilitated further dissection of the major QTL *qBWRB02.1* into two adjacent genomic regions, *qBWRB02.1a* (2.81-4.24 Mb) and *qBWRB02.1b* (6.54-8.75 Mb), significantly associated with BWR ($P<0.001$). Mapping of newly developed Kompetitive Allele-Specific PCR (KASP) markers on the genetic map confirmed their stable expressions across five environments, and the effects of *qBWRB02.1a* (49.43%-68.86% PVE) were much higher than *qBWRB02.1b* (3.96%-6.48% PVE). A total of 19 putative candidate genes that affected by 49 non-synonymous SNPs were identified for *qBWRB02a*, and ten of them were predicted to code for disease resistance proteins. The major QTL *qBWRB02.1a* and validated KASP markers could be deployed in genomics-assisted breeding (GAB) to develop improved peanut varieties with enhanced BWR.

5.26 Evaluation of groundnut genotypes for resistance to pre-harvest *Aspergillus flavus* and aflatoxin contamination in Ghana

Kwabena Asare Bediako[1, 2], James Yaw Asibuo[2], Daniel Dzidzienyo[1], Kwadwo Ofori[1], Samuel Kwame Offei[1], Zippora Appiah-Kubi[2]

[1] *West Africa Centre for Crop Improvement, University of Ghana, Legon, Accra, Ghana*
[2] *CSIR-Crops Research Institute, P. O. Box 3785, Kumasi, Ghana*

***Author for correspondence: jyasibuo@gmail.com**

Groundnut production in Ghana is mainly concentrated in the regions bedeviled with periodic drought and high risk of aflatoxin contamination with attendant acute and chronic toxicities in humans and animals. The present study was conducted to identify groundnut genotypes with low *Aspergillus flavus* infection and aflatoxin contamination in the field. Twenty-seven groundnut genotypes were evaluated at Fumesua and Nyankpala under artificial inoculation with *A. flavus* and terminal drought conditions in a Lattice design with three replications. The results revealed significant genotype and genotype x location effects for kernel *A. flavus* infection and aflatoxin contamination in the pooled analysis. Aflatoxin contamination ranged from 11.24 to 77.79 ng/g (mean = 27.37 ng/g) at Fumesua, whereas levels obtained at Nyankpala varied from 9.97 to 140.28 ng/g (mean = 71.27 ng/g). Kernel *A. flavus* infection was in the range of 8.09 to 36.26% (mean = 22.10%) for Fumesua and 4.05 to 69.65% (mean = 39.31%) for Nyankpala. Genotypes ICGV 02171, ICG 15396, ICGV 03331, ICGV 03401 and ICG 4729 appeared consistently among the top 10 aflatoxin resistant genotypes at Fumesua and Nyankpala, indicating their stability across the two locations. However, ICG 4729, ICGV 03331 and ICGV 03401 showed aflatoxin concentrations in conformity with the European Union Standard (15 ng/g) and the Ghana Standards Authority standard (20 ng/g). These genotypes were also found to support low levels of *A. flavus* growth in this study and could therefore be exploited for aflatoxin resistance breeding in Ghana.

Keywords: Resistance; aflatoxin breeding; kernel infection; drought; groundnut

6.1 Peanut shovelomics phenotyping root architecture and nodulation in the field

Qian Li[1], Lijie Li[1], Bin Wang[1], Zhiyong Zhang[1*], Baohong Zhang[2]

[1]Henan Collaborative Innovation Center of Modern Biological Breeding and Henan Key Laboratory for Molecular Ecology and Germplasm Innovation of Cotton and Wheat, Henan Institute of Science and Technology, Xinxiang, Henan 453003, China.
[2]Department of Biology, East Carolina University, Greenville, NC 27858, US.

***Author for correspondence: z_zy123@163.com**

Root shovelomics (all root architectural traits and other characteristics such as root nodule incubation being showed after shovel digging plants) not only is an easy way to investigate root architecture traits, but also is used in study root traits in relation to nutrient and water absorbance, and plant nutrient and water managements in the field. In this study, with 89 different types of peanuts were used to study the peanut root shovelomics variance and stability at harvest stage, specific root trait relationship with shoot growth, and some root traits coincidence between mature plants in the field and just emerging seedlings at the laboratory with paper pouch experiments. The results showed that the plant growth and root traits of the 89 different types of peanuts were variable to some extent in each year and were stable between two years of field experiments. For example, root dry weight varied from 0.48 to 2.31g in 2017, from 0.86 to 3.35g in 2018, and the coefficient of variation is 26.18% and 30.34%, respectively; nodule numbers varied from 18 to 198 per plant, from 15 to 201 per plant in 2018, and the coefficient of variation is 42.47% and 48.51%, respectively; lateral root angle varied from 45.94 to 90.99degree, from 42.69 to 94.75degree in 2018, and the coefficient of variation is 13.23% and 12.68%, respectively. At the same time, we found that the strong stability of dry weight of shoot and root and nodule numbers of different varieties during the two years. The correlation results showed that the dry weight of shoots and roots were significantly correlated with total root length, root surface area, total root volume and nodule number, indicating that the root structure is closely related to plant growth. The results of laboratory experiments showed that shoot dry weight of different varieties varied from 0.32 to 1.04g, and the coefficient of variation is 24.46%; root dry weight varied from 0.03 to 0.20g, and the coefficient of variation is 28.23%, total root length varied from 15.37 to 178.46cm, and the coefficient of variation is 50.60%; and root branching density varied from 5.73 to 11.75cm-1 and the coefficient of variation is 17.83%.As root architecture is closely related to plant uptake of nutrients, especially N, P, and K, which are the most universally limiting nutrients in agricultural soil, and water managements in the field, this study of peanut root characteristics can provide guidance for directing the cultivation and production of different genotypes depending on their respective root traits demonstrated by shovelomics.

Key words: Peanut (*Arachis hypogaea* L.); shovelomics; root system architecture; root nodulation.

6.2 Effects of superabsorbent polymer application on yield and quality of peanut (*Arachis hypogaea* L.) under un-mulching cultivation

Guanghui Li, Changsheng Li, Xingjun Wang, Chuanzhi Zhao, Han Xia, Shuzhen Zhao, Aiqin Li, Lei Hou*

Biotechnology Research Center, Shandong Academy of Agricultural Sciences; Shandong Provincial Key Laboratory of Crop Genetic Improvement，Ecology and Physiology, Jinan, Shandong, 250100

***Author for correspondence: houlei9042@163.com**

Mulching film could remarkably increase peanut yield, meanwhile, causing serious pollution. Superabsorbent polymer, with efficient water absorption and water-retaining property, has become a new technology for water-saving in many crops. In this work, a field study was conducted to investigate pod plumpness, yield, nutrition quality under un-mulching (UM), mulching film (FM) and superabsorbent polymer (SP) condition to explore effect of FM and SP on water-saving, yield and quality in peanut. The results showed that pod yield under SP (75~225kg·hm^{-2}) was 3.48 %~16.01 % higher compared with UM. When the SP amount applied increased, the yield increased first and then decreased. The yield was the highest when 150 kg·hm^{-2} of SP (SP150) was applied. The yield of the SP150 was no significant (P>0.05) difference from FM. Compared with UM, the plump rate of pods and seeds significantly increased under FM, it was 14.62 % and 14.11 % higher. The plump rate of pods and seeds gradually increased before SP150 was applied, then decreased with the amount of SP increased continuously. It was 10.99 % and 15.99 % higher than UM when the SP150 condition. Quality analysis demonstrated that quality traits including fat, oleic acid, the ratio of oleic acid to linoleic acid (O/L) of all seeds under FM and SP treatments were higher compared with UM. The general sample including all seeds with economic value increased more than the typical sample containing only plump and consistent seeds. The fat and oleic acid content, O/L of general sample increased by 9.66 %, 12.27%, 23.08 % compared with UM when SP150 was applied. It was no significant difference from FM. All these results indicate that SP had positive effect on yield and quality of peanut. The SP application of 150 kg·hm^{-2} improved most pod plumpness and yield, increased quality traits of peanut seeds mainly by the general sample. It was basically the same as FM. This study provided a theoretical basis for rational application of superabsorbent polymer and developing a new technology for water-saving in dry region peanut.

Key words: peanut, superabsorbent polymer, plumpness, yield, quality

6.3 Research on diversity of rhizosphere microorganism in peanut //maize intercropping system

Xiaoshu Chen[1a], Zhengkun Zhang[2a], Hailong Liu[1], Qiyun Li[2*], Yongchao Lv[1], Huayuan Gao[1*], Shaolun Wang[1], Qia Ning[1], Chunyu Li[1] & Xiaopin Sun[1]

[1]Peanut Research Institute, Jilin Academy of Agricultral Sciences, Gongzhuling 136100, China
[2]Institute of Plant Protection, Jilin Academy of Agriculture Science, Gongzhuling 136100, China
[a] These authors contributed equally to this work.

***Author for correspondence: ghy6413@163.com**

Intercropping is a comprehensive and efficient crop cultivation method which can not only increase the quantity of soil microorganisms, but also change the community structure of soil microorganisms and increase the biodiversity of farmland. In order to reveal the changes of rhizosphere soil microbial community structure and diversity in peanut //maize 6:6 intercropping mode, the rhizosphere soil of intercropping peanut, intercropping maize, monoculture peanut and monoculture maize in five growth stage were sequenced by high throughput sequencing. The results showed that, whatever monocropping or intercropping, Shannon index was first increased and then decreased of five growth period, and the highest value at maize flare opening stage and peanut pod setting stage, respectively. The distribution of microbial communities at different growth stages by 16SrDNA and ITS analysis was carried out, and Alphaproteobacteria was the dominant groups both in monocropping and intercropping, and gradually increase along with growing. The relative abundance of major bacterial species in soil samples at different growth stages was similar. There were significant differences in the distribution of fungal communities, Mortierellomycetes, Sordariomycetes and Tremellomycetes had significant changes compared to seedling stage. Peanut//maize intercropping can change bacterial and fungal composition structure in rhizophere soils, bacterial composition structure in intercropping and monoculture soils was similar, fungal diversity of intercropping was more abundance than monoculture.

6.4 The molecular and ecological mechanism of improving iron nutrition in peanuts intercropped with maize in calcareous soil

Yuanmei Zuo*, Hongchun Xiong, Xiaotong Guo, Wei Qiu, Nanqi Wang

Department of Plant Nutrition, Key Laboratory of Plant-Soil Interactions, Ministry of Education, China Agricultural University, Beijing 100193, P. R. China

***Author for correspondence: zuoym@cau.edu.cn**

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Peanut (*Arachis hypogaea*) is the fifth important oilseed crop in the world and is accounting for 30% of the total oilseed production in China. However, iron deficiency frequently limits both crop yield and quality for monocropped peanut grown in calcareous soils. Peanut/maize intercropping is a sustainable and effective agroecosystem that evidently enhances the iron nutrition of peanuts in calcareous soils. Significant progress has been made in Fe improvement of peanut intercropped with maize in last decade. First, our results indicated that phytosiderophores (PS) secreted by maize not only satisfied the demand of Fe for itself, but also significantly played a key role of phytosiderophores in improving the Fe nutrition of intercropped peanut at the molecular and ecological level. Second, we identified iron transport AhNRAMP, AhYL1, AhIRT1 and AhFRO1 gene in peanut, and importantly AhYL1 gene showed novel gene function which could uptake Fe(III)–DMA. Finally, In our recent study, the proteomics and transcriptomes analysis suggested that six key genes expression were significantly upregulated in jasmonate biosynthesis and jasmonate concentration were also increased in the maize roots of the intercropping system. These results imply that jasmonate may act as a signaling molecule, playing an important role in intercropping through rhizosphere interaction. Our results will illusate the ecological significance of peanut/maize intercropping for improving the adaptation of plants to environmental stress and the possible molecular mechanism of intercropping improvement in iron nutrition of crops. Our study would also provide scientific and technical evidence for improvement resources efficiency and high crop production and food security through plant interaction in intercropping systems. Further investigations are needed to clarify the contributions of other processes to Fe uptake and the transitions of peanuts in intercropped systems.

Key words: Intercropping of maize and peanut, iron improvement, novel gene function, molecular and ecological regulation.

6.5 Differences in drought tolerance and physiological response of peanut at seedling stage

Jingyao Ren, Jing Wang, Chunji Jiang, Xinhua Zhao, Xiaoguang Wang, Shuli Zhao, Xibo Liu, Chao Zhong, Haiqiu Yu*

Shenyang Agricultural University, Shenyang, 110161, China

***Author for correspondence: yuhaiqiu@syau.edu.cn**

Peanut is an important oil crop, with an average annual sown area of more than four million hectares in China. However, most of them grow in arid or semi-arid areas, where water stress has a great impact on their quality and yield. Therefore, the research on drought resistance is of great significance to the production of peanut. In this study, 20% PEG was used to simulate drought stress, and seven indexes such as relative plant fresh weight, relative water content, leaf weight, water loss rate of detached leaves, damage rate, withered index and proline contents were taken as drought tolerance evaluation criteria. Four varieties (two drought tolerant varieties and two sensitive varieties) were selected by comprehensive membership function to explore the physiological regulation mechanism to drought stress. Through the determination of physiological indexes, it is found that the protective enzyme activity of drought tolerance varieties was usually higher than the sensitive varieties, they accumulate more osmotic substances, regulate the biosynthesis of secondary metabolites to strengthen the ability of self-regulation and maintain internal environmental stability. Five genes related to drought tolerance were determined in the study, and the results showed that most of the genes were highly expressed in drought tolerant varieties, while the expression of AhNCED1 was higher in sensitive varieties at the early stage but decreased quickly. The physiological mechanism of peanut to deal with drought environment was discussed in this study, which enriched the physiological research of peanut drought tolerance and played a guiding role in field production.

6.6 Roles of fertilizer in peanut development and fertilization practice

Xinguo Li[1,2*], Jialei Zhang[1,2], Feng Guo[1,2], Shubo Wan[1]

[1]Biotechnology Research Center of Shandong Academy of Agricultural Sciences, Ji'nan, 250100, China;
[2]Shandong Provincial Key Laboratory of Crop Genetic Improvement, Ecology and Physiology, Ji'nan, 250100, China

***Author for correspondence: xinguol@163.com**

Large consumption and low utilization rate of agricultural fertilizer are the main problems in China. As to peanut cultivation, averagely more than 10kg of pure nitrogen per ha was used in China, which is much higher than other countries. Conventionally, excessive quick-acting fertilizer would inhibit rhizobia develop, and cause environmental pollution. How to apply fertilizer and what's kind of fertilizer, which can both benefit nitrogen fixation of rhizobia, and meet the request of seedling and pod filling stages?

Generally, the growth stage of peanut is divided into five stages: germination stage, seedling stage, flowering stage, pod-bearing stage and fruiting stage. During seedling stage, the root system is developing, and the rhizobia is in infection and nodule is in development. Exogenous nitrogen fertilizer is needed for growth and nodule formation; during flowering stage and pod-bearing stage, Rhizobia have strong nitrogen fixation ability. Fixed nitrogen through rhizobia about 6kg/mu, accounting for more than 70% of the total nitrogen needed; during middle to late pod-bearing stage and fruiting stage, nodule is senescent and lost nitrogen fixation ability. Our previous studies showed that calcium can not only improve peanut resistance to environmental stress but also improve pod filling. Additionally, low nitrogen application can induce significantly decrease of nitrogen fixation of root nodules. Based on previous studies, we put forward whole-period controllable fertilization. Initiating nitrogen for early stages, calcium for middle stages and controllable nitrogen for late stages. Controllable fertilizer combining with quick-acting ones to need all stages request. The key techniques of whole-period controllable fertilization was established based on Double layer fertilizer techniques and layered fertilization technique. In recent years, the results of multi-region and multi-site experiments show that the nitrogen fixation capacity of root nodules can be effectively improved. An average yield increases more than 450kg per ha.

6.7 Effects of maize root exudates on allelopathy of phenolic acids in continuous cropping peanut soil

Ping Liu[1], Qingkai Li[2,3], Haijun Zhao[4], Feng Guo[2,3], Jialei Zhang[2,3], Zhaohui Tang[2,3], Xinguo Li[2,3], Shubo Wan[3,4*]

[1]Institute of Agricultural Resources and Environment, Shandong Academy of Agricultural Sciences, Jinan 250100, China;
[2]Biotechnology Research Center, Shandong Academy of Agricultural Sciences, Jinan 250100, China;
[3]Key Laboratory of Crop Genetic Improvement and Ecological Physiology of Shandong Province, Jinan 250100, China;
[4]Shandong Academy of Agricultural Sciences, Jinan 250100, China.

*** Author for correspondence: wanshubo2016@163.com**

To explore the mechanism of maize//peanut intercropping alleviate peanut continuous cropping obstacles, effect of maize root exudates was explored in maize//peanut intercropping system on allelopathy of phenolic acids in soil of continuously cropped peanut. Maize root exudate was extracted at tasseling stage by CH_2Cl_2 (dichloromethane). Then it was added into soil containing different concentrations of 3 main phenolic acid compounds mixture (cinnamic acid, phthalic acid and p-hydroxybenzoic acid). Soil micro-environment was investigated. Results demonstrated allelopathic inhibition by phenolic acids on soil microbial biomass, microbial activity, enzyme activity and nutrient content. While the addition of corn root exudates increased respiration rate, enzyme activity, microbial biomass and nutrient content of the phenolic acids-treated soils, especially the low concentration phenolic acid treatments, which increased by 7.58%, 6.73%, 7.72% and 4.90% on the average, respectively, compared with the treatment of phenolic acids during the whole culture period. The root exudates of maize reduced the allelopathic index of phenolic acids on various indexes of soil with a larger decrease in the treatment of low concentration, and the allelopathic index of soil microbial biomass carbon and nitrogen content, microbial activity, enzyme activity and nutrient content treated with maize root exudates decreased by 21.57%, 21.19%, 26.32% and 20.95% on the average, respectively. Three times of sampling, the allelopathic effects of phenolic acids first increased and then weakened, and each treatment reached the strongest on the 10th day; while the effect of maize root exudates on the allelopathic effect of phenolic acids was the strongest on the 5th day, and then showed a weakening trend. All above indicated that the root exudates of maize could alleviate the allelopathic effect of phenolic acids on soil micro-ecological environment to a certain extent, which provides a theoretical basis for the technology of maize//peanut intercropping to alleviate peanut continuous cropping obstacles.

Key words: maize root exudates; maize//peanut intercropping; peanut; phenolic acid; allelopathy; continuous cropping obstacle

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Patent number：ZL 2014 1 0463583.1 ZL 2014 1 0251829.9 Patent type：Invention patent

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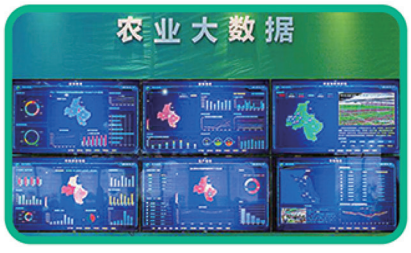

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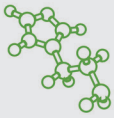

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建库测序

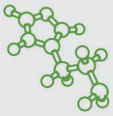
动植物基因组

动植物重测序

人类疾病

微生物基因组

转录调控


蛋白质组

分子育种

基因编辑

- 国际领先的基因组学研究中心
  软件著作权149项，专利22项，首款NGS多基因检测试剂盒获批上市
- 中国最高通量基因测序中心
  全球运行NovaSeq、PacBio Sequel、PromethION、HiSeq X、HiSeq 2000/2500/4000、MiSeq、10x Genomics Chromium ™、NextSeq 500、Life Ion Proton（DA8600）、S5XL 和 Q ExactiveTMHF-X 测序平台，可提供多种测序读长、通量和时间周期选择，满足各类科研及应用对成本和速度的差异化需求。
- 发表SCI论文400+，IF 2626+
  已发表Nature、Science 及Cell系列文章34余篇

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400-658-1585
service@novogene.com www.novogene.com

弥生生物
GENE MISSION

上海弥生生物科技有限公司 Tel: +86 18217269800
Email: tech@peanutedit.com Web: www. peanutedit. com

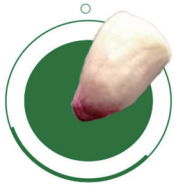
弥生生物 GENE MISSION | 花生基因编辑 PEANUTEDIT

提供专业化的花生基因编辑解决方案

Leading Specialized Gene-editing Services & Solutions

花生基因编辑突变体库计划

The Great Project of the Gene-editing Peanut Mutant Library

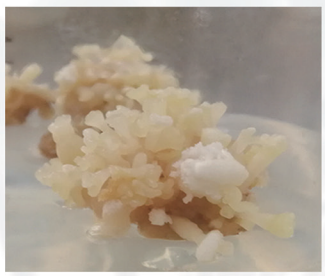
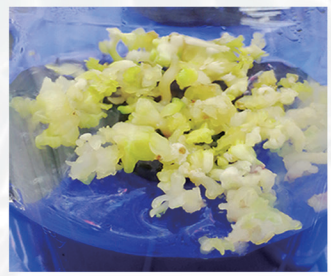
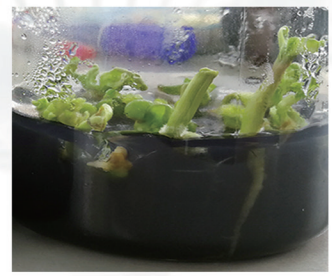


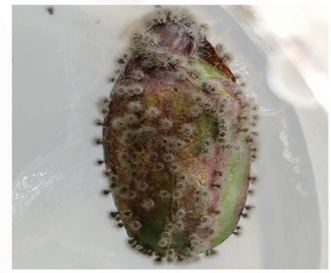
花生基因编辑技术服务

The Specialized Gene-editing Services & Solutions in peanut

花生遗传转化技术服务

The Specialized Gene-transformation Services & Solutions in peanut



本册封面图片由弥生生物提供

上海弥生生物科技有限公司 | GENE MISSION Tel:+86 18217269800 Email: tech@peanutedit.com Web: www.peanutedit.com

Qingdao Foodlink Co.,Ltd

Qingdao Foodlink Co.,Ltd was established in 2000 , it's building area is more than 30,000 square meters. Foodlink is a professional enterprises engaged in peanut and peanut products, pumpkin kernels, sunflower inshells and roasted sunflower inshells production. Foodlink has many years food processing and export experience, and has been Shandong Province NO.1 enterprise at the aspect of peanuts export business in Europe for many years.In recent years, we has vigorously exploited sunflower products, taking into account
both export and domestic sales, with annual sales increasing by more than 30%.

Thanks to our strict quality and food safety control, rick and reliable product knowledge, Foodlink has grown very quickly to become a very important nuts supplier in the domestic and international market ,and has a good reputation and reputation in peanuts and sunflowers industry. Foodlink has been the leader of Qingdao peanut import and Export Industry Association since 2013.

Since Foodlink establishment, we always regard "Quality is the lifeline of the enterprise" as our value. With the development of the company, a complete set of scientific and perfect quality management system has been gradually formed. Since 2005, Foodlink has passed HACCP, KOSHER, BRC and IFS and organic food authentication and so on.

On the premise of strengthening the quality control of the production process, Foodlink has achieved a new breakthrough in the supply of raw materials. We took the lead in establishing our own raw material bases in the main peanut planting areas (Shandong and Liaoning province) in China, and fundamentally guaranteed the safety of raw materials.At the same time, Foodlink introduced high oleic acid peanuts varieties from the United States since 2013. Because of its high "Oleic acid-linoleic acid" ratio, this variety is healthier and more durable than traditional peanuts, prolonging the shelf life of the products, and has become a new choice for many Chinese manufacturers.

Our own brand ″SAFELAND ″, has occupied a place in the domestic market after many years efforts. Quality, reputation, health and safety are the cores of our company' s business philosophy. The brand ″SAFELAND″ implies the paradise of safe
food. Chinese brand "Suifu Garden" : "Sui"means to follow
and guide the concept of healthy consumption;
"Fu"means healthy and happy; "Garden" is taking the
product as a medium, dealers as a bridge, and to build food safety paradise together with consumers .
"SAFELAND" and "Suifu Garden" are not only the responsibility and obligation of our company, bu t also our pursuit and commitment.

INTERNATIONAL COMPETENCE CENTER FOR THE ASSESSMENT OF RESPONSIBLE BUSINESS PRACTICES

ENAC ACERTA Leaders in reliability Líderes en fiabilidad

Certification body accredited by ENAC against UNE-EN ISO/IEC 17065 with n°332/C-PR066 for BRC certification, and having signed an agreement with the BRC owners

awards this

CERTIFICATE

To

QINGDAO FOODLINK CO., LTD.

BRC site code: 2387263

No.12 Century Avenue, Fengtai Zone, Pingdu, Qingdao City, Shandong Province, China

Which has been evaluated and found to meet the requirements of

Global Standard for Food Safety

ISSUE 7: JANUARY 2015

Scope:	De-stoning, sorting, blanching, roasting of peanut products (groundnut in shells, groundnut kernels, blanched peanuts, Chinese roasted peanuts, etc.), De-stoning, sorting, roasting of sunflower seeds products (sunflower seeds in shells, roast sunflower seeds, etc.), De-stoning, sorting of Pumpkin seeds and Goji berry in plastic bags.
Voluntary Modules	None
Exclusions from scope:	None
Product Categories:	Category 5: Fruits, vegetables and nuts Category 15: Dried food and ingredients
Achieved Grade:	B
Audit programme:	Announced

Certificate number:	CC-PBR-180/18
Certificate issue date:	2018/06/22
Certificate expiry date:	2019/05/30
Date(s) of audit:	2018/05/13 & 14
Re-audit due date: from	2019/03/21 to 2019/04/18
Lead Auditor number:	080022

Authorized by:

Signed by: Mat°as Romero Olmedo
CEO – Managing director

Rev. 17

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ACERTA H.O. • Calle Aracena , 15 – 28023 Madrid (Spain) • Tel.: (+34) 91 740 2660 • Fax: (+34) 91 740 2661 – info@acerta-cert.com

CQC

HACCP SYSTEM CERTIFICATE

Certificate No.: 001HACCP1600769

THIS IS TO CERTIFY THAT

QINGDAO FOODLINK CO., LTD.

Registered address: No.12 Century Avenue, Fengtai Zone, Pingdu City, Qingdao City, Shandong Province, P.R.China
Produced address: No.12 Century Avenue, Fengtai Zone, Pingdu City, Qingdao City, Shandong Province, P.R.China
South Side of West End, Liangan Road, Tonghe Zone, Pingdu City, Qingdao City, Shandong Province, P.R.China

HACCP SYSTEM

has been awarded the certificate for compliance with
GB/T 27341-2009 Hazard Analysis and Critical Control Point (HACCP) System—General Requirements for Food Processing Plant
GB 14881-2013 General Hygienic Regulation for Food Manufacturing

The HACCP System Applies in the Following Area:

No.12 Century Avenue, Fengtai Zone, Pingdu City, Qingdao City, Shandong Province, P.R.China: Processing of groundnut in shells, groundnut kernels, blanched peanuts, Chinese roasted diced blanched peanuts, sunflower in shells, Chinese roasted peanuts, Chinese roasted groundnut kernels, Chinese roasted sunflower seeds, Pumpkin seeds and kernels; Repacking of goji berries
South Side of West End, Liangan Road, Tonghe Zone, Pingdu City, Qingdao City, Shandong Province, P.R.China: Processing of sunflower in shells

Certified since: December 19, 2016 Valid from: December 19, 2016 Valid until: December 18, 2019

CQC No. : 0011602206080R0M/3700

After a surveillance cycle, the certificate is valid only when used together with an Acceptance Notice of Surveillance Audit issued by CQC. Please access http://food.cnca.cn for checking validity of the certificate and information of specific production places, workshops etc.

CNAS 中国认可 管理体系 MANAGEMENT SYSTEM CNAS C001-M

Signed by: Wang Kejiao

CHINA QUALITY CERTIFICATION CENTRE

Section 9, No.18A, Hanadaxiaolie South Fourth Ring Road, Xiba'Nkou Road), Beijing 100073,China
http://www.cqc.com.cn

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2015年版

INTERNATIONAL COMPETENCE CENTER FOR THE ASSESSMENT OF RESPONSIBLE BUSINESS PRACTICES

ENAC ACERTA Leaders in reliability Líderes en fiabilidad

Certification body accredited for IFS certification and having signed an agreement with the IFS owners

awards this

CERTIFICATE

To

QINGDAO FOODLINK CO., LTD

COID: 32633

Site address: No.12 Century Avenue, Fengtai Zone, Pingdu, Qingdao City, Shandong Province, China
Veterinary agreement number: 3700D13319

Which has been evaluated and found to meet the requirements of

IFS Food Version 6, April 2014

and other associated normative documents

Audit scope:	De-stoning, sorting, blanching, roasting of peanut products (groundnut in shells, groundnut kernels, blanched peanuts, Chinese roasted peanuts, etc.), De-stoning, sorting, roasting of sunflower seeds products (sunflower seeds in shells, roast sunflower seeds, etc.), De-stoning, sorting of Pumpkin seeds and Goji berry in plastic bags.
Product scope(s):	5. Fruit and vegetables
Technology scopes:	D/E /F
Level achieved:	Higher
Audit Programme:	Announced

Certificate number:	CC-IFS-119/18
Audit date:	2018/05/14
Certificate issue date:	2018/06/22
Certificate valid until:	2019/07/24
Next audit: between:	2019/04/04
and:	2019/06/13
	or unannounced

In Madrid, June 22nd, 2018

Signed by: Mat°as Romero Olmedo
CEO – Managing director

Rev.10

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青岛福德隆食品有限公司

青岛福德隆食品有限公司成立于2000年，建筑面积30000多平方米，专业从事花生及制品、南瓜籽仁、生熟葵花籽的生产。公司拥有多年食品加工与出口经验，连续多年保持山东省出口欧洲花生销量第一。近年来，大力开拓葵花籽产品，出口和内销同时兼顾，每年销量递增30%以上。公司基于严格的质量、食品安全控制，丰富且可靠的产品知识，现已成为国际/国内市场上重要的果仁供应商，并在本行业内具有很好的知名度与美誉度，从2013年起连续担任青岛花生进出口行业协会会长单位。

公司自成立之日起，始终把“质量是企业的生命线”作为企业的价值观。随着公司的发展，逐步形成了一整套科学、完善的质量管理体系。自2005年开始，先后通过了HACCP、有机产品、KOSHER、BRC和IFS等认证。

在强化过程质量控制的前提下，我司在原材料的供应上又实现了新的突破，率先在全国的主要花生产地（山东、辽宁）建立了自己的原料基地，从根本上保证了原材料的安全。同时自2013年开始，从美国引进高油酸品种，该品种因其高油亚比的特性，比传统花生更健康、更耐贮藏，延长了产品的货架期，已成为众多厂家的新选择。

我司自有品牌“SAFELAND随福园”，经过多年耕耘，已经在国内市场占据一席之地。质量、信誉、健康、安全是我公司经营理念的核心，英文品牌“SAFELAND”寓意为安全食品的乐土，体现了民以食为天，食以安为先的精神。中文品牌“随福园”中：随，是对健康消费理念的追随和引领；福，是健康、幸福；园，是以产品为媒介，以经销商为桥梁，与消费者共建食品安全的乐土。“SAFELAND”和“随福园”，既是我公司的责任和义务，也是我们的追求和承诺。

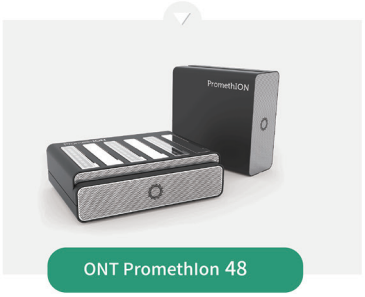
食品安全与检测中心
Food Safety & Inspection Center

质 量 管 理

GrandOmics RESEARCH SERVICE

Grandomics Biosciences Co., Ltd is a professional third-generation sequencing research service provider. Grandomics own a young but highly talented team with sophisticated genome sequencing and application experience. 150+ employees, 30+ long reading sequencing machines and terabase-scale supercomputer groups are working for a better genome sequencing service. It’ s open for all genomic scientists and labs to obtain a golden reference genome for nearly all species with NextOmics. With global collaboration, we have finished hundreds of pilot projects and participated in several influential articles in human, plant, animal, insects, bacteria genome and transcriptome, such as the genome of cultivated peanut Nature Genetics article. NextOmics sincerely welcome scientists from all over the world to work with us to climb the huge and complex genome mountain and discover the mystery of the unknown genome knowledge with long read sequencing technology!

GrandOmics Sequencing Plaform

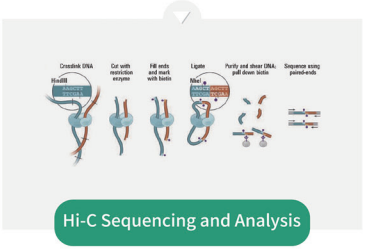


ONT PromethIon 48

PacBio Sequel

BioNano Saphyr

MGISEQ-2000



Hi-C Sequencing and Analysis

Supercomputing Groups

Star Products

Plant&Animal Genome	Microbial Genome	Transcriptome Rsearch	Modification Profile
de novo	Bacteria Complete Genome	Iso-seq	DNA methylation
Resequencing	Fungi Nearly-complete Genome	Direct RNA-seq	RNA methylation
Structural variants Analysis	16S/18S/ITS Amplicon Sequencing	RNA-seq	
	Metagenome	ONT RNA-seq	

GrandOmics Publications in TGS Genomics and Transcriptomic Fields

Grandomics Biosciences Co., Ltd

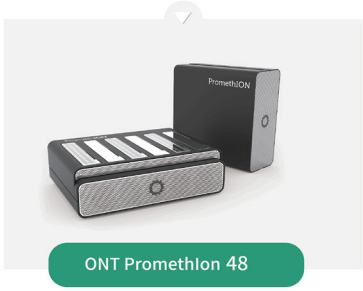
Add：19th Floor, Building C11, No.9 Huacheng Avenue, Wuhan, China

027-87782123 | sales-support@grandomics.com | www.nextomics.cn | www.grandomics.com

北京希望组——专业的三代测序科研服务提供商

自成立以来不断突破三代测序数据算法的壁垒，解决了复杂动植物基因组、超大型基因组、微生物基因组、全长转录组、微生物群体研究及人类基因组变异检测等领域的多项技术瓶颈。因为专注于三代测序技术开发和应用推广，拥有强大的交付能力、精准的市场定位以及精良的服务品质，成为众多科研机构优先合作的三代测序基因组中心，已完成了栽培花生基因组、苹果基因组、华夏一号基因组等在内的数百个三代测序科研项目，相关成果发表在 Nature Genetics、Nature Communications、Molecular Cell、Developmental Cell 等国际顶级期刊，累计影响因子超过 350。

希望组测序平台

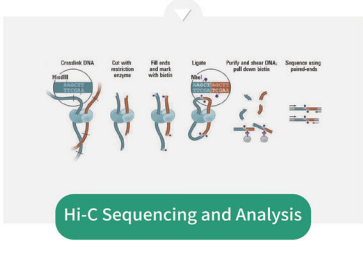


ONT PromethION 48

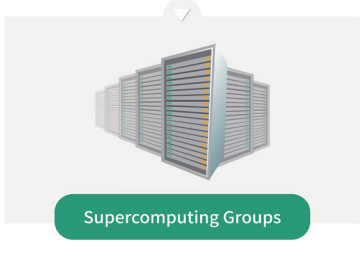
PacBio Sequel

BioNano Saphyr

MGISEQ-2000



Hi-C Sequencing and Analysis



Supercomputing Groups

明星产品

动植物基因组	微生物基因组	转录组研究	表观遗传研究
三代基因组 *de novo* 超大型基因组 基因组结构变异检测	细菌基因组完成图 真菌基因组近完成图 16S/18S/ITS 全长扩增子 宏基因组	ONT 全长转录组 Iso-Seq Direct RNA-Seq	DNA/RNA 甲基化修饰

希望组三代基因组、转录组代表性文章

希望组科服

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智惠仪器
Wisdom Instrument

Peanut NIR technology integrated solution

Shandong wisdom instrument Co., Ltd. commit to the promotion and application of international advanced scientific instruments and equipment, which is high-tech information enterprise that has research and development, sales and service. At present, we have reached a cooperation agreement with CARL ZEISS SPECTROSCOPY GMBH, focusing on the overall solution of ZEISS near infrared spectrometer and its related applications. As one of the leaders of the global optics and optoelectronics industry, ZEISS spectrometer is based on the long optical background and depth understanding of the wavelength-dependent nature of light to create high quality optical performance, robust and durable optical design and whole machine design to serve the users of various industries. For more than 170 years, the brand of ZEISS represents continuous innovation, precision manufacturing and superior quality. It sets standards for the industry with excellent products and services.

- Rapid quality evaluation of peanut purchase and storage
- Peanut screening before precision seeding
- Analysis of single/multi - grain peanut
- Measurement of peanut quality in processing

Calibration	Parameters
multi-peanut (Portable)	Fat、Protein、C16:0、C18:0、C18:1、C18:2、C20:0、C20:1、C22:0、C24:0、VLCFA、SFA
multi-peanut (table type)	Fat、Protein、C16:0、C18:0、C18:1、C18:2、C20:0、C20:1、C22:0、C24:0、VLCFA、SFA
single-peanut(table type)	Fat、Protein、C16:0、C18:0、C18:1、C18:2、C20:0、C20:1、C22:0、C24:0、VLCFA、SFA

Carl Zeiss Spectroscopy GmbH
Carl-Zeiss-Promenade 1007745 Jena
Phone：+49 3641 64-2838
Telefax：+49 3641 64-2485
F-Mail：info.spectroscopy@zeiss.com
www.zeiss.com/spectroscopy

山东智惠仪器有限公司
Shandong Wisdom instrument Co.,Ltd
山东省济南市历城区工业北路 58 号
Phone：+86 13964008535
E-Mail：sdwisdom@126.com
www.sdwisdom.cn

花生近红外技术整体解决方案

山东智惠仪器有限公司致力于国际先进科学仪器和设备的推广和应用，是集研发、销售和服务于一体的高科技信息企业。目前与德国 Carl Zeiss（卡尔·蔡司）公司达成合作协议，专注于 ZEISS 各类近红外光谱仪及配套应用的整体解决方案。德国卡尔·蔡司作为全球光学与光电行业的领先者，其光谱仪基于悠久的光学背景，凭借对光的波长相关性质的理解，其优质的光学性能，稳健耐用的光路设计和整机设计，服务于各个行业的用户。170 多年来，蔡司的品牌代表着持续创新、精密制造和优异质量，以卓越的产品和服务为业界订定了标准。

- 花生收储快速质量评价
- 单粒/多粒花生营养成分检测
- 精播育种前花生筛选
- 生产加工花生品质测量

定标	测量组份
多粒花生模型（便携式）	含油、蛋白、C16:0、C18:0、C18:1、C18:2、C20:0、C20:1、C22:0、C24:0、VLCFA、SFA
多粒花生模型（台式）	含油、蛋白、C16:0、C18:0、C18:1、C18:2、C20:0、C20:1、C22:0、C24:0、VLCFA、SFA
单粒花生模型（台式）	含油、蛋白、C16:0、C18:0、C18:1、C18:2、C20:0、C20:1、C22:0、C24:0、VLCFA、SFA

Carl Zeiss Spectroscopy GmbH
Carl-Zeiss-Promenade 1007745 Jena
Phone：+49 3641 64-2838
Telefax：+49 3641 64-2485
E-Mail：info.spectroscopy@zeiss.com
www.zeiss.com/spectroscopy

山东智惠仪器有限公司
Shandong Wisdom instrument Co.,Ltd
山东省济南市历城区工业北路 58 号
Phone：+86 13964008535
E-Mail：sdwisdom@126.com
www.sdwisdom.cn

百世兴食品
BAISHIXING FOOD

To be a benchmark of peanut food in China

20 years of dedicated attention

Established in 1998 with a registered capital of 10 million
A company integrating R&D, production and sales

Joy Go Peanut brand founder

National Joy Go Peanut trademark exclusive holder
the best-selling star products of BAISHIXING

Leading sales for 17 years

Combine mobile internet online marketing and offline integrated marketing
Sales are at the forefront of the industry

酒鬼花生

Quality Assurance

Selected raw materials, quality and safety

Big red coat peanuts from Henan, full of grains, fried with non-GMO small mustard seeds, and carefully seasoned with tribute salt from Sichuan, to achieve Joy Go Peanut.

Good taste, fine workmanship

Made by craftsmen with 20 years of work experience who precisely control oil temperature, taste, so that I meet you in the perfect way at the tip of the tongue.

Strict review for superior quality

Leading production process, maximally keep all kinds of basic nutrients in peanuts, golden color, moderate salty and sweet, fragrant, crisp.

Star Products

Original Flavor, Spicy Flavor

Original Flavor, Spicy Flavor, Spicy Chicken Flavor, crayfish Flavor

Original Flavor, Spicy Flavor, crayfish Flavor

Original Flavor, Spicy Flavor

Partial strategic partners

天猫 TMALL.COM
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BAISHIXING FOOD INDUSTRY CO,LTD SICHUAN
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Website: www.baishixing.com
400-028-8719
(9:00-17:00 Except holidays)

百世兴食品 BAISHIXING FOOD

成为中国花生食品的标杆企业

20载精诚专注
成立于1998年，注册资金1000万
集研发生产销售为一体的企业

酒鬼花生开创者
全国酒鬼花生商标独家持有者
百世兴畅销的明星产品

17年销量领先
结合移动互联网线上与线下整合营销
销量稳居行业前列

品质保障

精选原料 品质安全
源自河南的红衣大花生，粒粒饱满，采用非转基因小榨菜籽油炸制，再配以四川"贡盐"精心调味，成就酒鬼花生。

精工细作 味由心生
20年老师傅手工炒制，精准把控油温，调控口味，才让我以完美的方式和你相遇在舌尖。

严格把关 品质上乘
领先的生产工艺，最大地保留花生中的各种基础营养成分，色泽金黄，咸甜适中，香，酥，脆。

明星产品

原味 麻辣味

原味 麻辣味
辣子鸡味 小龙虾味

原味 麻辣味
小龙虾味

原味 麻辣味

部分战略合作伙伴

天猫 TMALL.COM　华润万家 vanguard　Carrefour 家乐福　盒马　METRO 麦德龙　中国石油　SINOPEC

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四川省百世兴食品产业有限公司
地址：成都市高新区天府一街两江国际B座1301
网址：www.baishixing.com
400-028-8719
(9:00-17:00 节假日除外)

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SHAN XI RUI AI DE SHANG MAO YOU XIAN GONG SI

农作物的种植推广
农产品的深加工
高油酸花生的培育
各类预包装食品

技术推广

种植培育

产业链接

领域研究

电话：18835546999

邮箱：sxczgwd@163.com

地址：山西省长治市太行西街政务中心C座605室

甄选花生 品质保证

甄选原产地优质花生
颗粒饱满 大小均匀
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高端品质享受

口感细腻
果色怡人
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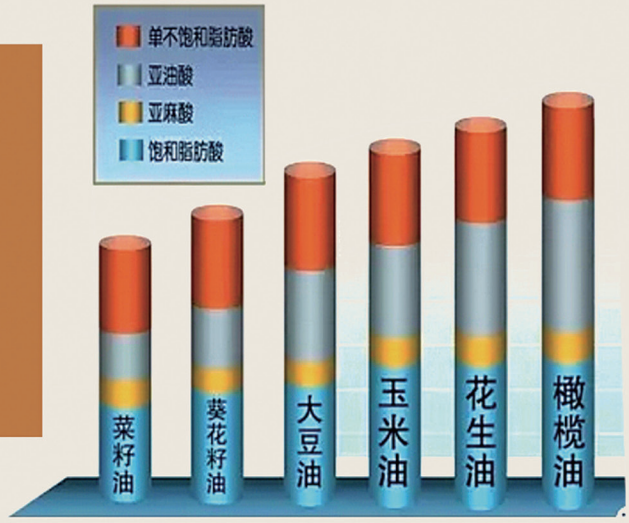
高油酸花生油与健康

优选高品质
花生新品种
油品达到橄榄油水平



品质之选

放心之选

山西瑞霭德商贸有限公司
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