

International Peanut Genome Initiative & the Peanut Genome Project Program Index

IPGI Strategic Plan Goal	PGP Component	Collaborative Research Projects
1	2	<u>Employing Microsatellite and SNP Markers to Track Functional Mutations and Evaluate Genetic Diversity in the USDA <i>Arachis</i> Germplasm Collection</u> , NA Barkley1*, ML Wang1, HT Stalker, 1USDA ARS Plant Genetic Resources Conservation Unit, Griffin, GA; 2Department of Crop Science, North Carolina State University, Raleigh, NC
1	2	<u>Advances on the scientific knowledge and use of peanut wild relatives in Brazil</u> , JFM Valls, Embrapa Genetic Resources and Biotechnology, Brasília, Brazil
1	2	<u>Capturing genetic diversity from peanut wild relatives: Advanced Backcross QTLs analysis and CSLL construction</u> , D Foncéka1*, T Hodo-Abalo2, R Rivallan1, H Vignes1, I Faye2, O. Ndoye2, B Courtois1 & JF. Rami1. 1 CIRAD, Montpellier, France. 2I SRA/CERAAS, Thiès Escalé, Senegal.
1	2	<u>Broadening the genetic base of peanut: Introgression of wild <i>Arachis</i> resistance genes using the Tetraploid Route with the aid of molecular and cytogenetic markers</u> . SCM Leal-Bertioli1*, MC Moretzsohn1, PM Guimarães1, SP Santos2,3, S Nielsen1, ACG Araujo1, ACM Brasileiro1, CV Morgante1,4, DJ Bertioli2,3. Embrapa Genetic Resources and Biotechnology, Brasília, Brazil. 2University of Brasília, Campus Darcy Ribeiro, Brazil. 3Catholic University of Brasília, Brasília, Brazil. 4Embrapa Semi-Arid, Petrolina, Brazil.
1	2	<u>Potential of new <i>Arachis</i> amphidiploids as sources of resistance to leafspots and rust</u> . AP Fávoro1*, MD Michelotto2, JF Santos3, ALM Martins2 & IJ Godoy3. 1Embrapa Pecuária Sudeste, São Carlos-SP, Brazil, 2APTA, Pólo Regional Centro-Norte, Pindorama-SP, Brazil 3Instituto Agronômico de Campinas, Campinas-SP, Brazil.
1	2	<u>The haplotypes of <i>Arachis correntina</i> and <i>A. villosa</i> reflects an associated history with the alluvial fan of the Parana River during the Upper Quaternary</u> . M Grabiele, LMI Chalup, G Robledo & G Seijo*. Instituto de Botánica del Nordeste y FaCENA, Universidad Nacional del Nordeste, Argentina.
1	2	<u>Unlocking the genetic diversity of peanut's wild relatives with genomic and genetic tools</u> . J. Valls, EMBRAPA, D. Bertioli, UCB, Brazil, S. Braconnier, CERAAS, Senegal; J. Crouch ICRISAT Kenya; P. Piffanelli, CIRAD, France; G. Seijo, IBONE, Argentina; J. Stougaard, Aarhus, Denmark; V Valdez, ICRISAT, India
1	5	<u>Developing Introgression Pathways for Gene Transfer to <i>Arachis hypogaea</i> L.</u> , CE Simpson1*, MD Burow2 & JL Starr3, 1Texas AgriLife Research, Texas A&M System, Stephenville, TX
1	5	<u>Carbon isotope discrimination of representative Brazilian cultivars under drought stress</u> . GG Brito & TMF Suassuna* 1Embrapa Cotton / Advanced Savannah Nucleus, Santo Antônio de Goiás, GO, Brazil.
1	6	<u>Some biogeographic, genomic and speciation considerations on section <i>Arachis</i></u> . G Seijo*, G Robledo, M Grabiele, D Carisimo, S Samoluk & G Lavia. Instituto de Botánica del Nordeste / FACENA Universidad Nacional del Nordeste, Corrientes, Argentina.
1	6	<u>The races of peanuts of Peru</u> . A Krapovickas1*, R Vanni1, J Pietrarello2, CE Simpson3. 1Instituto de Botánica del Nordeste IBONE, Corrientes, Argentina, 2Estación Experimental INTA, Manfredi, Córdoba, Argentina, 3Texas & University, Stephenville, TX
2	1	<u>Apply Next Generation Sequencing into Peanut Research</u> , X Xu1*, B Yang1.BGI- Shenzhen, Shenzhen, China
2	1	<u>BAC clone selection using a 3D pooling strategy in <i>Arachis</i></u> . BS Vidigal1*, LP Muniz2, SCM Leal-Bertioli3, DJ Bertioli1 & PM Guimarães3. 1University of Brasília, Campus Darcy Ribeiro, Brasília, Brazil. 2Catholic University of Brasília, Campus I, Taguatinga, Brasília, Brazil. 3Embrapa Genetic Resources and Biotechnology, Brasília, Brazil.
2	2	<u>Retrotransposons in <i>Arachis</i> – structure, genomic context, and phylogenetic classification</u> , S Nielsen1*, B Vidigal dos Santos2, S Leal-Bertioli1, P Guimarães1 & D. Bertioli2, 1Embrapa Recursos Genéticos e Biotecnologia, Brasília-DF, Brazil. 2Universidade de Brasília, Brasília, DF, Brazil.
2	2	<u>Dispersed and other repetitive DNA sequences in the peanut genome shown by BAC-FISH</u> . ACG Araujo1*, J Bailey2, T Schwarzacher2, PM Guimaraes1, S Leal Bertioli1, DJ Bertioli3, C Kim4, A Paterson4 & P Heslop-Harrison2. 1Embrapa Genetic Resources and Biotechnology, Brasília, Brazil. 2Department of Biology, University of Leicester, UK. 3University of Brasília, DF, Brazil. 4University of Georgia, Athens, GA
2	2	<u>Towards ultra-dense genetic maps of peanut generated by sequencing diploid and tetraploid RIL populations and a peanut diversity panel</u> L Froenicke1, M Pandey2, H Upadhyaya2, MC Moretzsohn3, P Guimaraes3, S Leal-Bertioli3, RK Varshney2, D Bertioli3 & RW Michelmore1. 1Genome Center, University of California Davis, Davis, CA; 2International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Greater Hyderabad, Andhra Pradesh, India. 3Embrapa Recursos Genéticos e Biotecnologia, Brasília, DF, Brazil.
2	2	<u>Development of genetic linkage maps for the A and B genomes of <i>Arachis</i> using RIL populations</u> . EG Gouveia1,2*, SCM Leal-Bertioli1, V Penmetsa2, D Cook2, S Senthilvel3, RK Varshney3, DJ Bertioli4 & MC Moretzsohn1. 1Embrapa Recursos Genéticos e Biotecnologia, Brasília-DF, Brazil. 2University of California, Davis, CA. 3International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad, India. 4Universidade de Brasília, Instituto de Ciências Biológicas, Brasília-DF, Brazil.
2	3	<u>Global transcriptome analysis of peanut wild species under biotic and abiotic stress</u> . PM Guimarães1*, ACM Brasileiro1, CV Morgante1,2, PA Roberts3, GJ Pappas Jr1, OB Silva Jr1, SCM Leal-Bertioli1, A Martins4 & D Bertioli4. 1Embrapa Genetic Resources and Biotechnology, Brasília, Brazil. 2Embrapa Semi-Arid, Petrolina, Brazil, 3University of California, Riverside, CA. 4University of Brasília, Brasília, Brazil.
2	3	<u>Denovo characterization of peanut transcriptome during gynophore development</u> . CZ Zhao1,2, XJ Wang1,2*, AQ Li1,2, CS Li1,2. 1High-Tech Research Center, Shandong Academy of Agricultural Sciences, Key Laboratory for Genetic Improvement of Crop Animal and Poultry of Shandong Province, Ji'nan, China. 2Key Laboratory of Crop Genetic Improvement and Biotechnology, Huanghuaihai, Ministry of Agriculture, Ji'nan, China
2	3	<u>Identification of peanut (<i>Arachis hypogaea</i> L.) miRNA targets through degradome sequencing</u> . M Li1,2, XJ Wang1,2*, CZ Zhao1,2 & H Xia1,2. 1High-Tech Research Center, Shandong Academy of Agricultural Sciences, Key Laboratory for Genetic Improvement of Crop Animal and Poultry of Shandong Province, Ji'nan. 2Key Laboratory of Crop Genetic Improvement and Biotechnology, Huanghuaihai, Ministry of Agriculture, The People's Republic of China, Ji'nan.
2	6	<u>Advance of Peanut Omics and Biotechnology in China</u> . XJ Wang 1,2*, H Xia 1,2, CZ Zhao 1,2, AQ Li 1,2, CS Li 1,2. 1Bio-Tech Research Center, Shandong Academy of Agricultural Sciences, Key Laboratory for Genetic Improvement of Crop, Animal and Poultry of Shandong Province, Ji'nan China. 2Key Laboratory of Crop Genetic Improvement and Biotechnology, Huanghuaihai, Ministry of Agriculture, Ji'nan, China.

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3	2	<p><u>Identification of candidate genes in <i>Arachis stenosperma</i> involved in the interaction with root-knot nematode (<i>Meloidogyne arenaria</i>).</u> LL Bride^{1,2*}, ACM Brasileiro¹, CV Morgante³, PA Roberts⁴, SCM Leal-Bertioli¹, DJ Bertioli² & PM Guimarães¹. ¹Embrapa Recursos Genéticos e Biotecnologia, Brasília, DF. ²Universidade de Brasília, Brasília, DF. ³Embrapa Semiárido, Petrolina, PE. ⁴University of California, Riverside, CA.</p>
3	3	<p><u>Cloning and expression analysis of flowering regulating genes in peanut.</u> H Xia^{1,2}, XF Zhai^{1,2}, SB Wan^{1,2*} & XJ Wang^{1,2*}. ¹Bio-Tech Research Center, Shandong Academy of Agricultural Sciences, Key Laboratory for Genetic Improvement of Crop, Animal and Poultry of Shandong Province, Ji'nan, China, ²Key Laboratory of Crop Genetic Improvement and Biotechnology, Huanghuaihai, Ministry of Agriculture, Ji'nan, China</p>
3	3	<p><u>Tagging of rust and late leaf spot disease resistance gene and identification of functional diversity with genic molecular markers in cultivated groundnut.</u> S Mondal^{1*}, AM Badigannavar¹ & SF D'Souza¹. ¹Nuclear agriculture and Biotechnology Division, Bhabha Atomic Research Centre, Mumbai, India.</p>
3	3	<p><u>Gene-expression profile of five runner peanut genotypes. response to short-term water deficit utilizing controlled rainout shelters.</u> PM Dang^{1*}, CY Chen¹, RB Sorensen¹, MC Lamb¹ & CC Holbrook². ¹USDA-ARS, National Peanut Research Laboratory (NPRL), Dawson, GA. ²USDA-ARS, Crop Genetics and Breeding Research, Tifton, GA.</p>
3	3	<p><u>Large scale transcriptome analysis of wild peanut (<i>Arachis stenosperma</i>) inoculated with <i>Passalora personata</i>, the causal agent of Late Leaf Spot.</u> ACQ Martins^{1,2*}, CV Morgante³, AK Silva², IC Galhardo¹, GJ Pappas Jr², OB Silva Jr², SCM Leal-Bertioli², DJ Bertioli¹, RNG Miller¹, ACM Brasileiro² & PM Guimarães². ¹University of Brasília, Campus Darcy Ribeiro, Brasília, Brazil. ²Embrapa Genetic Resources and Biotechnology, Brasília, Brazil. ³Embrapa Semi-Arid, Petrolina, Brazil.</p>
3	3	<p><u>Differential gene expression study of wild <i>Arachis</i> under a water deficit induction system.</u> TN Oliveira^{1,2*}, PM Guimarães¹, M Passos¹, F Rodrigues³, A Nepomuceno³, DJ Bertioli², SCM Leal-Bertioli¹ & ACM Brasileiro¹. ¹Embrapa Genetic Resources and Biotechnology – Brasília-DF, Brazil, ²University of Brasília – Brasília-DF, Brazil, ³Embrapa Soybean – Londrina-PR, Brazil.</p>
3	5	<p><u>Markers, Maps and Molecular Breeding in Cultivated Groundnut,</u> RK Varshney, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India.</p>
3	5	<p><u>Mining for induced and natural variation in peanut genes,</u> P Ozias-Akins^{1*}, JE Knoll¹, ML Ramos¹ & CC Holbrook². ¹University of Georgia and ²USDA-ARS, Tifton, GA</p>
3	5	<p><u>Identification of QTLs for drought tolerance across different locations and seasons using recombinant inbred lines in peanut (<i>Arachis hypogaea</i> L.).</u> I Faye^{1*}, F Hamidou², A Rathore³, M Pandey³, B Gautami³, V Vadez³ & R.K. Varshney³. ¹Institut Sénégalais de Recherches Agricoles (ISRA)-CNRA, Bambey, Sénégal. ²International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Sahelian Center, Niamey, Niger. ³International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India.</p>
3	5	<p><u>Toward understanding molecular mechanism of peanut resistance to <i>Ralstonia solanacearum</i>.</u> WJ Zhuang^{1*}, DR Cook², C Zhang¹, H Chen¹, GH He³, BJ Jiang¹, JB Zheng¹, CH Zhuang¹. Fujian Province Key Lab of Plant Molecular and Cell Biology, Fujian, Agriculture and Forestry University, Fuzhou, Fujian, China. ²Department of Plant Pathology, University of California, Davis, CA. ³Department of Agricultural Science, Tuskegee University, Tuskegee, AL</p>
3	5	<p><u>Peanut gene expression induced by infection of <i>Ralstonia solanacearum</i>.</u> B Liao^{1*}, J Huang¹, L Yan¹, Y Lei¹ & H Jiang¹. ¹Oil Crops Research Institute of Chinese Academy of Agricultural Sciences, Key Laboratory of Oil Crop Biology of the Ministry of Agriculture, Wuhan, China.</p>
3	6	<p><u>Genetic mapping of cultivated peanut with genomic SSR and transposon markers screened by <i>in silico</i> polymorphic analysis,</u> K Shirasawa^{1*}, H Hirakawa¹, M Hasegawa², H Kiyoshima², S Kuroda², C Kuwata², S Suzuki², Y Naito³, T Kuboyama⁴, S Tabata¹ & S Isobe¹, ¹Kazusa DNA Research Institute, Chiba 292-0818, Japan. ²Chiba Prefectural Agriculture and Forestry Research Center, Chiba, Japan. ³Mitsubishi Chemical Medicine Corporation, Tokyo, Japan. ⁴Ibaraki University, Ibaraki, Japan</p>
3	6	<p><u>Isolation and characterization of important genes related to embryo development.</u> H Chen¹, C Zhang¹, DR Cook², BJ Jiang¹, GH He³, JB Zeng¹, CH Zhuang¹, TC Cai¹, WJ Zhuang^{1*}. ¹Fujian Province Key Lab of Plant Molecular and Cell Biology, Fujian Agriculture and Forestry University, Fuzhou, Fujian, China. ²Department of Plant Pathology, University of California, Davis, CA ³Tuskegee University, Tuskegee, AL</p>
4	1	<p><u>Characterization of duplicate genes involved in oil pathways of polyploid peanut.</u> Y Brand¹, F Shilman¹ & R. Hovav¹. ¹Department of Field Crops, Plant Science Institute, ARO, Bet-Dagan, Israel.</p>
4	2	<p><u>Screening of groundnut (<i>Arachis hypogaea</i> L.) minicore collection for mutant allele of Oleoyl-PC desaturase to identify high oleic accessions.</u> G Mukri¹, HL Nadaf^{1*} & HD Upadaya². ¹Dept. of Genetics & Plant breeding, University of Agricultural Sciences Dharwad, Karnataka, India. ²International Crops Research Institute for the Semi-Arid tropics (ICRISAT), Patancheru, Hyderabad, India.</p>
4	3	<p><u>Peanut genes involved in oleic acid biosynthesis expression profiling in developing seeds at different reproduction stages.</u> HC Liu^{1,2}, XP Chen¹, HY Liu¹, EH Zhan¹ & XQ Lian^{1*}. ¹Crops Research Institute, Guangdong Academy of Agricultural Sciences, Guangzhou; ²College of Life Science, South China Normal University, Guangzhou, China.</p>
4	3	<p><u>Genetic enhancement of nutritional quality traits with induced mutagenesis in groundnut (<i>Arachis hypogaea</i> L.).</u> HL Nadaf¹, C Channayya¹, BS Kaveri¹, KG Parameshwarapp¹. ¹Depart of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Karnataka, India.</p>
4	5	<p><u>Identification of QTLs for Oil Content and Fatty Acid Composition in Cultivated Peanut (<i>Arachis hypogaea</i> L.).</u> X Zhang^{1,2}, S Han^{1,2}, F Tang^{1,2}, W Dong¹, J Xu¹, M Yan², H Liu². ¹Industrial Crops Research Institute, Henan Academy of Agricultural Sciences ²Henan Provincial Key Laboratory for Genetic Improvement of Oil Crops, Zhengzhou, China.</p>

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4	5	<u>Isolation and characterization of important genes toward improvement peanut resistance to <i>Aspergillus flavus</i></u> . WJ Zhuang *1, H Chen 1, PK Nancy 2, BJ Jiang1, JB Zeng1, C Zhang1, XY Chen1, Y Deng 1 & TC Cai1. 1Fujian Province Key Lab of Plant Molecular and Cell Biology, Fujian Agriculture and Forestry University, Fuzhou, Fujian, China. 2Department of Medical Microbiology and Immunology, Department of Plant Pathology, University of Wisconsin, Madison, WI
4	5	<u>Prevalence of aflatoxin contamination in groundnut value chains and strategies to enhance food safety in Mali</u> . F Waliyar1*, A Traore1, V Reddy1, B Diarra2, O Kodio2 & H Sudini1. 1International Crops Research Institute for the Semi-Arid Tropics, Niamey, Niger. 2Institut d Economie Rural, Bamako Mali.
4	6	<u>Genetic diversity of the gene Resveratrol Synthase in <i>Arachis</i> spp. from Embrapa active germplasm bank</u> . ALR Santana-Pereira1*, ACM Brasileiro2, DJ Bertoli1,2, CV Morgante2,3, MA Gimenes2 & SCM Leal-Bertoli1. 1Embrapa Genetic Resources and Biotechnology, Brasília, Brazil. 2University of Brasília, Brasília, Brazil. 3Embrapa Semi-Arid, Petrolina, Brazil
4	6	<u>Methodology adaptation for the determination of resveratrol in peanut leaves</u> . RM Lopes1,2, D Silveira1, MA Gimenes2, PS Vasconcelos1,3 & TS Agostini-Costa2*. 1Faculdade de Ciências da Saúde - Universidade de Brasília. 2Embrapa Recursos Genéticos e Biotecnologia. 3Universidade Estadual Paulista Julio de Mesquita Filho, Brazil
5	5	<u>Current progress in drought tolerance work in peanut – Field and lysimetric assessments of germplasm</u> , V Vadez1*, F Hamidou2, P Ratnakumar1, O Halilou2, O Mponda3, T. Kapewa4, E Monyo4, I Faye5, B Ntare6, SN Nigam1 & HD Upadhyaya1, 1 International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru India. 2 International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Sahelian Center, Niamey, Niger; 3 Nalendiele Research Station, Mtwara, Tanzania, 4 Chitedze Research Station, Lilongwe, Malawi. 5 CNRA Bambey, Senegal, 6 ICRISAT Bamako, Mali
5	5	<u>Genetic engineering of groundnut for crop improvement: Current status and future prospects</u> . KK Sharma1*, P Bhatnagar-Mathur1, V Vadez1, H Sudini1 & FW. Waliyar1. 1International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, India.
5	5	<u>Conventional breeding approaches to speed up release of new peanut varieties</u> . GC Wright1*, D Fleischfresser2, GA Baker1 & D O'Connor1. 1Peanut Company of Australia, Kingaroy, Qld, Australia, 2AgriSciences Queensland, Department of Employment, Economic Development and Innovation, Kingaroy, Queensland, Australia.
5	5	<u>Developing transgenic resistance in cultivated peanut (<i>Arachis hypogaea</i> L.) to peanut-stem- and peanut-budnecrosis viruses</u> . T Radhakrishnan1*, M Reetu1, Y Reena1, K Abhay1, JR Dobaría1, Thirumalaisami1 & RK Jain2. 1Directorate of Groundnut Research, PO Box 5, Jungadh, Gujarat, India. 2Indian Agricultural Research Institute, New Delhi, India .
5	5	<u>Peanut breeding program for drought resistance tolerance</u> . S Soave1*, P Faustinelli1,2 & MI Buteler1 1Criadero El Carmen. General Cabrera, Córdoba, Argentina. 2Universidad Católica de Córdoba. Córdoba, Argentina.
5	6	<u>Molecular breeding for foliar disease resistance and quality-related traits in cultivated groundnut</u> . MVC Gowda1*, V Sujay1, G Mukri1, H L Nadaf1, RS Bhat2 & R. K. Varshney3. 1Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, India. 2Department of Biotechnology, University of Agricultural Sciences, Dharwad, India. 3International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Greater Hyderabad, India .
5	6	<u>Development and Use of Molecular Markers to Accelerate Peanut Cultivar Development</u> CC Holbrook1, P Ozias-Akins2* & Y Chu2. 1USDA-ARS, Tifton, GA. 2University of Georgia, Tifton, GA.
5	6	<u>Molecular and physiological approaches to improve abiotic stress tolerance in groundnut (<i>Arachis</i> sp.)</u> . P Payton1, 1USDA-ARS Cropping Systems Research Laboratory, Lubbock, TX
5	6	<u>Identification and introgression of a major QTL for rust resistance in elite cultivated groundnut cultivars through marker-assisted selection</u> . MK Pandey1, SN Nigam1, MVC Gowda2, Y Khedekar1,2, M Sriswathi1, M Govil1, V Sujay1,2, B Gautami1, HD Upadhyaya1, RK Varshney1,3*. 1International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India; 2University of Agricultural Sciences (UAS)-Dharwad, India; 3Generation Challenge Programme (GCP), c/o CIMMYT, Mexico DF, Mexico.
5	6	<u>Selection of <i>Arachis hypogaea</i> breeding lines for resistance to multiple foliar diseases</u> . JF Santos1*, IJ Godoy1, MD Michelotto2, EL Finoto2 & ALM Martins2. 1Instituto Agronômico, Campinas, SP, Brazil. 2Polo Regional APTA Centro Norte, Pindorama, SP, Brazil