

May 30 - June 1, 2018
Conrad Seoul
Seoul, South Korea



PAG ASIA 2018

**THE INTERNATIONAL CONFERENCE ON THE STATUS
OF PLANT & ANIMAL GENOME RESEARCH**

FINAL PROGRAM, ABSTRACT & EXHIBIT GUIDE

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NIST, USA

SUK-HA LEE
Seoul National University, South Korea

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Huazhong Agricultural University, China

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MEETING MANAGEMENT

Scherago International
101 Hudson St., Suite 2100
Jersey City, NJ 07302, USA
Phone: +1 201-653-5141
Email: pagasia@scherago.com
Website: www.intlpagasia.org

MEDIA PARTNERS

- ▶ Canadian Science Publishing
- ▶ Cytogenetic and Genome Research
(Karger Publishing)
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Mark Your Calendar for:

Plant & Animal Genome XXVII
January 12-16, 2019
Town & Country Hotel
San Diego, CA

Plant & Animal Genome Asia 2019
June 2019
Futian Shangri-La Hotel
Shenzhen, China

Plant & Animal Genome Asia 2018

Registration & Meeting Schedule

Registration – GRAND BALLROOM FOYER

Wednesday - Thursday	May 30-31	8:00am - 5:00pm
Friday	June 1	8:00am - 12:00pm

Plenary Lectures – GRAND BALLROOM

Wednesday - Friday	May 30-June 1	9:00am - 10:30am
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Scientific/Industry Workshops - GRAND BALLROOM 1, 2, 3

Wednesday - Friday	May 30-June 1	11:15am - 1:00pm 2:00pm - 3:45pm 4:30pm - 6:15pm
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Meeting ends at 3:45pm on Friday, June 1.

Lunch - GRAND BALLROOM FOYER

Wednesday - Friday	May 30-June 1	1:00pm - 2:00pm
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Poster Sessions - GRAND BALLROOM FOYER

Thursday	May 31	10:30am - 11:15am 3:45pm - 4:30pm
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ALL POSTERS MUST BE REMOVED BY 3:00PM WEDNESDAY, JUNE 1.

Exhibit & Poster Hours - GRAND BALLROOM FOYER

Wednesday-Thursday	May 30-31	10:30am - 4:30pm
Friday	June 1	10:30am - 2:00pm

Wednesday - May 30, 2018

8:00am - 9:00am	Coffee - GRAND BALLROOM FOYER
8:00am - 5:00pm	Registration - GRAND BALLROOM FOYER
9:00am - 9:45am	Plenary Lecture: Doil Choi - "Multiple Genomes of Hot Pepper Provide Insight into Massive Emergence of Disease Resistance Genes in Solanaceae Plants" - GRAND BALLROOM Co-chairs: Suk-Ha Lee, Seoul National University and Shuhong Zhao, Huazhong Agricultural University
9:00am	Doil Choi, Dept of Plant Science Seoul National University "Multiple Genomes of Hot Pepper Provide Insight into Massive Emergence of Disease Resistance Genes in Solanaceae Plants"
9:45am - 10:30am	Plenary Lecture: Ben Hayes - "Integrating Genomic and Microbiome Information to Predict Future Phenotypes for Key Production and Environmental Traits in Livestock" - GRAND BALLROOM Co-chairs: Suk-Ha Lee, Seoul National University and Shuhong Zhao, Huazhong Agricultural University
9:45am	Ben J. Hayes, The University of Queensland "Integrating Genomic and Microbiome Information to Predict Future Phenotypes for Key Production and Environmental Traits in Livestock"
10:30am - 11:15am	Coffee Break / Exhibits / Posters - GRAND BALLROOM FOYER
10:30am - 4:30pm	Exhibits & Posters - GRAND BALLROOM FOYER
11:15am - 1:00pm	Modern SNP Technologies in Plants: Research and Commercial Applications - GRAND BALLROOM 1 Organizer: Yuri Shavrukov, Flinders University
11:15am	Awais Rasheed, CIMMYT, CAAS "From KASP to 'Traitbreed Array' and 'Triticum-Genesizer': Multiple Genotyping Platforms for Wheat Breeding and Allele-Discovery" (W031)
11:35am	Kenta Shirasawa, Kazusa DNA Research Institute "Genome-Wide SNP Genotyping by Whole-Genome Resequencing of a Recombinant Inbred Line Population in Tomato" (W032)
11:55am	Antonina A. Kiseleva, Institute of Cytology and Genetics SB RAS "Application of SNP Markers for Anchoring New Heading Time Determinants in Wheat" (W033)

Wednesday - May 30, 2018

- 12:15pm Piergiorgio Stevanato, University of Padova
"Developing SNP Assays to Improve Rhizomania Resistance in Sugar Beet" (W034)
- 12:35pm Yuri Shavrukov, Flinders University and University of Adelaide
"Amplifluor-like SNP Markers in Plant Genotyping" (W035)
- 11:15am - 1:00pm 10x Genomics - Understanding True Biology with Comprehensive Genomics and Transcriptomics - GRAND BALLROOM 3
Organizer: Anushka Brownley, 10x Genomics**
- 11:15am Anushka Brownley, 10x Genomics
"A Comprehensive View of Genomes and Transcriptomes with 10x Genomics"
- 11:45am Chui Li, Dovetail Genomics
"Confirmation Capture Technology for Chromosome Scale Genome Assembly"
- 12:15pm Jei Li, UC Davis Bioinformatics Core
"Towards Chromosome Scale Haplotype Assemblies"
- 11:15am - 1:00pm Solanaceae Genomics and Molecular Genetics - GRAND BALLROOM 2
Organizer: Byoung-Cheorl Kang, Seoul National University**
- 11:15am Guy Kol, NRGENE
"Creating a Pan Genome and Haplotype Database for Potato" (W044)
- 11:35am Eiji Yamamoto, Kazusa DNA Research Institute
"Genome-Wide Association Study, Genomic Selection and Other Technologies for Efficient Tomato Breeding" (W045)
- 11:55am Je Min Lee, Kyungpook National University
"Toward Identifying Hidden Genetic Regulation of Carotenogenesis in Tomato" (W046)
- 12:15pm Hyo-Bong Jeong, Seoul National University
"Single-Molecule Real-Time (SMRT) Sequencing Reveals Diverse Allelic Variations in Carotenoid Biosynthetic Genes in Pepper (*Capsicum spp.*)" (W047)
- 12:35pm Feng Li, Huazhong Agricultural University
"PacBio Sequencing of Full Length cDNA Reveals Broad Role for NAT Gene Pairs in Pepper Development and Stress Responses" (W048)
- 1:00pm - 2:00pm Lunch - GRAND BALLROOM FOYER**

Wednesday - May 30, 2018

- 2:00pm - 3:45pm** **LGC - Overcoming AgBio challenges: new solutions to SNP genotyping - GRAND BALLROOM 3**
Organizer: Jill Walerius, LGC
- 2:00pm Marcus Wills, LGC
 "Solutions for Challenges throughout the Agbio Workflow; From Sample Collection to DNA Extraction, Marker Discovery, Validation, Screening and Data Analysis"
- 2:20pm Guy Kol, NRGENE
 "Using Haplotypes to Reduce Costs in Large Scale Genotyping Projects."
- 2:40pm Sukganah Apparow, Sime Darby Technology Centre Sdn. Bhd.
 "Challenges and Opportunities for Oil Palm Breeding in the Era of Big Data"
-
- 2:00pm - 3:45pm** **Wheat Genomics in Agriculture: Building on IWGSC RefSeq v1.0 - GRAND BALLROOM 1**
Organizer: Rudi Appels, University of Melbourne
- 2:00pm Song Weining, Northwest A&F University
 "Comparative Analysis of Ta7DL and Ae7DL Chromosome Provides Insights into the Structure and Evolution of Bread Wheat" (W069)
- 2:20pm Philippa Borrill, John Innes Centre
 "Variation in Homoeolog Expression in Wheat" (W070)
- 2:40pm Long Mao, Chinese Academy of Agricultural Sciences
 "Wheat Inflorescence Transcriptomes: From Development to Yield" (W071)
- 3:00pm Huixian Zhao, College of Life Sciences, Northwest A & F University
 "Global Transcriptome Analysis Uncovers the Gene Co-Expression Regulation Network and Key Genes Involved in Grain Development of Wheat (*Triticum aestivum* L.)" (W072)
- 3:20pm Xigang Liu, Center for Agricultural Research Resources, CAS, China
 "New Insights on the GA Signaling in C3 and C4 Plants" (W073)
- 3:40pm Meng Ma, College of Life Sciences, Northwest A & F University
 "Roles of TaCYP78As in Wheat Grain Size" (W074)
-
- 2:00pm - 3:45pm** **Plant Omics - GRAND BALLROOM 2**
Organizers: Kentaro Yano, Meiji University, Hajime Ohyanagi, King Abdullah University of Science and Technology and Yasukazu Nakamura, DNA Data Bank of Japan
- 2:00pm Kentaro Yano, Meiji University
 "Statistical Analyses, Text-Mining and Web Databases for Plant Science" (W036)
- 2:05pm Andrea Ghelfi, Kazusa DNA Research Institute
 "Hayai-Annotation: An Ultra-Fast and Comprehensive Gene Annotation System in Plants" (W037)

Wednesday - May 30, 2018

- 2:30pm Yuriko Osakabe, Tokushima University
"Genome Editing for Improvement of Plant Responses to Environmental Conditions" (W038)
- 2:55pm Yong-Min Kim, Korea Bioinformation Center (KOBIC), KRIBB
"Transposase-Derived Transcriptional Factor, FAR1 Provides Insights of Gene Evolutions in Plants" (W039)
- 3:20pm Hajime Ohyanagi, King Abdullah University of Science and Technology
"Asian Rice Domestication: Recent Controversy in Rice Genomics" (W040)
- 3:45pm - 4:30pm Coffee Break / Exhibits / Posters - GRAND BALLROOM FOYER**
- 4:30pm - 6:15pm The IDT CRISPR Toolbox (IDT - Integrated DNA Technologies) - GRAND BALLROOM 3
Organizer: Jonggeun Park, IDT Korea**
- 4:30pm Allen Nguyen, Integrated DNA Technologies
"Innovative Solutions for Genotyping, Amplicon Sequencing and CRISPR Genome Editing"
- 4:50pm Jin Ngee Chia, IDT - PTE
"The Idt CRISPR Toolbox"
- 5:10pm Piergiorgio Stevanato, University of Padova
"Using Rhamp Technology for SNP Genotyping in Plants"
- 4:30pm - 6:15pm Genomic Annotation Resources at the EBI - GRAND BALLROOM 1
Organizer: Laura Huerta, European Bioinformatics Institute (EMBL-EBI)**
- 4:30pm Benjamin Moore, EMBL-EBI
"Accessing Genomic Data with Ensembl and Ensembl Genomes" (W010)
- 5:35pm Laura Huerta, European Bioinformatics Institute (EMBL-EBI)
"Integrating and Displaying Plant and Animal Gene Expression in Expression Atlas" (W011)

Wednesday - May 30, 2018

- 4:30pm - 6:15pm** **Livestock Genomic Adaptation to Climate Change - GRAND BALLROOM 2**
Organizer: Jian-Lin Han, The International Livestock Research Institute, CGIAR
- 4:30pm Introductory Remarks
- 4:35pm Jian-Lin Han, The International Livestock Research Institute, CGIAR
"Livestock Genomic Adaptation to Climate Changes Via Long-Term Natural Selection within and/or Historical Introgression between Species" (W026)
- 4:50pm Olivier Hanotte, ILRI/University of Nottingham
"Genomic Signatures in African Livestock for Adaptation to Climatic Changes" (W027)
- 5:15pm Neena Amatya Gorkhali, Animal Breeding Division-NARC
"Identification of Genomic Regions in Sheep Responsible for High-Altitude Adaptation" (W028)
- 5:35pm Zewdu Edea Bedada, Chungbuk National University
"Genome-Wide Scan Reveals Divergent Selection Among Taurine and Zebu Cattle Populations from Different Regions" (W029)
- 5:55pm Yi Zhang, China Agricultural University
"Genomic Signatures Associated with Adaptation of Buffaloes to Climate Change" (W030)

Thursday - May 31, 2018

8:00am - 9:00am	Coffee - GRAND BALLROOM FOYER
8:00am - 5:00pm	Registration - GRAND BALLROOM FOYER
9:00am - 9:45am	Plenary Lecture: Hiroyoshi Iwata - "Selection 4.0: Next Revolution of Breeding Will be Model-Based Development (MBD)" - GRAND BALLROOM Co-chairs: Sachiko Isobe, Kazusa DNA Research Institute and Kwan-Suk Kim, Chungbuk National University
9:00am	Hiroyoshi Iwata, The University of Tokyo "Selection 4.0: Next Revolution of Breeding Will be Model-Based Development (MBD)"
9:45am - 10:30am	Plenary Lecture: Yanfang Wang - "Genetic Response of Adipose Tissues to Cold-Stimulated Thermogenesis in Mice and Pigs" - GRAND BALLROOM Co-chairs: Kwan-Suk Kim, Chungbuk National University and Sachiko Isobe, Kazusa DNA Research Institute
9:45am	Yanfang Wang, Institute of Animal Science, CAAS "Genetic Response of Adipose Tissues to Cold-Stimulated Thermogenesis in Mice and Pigs"
10:30am - 11:15am	Coffee Break / Poster Session 1 - GRAND BALLROOM FOYER
10:30am - 4:30pm	Exhibits & Posters - GRAND BALLROOM FOYER
11:15am - 1:00pm	Prioritizing SNPs and Variants from Next Generation Sequencing Data - GRAND BALLROOM 2 Organizers: Prashanth Suravajhala, Birla Institute of Sc. Res and Haja N Kadarmideen, Technical University of Denmark
11:15am	Prashanth Suravajhala, Birla Institute of Sc. Res "Challenges in Prioritizing SNPs and Variants from NGS Data" (W041)
11:15am	Haja N Kadarmideen, Technical University of Denmark "Systems Genomic Challenges for Analyzing Variants" (W042)
11:15am	Santhi N, Department of Biochemistry "Meta-Analysis in Genomics: A Case Study on Obesity" (W043)

Thursday - May 31, 2018

- 11:15am - 1:00pm** **Aquaculture and Genomics - GRAND BALLROOM 1**
Organizer: Shannon Clarke, AgResearch, Invermay Agricultural Centre
- 11:15am Shannon Clarke, AgResearch, Invermay Agricultural Centre
 "Cost Effective Genotyping for Aquaculture Management and to Drive Genetic Gain" (W001)
- 11:35am Bo-Hye Nam, National Institute of Fisheries Science
 "Genome and Transcriptome Analyses for Identification of Genes Related to Immune Responses of the Rock Bream, *Oplegnathus Fasciatus*" (W002)
- 11:55am William Chow, Wellcome Sanger Institute
 "High Quality *de novo* Assemblies for All Teleosts" (W003)
- 12:15pm Rachael Ashby, AgResearch, Invermay Agricultural Centre
 "Implimentation of Genomic Tools for the New Zealand Greenshell™ Mussel Industry" (W004)
- 12:35pm Michelle T.T. Crown, Fisheries and Oceans Canada, West Vancouver Laboratory and Simon Fraser University
 "Identification of Genomic Loci Associated with Maturation in Pacific Coho Salmon (*Oncorhynchus kisutch*)" (W005)
- 11:15am - 1:00pm** **PacBio - Building Better Genomes. Enabling Breakthrough Discoveries - GRAND BALLROOM 3**
Organizer: Mio Tonouchi, PacBio
- 11:15am Michelle Vierra, PacBio
 "SMRT Sequencing: Long Reads for High-Accuracy Plant and Animal Genomics "
- 11:35am Stephen Moore, Centre for Animal Science, QAAFI
 "Sequencing Australian Brahman Cattle, an Insight into the Breeds Diversity"
- 12:05pm Kenta Shirasawa, Kazusa DNA Research Institute
 "Plant Genome Sequencing and Assembly with Long-Read Technology"
- 12:35pm Gregory T Concepcion, Pacific Biosciences
 "Beyond the Reference Genome"
- 1:00pm - 2:00pm** **Lunch - GRAND BALLROOM FOYER**
- 2:00pm - 3:45pm** **BGI - Law of Life Behind Genomics - GRAND BALLROOM 3**
Organizers: Xun Xu, BGI Genomics
- 2:00pm Xiaodong Fang, BGI Genomics
 "Genomics Study for Model and Non-Model Organisms"
- 2:30pm Long Mao, Chinese Academy of Agricultural Sciences, Beijing, China
 "Novel Mechanisms to Regulate Flowering Locus T in Temperate Grasses"
- 3:00pm Leslie A. Lyons, University of Missouri-Columbia
 "Genomic Arrays and Genomes of Felids"

Thursday - May 31, 2018

- 2:00pm - 3:45pm** **Legumes Genomics - GRAND BALLROOM 2**
Organizers: Suk-Ha Lee, Seoul National University /
Rajeev Varshney, ICRISAT
- 2:00pm Jungmin Ha, Seoul National University
 "Transcriptomic Profiling of Genes Involved in Proanthocyanidin
 Biosynthesis Pathway in *Glycine* Species " (W021)
- 2:20pm Taehwan Jun, Pusan National University
 " Development of SNP-Based Molecular Markers and its
 Applications in Peanut" (W022)
- 2:40pm Sailaja Bhogireddy, ICRISAT
 "New Insights of Gene Expression Regulation by Noncoding RNAs
 during Heat Stress in Chickpea (*Cicer arietinum* L.)" (W023)
- 3:00pm Sachiko Isobe, Kazusa DNA Research Institute
 "Phenotype Substitute Environment (PE) Value: Toward a
 G x E Research in Legumes" (W024)
- 3:20pm Guy Kol, NRGENE
 "Using Haplotypes to reduce costs in large scale genotyping projects"
- 2:00pm - 3:45pm** **Genomic Characterization of Ruminants in Asia - GRAND BALLROOM 1**
(Supported by the project from "National Research Foundation of Korea")
Organizer: Kwan-Suk Kim, Chungbuk National University
- 2:00pm Shannon Clarke, AgResearch, Invermay Agricultural Centre
 "Genomic Technologies to Support Ruminant Research and
 Industry Application" (W012)
- 2:20pm P. Olof Olsson, Sooam Biotech Research Foundation
 "Endangered and Extinct Species Progress and Potential" (W013)
- 2:40pm Zewdu Edea Bedada, Chungbuk National University
 "Signatures of Altitude Adaptation in Ethiopian Sheep Populations"
 (W014)
- 3:00pm Neena Amatya Gorkhali, Animal Breeding Division-NARC
 "Biodiversity of Indigenous Goats in Nepal" (W015)
- 3:20pm Kwondo Kim, Seoul National University
 "Genetic Structure and Introgression Signatures of African
 Cattle Genome" (W016)
- 3:40pm Kwan-Suk Kim, Chungbuk National University
 "Genomic Study of Domestic Animals Adapted to Extreme
 Environments" (W017)
- 3:45pm - 4:30pm** **Coffee Break / Poster Session 2 - GRAND BALLROOM FOYER**

Thursday - May 31, 2018

- 4:30pm - 6:15pm** **Swine Genomics - GRAND BALLROOM 2**
Organizers: Shuhong Zhao, Huazhong Agricultural University and Xuewen Xu, Huazhong Agricultural University
- 4:30pm Thong M Le, Konkuk University
 "Predicting the Efficacy of Adaptive Immunity Response by Understanding the Genetic Diversity of SLA and Analyzing Peptide-SLA Binding Affinity" (W059)
- 4:50pm Damarius S. Fleming, ORAU, USDA National Animal Disease Center, Texas A&M
 "ePIGenetics: Porcine miRNA and tRNA Expression during Highly Pathogenic PRRSV Infections" (W060)
- 5:10pm Xuewen Xu, Huazhong Agricultural University
 "Genome-Wide eQTL Analysis of *Porcine longissimus* Muscle Based on RNA-Sequencing Data" (W061)
- 5:30pm Ming Fang, Fisheris-Jimei University-China
 "Bayes-Poly: A Software for Fine Mapping Causitive Variants for Big Related Populations " (W062)
- 5:50pm Junchul David Yoon, Institute for Stem Cell & Regenerative Medicine
 "Growth Differentiation Factor 8 Modulate Porcine Immature Oocyte Maturation and Embryonic Development *in Vitro*" (W063)
-
- 4:30pm - 6:15pm** **Illumina - Accelerating Plant and Animal Genomic Breakthroughs. A history of progress. A future of promise. - GRAND BALLROOM 3**
Organizers: Casie Chislett, Illumina and Eli Mrkusich, Illumina
- 4:30pm Evgeny Glazov, Illumina
 "Accelerating Agrigenomic Breakthroughs. Driving Innovation in Agriculture."
- 4:55pm Seung-Hwan Lee, Chungnam National University
 "Thirty Years on - Implementation of a Breeding Program on Hanwoo (Korean Cattle)"
- 5:20pm Shannon Clarke, AgResearch, Invermay Agricultural Centre
 "Delivering Genomic Solutions to New Zealand's Biological Economy"
- 5:45pm André Eggen, Illumina
 "Genomics, a Molecular Microscope Finding His Way in Agriculture Research and Industry "

Friday - June 1, 2018

8:00am - 9:00am	Coffee - GRAND BALLROOM FOYER
8:00am - 12:00pm	Registration - GRAND BALLROOM FOYER
9:00am - 9:45am	Plenary Lecture: Xun Xu - "Big Data in Plant Genomics" - GRAND BALLROOM Organizers: Rudi Appels, University of Melbourne / Rajeev Varshney, ICRISAT
9:00am	Xu Xun, Beijing Genomics Institute (BGI) "Big Data in Plant Genomics"
9:45am - 10:30am	Plenary Lecture: Philippa Borrill - "The Transcriptome of Polyploid Wheat" - GRAND BALLROOM Organizers: Rudi Appels, University of Melbourne / Rajeev Varshney, ICRISAT
9:45am	Philippa Borrill, John Innes Centre "The Transcriptome of Polyploid Wheat"
10:30am - 11:15am	Coffee Break / Exhibits / Posters - GRAND BALLROOM FOYER
10:30am - 2:00pm	Exhibits & Posters - GRAND BALLROOM FOYER
11:15am - 1:00pm	Translational Genomics for Agriculture - GRAND BALLROOM 2 Organizer: Rajeev Varshney, ICRISAT
11:15am	Yong Pyo Lim, Chungnam National University "Secondary Metabolites Improvement and Human Health Effects through Crop Breeding" (W064)
11:35am	Marco Maccaferri, University of Bologna, DISTAL "Development of Resources for Mapping, GWAS and Allele Mining in Tetraploid Wheat Based on Svevo Durum Reference Sequence" (W065)
11:55am	Mahendar Thudi, ICRISAT "Simplifying Complex Traits using Whole Genome Resequencing in Chickpea (<i>Cicer arietinum</i> L.)" (W066)
12:15pm	Awais Rasheed, CIMMYT C/o. CAAS "Translating Wheat Genomics Knowledge for Applied Breeding" (W067)
12:35pm	Parwinder Kaur, Univ. of Western AU "Chromosome-length Scaffolds Solution to the <i>de novo</i> Assembly Challenge for Plant Community" (W068)

Friday - June 1, 2018

- 11:15am - 1:00pm High-Throughput Genetics: Lab to Landscape - GRAND BALLROOM 3**
Organizer: Parwinder Kaur, Univ. of Western AU
- 11:15am Rudi Appels, University of Melbourne
"The Wheat Genome Reference Sequence As a Tool for Documenting the Allergens and Immune-Responsive Proteins" (W018)
- 11:35am Philippa Borrill, John Innes Centre
"Gene Regulatory Network Modelling Identifies Novel Transcription Factors Regulating Senescence in Wheat" (W019)
- 11:55am Rajeev K Varshney, ICRISAT
"4Gs in Crop Breeding for Pulses Improvement in Developing Countries" (W020)
- 12:15pm Chui Li Leaw, Dovetail Genomics
"Using Genomics in Crops Improvement"
- 11:15am - 1:00pm Soybean Genomics - GRAND BALLROOM 1**
Organizer: Kyung Do Kim, Corporate R&D, LG Chem
- 11:15am Kyung Do Kim, Corporate R&D, LG Chem
"DNA Methylation and Paralog Evolution in Soybean" (W049)
- 11:35am Sungyul Chang, Korea Institute of Science and Technology
"What Do We Learn from *Glycine Latifolia*, a Perennial Wild Relative of Soybean?" (W050)
- 11:55am Young B. Cho, USDA-ARS/UIUC-IGB
"Structural Variation at Soybean Loci Regulating Small RNAs and Seed Color" (W051)
- 12:15pm Sangrea Shim, Seoul National University
"Identification of QTLs for Number of Branches in *Glycine max*" (W052)
- 1:00pm - 2:00pm Lunch - GRAND BALLROOM FOYER**
- 2:00pm - 3:45pm Genomic and Genetic Analysis in Polyploid Species - GRAND BALLROOM 2**
Organizer: Sachiko Isobe, Kazusa DNA Research Institute
- 2:00pm Rajeev K Varshney, ICRISAT
"A Journey of Genes from Genome to Fields in Groundnut" (W006)
- 2:20pm Ung-Han Yoon, National Institute of Agricultural Sciences, RDA
"Strategy and Progress of Sweetpotato Genome Project By TRAS" (W007)
- 2:40pm Andrew G. Griffiths, AgResearch
"Sequencing White Clover and its Progenitors - Two Genomes Gone Global." (W008)
- 3:00pm Hiroyuki Enoki, Toyota Motor Corporation
"New Genotyping Technology, GRAS-Di, using Next Generation Sequencer" (W009)

Friday - June 1, 2018

- 2:00pm - 3:45pm** **Student Workshop - GRAND BALLROOM 3**
Organizer: Kwan-Suk Kim, Chungbuk National University
- 2:00pm Chul Lee, IPBI, Seoul National University
 "Convergent Amino Acid Substitutions of Avian Vocal Learning Clades – Not How Many Genes, but Who" (W053)
- 2:20pm JongWon Kang, Chungbuk National University
 "Heterotic Grouping and F1 Hybrid Selection Based on Molecular Marker Heterozygosity in Waxy Corn Inbred Lines" (W054)
- 2:40pm Kun Han, HuaZhong Agricultural University
 "Genome-Wide Analysis of Histone Modifications in Porcine Placentas" (W055)
- 3:00pm Julianne A. Vilela, University of the Philippines
 "Draft De Novo Genome Assembly of the Philippine Endemic Abaca (Musa textilis Nee.)" (W056)
- 3:20pm John Bwalya, Seoul National University
 "Response of Soybeans Cultivars to Drought Stress" (W057)
- 3:40pm Subhankar Bera, Osaka Prefecture University
 "Long-Distance Movement of Naturally Occurring Small RNAs in a Host-Parasite Plant Complex" (W058)

Corporate Sponsors

**Thanks to our Corporate Sponsors for their support of
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Exhibitor Descriptions

Company	Booth#
BGI Genomics Co.,Ltd. BGI was founded in 1999 as a nonprofit research organization to support the human Genome Project. Over the years, BGI has grown into a multinational genomics company with significant global operations, including sequencing laboratories based in the US, Europe, Hong Kong and mainland China.	1
Bioline Bioline is an ISO 13485 certified primary manufacturer of specialized bio-research reagents that simplify, accelerate and improve life sciences research. We are part of the Meridian Bioscience group, providing clinical diagnostic and molecular research solutions used by molecular biologists and other research scientists to perform test-assays and research in many fields from medical, biotechnology and marine biology to food and agriculture technology as well as forensic and environmental sciences, where life scientists have come to depend upon the outstanding quality and reliability of our reagents. Our portfolio of more than 300 reagents and kits, many of them proprietary, are developed for molecular biology, cell analysis and nucleic acid and protein separation and purification. Bioline also offers a broad range of custom solutions, which can be tailored to meet your individual needs. Details on our new products as well as current offers are available from our friendly Sales Team at the Bioline booth.	17
Bionano Genomics Bionano Genomics, Inc. offers whole genome analysis tools to better understand the genome and its structure. Its high-throughput system Saphyr provides comprehensive structural variation (SV) calls with high sensitivities and when combined with orthogonal sequencing data, Bionano maps can provide the correct structure, order, and orientation to assemble reference-quality genomes.	4
Diagenode Diagenode is a leading global provider of complete solutions for epigenetics research, biological sample preparation, and diagnostics assays based in Liege, Belgium and NJ, USA. The company has developed a comprehensive approach to gain new insights into epigenetics studies. The company offers innovative Bioruptor® shearing and IP-Star® automation instruments, reagent kits, and high quality antibodies to streamline DNA methylation, ChIP, and ChIP-seq workflows. The company's latest innovations include a unique, full automation system, the industry's most validated antibodies, the Megaruptor shearing system for long fragment generation in sequencing, and epigenetics assay services.	15

DNA Link 18

DNA Link Sequencing Lab aims to provide the latest technologies of high-quality DNA sequencing service to the researchers and scientists all over the world, and have been keeping itself equipped with the sequencers with the most up-to-date technologies. Our fleet of sequencers include both second and third generation platforms including HiSeq and NextSeq from illumina , Sequel and RSII from Pacific Biosciences, and ion torrent and S5 from Thermo Fisher Scientific. From genotyping by microarray to the most recent technologies of next and third generation sequencing, DNA Link Sequencing Lab is equipped with all diverse platforms with which it can provide a suited sequencing service to the researchers.

Dovetail Genomics LLC 2

Dovetail is transforming the life sciences by profiling the 3-dimensional structure of the genome. Dovetail’s proprietary in vitro proximity ligation approach and assembly algorithms enable researchers and clinicians to solve complex problems involving de novo assembly, structural variation, microbiome analysis, TAD analysis, cancer research, phasing analysis and more.

GeneSeek, A Neogen Company 10

As an industry founder, Neogen GeneSeek’s innovation and global leadership delivers reliable data, quick service and affordable technologies that empower your decisions in food security, animal care and life sciences. We make cutting-edge genomics part of your world. GeneSeek Genomic Profiles provide you with the most advanced genomic solutions, empowering your decisions in genomic selection, health management and research.

GENEWIZ 14

Specialized in genomic services, GENEWIZ has a comprehensive product portfolio, including Next Generation Sequencing, Gene Synthesis, Sanger Sequencing and Molecular Genetics. GENEWIZ has maintained an unwavering commitment to increase research productivity through fast, reliable delivery of quality results, competitive prices, excellent project management, and easy access to expert technical support.

Illumina 5,6

Illumina provides innovative sequencing and array-based solutions for genotyping, copy number variation analysis, methylation studies, gene expression profiling, and low-multiplex analysis of DNA, RNA, and protein. Our agrigenomics technologies help plant and animal breeders and researchers identify desirable traits, leading to healthier and more productive crops and livestock.

JCBio 12

Oxford Nanopore has developed the world's first and only nanopore DNA sequencer, the MinION. The MinION is a portable, real-time, long-read, low-cost device that has been designed to bring easy biological analyses to anyone, whether in scientific research, education or a range of real-world applications

JN Medsys 11

Adopting an innovative tube-strip design, the Clarity™ digital PCR system offers a new paradigm in the absolute quantification of target nucleic acids with high precision, accuracy and sensitivity.

KeyGene 8

KeyGene - The crop innovation company KeyGene is the go-to AgBiotech company for higher crop yield & quality. With our intellectual capital, solution driven approach and collaborative spirit, we work for the future of global agriculture with partners in the AgriFood sector. Using our proprietary technologies and non-GM approaches, we support customers with the development of new and improved crops. Our goal is to help organizations with their toughest R&D challenges, combining our cutting edge breeding technologies, bioinformatics & data science expertise and plant-based trait platforms. At KeyGene, we work in an international environment with more than 140 professionals from all over the world. Our company is based in Wageningen, Netherlands and Rockville, MD, USA. www.keygene.com

LGC 9

LGC is an international leader in the laboratory services, measurement standards, reference materials, genomics and proficiency testing marketplaces. We are a global leader in delivering genomic solutions for research, diagnostics, and applied markets. LGC's product portfolio provides best-in-class reagents, instruments, and services supporting quantitative and end-point PCR. We offer reagents such as KASP, BHQ® probes, and Array Tape® to complement robust instrumentation including the Nexar®, SNPLINE, and Oktopure™ for extraction and genotyping, and the IntelliQube®, a fully integrated liquid handling and PCR platform. Our innovative technologies also power lab services for genotyping, DNA extraction, arrays, Genotyping by Sequencing (GBS), Sanger sequencing, and NGS. LGC operates out of 21 countries, which encompasses our Genomics division's network of 9 manufacturing facilities and 3 service labs creating a geographic footprint to support customers in all major markets worldwide.

MacroGen 21

The slogan of MacroGen has the same meaning as the philosophy of humanitarianism, benefitting humanity, by offering personalized medicine according to the individual genetics of each patient based on human genome information and data analysis technology.

Mbiotech an IDT company	19
<p>Integrated DNA Technologies, Inc. (IDT) is recognized widely as the industry leader in the manufacture of custom oligonucleotides for molecular biology applications. We have developed proprietary technologies for genomics applications, such as Next Generation Sequencing, CRISPR genome editing, qPCR, and RNA interference. Through our GMP services, we manufacture products used in diagnostic tests for many forms of cancer and most inherited and infectious diseases.</p>	
Nextomics Biosciences Co., Ltd	3
<p>Nextomics Biosciences Co., Ltd is a world leading PacBio Sequencing Genome Center, focusing on the applications of Single-Molecular Real-Time technology. Nextomics has purchased 6 PacBio Sequel sequencers in 2016, which can yield 2T data per month steadily. Nextomics has completed thousands of projects so far, ranging from genome de novo assembly to Iso-seq analysis.</p>	
NRGene	16
<p>NRGene is a leading genomic big data company, develops advanced computational tools and cutting-edge algorithmic models to facilitate optimal trait discovery for seed companies, animal breeders, and academia. With NRGene, a process that used to be notoriously expensive, laborious and time consuming has become turnkey, predictable, quick and affordable. www.nrgene.com</p>	
PacBio	7
<p>PacBio is the leader in long-read sequencing and your partner in life science exploration. PacBio Sequencing Systems provide the most comprehensive view of genomes, transcriptomes, and epigenomes. Our Single Molecule, Real-Time (SMRT®) technology delivers long continuous reads, high consensus accuracy, uniform coverage, and simultaneous epigenetics characterization.</p>	
VHLGenetics	20
<p>VHLGenetics is a leading genetic service provider with business units in The Netherlands, Germany and in Belgium. For more than 25 years, DNA has been the core of the organization, serving clients with research and routine tests. Providing good genotyping results in a reliable high quality is our profession. The offered tests are focused on all species of animals, plants and microorganisms, where our expertise is. As a group, we continually improve technology and instruments in our laboratories, being steadily on the state-of-the-art. Please visit our website www.vhlgenetics.com and www.snpexpert.com for more information.</p>	
Walz	13
<p>The current product line ranges from the well known PAM chlorophyll fluorometers and light measuring equipment to gas-exchange systems for physiological and ecophysiological research. Dewpoint-mirror measuring systems as well as cold traps and measuring-gas coolers complement the line of products. In our field of expertise, we provide custom made solutions, reaching from small specialized accessories to complete measuring stations. A network of distributors in many countries provides close contact and technical advice to customers throughout the world.</p>	

W001: Aquaculture and Genomics

Cost Effective Genotyping for Aquaculture Management and to Drive Genetic Gain

Shannon Clarke, AgResearch, Invermay Agricultural Centre, Mosgiel, New Zealand

High-throughput molecular genotyping methods coupled with efficient tissue sampling through to the bioinformatic and statistical analyses have enabled development and implementation of genomic tools for aquaculture species. Genotyping by sequencing (GBS), a simultaneous genotyping and SNP discovery platform, has emerged as an alternative technology to array based genotyping for genetic diversity and genetic mapping studies as well as industry implementation of genomic selection in aquaculture. AgResearch developed a generic algorithm that produces bias free genomic relationship matrices (GRM) based on allele read depths from GBS data. This overcomes missing genotypes and genotype calling accuracy at low coverage when SNP density and samples numbers per lane are maximised. The GRM produced can be interrogated to estimate: breed composition, pedigree, traceability, inbreeding and co-ancestry as well as be included directly in existing mixed models to estimate breeding values. Furthermore, imputation nor genome sequence are not required. I will present the use of GBS in both Pacific (Chinook) and Atlantic salmon for use in aquaculture management and to drive genetic gain.

W002: Aquaculture and Genomics

Genome and Transcriptome Analyses for Identification of Genes Related to Immune Responses of the Rock Bream, *Oplegnathus Fasciatus*

Bo-Hye Nam, National Institute of Fisheries Science, Busan, Korea, Republic of (South)

W003: Aquaculture and Genomics

High Quality *de novo* Assemblies for All Teleosts

William Chow, Wellcome Sanger Institute, Cambridge, United Kingdom and Vertebrate Genomes Project Assembly Group

The mission of the Genome10K Vertebrate Genomes Project is to create near-gapless, phased, chromosomal level reference assembly for all vertebrate species. The first phase of this international endeavor targets on completing one select representative for each vertebrate order, with the Wellcome Sanger Institute focusing on teleosts, caecilians and select rodents.

Applying a strategy involving PacBio long reads, 10X linked reads, Bionano optical maps and Arima HiC libraries to build the assemblies, the goal is to reach a quality standard of 1Mb+ ContigN50, 10Mb+ ScaffoldN50, over QV40 average and 90% sequence assignment to chromosomes.

In addition to targeting a representative for each vertebrate order, the generation of datasets has been expanded to include other cyprinids, cichlids, notothenioid and anabantoid fishes of scientific interest.

Whilst there are workflows and ever evolving pipelines available for assembling new genomes, the challenge remains that results which work favourably for one species may not work on another. This may be attributed to varying genome complexity and structure (e.g. heterozygosity and repeat content).

Because of this, additional manual curation was applied to the Sanger Institute assemblies to improve the overall quality and contiguity whilst identifying the shortcomings of various points in the workflow. Interrogation of the various data types used in the assembly process was facilitated by the genome evaluation tool gEVAL (geval.co.uk) during this manual curation process to resolve the issues that may have lingered or even been introduced during the assembly and scaffolding process such as false joins, incomplete gene structure and duplicated components.

The lessons learned from this are relayed back to our technical collaborators to further improve on data generation/quality and assembly strategy, whilst allowing the Vertebrate Genome Project to create an improved workflow.

Interested parties can find updates on progress and species involved on the website: <http://www.sanger.ac.uk/science/data/vertebrate-genomes-project>.

W004: Aquaculture and Genomics

Implementation of Genomic Tools for the New Zealand Greenshell™ Mussel Industry

Rachael Ashby¹, Andrew S Hess¹, Hayley Baird¹, Rudiger Brauning¹, Rodney Roberts², Nick King³, Jane Symonds³, Neil Gemmill⁴ and Shannon Clarke¹, (1)AgResearch, Invermay Agricultural Centre, Mosgiel, New Zealand, (2)SPATNZ, Nelson, New Zealand, (3)Cawthron Institute, Nelson, New Zealand, (4)University of Otago, Department of Anatomy, Dunedin, New Zealand

Aquaculture is a growing industry globally, however genomic resources are only available for a few key species. The Greenshell™ Mussel (GSM) is an endemic species of economic importance to the New Zealand aquaculture industry and is currently the largest industry by export volume and value. The development of a purpose-built mussel hatchery has allowed family-based selective breeding of GSM, reducing the industry's reliance on wild-caught juveniles and also enabling genomic selection.

Lower sequencing costs have allowed us to assemble the GSM genome and develop transcriptome resources. Subsequently a genotyping-by-sequencing (GBS) pipeline has been developed to provide a cost effective method for SNP genotyping. We are now using the GBS pipeline to aid mussel farming by providing a low-cost parentage test and assess the genetic diversity in established broodstock. Pooled family rearing with genotyping is also being evaluated as a method for future family production. In addition, we are utilising the data to investigate genomic selection with the aim of optimising commercial trait selection and deliver benefits for New Zealand's economy.

W005: Aquaculture and Genomics

Identification of Genomic Loci Associated with Maturation in Pacific Coho Salmon (*Oncorhynchus kisutch*)

Michelle T.T. Crown^{1,2}, Kris A. Christensen¹, Krzysztof P. Lubieniecki², Ruth E. Withler³, Janine Supernault³, Eric B. Rondeau^{1,4}, Ben F. Koop⁴, Robert H. Devlin¹ and William S. Davidson², (1)Fisheries and Oceans Canada, West Vancouver Laboratory, West Vancouver, BC, Canada, (2)Simon Fraser University, MBB Department, Burnaby, BC, Canada, (3)Fisheries and Oceans Canada, Pacific Biological Station, Nanaimo, BC, Canada, (4)University of Victoria, Victoria, BC, Canada

Reproductive success of salmon is influenced by multiple morphological features, physiological performance, and behavioural mating strategies. While certain male-specific traits such as sperm quality can clearly affect reproductive success, precocious sexual maturation (maturing one year early, smaller body size and absent secondary sexual characteristics) is an interesting example of an evolutionary stable strategy where the fitness is balanced between precocious and full adult males. The genetic basis of early maturation (termed jacking in Pacific salmon and grilising in Atlantic salmon) is thought to be polygenic, but recent work has found that 39.4% of the phenotypic variation can be explained by a single locus (vestigial-like-family-member-3; *vgl13*) in regulating maturation onset in Atlantic salmon. Our current study aims to identify loci associated with jacking and survival in Pacific coho salmon, *Oncorhynchus kisutch*. We conducted a genome-wide-association-study and mapping analysis on six families from a hatchery population (Inch Creek), three of which possessed a high proportion of jacks and three that had a low proportion. Using a Genotype by-Sequencing (GBS) approach, EcoT22I reduced representation libraries were generated for 716 individuals and sequenced on the Illumina HiSeq platform. GBS data was aligned to the published version of the coho genome with BWA, and variants were called with STACKS. To enhance the power of our genome-wide-association analysis, we then used the resultant 45,716 SNPs to impute missing genotypes with BEAGLE. Data analysis to date reveal that genomic loci associated with jacking in coho salmon are distinct from *Vgl13*. Using this population of coho salmon as a model, these data suggest that the molecular mechanisms determining age of male maturation are not fully conserved between Atlantic salmon and Pacific coho salmon.

W007: Genomic and Genetic Analysis in Polyploid Species

Strategy and Progress of Sweetpotato Genome Project By TRAS

Ung-Han Yoon¹, Qinghe Cao², Kenta Shirasawa³, Hong Zhai⁴, Jae Cheol Jeong⁵, Masaru Tanaka⁶, Hideki Hirakawa³, Hideki Nagasaki³, Xiangfeng Wang⁴, Tae Ho Kim¹, Dai-fu Ma², Yoshihiro Okada⁷, Jang-ho Hahn¹, Sang-Soo Kwak⁸, Qingchang Liu⁴ and Sachiko Isobe³, (1)National Institute of Agricultural Sciences, RDA, Jeonju, South Korea, (2)Sweetpotato Research Institute, CAAS, Xuzhou, China, (3)Kazusa DNA Research Institute, Kisarazu, Japan, (4)China Agricultural University, Beijing, China, (5)Korea Research Institute of Bioscience and Biotechnology, South Korea, (6)Kyushu Okinawa Agricultural Research Center, NARO, Miyakonojo, Japan, (7)Kyushu Okinawa Agricultural Research Center, NARO, Okinawa, Japan, (8)Korea University of Science and Technology, Daejeon, Korea, Republic of (South)

Sweetpotato (*Ipomoea batatas*(L.) Lam) grows well in harsh environmental conditions, and has been cultivated as one of the top seven food crops in the world. Recently, sweetpotato is drawing interest of people as a healthy food because it has higher dietary fiber, vitamins, carotenoids and overall nutrition value.

For the complete genome sequencing of diploid sweetpotato Mx23Hm (*Ipomoea trifida*, 2n=2x=30, 515.8 Mb), we used Illumina HiSeq and single-molecule real-time (SMRT) sequencing platform. *De novo* whole genome assembly was conducted with 58.19 Gb PacBio reads using HGAP 2.0 assembler. Subsequently, chromosome-scale scaffolding was performed with 582 PacBio scaffolds using Hi-C method. As a result, total number of scaffolds was 520, N50 scaffold length was 30.854 Mb, and total size of scaffolds was 497.197 Mb. Gene prediction was performed by evidenced gene model and predicted gene model pipelines. As a result of this annotation, 37,100 gene models were predicted. Also, we performed the whole genome sequencing of hexaploid sweetpotato Xushu 18 (2N=6x=90, 3 Gb) using Illumina HiSeq, SMRT sequencing platforms. *De novo* whole genome assembly with 181.5 Gb PacBio reads of hexaploid Xushu 18 was performed using Falcon-unzip assembler. Chromosome-scale scaffolding was performed with 5,680 PacBio scaffolds using Bionano and Hi-C method. As a result, total number of scaffolds was 3,965, N50 scaffold length was 42.586 Mb, total size of scaffold was 1.735 Gb, and 93.52% of the assembled genome was contained in 45 cluster. We are conducting whole genome assembly of Xushu 18 using DenovoMAGIC. Currently, we are building pseudomolecules based on the high-density SNP genetic map.

W006: Genomic and Genetic Analysis in Polyploid Species A Journey of Genes from Genome to Fields in Groundnut

Rajeev K Varshney, ICRISAT, Hyderabad, India

Groundnut (*Arachis hypogaea*), also known as peanut, is one of the major oilseed and confectionary crop grown in ~ 25.4 million hectares across 100 countries achieving a global production of 42.4 Million tons. The crop is mainly consumed as confectionary and edible ingredients in various food products in western countries while used dual purpose (cooking oil and confectionary/table purpose) in the Indian subcontinent. Exposure of the crop to different biotic and abiotic stresses in marginal environments results in low crop productivity in developing countries. Until recently, very limited genomic resources were available in this crop. Traditional breeding approaches, however, could not be effective for enhancing crop productivity. A number of omics approaches have been deployed to understand the genome architecture, complexity of trait and apply genome diversity in breeding for groundnut improvement. For instance, various genomic resources including high-density genetic maps, reference genomes have been developed. In addition, 300 lines of the reference set and several mapping populations have been re-sequenced to identify millions of sequence variants. Modern trait mapping approaches such as genotyping-by-sequencing, QTL-Seq have been used to map a number of agronomic traits. RNA-seq approach has been used to develop gene expression atlas and identify differentially expressed genes for several traits. In parallel, marker-assisted backcrossing approach has been used to develop the superior lines with enhanced resistance to foliar diseases and also with increased oleic acid content. Several introgression lines for foliar disease, under multi-location trials, have shown yield advantages from 39- 79% as compared to the recurrent parents. Similarly introgression lines for oleic acid have shown enhancement of oleic acid contents upto 79%. We anticipate release of several superior varieties for both foliar diseases and high oleic acid content.

W008: Genomic and Genetic Analysis in Polyploid Species

Sequencing White Clover and its Progenitors - Two Genomes Gone Global

Andrew G. Griffiths, AgResearch, Palmerston North, New Zealand

**W009: Genomic and Genetic Analysis in Polyploid Species
New Genotyping Technology, GRAS-Di, using Next Generation Sequencer
Hiroyuki Enoki, Yoshie Takeuchi and Kazuyo Suzuki, Toyota Motor
Corporation, Aichi, Japan**

We developed new genotyping technology, Genotyping by Random Amplicon Sequencing-Direct (GRAS-Di). This technology consisted of sample preparation using high concentration random primer, NGS and data analysis. The sample preparation was very simple. It was not necessary to do primer design, enzyme digestion, fragmentation, size selection, adaptor ligation, and normalization. It was only two steps PCR for NGS library with sequence adaptor without specialized equipment. Rice BIL population was used for evaluation of genotyping ability of GRAS-Di, with HiSeq2500 for 96 samples / lane. The number of reads for each amplicon was highly reproducibility, $r > 0.99$ with repetition. Over ten thousand SNPs were detected among the BIL population. The SNPs were distributed uniformly rice genome. The ratio of missing value was very low, 1.5%. The reproducibility of SNP was 99.99% with repetition. If there was no reference sequence, genotype data could be detected by GRAS-Di using original algorithm based on amplicon analysis. Theoretically, the technology is also applicable to other species, including highly polyploidy species. We performed the applicability test for several species. The result of the test shown that the technology was applicable for all sixty species, including wheat, strawberry, sugarcane, cow, pig, chicken, tuna and human. Several sequence adaptors with index were designed. They could be provided over 60,000 multiplex sequencing. We think that GRAS-Di would be very powerful technology for genome wide genotyping in many species.

**W011: Genomic Annotation Resources at the EBI
Integrating and Displaying Plant and Animal Gene Expression in
Expression Atlas**

Laura Huerta, European Bioinformatics Institute (EMBL-EBI), Hinxton, United Kingdom
Expression Atlas (www.ebi.ac.uk/gxa) is a database and web-service at EMBL-EBI that selects, curates, re-analyses and displays gene expression data in a baseline context, e.g. to find genes expressed in different tissues in chicken, and in a differential context, e.g. to find up-regulated genes in response to stripe rust and powdery mildew in wheat. Experiments from ArrayExpress, GEO and SRA/ENA/DDBJ are selected for curation and analysis. Data curation involves enriching sample annotation with additional metadata, annotating metadata with Experimental Factor Ontology (EFO) terms and deciding comparisons for differential expression analysis based on associated publications and correspondence with the original researchers. Data analysis is performed using open source tools for microarray data and our standardized pipeline iRAP (github.com/nunofonseca/irap) for RNA-seq data. Currently, we provide gene expression analysis results for more than 3300 experiments across 50 different species. Expression Atlas can be searched by gene, gene set and biological condition queries. The use of EFO annotations allows efficient search via ontology-driven query expansion and facilitates data integration across multiple experiments. We offer downstream analysis and visualization such as gene co-expression, biological variation among replicates, transcript quantification, visualization of gene expression in Ensembl and Gramene genome browsers and enrichment of Gene Ontology terms and Reactome pathways. Finally, we have developed an automatic pipeline that discovers new RNA-seq data at ENA for 200 different species, performs quality control, alignment to the genome reference in Ensembl and quantification of gene and exon expression. The analysis results are available via our RNaseq-er API (www.ebi.ac.uk/fg/rnaseq/api/).

**W010: Genomic Annotation Resources at the EBI
Accessing Genomic Data with Ensembl and Ensembl Genomes
Benjamin Moore**, EMBL-EBI, Hinxton, United Kingdom

'Accessing genomic data with Ensembl and Ensembl Genomes' will include an introduction to the Ensembl browsers, demonstrate key views in browsing genomes, and show you how to use tools for accessing genomic data and analysing your own, BioMart and the Variant Effect Predictor (VEP). Ensembl (www.ensembl.org) provides an interface and an infrastructure for accessing genomic information covering over 100 vertebrate species, including cow, pig, sheep, goat and chicken. Its sister project, Ensembl Genomes (www.ensemblgenomes.org), consists of five sub-portals (bacteria, protists, fungi, plants, and invertebrate metazoa) which contain data for over 700 eukaryotic (including wheat, barley, tomato and brassicas) and over 40,000 prokaryotic genomes. All species in Ensembl and Ensembl Genomes have gene annotation and comparative genomics analyses within the taxa (excluding bacteria). For many of these genomes, we also provide annotation of variants, such as SNPs and CNVs. All these data can be accessed via our browser websites, BioMart (for protists, fungi, plants, and animals), FTP, Perl APIs, REST API, and MySQL. Furthermore, the Variant Effect Predictor (VEP) is a powerful tool for analysing sets of genomic variants, available for all species in Ensembl and Ensembl Genomes.

Highlights of the past year include;

- Over 30 new and updated rodent and primate genomes now available, as well as new assemblies and genebuilds for goat, pig and cat.
- New plant species: jute, cassava, yam, sunflower, cotton, bean and cucumber. New assembly for barley, and updated assemblies and annotation for sorghum bicolor, soybean, peach, rice and maize. New polyploid view for wheat.

**W012: Genomic Characterization of Ruminants in Asia
Genomic Technologies to Support Ruminant Research and Industry
Application**

Shannon Clarke, AgResearch, Invermay Agricultural Centre, Mosgiel, New Zealand
To enable and enhance genomic research and industry application for ruminants, AgResearch has developed a suite of genomic tools. In addition to developing several SNP array based genotyping tools, AgResearch has also invested in genotyping by sequencing (GBS) methods, both targeted and restriction enzyme based. For restriction enzyme based GBS, combining low-depth sequencing with algorithms that produce bias free genomic relationship matrices we can estimate: breed composition, pedigree, traceability, inbreeding and co-ancestry as well as using directly in existing mixed models (GBLUP) to estimate breeding values. In addition, further developments for GBS analysis has established methods to undertake GWAS, linkage mapping, estimation of linkage disequilibrium and derivatives such as Ne. I will present how the developed genomic technologies can support ruminant research and industry application.

**W013: Genomic Characterization of Ruminants in Asia
Endangered and Extinct Species Progress and Potential**

P. Olof Olsson, Soom Biotech Research Foundation, Seoul, South Korea
Currently more species are endangered than have ever been before and largely due to direct and indirect human influence. A question often posed when discussing animal conservation, especially work on restoration of extinct species, is what the motivation. Why should we extend the effort to save and restore animal species or populations that have died out? Our answer depends in large part on our views about our role in the equation, the reason for extinction, the species itself and the effect on the ecosystem. Whether the intrinsic and extrinsic value of the species of question warrants the effort, basically should we do it and is it worth the cost? Once we agree to intervene the question becomes how. To answer this we address the methods of population management, captive breeding and, discussed herein, assisted reproductive technologies.

Aside from conventional reproductive means for endangered species, including the often unsuccessful, *in vitro* fertilization (IVF). The approach using somatic cell nuclear transfer (SCNT) using similar species, which has not largely been pursued, is the. Our approach illustrates a number of the successes and difficulties using interspecies SCNT and embryo transfer. We are moving forward to include cell and molecular techniques to better the efficiencies and enable the development of embryos to term. New technologies, most notably including genome manipulation and synthesis, may make the potential for extinct species restoration more obtainable than previously imagined. Although to date only bacteria have been produced solely by this method. We have shown that SCNT is a viable method for the cloning of similarly related species. Preliminary success in restoration techniques has been achieved by us in related members of the canine family, wolves and coyotes, as well as by others in related bovine species, cattle, guar. Success has however been limited to the closely related species and is thought primarily to be due to maternal- fetal or genomic-mitochondrial incompatibilities. Our failures have been equally instructive in the requirements for further attempts and the need for specific modifications and advancements to established technologies.

Preliminary conclusions are positive, illustrating the potential for further progress. More work is required to expand current and introduce new technologies to this field. International regulatory roadblocks remain an obstacle for the transfer of material.

**W015: Genomic Characterization of Ruminants in Asia
Biodiversity of Indigenous Goats in Nepal**

Neena Amatya Gorkhali, Animal Breeding Division-NARC, Kathmandu, Nepal

**W014: Genomic Characterization of Ruminants in Asia
Signatures of Altitude Adaptation in Ethiopian Sheep Populations**

Zewdu Edea Bedada, Chungbuk National University, Chungcheongbuk-do, Korea, Republic of (South), Dessie Tadelle, International Livestock Research Institute, Addis Ababa, Ethiopia, Hailu Dadi, Addis Ababa Science and Technology University, Addis Ababa, Ethiopia and Kwan-Suk Kim, Chungbuk National University, Chungcheongbuk, Korea, Republic of (South)
Ethiopian sheep populations such as Menz (MZ, short fat-tailed), Arsi-Bale and Horro sheep (LFT, long fat-tailed) are adapted to the high-altitude (2000-3200m), whereas Blackhead Somali sheep (BHS) thrive well in a hot/dry climate (<1500m); and such variation in altitude can offer an opportunity for investigating livestock species genetic adaptation to extreme environments. However, there have been no studies conducted to identify signatures of selection for environmental adaptation in Ethiopian sheep populations. In this study, we genotyped a total of 60 animals sampled from high- versus low-altitude environments using an Ovine 600K chip; and scanned for genomic regions showing evidence of selection for environmental adaptation. Several signatures of selection was detected in genes known to be associated high altitude adaptation for MZ (*PRKAA1*, *SOCS2*, *TUBB3*, *CSRP2BP*, *TUBB3*, *SKIV2L2*, *DNAH9*, *PPP1R12A*, *SKA3*, and *TRHDE*) and for LFT (*ADRBK1*, *VAV3*, *HSF2*, *KIT*, *MC1R*, *ARHGAP28*, *CSRP2BP*, *BMP2*, *RNMT*, *LEP*, and *LEMD3*). Fourteen of the genes (*MITF*, *FGF5*, *PARP4*, *OVOL2*, *SLAIN1*, *IFT88*, *MMP28*, *PGD*, *RABGAP1L*, *SNX5*, *PAX1*, *TRHDE*, *BPIFB2*, and *SAMHD1*) were shared between the two sheep populations. Further functional enrichment analysis reveals that the candidate genes have GO terms relevant to adaptation under extreme environments, including regulation of metabolic process, response to nutrient levels, regulation of apoptosis and pigmentation. Altogether, our results aid further understanding and exploitation of the underlying genetic mechanisms for sheep and other livestock species adaptation to high-altitude environments.

Keywords: Adaptation, Ethiopian sheep, high-altitude, selection signatures

**W016: Genomic Characterization of Ruminants in Asia
Genetic Structure and Introgression Signatures of African Cattle Genome**

Kwondo Kim, Seoul National University, Seoul, South Korea, Dajeong Lim, National Institute of Animal Science, Suwon, Korea, Republic of (South) and Hee-bal Kim, Seoul National University, Seoul, Korea, Republic of (South)
African continent, where more than 150 breeds reside, is a reservoir of diverse cattle breeds; hence, the genetic diversity of cattle is well preserved in contrast to other regions. One of the factors that give rise to this diversity is interbreeding between populations, especially between taurine and indicine cattle (zebu). Since the introduction of two subspecies, the continent has experienced dynamic admixture. However, the complex structure of African cattle genome is not fully elucidated at a genome-wide level. In this ongoing study, the complex population structure of 15 African cattle breeds was inferred by the whole genome sequence of 217 individuals, which demonstrated extensive admixture among zebu breeds. The degrees of taurine introgression were highly diverse between zebu breeds, reflecting different population history for each breed. Nevertheless, there was one particular region that is significantly introgressed from taurine cattle in all zebu breeds. The region is associated with gamma-aminobutyric acid (GABA), the main inhibitory neurotransmitter in the mammalian central nervous system, which suggest the tameness of indicine cattle through interbreeding with taurine cattle. The results of this study will extend our understanding of the complex history of African cattle breeds and might give insight into the influence of admixture on the traits of cattle subspecies.

W017: Genomic Characterization of Ruminants in Asia
Genomic Study of Domestic Animals Adapted to Extreme Environments
Kwan-Suk Kim, Chungbuk National University, Cheongju, South Korea

W018: High-Throughput Genetics: Lab to Landscape
The Wheat Genome Reference Sequence As a Tool for Documenting the Allergens and Immune-Responsive Proteins

Rudi Appels, University of Melbourne, Melbourne, Australia
The wheat genome reference sequence as a tool for documenting the allergens and immune-responsive proteins.
Angela Juhasz, Rudi Appels,
Murdoch University, Perth, Western Australia
Wheat is an important staple grain for human-kind globally because of its end-use quality and nutritional properties and its adaptability to diverse climates. Specific wheat proteins can trigger adverse immune responses and clinical manifestations such as celiac disease, wheat allergy, baker's asthma and wheat-dependent exercise-induced anaphylaxis (WDEIA). Establishing the content and distribution of the immune-stimulatory regions in wheat has been hampered by the complexity of the wheat genome and lack of complete genome sequence information. A comprehensive analysis and annotation of the wheat Prolamin Pfam clan grain proteins implicated in these disorders using the new IWGSC RefSeq v1.0 genome sequence of bread wheat has now established a new reference map for immune-stimulatory wheat proteins and provides a new basis for selecting wheat lines and developing diagnostics for products with more favorable consumer attributes.

W019: High-Throughput Genetics: Lab to Landscape
Gene Regulatory Network Modelling Identifies Novel Transcription Factors Regulating Senescence in Wheat

Philippa Borrill, John Innes Centre, Norwich, United Kingdom
Monocarpic senescence in crops is essential to enable nutrient remobilisation from photosynthetic tissues to the grain. This process must be tightly regulated to prevent premature senescence adversely affecting yields, however few genes controlling senescence have been identified in wheat.
We are using a combination of approaches to identify novel regulatory genes affecting the early processes controlling senescence. We have generated a high-resolution RNA-Seq time-course of ten time-points from anthesis until the first visible signs of flag leaf senescence. To understand the key genes driving transcriptional changes, we used a combination of gene regulatory network analyses to identify modules of co-expressed genes and hub genes regulating the transcriptional processes across this time-course.
From these networks, we selected ten transcription factors as candidate genes for further characterisation. We have generated double knock-out mutants of these candidate genes using the sequenced tetraploid TILLING population. Preliminary results show that two out of five candidate genes tested to date have roles in monocarpic senescence. Further studies are in progress to characterise the effects of these novel senescence regulators on nutrient remobilisation.
The availability of new genomic resources for wheat, such as high-quality genome sequences and TILLING knock-out mutants, has enabled the study of genes regulating senescence at an unprecedented resolution. These genes may represent new breeding targets to adapt senescence to the environment and to modulate grain nutrient content which is influenced by the rate of senescence.

W020: High-Throughput Genetics: Lab to Landscape
4Gs in Crop Breeding for Pulses Improvement in Developing Countries

Rajeev K Varshney, ICRISAT, Hyderabad, India
Pulses are rich sources of dietary protein (20-30% of total weight), carbohydrates (55-65%), essential amino acids and significant amount of micronutrients with very low calories. These crops play an important role in global food and nutritional security, especially in the context of climate change and limited water availability for agriculture. However, the crop productivity of pulses has been less than 1 ton per hectare. Various biotic and abiotic stresses are the major constraints leading to significant yield losses in pulse production. In this context, 4Gs i.e. germplasm, genomes, genes/markers and genomics and their integrated use hold great potential for bringing much needed disruptive change in crop improvement. Germplasm (1st G) collections stored in genebanks should be well characterised preferably in extreme conditions for future breeding traits. Superior germplasm lines may be useful for introgressing desired traits as well as enhancing genetic base of cultivated gene pool. Genomes (2nd G) and their sequencing and re-sequencing can provide superior alleles and markers with higher prediction value for target traits by using genome-wide association study and linkage mapping approaches. Genes (3rd G) with causal effect can be identified by using functional genomics and systems biology approaches. Genomics (4th G) technologies should become the integral part of crop improvement programs by deploying genomics-assisted breeding approaches such as early generation screening, marker-assisted backcrossing, genomic selection and genome editing. While discussing the role of the above mentioned 4Gs, some examples of integrated use of 4Gs in pulses improvement for developing countries will be presented. In summary, accelerated deployment of 4Gs is expected to enhance, precision, efficiency and effectiveness of breeding programs to deliver climate-resilient varieties and higher genetic gains in developing countries.

W021: Legumes Genomics

Transcriptomic Profiling of Genes Involved in Proanthocyanidin Biosynthesis Pathway in *Glycine* Species

Jungmin Ha, Seoul National University, Seoul, South Korea

Proanthocyanidins are oligomeric or polymeric end products of flavonoid metabolic pathways starting with the central phenylpropanoid pathway.

Although soybean (*Glycine* spp.) seeds represent a major source of nutrients for the human diet as well as components for the cosmetics industry due to their high levels of flavonoid metabolites, including isoflavonoids, anthocyanins, and proanthocyanidins, the genetic regulatory mechanisms underlying proanthocyanidin biosynthesis in soybean remain unclear. We evaluated interspecific and intraspecific variability in flavonoid components in soybean using 43 cultivars, landraces, and wild soybean accessions. We performed transcriptomic profiling of genes encoding enzymes involved in flavonoid biosynthesis using three soybean genotypes, Hwangkeum (elite cultivar), IT109098 (landrace), and IT182932 (wild accession) in seeds. We identified a *G. max* landrace, IT109098, with a proanthocyanidin content as high as that of wild soybean. Different homologous genes for anthocyanidin reductase, which is involved in proanthocyanidin biosynthesis, were detected as differentially expressed genes (DEGs) between IT109098 and IT182932 compared to Hwangkeum. We detected major differences in the transcriptional levels of genes involved in the biosynthesis of proanthocyanidin and anthocyanin among genotypes beginning at the early stage of seed development. Our results provide insights into the underlying genetic variation in proanthocyanidin biosynthesis among soybean genotypes.

W023: Legumes Genomics

New Insights of Gene Expression Regulation by Noncoding RNAs during Heat Stress in Chickpea (*Cicer arietinum* L.)

Sailaja Bhogireddy, ICRISAT, Greater Hyderabad, India

Chickpea is an important leguminous crop with nutritional value and widely grown in semi-arid tropics. The crop is sensitive to extreme temperature regimes and exposure to high temperatures (>35°C) during reproductive stage leading to limited crop productivity. Consequently there is a prerequisite to develop heat-tolerant chickpea varieties to cope up with changing climatic conditions. Besides global gene expression, high throughput technologies paved the way to identify non-coding RNAs (ncRNAs), which tend to play a crucial role in gene expression regulation at transcriptional and post transcriptional level. Particularly, to understand the role of long intergenic noncoding RNAs (lincRNAs) in heat stress, the present study was undertaken by constructing 24 RNA-seq libraries from vegetative and reproductive tissues (roots and leaves) of three heat stress responsive chickpea (two tolerant- ICC 15614, ICC 1356 and one sensitive-ICC 4567) genotypes. A total of 236 million reads were generated and about 98% of total reads were aligned to genome. Expression analysis results in identification of 31580 lincRNAs in which 5525 lincRNAs were differentially expressed. Reciprocal expression of three lincRNA genes, XLOC_003252, XLOC_003259 and XLOC_011985 in tolerant and sensitive genotypes provided a clue in heat stress response. LincRNA-mRNA co-expression analysis revealed the association of lincRNA (XLOC_003252) with coding mRNA for pleiotropic drug resistance, the member of the Hsp70 and J-protein chaperone family suggesting regulatory mechanism of lincRNA in heat stress. Validation of the identified lincRNAs is in progress. Further, these lincRNAs can be deployed in crop improvement programs through effective breeding strategies after thorough validation and characterisation.

W022: Legumes Genomics

Development of SNP-Based Molecular Markers and its Applications in Peanut

Taehwan Jun, Pusan National University, MIRYANG, South Korea

Peanut or groundnut (*Arachis hypogaea* L.) is a major economic legume crop widely cultivated in tropical and subtropical regions of the world and an important source of protein and vegetable oil especially unsaturated fatty acid (such as oleic acid) for human nutrition. Cultivated peanut is an allotetraploid (AABB; 2n=4x=40) with a relatively large genome size of 2800 Mb/1C, which is presumed to have derived from a single recent hybridization event between two diploid ancestors of *A. duranensis* (the A genome) and *A. ipaensis* (the B genome). We resequenced two Korean peanut cultivars "K-OI" (*Arachis hypogaea* ssp. *fastigiata* L.) and "Pungan" (*Arachis hypogaea* ssp. *hypogaea* L.), which were developed at the National Institute of Crop Science (NICS), RDA in Milyang. The whole genome re-sequencing for the two cultivars was performed to produce sequences of 35.3×10⁹ bp with 350×10⁶ reads and 32.0×10⁹ bp with 318×10⁶ reads, respectively. As compared with the peanut reference genomes, the distribution of homozygous and heterozygous SNPs on each chromosome showed very similar patterns between 'K-OI' and 'Pungan', and most of them were in intergenic-region regardless of the peanut cultivars and reference genome type. The SNPs identified between the two peanut cultivars were evenly distributed across chromosomes of peanut diploid A and B reference genomes. This result indicates that these SNPs could be available to construct a genetic map using the segregating population derived from a cross between 'K-OI' and 'Pungan'. We also identified various types of genetic markers including single nucleotide polymorphisms (SNPs), insertions/deletions (Indels), simple sequence repeats (SSRs), and Cleaved Amplified Polymorphic Sequences (CAPS). To verify the availability of markers found in the study, we screened 30 polymorphic markers across 96 peanut varieties that are made up of 5 different origins including South Korea, China, and three South American countries. The 96 peanut genotypes evaluated were divided into two main groups using Neighbor-joining tree construction based on the Maximum Composite Likelihood method. Results indicated that most of Korean genotypes grouped in second cluster, only eight exceptions originated from Korea were grouped in the first cluster including most of South American genotypes. Further studies should be carried out, our results are likely to provide a valuable resource for the peanut breeders and researchers.

W024: Legumes Genomics

Phenotype Substitute Environment (PE) Value: Toward a G x E Research in Legumes

Sachiko Isobe¹, Takanari Tanabata², Atsushi Hayashi², Hidenori Tanaka³, Masatsugu Hashiguchi³, Shusei Sato⁴, Akihiro Nakaya⁵, Mai Hasegawa⁶, Sayuri Tanabata⁷ and Ryo Akashi³, (1)Kazusa DNA Research Institute, Kisarazu, Japan, (2)Kazusa DNA Research Institute, Chiba, Japan, (3)University of Miyazaki, Miyazaki, Japan, (4)Tohoku University, Sendai, Japan, (5)Graduate School of Medicine, Osaka University, Suita, Osaka, Japan, (6)Osaka University, Suita, Osaka, Japan, (7)Ibaraki University, Ibaraki, Japan Investigation of genotype × environment interaction (G×E) is becoming more important in plant molecular genetics. While genotype data is able to be obtained in whole genome with the recent NGS technologies, comprehensive environmental data is difficult to obtain even we use multiple sensors. The imbalance quality and quantity of data between genome and environmental values makes G×E studies incomplete.

In order to obtain comprehensive environmental value (E) during the plant growing season, we propose a new parameter, PE (Phenotype substitute for Environment). PE is a parameter generated from phenotypic values of each plant during a growing period, obtained by traditional and/or digital measurement methods such as image analysis. It substitutes environmental factors that cannot be measured by sensors set in the test space. It complements E together with measured environmental values (ME) obtained by sensors.

To substantiate the concept of PE, we are developing semi-automated imaging system for obtaining phenotype and environmental data. Four Soybean varieties used for the model materials to investigate the G x E analysis, and grown in the fields located across Japan (Miyazaki, Chiba and Miyagi). The seeds yield per a plant were segmented in each phytomere, and network analysis was performed with other morphological traits for generation of PE values. The degree of independence is considered to be one of the important index for generation of PE values, and the numbers of primary branch generated from middle part of the main stems were selected as candidate PE values.

W025: Legumes Genomics

Using Haplotypes to reduce costs in large scale genotyping projects

Guy Kol, NRGene, Ness-Ziona, Israel

In any large-scale breeding effort, the challenge of capturing genomic similarities and differences of large number of individuals is often a main cost driver. The talk will feature NRGene's cost effective, sequence-based method to analyze the genomic content of many, often very diverse genomes and allows that information to be efficiently used for understanding that genomic complexity and design an efficient genotyping approach for it.

The talk will include specific example of applying the approach to maize and wheat breeding and will demonstrate novel query and visualization tools. NRGene and LGC are integrating the above computational approach with the of design of low resolution, cost effective and imputation optimized genotyping assays. The combination of the technologies will allow successful imputation to high resolution genotyping and the predicted effect on cost and predictability of genomic selection in maize, wheat and other organisms will be discussed.

W026: Livestock Genomic Adaptation to Climate Change

Livestock Genomic Adaptation to Climate Changes Via Long-Term Natural Selection within and/or Historical Introgression between Species

Jian-Lin Han, The International Livestock Research Institute, CGIAR, Nairobi, Kenya

Livestock contributes to and is also affected by climate change. While the demand for animal-sourced food has been consistently growing, climate change is becoming a major threat to the sustainability of extensive livestock systems where indigenous animal genetic resources still play an important role in Asian and African developing countries. Heat stress from climate change has been leading to the most significant, negative impact on livestock productivity, e.g. reduced milk, meat and egg production as well as impaired reproductive efficiency and immunity. Climate change also affects intensified livestock production systems via limited availability of feeds and water resources. On the other hand, methane emissions from intensive livestock production systems have shed significantly negative impact on animal agriculture. It is highly expected that the application of new technologies, including genomic selection and advanced reproductive technologies, will play an important role in addressing these challenges. There have been tremendous achievements in the past a few years on the improved understanding on genomic adaptation of major livestock and poultry species to adverse environmental challenges, e.g. heat/cold stress and hypoxia at high-altitudes. Several large geographic scale and deep genome-coverage re-sequencing data from indigenous animal genetic resources in Asia and Africa have been generated and published through international intensive collaborations. Genomic signature analyses support long-term natural selection within a species and historical hybridization or introgression between species towards the accumulation of advantageous genotypes or alleles responsible for the enhanced genetic tolerance to heat/cold and hypoxia challenges.

W027: Livestock Genomic Adaptation to Climate Change

Genomic Signatures in African Livestock for Adaptation to Climatic Changes

Olivier Hanotte, International Livestock Research Institute (ILRI - Ethiopia) and The University of Nottingham (UK)

BBY 2100, it is predicted that the global average earth temperature will increase by 1.4°C to 5.8°C. Global average annual precipitation will also increase with significant variation between regions. Extreme climatic events will become more common.

Overall, we will be living in a hotter but also a more humid planet. Moreover, human population will continue to increase with estimation around 7 to 15 billion people by 2100. Not only will our livestock and crops need to adapt but they will need to produce more and sustainably. Fortunately, livestock species, breeds or/and populations, throughout their genetic history have become adapted to nearly all agro-ecologies and environments. Livestock genetic diversity is a treasure trove of adaptation to environmental challenges, which, when characterised will represent major entry points to mitigate the impact of climatic changes. This is particularly true for the African continent which displays a north-south orientation, with the equator at its middle and landscapes from below sea levels to above 4000 meters asl. Combined with ancient trading networks linking the African civilisations to the Middle-East and Asia, the continent is now hosting a large section of the diversity of the major Eurasian domesticates, namely cattle, sheep, goat and chicken. Adaptation to climatic challenges in these species is an essential component of their functional diversity. The genetic mechanisms of such adaptation are expected to be complex. They should not only be understood as an adaptation to temperature and water availability but also an adaptation to the consequence of these two, such as changes in infectious and parasitic diseases distribution, forage availability and changes in vegetation cover and/or plant species etc. Similarly, heat tolerance is a physiological trait dependent on the complex interactions between many factors, including properties of the skin and hair, sweating and respiration capacity, metabolic heat production, behaviours etc. Here, I will present some of our work in collaboration with institutions in Europe and Asia, aiming to understand the unique adaptation of African livestock (cattle, sheep and chicken) to the direct and indirect challenges of climates.

W028: Livestock Genomic Adaptation to Climate Change

Identification of Genomic Regions in Sheep Responsible for High-Altitude Adaptation

Neena Amatya Gorkhali, Animal Breeding Division-NARC, Kathmandu, Nepal and Jian-Lin Han, The International Livestock Research Institute, CGIAR, Nairobi, Kenya

Domestic sheep is one of the first livestock species being domesticated around 10,000 years ago in the Fertile Crescent. From there they spread west throughout Europe, south into Africa and east into Asia. Sheep living at the Himalayas serves as an outstanding model for the study of the genetic mechanism of high-altitude adaptation. The Himalayas extends to the Qinghai-Tibetan Plateau on the north and east; and is bordered by the Indo-Gangetic Plain on the south. Nepal lies in the south slope of the Himalayas and between these unique geographic wonders, it thus has a spectacular altitudinal range from 80 m above sea level (masl) in the south to 8,848 masl in the north. There are four indigenous sheep breeds including Bhyanglung, Baruwai, Kage and Lampuchhre distributed at various altitudes ranging from 4500 to 80 masl in Nepal. To identify potential functional genes underlying the adaptation of indigenous sheep to high-altitudes, we genotyped genome-wide single nucleotide polymorphisms (SNPs) of these four breeds and downloaded relevant SNP array data from additional Asian and Middle East breeds. A genomic comparison between four high-altitude and eight lowland Asian breeds revealed the most differentiated variants at the locus of *FGF-7* (*Keratinocyte growth factor-7*). A SNP mapped to the upstream of *FGF-7* seemed to contribute to the divergence signature. We hypothesized that *FGF-7* gene probably enhances lung function by regulating its expression level in high-altitude sheep through altering its binding of specific transcription factors, implying a novel adaptive mechanism to high altitudes in sheep.

W029: Livestock Genomic Adaptation to Climate Change
Genome-Wide Scan Reveals Divergent Selection Among Taurine and Zebu Cattle Populations from Different Regions
Zewdu Edea Bedada, Chungbuk National University, Chungcheongbuk-do, Korea, Republic of (South)

W030: Livestock Genomic Adaptation to Climate Change
Genomic Signatures Associated with Adaptation of Buffaloes to Climate Change

Yi Zhang, China Agricultural University, Beijing, China and Jian-Lin Han, The International Livestock Research Institute, CGIAR, Nairobi, Kenya
The Asian water buffalo (*Bubalus bubalis*) is one of the most important domestic animals in tropical and subtropical regions. Morphological and performance traits differentiate two types – the dairy river buffalo of the Indian sub-continent and west to the Balkans, Italy and Egypt, and the swamp buffalo whose main use is as a draft animal in the region from Assam of India in the west through Southeast Asia to the Yangtze valley of China in the east. Within each type, various local breeds have adapted themselves to different environments, which offer an opportunity to us to understand the drivers of adaptation traits in terms of genomic variations. Most recently the river buffalo genome was successfully assembled by International Buffalo Genome Consortium (IBGC). Taking this advantage, we performed a large-geographic-scale genomic population analysis of Asian water buffaloes using next generation sequencing data of well-represented buffalo breeds/populations, with focuses on the genetic differentiation and genome-wide scan of selection signatures to identify genomic regions and linked functional genes/alleles that are associated with the adaptation traits in buffaloes.

W031: Modern SNP Technologies in Plants: Research and Commercial Applications

From KASP to ‘Traitbreed Array’ and ‘Triticum-Genesizer’: Multiple Genotyping Platforms for Wheat Breeding and Allele-Discovery

Awais Rasheed, CIMMYT, CAAS, Beijing, China

Development of efficient, low-cost and high-throughput genotyping platforms for various wheat breeding and genetics objectives is challenging and there is no 'one shoe fits all' approach. Given these challenges and multiple objectives, our research has resulted in i) development of new 55K SNP chip array with improved SNP calling rate irrespective of genetic backgrounds for genome-wide genotyping, ii) conversion of all functional markers into KASP format to facilitate high-throughput automated genotyping in wheat breeding research, and iii) development of targeted-GBS platform (Triticum-Genesizer) to precisely identify causal variations in homoecologous copies of more than 200 functional genes. These assays can greatly benefit mapping experiment, characterization of crossing parents and advanced lines as well as marker-assisted selection in wheat breeding programs.

W032: Modern SNP Technologies in Plants: Research and Commercial Applications

Genome-Wide SNP Genotyping by Whole-Genome Resequencing of a Recombinant Inbred Line Population in Tomato

Kenta Shirasawa¹, Makoto Endo², Kazuyuki Tanaka², Eiji Yamamoto¹, Makoto Hatanaka² and Sachiko Isobe¹, (1)Kazusa DNA Research Institute, Kisarazu, Japan, (2)Takii & Co., Ltd., Japan

As genome-wide SNP genotyping is enabled by sequencing analysis, reduced represent sequencing techniques including genotyping by sequencing and restriction-site associated DNA sequencing (RAD-Seq) have recently become popular. Sequencing cost is continuously decreasing due to the great advance in next-generation sequencing technology. It has been already possible to apply whole-genome resequencing (WGRS) analysis on segregating populations to obtain whole-genome SNP genotyping data. We employed the WGRS for genotyping analysis of 173 recombinant inbred lines (RILs) derived from a cross between two F1 commercial varieties. The number of SNPs obtained from WGRS were as many as one million, which was 1000 times larger than that from RAD-Seq. As the result, mapping resolutions of association studies were dramatically improved. Furthermore, recombination breakpoints in chromosomes were finely identified. Besides, *de novo* mutations not presented in the parental lines were found in the genomes of the RILs. The whole-genome SNP data gave a new insight into genetics, genomics, and molecular breeding in tomato, and this would be applicable to both model and non-model plants, including crops.

W033: Modern SNP Technologies in Plants: Research and Commercial Applications

Application of SNP Markers for Anchoring New Heading Time Determinants in Wheat

Antonina A. Kiseleva, Andrey B. Shcherban, Irina N. Leonova and Elena A. Salina, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russian Federation

In this study we used the Illumina Infinium 15k SNP Wheat platform to detect new determinants of heading time on 5B chromosome in the substitution line of Chinese Spring with 5B chromosome from *T. dicoccoides* (CS-5Bdic), different from Chinese Spring (CS) in heading time by two weeks.

To ascertain the loci determining heading time difference, a set of 116 recombinant inbred 5B chromosomal lines as a result of hybridization of CS with CS-5Bdic were developed and their heading dates were estimated. Lines were different in their heading time when they were not vernalized. Genotyping was performed using 15k SNP array. 409 5B-specific polymorphic markers were detected and a genetic map with 85 skeletal SNP markers was constructed. QTL analysis of heading time variation demonstrated that locus in the pericentromeric region of 5B chromosome is significantly associated with heading time. This locus included 5 skeletal markers (79 SNP markers in total). Based on SNP sequences and synteny with model crop genomes we identified the four best candidate genes: *WRKY*, *ERF/AP2*, *FHY3/FAR1* and *ELF4*, known to be involved in flowering time modulation. Contribution of *FHY3/FAR1* in flowering pathways was shown in further experiments. Acknowledgements. This study was supported by the RSF (Project No. 14-14-00161).

W035: Modern SNP Technologies in Plants: Research and Commercial Applications

Amplifluor-like SNP Markers in Plant Genotyping

Yuri Shavrukov^{1,2}, Satyvaldy Jatayev³, Lyudmila Zotova³, Gulmira Khasanova³, Dan Cu¹, Peter Langridge² and Kathleen Soole¹, (1)Flinders University, Adelaide, Australia, (2)University of Adelaide, Adelaide, Australia, (3)S. Seifullin Kazakh AgroTechnical University, Astana, Kazakhstan

Single nucleotide polymorphisms (SNP) represent a very useful tool, successfully used for plant genotyping. There are various methods for SNP analyses, most of which have been commercialised. The Amplifluor (Amplification with Fluorescence) SNP method is based on competitive allele-specific PCR, similar to those applied in KASP markers. Two assays are required to carry out Amplifluor SNP analyses: PCR using Universal probes (UPs) and Gene-specific primers (GSPs), which are developed independently. Each of the two UPs contains a fluorophore and a quencher with a 'hair-pin' fragment in-between. During PCR with a DNA template containing one of two alleles at the SNP position, the amplification with GSPs will result in the release of fluorescence from one of the UPs. The two UPs are relatively expensive, but their 'universality' allows for their purchase as a 'one-off' order that provides a stock for all further SNP analyses. This makes the application of the UP mixture much cheaper since GSPs for each SNP cost the same as ordinary oligos. Unlike the commercial product 'Amplifluor', a trademark of Merck-Millipore, the 'Amplifluor-like' SNP markers can be developed by any researcher based on published data without restrictions. Therefore, scientists have the choice of purchasing either commercial products for Amplifluor / KASP assays or ordering self-designed Amplifluor-like SNP markers. In the latter case, a wide range of modifications and adjustments are possible in UPs, GSPs, PCR conditions, use of instruments, signal reading and interpretation. The significantly lower cost of Amplifluor-like SNP markers is accompanied by a high degree of freedom, completely 'in the minds' and 'in the hands' of researchers. Examples of various SNP genotyping studies using self-designed Amplifluor-like markers will be presented for wheat, barley, crested wheatgrass, sugar beet and chickpea; all of which provide useful 'fuel' for further candidate gene studies and Marker-assisted selection.

W034: Modern SNP Technologies in Plants: Research and Commercial Applications

Developing SNP Assays to Improve Rhizomania Resistance in Sugar Beet

Claudia Chiodi¹, Chiara Broccanello¹, Samathmika Ravi¹, Somaieh Moshari², J. Mitchell McGrath³, Andrew J. Funk³, Paul Galewski³ and Piergiorgio Stevanato¹, (1)University of Padova, Legnaro (Padova), Italy, (2)University of Zanjan, Zanjan, Iran (Islamic Republic of), (3)Michigan State University, East Lansing, MI

Abstract

Rhizomania virus (BNYVV) is well-known as the most dangerous one for sugar beet cultivation. Many genetic resistance sources and many SNP markers are available for sugar beet protection against this disease. But the research cannot stop and be satisfied with this result: the virus is mutating and evolving, as demonstrated from IV-BNYVV and AYPR strains. For this reason, sugar beet breeders continuously need new resistance sources and new markers. Since rhizomania resistance is a polygenic character, the best resistance level can be achieved pyramiding the highest number of reliable markers. The aim of this research was to validate new SNPs for rhizomania resistance. These SNPs have been genotyped using rhAmp technology (IDT, Iowa), the latest kind of assay available on market. This technology is able to provide high-trustworthy genotyping data. 18 SNPs located on Rz1 flanking regions have been genotyped on a F₂ population by means of QuantStudio 12K Flex Real-Time PCR System (Life Technologies, CA) by using rhAmp assays. Among those SNPs, 5 markers showed significant association with rhizomania resistance. The result emphasizes the importance of chromosome 3 on rhizomania resistance and the need of new markers for sugar beet breeders.

W036: Plant Omics

Statistical Analyses, Text-Mining and Web Databases for Plant Science

Shizuka Koshimizu¹, Aria Hisaoka¹, Misao Senbokuya¹, Yukino Nakamura¹, Misa Saito¹, Maasa Kanno¹, Eiji Nambara², Hajime Ohyanagi³ and Kentaro Yano¹, (1)Meiji University, Kawasaki, Japan, (2)Dept. of Cell & Systems Biology, University of Toronto, Toronto, ON, Canada, (3)King Abdullah University of Science and Technology, Thuwal, Saudi Arabia

Comprehensive integration of large-scale omics resources such as genomes, transcriptomes and metabolomes will provide deeper insights into broader aspects of molecular biology. For better understanding of plant biology, we aim to develop statistical methods for large-scale omics data and web databases providing the comprehensive omics information. Here we introduce the statistical methods and three web databases: PODC (Plant Omics Data Center; <http://plantomics.mind.meiji.ac.jp/podc/>), TOMATOMICS (<http://plantomics.mind.meiji.ac.jp/tomatomics/>) and CATchUP (<http://plantomics.mind.meiji.ac.jp/CATchUP/>). To easily and quickly mine gene candidates from large-scale expression data, we have developed a GUI application 'CA_Plot_Viewer' on the basis of correspondence analysis. A database PODC provides the information on the gene expression networks which were constructed by 'CA_Plot_Viewer', knowledge-based functional annotations of genes, transcription factors and cis-regulatory elements in eleven plant species. The knowledge-based functional annotations, which are obtained with natural language processing (NLP) techniques and manual curation from published literature, are updated every month. TOMATOMICS stores the tomato omics information such as the genome annotations and experimental resources including Micro-Tom cDNA clones. The information on spatiotemporally expressed genes is freely available from the other database CATchUP. Our tool 'heap' for the SNP calling with RAD-Seq data is also downloadable from our web site.

W037: Plant Omics

Hayai-Annotation: An Ultra-Fast and Comprehensive Gene Annotation System in Plants

Andrea Ghelfi, Kazusa DNA Research Institute, Kisarazu, Japan

The main target in plant breeding is to increase crop productivity and quality through improving biotic and abiotic stress tolerance. In order to achieve it, it would be critical for molecular breeders to broadly and accurately understand gene profiles in genomes. Since genome sequencing are becoming faster and cheaper, a high throughput workflow is required. Here, we propose, automated, fast, and accurate gene annotation system for plant species, i.e., Hayai-Annotation, a graphical user interface R-package. The workflow is based on sequence similarity searches using USEARCH to a database of UniprotKB, taxonomy Embryophytes. Hayai-Annotation provides six levels of annotation: 1) gene name; 2) gene ontology consisting of three main categories (Biological Process, Molecular Function and Cellular Component); 3) enzyme commission code; 4) protein evidence level; 5) evidence type; 6) and database name. Regarding speed Hayai-Annotation identified and properly annotate 39,296 SwissProt sequences in 14.9 minutes (6Gb RAM, i5-2450M) with an accuracy of 0.988. We applied Hayai-Annotation to perform the annotation of five plant species, three Rosaceae (*Prunus avium*, *Prunus persica*, *Fragaria vesca*), one Moraceae (*Ficus carica*) and one Brassicaceae (*Arabidopsis thaliana*). The comparison between three domains of GO terms (gene level, ancestor level) and EC codes were performed with two main purposes. The first one was the analysis under an evolutionary approach. The other was the comparison of different gene prediction methodologies. Hayai-Annotation was an efficient and accurate method for annotation of protein sequences in plants.

W039: Plant Omics

Transposase-Derived Transcriptional Factor, FAR1 Provides Insights of Gene Evolutions in Plants

Yong-Min Kim, Korea Bioinformatics Center (KOBIC), KRIBB, Daejeon, South Korea

Far-red impaired response1 (FAR1) is a Mutator-like element (MULE)-derived transcriptional factor and plays central roles in light signaling in plants. MULEs are widespread in plants, fungi and animals and are known as active and mutagenic transposons. Here, we report inter-kingdom analysis of FAR1 family known as molecular domesticated genes by DNA transposons. Genes of FAR1 family in *Arabidopsis thaliana* belonged to plant-specific subtypes and two kingdom-specific subtypes of FAR1 family were identified from subtype analysis. Investigation of domain architectures of molecular domesticated genes suggested that MULE-derived genes (MDGs) were significantly increased in plant and almost of MDGs were DNA-binding domain-containing genes. Furthermore, lineage-specific DNA transposons and their fusion domains implicated lineage-specific evolutionary roles of molecular domesticated genes by each DNA transposon. Further domain deletion analysis revealed a role of MULE domain in evolution of FAR1 family. Collectively, our study suggested the evolution of FAR1 family and evolutionary roles of DNA transposons.

W038: Plant Omics

Genome Editing for Improvement of Plant Responses to Environmental Conditions

Yuriko Osakabe, Tokushima University, Tokushima-city, Japan

Recent advances in genome editing with engineered nucleases such as CRISPR/Cas9 provide a platform with the powerful tool in targeted gene modification in wide variety organisms. To utilize genome editing to a broad range of plant species, we have developed the highly efficient CRISPR/Cas9 system using the combination of codon-optimized Cas9 and several types of promoters for Cas9 expression, and gRNA-designing strategy via in silico analysis. Using selected gRNAs with low off-target effects, our CRISPR/Cas9 system has been utilized in *Arabidopsis*, rice, tomato, apple, potato, strawberry, etc., to modify the target genes that function in signal transduction pathways and stress responses and are also important in molecular breeding. The high mutation rates on the target loci including bi-allelic mutations in T0 generation of transgenic plants generated using tissue culture or T2 generation of *Arabidopsis* were obtained. I will discuss how these current techniques and further applications can provide insights into future plant genomics and biotechnology, and especially genetic improvement of plants for enhanced productivity in stressful environments.

Ref. (Osakabe et al., Sci Rep. 2016), (Nishitani et al., Sci Rep. 2016), (Ueta et al., Sci Rep. 2017), (Osakabe Y, Osakabe K. Prog Mol Biol Transl Sci. 2017), (Takahashi et al., Nature 2018).

W040: Plant Omics

Asian Rice Domestication: Recent Controversy in Rice Genomics

Hajime Ohyanagi, Kosuke Goto, Katsuhiko Mineta and Takashi Gojobori, King Abdullah University of Science and Technology, Thuwal, Saudi Arabia

Asian Rice (*Oryza sativa*) domestication is particularly interesting and important evolutionary event in human history. Recent accumulation of genomic big data in wild and cultivated Asian rice accessions caused a big controversial issue again in rice domestication, namely a single domestication event or multiple domestication events. In this talk we would like to review the background information of Asian rice history and update the recent publication in Asian rice domestication.

W041: Prioritizing SNPs and Variants from Next Generation Sequencing Data
Challenges in Prioritizing SNPs and Variants from NGS Data
Prashanth Suravajhala, Birla Institute of Sc. Res, Jaipur, India

W042: Prioritizing SNPs and Variants from Next Generation Sequencing Data
Systems Genomic Challenges for Analyzing Variants
Haja N Kadarmideen, Technical University of Denmark, Kgs. Lyngby, Denmark

W043: Prioritizing SNPs and Variants from Next Generation Sequencing Data

Meta-Analysis in Genomics: A Case Study on Obesity

Santhi N, Department of Biochemistry, Coimbatore, India

Meta-analysis is the process of integrating the results of many studies, a systematic review to arrive a conclusion. The outcome may include the risk factor for the disease or the assessment of the treatment than any individual research contributing to the pooled analysis. Obesity is considered as the risk factor for diseases like cardiovascular, diabetes, hypertension, dyslipidemia, gallbladder disease, osteoarthritis, musculoskeletal issues, and psychological issues. A meta-analysis of the pooled data was carried out to find the association of significant SNPs in Fat, Mass and Obesity (FTO) region with increased BMI and obesity risk in different population groups using Comprehensive Meta-Analysis Software.

A literature survey was carried out to obtain the raw clinical data from PubMed using the keywords "FTO polymorphism" and "obesity". Out of 93 hits, nine research papers were selected based on inclusion criteria, such as a minimum number of FTO variants in each research paper should be two, and the studies related to only genetic association with obesity and BMI. In this study, all the four SNP variants rs9939609 (OR=1.130; 95% CI=1.060 to 1.204), rs8050136 (OR=1.494; 95% CI=1.127 to 1.981), rs3751812 (OR=1.420; 95% CI=1.225 to 1.645) and rs1421085 ((OR=1.107; 95% CI=1.059 to 1.157), were strongly associated with obesity risk and increased BMI which also exhibited heterogeneity

W044: Solanaceae Genomics and Molecular Genetics
Creating a Pan Genome and Haplotype Database for Potato

Guy Kol, NRGene, Ness-Ziona, Israel

NRGene is participating in an international effort led by Wageningen university to create a comprehensive and high-quality Pan Genome for potato. Several potato assemblies have already been completed and are going through a comprehensive QA. The talk will describe the unique Pan Genome approach and some of the findings so far.

The second part of the talk will present a haplotype-based diversity analysis approach in potato. A specific approach for haplotype based analysis of a large collection of potato genomes will be presented. Such system should enable a high quality yet cost effective genotyping scheme for potato breeding.

**W045: Solanaceae Genomics and Molecular Genetics
Genome-Wide Association Study, Genomic Selection and Other
Technologies for Efficient Tomato Breeding**

Eiji Yamamoto, Kazusa DNA Research Institute, Kisarazu, Japan
Simultaneous improvement of multiple traits is important for modern breeding. In big-fruited tomato, increase of both fruit sugar content and yield performance is one of the most important breeding objectives. For this objective, we performed simulation-based breeding design that uses genomic selection models. The result indicated that cycles of recurrent selections are necessary to simultaneously improve these traits. We are now conducting the demonstration experiment. Through the experiment, we found several theoretical and practical problems. Decrease of predictability during the breeding cycle is especially problematic for crops that require large effort for phenotyping. Appropriate variable selection for model construction is an efficient solution. We performed whole-genome sequencing based association study to identify genes and loci that contribute phenotypic variation. Environmental bias is another serious problem. For precise evaluation of environmental condition on each plant, we developed high-density environmental sensing system. Using these technologies, we are aiming at efficient tomato breeding.

**W046: Solanaceae Genomics and Molecular Genetics
Toward Identifying Hidden Genetic Regulation of Carotenogenesis in
Tomato**

Je Min Lee, Kyungpook National University, Daegu, South Korea
Carotenoids are essential for plant and animal nutrition, and are important factors in the variation of pigmentation in fruits, leaves, and flowers. Tomato is a model crop for studying the biology and biotechnology of fleshy fruits, particularly for understanding carotenogenesis. Carotenoid biosynthetic pathway has been well studied for decades, however, hidden genetic mechanisms are still resided in the pathway. We developed chemotyping and genotyping pipelines in order to classify fruit color variations from germplasms and introgression lines of wild species and mine unidentified variations. *yellow flesh*, *tangerine*, *apricot*, *Beta*, and *Delta* among germplasm collections were clearly distinguishable based on carotenoid profiles and their genotypes. A couple of new variations were selected by the pipelines and are being characterized. Quantitative carotenoid variations existed in wild species are being identified as well. This talk will highlight the usefulness of metabolic profiling and simple genotyping for inferring the genetic determinants of fruit color and excavating new factors.

**W047: Solanaceae Genomics and Molecular Genetics
Single-Molecule Real-Time (SMRT) Sequencing Reveals Diverse Allelic
Variations in Carotenoid Biosynthetic Genes in Pepper (*Capsicum* spp.)**

Hyo-Bong Jeong, Seoul National University, Seoul, South Korea
The diverse colors of mature pepper (*Capsicum* spp.) fruit result from the accumulation of different carotenoids. The carotenoid biosynthetic pathway has been well elucidated in Solanaceous plants, and analysis of candidate genes involved in this process has revealed variations in carotenoid biosynthetic genes in *Capsicum* spp. However, the allelic variations revealed by previous studies could not fully explain the variation in fruit color in *Capsicum* spp. due to technical difficulties in detecting allelic variation in multiple candidate genes in numerous samples. In this study, we uncovered allelic variations in carotenoid biosynthetic genes, including phytoene synthase (*PSY1*), lycopene β -cyclase (*Lcyb*), β -carotene hydroxylase (*CrtZ-2*), and capsanthin-capsorubin synthase (*CCS*) genes, in 94 pepper accessions by single-molecule real-time (SMRT) sequencing. To investigate the relationship between allelic variations in the candidate genes and differences in fruit color, we performed ultra performance liquid chromatography (UPLC) analysis using 43 accessions representing each allelic variation. Different combinations of dysfunctional mutations in *PSY1* and *CCS* could explain variation in the compositions and levels of carotenoids in the accessions examined in this study. Our results demonstrate that SMRT sequencing technology can be used to rapidly identify allelic variation of target genes in various germplasms. The newly identified allelic variants will be useful for pepper breeding and for further analysis of carotenoid biosynthesis pathways.

**W048: Solanaceae Genomics and Molecular Genetics
PacBio Sequencing of Full Length cDNA Reveals Broad Role for NAT
Gene Pairs in Pepper Development and Stress Responses**

Feng Li, Huazhong Agricultural University, Wuhan, China

W049: Soybean Genomics

DNA Methylation and Paralog Evolution in Soybean

Kyung Do Kim, Corporate R&D, LG Chem, Seoul, South Korea
DNA methylation can contribute to the regulation of gene expression in plants. While methylation of genes in the CG context is generally associated with active transcription; the methylation of transposable elements (TEs) concomitantly in three different sequence contexts (CG, CHG, and CHH, H = A, T, or C), results in transcriptional silencing. To a lesser extent, genes can also have TE-like repressive methylation in the gene body and/or promoter regions. Most plants are polyploid, that is they have duplicated genes due to genome duplications. The origin, extent and consequences of gene C-methylation (CG, CHG and CHH) in transcriptional divergence of duplicated genes in a paleopolyploid, such as soybean, and among closely related species and within populations remains unclear. To answer these questions, we generated high-resolution methylation maps of nine domesticated and seven wild soybean accessions. We found that a subset, ~7%, of genes in soybean are methylated in all three sequence contexts, CG, CHG and CHH, and are either not transcribed or at very low levels. Most of those genes are in close proximity with TEs suggesting a role for TEs and genic C-methylation. These epigenetically repressed genes were enriched in pericentromeric, TE-rich regions. Additionally, we show that C-methylated genes associated with proximal TEs are dynamic—likely shaping the epigenetic and transcriptional fates of duplicated genes within and between species. Our study provides evidence that this process likely contributed to the elimination of genetic redundancy of polyploidy-derived gene paralogs and to the sub-functionalization of paralogs (e.g. tissue specificity).

W051: Soybean Genomics

Structural Variation at Soybean Loci Regulating Small RNAs and Seed Color

Young B. Cho, USDA-ARS/UIUC-IGB, Urbana, IL and Lila Vodkin, University of Illinois, Urbana, IL

In soybean, seed color is determined by a specific class of small RNAs known as short interfering RNAs (siRNAs). The dominant *i*¹ allele of the *I* (inhibitor) locus is composed of an inverted-repeat cluster of six chalcone synthase (*CHS*) genes on chromosome 8 whose unique arrangement generates *CHS* siRNAs that downregulate target *CHS7* and *CHS8* genes on non-linked chromosomes resulting in yellow seed coats. We determine the extent of naturally occurring deletions resulting in pigmented seed coats using genomic resequencing and copy number determination by digital PCR. Two size deletions (130 kb and 22 kb) were discovered that each eliminate part of the 27-kb inverted repeat *CHS* cluster resulting in black seed coats. This study demonstrates the importance of the correct representation of the target region in repetitive regions for determining structural variation since both of the current versions of the soybean reference genome (Wm82.a1 and Wm82.a2) have inversions and gaps and do not accurately represent the *i*¹ allele. We also show the interaction of the unlinked *k1* mutation that modifies the distribution of *CHS* siRNAs in the seed coat resulting in a pigment pattern phenotype. Using RNA-Seq and genomic resequencing coupled with genetic marker information, a 129 bp deletion was discovered in a gene (Glyma.11G190900) encoding a member of the argonaute family of proteins (AGO5) that identifies the *k1* mutation and leads to a non-functional protein.

W050: Soybean Genomics

What Do We Learn from *Glycine Latifolia*, a Perennial Wild Relative of Soybean?

Sungyul Chang, Korea Institute of Science and Technology, Gangneung, South Korea, Qiong Liu, University of Illinois, Urbana, IL and Leslie Domier, USDA-ARS, Urbana, IL
Crop wild relatives (CWRs) possess genetic diversity and agronomically favorable traits that are lacking in cultivated crops. However, genetic and genome sequence data of CWRs rarely are available in the public domain. *Glycine latifolia* (Benth.) Newell & Hymowitz ($2n=40$) is one of the 28 CWRs of soybean, *Glycine max*(L.) Merr. Hence, we built genetic and genomic information for *G. latifolia* including F₂ and F₅ genetic maps and next-generation sequencing data. The genetic maps showed extensive inter-chromosomal rearrangements in *G. latifolia* relative to *G. max*. Later, we assembled a 939-Mb draft genome of *G. latifolia* (PI 559298). Nearly 41% of the *G. latifolia* genome was repetitive, of which long terminal repeat retrotransposons were the predominant component. Twenty chromosome-scale pseudomolecules were constructed using two genetic maps and the *G. max* genome sequence as guides. Different from the soybean genome, which contains a single pair of acrocentric chromosomes, *G. latifolia* was predicted to have two pairs of acrocentric chromosomes. Predicted pericentromeric regions of *G. latifolia* chromosomes contained repeated sequences similar to soybean's 91-bp centromeric repeats but not soybean's 92-bp centromeric repeats. Gene content analysis indicated that the assembly was about 94% complete. Annotation of the *G. latifolia* genome assembly identified 54,475 high confidence protein-coding loci. In comparative analysis with five legume species, genes related to defense responses were significantly overrepresented in *Glycine*-specific orthologous gene families. The *G. latifolia* genome contained 304 putative nucleotide-binding site (NBS)-leucine-rich-repeat (LRR) resistance gene homologues, with a scarcity of TIR-NBS-LRR genes relative to other legume species. The whole genome sequence and annotation of *G. latifolia* provides insights into the evolution of the genus *Glycine* and is a valuable source of alternative alleles and novel genes for soybean improvement.

W052: Soybean Genomics

Identification of QTLs for Number of Branches in *Glycine max*

Sangrea Shim¹, Moon Young Kim², Jungmin Ha¹ and Suk-Ha Lee³, (1)Seoul National University, Seoul, South Korea, (2)Plant Genomics and Breeding Institute, Seoul, South Korea, (3)Department of Plant Science and Research Institute, Seoul, South Korea

Branch number is a yield factor affecting the number of pods and seeds per plant. Various environmental factor affecting branch development in soybean. Up to date, low number of genetic factor controlling branch development has been reported due to the environmental influences. In this study, QTLs conferring branching were identified based on the high-density genetic map based on the genotypes analyzed using BARCSoySNP6K chip. Additionally, correlation between branching and total pod number per plant was also investigated. Although there were already known QTLs for branch number and total pod number on the same chromosomes we identified the QTLs, we narrowed down the QTL regions from 0.7 Mb to 0.1 Mb at least, from 26 Mb to 0.5 Mb at most so that we could identify promising candidate genes. The *BRANCHED1* (*BR1*) gene, which encodes TEOSINTE-BRANCHED1/CYCLOIDEA/PCF (TCP) transcription factor, and genes which regulate developmental growth associated with auxin signaling were identified as candidate genes for branching. This study will help breeders improve soybean yield using marker assisted selection (MAS) of branch number and will facilitate identification of the causative genes for the traits in the near future.

W053: Student Workshop**Convergent Amino Acid Substitutions of Avian Vocal Learning Clades – Not How Many Genes, but Who**

Chul Lee, IPBI, Seoul National University, Seoul, South Korea, Erich D. Jarvis, The Rockefeller University, New York, NY; Howard Hughes Medical Institute, New York, NY and Heebal Kim, Seoul National University, Seoul, Korea, Republic of (South)

Vocal learning, the ability to imitate vocalizations based on auditory experience, is a convergent trait observed in independent lineages of birds (songbirds, parrots, hummingbirds) and mammals (human, bat, elephant, cetaceans, pinnipeds). It has now become possible to perform proteome-wide molecular analyses across vocal learners and vocal non-learners with the recent expansion of avian genome data. Here we analyzed whole genomes of avian species that belong to the three vocal learning clades to determine if behavior and neural convergence is associated with molecular convergence. In all species combinations, with or without vocal learners, we found molecular convergences is correlated to the product of origin branch lengths of each major lineage. Vocal learners do not have more convergent amino acid substitutions compared to species of control sets. Nevertheless, the function of convergent genes specific to vocal learners was enriched for learning, and was involved in cAMP-based mechanisms. The candidate genes also showed human-specific substitutions compared to non-human primates in same functional domains. Of the convergent genes in vocal learning birds, the dopamine receptor D1B was supported by multiple pieces of evidence associated with vocal learning. By applying genome editing techniques for the key gene in future, we believe phenotypic changes in transgenic birds will give us insights into macro-evolution of a complex behavioral trait, vocal learning.

W054: Student Workshop**Heterotic Grouping and F1 Hybrid Selection Based on Molecular Marker Heterozygosity in Waxy Corn Inbred Lines**

JongWon Kang, Chungbuk National University, Cheongju, South Korea

W055: Student Workshop**Genome-Wide Analysis of Histone Modifications in Porcine Placentas**

Kun Han, HuaZhong Agricultural University, China, China
The placenta is of utmost importance for intrauterine fetal development and growth. The formation of dense networks of blood vessels and complex placental folds structure is important to improve placenta efficiency and support successful pregnancy. However, little is known about the cis-regulatory mechanisms underlying this important process. Here, we generated the genome-wide maps of H3K4me3 and H3K27ac of Meishan pig placenta on day 50 and 95 of gestation using ChIP-seq and RNA-seq. ChIP-seq analysis identified thousands of H3K4me3 regions and H3K27ac regions on day 50 and 95 of gestation, respectively. Moreover, differential enrichment analysis indicated that a large amount of H3K4me3 and H3K27ac regions were differentially modified in day 50 and 95 of gestation. Finally, we found that many differential expression genes were regulated by histone modification. Further function enrichment analysis revealed those genes were associated with the placental angiogenesis. Taken together, our work identified that histone modification status changes in pig placentas during placental development. The main changes of histone modifications are involved in gene expression associated with angiogenesis. Our results can provide new insights for understanding the mechanism involved in placental development.

W056: Student Workshop**Draft De Novo Genome Assembly of the Philippine Endemic Abaca (*Musa textilis* Nees)**

Julianne A. Vilela, University of the Philippines, Los Banos, Philippines

W057: Student Workshop
Response of Soybeans Cultivars to Drought Stress
John Bwalya, Seoul National University, Seoul, South Korea

W058: Student Workshop
Long-Distance Movement of Naturally Occurring Small RNAs in a Host-Parasite Plant Complex

Subhankar Bera, Osaka Prefecture University, SAKAI, Japan and Kohki Shimizu¹, Keisuke Tanaka², Shunsuke Yajima², Koh Aoki¹ | Osaka Prefecture University, 2NODAI Genome Research Center, Tokyo University of Agriculture.

Cuscuta spp. are holo-parasitic plants that uptake water and nutrients for their survival and growth. Plant endogenous mRNAs and proteins have been known to move bidirectionally through the parasitic junction. It has been shown recently that parasitization triggers accumulation of small RNAs (sRNAs) in parasitic tissues and they move from parasite to host plant to control trans-species gene regulation and/or secondary siRNA production. However, there have been no direct evidence for the sRNA movement from host to parasite plants and control of gene expression. In this work, we explored naturally occurring sRNAs that move long distance and regulate trans-species genes in bidirectional manner. We chose *Cuscuta japonica* and *Glycine max* as a parasitic model for our study. sRNA-seq of non-parasitic and parasitic tissues of *C. japonica* and *G. max* allowed us to prioritize several sRNA candidates of *C. japonica* that possibly moved to *G. max* tissue, and vice-versa. We confirmed the presence of these sRNA candidates system-loop PCR followed by Sanger sequencing. By cross-species detection of sRNAs, we confirmed that long-distance movement of sRNA occurs in bidirectional manner. We are currently identifying their trans-species target genes and target tissues. These results suggest that mobile sRNAs control trans-species gene regulation and secondary sRNA accumulation. This work was partly supported by the Cooperative Research Grant of the Genome Research for BioResource (NODAI Genome Research Center, Tokyo University of Agriculture), and Scientific Research on Innovative Areas “The Plant Cell Wall as Information Processing System” (MEXT, Japan).

W059: Swine Genomics
Predicting the Efficacy of Adaptive Immunity Response by Understanding the Genetic Diversity of SLA and Analyzing Peptide-SLA Binding Affinity
Thong M Le¹, Le Van Chanh Quy², Hae-Jung Lee² and Chankyu Park³,
(1)Konkuk University, Seoul, South Korea, (2)Konkuk university, Seoul, South Korea, (3)Department of Animal Biotechnology, Konkuk University, Seoul, Korea, Republic of (South)

Understanding the differences in immune responses attributed to genetic differences should provide means to enhance host capacity to control disease causing agents. Swine leukocyte antigens (SLA), the major histocompatibility complex (MHC) of pigs and the most polymorphic genes of the pig genome, code for molecules that present self and non-self antigens to T cells. MHC triggers specific immune responses, thereby playing a crucial role in the immune system. We performed high resolution typing for more than 500 pigs of 7 different breeds and characterize the genetic characteristics and diversity of the pig MHC system including SLA-1, -2, and -DQA, -DQB1 and -DRB1 using the genomic-sequence-based typing (GSBT) method. We identified new alleles and characterized them in collaboration with the SLA nomenclature committee of international society of animal genetics (ISAG). There was difference in allele frequency or distribution of MHC genes among different pig breeds. Porcine alveolar macrophage (PAM) is one of major antigen presenting cells (APC) and releases cytokines to affect other cells in the body. They can interact with many antigen proteins by MHC, the antigen receptor, and present to T lymphocytes. We developed two stable PAM cell lines with known SLA haplotype information and synthesized biotin labelled antigenic peptides of porcine corona virus 2 (PCV2). Then, we carried out the binding affinity assay between SLA class II molecules and the peptide. We successfully showed difference in binding affinity MHC molecules of specific MHC class II haplotypes and the antigenic peptide. The reported method in this study could contribute to vaccine development and animal breeding to improve the genetic potential of the disease resistance of pigs against specific pathogens.

W060: Swine Genomics
ePIGenetics: Porcine miRNA and tRNA Expression during Highly Pathogenic PRRSV Infections

Damarius S. Fleming, ORAU, USDA National Animal Disease Center, Texas A&M, Ames, IA and Laura C. Miller, NADC-ARS-USDA, Ames, IA
Porcine respiratory and reproductive syndrome virus (PRRSV) is a single stranded RNA virus member that infects pigs and causes losses to the commercial industry reaching upwards of a billion dollars annually in combined direct and indirect costs. The virus can be separated into etiologies that contain multiple heterologous low and highly pathogenic strains. Recently the United States has begun to see an increase in heterologous type 2 PRRSV strains of higher virulence. The high pathogenicity of these strains can drastically alter host immune responses and the ability of the animal to maintain homeostasis. The loss of homeostasis denotes underlying changes in gene and regulatory element expression profiles. What is less understood, however, are the actions of small non-coding regulatory RNAs (sncRNA) and how they influence host immunologic and metabolic functions to skew away from homeostasis during PRRSV infections.

In order to investigate the impact sncRNA expression has on homeostasis, the study examined host differential expression of miRNA and tRNA molecules during infection with a highly pathogenic PRRSV (HP-PRRSV) strain. We accomplished this using transcriptomic analysis of whole blood taken from either control or infected pigs at several timepoints.

The analysis returned a total of 149 statistically significant ($FDR < 0.15$) miRNAs and tRNAs that were evaluated for possible pro and anti-viral effects. The results indicated that HP-PRRSV infection effects host homeostasis at the epigenetic level through changes in miRNA and tRNA expression that target and influence the function of host immune, metabolic, and structural pathways.

W061: Swine Genomics

Genome-Wide eQTL Analysis of *Porcine longissimus* Muscle Based on RNA-Sequencing Data

Yan Liu, Tingting Ma, Ying Liu, Shuhong Zhao and Xuewen Xu, Huazhong Agricultural University, Wuhan, China

Genetic analysis of gene expression level is a promising approach for characterizing of functional genes and regulatory networks of complex traits like meat quality. In the present study, we conducted eQTL analysis based on the SNP chip genotyping and RNA-sequencing of 197 porcine longissimus muscle from the offspring individuals of Duroc boar crossed with Luchuan sows. With single-marker analysis using MatrixEQTL, we identified 18,018 cis-eQTL ($p \leq 1e-2$) and 134,057 trans-eQTL ($p \leq 1e-5$), and with GWAS, we identified 10,462 cis-eQTL ($p \leq 1e-2$) and 236,442 trans-eQTL ($p \leq 1e-3$). Overlapping analysis identified 7,983 cis-eQTL ($p \leq 1e-2$), including 612 genome-wide significant cis-eQTL ($p < 1e-5.63$) that are involved in 184 transcripts. Three cis-eQTL hotspots have been identified: SSC2: 5.5Mb-7.5Mb, SSC12: 4.5Mb-6.5Mb, SSC7:23.2Mb-25.3Mb. Interestingly, some significant cis-eQTL are associated with myofiber-type related functional genes, such as MYLPF ($p=1.99e-8$), TNNC2 ($p=5.62e-9$), TNNI1 ($p=1.57e-11$), and TNNI2 ($p=3.93e-3$), TNNI1 ($p=5.33e-3$), TNNI2 ($p=7.98e-4$). Correlation analysis of gene expression level and the value of muscle fiber density identified 842 significantly correlated genes ($p < 0.01$), of which 16 genes are related with genome-wide significant eQTL signals ($p < 1e-5.63$), such as MYLPF ($r=0.22$, $p=0.0016$) and CTSC ($r=0.21$, $p=2.99e-3$). Characterization of causative mutations for the myofiber-related cis-eQTL was undergoing. In conclusion, the present study provided new clues of candidate genes and functional mutations for genetic analysis of meat quality traits.

W063: Swine Genomics

Growth Differentiation Factor 8 Modulate Porcine Immature Oocyte Maturation and Embryonic Development *in Vitro*

Junchul David Yoon, Institute for Stem Cell & Regenerative Medicine, Cheongju, South Korea and Sang-Hwan Hyun, Chungbuk National University, Cheongju, South Korea
Growth differentiation factor8 (GDF8) is a member of transforming growth factor- β (TGF- β) that has been identified as a strong physiological regulator. SB431542 (SB) is a specific inhibitor of transforming growth factor-beta superfamily type I activin receptor-like kinase (ALK) receptors. The purpose of this study is the effects of GDF8 and SB on porcine oocytes *in vitro* maturation (IVM) and subsequent embryonic development after *in vitro* fertilization (IVF). We were investigated the effect of GDF8 and SB treatment during IVM on nuclear maturation, intracellular glutathione (GSH), reactive oxygen species (ROS) levels, analyzed specific gene transcription levels and TGF- β related factor translation levels in cumulus cells after IVM, and embryonic development and transcription pattern after IVF. Data were analyzed by on way ANOVA followed by Duncan using SPSS. The 1.318 ng/mL of GDF8 and 5ng/mL of SB were added during IVM followed experiment design as control, SB, SB+GDF8, and GDF8 treatment groups. After 44 h of IVM, GDF8 group (90.4%) showed significantly increased nuclear maturation than control and SB+GDF8 groups (85.4% and 81.7%), compared to SB group (78.9%) was significantly lower than control ($p < 0.05$). The GDF8 treatment group showed a significant ($P < 0.05$) decrease in intracellular ROS and increased GSH levels compared with other groups. Also SB+GDF8 treatment group showed significantly better cytoplasmic maturation than SB treatment group. The GDF8 treatment showed highly increased *PCNA* and *Nr12* and cumulus expansion factor *COX-2*, *Has2*, *Ptg3* and *TNFAIP6* mRNA expression levels from cumulus cells after IVM. In protein expression level, GDF8 group showed significantly increased phosphorylated SMAD 2/3 per SMAD 2/3 ratio than control ($p < 0.05$) even though GDF8 specific type I receptor ALK4 and ALK5 expression levels from cumulus cells after IVM showed no significant. In IVF embryonic development, respectively 0, 0.2, 2 and 20 ng/mL of GDF8 were added during IVF followed experiment design. After additional 120hr of embryo culture, 0.2 group was shown significantly ($p < 0.05$) higher than control in blastocyst formation rate and total cell number (32.5% and 88.0 \pm 7.3 VS 40.4% and 118.4 \pm 12.7, respectively). Moreover, in immune-stain result the 0.2 supplement group showed significantly SOX2 expressing cell number and SOX2 per CDX2 ratio than control. In conclusion, treatment of GDF8 during IVM significantly improved the matured oocytes developmental competence and the supplementation of 0.2 ng/ml GDF8 during IVF significantly improved embryonic developmental potential via regulating embryo developmental competence markers.

Keywords: porcine, oocyte, *in vitro* production, GDF8, SMAD2/3

*Corresponding author: shhyun@cju.ac.kr

Acknowledgement

This work was supported, in part, by a grant from the "Korea Institute of Planning and Evaluation for Technology in Food, Agriculture, Forestry and Fisheries (IPET) through Advanced Production Technology Development Program, funded by Ministry of Agriculture, Food and Rural Affairs (MAFRA) (Grant number: 1545013816)" and "The Global Research and Development Center (GRDC) Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education, Science and Technology (2017K1A4A3014959)", Republic of Korea.

W062: Swine Genomics

Bayes-Poly: A Software for Fine Mapping Causative Variants for Big Related Populations

Ming Fang, Fisheris-Jimei University-China, Xiamen, China

W064: Translational Genomics for Agriculture

Secondary Metabolites Improvement and Human Health Effects through Crop Breeding

Yong Pyo Lim, Chungnam National University, Daejeon, South Korea and Byeong Hwa Jeon, School of Medicine, Chungnam National University, Daejeon, South Korea

The B. rapa subspecies has wide genetic and morphological diversity which grown as leafy vegetables, vegetable oils, turnip greens, turnip roots, turnip tops and as a fodder crop. In general plant secondary metabolites play vital roles during different stages of growth and development. These functional compounds like glucosinolates, anthocyanins, vitamin C, total sugars, and calcium add high nutritional value to humans. We have generated double haploid (DH) lines through micro spore culture from the collected germplasm accessions with high functional compounds. For glucosinolates we have performed a conventional QTL analysis using $F_{2,3}$ mapping population of *B. rapa* combined with candidate gene association approach by using natural population in order to identify the genomic region and genes regulating glucosinolates biosynthesis in *B. rapa* crops. Results suggest several alleles with very high association for important compounds. Additionally the comparative analyses of several association results were completely matching with previous analyzed QTL maps. The further analysis will be done to study the identified candidate genes related to glucosinolates enhancement. Similarly Anthocyanins, the most prevalent flavonoids in red/purple crops, are known to improve immune responses and reduce chronic disease risks. The anti-inflammatory activities were tested based on its inhibitory effects in cultured endothelial cells and hyperlipidemic apolipoprotein E-deficient mice using anthocyanin-rich extract from red Chinese cabbage. The results suggest that the consumption of anthocyanin-rich red Chinese cabbage is closely correlated with lowering the risk of vascular inflammatory diseases.

W065: Translational Genomics for Agriculture**Development of Resources for Mapping, GWAS and Allele Mining in Tetraploid Wheat Based on Svevo Durum Reference Sequence**

Marco Maccaferri, University of Bologna, DISTAL, Bologna, Italy; University of Bologna, Bologna, Italy

The assembled Svevo durum wheat genome and the iSelect wheat 90K SNP array were used as a base to characterize a world-wide tetraploid wheat collection. We report on the diversity pattern of 1,854 non-redundant accessions from all known *Triticum turgidum* subspecies. The genetic diversity survey relied on a common genotype-calling pipeline from AgriBio supported by 17 tetraploid linkage maps. The pipeline yielded 17,416 informative single-locus SNPs anchored to the Svevo genome. Among the wild emmer (WEW), domesticated emmer (DEW), durum wheat landraces (DWL) and durum wheat cultivars (DWC), WEW showed the highest and uniform diversity across the whole genome, providing a reference for cross-comparison with DEW, DWL and DWC. Extended diversity depletions associated to domestication were found particularly in pericentromeric regions. Some 38.2% of DW genome was affected by strong genetic bottleneck/selection events leading to diversity depletions. Six extended regions showed increased genetic diversity associated to DEW-DWL and DWL-DWC transitions. Population structure revealed multiple subsequent events of population differentiation associated to human-driven dispersal routes. This analysis provides the basis for a more informative re-sequencing towards a tetraploid pan-genome. Sub-panels have already been used for GWAS analysis, allowing us to identify GWAS-QTL that can be readily used in breeding. GWAS-QTLs for grain yield components (grain size and grain number per spike) have been identified using a subpanel of Mediterranean DW landraces. These resources allowed us to map QTLs at an improved resolution (1 cM confidence interval) and readily scan the genome for underlying candidate genes.

W067: Translational Genomics for Agriculture**Translating Wheat Genomics Knowledge for Applied Breeding**

Awais Rasheed, CIMMYT C/o. CAAS, Beijing, China

W066: Translational Genomics for Agriculture**Simplifying Complex Traits using Whole Genome Resequencing in Chickpea (*Cicer arietinum* L.)**

Mahendar Thudi and Rajeev K Varshney, ICRISAT, Hyderabad, India
Chickpea (*Cicer arietinum* L.) is the second most important grain legume cultivated by resource poor farmers in arid and semi-arid regions across the globe. Chickpea production in the climate change scenarios is hampered by several biotic and abiotic stresses. Reduced cost of sequencing in recent years, brought a paradigm shift in trait mapping approaches. The “*QTL-hotspot*”, spanning 29 cM, responsible for drought tolerance, has been fine mapped into two smaller regions viz. “*QTL-hotspot_a*” (139.22 kb) and “*QTL-hotspot_b*” (153.36 kb) on the genome using Genotyping-by-sequencing, restriction-site associated DNA sequencing, Skim sequencing GBS, RAD-seq and Skim sequencing approaches. Further QTL-seq, MutMap and TILLING by sequencing approaches are being employed to identify the causal SNPs, candidate genes and their functional validation for traits like heat tolerance, Fusarium wilt, Ascochyta blight and dry root rot resistance. WGRS 129 of release varieties provided insights into the spatial and temporal trends in diversity and 4.9 million single nucleotide polymorphisms, 596,100 Indels, 4,931 copy number variations, 60,742 presence absence variations and 70,159 structural variations. Further, resequencing of reference set provided 207 significant marker trait associations for drought and heat tolerance related traits. In addition, the analysis provided insights into population structure, genetic diversity, gene loss, domestication and selection sweeps in this crop that is important for global food security in developing countries. Resequencing of multi-parent advanced generation intercross (MAGIC) population enabled fine mapping and identification of markers associated with drought tolerance.

W068: Translational Genomics for Agriculture**Chromosome-length Scaffolds Solution to the *de novo* Assembly Challenge for Plant Community**

Parwinder Kaur, Univ. of Western AU, Perth, WA, Australia
Genome sequencing is now affordable, but assembling plant genomes *de novo* remains challenging. Here we assess the state of the art of Hi-C sequencing-based approach for assembling chromosome-length scaffolds for a legume genome to find a solution to the *de novo* assembly challenge for the plant community. An improved Hi-C protocol adapted for plants demonstrated use of Hi-C genome-wide chromosomal contact data to overcome the fragmented assembly limitations, and present an assembly approach that determines the most likely genome structure. In this study, we combine Hi-C data with existing draft assembly to generate chromosome-length scaffolds. The genome assembly procedure we describe is fast, inexpensive, accurate, and can be applied across many species for assembling whole chromosomes including resolving misassemblies in the draft assembly. Knowing how to assemble genomes accurately and how to perform these applications at a fast pace with the lowest cost are crucial to drive the understanding of the dynamic plant kingdom filled with amazing diversity and significance.

W069: Wheat Genomics in Agriculture: Building on IWGSC RefSeq v1.0 Comparative Analysis of Ta7DL and Ae7DL Chromosome Provides Insights into the Structure and Evolution of Bread Wheat
Song Weining, Northwest A&F University, Shaanxi, China

W070: Wheat Genomics in Agriculture: Building on IWGSC RefSeq v1.0 Variation in Homoeolog Expression in Wheat

Philippa Borrill, John Innes Centre, Norwich, United Kingdom

Polyploidy is common amongst major crop species and has been proposed to confer adaptive plasticity. The presence of duplicated genes within polyploids may provide extra flexibility to adapt and evolve new patterns of gene expression and function for homoeologous gene copies. Despite the potential importance of changes in gene expression within polyploids, we have a limited understanding of how similar expression patterns are between homoeologs, how these vary across tissues and development, or across environmental conditions.

In this study we analyse 850 RNA-seq samples from diverse tissues, developmental stages, stress conditions and varieties to explore global gene expression in wheat. The recent release of the highly complete and annotated IWGSC RefSeqv1.0 genome sequence for wheat has enabled homoeolog-specific gene expression analysis at an unprecedented level of detail. Here we will discuss the extent of the co-ordination of homoeolog expression patterns across diverse tissues, stress conditions and wheat varieties.

W071: Wheat Genomics in Agriculture: Building on IWGSC RefSeq v1.0 Wheat Inflorescence Transcriptomes: From Development to Yield
Long Mao, Chinese Academy of Agricultural Sciences, Beijing, China

W072: Wheat Genomics in Agriculture: Building on IWGSC RefSeq v1.0 Global Transcriptome Analysis Uncovers the Gene Co-Expression Regulation Network and Key Genes Involved in Grain Development of Wheat (*Triticum aestivum* L.)

Huixian Zhao, College of Life Sciences, Northwest A & F University, Shaanxi 712100, China

**W073: Wheat Genomics in Agriculture: Building on IWGSC RefSeq v1.0
New Insights on the GA Signaling in C3 and C4 Plants**

Xigang Liu, Center for Agricultural Research Resources, CAS, China,
Shijiazhuang, China

Phytohormone Gibberellin (GA) plays very important roles in plant growth and development. GA-GID1-DELLA complex are key components in GA signaling transduction. The GA signaling is well characterized in rice (*Oryza sativa*) and wheat (*Triticum aestivum*) (represent Ehrhartoideae and Pooideae of C₃ plants, respectively). However, little is known about GA transduction in Panicoideae, even though this clade includes the most C₄ plants. Here, we demonstrated that the SiGID1 from foxtail millet (*Setaria italica*) interacts with DELLA in a GA-independent manner through two N-terminal regions. Moreover, the GA-independent GID1 has been evolved with many other Panicoideae grasses including C₄ and their close C₃ grasses. SiGID1, compared to GA-dependent GID1 such as OsGID1, could partially rescue the dwarf of GA-deficient *gal-3* mutant by GA-independent degradation of DELLA protein. SiGID1 transgenic Brachypodium was more drought-resistant than TaGID1 transgenic plants. Moreover, *SiGID1* driven by *OsGID1*'s promoter not only completely rescued the dwarf of rice *gid1* mutant under normal condition but also significantly enhanced plant adaption to high intensity light stress compared with wild type. Our results reveal the conservation and divergence of GA signaling in foxtail millet of C₄ plants and in rice and wheat of C₃ plants.

**W074: Wheat Genomics in Agriculture: Building on IWGSC RefSeq v1.0
Roles of TaCYP78As in Wheat Grain Size**

Meng Ma, College of Life Sciences, Northwest A & F University, Yangling, Shaanxi, China, Ruilian Jing, Chinese Academy of Agricultural Sciences, Beijing, China, Zhensheng Kang, Northwest A&F University, Yangling, China and Huixian Zhao, College of Life Sciences, Northwest A & F University, Shaanxi 712100, China

Grain size is one of the key agronomic traits that determine grain yield. However, the mechanisms underlying grain size control in wheat remain elusive. Here we demonstrated that cytochrome P450 78A family members (*TaCYP78As*) positively regulates grain size in wheat. There are four members of *TaCYP78A* family, *TaCYP78A3*, *TaCYP78A5*, *TaCYP78A12* and *TaCYP78A16*, encoding *CYP78A* family proteins in wheat. All *TaCYP78As* were detectable in young spike and grain in wheat, and their activities were positively correlated with the final grain size. *TaCYP78As* silencing caused a reduction in grain size of wheat, whereas *TaCYP78As* over-expression induced an increase in grain size of transgenic *Arabidopsis* or wheat. Then, we focused on functional characterization of *TaCYP78A3* and *TaCYP78A5*. Cytological study showed that the cell numbers of the final grain coat was affected by *TaCYP78A3/5* expression level that affected the extent of integument cell proliferation in the developing ovule and grain, and ultimately appeared to determine the final grain size in wheat and *Arabidopsis*. Moreover, ectopic expression of *TaCYP78A3/5* in *Arabidopsis* led to a reduction in grain yield because of causing a reduced grain set due to an ovule developmental defect. Fortunately, the grain set reduction was not observed in transgenic wheat. *TaCYP78A3/5* over-expression caused an increase in wheat grain yield by approximately 5-15%, compared to the control. Furthermore, association analysis showed that alleles of *TaCYP78A5* and *TaCYP78A16* significantly associating with 1,000-grain weight in 323 wheat varieties under 16 environments. In summary, our results indicated that *TaCYP78As* play critical roles in influencing wheat grain size.

P0001: Aquaculture

Identification of Genomic Loci Associated with Maturation in Pacific Coho Salmon (*Oncorhynchus kisutch*)

Michelle T.T. Crown^{1,2}, Kris A. Christensen², Krzysztof P. Lubieniecki¹, Ruth E. Withler³, Janine Supernault³, Eric B. Rondeau^{2,4}, Ben F. Koop⁴, Robert H. Devlin² and William S. Davidson¹, (1)Simon Fraser University, MBB Department, Burnaby, BC, Canada, (2)Fisheries and Oceans Canada, West Vancouver Laboratory, West Vancouver, BC, Canada, (3)Fisheries and Oceans Canada, Pacific Biological Station, Nanaimo, BC, Canada, (4)University of Victoria, Victoria, BC, Canada

Reproductive success of salmon is influenced by multiple morphological features, physiological performance, and behavioural mating strategies. While certain male-specific traits such as sperm quality can clearly affect reproductive success, precocious sexual maturation (maturing one year early, smaller body size and absent secondary sexual characteristics) is an interesting example of an evolutionary stable strategy where the fitness is balanced between precocious and full adult males. The genetic basis of early maturation (termed jacking in Pacific salmon and grilising in Atlantic salmon) is thought to be polygenic, but recent work has found that 39.4% of the phenotypic variation can be explained by a single locus (vestigial-like-family-member-3; *vgl3*) in regulating maturation onset in Atlantic salmon. Our current study aims to identify loci associated with jacking and survival in Pacific coho salmon, *Oncorhynchus kisutch*. We conducted a genome-wide-association-study and mapping analysis on six families from a hatchery population (Inch Creek), three of which possessed a high proportion of jacks and three that had a low proportion. Using a Genotype by-Sequencing (GBS) approach, EcoT22I reduced representation libraries were generated for 716 individuals and sequenced on the Illumina HiSeq platform. GBS data was aligned to the published version of the coho genome with BWA, and variants were called with STACKS. To enhance the power of our genome-wide-association analysis, we then used the resultant 45,716 SNPs to impute missing genotypes with BEAGLE. Data analysis to date reveal that genomic loci associated with jacking in coho salmon are distinct from *Vgl3*. Using this population of coho salmon as a model, these data suggest that the molecular mechanisms determining age of male maturation are not fully conserved between Atlantic salmon and Pacific coho salmon.

P0003: Brassicas, Arabidopsis, and related

Discovery of Long Intergenic Non-Coding RNAs (lincRNAs) That Influence Root Radial Growth in Radish (*Raphanus sativus*)

Nam V. Hoang¹, Goh Choe², Yi Zheng³, Zhangjun Fei³ and Ji-Young Lee², (1)Seoul National University, Seoul, South Korea, (2)School of Biological Sciences, Seoul National University, Seoul, South Korea, (3)Boyce Thompson Institute, Cornell University, Ithaca, NY

Long intergenic noncoding RNAs (lincRNAs) have been shown to be important regulators in various biological processes including transcriptional and post-transcriptional regulations of protein-coding genes in both animals and plants. Recent advances in sequencing technologies allow large transcriptome data to be generated, facilitating the discovery of novel transcripts. Radish, a close relative of Brassica, is one of the most cultivated root crops in eastern Asia, for its remarkable root biomass production capacity within short growth period. Radish root radial growth and yields are found to be strongly influenced by the formation of cambium tissue, which highlights the importance to understand the transcripts involve in regulation of cambium establishment and root biomass accumulation. We recently generated transcriptome data for cambium and neighboring tissues in the radish roots, 5, 7 and 9 weeks post seed planting, from two radish inbred lines of contrasting root radial growth and yields. Besides protein-coding transcripts, a total of 14,202 novel lincRNAs were identified within a distance >500 nt to the nearest protein coding genes either upstream or downstream. In general, the radish lincRNAs exhibit a shorter length, lower expression level and more tissue specific, in comparison with protein coding transcripts. We identified several pairs of lincRNAs – nearby coding genes, *trans*-natural antisense transcripts – coding transcripts and miRNA-encoding lincRNAs – target genes, that their co-expression likely to influence cambium tissue formation, and hence, root radial growth, in radish. Our results provide a novel insight into the yield-related lincRNAs in this representative root crop system.

P0002: Brassicas, Arabidopsis, and related

Gene Regulatory Networks of Inner and Rosette Leaves in Brassica rapa

Man-Sun Kim, Chungnam National University, Daejeon, South Korea

Chinese cabbage is one of the most important crops in Asian countries. In the heading formation of Chinese cabbage, differential regulation of production and growth between inner and rosette leaves is the most important developmental process. In general, it is well known that the developmental process is determined by complex interactions among genes. Therefore, it is very important to understand the developmental process of Chinese cabbage by studying the essential genes in the cells constituting the two types of cabbage leaves, and to clarify its dynamical characteristics. According to recent results, the gene expression patterns of inner and rosette leaves are quite different. However, there is no investigation to identify the tissue-specific gene regulatory networks of the two types of leaves. Based on the tissue-specific RNA sequencing profiles, we identified differentially expressed genes in each type of leaf. Based on the gene regulatory network of *A. thaliana*, we identified tissue-specific regulatory networks of inner and rosette leaves.

P0004: Brassicas, Arabidopsis, and related

Developing DNA Marker to Select Clubroot Disease Resistant Breeding Materials in Kimchi Cabbage (Chinese cabbage)

Suhyoung Park¹, Hayoung Jang², Min Young Park², Seok-Woo Jang² and Seung-Kook Choi², (1)National Institute of Horticultural & Herbal Science, RDA, Wanju, South Korea, (2)NIHHS, Wanju, South Korea

Kimchi cabbage (Chinese cabbage; *Brassica rapa* L.) is one of major Brassicaceae vegetables in Korea. Koreans like tasting Kimchi in every meal as a side dish. As Kimchi cabbage cultivated continuously in the same place, clubroot disease spreaded very fast in Korea. Even though a disease resistant cultivar became sensitive in many fields at Gang-Won province. We tried to use reported DNA markers of *Crr1a*, *Crr2*, *CRb*, *Cra*, *Crr3*, and *Crc* for selecting clubroot resistant breeding materials in Kimchi cabbage. Total 192 materials tested using these 6 markers. Among them, 86 materials were artificially inoculated using Yeon-Cheon(YC) inoculum and 17 materials failed matching the phenotype and genotype. After Genome-Wide Association Analysis (GWAS) analysis using Genotyping-by-Sequence (GBS) method, 20,540 single-nucleotide polymorphism (SNP) genotypes were selected using 96 breeding materials. We developed 9 candidate of Cleaved Amplified Polymorphic Sequence (CAPS) markers. One marker can distinguish between YC clubroot sensitive and resistant materials. Together with various clubroot resistant DNA markers, this novel DNA marker can be used for selecting disease resistant materials in Kimchi cabbage.

P0005: Brassicas, Arabidopsis, and related

Characterization of Mutation Induced By Proton Beam Irradiation in *Arabidopsis thaliana*

Sang Woo Lee^{1,2}, Sang Hoon Kim¹, Se Won Kim¹, Sun-Young Kim^{1,2}, Jin-Baek Kim¹, Si-Yong Kang¹ and Yeong Deuk Jo¹, (1)Korea Atomic Energy Research Institute, Jeongup, South Korea, (2)Chonnam National University, Gwangju, South Korea

Mutation breeding technologies based on irradiation have advanced for last ninety years. Although X- and gamma-rays have been mainly used so far, mutation breeding researches using diverse radiation sources such as heavy ion beams are increasing recently. However, few researches have been performed on breeding using proton beam which has the characteristics of particles, but has much lower LET (Linear Energy Transfer) compared to heavy ion beams. Therefore, in order to establish a mutation breeding system using proton beam, we irradiated proton beams at various doses on *Arabidopsis* seeds, and investigated survival and growth rates, respectively. In order to determine the most effective dose for mutation induction, 400 M₂ lines for 500, 800 (Dq, shoulder of the survival curve) and 1,000 (near Lethal Dose, 50%), respectively, were cultivated and rates for emergence of mutant phenotypes including leaf discoloration, and leaf shape alterations were investigated. As a result, among the three irradiated doses, 800 Gy, which corresponds to Dq value, showed the highest mutation rate. We are performing complete sequencing for M₂ plants selected from each dose to analyze mutation pattern and frequency in genomic level. Comparison of mutations in both phenotypic and genomic levels between different irradiation doses will provide information for determination of effective irradiation dose for practical breeding using proton beam. In addition, comparison of mutation characteristics between proton beam and other radiation sources will be useful for characterization of proton beam as a new mutagen for mutation breeding.

P0007: Brassicas, Arabidopsis, and related

Analysis of Self-Incompatibility Genes Using DNA Markers in Radish (*Raphanus sativus*) Cultivars in Korea

Seung-Kook CHOI, Suhyoung Park and Suk-Woo Jang, National Institute of Horticultural & Herbal Science, RDA, Wanju, South Korea
Radish (*Raphanus sativus* L., 2n=18), a member of the family Brassicaceae has self-incompatibility (SI) determined by multiple alleles in a single locus called the S locus. The SI expression of radish is controlled by expression of S-locus glycoprotein (called SLG) and S-locus receptor kinase (called SRK) in the stigma and by expression of S-locus cysteine-rich protein (called SCR) in the pollen. Analysis using 23 S-haplotype-specific sequences characterized amplified region (SCAR) markers from Genbank database and previous reports showed that S-haplotypes s4, s21, and s29 were the most abundant and the S-haplotypes s18, s20, s23 were the least popular in radish inbred lines. The same SCAR marker indicated that the S-haplotypes s5, s8, s16 were the most popular in commercial radish cultivars in South Korea. In addition, new SCAR markers with standard DNA pool were developed for specific detection of S-haplotypes s6, s9, and s29 that were not available for radish, resulting in successful SI differentiation in radishes.

P0006: Brassicas, Arabidopsis, and related

Tissue Specific Transcriptome Analysis Associated with the Secondary Growth of Radish Root (*Raphanus sativus* L.)

Goh Choe¹, Ana Cecilia Aliaga Fandino¹, Yi Zheng², Zhangjun Fei² and Ji-Young Lee¹, (1)School of Biological Sciences, Seoul National University, Seoul, South Korea, (2)Boyce Thompson Institute, Cornell University, Ithaca, NY

Root system has two important functions for plants, providing mechanical support to the aerial parts of the plant by anchoring the plant body to the ground; and absorbing nutrients and water from the soil. Crop species, including sweet potato, cassava, and radish also utilize roots for storage in the form of carbohydrates. Therefore, they are recognized as important food sources for humans and livestock animals. Among them, radish is characterized by rapid and vigorous root growth. However, the underlying molecular mechanism is still elusive. To understand the gene expression dynamics involved in the secondary growth of radish root, we analyzed transcriptome profiles of root tissues including cambium, its neighboring tissues in the phloem side (cortex) and xylem side (parenchyma) that were dissected using the laser capture microdissection technique. We identified 50,029 protein-coding transcripts including 3,515 novel transcripts from *de novo* transcriptome assembly from two radish inbred lines showing contrasting root growth behavior. 4,602 transcripts were further characterized as differentially expressed genes in cambium tissues. Analysis of transcriptome profiling revealed that conserved hormone regulatory pathways for vascular tissue differentiation are activated during the secondary growth in radish roots. Clustering based on the transcript co-expression patterns showed that the enriched biological processes are different in the two radish inbred lines. Overall, our transcriptome profiling analysis will provide valuable resources to understand root secondary development processes and to improve root characteristics for yield increase.

P0008: Brassicas, Arabidopsis, and related

Identification of Structural Variation in Chloroplast Genome of *Arabidopsis thaliana*

Eunbi Jo¹, Jungmin Ha¹, Min Young Yoon² and Suk-Ha Lee³, (1)Seoul National University, Seoul, South Korea, (2)Seoul National University, Seoul, Korea, Republic of (South), (3)Department of Plant Science and Research Institute, Seoul, South Korea
The chloroplast is a crucial plant organelle that sustains life by converting solar energy to carbohydrates through photosynthesis process. The chloroplast genome encodes many proteins that are involved in photosynthesis and other metabolic processes. The chloroplast genome of land plants generally has a highly conserved structure. However, structural variation of chloroplast genomes between *Glycine max* and *Arabidopsis thaliana* has been reported; a single, large inversion of 51 kilobases (kb) is present in the chloroplast genome of *Glycine max*. We designed primer sets on boundaries of the 51 kb inversion using reference sequences of PI437654 in *Glycine max* and Columbia in *Arabidopsis thaliana* available at NCBI. PCR was performed using DNA samples from Williams82 and Columbia, reference accessions of each species, and we confirmed the inversion of 51 kb between *Glycine max* and *Arabidopsis thaliana*. There was no significant difference in the chloroplast genome sequences between Williams82 and PI437654, but an insertion of ~500 bp was identified between the reference genome sequence and actually amplified and sequenced region in *Arabidopsis*. We will verify the 500 bp insertion in the reference chloroplast sequence of *A. thaliana* and provide an evidence to improve the reference sequence.

P0009: Canine

Primary Culture of Canine Mammary Tumor Cells

Mirae Kim, Seon-Ung Hwang and Sang-Hwan Hyun, Chungbuk National University, Cheongju, South Korea

Mammary tumors are one of the most common cancers in female dogs. Because dogs share the same environmental factors with humans, canine mammary tumors (CMT) are similar pathologically and histologically to human mammary tumors. A total of three primary tumor cell lines were obtained from three different mammary tumor patients. To obtain primary CMT cells from mammary tumors and normal mammary tissues, these tissues were mechanically isolated and enzymatically dissociated by 0.25% trypsin-EDTA and 1mg/mL collagenase type IV. After digestion, trypsin-collagenase mixture was inactivated and then enzyme dissociated tumor cells were cultured in Advanced DMEM containing 0.5% FBS, 1x Glutamax 1x MEM NEAA and 1x Antibiotic-antimycotic. At passage 1, Advanced DMEM medium was replaced with serum-free DMEM (low glucose) supplemented 4ng/mL bFGF and 10ng/mL EGF. Interestingly, two days later, tumorspheres were formed from CMT cell lines. The tumorsphere size became larger and proliferation rate was increased. However, the number of tumorspheres was lower in serum conditions than in serum-free conditions. As a result, it seems that serum-free conditions are more suitable for culture of tumorspheres. Although further studies will be needed, these results will be helpful for establishment of cancer stem cells in the CMT cell lines.

Acknowledgement

This work was supported, in part, by the "National Research Foundation of Korea Grant funded by the Korean Government (NRF-2017R1A2B4002546, GRDC-2017K1A4A3014959)" and "Business for Cooperative R&D between Industry, Academy, and Research Institute funded Korea Small and Medium Business Administration in 2017 (Grants No. 2017020681010101)", Republic of Korea.

P0011: Cattle

Genetic Structure and Introgression Signatures of African Cattle Genome

Kwondo Kim, Seoul National University, Seoul, South Korea, Dajeong Lim, National Institute of Animal Science, Suwon, Korea, Republic of (South) and Hee-bal Kim, Seoul National University, Seoul, Korea, Republic of (South) African continent, where more than 150 breeds reside, is a reservoir of diverse cattle breeds; hence, the genetic diversity of cattle is well preserved in contrast to other regions. One of the factors that give rise to this diversity is interbreeding between populations, especially between taurine and indicine cattle (zebu). Since the introduction of two subspecies, the continent has experienced dynamic admixture. However, the complex structure of African cattle genome is not fully elucidated at a genome-wide level. In this ongoing study, the complex population structure of 15 African cattle breeds was inferred by the whole genome sequence of 217 individuals, which demonstrated extensive admixture among zebu breeds. The degrees of taurine introgression were highly diverse between zebu breeds, reflecting different population history for each breed. Nevertheless, there was one particular region that is significantly introgressed from taurine cattle in all zebu breeds. The region is associated with gamma-aminobutyric acid (GABA), the main inhibitory neurotransmitter in the mammalian central nervous system, which suggests the tameness of indicine cattle through interbreeding with taurine cattle. The results of this study will extend our understanding of the complex history of African cattle breeds and might give insight into the influence of admixture on the traits of cattle subspecies.

P0010: Cattle

The Brahman Genome

Elizabeth Ross, QAAFI - University of Queensland, Brisbane, Australia, Ben J. Hayes, The University of Queensland, Brisbane, Australia, Brian Burns, QAAFI - The University of Queensland, Rockhampton, Australia, Russell E Lyons, School of Veterinary Sci., The University of Queensland, Gatton, Australia and Stephen Moore, University of Queensland, Brisbane, Australia Just 15 years after the massive undertaking that was the Human Genome Project, we have now reached a point where technological advances make it possible to sequence and assemble a de-novo genome in under one year to a reference standard. This may be the tipping point where it is now viable for economically important species to have their own reference quality genome sequence. Sequencing of a Brahman genome (*Bos indicus*) for use as a reference was identified as an industry goal, to ensure that cattle with *B. indicus* genomic content can fully benefit from the full suite of genomics technologies (e.g. GWAS) that are available for trait improvement and understanding. Here we present the Brahman reference genome. In total 195GB of sequence data was obtained from the PacBio Sequel. The sequence reads were error corrected using the DAZZler scrubber suite and then assembled with the Falcon assembler. The assembly yielded 1867 contigs, with an N50 of 11MB. The assembled contigs were error corrected with Arrow, and then scaffolded using Hi-C and Chicago data (Dovetail Genomics). After scaffolding the assembly consisted of 843 scaffolds with an N50 of 62MB, and L50 of 13 with 1106 gaps. The scaffolds then underwent several rounds of gap filling using PBJelly and Arrow. After gap filling and polishing the assembly consists of 835 scaffolds, which contain only 443 gaps in total. Eighteen of the 30 chromosomes are present at >95% length in a single scaffold, including the notoriously hard to assemble X chromosome.

P0012: Cattle

Detection of Candidate Polymorphisms in the QTL for Oleic Acid Percentage on BTA9 Based on Whole-Genome Resequencing Data

Fuki Kawaguchi¹, Hiroto Kigoshi¹, Namiko Kohama², Takayuki Akiyama², Moriyuki Fukushima², Emi Yoshida³, Eiji Kobayashi⁴, Kenji Oyama⁵, Hideyuki Mannen¹ and Shinji Sasazaki¹, (1)Kobe University, Kobe, Japan, (2)Hyogo Prefectural Hokubu Agricultural Institute, Asago, Japan, (3)Hyogo Prefectural Agricultural Institute, Kasai, Japan, (4)National Agriculture and Food Research Organization, Tsukuba, Japan, (5)Kobe university, Kasai, Japan In our previous study, we identified a QTL for oleic acid percentage (C18:1) on BTA9 by GWAS in Japanese Black cattle. The objective in the current study was to detect the candidate polymorphisms for the QTL by whole-genome resequencing.

We selected eight animals, four samples with high C18:1 and four samples with low C18:1, from 1836 animals used in the GWAS. Whole-genome resequencing was performed and all polymorphisms in the candidate region (BTA9: 64.9 ~ 74.9 Mbp) were detected by comparison among nine animals including the reference genome sequence (UMD3.1.1). Among them, we selected three putative candidate polymorphisms, (i) *CYB5R4* c.*349G>T, (ii) *MED23* c.3700G>A, and (iii) *VNN1* c.197C>T, in terms of positions, gene functions, and genotypes in eight animals. These SNPs were genotyped in a Japanese Black population (n = 899) to investigate the effect on C18:1 using ANOVA and Tukey-Kramer's HSD test.

ANOVA revealed the significant association between three SNPs and C18:1 ($p =$ (i) 0.0018, (ii) 0.0064, and (iii) 0.0039). Tukey-Kramer's HSD test showed that the significant differences between genotypes were also observed and the differences of least square mean values between homozygous were (i) 1.47, (ii) 1.51, and (iii) 1.88. These results indicated that they might be the useful markers for C18:1 improvement. We additionally conducted ANOVA using an analytical model including genotypes of three SNPs as effects. As the result, *CYB5R4* c.*349G>T showed the lowest p -value ($p = 0.069$) of three SNPs, suggesting that it would be the most possible candidate polymorphism for the QTL.

P0013: Cattle

Effect of SLC27A6 Gene K81M Polymorphism on Fat Percentage in Rib-Eye Area in Japanese Black Cattle

Shintaro Toyomoto¹, Namiko Kohama², Takayuki Akiyama², Moriyuki Fukushima², Emi Yoshida³, Eiji Kobayashi⁴, Kenji Oyama⁵, Hideyuki Mannen¹ and Shinji Sasazaki¹, (1)Kobe University, Kobe, Japan, (2)Hyogo Prefectural Hokubu Agricultural Institute, Asago, Japan, (3)Hyogo Prefectural Agricultural Institute, Kasai, Japan, (4)National Agriculture and Food Research Organization, Tsukuba, Japan, (5)Kobe university, Kasai, Japan

Fat percentage in rib-eye area (FPR) is highly correlated to beef marbling and therefore is one of the most important traits in beef industry. In our previous study, we detected a QTL for FPR on BTA7 by GWAS in Japanese Black cattle, and determined 10-30Mbp on BTA7 as a candidate region. The aim of our study is to identify candidate polymorphisms for the QTL.

We conducted whole-genome resequencing using eight animals including four animals with high FPR and four animals with low FPR. Comparing the sequences of the eight animals and reference genome sequence, we detected 127,090 polymorphisms within the region. Based on the resequencing data, we selected 47 polymorphisms in eight genes according to their gene functions and linkage disequilibrium with the most significant SNP in GWAS (No.1 SNP). We focused on *SLC27A6* genes with the function as fatty acid transport, and selected a nonsynonymous substitution K81M as a putative candidate polymorphism. We genotyped the SNP in a Japanese Black population (n = 904) to investigate the effect on FPR using analysis of variance (ANOVA) and Tukey-Kramer's HSD test.

The statistical analysis revealed *SLC27A6* K81M showed lower *p*-value (*p* = 1.04E-5) than No.1 SNP (*p* = 4.05E-4), suggesting that it would be a possible candidate polymorphism for the QTL. Considering the function of *SLC27A6* gene, the SNP might change acyl CoA synthase activity and fatty acid uptake efficiency. These results suggested that the *SLC27A6* K81M might be responsible polymorphism for FPR and it could be useful as selective marker for beef marbling in Japanese Black cattle.

P0015: Fruit Species

The Chloroplast Genome Based Indel Markers in Niitaka (*Pyrus pyrifolia*) and Its Application

Jung Sun Kim, Ho Yong Chung and So Youn Won, National Institute of Agricultural Sciences, RDA, Jeonju, South Korea
Pears (*Pyrus* spp.) are one of the most important fruit crops in temperate regions and are self-incompatible. Therefore, high numbers of interspecific hybrids occur naturally and, have been artificially produced in breeding programs. Pears have been cultivated through natural recombination in breeding programs; however, there are several pear varieties, cultivated long ago, for which an accurate breeding history remain unavailable. The complete chloroplast (cp) genome of the *P. pyrifolia* cultivar 'Niitaka', which is the major pear variety produced in South Korea, was sequenced using Illumina sequencing technology. The cp genome has a total of 133 genes, including predicted 93 protein-coding genes, 32 tRNA genes, and eight rRNA genes. We found many SNPs in the 'Niitaka' cp genes when compared with that in the Korean cultivar 'Wonwhang' (BioSample SAMN05196235). The primer sets for six genes that had more than two SNPs in their sequence were used to amplify and sequence 29 *Pyrus* and one *Malus* cultivar. Of these, we found dramatic InDel polymorphisms in the *ndaA* and *clpP* genes. Phylogenetic relationships using the sequences of these two genes in 30 samples showed that they could mainly be classified into two groups of *P. pyrifolia*. Group I constitutes Niitaka and all cultivars that maternally inherited chloroplast from Niitaka, and group II constitutes the other cultivars of *P. pyrifolia*. We have developed a useful polymorphic molecular marker to confirm the maternal parent in the interspecific hybrids of Niitaka and previous mothers of Niitaka, (such as Amanogawa). Furthermore, these two genes could identify and greatly aid in understanding the *subsp* criteria in *Pyrus*.

P0014: Cattle

Genomic Characterization of Korean Cattle Breeds Using High-Density (600K) Affymetrix Array

Kwan-Suk Kim¹, Byeonghwi Lim¹ and Zewdu Edea Bedada², (1)Chungbuk National University, Cheongju, South Korea, (2)Chungbuk National University, Chungcheongbuk-do, Korea, Republic of (South)

Korea is endowed with three phenotypically distinct cattle breeds. To elucidate the genetic diversity and relationship among three Korean cattle populations based on color (brown, black and brindle). we analyzed 284 animals genotyped for 630, 973 SNPs. After applying quality control criteria of call rate >0.90, MAF > 0.05 and Hardy-Weinberg equilibrium (HWE) >0.001, a total of 304,104, 293,909 and 358,829 SNPs were left for brindle, black, and brown cattle, respectively; and used for further analyses. The mean allele frequencies were 0.14, 0.13 and 0.16, respectively. The levels of inbreeding coefficients were found to be -0.060, -0.090 and -0.005, respectively. The largest genetic differentiation (*F_{st}* = 0.13) was observed between brindle and black followed by between brown, and black (*F_{st}* = 0.07). These differences could be attributed to demographic events. The overall mean *r*² values were 0.37, 0.40, and 0.27 in brindle, black, and brown cattle, respectively. Principal components analysis further separated the study population clustered according to their phenotypic classification. The SNPs which were significantly differentiated among the three cattle breeds could be used for breed and product discrimination.

P0016: Gene Editing/CRISPR

Agrobacterium Mediated Transformation and Genome Edition in *Solanum nigrum*: Applicable Tools for Molecular Breeding of Medicinal Plant

Jabamala Anitha¹, Seunghye Park², Heo Jung³, Jae Cheol Jeong⁴, Woo Young Bang⁵ and Soon Ju Park¹, (1)Institute for Basic Science, Wonkwang University, Jeonbuk, South Korea, (2)Institute for Basic Science, Wonkwang University, Iksan, South Korea, (3)Institute for Basic Science, Jeonbuk, South Korea, (4)Korea Research Institute of Bioscience and Biotechnology, South Korea, (5)National Institute of Biological Resources (NIBR), South Korea
Numerous research activities have been carried out on Solanaceae species such as *Solanum tuberosum*, *Solanum lycopersicum*, *Solanum melongana* but still, molecular breeding activity on *Solanum nigrum* is necessary, it is an important medicinal plant and possess various therapeutic properties. In the present work, genetic engineering study ranging from gene transformation to gene editing technique has been carried out on *Solanum nigrum*.

We optimized the preincubation and regeneration method, resulted in shortening the *Agrobacterium* mediated transformation period to 8 weeks in *S. nigrum*. After evaluation of the method with 35S::GUS in *Solanum nigrum*, 72076 predicted CDS from RNA seq were assembled using Trinity platform. Among that one of CDSs is homologue of *SELF PRUNING (SP)*, considered to be the shoot growth regulator in tomato. *SnSP* locus was edited using CRISPR/Cas9 system.

A successful partial gene deletion in *SnSP* locus of T0 plant was obtained, which show relatively short stem length phenotype. Currently our results showed that the exogenous transformation and genome edition is applicable to the medicinal plant of *Solanum nigrum*.

P0017: General Comparative**Convergent Amino Acid Substitutions of Avian Vocal Learning Clades – Not How Many Genes, but Who**

Chul Lee, IPBI, Seoul National University, Seoul, South Korea, Erich Jarvis, The Rockefeller University, New York, NY and Heebal Kim, Seoul National University, Seoul, Korea, Republic of (South)

Vocal learning, the ability to imitate vocalizations based on auditory experience, is a homoplastic characteristics observed in different independent lineages of animals such as songbirds, parrots, hummingbirds and human. It has now become possible to perform proteome-wide molecular analyses across vocal learners and vocal non-learners with the recent expansion of avian genome data. Here we analyzed the whole genome of avian species that belong to one of the three vocal learning clades. We aimed to determine if behavior and neural convergence is associated with molecular convergence in polyphyletic avian vocal learners. We found molecular convergences are correlated to products of original branch lengths. We uncovered vocal learners do not need more number of convergent substitutions compared to control sets, illuminated the function of homoplastic genes specific to vocal learners was enriched for learning, and suggested a novel cAMP-based vocal learning pathway. Especially, candidate genes share human-specific substitutions compared to non-human primates in same functional domains. Out of the convergent genes of vocal learning birds, DRD5 was validated as the key candidate gene supported by multiple evidences associated with vocal learning. By applying genome editing techniques for the key gene in future, we believe phenotypic changes in transgenic birds give us insights into macro-evolution of the complex behavioral trait, vocal learning.

P0019: General Comparative**Mining Comparative Plant Data in Gramene**

Marcela Karey Tello-Ruiz¹, Andrew Olson¹, Sharon Wei¹, Justin Preece², Joshua Stein¹, Sushma Naithani³, Yinping Jiao⁴, Bo Wang¹, Sunita Kumari¹, Young Kyoung Lee⁵, Vivek Kumar¹, Demitri Muna⁶, Dan Bolser⁷, Irene Papatheodorou⁸, Paul J. Kersey⁷, Pankaj Jaiswal² and Doreen Ware⁹, (1)Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, (2)Botany & Plant Pathology, Oregon State University, Corvallis, OR, (3)Oregon State University, Corvallis, OR, (4)USDA-ARS/Cold Spring Harbor Laboratory, Lubbock, TX, (5)Wonkwang University, Iksan, South Korea, (6)Cold Spring Harbor Lab, Cold Spring Harbor, NY, (7)EMBL - The European Bioinformatics Institute, Cambridge, United Kingdom, (8)European Bioinformatics Institute (EMBL-EBI), Hinxton, United Kingdom, (9)USDA/ARS - Cold Spring Harbor Laboratory, Cold Spring Harbor, NY

Have you ever needed to know if the plant gene you work on has an ortholog in rice, maize or Arabidopsis? Has the gene family that you are working on expanded in a crop species? Is the biochemical pathway you work on conserved in sorghum and soybean? If so, you may want to explore these questions in the Gramene database. Gramene (<http://www.gramene.org>) is an integrated resource for comparative functional analysis in plants. Gramene provides researchers with access to 53 genomes, and pathways for 75 plants species. The current release features a polyploid genome view for wheat. Gramene provides powerful phylogenetic approaches, including protein-based gene trees with stable IDs and whole-genome DNA alignments, enable traversing across plant species. We provide integrated search capabilities and interactive views to visualize gene features, gene neighborhoods, phylogenetic trees, genetic variation, gene expression profiles, pathways, and cross-references and host curated rice pathways, and uses these curated pathways to generate orthology-based projections for other species. Gramene builds upon Ensembl and Reactome software, and is committed to open accesses and reproducible science based on the FAIR principles, providing both human and machine access to the data.

Gramene is supported by an NSF grant IOS-1127112, and from USDA-ARS (1907-21000-030-00D).

P0018: General Comparative**The Genome10K Vertebrate Genomes Project Phase 1: Building De Novo Reference Genomes for All Vertebrate Orders**

Arang Rhie¹, Sergey Koren¹, Erich Jarvis², Adam M. Phillippy¹ and The Genome 10K VGP Assembly Working Group, (1)NHGRI, NIH, Bethesda, MD, (2)The Rockefeller University, New York, NY

High-quality genome assemblies are needed to address fundamental questions in biology and disease, to identify species most genetically at risk for extinction, and to preserve genetic information for posterity. However, most vertebrate genomes are lacking such a reference. The Genome10K (G10K) consortium's Vertebrate Genomes Project (VGP) is an international effort, spanning over 50 institutions on nearly all continents, to create a digital open-access genome library of all extant vertebrate species. The VGP aims to construct high-quality, near-gapless, phased and annotated chromosomal-level assemblies. Phase 1 of this project is focused on generating assemblies of one species from each vertebrate order defined at 50 million years or more from a common ancestor, totaling 260 individual species, to a quality standard of >1 Mb N50 contig size, >10 Mb N50 scaffold size, average bp quality >QV40, 90% of the sequence assigned to chromosomes, and haplotype phased. The VGP has begun collecting, sequencing, and assembling ordinal samples using 4 emerging technologies that we have found gives us the most contiguous assemblies to date: PacBio long reads, 10X Genomics linked reads, Bionano optical maps, and Arima Genomics Hi-C libraries. The VGP assembly working group has been comparing and evaluating assembly strategies using an initial set of ~16 species including 4 mammals, 4 birds, 1 reptile, 1 amphibian, and 7 fishes, each of which responds differently to assembly due to differences in genome size, heterozygosity, and repeat content. For highly heterozygous genomes, we have also trialed a new approach for haplotype phasing, called trio binning, that uses parental genomes to partition long reads from the child into separate haplotype bins prior to assembly. An improved, comprehensive strategy to enable phased assembly for all genomes is under continued development. All raw data and version 1 assemblies will be uploaded at the time of generation to the "GenomeArk" and can be accessed under the terms of the associated G10K Data Use Policy (<http://genomeark.s3.amazonaws.com>).

P0020: Insects**Differential Proteomics Analysis of Pea Aphids, *Acyrtosiphon pisum*, Between Alate and Apterous Morphs**

Liping Ban and Limei Song, China Agricultural University, Beijing, China
Wing dimorphism is a widespread phenomenon in insects, with an associated trade-off between flight ability and fecundity. However, the mechanism at the molecular level of phenotypic plasticity is not entirely understood. In this study, we focused on the differential proteomics profiles between alate and apterous morphs of pea aphid, *Acyrtosiphon pisum*, using isobaric tags for relative and absolute quantitation (iTRAQ). A total of 5560 proteins were identified and quantified in the three biological replicates, of which 846 were differentially expressed between alate and apterous morphs. A bioinformatics analysis of differentially expressed proteins (DEPs) was performed based on GO Slim and KEGG. To validate the proteomics results, the transcriptional expression of 28 DEPs from iTRAQ were verified by quantitative real-time PCR (qRT-PCR). The results showed that the expression patterns of 82.14% of the genes agreed with the expression patterns of the corresponding proteins. In addition, we found that significant changes in several genes were associated with odorant-binding and chemosensory reception in alate morphs. qRT-PCR revealed the tissue- and morph-biased expression patterns. The comparative proteomic analysis between alate and apterous morphs of pea aphid will help to improve our understanding of molecular mechanisms underlying wing development in aphids.

P0021: Insects

Niemann-Pick C2 Gene in Moth *Helicoverpa armigera*

Liping Ban and Limei Song, China Agricultural University, Beijing, China
Niemann-Pick proteins type C2 (NPC2) are carriers of cholesterol in vertebrates, with a single member in each species. The high sequence conservation between mammals and across vertebrates is related to their common function. In contrast, NPC2 proteins in arthropods have undergone extensive duplication and differentiation, probably under environmental pressure, and are likely to have different functions. Recent studies have suggested that in arthropods these proteins might act as carriers for semiochemicals and other hydrophobic compounds. In this study we focused on the function of a specific NPC2 gene in the moth *Helicoverpa armigera* (HarmNPC2-1). This protein binds several flavonoids with micromolar dissociation constants. The best ligand was gossypol, present in cotton, one of the main host plants for *H. armigera*. Western blot revealed the presence of HarmNPC2-1 in different parts of the body, including the antennae, proboscis, and abdomen. In the antennae, *in situ* hybridization experiments produced strong staining in auxiliary cells at the base of sensilla trichodea, basiconica, coeloconica, and chaetica. Immunocytochemistry confirmed the expression of the protein in sensilla chaetica. Our results support a role of semiochemical carriers for NPC2 proteins in insects and indicate such proteins as new targets for insecticide-free pest population control.

P0023: Insects

Taxonomy of Korean *Apis cerana* Inferred from the Complete Mitochondrial Genome Sequence

Dong In Kim, Division of Life Sciences, Incheon National University, Yeonsu-gu, Incheon, South Korea
Apis cerana is Eastern honeybee species distributed across all Eastern Asia, and has 2 proved subspecies only (*A. c. cerana*, *A. c. japonica*). Eastern honeybee species *A. cerana* is a closely related to Western honeybee species *Apis mellifera* distributed across all Africa, Europe and Western Asia, and subdivided into 30 proved subspecies. Currently, honeybee *A. cerana* is endangered bee species in contrast to *A. mellifera*. We sequenced and annotated the whole mitochondrial genome of *A. cerana* from Jeollanam-do province of South Korea and uploaded to database DDBJ/Genbank (AP018431). MtDNA sequence has 15,925 bp length, AT-content 84% and GC-content 16% and contains 22 tRNA genes, 13 protein-coding genes, 2 ribosomal RNA genes, 1 AT-rich region and 4 non-coding intergenic regions (NC1-4). All protein-coding genes are started by ATT and ATG codons, excepting the start codon of ATP8 gene, which ATC, and are stopped by the common stop codons TAA and TAG. A comparative analysis of whole mtDNA sequences of *A. cerana* from Korea, Taiwan, China (*A. c. cerana*) and Japan (*A. c. japonica*) showed that genetic divergence of Korean (2.58%) and Taiwanese (4.40%) *A. cerana* samples from subspecies *A. c. cerana* and *A. c. japonica* matched to the level of genetic divergence of mtDNA between animal subspecies (1-10%). Samples of Korean and Taiwanese *A. cerana* located separately from all other *A. cerana* samples on both the phylogenetic tree and the median network. According this data, we assumed that Korean and Taiwanese *A. cerana* samples are representatives of two distinct subspecies, which can be named in future as *Apis cerana koreana* and *Apis cerana taiwanensis* after additional genetic, biochemical and morphological evidences. As well, additional samples of Korean and Taiwanese *A. cerana* must be analyzed to prove these assumed subspecies.

P0022: Insects

Improvement of *Dermatophagoides farinae* Genome By Third-Generation Sequencing

Angel Tsz-Yau Wan, Ming-Qiang WANG and Stephen Kwok-Wing Tsui, Faculty of Medicine, The Chinese University of Hong Kong, Hong Kong, Hong Kong

Dermatophagoides (D.) farinae, commonly known as American house dust mite (HDM), is one of the predominant sources of inhalant allergens. More than 50% of allergic diseases are attributed to HDM, so the identification of allergen genes and structure in this species is important for clinical diagnosis and further allergen-specific immunotherapy. Previously, we have published a *D. farinae* draft genome and transcriptome using high-throughput sequencing. In this study, we aim to improve the quality of *D. farinae* reference genome to find known canonical allergens and identify novel allergen genes using third-generation sequencing. A total of 14 Gb raw data presenting about 175-fold coverage of this genome with average read length of 8.36 Kb was generated on PacBio SEQUEL. The 79.8 Mb *D. farinae* genome was achieved after genome assembly, scaffolding, gap filling and polishing. The genome contained 1139 contigs and 506 scaffolds, with the contig and scaffold N50 being 221.7 kb and 589.8 kb respectively. The completeness of the genome was assessed using BUSCOs (Benchmarking Universal Single-Copy Orthologs). The results contained 91.3% BUSCO core genes from arthropoda_odb9 dataset that represented a good completeness. This result showed a great improvement of contig N50 compared to previous assembled genome.

This study paves the way for assembling a complete genome of *D. farinae* and provides genetic resources for further development of specific immunotherapy, therefore saving patients from allergic reactions induced by dust mite allergens.

P0024: Legumes, Soybean, Common Bean, and related Selection of Soybean Mutants with Alteration in Seed Fatty Acid Composition and Their Gene Expression

Min Jeong Hong¹, Young Eun Jang¹, Dong-Gun Kim^{1,2}, Hong-Il Choi¹, Yeong Deuk Jo¹, Sang Hoon Kim¹, Joon-Woo Ahn¹, Jin-Baek Kim¹ and Soon-Jae Kwon¹, (1)Korea Atomic Energy Research Institute, Jeongeup, South Korea, (2)Sunchon National University, Sunchon, South Korea
Soybean seeds contain 18-24% lipid comprising 85% polyunsaturated fatty acid with two essential fatty acids (Linoleic and linolenic acid), which are not synthesized in human and other animals. One of breeding programs in soybean is development of inherently low levels of linolenic acid to improve resistance to oxidation and stability during cooking process. However, linolenic acid plays vital roles to maintain brain functions and provide a source of retinal and nerve tissue DHA; hence, the physiological functions of linolenic acid has been drawing attention. In this study, we developed mutant populations using Korea elite soybean cultivars, Danbaek (DB) and Daepung (DP), by gamma irradiation. To select high linolenic acid mutant lines, 78 and 154 M₃ mutant progenies were evaluated for fatty acid concentration. Each 10 mutant lines from two original cultivars which have highest linolenic acid were selected first, and four mutant lines were selected from two years investigation of unsaturated fatty acid. Selected mutant lines showed increase linolenic acid approximately from 2 to 4 % over their original cultivars. To investigate whether *FAD* genes in linolenic biosynthesis were involved the differences of the fatty acid composition among mutant lines, we examined the expression level of *FAD* genes in developing seed by qRT-PCR. Each genes in *FAD* families showed different expression patterns during seed development. Selected mutants would be used as beneficial genetic resources for providing basic research information and genetic diversity of soybean.

**P0025: Legumes, Soybean, Common Bean, and related
Current Status of Legume Experimental Resources of Japan: The National
Bioresource Project *Lotus* and *Glycine***

Shusei Sato, Graduate School of Life Sciences, Tohoku University, Sendai, Japan
The National BioResource Project (NBRP) was launched by the Japanese government in 2002 with the aim to construct the framework for collection, conservation and distribution of bio-resources. The NBRP project has entered into 4th phase from April 2017, and the program of legume bio-resources, *Lotus japonicus* and *Glycine max*, renewed its web database, "LegumeBase" (<https://www.legumebase.brc.miyazaki-u.ac.jp/>), as a kickoff of the new phase. In the phase 4 of NBRP *Lotus* and *Glycine*, we are continuing our efforts on providing the material resources, such as seeds of experimental strains, wild accessions and recombinant inbred lines (RILs) of *L. japonicus*, wild accessions of *G. soja*, RILs of *G. max*, full-length cDNA clones of *L. japonicus* and *G. max*, and signature tagged mutant lines of *Mesorhizobium loti*, a symbiont of *L. japonicus*. In addition, we are going to provide the information resources, such as updated reference genome sequence of *L. japonicus* experimental strain "Gifu; B-129", and genome resequence-based genotype information of RILs and wild accessions of *L. japonicus*. Also we are going to improve our material resources by increasing the number of native retrotransposon (*LORE1*) insertion tag lines of *L. japonicus*, collecting the published symbiotic mutant lines of *L. japonicus* and *G. max*, and establishing the collection of the pairs of wild accession of *L. japonicus* and its natural symbionts. In the presentation, we will introduce the examples of application of updated information resources and how to access the resources.

**P0027: Legumes, Soybean, Common Bean, and related
Investigation of Genetic Variations of Sucrose Transporters in Soybean
Cultivars Differing in Seed Sucrose Content**

Eunsam Park¹, Suk-Ha Lee², Jungmin Ha¹ and Moon Young Kim³, (1)Seoul National University, Seoul, South Korea, (2)Department of Plant Science and Research Institute, Seoul, South Korea, (3)Plant Genomics and Breeding Institute, Seoul, South Korea
High sucrose content in soybean seeds (*Glycine max* (L.) Merr) has been a desirable factor in soybean breeding programs because it improves sweetness and flavor of soyfood. We screened five soybean cultivars and identified two genotypes with high and low sucrose contents, Taekwang and Danbeak, respectively. Sucrose transporters (SUTs) have been reported as one of the major factors for sucrose transport and accumulation in *Arabidopsis thaliana*. We carried out a phylogenetic analysis of SUT homologous genes in soybean and other model plants to gain evolutionary characterization. Also, we selected several SUTs as candidates based on previous reports to identify genetic factors affecting sucrose content in soybean seeds. To investigate the physiological functions of SUTs in soybeans, we performed comparative analysis of gene structure and gene expression level between Taekwang (high sucrose) and Danbeak (low sucrose). Further, based on the results in this study, we will perform quantitative trait loci analysis using F6 recombinant inbred line population derived from a cross between Taekwang and Danbeak to identify genetic factors affecting sucrose content in soybean. The identification of candidate genes related to high sucrose content will help improve the quality of soybean seeds.

**P0026: Legumes, Soybean, Common Bean, and related
Identifying the Causal Agents of Leaf Spot Disease of Mungbean (*Vigna
radiata* (L.) R. Wilczek)**

Jun Hee Jung¹, Jungmin Ha¹, Moon Young Kim², Jung-Eun Kim³, Hokyong Son³ and Suk-Ha Lee¹, (1)Seoul National University, Seoul, South Korea, (2)Plant Genomics and Breeding Institute, Seoul, South Korea, (3)Seoul National University, South Korea
Mungbean (*Vigna radiata* (L.) R. Wilczek) is an important crop as it is an excellent source of protein and other micro and macronutrients. Despite its importance, little is known about mungbean as a host of other organisms. Data from Korean Agricultural Culture Collection indicate mungbean is host to only 14 species. Our aim is to isolate the disease-causing agent of the leaf spot disease, one of the major factors affecting mungbean yield negatively. The infected leaves were surface sterilized and fungi were isolated from the symptomatic regions. DNA of isolated fungi was extracted and Internal Transcribed Spacer 1 and 2 regions was PCR amplified and four species were identified using BLASTn. Identified species were: *Alternaria alternata*, *Plectosphaerella cucumerina*, *Stagonosporopsis cucurbitacearum* and *Fusarium equiseti*. Fungi were grown in Potato Dextrose Agar under no light and 25 °C conditions. Under these conditions, conidiogenesis was successfully induced for *A. alternata* and *P. cucumerina*. Single spore isolation was carried out for two previous mentioned species and are used to fulfill Koch's postulate using both *in vivo* and *in vitro* tests. To our knowledge, there was no other researches indicating that any of the four isolates caused diseases in mungbean in Korea. This isolation will give a good insight into the role of mungbean as host of various fungi. Once Koch's postulate is fulfilled, we intend to use the isolates to identify Qualitative Trait Loci and candidate pathogen resistance genes. Genes identified via this method can be used to breed resistant cultivars.

**P0028: Legumes, Soybean, Common Bean, and related
Inflorescence Architecture and Synchronous Pod Maturity in Mungbean
Jungmin Ha¹, Eunsoo Lee¹, Moon Young Kim² and Suk-Ha Lee³, (1)Seoul
National University, Seoul, South Korea, (2)Plant Genomics and Breeding
Institute, Seoul, South Korea, (3)Department of Plant Science and Research
Institute, Seoul, South Korea**

Mungbean (*Vigna radiata* (L.) R. Wilczek) is one of legume crops primarily cultivated in South, East and Southeast Asia. Both production and consumption of mungbean have increased steadily around the world. One of the challenges interfering with an efficiency of harvesting is a non-synchronous pod maturity requiring more time and labor. In this study, we found an association of inflorescence architecture traits with synchrony in mungbean by investigating growth and developmental habits of inflorescence architecture. Typically, mungbean has a compound raceme inflorescence architecture consisting of a primary branch and multiple secondary branches that can produce flowers. However, a genotype named 'Binh khe D.X.' has a simple raceme inflorescence architecture where flowers are produced only from the primary branch and show relatively synchronous pod maturity. By comparing Binh khe D.X. with Seonhwanogdu, which had the compound raceme inflorescence architecture and non-synchronous pod maturity, we found the difference between synchronous and non-synchronous pod maturity was caused by the degree of indeterminate characters. This study suggests a preferable standard for inflorescence architecture traits for future breeding, as well as for genetic research in mungbean pod maturity synchrony.

P0029: Legumes, Soybean, Common Bean, and related Phenotypic and Genetic Variation between SS2-2 and Taekwang Under Drought Stress

Hakyung Kwon¹, Xuefei Yang², Jungmin Ha¹, Min Young Yoon³ and Suk-Ha Lee⁴, (1)Seoul National University, Seoul, South Korea, (2)Seoul National University, South Korea, (3)Seoul National University, Seoul, Korea, Republic of (South), (4)Department of Plant Science and Research Institute, Seoul, South Korea

Drought is one of the major constraints which significantly reduces crop productivity. As so, many efforts have been made to overcome negative effects of drought on productivity by studying the physiological or molecular responses of various model plants under water deficit conditions. Several drought-responsive mechanisms including rapid stomata conductance to reduce water loss and continuation of root elongation to reach to water sources have been revealed, and phytohormones, like ABA, JA, ethylene, and etc., are involved in this mechanism. However, drought-resistant mechanisms of soybean at genetic level have not been fully understood yet. Two QTLs for drought tolerance on soybean have been reported; one on drought tolerance (Resistance to damage by water restriction), and the other on drought susceptibility index, and several transcriptome analyses have been conducted. Here, we screened two soybean genotypes, Taekwang and SS2-2, which were drought susceptible and resistant respectively, and selected three candidate genes which might be involved in the drought-tolerance trait by comparing drought-related QTL regions with differentially expressed genes under water stress previously reported. qRT-PCR is being performed to evaluate the expression levels of three candidate genes in Taekwang and SS2-2 under water deficit condition. Their putative promoter regions of the candidate genes showing different expression level would be sequenced. Furthermore, we would also compare plant hormone levels between the cultivars and their genomic sequences.

P0031: Maize, Sorghum, Millet, Sugar Cane, and related Characterizing the Pan-Genome of Maize with PacBio SMRT Sequencing
Michelle Vierra, Gregory Concepcion, Aaron Wenger, David Rank and Paul Peluso, PacBio, Menlo Park, CA

Maize is an amazingly diverse crop. A study in 2005 demonstrated that half of the genome sequence and one-third of the gene content between two inbred lines of maize was not shared. This diversity, which is more than two orders of magnitude larger than the diversity found between humans and chimpanzees, highlights the inability of a single reference genome to represent the full pan-genome of maize and all its variants. Here we present and review several efforts to characterize the complete diversity within maize using the highly accurate long reads of PacBio Single Molecule, Real-Time (SMRT) Sequencing for *de novo* assembly, structural variation detection, genome annotation, and isoform discovery. These methods provide a framework for a pan-genomic approach that can be applied to studies of a wide variety of important crop species.

P0030: Legumes, Soybean, Common Bean, and related Response of Soybeans Cultivars to Drought Stress

John Bwalya¹, Jungmin Ha¹, Moon Young Kim², Min Young Yoon³ and Suk-Ha Lee⁴, (1)Seoul National University, Seoul, South Korea, (2)Plant Genomics and Breeding Institute, Seoul, South Korea, (3)Seoul National University, Seoul, Korea, Republic of (South), (4)Department of Plant Science and Research Institute, Seoul, South Korea

Soybeans (*Glycine max* L. Merrill) is one of the world's foremost providers of protein and oil. Soybean's consumption as food products and animal feeding materials has grown worldwide because of its health-related benefits. However, soybean supply does not meet worldwide demand due to low soybean productivity caused by drought stress. Drought stress is the condition where a plant's water potential and turgor pressure decrease enough to inhibit normal plant function. Drought stress is a major global constraint for crop production, therefore, improving crop tolerance to drought is of critical importance. Crop physiology can play a major role for improving drought tolerance through the identification of traits associated with drought tolerance that can be used in a breeding program. In this study, we evaluated the response of two soybean cultivars, Buseok and Cheongja3 and RILs population derived from a cross between two cultivars under drought stress induced by mannitol and NaCl. We will identify QTLs that contribute to drought tolerance in RILs population and propose candidate genes involved in the mechanism of drought tolerance in soybean. The detection of the QTLs in cultivars provides a potential target for marker assisted selection in developing varieties with drought tolerance.

P0032: Maize, Sorghum, Millet, Sugar Cane, and related In Planta Yielded Recombinant Hyperthermostable GH10 Xylanase Xyl10B Enables to Increase the Efficiency of Hydrolysis of Sugarcane Xylan to Fermentable Sugars for Biofuel Production

Sangyong Park, Kongju National University, Yesan, South Korea
Sugarcane is one of the most efficient photosynthesizer in the plant kingdom, able to convert as much as 2% of incident solar energy into biomass. A large amount of lignocellulosic biomass such as leaf litter residues and bagasse are generated during the sugarcane harvest or after the sugar refining process, respectively. Therefore, lignocellulosic biomass from leaf and processing residues will likely become a valuable feedstock for biofuel production. Recent efforts focus on the integration of first and second generation bioethanol conversion technologies for sugarcane to increase biofuel yields. This integrated process will utilize both the cell wall bound sugars of the abundant lignocellulosic sugarcane residues in addition to the sucrose from stem internodes. Enzymatic hydrolysis of lignocellulosic biomass into its component sugars requires significant amounts of cell wall degrading (CWD) enzymes. *In planta* production of xylanases has the potential to reduce costs associated with enzymatic hydrolysis but has been reported to compromise plant growth and development. To address this problem, we expressed a hyperthermostable GH10 xylanase, *xyl10B* in transgenic sugarcane which displays optimal catalytic activity at 105°C and only residual catalytic activity at temperatures below 70°C. Transgene integration and expression in sugarcane were confirmed by Southern blot, RT-PCR, ELISA and western blot following biolistic co-transfer of minimal expression cassettes of *xyl10B* and the selectable *nrpII*. Xylanase activity was detected in 17 transgenic lines with a fluorogenic xylanase activity assay. Up to 1.2% of the total soluble protein fraction of vegetative progenies with integration of chloroplast targeted expression represented the recombinant Xyl10B protein. Xyl10B activity was stable in vegetative progenies. Tissues retained 75% of the xylanase activity after drying of leaves at 35°C and a 2 month storage period. Transgenic sugarcane plants producing Xyl10B did not differ from non-transgenic sugarcane in growth and development under greenhouse conditions. Sugarcane xylan and bagasse were used as substrate for enzymatic hydrolysis with the *in planta* produced Xyl10B. TLC and HPLC analysis of hydrolysis products confirmed the superior catalytic activity and stability of the *in planta* produced Xyl10B with xylobiose as a prominent degradation product. These findings will contribute to advancing consolidated processing of lignocellulosic sugarcane biomass.

Acknowledgement: This work was carried out with the support of "Cooperative Research Program for Agriculture Science and Technology Development (Project No. PJ013159)" Rural Development Administration, Republic of Korea.

P0033: Maize, Sorghum, Millet, Sugar Cane, and related Chloroplast Genomes and Microbiome of Medieval Broomcorn Millet
Stephen Richards, University of Adelaide, Adelaide, Australia
Millets are among the first cultivated crops including broomcorn (*Panicum miliaceum*) and foxtail (*Setaria italica*) millet, which were domesticated in the arid regions of northeastern China at least 7,000 years ago. Millets were important crop in the ancient world and remain an essential food source for many regions of the world today. The movement of domesticated broomcorn and foxtail millet out of China is poorly understood. Archaeobotanical specimens are a unique resource as these materials can be used to investigate the history of domesticated crops through ancient DNA. To this end, we extracted ancient DNA from millet grains excavated in the Areni-1 cave of southern Armenia and were carbon dated to 873 ± 36 and 1118 ± 35 BP. We generated near complete chloroplast genomes (sans inverted repeats) and identified the Armenian grains as a close relative of broomcorn millet. Further, a metagenomic analysis was performed and ancient DNA from the endophytic fungus, *Chaetomium globosum*, was identified in one of the grains. The presence of ancient DNA from *C. globosum* presents the possibility of investigating endophyte evolution.

P0035: Maize, Sorghum, Millet, Sugar Cane, and related Molecular Marker Heterozygosity of Commercial Maize Hybrids and Its Implication for the Development of New Hybrid Cultivars
Taichoon Park, Seunghyun Wang, JongWon Kang and Yoon-Sup So, Chungbuk National University, Cheongju, South Korea
Heterosis is unlikely explained by a single mechanism such as dominance theory. Nevertheless, breeders avoid crosses among related inbred lines. The objective was to estimate molecular marker heterozygosity in commercially available maize hybrids around the world with Illumina MaizeLD Genotyping BeadChip with 3047 SNPs. The molecular marker heterozygosity among 79 commercial hybrids ranged from 14.9% to 47.57% with the average of $26.4 \pm 5\%$. There were seven hybrids from the tropics, one of which was a field corn (32.8%), three were sh2-based supersweet corns and the other three were waxy corns. The tropical waxy corns, one from the Philippines and two from Vietnam had the range of 31.5–36.7%. Two tropical super sweet hybrids had similar heterozygosity at around 30% while the third one had only 15.5%. This hybrid was recently released and outperformed the old but still leading hybrid with 31.3% from the same company. The 72 hybrids were sold in temperate regions, among which 54 hybrids were broadly classified as temperate sweet corn since different genes (*su*, *se*, *sh2*) were involved independently or in combination. The average heterozygosity in this class was $23.7 \pm 2.7\%$ with the range of 14.9–30.1%. The six temperate field corn and twelve temperate waxy hybrids, however, had much higher average of $36 \pm 3.3\%$ and $31.8 \pm 7.4\%$, respectively. The lower average of heterozygosity in temperate sweet corns may indicate that the genetic distance among temperate sweet corn breeding materials is narrower but still breeders were able to produce quality hybrids with less emphasis on yield.

P0034: Maize, Sorghum, Millet, Sugar Cane, and related Building High Quality, Chromosome-Scale, De Novo Maize Genome Assemblies By Scaffolding Next-Generation Sequencing Assemblies with Bionano Maps Generated with the New Direct Labeling Enzyme
Goran Pljevaljcic, Bionano Genomics, San Diego, CA
Compared to human and a few other model organisms, genomic and genetic studies of plant species with complex genomes have lagged behind. Most of the economically important crops still lack a gold-standard reference genome assembly, crucial to understanding their biology. Plant genomes are often complex and highly repetitive; and in the absence of long-range structural DNA information, generating high-quality genome assemblies with next-generation sequencing (NGS) alone, can be very costly if not impossible. Bionano genome mapping, using nickase-based labeling, has been an indispensable tool for genome assembly in plants and animals. A new direct labeling enzyme and protocol has shown orders of magnitude improvement in contiguity, while also improving the amount of NGS data that can be scaffolded. This is achieved by the elimination of systematic double-stranded breaks that nickases introduce. The new labeling approach maintains the integrity of long DNA and allows the production of affordable, contiguous, and accurate chromosome-scale genome assemblies that can span most repeat regions.
Here, we present the workflow for direct labeling of genomic DNA of plants and animals for the Bionano Saphyr system and show some exemplary results on maize B73 genome assembly. With the new direct labeling enzyme and protocol, the *de novo* assembly produced very contiguous genome maps with an N50 of 99.5 Mbp, which covered the whole B73 reference across all 10 chromosomes. Scaffolding with a PacBio NGS dataset with a N50 of 1.18 Mbp generates a hybrid assembly with an N50 of >100 Mbp where >95% of the NGS sequences are anchored.

P0036: Maize, Sorghum, Millet, Sugar Cane, and related Heterotic Grouping and F1 Hybrid Selection Based on Molecular Marker Heterozygosity in Waxy Corn Inbred Lines
JongWon Kang, Seunghyun Wang, Taichoon Park and Yoon-Sup So, Chungbuk National University, Cheongju, South Korea
The number of possible F1 hybrid combination increases drastically as new inbred lines develop, especially when inbreds developed are not classified for well-defined heterotic groups and there are no elite tester lines available from them. We attempted to group total of 75 newly developed waxy corn inbreds from commercial F1s and Korean landraces via molecular marker genotypes from Illumina MaizeLD Genotyping BeadChip with 3047 SNPs. Neighbor-joining cluster analysis grouped the 75 inbreds into 7 different clusters. Haploid genotypes excluding residual heterozygous marker genotypes were then taken and the total of 2,775 F1 combination were created virtually in a computer. The molecular marker heterozygosity of the virtual 2,775 F1 hybrids had the average of $23.7 \pm 6.3\%$ with the range between 0.3% and 35.3%. We also genotyped 9 leading commercial F1 waxy corn hybrids developed and being marketed in South Korea. Heterozygosity of the 9 commercial hybrids had the average of $28.9 \pm 5.3\%$ with maximum of 34.2%. There were 543 virtual F1 hybrids (19.6%) with over 30% heterozygosity out of 2,775 F1s. We identified some closely related inbred lines based on the low F1 heterozygosity less than 4%. Top 50 F1 hybrids with the most marker heterozygosity are being tested in the field and we will attempt to correlate the field performance to the observed marker heterozygosity. Although dominance theory of heterosis mechanism cannot be thoroughly translated into hybrid field performance, genome-wide molecular marker genotyping would in part help breeders reduce the number of hybrids to be tested in the field.

**P0037: Maize, Sorghum, Millet, Sugar Cane, and related
Determining Heterotic Groups in Tropical Super Sweet Corn Inbreds**

Seunghyun Wang, Taichoon Park, JongWon Kang and Yoon-Sup So,
Chungbuk National University, Cheongju, South Korea

There are no well-defined heterotic patterns for tropical super sweet corns. Understanding genetic relationship among inbred lines is an important step forward F1 hybrid development. Ninety-two newly developed tropical super sweet corn inbred lines through pedigree selection method were genotyped using Illumina MaizeLD Genotyping BeadChip with 3047 single nucleotide polymorphism(SNP) markers to determine possible heterotic groups. Call rate of per-sample basis ranged between 90.7% and 99.8% with the median of 98.6 and the mean of 98.5% indicating that the Illumina MaizeLD kit developed from field corn materials can be also applicable to tropical super sweet corn materials. There were 190 SNPs with per-SNP call rate less than 95%. Minor allele frequency(MAF) was also determined and total of 875 SNPs had less than 5% MAF, of which 653 SNPs were monomorphic (MAF=0). Molecular marker homozygosity level of the inbreds was at around 2.5% median with B73 being 1.7%. Nine inbred lines were identified as yet to be fixed due to still high heterozygosity of more than 10%. About 86.3% of pairs of lines had shared allele distance of 0.3-0.4. Neighbor-joining cluster analysis revealed that there are 8 possible heterotic groups and the grouping in general agreed with pedigree.

P0038: Methods: Bioinformatics

Hayai-Annotation: An Ultra-Fast and Comprehensive Gene Annotation System in Plants

Andrea Ghelfi, Kenta Shirasawa, Hideki Hirakawa and Sachiko Isobe, Kazusa DNA Research Institute, Kisarazu, Japan

The main target in plant breeding is to increase crop productivity and quality through improving biotic and abiotic stress tolerance. In order to achieve it, it would be critical for molecular breeders to broadly and accurately understand gene profiles in genomes. Since genome sequencing are becoming faster and cheaper, a high throughput workflow is required. Here, we propose, automated, fast, and accurate gene annotation system for plant species, i.e., Hayai-Annotation, a graphical user interface R-package. The workflow is based on sequence similarity searches with usearch to a database of UniprotKB, taxonomy Embryophytes. Hayai-Annotation provides six levels of annotation: 1) gene name; 2) gene ontology consisting of three main categories (Biological Process, Molecular Function and Cellular Component); 3) enzyme commission code; 4) protein evidence level; 5) evidence type; 6) and database name. Hayai-Annotation identified and properly annotate 39,296 SwissProt sequences in 14.9 minutes (6Gb RAM, i5-2450M) with an accuracy of 0.988. We applied Hayai-Annotation to sweet cherry (*Prunus avium*), in which genome sequences 43,349 gene structures were predicted. Out of them, 29,826 genes were successfully annotated with Hayai-Annotation using the following criteria for the similarity search: local alignment; 70% minimum sequence identity and e-value of 1e-6. There were 84 genes at a protein evidence level, 2,991 at a transcript level, 5,924 at a homology level, and 26,977 at a predicted level. GO categories of 4,136 unique Biological Process, 3,544 Molecular Function, and 866 Cellular Component were found. Hayai-Annotation was an efficient and accurate method for annotation of protein sequences in plants.

P0039: Methods: Bioinformatics

Development of Novel EST-SSRs from a Partial Coconut (Cocos nucifera L.) Transcriptome Assembly

Christian John S. Robiso¹, Edward A. Barlaan², Cynthia P. Saloma³, Ma. Anita M. Bautista³, Andrea Danna S Camiring⁴, Maria Adelina Marzan Facun⁵, Ma. Regina G. Punzalan⁵, Gamaliel Lysander B. Cabria⁶ and Ian Kendrick C. Fontanilla⁷, (1)PGC/IB - University of the Philippines, NCR / METRO MANILA, Philippines, (2)University of Southern Mindanao - Kabacan, Philippines, (3)Philippine Genome Center, Quezon City, Philippines, (4)Institute of Biology, University of the Philippines, Quezon City, Philippines, (5)Institute of Biology University of the Philippines, Quezon City, Philippines, (6)National Institute of Molecular Biology & Biotechnology, Quezon City, Philippines, (7)PGC/ IB - University of the Philippines, Quezon City, Philippines

Simple sequence repeats (SSRs) remain as one of the most versatile molecular markers in plant breeding due to their high availability and reproducibility. In this study, a partial transcriptome assembly of coconut was utilized to develop novel EST-SSRs for downstream analysis on coconut genomics and genetics. Three SSR search tools (MISA, Mreps, and SciRoKo) were used to search for potential EST-SSRs from 68,138 transcriptome contigs. The results from each software were then dereplicated to produce a non-redundant SSR loci dataset containing a total of 6,806 potential EST-SSRs. Among the 6,806 markers, 931 (13.68%) were found to be ambiguous and thus cannot be used for subsequent analyses. From the remaining 5,875 (86.32%) perfect SSRs, majority of the repeat motifs identified were dinucleotide (52.94%) and trinucleotide (44.27%) repeats, with only 2.79% comprising tetra-, penta-, and hexanucleotide repeats. Primer3 was then employed to develop primers with the following properties: amplicon length of 100-500 bp, 20 bases optimal primer length, 55°C optimal melting temperature, GC content of 50% and higher, and the homopolymer stretch should be no longer than three bases. The development of these SSRs proved the efficiency of transcriptomics in generating novel molecular markers which can be utilized in coconut marker-assisted breeding programs for mapping economically important genes, evaluating diversity and population structure, and genotyping coconut varieties for germplasm conservation.

P0040: Methods: Bioinformatics

Structural Variant Detection in Crops Using PacBio SMRT Sequencing

Gregory T Concepcion, Pacific Biosciences, Menlo Park, CA
Structural variants (genomic differences ≥ 50 base pairs) contribute to the evolution of traits and disease. Most structural variants (SVs) are too small to detect with array comparative genomic hybridization and too large to reliably discover with short-read DNA sequencing. While *de novo* assembly is the most comprehensive way to identify variants in a genome, recent studies in human genomes show that PacBio SMRT Sequencing sensitively detects structural variants at low coverage¹. Here we present SV characterization in two major crop species grown worldwide, *Zea mays* (Maize) and *Glycine max* (Soy).

P0041: Methods: Cellular Processes and Regulatory Networks
Synergistic Effects of Tgfb2, Wnt9a, and Fgfr4 Signals Attenuate Satellite Cell Differentiation During Skeletal Muscle Development

Weiya Zhang, Huazhong Agricultural University, Wuhan, China
Satellite cells play an important role in aging, generation, and damage repair of skeletal muscle. The molecular mechanism of satellite cells in these processes was still largely unknown. This study systematically investigated the characteristics of satellite cells at 10 ages of mouse for the first time. The result indicated that the number and the differentiation capacity of satellite cell decreased with age during skeletal muscle development. Meanwhile, transcriptome analysis showed that 2907 genes were differentially expressed between 6 time points postnatal. Among them 1739 differentially expressed genes (DEGs) were mainly involved in skeletal muscle development processes based on Weighted Gene Co-expression Network Analysis (WGCNA) and Gene Ontology (GO) analysis. Moreover, the result of WGCNA and protein interaction analysis demonstrated that Tgfb2, Wnt9a, and Fgfr4 were the key genes related to differentiation of satellite cells. Finally, functional analysis indicated that Tgfb2 and Wnt9a inhibited the differentiation of the satellite cells, while Fgfr4 promoted the differentiation. Moreover, each two of them had regulatory relationship at protein level. Therefore, we conclude that the synergistic effects of Tgfb2, Wnt9a, and Fgfr4 were responsible for attenuation of the differentiation of aging satellite cells during skeletal muscle development. This study provides new insights into molecular mechanism of satellite cells development. The target genes and signaling pathways would be useful for improvement of muscle growth of livestock or muscle disease cure in clinic.

P0043: Methods: Markers

Evaluating the Genetic Diversity and Population Structure of Cultivated Coconut (*Cocos nucifera* L.) in the Philippines Using Novel EST-SSRs

Christian John S. Robiso, PGC/IB - University of the Philippines, NCR / METRO MANILA, Philippines, Edward A. Barlaan, University of Southern Mindanao - Kabacan, Philippines, Ian Kendrick C. Fontanilla, PGC/IB - University of the Philippines, Quezon City, Philippines, **Andrea Danna S Camiring**, Institute of Biology, University of the Philippines, Quezon City, Philippines and Maria Adelina Marzan Facun, Institute of Biology University of the Philippines, Quezon City, Philippines

The Philippines rank first in total land area and second to global production in coconuts. Knowledge of the existing germplasm in the country is therefore essential in making decisions towards genetic improvement and conservation. In this study, 27 novel SSRs developed from a partial coconut transcriptome assembly were used to assess the genetic diversity and population structure of 16 cultivated coconut varieties (eight native and eight introduced) in the Philippines. Out of 27 markers, 19 did not show amplification or were monomorphic across the varieties tested and were discarded. Of the remaining, 21 alleles were detected across eight loci, with an average of 2.6 alleles per locus. The microsatellites displayed low to high degree of genetic diversity across populations: heterozygosity ranged from 0 to 0.635 (average 0.124) while gene diversity varied from 0.2 to 0.469 (average 0.234). The resulting UPGMA tree clustered the populations into two major subgroups, with the first subgroup further subdivided into three subpopulations. The Philippine native dwarfs clustered with the Laguna Tall, indicating their close relationship and possible shared ancestry. Interestingly, the introduced dwarfs from Southeast Asia grouped separately with Equatorial Guinea Green Dwarf (Africa). All other Philippine tall clusters separately and revealed high degree of genetic variation to Laguna Tall and Bago Oshiro Tall that suggests more than one possible event of introduction or origin. The study demonstrated the potential of using SSRs developed from transcriptomes as a tool in analyzing genetic diversity and population structure of coconut varieties.

P0042: Methods: High-throughput Methods
Analysis Method Pipeline Construction That Identifies and Visualize Sequence Variations from Next-Generation Sequencing Data

Dong Jun Lee¹, Dowan Kim², Jae Hyeon Oh³, Minseok Jung², Chang-Kug Kim⁴ and Tea-Ho Lee⁵, (1)National Institute of Agricultural Sciences(NAS), Jeonju-si, South Korea, (2)National Institute of Agricultural Sciences, RDA, Jeonju-si, Korea, Republic of (South), (3)National Institute of Agricultural Sciences, RDA, Jeonju-si, Jeollabuk-do, Korea, Republic of (South), (4)National Institute of Agricultural Sciences (NAS), Jeonju, Korea, Republic of (South), (5)National Institute of Agricultural Sciences, RDA, Jeonju, Korea, Republic of (South)

Recent, biology research is increasing big data with next-generation sequencing(NGS) methods that technology that produces large amounts of data. Mainly, it is rapidly developing for data storage technology, analysis, and processing method to support NGS. We have developed a pipeline that able to visualize and analyze differences in nucleotide sequence variations between two genomes by comparing new NGS data with reference genomic data. As a result, the advantage of this method is that it has developed a pipeline that can be analyzed and visualized in one-step automatically method better than the existing manual method.

P0044: Methods: Markers

Development SNP Marker Set for Mab (Marker-assisted Backcross) System in Cucumber

Eun Su Lee¹, Jinhee Kim², Hye-Eun Lee³, Jong Pil Hong⁴, Abinaya Manivannan⁵, Ji-Hye Moon¹ and Dosun Kim⁶, (1)National Institute of Horticultural and Herbal Science, Wanju-gun, South Korea, (2)National Institute of Horticultural and Herbal Science, Wanju-gun, Jeollabuk-do, South Korea, (3)National Institute of Horticultural & Herbal Science, South Korea, (4)National Institute of Horticultural and Herbal Science, Wanju-gun, Korea, Republic of (South), (5)National Institute of Horticulture & Herbal Science, RDA, Jeonju, South Korea, (6)The institute of horticulture and herbal science, Wanju, South Korea

Cucumbers are widely cultivated plants in the world and scientifically known as *Cucumis sativus*. They provide us with numerous nutrients such as vitamin C, polyphenols and several detoxifying compounds. Breeding of cucumber is constantly evolving and breeding technique using molecular marker gets a lot of attention recently. Among the molecular markers, single nucleotide polymorphism (SNP) is mostly used in genetic diversity analysis due to its abundance. To develop high-throughput SNP marker for analyzing genotype, we selected 38 cucumber lines with diverse traits such as heat tolerance, nodal bearing, color of flesh, protuberance and powdery mildew resistance etc. Then, we sequenced the transcriptomes of 38 lines by using Illumina HiSeq4000. The average transcriptome size was 3,602,733,209bp (35,990,890 reads), the average of Q30 level and GC content was 96% and 46% respectively. We performed the comparison with transcriptome sequences and identified 426,176 SNPs. The filtering criteria were depth, segregation ratio, distinguishable species, lack of adjacent SNP and copy number. We chose SNPs that cover the whole cucumber genome. Selected SNPs are schedule to be used in species classification and marker-assisted backcross (MAB), development of genetic map etc. Moreover the molecular marker set can be analyzed in Fluidigm system for a variety of purposes. Hence, the SNP marker set can be applied in the various cucumber breeding system.

P0045: Methods: Other Genome Methodology
Building High Quality, Chromosome-Scale, De Novo Genome Assemblies By Scaffolding Next-Generation Sequencing Assemblies with Bionano Genome Mapping

Goran Pljevaljcic, Bionano Genomics, San Diego, CA

With the exception of a few model organisms, many biologically and economically important plants and animals still lack a reference-quality genome assembly that is crucial for understanding their biology. With genomes that are often complex and highly repetitive, constructing high-quality assemblies from next-generation sequencing (NGS) alone, without access to long-range structural information, is extremely difficult or not possible.

Bionano's genome mapping technology provides a solution to reconstruct the full genomic architecture of large and complex genomes.

Here, we present a novel direct enzymatic labeling approach which maintains the integrity of the DNA and allows us to create very contiguous Bionano maps which can then be used to scaffold NGS sequence assemblies to produce highly contiguous and structurally accurate hybrid assemblies that can span most repeat regions. This direct labeling method is compatible with a vast array of organisms

On the human NA12878 genome, we produced hybrid assemblies with N50 up to 80 Mbp from NGS assemblies ranging from 0.18 – 14.5 Mbp. Chromosome-arm length scaffolds were assembled in 20 out of 23 chromosomes with over 99% scaffolding accuracy. We will also show equally impressive scaffolds for a variety of plants and animals. The scaffolds generated with this data have set a new standard for genome assembly that can be accomplished in less than one week.

P0047: Microbes and Pathogens

Pan-Genome Analysis of *Ralstonia solanacearum* Isolated from Potato Bacterial Wilt in Korea

Heejung Cho, Young Kee Lee, Seungdon Lee, Ji Yeon Park, Jeong-Gu Kim and Dong Suk Park, National Institute of Agricultural Sciences, RDA, Jeonju, South Korea

Soil-borne pathogenic *Ralstonia solanacearum* is economically destructive phytopathogens in worldwide with broad host range - various solanaceae plants, banana, ginger, sesame, clove, sunflower, etc. This bacterium distributed worldwide encompassing tropical, subtropical, and temperate region. With these features, this species are very diverse and complex and call as pathogenic *Ralstonia solanacearum* species complex (RSSC). Here, we sequenced the genomes of twenty-five Korean *R. solanacearum* strains based on host range. The newly sequenced genomes were analyzed the phylogenetic relationship with ANI values and structurally compared multiple genome alignment using Mauve software. As the results, Korean genomes were usually conserved in the phylotype, but more divergent between phylotype I and IV. After that, to investigate candidate genes responsible for host specificity, functional genome comparisons were performed by analyses of pan-genome orthologous group (POG) and type III secretion system effectors (T3Es). In the POG analysis, total 128 genes shared only in tomato-nonpathogenic strains, 8 genes in tomato-pathogenic strains, 5 genes from eggplant-nonpathogenic strains, 7 genes from eggplant-pathogenic strains, one gene from pepper-nonpathogenic strains, and 34 genes from pepper-pathogenic strains. In the T3Es prediction, it was found three host specific effectors; RipS3 (Skwp3) and RipH3 were found only in the tomato-pathogenic strains and RipAC (PopC) were only in the eggplant pathogenic strains. This study showed that the host range of *R. solanacearum* required comprehensive actions of various virulence factors involving effectors, secretion systems, attachment, and enzymes, etc.

P0046: Methods: Sequencing
Molecular Identification of Cyanobacteria from Some Mining Sites in Benguet, Philippines Using Metagenomic and PCR-Based 16S rRNA GENE Sequencing

Ernelea P. Cao, Institute of Biology-University of the Philippines, Quezon City, Philippines; Natural Sciences Research Institute, U.P. Diliman, Quezon City, Philippines and Amor II M. Damatac, Natural Sciences Research Institute- U.P. Diliman, Quezon City, Philippines; Institute of Biology, University of the Philippines, Quezon City, Philippines

Cyanobacteria belong to the ancient group of plant-like organisms that are capable of oxygenic photosynthesis. They are ubiquitous in nature and have been reported to survive even in extreme environments. In this study, cyanobacteria present from some mining areas in Benguet, Philippines were identified using isolation-dependent and -independent approaches. Soil samples from four mining sites (Acupan, Ampucao, Philex TSF1 and Philex TSF3) were processed for cyanobacteria enrichment. The consortia were directly subjected to DNA extraction followed by 16s rRNA gene-based metagenomic sequencing, while the remaining samples were used to isolate unialgal cultures of cyanobacteria, which were likewise subjected to DNA extraction followed by 16s rRNA gene amplification and sequencing. Alignment in NCBI and SILVA databases revealed six Operational Taxonomic Units (OTUs). Crocococcales were found in all sites, while Nostocales (*Nostoc* sp.) and Stigonematales (*Calothrix* sp.) were found only in Philex TSF1 and TSF3. Members of Pseudoanabaenales (*Arthronema africanum* and *Leptolyngbya* sp.) were found in all sites, while some members of Oscillatoriales (*Phormidium* sp. and *Planktothrix* sp.) and Sinechococcales (*Acaryochloris* sp. and *Thermosynechococcus* sp.) were only present in specific sites, indicating that certain cyanobacteria can uniquely thrive in certain environments. Characterization of the genomes of these cyanobacteria may lead to the discovery of genes or gene clusters for metal tolerance and other stress-related adaptations, which may be harnessed for potential bioremediation of waters with high levels of heavy metal contamination.

P0048: Oilseeds, Sunflower, and related

Genomic Resources for the Development of High Copra Yield Gene Markers in Philippine Coconut Palms

Ma. Anita M. Bautista^{1,2}, Ma. Regina G. Punzalan¹, Gamaliel Lysander B. Cabria², Ramon L. Rivera³, Susan M. Rivera³, Ernesto E. Emmanuel³ and Cynthia P. Saloma^{1,2}, (1)Philippine Genome Center, Quezon City, Philippines, (2)National Institute of Molecular Biology & Biotechnology, Quezon City, Philippines, (3)Philippine Coconut Authority - Zamboanga Research Center, Zamboanga City, Philippines

The growing demand for coconut oil in the world market puts a pressure for coconut-producing countries to increase copra production. According to the Philippine Coconut Authority, the Baybay Tall variety has the highest copra yield among all cultivars of Philippine coconuts. However, genomic studies associated with nut yield are lacking; hence, coconut breeders still resort to traditional breeding techniques. In order to improve breeding strategies for increased copra production, RNA-seq with subsequent differential gene expression analysis on Baybay Tall was performed. High quality RNA was isolated from the endosperm and endocarp of tagged high-yielding and low-yielding coconut palms. RNA-seq was performed using Illumina HiSeq 2000 followed by *de novo* transcriptome assembly using Trinity. Expression data was obtained using Corset and differentially expressed genes were identified using edgeR. In total, 1,945 genes were found to be differentially expressed (FDR < 0.05) from the nut tissues. Annotation of the transcripts revealed that only 82 of the differentially expressed genes have significant annotation. Copra yield has been found to be influenced by several biological pathways as evidenced by the high number of differentially expressed genes observed. It also appears that high copra yield is attributed to three main events during seed development: cell division, cell expansion, and cell wall modification. Gene-targeted markers were designed for 64 genes which can be used in crop breeding technologies for selecting high-yielding palms.

P0049: Other Plant Species

RNA-Seq, De Novo Transcriptome Assembly, and Functional Genomics Studies of *Cocos nucifera* Var. Catigan Dwarf

Dianne J. Acoba^{1,2}, Ramon L. Rivera³, Susan M. Rivera³, Ernesto E. Emmanuel³, Cynthia P. Saloma^{1,2} and Ma. Anita M. Bautista^{1,2}, (1)National Institute of Molecular Biology & Biotechnology, Quezon City, Philippines, (2)Philippine Genome Center, Quezon City, Philippines, (3)Philippine Coconut Authority - Zamboanga Research Center, Zamboanga City, Philippines
The Philippines remains the top producer and exporter of coconut oil worldwide. Coconut oil is extracted from copra, the dried meat of mature coconuts, making *Cocos nucifera*, commonly known as the coconut palm, the most prominent and highly valued palm in the Philippines. Despite its significance, there is a severe paucity of genomic and genetic research and data on the coconut palm. In this study, we report a coconut transcriptome profile by performing *de novo* transcriptome assembly from RNA-seq data and gene expression analysis in six coconut tissues: endosperm, endocarp, mesocarp, leaf, male flower, and female flower. RNA extracted from tissues of the Catigan Dwarf, a traditional Philippine coconut variety, were sequenced using Illumina HiSeq 2000 and assembled *de novo* via Trinity. Illumina short reads were multi-mapped back to the assembly using Bowtie, followed by clustering analysis. Annotation was done by BLASTX against the nr protein database and other annotated sequences from related species. The annotated unigenes were then further classified by querying in the GO and KEGG databases. Gene expression analyses and functional genomics studies were also performed. Lastly, assembly and gene expression validation were done using quantitative RT-PCR. The extensive genomic information generated by the study could be a valuable resource for further molecular studies, varietal improvement, and breeding of the coconut palm.

P0051: Other Plant Species

De Novo Genome Sequencing and Transcriptomes Identification of *Bienertia sinuspersici*, a Single Cell C₄ (SCC₄) Non-Krantz Photosynthetic Plant

Soundararajan Prabhakaran, So Youn Won, Seung Ah Choi and Jung Sun Kim, National Institute of Agricultural Sciences, RDA, Jeonju, South Korea
Bienertia sinuspersici is an important C₄ model plant with dimorphic chloroplast on single chlorenchyma cells. Subcellular-compartmentalization of peripheral compartment chloroplast (PCC) and central compartment chloroplast (CCC) in the single cell is utilized for carbon fixation. However, till date none of the DNA sequencing or genomics study has been conducted on C₄ plants without Krantz anatomy. Genome sequencing and full length gene prediction were performed using PacBio Single Molecule Real Time (SMRT) sequencing and PacBio Iso-Seq technology, respectively. Benchmarking Universal Single-Copy Orthologs (BUSCOs) was used for the assessment of genome assembly, gene set, and transcriptome completeness. Totally 53.77X depth coverage have been achieved with 18,792,719 numbers of reads. Final number of contigs assembled was 44,089 and the longest contig length is 10,539,932 bp. Total size of contig assembled using Falcon-Unzip Assembler was around 3.6 Gb. From 1,161 BUSCOs, 938 and 223 complete orthologs were identified as single and duplicated copies, respectively. Maximum number of genes showed homology with the *Beta vulgaris*, *Spinacia oleracea*, and *Vitis vinifera*. Gene ontology (GO) analysis predicted the higher number of genes involved in ATP binding, followed by metal ion binding, DNA binding, and so on. Interestingly, majority of genes located in the integral membrane and chloroplast. Biological process category of GO analysis signifies the maximum numbers of genes are involved in oxidation-reduction process. This draft assembly report provides deeper insights into the genome sequence, complete transcripts, orthologs, species distribution, and also functional category of identified genes in *B. sinuspersici*. Further functional annotation and evolutionary studies will provide more details about the adaptation of C₄ metabolism with non-krantz anatomy of *B. Sinuspersici*.

P0050: Other Plant Species

The Octoploid Strawberry SNP Discovery Using Genotyping By Sequencing Method for the Fruit Firmness Study

Jinhee Kim¹, Sun Yi Lee², Abinaya Manivannan³, Dosun Kim⁴, Eun Su Lee⁵, Hye-Eun Lee², Minjeong Park⁶ and Byoung-Cheorl Kang⁷, (1)National Institute of Horticultural and Herbal Science, Wanju-gun, Jeollabuk-do, South Korea, (2)National Institute of Horticultural & Herbal Science, South Korea, (3)National Institute of Horticulture & Herbal Science, RDA, Jeonju, South Korea, (4)The institute of horticulture and herbal science, Wanju, South Korea, (5)National Institute of Horticultural and Herbal Science, Wanju-gun, South Korea, (6)Seoul National University, Seoul, South Korea, (7)Seoul National University, Seoul, South Korea

The molecular genetic information of octoploid strawberry (*Fragaria x ananassa*) is still insufficient to develop effective markers for agronomic traits. In this study, we collected a set of high-quality single nucleotide polymorphisms (SNPs) using F₂ population to study strawberry firmness. To search a useful set of SNPs, we used the genotyping-by-sequencing (GBS) method. F₂ populations consisted of 150 plants were constructed using inbred lines developed in the Institute of Horticulture and herbal science. Chandler inbred line was used for the weak firmness parent (below 15 g/mm²) and Benihoppe inbred line was selected for the strong firmness parent (over 25 g/mm²). The phenotype data of firmness was collected from F₂ population in the spring season. By GBS method, 2,245 raw SNP was collected in the first place. The SNPs in the same scaffold was eliminated. Then several filtering criteria (SNP quality, read depth, genotype quality, etc.) were used to sort the qualified SNPs. Final remained 401 SNPs were mapped in the T137 linkage map using Carthagene software. The robust SNP discovery related to the firmness using GBS in this study can be a valuable source in accelerating strawberry molecular breeding.

P0052: Other Plant Species

Draft De Novo Genome Assembly of the Philippine Endemic Abaca (*Musa textilis* Nee.)

Julianne A. Vilela, University of the Philippines, Los Banos, Philippines
The Abaca (*Musa textilis* Nee.) is endemic to the Philippines and the country's most economically important fiber crop. Since 1980s, rapid decline in abaca production is reported due to destruction brought about by three major virus diseases, namely, abaca bunchy top (ABT), abaca mosaic (AM) and recently, abaca bract mosaic (BM). The resistant varieties identified from the abaca germplasm are often of inferior quality, while traditional varieties, although of superior fiber quality, are highly susceptible to these diseases. To address this problem, efforts in rehabilitating the abaca industry will be assisted by information from the abaca genome generated and assembled, which will allow detailed analysis of genes associated with virus resistance and superior fiber quality.

The Ion Semiconductor technology was used to generate short 250-300 bp single-end reads for whole genome sequencing of abaca. We present here the first draft genome assembly of the Philippine endemic abaca. With Mimicking Intelligent Read Assembler (MIRA), a total of 33730 contigs were generated. We further anchored and oriented the abaca genome assembly on ten chromosomes of *Musa acuminata* reference genome and found that approximately 30% of the genome is occupied by repetitive DNA sequences. Comparative genome analysis and annotation showed gene families associated to superior fiber quality and virus resistance thus, the abaca genome assembly will aide in marker assisted breeding of new and improved abaca hybrids.

P0053: Other Plant Species

Identification of Isoeogomaketone-Related Genes in New Radiation Mutant Cultivar of *Perilla frutescens* Var. *Crispa* By RNA-Seq

Soon-Jae Kwon¹, Min-Kyu Lee^{1,2}, Dong-Gun Kim^{1,3}, Jung Min KIM^{1,2}, Min Jeong Hong¹, Bo Mi Nam¹, Chang Hyun Jin¹, Hong-Il Choi¹, Bo-Keun Ha² and Jin-Baek Kim¹, (1)Korea Atomic Energy Research Institute, Jeongeup, South Korea, (2)Chonnam National University, Gwangju, South Korea, (3)Suncheon National University, Suncheon, South Korea

Perilla frutescens var. *crispa* (Labiatae), which is known as 'Cha-Jo-Ki' in Korea, 'Zi-Su-Ye' in China, and 'Shiso' in Japan, has been used as a medicinal herb. Recently, our research group developed a new mutation cultivar *P.*

frutescens var. *crispa* (vs. *Antisperill*) through gamma irradiated mutation breeding, which has a 25-fold higher content of isoeogomaketone (IK) than the wild type. We performed RNA sequencing with three growth stages to evaluate the molecular mechanisms that determine the differences in IK content between *Antisperill* and wild type. In total, 132,943 transcripts and 36,995 representative transcripts were identified. Of the 36,995 representative transcripts, 25,510 (69.96%) sequences had similarity with the GO, KOG, and KEGG amino acid sequences. We identified 65, 131, and 230 differentially expressed genes between the mutant and wild type in 70, 94, and 122 days after sowing, respectively. With the exception of redundancy, a clustering analysis was performed using 362 unigenes. Among these genes, 110 homologs of *P. frutescens* terpenoid biosynthesis pathway related genes were identified and seven genes were related to monoterpenoid biosynthesis, which is thought to be the pathway of IK. However, the correlation between the seven candidate genes and IK contents depending on the growth stage should be compared in a further study.

P0055: Other Plant Species

Transcriptome Sequencing and Identification of Putative Genes Involved in Flavonoid Biosynthesis in Kenaf (*Hibiscus cannabinus* L.)

Hong-Il Choi¹, JaiHyunk Ryu², Soon-Jae Kwon¹, Yeong Deuk Jo¹, Min Jeong Hong¹, Joon-Woo Ahn¹, Sang Hoon Kim¹, Si-Yong Kang¹ and Jin-Baek Kim¹, (1)Korea Atomic Energy Research Institute, Jeongeup, South Korea, (2)Chonnam National University, Gwangju, South Korea

Kenaf (*Hibiscus cannabinus* L.) is an annual herbaceous plant belonging to the Malvaceae family. As an industrial crop, kenaf has been cultivated for multiple purposes such as the stem fiber, livestock feed, and medicinal use. This study was conducted to obtain comprehensive transcriptome information and identify putative genes involved in flavonoid biosynthesis. A total of 39.6 Gb reads were generated for six kenaf accessions, and the de novo assembly of each accession resulted in 127,526 contigs of 145 Mb in total length and N50 of 1,618 bp, on average. Finally, 299,902 representative unigenes with an average length of 1,217 bp and N50 of 1,782 bp were constructed by clustering of whole transcriptome contigs. Among the unigenes, 231,825 (77.3%) had BLASTX hits against the various protein databases, 118,674 (39.6%) had gene ontology terms, 71,355 (28.3%) had COG terms, and 33,093 (11.0%) were matched against the KEGG database. An analysis of the gene expression level identified 6,592 unigenes that were differentially expressed among the three accessions, one original germplasm "C14," and two mutant varieties "Baekma" and "Jeokbong." Functional-annotation based identification revealed 213 putative unigenes involved in the phenylpropanoid and flavonoid biosynthesis pathways, including 17 differentially expressed unigenes. Our results provide broad transcriptional information and contribute to an understanding of the mechanism of biosynthesis and the accumulation of useful flavonoid derivatives in kenaf.

P0054: Other Plant Species

Cross-Species Transferability of EST-SSR Markers Derived From Kenaf Transcriptome and Their Application in Hibiscus Genus

Jung Min Kim^{1,2}, JaiHyunk Ryu¹, Min-Kyu Lee^{1,2}, Dong-Gun Kim^{2,3}, Min Jeong Hong², Jin-Baek Kim², Si-Yong Kang², Bo-Keun Ha¹, Joon-Woo Ahn² and Soon-Jae Kwon², (1)Chonnam National University, Gwangju, South Korea, (2)Korea Atomic Energy Research Institute, Jeongeup, South Korea, (3)Suncheon National University, Suncheon, South Korea

The hibiscus genus was composed of about 300 diverse species. However, an evaluation of the genetic relationship has not been investigated and studied. Hence, we assessed the genetic diversity and relationship through transferability of 102 EST-SSR markers derived from kenaf in 18 hibiscus species. One-hundred and one EST-SSR markers were completely amplified. Of them, 100 markers showed polymorphism to 94 genetic resources/cultivars in the hibiscus genus. As a result, cross-species transferability rates ranged from 82.35% (*H. trionum*) to 98.04% (*H. ponticus*) and the average of transferability rates revealed 89.02% in the hibiscus genus. A total of 827 alleles were generated from the use of 101 EST-SSR markers, and the number of alleles ranged from 1 to 16 and the average was 8.6. The PIC values ranged from 0 to 0.86, and the average PIC value was 0.5608. Moreover, we identified the genetic relationship among 18 hibiscus species. According to UPGMA clustering and a PCoA analysis, 18 hibiscus species were classified into three clusters. Cluster I contained one species (*H. acetosella*), cluster II included two species (*H. sabdariffa* and *H. radiates*), and the remaining 15 species were clustered in Cluster III. The population structure with 94 genetic resources/cultivars was divided into three groups as well. Overall, this study provides genetic diversity, the genetic relationship and transferability to unclear genetic resources in the hibiscus genus.

P0056: Other Plant Species

Identification of the Chloroplast Genome of Chrysanthemum Species and Phylogenetic Analysis

So Youn Won¹, Jae-A Jung² and Jung Sun Kim¹, (1)National Institute of Agricultural Sciences, RDA, Jeonju, South Korea, (2)Rural Development Administration, Wanju-gun, Korea, Republic of (South)

Chrysanthemum is a genus that includes about 50 species and belongs to the Asteraceae family. Its species are famous for their various types, colours and sizes of flowers, as shown in the commercial cultivar, *Chrysanthemum morifolium*. Several phylogenetic analyses were conducted on *Chrysanthemum* species by using the barcode sequences such as nucleus genes or chloroplast genes. Since the barcodes used were as short as hundred bases in length at the most analysis, however, the phylogenetic relationship of *Chrysanthemum* species needs to be clearly identified. To provide genomic information of and resolve the genetic relationship among *Chrysanthemum* species, we sequenced chloroplast (CP) genomes of 7 species and 16 individuals in *Chrysanthemum* by using Illumina HiSeq platform and also downloaded two CP genomes. Reference-guided genome assembly revealed that the CP genomes ranged from 150,995bp to 151,024bp in length and had a typical quadripartite structure with a large single copy region, a small single copy region and two inverted repeat regions. According to the Maximum-likelihood analysis, *Chrysanthemum* species formed a monophyletic group and their phylogenetic relationships were uncovered, suggesting that the complete CP genome serves as a useful genomic resource to understand the genetic relationships among the close species.

P0057: Other Plant Species

Mapping of Quantitative Trait Loci for Fruit Morphological Traits in Melon (*Cucumis melo* L.)

Fauziatul Fitriyah¹, Sachiko Isobe², Kenta Shirasawa² and Yosuke Yoshioka¹, (1)University of Tsukuba, Tsukuba, Japan, (2)Kazusa DNA Research Institute, Kisarazu, Japan

Melon (*Cucumis melo* L.) is one of the most important species of Cucurbitaceae family. Fruits at both mature and immature stages have been consumed in many ways, resulting in the tremendous diversity and distinctive features in fruit quality traits. The introduction of next-generation sequencing (NGS) methods has helped the genotyping of mapping populations for identification of candidate genomic regions for important agronomic traits. Here we report a high density genetic linkage map using restriction-site associated DNA sequencing (RAD-seq) and identification of QTLs for fruit morphological traits in melon.

A total of 2771 SNPs markers were detected by RAD-seq in the analysis of two cultivations, comprising of 273 F₂ population derived from a cross between weedy melon and muskmelon. The final map included 1833 SNPs distributed on 12 linkage groups (LGs) and was 1496.7 cM in length with average of 0.82 cM between adjacent markers. Using this map and phenotypic data, a total of 51 QTLs were found in first cultivation and 62 QTLs in second cultivation for ten fruit morphological traits by the composite interval mapping (CIM) using WinQTLCart v2.5. In the second cultivation, we evaluated seed and ovary traits, and detected 21 and 12 QTLs, respectively.

RAD-seq data was successfully used to rapidly construct high-density genetic map with SNP markers in F₂ population and to detect QTLs for important fruit morphological traits in melon.

P0059: Other Species

Long-Distance Movement of Naturally Occurring Small RNAs in a Host-Parasite Plant Complex

Subhankar Bera, Osaka Prefecture University, SAKAI, Japan, Koh Aoki, Osaka Prefecture University, Sakai, Japan and Kohki Shimizu¹, Keisuke Tanaka², Shunsuke Yajima^{2,3}, Koh Aoki¹ Osaka Prefecture University, 2NODAI Genome Research Center, Tokyo University of Agriculture, 3Department of Bioscience, Tokyo University of Agriculture.

Cuscuta spp. are holo-parasitic plants that uptake water and nutrients for their survival and growth. Plant endogenous mRNAs and proteins have been known to move bidirectionally through the parasitic junction. It has been shown recently that parasitization triggers accumulation of small RNAs (sRNAs) in parasitic tissues and they move from parasite to host plant to control trans-species gene regulation and/or secondary siRNA production. However, there have been no direct evidence for the sRNA movement from host to parasite plants and control of gene expression. In this work, we explored naturally occurring sRNAs that move long distance and regulate trans-species genes in bidirectional manner. We chose *Cuscuta japonica* and *Glycine max* as a parasitic model for our study. sRNA-seq of non-parasitic and parasitic tissues of *C. japonica* and *G. max* allowed us to prioritize several sRNA candidates of *C. japonica* that possibly moved to *G. max* tissue, and vice-versa. We confirmed the presence of these sRNA candidates by stem-loop PCR followed by Sanger sequencing. By cross-species detection of sRNAs, we confirmed that long-distance movement of sRNA occurs in bidirectional manner. We are currently identifying their trans-species target genes and target tissues. These results suggest that mobile sRNAs control trans-species gene regulation and secondary sRNA accumulation. This work was partly supported by the Cooperative Research Grant of the Genome Research for BioResource (NODAI Genome Research Center, Tokyo University of Agriculture), and Scientific Research on Innovative Areas "The Plant Cell Wall as Information Processing System" (MEXT, Japan).

P0058: Other Plant Species

Improving Nutritional Value of Lettuce While Adapting Lettuce to Low Nitrogen

Youngsook You¹, Linda K. Stroud¹ and David W. Still², (1)California State Polytechnic University, Pomona, Pomona, CA, (2)California State Univ. Agricultural Research Institute, Pomona, CA

Youngsook You, California State Polytechnic University, Pomona Lettuce is a much-consumed vegetable in the U.S., Europe and China and is a significant contributor of vitamins, antioxidants and other phytochemicals that may have health benefits. Lettuce requires high amounts of nitrogen (N) fertilizers to ensure size and quality. However, use of N fertilizers can lead to nitrates leaching into groundwater and the release of the potent greenhouse gas N₂O into the atmosphere. Thus, adapting lettuce cultivars to low N while improving nutritional density of is a goal of our laboratory.

Nitrogen has clear effects on growth, but it also affects complex biosynthetic pathways, including the phenylpropanoid and carotenoid pathways, which are responsible for key nutritional components of lettuce. We have observed large differences in nitrogen use efficiency and nutritional content in commercial cultivars, inbred genetic lines and sexually compatible wild germplasm. We have developed mapping populations and have identified major effect quantitative trait loci associated with these traits. In general, wild germplasm exhibits better nitrogen use efficiency and has greater nutritional content when grown under low N. Subsequently, alleles from wild germplasm are being introgressed into lettuce germplasm to improve these traits.

P0060: Poultry

Spleen RNA-Seq Reveals Host Immune Mechanism in Response to *Salmonella pullorum* Infection in Resistant and Susceptible Chicken Lines

Xinghua Li¹, Yaxiong Jia², Yu Chen³, Jianwei Zhang³, Yu Wang³, Zhonghua Ning¹ and Lujiang Qu¹, (1)China Agricultural University, Beijing, China, (2)Chinese Academy of Agricultural Sciences, Beijing, China, (3)Beijing Municipal General Station of Animal Science, Beijing, China

Background: *Salmonella Pullorum* (SP) is the causative agent of pullorum disease, a troublesome infectious disease threatening the poultry industry. Traditional purification measures are unable to eradicate the pathogen, owing to its complex transmission way. Selective breeding for improved host disease resistance is a promising alternative strategy for disease control. However, it has not been fully understood to date for host gene expression and immune mechanism after SP infection. Here, we study gene expression in the spleen between infected and mock-infected chicks, and between resistant and susceptible chicken lines, at three time points (4d, 10d and 21d) post-infection.

Results: We sequenced 36 spleen RNA libraries generated from the twelve different treatment groups with three replicates each, and obtained an average of 45 million pair-end, 150-bp strand-specific clean reads per library. Differentially expressed genes (DEGs) were detected between infected and mock-infected treatments within lines at a given time point. At 4 dpi, the results show that a lot of immune genes and relevant pathways contributes to the host responses to SP infection at 4 dpi in both resistant and susceptible lines. However, the resistant chicks' immune system turned to be alike with the non-infected birds at 10 dpi and 21 dpi, while the susceptible chicks still presented many DEGs. These genes mostly belong to cytokine activities and toll-like receptor signaling. Among these DEGs, TLR4, IL18 and CCL110 are classic immune genes which have been reported and elucidated in many other salmonella infection models. Besides, a previously uncharacterized gene, avidin, was remarkably high-expressed after infection, which indicates that it may play an important role during SP infection.

Conclusion: The spleen is the major location where SP survive and reproduce. These identified DEGs are representative of host immune activation and defense strategy. Our result reveals the host immune responses and provides candidate genes for future selective breeding. We firstly detected that the avidin, which was formerly found to deposited in the whites of eggs, might possess the antimicrobial function.

P0061: Poultry

Genome-Wide Association Study Revealed Genomic Regions Related to White/Black Tail Feather Color Trait in the Dwarf Chickens

Changsheng Nie¹, Liang Qu², Yaxiong Jia³, Yu Chen⁴, Chuanwei Zheng⁵, Zhonghua Ning¹, Kehua Wang² and Lujiang Qu¹, (1)China Agricultural University, Beijing, China, (2)Jiangsu Institute of Poultry Science, Yangzhou, China, (3)Chinese Academy of Agricultural Sciences, Beijing, China, (4)Beijing Municipal General Station of Animal Science, Beijing, China, (5)Bei Nong Da Science and Technology Co., Ltd., Beijing, China

Tail feather color is a naturally and artificially selected in chicken. Blackness and whiteness are predominant feather color in chicken, and in some breeds, chickens also present with red, blue, yellow, purple or colorful tail feathers. Tail feather color is selected by human for keeping the breed characteristics. In the present study, we performed genome-wide association (GWA) analysis to explore the candidate genomic regions underlying chicken tail feather color phenotypes in one inbred population of dwarf chickens in which the tail feather present blank and white. We used hens with black tail feather and hens with white tail feather for case-control analysis by Illumina 600K SNP arrays. The GWA results showed that a genomic region (5.76Mb) being 5%genome-wide significance on chromosome 20 were significantly correlated to tail feather color. Candidate genes around peak SNP (rs312649884) on Chromosome 20 were found in the region including *SLC2A10*, *TP53RK* and *SLC13A3*.

Causative gene *SLC45A2* encoding SLC protein can translocated cysteine further regulate pigment synthesis in silver feather color chicken. Out of the candidate genes, *SLC2A10* and *SLC13A3* belongs to SLC gene family may have its special function in tail feather color formation. Tyrosine is a precursor in melanin formation. *NTRK2* is a member of the tyrosine protein kinase family.

P0063: Rice

Jacalin-Related Lectin Regulates DNA Damage Response Induced By Gamma-Radiation

Joon-Woo Ahn, In Jung Jung, Soon-Jae Kwon, Hong-Il Choi, Min Jeong Hong and Jin-Baek Kim, Korea Atomic Energy Research Institute, Jeongseup, South Korea

Jacalin-related lectins containing lectin domain are play a key role in plant defense and development. In this study, we characterized rice Jacalin-related lectin (OsJAC1) function in response to gamma radiation. To identify expression pattern of *OsJAC1* in response to gamma radiation, quantitative RT-PCR analysis was performed using gamma-irradiated rice seedlings. Interestingly, time course- and dose-dependent changes of *OsJAC1* expression were detected after gamma irradiation in rice. *OsJAC1* expression was significantly down-regulated after gamma irradiation, however gradual induction of *OsJAC1* expression was detected until 24 h. After 7 days of gamma irradiation, over 30-fold induction of *OsJAC1* transcript was found in the rice seedlings irradiated with 100 Gy. To determine molecular insight of DNA damage response on OsJAC1 function, transcriptome analysis was carried out using OsJAC1-overexpressing *Arabidopsis* transgenic lines after gamma irradiation. OsJAC1-overexpression induced transcriptional accumulations of *MCMs* which are DNA replication factors; especially *MCM6* expression was significantly up-regulated with and without gamma irradiation in OsJAC1-overexpressing lines. Transcripts of replication factors *A1* (*RPA70D*) and *A2* were induced in response to gamma irradiation. Induction of double strand break repair protein (*MER11*) expression was found in OsJAC1-overexpressing lines. Furthermore, *Ataxia telangiectasia mutated family protein* (*ATM*) transcript was significantly induced without gamma-irradiation, however gamma-irradiation resulted in reduction of *ATM* transcript in OsJAC1-overexpressing lines. These results suggest that OsJAC1 may be associated with DNA damage response such as DNA replication and homologous recombination repair in plants.

P0062: Rice

Genetic Dissection of Antioxidant Activity in Indica Rice Grains using Genome-Wide Association Analysis

Jaesung Lee¹, Dmytro Chebotarov¹, Kenneth McNally¹, Myrlish Pacleb¹, Chia-Hsing Huang², Ruairaidh S Hamilton¹, Fiona Hay³ and Hei Leung¹, (1)International Rice Research Institute, Los Baños, Philippines, (2)Hualien District Agric. Research and Extension Station, Council of Agriculture, Taiwan, (3)Department of Agroecology, Aarhus University, Forsøgsvej 1, 4200 Slagelse, Denmark

Rice contains variable concentrations of bioactive compounds such as oryzanol, phenolics, and vitamin E. These compounds act as antioxidants, scavenging free radicals in human cells and thus preventing cellular damage that leads to disease. Identification of genetic markers associated with grain-antioxidants will be useful in breeding for functional rice.

In this study, we screened antioxidant activity in the grains of 240 Indica rice accessions held in the International Rice Genebank (IRG) at the International Rice Research Institute (IRRI). Seeds were harvested at 38 and 45 days after heading (DAH) to take into account the effect of maturity on grain-antioxidants. Through seed storage experiments, the sample with greatest longevity (or storability) was considered as physiologically-matured seeds and used for the antioxidant assay. A genome-wide association (GWA) mapping was conducted using the high-density single nucleotide polymorphism (SNP) data generated from the rice 3000 genome project.

Our initial results showed that a consistent major peak on chromosome 7 was associated with grain antioxidant activity. However, this peak is also strongly associated with seed pigmentation, reflecting relatively higher antioxidant activity of coloured rice than of non-coloured rice. We correct the confounding effects of the grain colour grouping and unravel novel candidate regions that were shadowed by the chromosome 7 peak.

P0064: Rice

Analysis of Genome Methylation and Gene Expression Associated with the Primary Seed Dormancy Release of Rice By Heat Stress

Suyeon Kim, Beom Gi Kim and In SUN Yoon, National Institute of Agricultural Sciences, Jeonju, South Korea

Seed dormancy is a highly variable agronomic trait affected by genetic and environmental factors. It has been known that acquisition and release of seed dormancy is affected by temperature changes. However, the molecular mechanism underlying the thermal regulation of seed dormancy is largely unknown. We previously found that the strong primary seed dormancy of rice seeds at 25 day after heading (DAH) is released by heat treatment and ripening. Transcriptomic analysis indicated that 28% of total 40,309 probes showed at least two-fold changes by heat stress in the seed embryos at 25 DAH, suggesting that global transcriptomic changes were induced by heat stress. DNA methylation is an epigenetic mechanism to control gene expression in response to environmental changes. Using BiSeq, a DMR (differentially methylated region) detecting approach within target regions, we identified DMRs in heat-stressed seed embryos at 25 DAH. The integrative analysis of transcriptome and genome-wide DNA methylation revealed that 57% of differentially expressed genes (DEGs) in heat-stressed seed embryos were associated with DMRs, and hypermethylated genes generally exhibited down-regulated tendency. Among the DMRs-associated DEGs, 2,367 genes were negatively correlated with methylation status, and further transcriptome analysis between 25 and 60 DAH seed embryos revealed that 12% of these genes also differentially expressed under seed ripening conditions. This suggests that these genes are potentially correlated with the primary seed dormancy release by changing DNA methylation status under both heat-stressed and seed ripening conditions. Supported by a grant PJ01321801.

P0065: Rice**Updates on Evolutionary Studies of Cultivated and Wild Rice Using Chloroplast Genome Sequencing**

Lin Cheng and Yong-Jin Park, Kongju National University, Chungnam, South Korea

Cultivated rice is divided in two subspecies, indica and japonica. The two hypotheses about their origin hold that they have independent and single origins, respectively. Many researches on the origin of rice have been conducted but have yet to draw a consensual conclusion on the origins of cultivated rice. We recently discovered interesting results supporting the independent origin hypothesis through a phylogenetic study of rice mitochondrial and chloroplast genomes, and we explored further to make more detailed observations. We sequenced chloroplast genomes of 60 cultivars including indica and japonica, 30 weedy and 74 wild rices, and identified 840 SNVs and 148 InDels. The phylogenomic analyses indicated that japonica and indica were clearly separated from wild rice by six diploid genome types, and evolutionary analyses revealed specific selection signatures on different and distinct regions of their chloroplast genomes, suggesting that different selection signatures might have been exerted upon indica and japonica during domestication.

P0067: Rice**Large-Scale Web Mining for Phenotypic Assessment of Korean Rice Genetic Stocks' Response to Rice Bacterial Blight**

Kyu-Won Kim and Yong-Jin Park, Kongju National University, Chungnam, South Korea

Rice bacterial blight is a disease caused by the bacterium *Xanthomonas oryzae pv. oryzae*, which occurs extensively throughout the world, especially in Southeast Asia. Genes associated with resistance to rice bacterial blight *Xa1*, *Xa5*, *Xa13*, *Xa21*, *Xa3/Xa26* and *Xa27* have been cloned and *Xa2*, *Xa4*, *Xa7*, *Xa30* and *Xa38* have been found on the rice genome. Among them, *Xa21* is known to be an RLK type and *Xa1*, *Xa27*, *Xa5* and *Xa13* are NBS-LRR types. As a preliminary study on the use of these resistance genes in bacterial blight resistance breeding, we collected large-scale data on the phenotypic assessment of rice bacterial blight using web data mining and obtained 1,380,564 phenotypic characteristics of 34,217 rice entities from public data sources. A total of 28,410 cumulative rice accessions had assessment data on K1, K2, K3, K3a and unknown strains. Most accessions were found to be susceptible to bacterial blight with leaf lesion lengths of 10.1cm or longer and there was no significant difference in susceptibility by year or strain, while a few resistant resources showed strong resistance with no lesions.

P0066: Rice**Indel Identification of Whole Genome and Related Alleles in Agricultural Traits from Next-Generation Resequencing Data of 294 Korean Rice Core Accessions**

Jungrye Nam and Yong-Jin Park, Kongju National University, Chungnam, South Korea

Indel in a gene is a sequence variation that is likely to cause functional change of the gene because it can cause frame shift in coding region. Therefore, indel information is of considerable importance in studies of gene function. Especially it is necessary to refer to the indel information in order to identify functional variants in the candidate gene after identifying the statistically related candidate genes from the genome-wide association study using SNPs. We identified the indel variants from the NGS resequencing data of 294 Korean rice core accessions (KRICE_CORE). In addition, 28 major genes controlling traits of agronomic importance in rice, such as grain size and yield, were selected and the indels in the genes were identified and characterized. The results showed that a large number of indels were identified in the genic region as well as in major genes related to agricultural traits such as yield and eating quality. Some of those indels in the major genes made frame shifts that can affect gene function.

P0068: Sheep**Signatures of Altitude Adaptation in Ethiopian Sheep Populations**

Zewdu Edea Bedada, Chungbuk National University, Chungcheongbuk-do, Korea, Republic of (South), Kwan-Suk Kim, Chungbuk National University, Cheongju, South Korea, Hailu Dadi, Addis Ababa Science and Technology University, Addis Ababa, Ethiopia and Dessie Tadele, International Livestock Research Institute, Addis Ababa, Ethiopia

Ethiopian sheep populations such as Menz (MZ, short fat-tailed), Arsi-Bale and Horro sheep (LFT, long fat-tailed) are adapted to the high-altitude (2000-3200m), whereas Blackhead Somali sheep (BHS) thrive well in a hot/dry climate (<1500m); and such variation in altitude can offer an opportunity for investigating livestock species genetic adaptation to extreme environments. However, there have been no studies conducted to identify signatures of selection for environmental adaptation in Ethiopian sheep populations. In this study, we genotyped a total of 60 animals sampled from high- versus low-altitude environments using an Ovine 600K chip; and scanned for genomic regions showing evidence of selection for environmental adaptation. Several signatures of selection was detected in genes known to be associated high altitude adaptation for MZ (*PRKAA1*, *SOCS2*, *TUBB3*, *CSRP2BP*, *TUBB3*, *SKIV2L2*, *DNAH9*, *PPP1R12A*, *SKA3*, and *TRHDE*) and for LFT (*ADRBK1*, *VAV3*, *HSF2*, *KIT*, *MC1R*, *ARHGAP28*, *CSRP2BP*, *BMP2*, *RNMT*, *LEP*, and *LEMD3*). Fourteen of the genes (*MITF*, *FGF5*, *PARP4*, *OVOL2*, *SLAIN1*, *IFT88*, *MMP28*, *PGD*, *RABGAP1L*, *SNX5*, *PAX1*, *TRHDE*, *BPIFB2*, and *SAMHD1*) were shared between the two sheep populations. Further functional enrichment analysis reveals that the candidate genes have GO terms relevant to adaptation under extreme environments, including regulation of metabolic process, response to nutrient levels, regulation of apoptosis and pigmentation. Altogether, our results aid further understanding and exploitation of the underlying genetic mechanisms for sheep and other livestock species adaptation to high-altitude environments.

Keywords: Adaptation, Ethiopian sheep, high-altitude, selection signatures

P0069: Swine**Genome-Wide Analysis of Histone Modifications in Pig Placental**

Kun Han¹, Mei Yu² and Shuhong Zhao², (1)Huazhong Agricultural University, China, China, (2)Huazhong Agricultural University, Wuhan, China
The placenta is of utmost importance for intrauterine fetal development and growth. The formation of dense networks of blood vessels and complex placental folds structure are important to improve placenta efficiency and support successful pregnancy. However, little is known about the cis-regulatory mechanisms underlying this important process. Here, we generated the genome-wide maps of H3K4me3 and H3K27ac of Meishan pig placenta trophoblast in day 50 and 95 of gestation using ChIP-seq and their high-coverage transcriptomes using RNA-seq. ChIP-seq analysis shown that in day 50 of gestation, 39,673 H3K4me3 and 15,268 H3K27ac regions were identified, and in day 95 of gestation, 26,101 H3K4me3 and 23,745 H3K27ac regions were identified. Differential enrichment analysis indicated that H3K4me3 and H3K27ac signals in many genomic regions was increased in day 95 of gestation, but decreased in only a few regions. There are 5,135 H3K4me3-increased regions located in the promoter regions (3 kb upstream or downstream of the transcription start site) and 1,823 H3K27ac-increased regions were located in enhancer regions (filtered out H3K27ac regions overlapping promoters of Ensembl genes (± 1 kb from transcription start sites/TSS), exons of known genes, and H3K4me3-enriched peaks (potential promoters) to define enhancer region). Finally, integration of RNA-seq data found that 1,993 promoter regions and 646 enhancer regions were involved in the regulation of gene expression. Further function enrichment analysis revealed genes with the promoter or enhancer regions were associated with the placental angiogenesis. Taken together, our work identified histone modification statuses on a genome-wide basis change in pig placenta trophoblast during placental development. The main changes of histone modifications are involved in gene expression associated with angiogenesis. Our results can provide new insights for placental development mechanism.

P0070: Swine**Production of Tumor-Inducible Piglets with EGFP Expression**

Seon-Ung Hwang¹, Kiyoung Eun², Junchul D. Yoon¹, Hyunggee Kim² and Sang-Hwan Hyun¹, (1)Chungbuk National University, Cheongju, South Korea, (2)Korea University, Seoul, South Korea
Large animal cancer models are needed to develop innovative and clinically applicable tumor diagnostic, therapeutic and monitoring technologies. In this study, we developed a genetically modified porcine model of cancer based on a CreER^{T2} (a Cre recombinase fused to the mutated ligand-binding domain of the human estrogen receptor) induction system. We made a vector structure. This is a 2A peptide-dependent polysitronic expression construct carrying the DsRed, SV40LT and HrasV12 genes after CreER^{T2}-related recombination. The vector was transfected into fetal yucatan mini-pig cell line. Whether the introduction of the transgenes are confirmed by PCR. The somatic cell nuclear transfer was performed using the transgenic (TG) cell line and then embryo transfer into a surrogate mother pig. As a result, five transgenic piglets were born. Analysis of umbilical cord gDNA showed that all 5 piglets were transfected. EGFP expression was confirmed in all cell lines established by primary culture of umbilical cord tissue. Expression was also confirmed in live TG piglets. This means that the system has been introduced in all transgenic piglets and the oncogenes are not yet expressed. Further studies are needed to induce oncogene expression by *in vitro* and / or *in vivo* editing via the Cre/LoxP inducible system.
This work was supported by a grant from the “National Research Foundation of Korea Grant funded by the Korean Government (NRF-2017R1A2B4002546)” and “The Global Research and Development Center (GRDC) Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education, Science and Technology (2017K1A4A3014959)”, South Korea.

P0071: Tomato, Potato, Pepper, and related**Exploring Genetic Diversity of Ethiopian Capsicum Landrace Collection**

Solomon A. Mekonnen, SNU (Seoul National University), Seoul, South Korea
Knowledge on population structure and genetic diversity is essential for association mapping studies and genomic selection. A collection of 142 genotypes from different geographical areas of Ethiopia was established with the aim of capturing a wide diversity. Nineteen morphological traits related to mainly growth features were evaluated. Significant differences within most measured growth parameters were detected among pepper lines. Architecturally, while the majority of germplasm (73%) have spreading to half spreading growth habit, 26% were erect. One line showed fasciculate growth habit. Genotypes were classified into three groups based on plant height: group I (28% of the total) measured 48-89 cm, the majority (62%) belongs to group II (90-131 cm) and the remaining 14% belongs to group III (132-175 cm). The result of the principal component analysis (PCA) showed that the first five principal component axes explained 50.4% of the total variations in the capsicum accessions. The first component (PC1) explained 16.1% of the variation and was mainly associated to plant height, internode length, stem thickness and main stem length. The second component (PC2) explained 11.2% of the total variation and was basically defined by petal length, petal width, number of petal, stem thickness and color. Sixteen fruit quality related traits have also been studied, and genotyping-by -sequencing was employed to evaluate the genetic basis of variation between Ethiopian *Capsicum* lines. Morphological and genetic diversity of the present collection can be further exploited as potential resources in future.

P0072: Tomato, Potato, Pepper, and related**Development of Gene-Based Markers for the Ovate Gene in Cultivated Tomato**

Hyunjung Kim, Yonam College, South Korea

Tomato fruit shape, which is the most visible characteristic among the other fruit trait, is considered to have a substantial influence on consumers. *OVATE* determines the conversion from round to pear-shaped fruit in tomato. It is caused by a single non-sense, recessive, mutation which results in premature stop codon and elimination of the conserved C-terminal domain of its predicted protein, and consequently its loss-of-function. *OVATE* is expressed primarily in reproductive organs and its transcripts can be detected in flowers 10 days before anthesis and until 8 days after anthesis in developing fruit. However linked marker of *OVATE* had been reported, in this study we found SNPs within *OVATE* gene nucleotide sequence of the domestic breeding lines by re-sequencing and developed a derived cleaved amplified polymorphic sequence (dCAPS) markers. Developed dCAPS markers is helpful to discriminate of *OVATE* gene variation. These molecular markers are expected to enhance the efficiency and accuracy of selection round and pear-shaped fruit tomato breeding programs.

P0073: Tomato, Potato, Pepper, and related**Clarification of the Genome Structure of Micro-Tom, a Model Cultivar of Tomato (*Solanum lycopersicum*)**

Hideki Nagasaki¹, Kenta Shirasawa¹, Sachiko Isobe¹, Pierre Baldet², Christophe Rothan³, Mohamed Zouine⁴, Koh Aoki⁵ and Hideki Hirakawa¹, (1)Kazusa DNA Research Institute, Kisarazu, Japan, (2)Functional Genomics of Fruit Development, UMR 1332 – INRA, Villenave d'Ornon, France, (3)INRA UMR, Villenave d'Ornon, France, (4)INPT-ENSAT, Toulouse, France, (5)Osaka Prefecture University, Sakai, Japan

Micro-Tom is one of the cultivar of tomato (*Solanum lycopersicum*), which is known as a major crop and model plant in Solanaceae. Micro-Tom has phenotypic traits such as *dwarf*, and substantial EMS-mutagenized lines have been reported. There are two Micro-Tom varieties, which are Micro-Tom S9 and Micro-Tom MM, that have been maintained independently in Japan and France. Since the whole genome sequencing of Heinz 1706 had been determined, the genome sequence of Micro-Tom was determined by reference guided assembly using 454 FLX reads. To reveal detailed genome structure of Micro-Tom, we have conducted *de novo* assembly of Micro-Tom S9 by adding Illumina MiSeq reads. We obtained the 69M paired-end reads and 269M mate-pair reads. The total coverage was estimated as 63-fold of the Micro-Tom genome. The reads were assembled by MaSuRCA-2.3.2, and BAC end sequences of Micro-Tom S9 were used for scaffolding by SSPACÉ v2.0, and finally 2,925 scaffolds were constructed (named SLM_r1.1). On the other hand, the high quality pseudomolecule of Micro-Tom MM (Sol_mic1.0) has been built using the optical mapping of BioNano and long read sequencing of Chromium 10x and PacBio by INRA group of France. The scaffolds of SLM_r1.1 were mapped to Sol_mic1.0 by NUCmer in MUMer3.23, and 640 of them were chosen under the condition of 50% length coverage, and then we built a pseudomolecule of Micro-Tom S9. Furthermore we performed SNP and copy number variation (CNV) analyses between Sol_mic1.0 and the 5 Micro-Tom varieties (FRA, BRA, JPN, NIVTS, and USA).

P0075: Tomato, Potato, Pepper, and related**RNA-Seq Analysis of Pepper Containing the *Tsw* Gene at High Temperature Conditions Provides Insight into the Resistance Breaking Mechanism**

Joung-Ho Lee¹, Bong-Nam Chung², Min-Young Kang³ and Byoung-Cheorl Kang³, (1)Seoul National University, Seoul, Korea, Republic of (South), (2)National Institute of Horticultural & Herbal Science, Wanju, Korea, Republic of (South), (3)Seoul National University, Seoul, South Korea
Tomato spotted wilt virus (TSWV) is the threatening virus resulting in the great yield loss of pepper worldwide. For this reason, the TSWV resistance gene, *Tsw*, has been identified and used to breed TSWV resistant cultivars. However, this resistance is known to be broken at high temperature conditions. To dissect the resistance breaking mechanism of *Tsw* at high temperature, RNA-seq analysis was performed in two different temperature conditions, 25°C and 30°C for 'PI152225' carrying the *Tsw* gene. At 25°C hypersensitive resistance (HR) was observed, but not at 30°C upon TSWV inoculation. Comprehensive RNA-seq expression profiles revealed that 310 differentially expressed genes (DEGs) are involved in temperature dependent TSWV resistance together with several disease-resistance genes. Gene Ontology analysis showed that most of the DEGs were represented in DNA binding and catalytic activity for molecular function. Our analysis will uncover the molecular genetic pathways of the temperature-sensitive resistance breaking mechanism in pepper.

P0074: Tomato, Potato, Pepper, and related**Broad Role of Pepper Natural Antisense Transcripts in Development and Stress Response Revealed By PacBio Full-Length cDNA Sequencing**

Jubin Wang, Huazhong Agricultural University, Wuhan, China
Pepper (*Capsicum annuum*) is one of the most important vegetable crops in the world. Two major pepper reference genomes of variety CM334 and Zunla were published in recent years. Knowledge about complete transcript sequence is important in understanding gene regulation. However, previous annotations mostly pay attention to the coding protein region due to limitation in annotation methods and mRNA sequencing data. In this study, we used PacBio full-length cDNA sequencing to improve the annotation of pepper, and obtained more complete UTR region and more precise gene splice. Totally, we found 57204 PacBio isoforms containing 18368 previous zunla annotation genes and 5769 novel genes. Interestingly, among of them, 511 fusion genes were deemed to multiple partial transcripts, divided by long introns. Besides, 1765 cis-acting natural antisense transcripts (cis-NATs) paired-genes were detected. And 4369 trans-acting natural antisense transcripts (trans-NATs) gene groups were discovered through its partial complementary sequence, which has a largest proportion of TEs (43.1%, 2720 of 6308). Moreover, small RNA reads from various tissues were enriched in the overlapping regions. And RNA-seq data in various developmental stage, abiotic stress and phytohormone response, revealed that multiple genes function through natural antisense transcripts. By cis-NATs analysis of monocots species (rice) and eudicots species (*Arabidopsis*, tobacco, potato and tomato). We found that there were number of bursts between dicots (*Arabidopsis*) and Solanaceae (tobacco) in divergence of eudicots, and many ancient cis-NATs were conserved since the divergence between eudicots and monocots. Taken together, our results demonstrate that PacBio cDNA sequencing is highly powerful in discovery of functional NATs that regulating development, abiotic stress and plant hormone response.

P0076: Tomato, Potato, Pepper, and related**Fine Mapping of the *A2* Locus That Regulates Fruit-Specific Anthocyanin Regulation in Pepper**

Soyoung Jung¹, Koeun Han¹, Seungki Back², Jin-Kyung Kwon³ and Byoung-Cheorl Kang³, (1)Seoul National University, Seoul, Korea, Republic of (South), (2)Seoul National University, South Korea, (3)Seoul National University, Seoul, South Korea
Anthocyanins are natural flavonoid compounds found in leaves, flowers, and fruits. Because of their benefits for human being, a lot of research has been done on anthocyanin in various plants. In pepper (*Capsicum spp.*), the *A* gene, an R2R3 MYB transcription factor, has been identified to regulate anthocyanin accumulation in the foliage, flowers and immature fruits. However, we found the fruit-specific purple colored pepper in our germplasm. To identify the *A2* locus that regulates fruit-specific anthocyanin accumulation in pepper, we conducted genotyping-by-sequencing (GBS) using two different restriction enzymes, *EcoRI* and *MseI*. Total 279,865 SNPs were detected and high quality SNPs were called using GATK UnifiedGenotyper with minimum sequencing depth 3 and quality score 30. A total of 18,342 filtered SNPs were used to construct high-density genetic map. The *A2* locus was mapped to chromosome 10. Using the GBS data, we developed CAPS marker and HRM markers for the purple fruit color that co-segregate with phenotype. Markers linked to the fruit-specific anthocyanin accumulation will be useful to breed highly anthocyanin pigmented peppers.

**P0077: Tomato, Potato, Pepper, and related
Differential Expression Analysis of RNA-Seq with Respect to Capsaicinoid Biosynthesis in the Pericarp Tissue of *Capsicum chinense***

Minjeong Park¹, Joung-Ho Lee², Koeun Han², Byoung-Cheorl Kang³ and PAG author RNASeq, (1)Seoul National University, Seoul, South Korea, (2)Seoul National University, Seoul, Korea, Republic of (South), (3)Seoul National University, Seoul, South Korea

Pungency is a distinct characteristic of hot pepper fruits and is caused by the alkaloid compounds known as capsaicinoids. The biosynthesis of these compounds was known to exclusively occur in epidermal cells in the interlocular septa (placenta) in pepper fruits. However, extremely pungent pepper such as *C. chinense* 'Trinidad Moruga Scorpion' shows the accumulation of capsaicinoids in the pericarp tissue as well as the placenta, leading to the elevation of capsaicinoid content in the whole fruit. The goal of the present study was to identify putative genes involved in controlling capsaicinoid biosynthesis in the pericarp by analyzing changes in global gene expression patterns. RNA-seq was used to analyze the expression profiles in the pericarp tissue over three developmental stages of three *Capsicum* cultivars with different capsaicinoid content: a highly pungent cultivar *C. chinense* 'Trinidad Moruga Scorpion', a pungent cultivar *C. chinense* 'Habanero', and a non-pungent *C. annuum* 'Early Calwonder (ECW)'. Changes in gene expression patterns were determined by comparing two cultivars at each developmental stages: 18 days after pollination (DAP), 34 DAP, and 45 DAP. We identified genes differentially expressed in the pericarp of 'Scorpion' compared to 'Habanero' 1,437, and 1,717, and 676 were up-regulated while 1,195, 1,313, and 654 were down-regulated at 18, 34, and 45 DAP, respectively. Additionally, to functionally categorize DEGs, these DEGs were mapped to terms in the KEGG database. Furthermore, we analyzed the expression patterns of 12 genes of known function in the capsaicinoid biosynthesis pathway. Multiple genes including *Pun1*, *pAMT* and *KAS* were up-regulated in the pericarp of 'Scorpion'. Increasing capsaicinoid content is an important objective of pepper breeding. Our comprehensive transcriptional overview will be helpful for revealing genes involving capsaicinoid biosynthesis in the pericarp, and thus enhancing the capsaicinoid content in the whole fruit.

**P0079: Wheat, Barley, Oat, and related
Localization and Study of Interactions of B-Genome Genes Inducing Flowering of Common Wheat**

Antonina A. Kiseleva and Elena A. Salina, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russian Federation

The study of B-genome genes of common wheat, associated with flowering, the mechanisms of their regulation and interactions is important for wheat adaptation. Using different marker systems (SSR and SNP), loci on the B-genome of common wheat associated with flowering time were localized on the short arm of the 2B chromosome and in the pericentromeric region of 5B chromosome. The genes located in the identified loci were investigated.

Locus on the 2BS contains *Ppd-B1a^{emv}* allele, increased copy number of which accelerate flowering. Sequences of gene copies were equal, but the identified SNPs and indel distinguished the *Ppd-B1a^{emv}* and other *PPD-B1* alleles. In the locus on the pericentromeric region of 5B chromosome candidate genes *WRKY*, *ERF/AP2*, *FHY3/FAR1* and *ELF4* are identified. These genes are known to influence flowering in model species.

Analysis of the diurnal expression suggests that *Ppd-B1a^{emv}* is expressed during night period and positively regulates *PHYC* expression. Transcription factor *FHY3/FAR1*, located on 5B chromosome, may contribute to the interaction of *PPD-B1* and *PHYC* of common wheat. Therefore, we propose that there is a positive bidirectional regulation of *Ppd-B1a^{emv}* and *PHYC* with a putative *FHY3/FAR1* contribution.

Acknowledgements. This study was supported by the RSF (No. 14-14-00161).

**P0078: Tomato, Potato, Pepper, and related
Mutation Breeding Platform Based on Irradiation in Pepper**

Yeong Deuk Jo¹, Sang Woo Lee², Sang Hoon Kim³, Han Sol Kang³, Se Won Kim¹, Sun-Young Kim¹, Jaihyunk Ryu², Jin-Baek Kim¹ and Si-Yong Kang¹, (1)Korea Atomic Energy Research Institute, Jeongeup, South Korea, (2)Chonnam National University, Gwangju, South Korea, (3)Korea Atomic Energy Research Institute, South Korea

Mutation breeding systems have been widely used for development of useful genetic resources and cultivars in diverse crops. In pepper, we have been constructing mutation populations and optimizing mutation breeding technologies for development of an efficient mutation breeding platform. Firstly, mutant populations have been developed in *Capsicum annuum* and *C. chinense*, respectively, through irradiation of gamma-rays or carbon ion beams. These populations consist of a total of 4,490 and 1,666 M₂-M₃ individuals of *C. annuum* (original cultivar: Yuwolcho) and *C. chinense* (original cultivar: Habanero), respectively. Secondly, a TILLING system based on capillary electrophoresis has been optimized for efficient and less labor-intensive screening of mutants carrying mutations on the target genes. Using this system, the screening of mutants without using an acrylamide gel or labeled primers in 4-16x pools is possible according to the length of the target sequence. Finally, we are testing new radiation sources and target tissues subjected to irradiation to increase efficiency of mutation induction. We have developed pepper mutants by irradiation of a new radiation source, proton beam. In addition, we obtained M₃ populations derived from crosses using male or female reproductive tissues mutated by gamma-irradiation. GBS (genotyping by sequencing) analyses are on-going for plant materials from each study.

**P0080: Wheat, Barley, Oat, and related
Evaluations and Selections for Colored-Wheat Mutants Induced By Gamma Irradiation**

Min Jeong Hong¹, Dae Yeon Kim², Hong-Il Choi¹, Yeong Deuk Jo¹, Sang Hoon Kim¹, Soon-Jae Kwon¹, Joon-Woo Ahn¹ and Jin-Baek Kim¹, (1)Korea Atomic Energy Research Institute, Jeongeup, South Korea, (2)Korea University, Seoul, Korea, Republic of (South)

To improve human health and prevent diseases, aim of breeding program has mainly focused on increasing the antioxidant capacity such as anthocyanin and phenolic compounds in grains. Mutation breeding is a useful tool to generate new genetic resources by improving existing elite varieties. To broaden genetic diversity in colored-wheat seed (K4191; purple color), gamma-ray was used as physical mutagen in this study. Based on selection criteria such as grain color and agronomic trait, five novel mutant lines were selected from the population. The selected wheat mutant lines (L47, L85, L167, L567, and L925) showed a extensive variation in seed color, ranging from light to dark in purple color. Seeds of L925 were the darkest ($L^* = 17.32 \pm 3.16$), whereas those of 'Keumkang' (white color) ($L^* = 57.33 \pm 3.22$) were the lightest. The total anthocyanin contents of three mutant lines (L47, L167, and L925) were significantly higher than those of wild-type lines, including K4191 and 'Keumkang'. And also, radical scavenging activity was shown the highest in L925. Total phenol content of wheat mutants with dark-colored seeds was higher than that of light-colored seeds. Significant differences were observed in the concentrations of anthocyanin, total phenol and antioxidant activity among colored-wheat mutant with higher values obtained for seeds with purple colors, and a positive correlation between these parameters was found.

P0081: Wheat, Barley, Oat, and related

MSD1 Regulates Pedicellate Spikelet Fertility in Sorghum through the Jasmonic Acid Pathway

Young Koung Lee, Cold spring harbor lab., Cold spring harbor, NY; Wonkwang University, Iksan, South Korea, Yinping Jiao, USDA-ARS/Cold Spring Harbor Laboratory, Lubbock, TX, Nicholas Gladman, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, Ratan Chopra, USDA-ARS, Lubbock, TX, Shawn A. Christensen, USDA-ARS, Gainesville, FL, Soon Ju Park, Institute for Basic Science, Wonkwang University, Jeonbuk, South Korea, Zhanguo Xin, USDA ARS, Lubbock, TX and Doreen Ware, USDA/ARS - Cold Spring Harbor Laboratory, Cold Spring Harbor, NY Grain number per panicle (GNP) is a major determinant of grain yield in cereals. However, the mechanisms that regulate GNP remain unclear. To address this issue, we isolate a series of sorghum [*Sorghum bicolor* (L.) Moench] multiseeded (msd) mutants that can double GNP by increasing panicle size and altering floral development so that all spikelets are fertile and set grain. Through bulk segregant analysis by next-generation sequencing, we identify MSD1 as a TCP (Teosinte branched/Cycloidea/PCF) transcription factor. Whole-genome expression profiling reveals that jasmonic acid (JA) biosynthetic enzymes are transiently activated in pedicellate spikelets. Young msd1 panicles have 50% less JA than wild-type (WT) panicles, and application of exogenous JA can rescue the msd1 phenotype. Our results reveal a new mechanism for increasing GNP, with the potential to boost grain yield, and provide insight into the regulation of plant inflorescence architecture and development.

P0082: Wheat, Barley, Oat, and related

Development of Resources for Mapping, GWAS and Allele Mining in Tetraploid Wheat Based on Svevo Durum Reference Sequence

Marco Maceferri¹, Raj K Pasam², Anna-Maria Mastrangelo³, Elisabetta Mazzucotelli⁴, Reem Joukhadar⁵, Francesca Desiderio⁶, Sara G. Milner⁷, Danara Ormanbekova⁸, Silvio Salvi⁹, Roberto Tuberosa¹⁰, Neil Harris¹¹, Gabriella Sonnante¹², Benjamin Kilian¹³, Assaf Distelfeld¹⁴, Nicola Pecchioni¹⁵, Pasquale De Vita¹⁶, Curtis Pozniak¹⁷, Stephen Xu¹⁸, Shiaoanm Chao¹⁸, Matthew Hayden⁷ and Luigi Cattivelli¹⁹, (1)University of Bologna, DISTAL, Bologna, Italy, (2)DEDJTR, Biosciences Research, AgriBio, Melbourne, Australia, (3)CREA-MAC, SS42, 24126 Bergamo, Foggia, Italy, (4)CREA-GB, Fiorenzuola d'Arda, Italy, (5)DEDJTR, AgriBio, Bundoora, Australia, (6)CRA Genomics Research Centre, Fiorenzuola d'Arda, Italy, (7)IPK Gatersleben, Stadt Seeland, Germany, (8)DipSA, University of Bologna, Bologna, Italy, (9)DipSA - University of Bologna, Bologna, Italy, (10)DISTAL, University of Bologna, Bologna, Italy, (11)University of Alberta, Edmonton, AB, Canada, (12)IBBR, Italy, (13)The Global Crop Diversity Trust (GDCT), Bonn, Germany, (14)Tel Aviv University, Israel, Tel Aviv, Israel, (15)CREA - Research Centre for Cereal and Industrial Crops, Foggia, Italy, (16)CREA - Cereal Research Centre, Foggia, Italy, (17)University of Saskatchewan, Saskatoon, SK, Canada, (18)USDA-ARS, Fargo, ND, (19)CREA - Research Centre for Genomics and Bioinformatics, Fiorenzuola d'Arda, Italy The assembled Svevo durum wheat genome and the iSelect wheat 90K SNP array were used as a base to characterize a world-wide tetraploid wheat collection. We report on the diversity pattern of 1,854 non-redundant accessions from all known *Triticum turgidum* subspecies. The genetic diversity survey relied on a common genotype-calling pipeline from AgriBio supported by 17 tetraploid linkage maps. The pipeline yielded 17,416 informative single-locus SNPs anchored to the Svevo genome. Among the wild emmer (WEW), domesticated emmer (DEW), durum wheat landraces (DWL) and durum wheat cultivars (DWC), WEW showed the highest and uniform diversity across the whole genome, providing a reference for cross-comparison with DEW, DWL and DWC. Extended diversity depletions associated to domestication were found particularly in pericentromeric regions. Some 38.2% of DW genome was affected by strong genetic bottleneck/selection events leading to diversity depletions. Six extended regions showed increased genetic diversity associated to DEW-DWL and DWL-DWC transitions. Population structure revealed multiple subsequent events of population differentiation associated to human-driven dispersal routes. This analysis provides the basis for a more informative re-sequencing towards a tetraploid pan-genome. Sub-panels have already been used for GWAS analysis, allowing us to identify GWAS-QTL that can be readily used in breeding. GWAS-QTLs for grain yield components (grain size and grain number per spike) have been identified using a subpanel of Mediterranean DW landraces. These resources allowed us to map QTLs at an improved resolution (1 cM confidence interval) and readily scan the genome for underlying candidate genes.

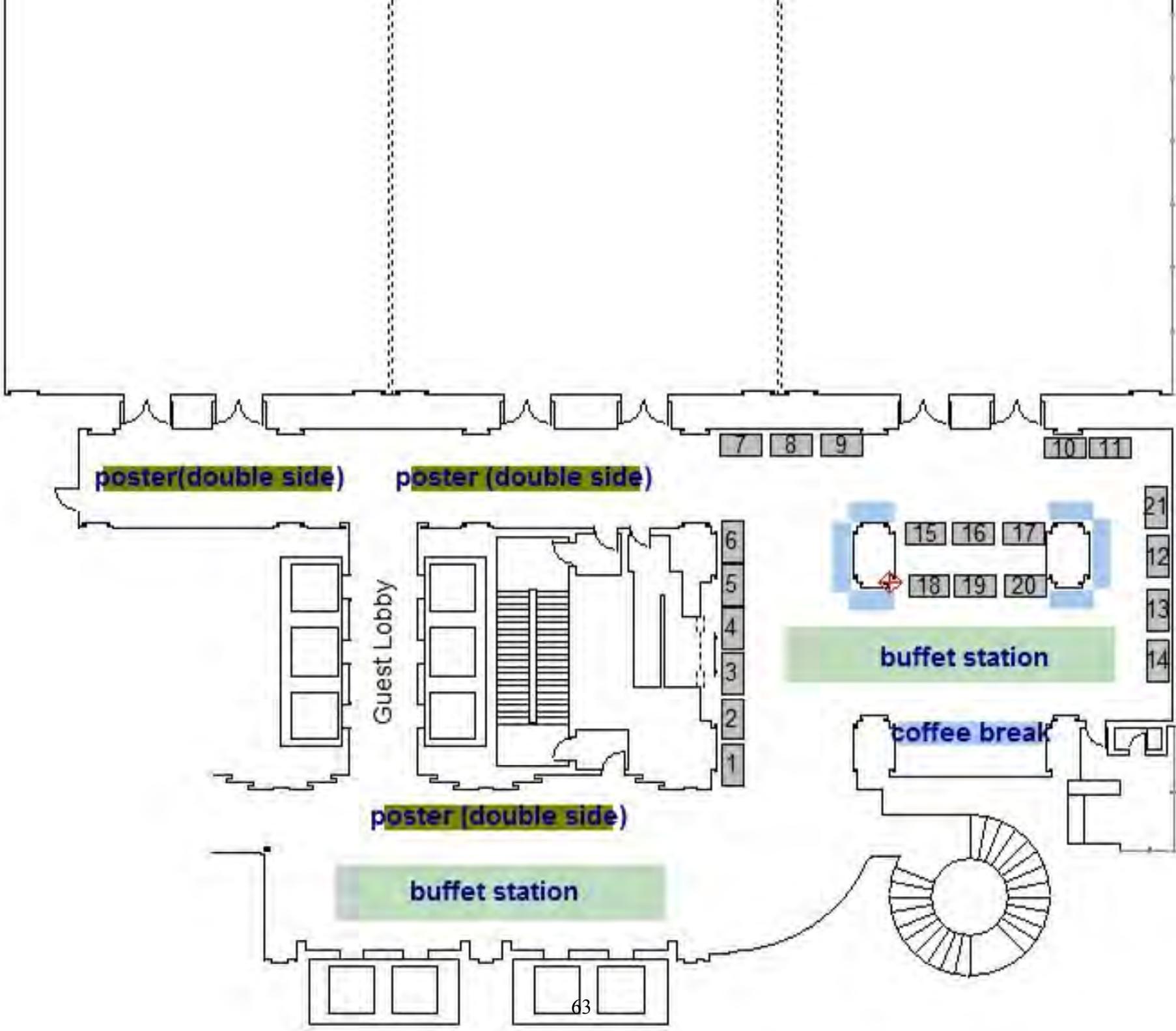
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