Co-Chairs

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NIH, USA

ZHONGLIN TANG
Agricultural Genome Research Institute, Chinese Academy of Agricultural Sciences (CAAS), China

XUN XU
BGI - Shenzhen, China

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USDA/ARS/CICGR, USA

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John Innes Centre, United Kingdom

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Iowa State University, USA

RAJEEV K. VARSHNEY
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India

QIFA ZHANG
Huazhong Agricultural University, China

SHU-HONG ZHAO
Huazhong Agricultural University, China

Corporate Sponsors

Berry Genomics
BGI
Dovetail Genomics
Genomeweb
Illumina
LGC, Biosearch Technologies
NRgene
PacBio
Thermo Fisher Scientific

MEETING MANAGEMENT
Scherago International
184 S. Livingston Ave, Ste 9, #184
Livingston, NJ 07039, USA
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Email: pagasia@scherago.com
Website: www.intipagasia.org
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Mark Your Calendar for:

Plant & Animal Genome XXVIII
   January 11-15, 2020
   Town & Country Hotel
      San Diego, CA

Plant & Animal Genome Asia 2020
   June 4-6, 2020
      Shenzhen, China
Registration – GRAND BALLROOM FOYER

Thursday - Friday       June 6-7       8:00am - 5:00pm
Saturday               June 8         8:00am - 12:00pm

Plenary Lectures – GRAND BALLROOM

Thursday - Saturday     June 6-8       9:00am - 10:30am

Scientific/Industry Workshops - GRAND BALLROOM 1, 2, 3

Thursday - Saturday     June 6-8       11:15am - 1:00pm
                        2:00pm - 3:45pm
                        4:00pm - 5:45pm (Sat only)
                        4:30pm - 6:15pm
                        6:30pm - 8:15pm (Thurs/Fri Only)

Meeting ends at 5:45pm on Saturday, June 8.

Lunch - GRAND BALLROOM FOYER

Thursday - Saturday     June 6-8       1:00pm - 2:00pm

Poster Sessions - GRAND BALLROOM FOYER

Friday                  June 7         10:30am - 11:15am
                        3:45pm - 4:30pm

ALL POSTERS MUST BE REMOVED BY 3:00PM WEDNESDAY, JUNE 8.

Exhibit & Poster Hours - GRAND BALLROOM FOYER

Thursday - Friday       June 6-7       10:30am - 4:30pm
Saturday               June 8         10:30am - 2:00pm
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<th>Time</th>
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<tr>
<td>8:00am - 5:00pm</td>
<td>Registration - GRAND BALLROOM FOYER</td>
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</table>
| 9:00am - 9:45am | Plenary Lecture: Xuewei Chen - "Exploration and Utilization of Rice Resources with Broad-Spectrum Resistance Against Blast Disease" - GRAND BALLROOM  
Chair: Shuhong Zhao, Huazhong Agricultural University |
| 9:00am        | Xuewei Chen, Sichuan Agricultural University                        |
|              | "Exploration and Utilization of Rice Resources with Broad-Spectrum Resistance Against Blast Disease" |
| 9:45am - 10:30am | Plenary Lecture: Ning Yang - "Genetic and Genomic Studies of Economically Important Traits of Chickens and Their Application to Breeding" - GRAND BALLROOM  
Chair: Xun Xu, BGI-Shenzhen |
| 9:45am        | Ning Yang, China Agricultural University                           |
|              | "Genetic and Genomic Studies of Economically Important Traits of Chickens and Their Application to Breeding" |
| 10:30am - 11:15am | Coffee Break / Exhibits / Posters - GRAND BALLROOM FOYER            |
| 10:30am - 4:30pm | Exhibits & Posters Open - GRAND BALLROOM FOYER                     |
| 11:15am - 1:00pm | Illumina: Accelerating plant and animal genomic breakthroughs - GRAND BALLROOM 3  
Organizers: Hui Guo, Illumina Trading (Shanghai) Co., Ltd. Beijing Branch and Youpei Cao, illumina China |
<p>| 11:15am       | Lisa G Eldridge, Illumina, Inc.                                    |
| 11:25am       | Fasong Zhou, Wuhan Greenfafa Institute of Novel Genechip R&amp;D Co., Ltd. |
|              | &quot;Applications of SNP Arrays to the Development of Green Super Rice&quot; |
| 11:50am       | André Eggen, Illumina                                              |
|              | &quot;The Power of Genomics in Agriculture&quot;                             |
| 12:10pm       | Zewdu Edea Bedada, Chungbuk National University                     |
|              | &quot;Genomics to Unravel the Genetic Diversity and Adaptation of Ruminants to Extreme Environments&quot; |
| 12:35pm       | Jason Cruz, Illumina                                               |
|              | &quot;Challenges and Opportunities with Genomic Tools in Agriculture.&quot;   |</p>
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<tr>
<th>Time</th>
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<tr>
<td>11:15am - 1:00pm</td>
<td>DNA Zoo - GRAND BALLROOM 1</td>
<td>Organizer: Parwinder Kaur, Univ. of Western AU Co-Chair: Erez Lieberman Aiden, Baylor College of Medicine</td>
</tr>
<tr>
<td>11:15am</td>
<td>Erez Lieberman Aiden, Baylor College of Medicine</td>
<td>&quot;Genome Assembly at the DNA Zoo: Affordable, Accurate and Open-Source&quot; (W011)</td>
</tr>
<tr>
<td>11:35am</td>
<td>Olga Dudchenko, Baylor College of Medicine</td>
<td>&quot;3D-DNA, an Automated Pipeline to Assemble Genomes&quot; (W012)</td>
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<tr>
<td>11:55am</td>
<td>Parwinder Kaur, Univ. of Western AU</td>
<td>&quot;DNA Zoo Australia&quot; (W013)</td>
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<tr>
<td>12:15pm</td>
<td>Lichun Jiang, Shanghai Tech</td>
<td>&quot;DNA Zoo China&quot; (W014)</td>
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<tr>
<td>12:35pm</td>
<td>Sarah Kocher, Princeton University</td>
<td>&quot;Convergent Evolution of Social Behavior in Sweat Bees&quot; (W015)</td>
</tr>
<tr>
<td>11:15am - 1:00pm</td>
<td>Translational Genomics - GRAND BALLROOM 2</td>
<td>Organizers: Rajeev K Varshney, ICRISAT and Xin Liu, Beijing Genomics Institute-Shenzhen</td>
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<tr>
<td>11:15am</td>
<td>Pei Xu, Zhejiang Academy of Agricultural Sciences</td>
<td>&quot;Leveraging Genomic Resources to Secure Quality and Climate-Resilient Vegetable Cowpea Breeding&quot; (W098)</td>
</tr>
<tr>
<td>11:35am</td>
<td>Weichang Yu, College of Life Sciences, Shenzhen University</td>
<td>&quot;Transcriptome Analysis of Genes Involving in Zn2+ Response during Peanut Seed Germination&quot; (W099)</td>
</tr>
<tr>
<td>11:55am</td>
<td>Ruilian Jing, Institute of Crop Science, CAAS</td>
<td>&quot;Genetic Dissection of Agronomic Traits and Multiple Abiotic Stress Tolerances at Terminal Stage in Wheat&quot; (W100)</td>
</tr>
<tr>
<td>12:15pm</td>
<td>Boshou Liao, Oil Crops Research Institute</td>
<td>&quot;Next Generation Sequencing Identified Genomic Region and Diagnostic Markers for Resistance to Bacterial Wilt in Peanut&quot; (W101)</td>
</tr>
<tr>
<td>12:35pm</td>
<td>Himabindu Kudapa, ICRISAT</td>
<td>&quot;A High Resolution Gene Expression Atlas in Chickpea: Implications in Crop Improvement&quot; (W102)</td>
</tr>
<tr>
<td>1:00pm - 2:00pm</td>
<td>Lunch - GRAND BALLROOM FOYER</td>
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Thursday - June 6, 2019

2:00pm - 3:45pm  Ruminants Genomics - GRAND BALLROOM 2
Organizer: Yi Zhang, College of Anim. & Tech., China Agricultural University

2:00pm  Jian-Lin Han, CAAS-ILRI Joint Lab, Inst. of Anim. Sci., CAAS
"Recent Advances in Yak Genomics" (W077)

2:15pm  Qingyou Liu, Guangxi University
"Comparison of Long Non-Coding RNA Expression Profiles of Cattle and Buffalo Differing in Muscle Characteristics" (W078)

2:30pm  Yi Zhang, College of Anim. & Tech., China Agricultural University
"Whole-Genome Resequencing Reveals Selection Signatures for Body Size in Chinese Buffalo" (W079)

2:45pm  Xuexue Liu, Institute of Animal Science, CAAS
"Whole-Genome Sequencing Reveals the Genetic Mechanisms Underlying the High-Altitude Adaptation in Tibetan Horses" (W080)

3:00pm  Kwan-Suk Kim, Chungbuk National University
"Strong Signatures of Selection in Three Korean Cattle Breeds Exposed to Different Selective Pressures" (W081)

3:15pm  Taehyung Kwon, Seoul National University
"Evolutionary Signatures of the Mitochondria – Nucleus Conflict in African Cattle Admixture" (W082)

2:00pm - 3:45pm  Wheat Genomics, Genetic Diversity, Evolution and Domestication History - GRAND BALLROOM 1
Organizers: Shifeng Cheng, Agricultural Genomics Institute at Shenzhen, CAAS and Hong-Qing Ling, Institute of Genetics and Developmental Biology, CAS

2:00pm  Shifeng Cheng, Agricultural Genomics Institute at Shenzhen, CAAS
"A Total Diversity Map for Polyploidy Crop: What It Looks like?" (W103)

2:20pm  Song Weining, Northwest A&F University
"Genome-Wide Sequence Analysis of Wild and Cultivated Emmer" (W104)

2:40pm  Hong-Qing Ling, Institute of Genetics and Developmental Biology, CAS
"The Genome of Triticum urartu and Its Comparative Analysis" (W105)

3:00pm  Zhengqiang Ma, Nanjing Agricultural University
"Map-Based Cloning of Fhb1 Revealed Unique Mutation of a Well-Conserved Gene Resulting in Resistance to Wheat Fusarium Head Blight" (W106)

3:20pm  Bao Liu, Northeast Normal University
"Genetic Instability in a Synthetic Tetraploid Wheat (AADD) Revealed By Genome Resequencing" (W107)
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<tr>
<th>Time</th>
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<tr>
<td>2:00pm - 3:45pm</td>
<td>PacBio: Sequence with Confidence - How SMRT Sequencing is Accelerating Plant and Animal Genomics - GRAND BALLROOM 3 Organizer: Zuwei Qian, PacBio</td>
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<td>3:45pm - 4:30pm</td>
<td>Coffee Break / Exhibits / Posters - GRAND BALLROOM FOYER</td>
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<td>4:30pm - 6:15pm</td>
<td>LGC, Biosearch Technologies: Together we innovate agrigenomics - GRAND BALLROOM 3 Organizer: Joy Kang, LGC, Biosearch Technologies</td>
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<td>4:30pm</td>
<td>Ai Ling Ong, Sime Darby Technology Centre Sdn Bhd</td>
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<td>&quot;An Improved Reference Genome and Multiple Genotyping Platforms for Better Marker-Assisted Breeding in Oil Palm&quot;</td>
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<tr>
<td>5:00pm</td>
<td>Zeng Qingdong, Northwest Agriculture and Forestry University</td>
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<td>&quot;The “Golden Standard” Reference Sequences for Most Complex Species&quot;</td>
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<td>5:30pm</td>
<td>Jason Hein, LGC</td>
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<td>&quot;BHQplex™ CoPrimers™ - Redefining Multiplex PCR&quot;</td>
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<td>4:30pm - 6:15pm</td>
<td>Sugar Beet - GRAND BALLROOM 1 Organizer: Piergiorgio Stevanato, DAFNAE, Università degli Studi di Padova</td>
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<td>4:30pm</td>
<td>Dayou Cheng, Harbin Institute of Technology</td>
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<td>&quot;Analysis of the Lncrna Related to Vernalization in Sugar Beet&quot; (W088)</td>
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<td>4:50pm</td>
<td>Gui Geng, Heilongjiang University</td>
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<td>&quot;Preliminary Study on the Physiology and Molecular Mechanisms of Alkali Tolerance in Sugar Beet &quot; (W089)</td>
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<td>5:10pm</td>
<td>Wei Wang, Inner Mongolia Agricultural University</td>
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<td>&quot;The Role of Bzr Transcription Factors in the Growth of Sugar Beet&quot; (W090)</td>
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<td>5:30pm</td>
<td>Jie Cui, Harbin Institute of Technology</td>
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<td>&quot;Function and Expression Pattern of Multiple Transcription Factors in Response to Salt Stress in Beta vulgaris&quot; (W091)</td>
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<td>5:50pm</td>
<td>XiaoDong Li, Inner Mongolia Academy of Agriculture and Husbandry Sci</td>
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<td>&quot;Establishing a Sugar Beet Core Germplasm Collections for Molecular Breeding&quot; (W092)</td>
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Thursday - June 6, 2019

4:30pm - 6:15pm  Non-Chinese Young Scientists Working on Animal Genomics - GRAND BALLROOM 2
Organizer: Jian-Lin Han, CAAS-ILRI Joint Lab, Inst. of Anim. Sci., CAAS

4:30pm  Hosein Salehian Dehkordi, Institute of Zoology (UCAS)
"Diversity and Association Study of Copy Number Variation in Worldwide Sheep Using Ovine High-Density 600 K SNP Array" (W067)

4:45pm  Haile Berihulay Gebereselasea, Institute of Animal Science, CAAS
"Whole Genome Re-Sequencing Reveals Selection Signatures Associated with Important Traits in Ethiopian Indigenous Goat Populations" (W068)

5:00pm  Endashaw T. Assegidaw, Addis Ababa University, CNS, MCMB
"Genome Adaptation of Indigenous Ethiopian Cattle to High Altitude and Heat Stress" (W069)

5:15pm  Abdulfatai Tijjani, LiveGene – CTLGH, ILRI
"Whole Genome Sequence Analysis of West African Taurine Reveals Their Unique Trypanotolerant Adaptation" (W070)

5:30pm  Jian-Lin Han, CAAS-ILRI Joint Lab, Inst. of Anim. Sci., CAAS
"Genomic Characterization and Introgression of Indigenous Cattle Breeds of Pakistan" (W071)

5:45pm  Gebremedhin Gebreselassie Hidaru, Institute of Animal science
"Genomic mapping identifies the causative gene MC1R for the coat color variation in Chinese Tan sheep" (W072)

6:30pm - 8:15pm  Advances in Swine Genomics - GRAND BALLROOM 2
Organizer: Mei Yu, Huazhong Agricultural University

6:30pm  Lo Ling-Ling, Chinese Culture University
"Genomic Selection Using Biochip in Swine Breeding" (W001)

6:50pm  Zhonglin Tang, Agricultural genomics Institute, CAAS
"Dynamic Atlas of DNA Methylation during Skeletal Muscle Development in Pigs" (W002)

7:10pm  Md. Rasel Uzzaman, Chungbuk National University
"Gene Co-Association Network Analysis of Conventional Genome Wide Association Study of Sow Reproductive Traits in Yorkshire Population" (W003)

7:30pm  Yunxia Zhao, Huazhong Agriculture University
"Comprehensive Annotation of Cis Regulatory Elements and 3D Architecture of the Pig Genome" (W004)

7:50pm  Xiao Wang, Institute of Zoology Chinese Academy of Sciences
"A Novel ABCA12 Mutation Cause Abnormal Lipid Homeostasis in the Skin and Can be Rescued By Acitretin Treatment" (W005)

8:10pm  Feiyu Wang, Huazhong Agricultural University
"ATAC-Seq on Laser Captured Uterine Lumen Epithelial Cells Identifies Key Regulatory Regions Involved in Embryo Implantation in Pigs"
**Thursday - June 6, 2019**

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<th>Time</th>
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<tr>
<td>6:30pm - 8:15pm</td>
<td>New England Biolabs - Enabling Transformative Crop Science Through Innovative Molecular Biology - GRAND BALLROOM 3</td>
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<td>Organizer: Andrew Barry, New England Biolabs</td>
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<td>6:30pm</td>
<td>Andrew Barry, New England Biolabs</td>
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<td>&quot;Novel NEBnext Solutions to Advance Agricultural Genomics&quot;</td>
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<td>6:50pm</td>
<td>Cynthia L. Hendrickson, Directed Genomics</td>
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<td>&quot;A Highly Multiplexed, Targeted NGS Approach for High-Throughput and Cost-Effective Genotyping&quot;</td>
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<td>6:30pm - 8:15pm</td>
<td>Crop Informatics - GRAND BALLROOM 1</td>
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<td>Organizer: Kenneth McNally, International Rice Research Institute</td>
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<td>6:30pm</td>
<td>Star Yanxin Gao, Cornell University</td>
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<td>&quot;Genomic Open-Source Breeding Informatics Tool Portal&quot; (W006)</td>
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<td>6:50pm</td>
<td>Shuhui Song, Beijing Institute of Genomics</td>
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<td>&quot;Rice Genome Reannotation and the Information Commons for Rice (IC4R)&quot; (W007)</td>
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<td>7:10pm</td>
<td>Hajime Ohyanagi, King Abdullah University of Science and Technology</td>
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<td>&quot;Explore Asian Rice Domestication: Issues on Outgroup, Genotype Density and Unwieldy Diversity&quot; (W008)</td>
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<td>7:30pm</td>
<td>Dmytro Chebotarov, International Rice Research Institute</td>
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<td>&quot;SNP-Seek Database for Rice Genomic Diversity&quot; (W009)</td>
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<td>7:50pm</td>
<td>Bingbing Wang, BioBin Data Sciences CO., LTD</td>
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<td>&quot;Biobin, a Cloud-Based Platform for Breeding Data Management and Analysis&quot; (W010)</td>
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<td>Time</td>
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<tr>
<td>8:00am - 5:00pm</td>
<td>Registration - GRAND BALLROOM FOYER</td>
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| 9:00am - 9:45am | Plenary Lecture: Paul Boettcher - "FAO’s Work on Applying Genomics In the Management of Animal Genetic Resources" - GRAND BALLROOM  
Chair: Kwan-Suk Kim, Chungbuk National University |
| 9:00am        | Paul Boettcher, Food and Agriculture Organization of the UN (FAO)               |
| 9:00am        | "FAO’s Work on Applying Genomics in the Management of Animal Genetic Resources" |
| 9:45am - 10:30am | Plenary Lecture: Yaofeng Zhao - "Immunoglobulins in Domestic Animals: Surprises and Applications" - GRAND BALLROOM  
Chair: Zhonglin Tang, Agricultural genomics Institute, CAAS  |
| 9:45am        | Yaofeng Zhao, China Agricultural University                                      |
| 9:45am        | "Immunoglobulins in Domestic Animals: Surprises and Applications"                |
| 10:30am - 11:15am | Coffee Break / Poster Session 1 - GRAND BALLROOM FOYER  |
| 10:30am - 4:30pm | Exhibits & Posters Open -                                                       |
| 11:15am - 1:00pm | Legumes Genomics - GRAND BALLROOM 1  
Organizers: Weijian Zhuang, Fujian Agriculture and Forestry University and Rajeev K Varshney, ICRISAT  |
| 11:15am       | Zheng Zheng, Henan Academy of Agricultural Sciences                             |
| 11:15am       | "Genomic Analysis Identifies Genomic Variation and History of Peanut Breeding" (W047) |
| 11:35am       | Weijian Zhuang, College of Plant Protection, FAFU                                |
| 11:35am       | "The Genome of Cultivated Peanut Reveals a Differential A and B Subgenome Evolution after Tetraploidization" (W048) |
| 11:55am       | Xiaoping Chen, Crops Research Institute, GAAS                                    |
| 11:55am       | "The Genomes of Cultivated Peanut and Its Suspected Wild Progenitors" (W049)     |
| 12:15pm       | Shusei Sato, Graduate School of Life Sciences, Tohoku University                 |
| 12:15pm       | "Genomic Basis for Environmental Adaptation Revealed By Resources of Lotus Japonicus" (W050) |
| 12:35pm       | Dongmei Yin, College of Agronomy                                                 |
| 12:35pm       | "Monticola Genome Abstract" (W051)                                               |
**Friday - June 7, 2019**

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<th>Time</th>
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| 11:15am - 1:00pm | **GsSnRK1 Interplays with Transcription Factor GsERF7 from Wild Soybean to Regulate Soybean Stress Resistance - GRAND BALLROOM 2**  
Organizer: Xiaodong Ding, Northeast Agriculture University |

Many SnRK kinases are well-known to regulate plant resistance to environmental stresses. From a wild soybean cDNA library, we identified a GsSnRK1 binding protein designated as GsERF7. GsERF7 gene dominantly expressed in wild soybean roots and demonstrated high response to ethylene, salt, alkaline. GsSnRK1 interacted and were co-localized with GsERF7 in nucleus, and phosphorylated GsERF7 at S36 residue. Moreover, GsERF7 phosphorylation by GsSnRK1 is required for its translocation from cytoplasm to nucleus and transactivation activity. To investigate the physiological functions, we co-expressed GsERF7 and GsSnRK1 in hair roots of soybean cotyledons mediated by Agrobacterium rhizogenes. All the transgenic roots showed similar growth on normal medium. However, the roots carrying GsERF7 and GsSnRK1(wt) demonstrated stronger growth than the ones carrying GsERF7 and GsSnRK1(K49M) on the media containing NaCl or NaHCO3, suggesting that the kinase activity of GsSnRK1 is indispensable for GsERF7 to regulate plant tolerance to abiotic stresses. Moreover, RT-qPCR determined the altered the transcription levels of representative abiotic stress-responsive and hormone-synthetic genes. These results will aid our further understanding of the mechanism of how SnRK1 kinase plays a cardinal role in regulating plant stress resistances through activating the biological functions of downstream factors.

| 11:15am - 1:00pm | **Arbor Biosciences: Advances in Targeted Sequencing & Visualizing Genome Organization - GRAND BALLROOM 3**  
Organizer: Matthew Hymes, Arbor Biosciences |

We will present the latest advances in targeted sequencing for both short- and long-read sequencing platforms including Illumina, PacBio, and Oxford Nanopore. New technologies utilizing CRISPR-driven techniques for capturing and sequencing very long genomic regions of 10MB or more. Additionally, advances in Fluorescence in situ hybridization (FISH) for visualizing genome organization and barcoding chromosomes will be presented. Finally, we will introduce the new myBaits Expert Wheat Exome Panel, which was developed in collaboration with the International Wheat Genome Sequencing Consortium (IWGSC), and related sequencing and bioinformatics services.

| 1:00pm - 2:00pm | **Lunch - GRAND BALLROOM FOYER** |
Friday - June 7, 2019

2:00pm - 3:45pm Genetic and Genomic Analysis in Polyploid Species - GRAND BALLROOM 1
Organizer: Sachiko Isobe, Kazusa DNA Research Institute

2:00pm Hyungtaek Jung, Queensland University of Technology
"Pan-Genome Engineering of Nicotiana Benthamiana highlights the Functional Difference between Laboratory and Other Wild Ecotypes " (W025)

2:20pm Qinghe Cao, Sweetpotato Research Institute, CAAS
"The Whole Genome of the Sweetpotato Tetraploid Relatives Ipomoea tabascana" (W026)

2:40pm Won Yim, University of Nevada - Reno
"Typical Genome Assembly and Beyond : Advanced Approaches for Genome Analysis in Diploid and Polyploid Plant Species" (W027)

3:00pm Takuya Wada, Fukuoka Agriculture and Forestry Research Center
"Uncovering Genetic Regions Controlling Strawberry Fruit Color By Genome-Wide Association Study" (W028)

3:20pm Eiji Yamamoto, Kazusa DNA Research Institute
"A Simple Approach for Genetic Mapping in Polyploids Based on Allelic Dosage Estimates from RAD-Seq Data" (W029)

2:00pm - 3:45pm Dovetail Genomics – Chromosome Level Genome Scaffolding - GRAND BALLROOM 3
Organizer: Chui Li Leaw, Dovetail Genomics, LLC

A contiguous and accurate genome assembly is a crucial first step in fully understanding the biology of any organism. A high-quality genome assembly will make any downstream analyses, like gene annotation, synteny, comparative genomics and population genetics far easier and more reliable. This has been shown in plant and animal breeding, conservation and preservation study, and evolutionary study.

Dovetail Genomics is the leading company for high quality genome assemblies. To date, we have completed more than 1000 projects, encompass more than 800 species.

Using our two complementary scaffolding methods, Chicago and Dovetail Hi-C, we help to increase the contiguity and accuracy of genome assemblies, enabling true, full-chromosome-length scaffolding.

2:00pm Shu-Miaw Chaw, Biodiversity Research Center
"Stout Camphor Tree Genome Fills Gaps in Understanding of Flowering Plant Evolution"

2:45pm Chui Li Leaw, Dovetail Genomics, LLC
"Building the Best Genome on Earth"
Friday - June 7, 2019

2:00pm - 3:45pm  Genomics Applied to Tropically Adapted Livestock - GRAND BALLROOM 2
Organizer: Stephen Moore, University of Queensland

2:00pm  Alfred de Vries, Bill and Melinda Gates Foundation  
"The Need for Higher Productivity of Tropically Adapted Livestock" (W035)

2:20pm  Olivier Hanotte, School of Life Sciences, University of Nottingham  
"The Unravelling of the Genomics – Environment Interactions in Tropical Chicken" (W036)

2:40pm  Joram M. Mwacharo, International Centre for Agricultural Research Dry Areas  
"Decoding Genetic Mechanisms for Adaptation in African Indigenous Sheep" (W037)

3:00pm  Alessandra Stella, National Research Council of Italy  
"Adaptmap Project: Exploring Worldwide Goat Diversity and Adaptation" (W038)

3:20pm  Ningbo Chen, College of Animal Sci and Technology, NW Ag and Forestry Uni  
"The Tropical and Subtropical Adaptation and Genetic Diversity of Chinese Local Cattle Based on the Whole-Genome Data" (W039)

3:40pm  Ben J. Hayes, Department of Environment and Primary Industries  
"Genomic Strategies to Accelerate Breeding for Productive, Tropically Adapted Cattle" (W040)

3:45pm - 4:30pm  Coffee Break / Poster Session 2 - GRAND BALLROOM FOYER

4:30pm - 6:15pm  BGI: Genome-wide Population Study in World's Most Important Staple Foods - GRAND BALLROOM 3
Organizer: Yu Wang, BGI Genomics Co., Ltd.

Staple foods constitute the majority of a particular diet, and generally supply most of the total intake of energy and nutrients. Culture, climate, and trade are all factors that determine the popularity of a certain food. Over 50,000 plants are edible, but very few of them make any significant contribution to the human food supply. The overwhelming majority of global staple foods are grains. Corn, rice, and wheat together make up 51% of the world’s caloric intake. Understanding the genetic architecture of grains has become a key objective of breeding programs. Based on Massively Parallel High-throughput sequencing technology, researchers can successfully identify genomic regions associated with complex traits in species and get a better comprehension of the phylogenetic history and demography of a population.
Friday - June 7, 2019

4:30pm - 6:15pm  HC Scientific LLC: Genematrix, a New Option to Help You Genotype - GRAND BALLROOM 2
Organizer: Sujie Yang, HC Scientific (Chengdu) L.L.C.

Genotyping in large scale breeding materials is an essential step in molecular-assisted-breeding (MAB). When doing so, researchers would evaluate numerous factors including accuracy, throughput, human labor, and especially cost considering the large amount of SNP typing data to be generated and analyzed. In this workshop, HC Scientific, a China startup enterprise would demonstrate its full automated high-throughput genotyping platform, GeneMatrix, which is capable of automatically preparing 384-well-plate for subsequent thermocycling in waterbath, and fluorescent detection and analysis. The patented design of microwell plate may hold a reaction volume as low as 1.5-2μL to dramatically save reagents and samples. The workshop would show the operation of the instrument, and would also show real data from current users.

4:30pm  Xiaohui Luan, HC Scientific
"Genematrix, a New Option to Help You Genotype."

4:30pm - 6:15pm  Modern SNP technologies in plants: From tools in laboratory to commercial service - GRAND BALLROOM 1
Organizer: Yuri Shavrukov, Flinders University

4:30pm  Vadim Khlestkin, Institute of Cytology and Genetics and Research Institute of Farm Animal Genetics and Breeding
"GWAS-Based Search for Significant SNPs and Target Genes for Development of Potato with Genetically Designed Starch Properties" (W052)

4:50pm  Changlong Wen, Beijing Vegetable Research Center (BVRC)
"Target SNP-Seq Technology and Its Application in Genetic Analysis of Cucurbits Crops Varieties" (W053)

5:10pm  Hidetoshi Ikegami, Fukuoka Agriculture and Forestry Research Center
"Development and Application of FcRAN1-Based SNP Marker for Fig Sex Identification" (W054)

5:30pm  Xiao Huang, Nanjing Agricultural University
"Climate Adaptation of Prunus mume, Native to China, Associated with Its Chilling Requirements" (W055)

5:40pm  Jason Hein, LGC, Biosearch Technologies
"SeqSNP Targeted Genotyping By Sequencing, an Alternative to Array Genotyping in Routine Breeding Programs" (W056)

6:00pm  Yuri Shavrukov, Flinders University
"Plant Genotyping with Application of Amplifluor-like SNP Markers" (W057)
<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Location</th>
<th>Organizer/Institution</th>
<th>Title</th>
<th>Code</th>
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<tbody>
<tr>
<td>6:30pm</td>
<td>Fruit Trees: Genomics and Molecular Genetics - GRAND BALLROOM 1</td>
<td>GRAND BALLROOM 1</td>
<td>Ji-Hong Liu, Huazhong Agricultural University</td>
<td>&quot;The Genetic Basis of Domestication and Improvement in Pear&quot; (W019)</td>
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<td>6:30pm</td>
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<td>Jun Wu, Nanjing Agricultural University</td>
<td>&quot;The Genetic Basis of Domestication and Improvement in Pear&quot; (W019)</td>
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<td>6:45pm</td>
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<td>Yuepeng Han, Wuhan Botanic Garden of Chinese Academy of Sciences</td>
<td>&quot;Genetic Basis of Anthocyanin Coloration in Peach&quot; (W020)</td>
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<td>7:00pm</td>
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<td>Qingmei Guan, Northwest A&amp;F University, China</td>
<td>&quot;Apple Genome and Genomics: In Terms of Stress Response&quot; (W021)</td>
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<td>7:15pm</td>
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<td>Xueren Yin, Zhejiang University</td>
<td>&quot;Transcriptome-Based Elucidation of Network on Persimmon Astringency Removal and Softening&quot; (W022)</td>
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<td>7:30pm</td>
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<td>Chunyu Li, Guangdong Fruit Tree Institute</td>
<td>&quot;Fusaric Acid Is a Vanward Molecule of Foc TR4 and Modulates Its Invasion in Banana&quot; (W023)</td>
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<td>7:45pm</td>
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<td>Qiang Xu, Huazhong Agricultural University</td>
<td>&quot;Citrus Genome Sequencing and Its Application&quot; (W024)</td>
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<tr>
<td>6:30pm</td>
<td>Soybean Functional Genomics - GRAND BALLROOM 2</td>
<td>GRAND BALLROOM 2</td>
<td>Zhixi Tian, Institute of Genetics and Developmental Biology, CAS</td>
<td>Identifies Loci Controlling Adaptation in Chinese Soybean Landraces&quot; (W083)</td>
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<td>6:30pm</td>
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<td>Li-juan Qiu, Institute of Crop Science, CAAS</td>
<td>Identifies Loci Controlling Adaptation in Chinese Soybean Landraces&quot; (W083)</td>
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<tr>
<td>6:55pm</td>
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<td></td>
<td>Jin-Song Zhang, Institute of Genetics and Developmental Biology, CAS</td>
<td>Regulation of Seed Oil Accumulation in Soybean&quot; (W084)</td>
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<td>7:15pm</td>
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<td>Fanjiang Kong, Guangzhou University</td>
<td>Genomic and Genetic Elucidation of Low Latitude Adaptation in Soybean&quot; (W085)</td>
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<td>7:35pm</td>
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<td>Qingshan Chen, Agriculture-Northeast Agricultural University</td>
<td>Fine Mapping of Soybean Important Agronomic Trait QTLs with CSSL Population&quot; (W086)</td>
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<td>7:55pm</td>
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<td>Yuefeng Guan, Fujian Agriculture and Forestry University</td>
<td>Application of High-Throughput CRISPR-Cas9 for Multiplex Mutagenesis in Soybean&quot; (W087)</td>
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**Friday - June 7, 2019**

6:30pm - 8:15pm  Poultry Genomics and Biotechnology - GRAND BALLROOM 3  
Organizer: Zhi-Qiang Du, Northeast Agricultural University

6:30pm  Jae Yong Han, Seoul National University  
"Chicken Gene Editing and Model Development" (W073)

7:00pm  QinghuaNie, South China Agricultural University  
"circFOXO3 Acts As a Cerna in Regulating Global DNA Methylation By Sponging Mir-29-3p Family" (W074)

7:20pm  Guobin Chang, Yangzhou University, Yangzhou, Jiangsu, China  
"Functional Analysis of PIWI Protein and piRNAs during Chicken Spermatogenesis" (W075)

7:40pm  Zhi-Qiang Du, Northeast Agricultural University  
"Gene Expression Network Comparison Identifies Conserved Network Modules for Chicken Adipogenesis" (W076)

8:00pm  Shaopan Ye, South China Agricultural University  
"A Combined Reference Panel for Imputation to Whole Genome Sequence: A Case Study in a Chinese Indigenous Chicken Population"
<table>
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<tr>
<th>Time</th>
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<tr>
<td>8:00am - 2:00pm</td>
<td>Registration - GRAND BALLROOM FOYER</td>
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</table>
| 9:00am - 9:45am | Plenary Lecture: Takeshi Izawa - "Photoperiodic Flowering in Rice Under Natural Conditions" - GRAND BALLROOM  
Chair: Sachiko Isobe, Kazusa DNA Research Institute |
| 9:00am      | Takeshi Izawa, National Institute of Agrobiological Sciences  
"Photoperiodic Flowering in Rice Under Natural Conditions" |
| 9:45am - 10:30am | Plenary Lecture: Jane Loveland - "From Human Genome Annotation to Wheat Genome Analyses" - GRAND BALLROOM  
Chair: Rudi Appels, University of Melbourne |
| 9:45am      | Jane Loveland, EMBL-EBI  
"From Human Genome Annotation to Wheat Genome Analyses" |
| 10:30am - 11:15am | Coffee Break / Exhibits / Posters - GRAND BALLROOM FOYER |
| 10:30am - 2:00pm | Exhibits & Posters Open - GRAND BALLROOM FOYER |
| 11:15am - 1:00pm | Bionano Optical Genome Mapping Builds the Most Contiguous and Correct Genome Assemblies - GRAND BALLROOM 3  
Organizer: Lee Costa, Bionano Genomics Inc. |
| 11:15am      | Chad Collier, Bionano Genomics  
"Assemble the Highest-Quality Reference Genomes Using Bionano Genomics Optical Mapping" |
| 11:35am      | Chengzhi Liang, Institute of Genetics and Developmental Biology, CAS  
"High-Quality Genome Assembly and Comparative Genomic Analyses in Several Plants" |
| 11:55am      | Maojun Wang, Huazhong Agricultural University  
"Reference Genome Assemblies Facilitate the Exploitation of Favorable Genetic Variations for Superior Cotton Fibers" |
**Saturday - June 8, 2019**

**11:15am - 1:00pm**

IWGSC - Towards a Functionally Annotated Wheat Genome Reference Sequence - GRAND BALLROOM 1
Organizers: Rudi Appels, University of Melbourne
Kellye Eversole, IWGSC and Etienne Paux, INRA GDEC

11:15am Jiang Yu, CSIRO Animal, Food and Health Sciences  
"Frequent Intra- and Inter-Species Introgression Shape the Landscape of Genetic Variation in Bread Wheat" (W041)

11:32am Shun Sakuma, Faculty of Agriculture, Tottori University  
"Enhancing Grain Yield By Improving Floret Fertility in Wheat" (W042)

11:49am Nikolai V. Borisjuk, School of Life Science, Huaiyin Normal University  
"Control of Wheat Leaf Surface Structure Under Limited Water Conditions" (W043)

12:06pm Huixian Zhao, Northwest A & F University  
"Controlling Grain Size in Wheat" (W044)

12:23pm Xianchun Xia, Chinese Academy of Agricultural Sciences (CAAS)  
"Capture the New Genome Technologies for Wheat Breeding" (W045)

12:40pm Parwinder Kaur, Univ. of Western AU  
"The Wheat Cell Atlas (WCA) for a New View of the Wheat Plant" (W046)

**11:15am - 1:00pm**

Genome-Wide Association Studies and Genomic Selection for Plant and Animal - GRAND BALLROOM 2
Organizer: Xiaolei Liu, Huazhong Agricultural University Co-Chair: Xiaohui Yuan, Wuhan University of Technology

11:15am Zhengkui Zhou, Chinese Academy of Agricultural Sciences  
"What Are the Differences of GWAS in Plant and Animal?" (W031)

11:35am Joong Hyoun Chin, Sejong University  
"Genome-Wide Identification of the Genes Linked to Grain Nutritional Traits and Bacterial Leaf Blight Resistance in Colored Rice Population" (W032)

11:55am Congjiao Sun, China Agricultural University  
"Longitudinal Genome-Wide Association Analysis Revealed the Genetic Architectures for Dynamic Body Weights in Chickens" (W033)

12:15pm Xiaolei Liu, Huazhong Agricultural University  
"A Command-Line-Interface Based User Interactive and Learning-Costless Tool for Genome Wide Association Study and Genomic Selection" (W034)

**1:00pm - 2:00pm**

Lunch - GRAND BALLROOM FOYER
Oxford Nanopore Technologies - Closing the gap in plant and animal genomes - GRAND BALLROOM 3
Organizer: Iain MacLaren, Oxford Nanopore Technologies Ltd

This workshop will enable participants to gain valuable insight and understanding into how nanopore long-read sequencing is greatly advancing the field of plant and animal genome sequencing and assembly.

Plant and animal genomes are challenging to complete due to their large size and the prevalence of repeat regions. Plant genomes in particular are characteristically large, highly repetitive, and exhibit a variety of ploidy. Nanopore long and ultra-long reads enhance genome assembly, enabling downstream resolution of structural variants, repeat regions and transposable elements. With greater sequencing read overlap and fewer reads to complete the assembly jigsaw, nanopore long reads are closing the gaps in plant and animal genomes.

Participants will hear from scientists using nanopore sequencing on how these sequencing platforms are scalable to meet your requirements. In particular, the PromethION is becoming a game changer for assembling large genomes, with an output of up to 9,600 Gb of data across 48 flow cells.

Featuring presentations from BioMarker, BGITech and NextOomics

Modulating Plant MicroRNAs by Short tandem Target Mimic (STTM) For Crop Improvement - GRAND BALLROOM 1
Organizer: Guiliang Tang, Michigan Technological University Co-Chair: Jian-Kang Zhu, Purdue University

2:00pm Jian-Kang Zhu, Purdue University
"Application of Sttm in Rice" (W058)

2:20pm Guiliang Tang, Michigan Technological University
"A Resource for Inactivation of Micrornas Using Short Tandem Target Mimic Technology in Model and Crop Plants" (W059)

2:40pm Lin Liu, Shenzhen University
"An Update on the Application of STTM in Crops" (W060)

3:00pm Ting Lan, Shenzhen University
"Application of STTM Technology for Large miRNA Gene Families in Rice" (W061)

3:20pm Hui Zhang, Shanghai Normal University
"Application of Sttm in Rice for Agronomic Improvement" (W062)
### Plant Genomes for 10KP Project - GRAND BALLROOM 2
**Organizer:** Huan Liu, BGI-Research

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<tr>
<th>Time</th>
<th>Speaker</th>
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<tr>
<td>2:00pm</td>
<td>Michael Melkonian, Universität zu Köln</td>
<td>&quot;Algae Genome Research&quot;</td>
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<tr>
<td>2:20pm</td>
<td>Yang Liu, BGI</td>
<td>&quot;Tree of Life of Mosses in the Genomic Era&quot;</td>
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<tr>
<td>2:40pm</td>
<td>Gane Ka-Shu Wong, University of Alberta</td>
<td>&quot;From 1KP Green Plant Transcriptomes to 10KP Non-Animal Genomes&quot;</td>
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<td>3:00pm</td>
<td>Scott C Edmunds, BGI-Hong Kong/GigaScience</td>
<td>&quot;Big Data Storage, Handling and Sharing&quot;</td>
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<tr>
<td>3:20pm</td>
<td>Xin Liu, Beijing Genomics Institute-Shenzhen</td>
<td>&quot;10k Progress&quot;</td>
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### Nitrogen-fixing Root Nodule Symbiosis: Genetics, Evolution, and Engineering for Future Crops - GRAND BALLROOM 3
**Organizer:** Shifeng Cheng, Agricultural Genomics Institute at Shenzhen, CAAS

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<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
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<tr>
<td>4:00pm</td>
<td>Yiping Wang, Peking University</td>
<td>&quot;Synthetic Biology: Construction of a Minimal “Nif-Ome” for Engineering Nitrogen-Fixing Plants&quot; (W063)</td>
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<tr>
<td>4:25pm</td>
<td>Ting-Shuang Yi, Kunming Institute of Botany, Chinese Academy of Sciences</td>
<td>&quot;Plastid Phylogenomic Insights into the Evolution of Legumes&quot; (W064)</td>
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<td>4:50pm</td>
<td>Shifeng Cheng, Agricultural Genomics Institute at Shenzhen, CAAS</td>
<td>&quot;Pathway Discovery in Deep Convergence: Big Data in Phylogenomics for Nitrogen-Fixing Root Nodule Symbiosis&quot; (W065)</td>
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<td>5:15pm</td>
<td>Yu Zhang, Agricultural Genome Institute at Shenzhen, CAAS</td>
<td>&quot;Comparative &quot;Oomics&quot; of Nitrogen-Fixing Nodulated Plants&quot; (W066)</td>
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Saturday - June 8, 2019

4:00pm - 5:45pm Transforming Breeding through Integrated Data Management and Analysis - GRAND BALLROOM 2
Organizers: Star Yanxin Gao, Cornell University and Hima Bindu Kudapa, ICRISAT

4:00pm Eng Hwa Ng, Excellence in Breeding
"CGIAR Excellence in Breeding Platform" (W093)

4:20pm Yaw A. Nti-Addae, Genomic Open-Source Breeding Informatics Initiative
"Gobii System Overview" (W094)

4:40pm Rajaguru Bohar, ICRISAT
"Shared Genotyping Platform to Achieve Accelerated Genetic Gains in Crop Improvement in Sub-Saharan Africa and South Asia By Enabling Access to High Throughput Genotyping" (W095)

5:00pm Xuecai Zhang, CIMMYT
"Maize Genomic Selection Use Case and Galaxy Analysis Pipeline" (W096)

5:20pm Yi Zheng, Boyce Thompson Institute, Cornell University
"Cucurbit Genomics Database (CuGenDB): A Central Portal for Comparative and Functional Genomics of Cucurbit Crops" (W097)

Sunday - June 9, 2019

9:00am - 5:00pm EBI/IWGSC: Annotation of Gene Families in Animal and Plant Genomes - BGI
Organizer: Rudi Appels, University of Melbourne

9:00am Daowen Wang, Institute of Genetics and Developmental Biology and College of Agronomy
"New Opportunities for Efficiently Studying the Complex Glutenin and Gliadin Genes to Aid the Enhancement of Wheat End-Use Traits" (W016)

9:30am Rudi Appels, BioSciences, University of Melbourne
"The Gene Networks Involved in Wheat Drought Response" (W017)

10:00am Jane Loveland, EMBL-EBI
"Annotation of Animal and Plant Genomes" (W018)
Corporate Sponsors

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BGI

DoveTail Genomics

Illumina China

LGC, Biosearch Technologies

NRGene

PacBio

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## Exhibitor Descriptions

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<th>Company</th>
<th>Booth#</th>
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<tr>
<td><strong>Arbor Biosciences</strong></td>
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<tr>
<td>Arbor Biosciences is a development and services company founded by scientists to serve our peers in molecular biology applications. We are a passionate organization of scientists determined to deliver cost-effective, user-friendly products to researchers of genetics and agrigenomics. The team at Arbor Biosciences prides themselves on providing exceptional customer service and timely technical support to new or advanced users on our array of products. We routinely collaborate with our customers and research partners to develop innovative solutions to address their unique applications. From discussing the feasibility of a project to providing fast, reliable laboratory services, we are here to help. During the conference we will be introducing our new myBaits® Expert Wheat Exome Panel for next-generation sequencing of wheat developed in conjunction with the International Wheat Genome Sequencing Consortium (IWGSC). We will also feature our myNGS Guides™ gRNA pools for targeted sequencing of large genomic regions which can be difficult to resolve with conventional sequencing methods. We welcome the opportunity to collaborate and develop a custom solution for your unique research question.</td>
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<tr>
<td><strong>Beijing Ecotech Science and Technology Ltd</strong></td>
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<td>Beijing Ecotech Science and Technology Ltd. is located in Beijing city, and specialized in spectroscopy technology and drones. For 17 years, we are engaged in introduction, promotion, R&amp;D and integration of the advanced instrument and technology of the world - for plants, soil, animals, water and algae. Besides the instruments, we can also provide the service of planning &amp; design, solutions, system integration, measurement &amp; analysis, and consultation for ecological study, monitoring, restoration and protection.</td>
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<tr>
<td><strong>Benson Hill Biosystems</strong></td>
<td>23</td>
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<td>Our mission is to empower companies of any size across the agri-food value chain with the technologies, expertise and product development infrastructure they need to develop better food and feed ingredients. Benson Hill’s crop design platform, CropOS, uses proprietary and public data to fully leverage the natural genetic diversity of our partner's genetics, by putting it in the context of the global genetic diversity of a crop. This allows our partners to bring products to market faster through breeding, gene editing, and transgenics.</td>
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<tr>
<td><strong>Berry Genomics Corporation</strong></td>
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<td>Founded in May 2010, Berry Genomics is the leading genomics company specializing in developing and commercializing technologies for life sciences and clinical applications. Since we have the platform of PacBio Sequel/Sequel II, Bionano Saphyr, 10x Genomics, Illumina NovaSeq and Hi-C three-dimensional technology, We could provide comprehensive genomic solutions to meet the genome research of different species with different complexity.</td>
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BGI is a leading Global Genomic Services company, itself actively involved in genomic research to benefit agriculture, the environment and human health. We put our extensive NGS experience and capacity to work for your academic and industrial research projects. Our line of services is complete, starting from De Novo sequencing to Whole Genome Re-sequencing to RNA and Metagenomics sequencing. Our service laboratories are located around the world and operate under international quality systems. Come see us at PAG booth #14, to learn how BGI can support your research with affordable, high quality NGS data.

Bionano Genomics Inc.
Bionano Genomics is a life sciences instrumentation company in the genome analysis space. The Company develops and markets the Saphyr system which builds de novo maps of the genome by massively parallel imaging of the longest single DNA molecules in the industry. When combined with orthogonal sequencing data, Bionano maps can provide the correct structure, order, and orientation to quickly assemble reference-quality genomes like never before. The Saphyr system comprises an instrument, chip consumables, reagents and a suite of data analysis tools. For more information, visit us at www.BionanoGenomics.com.

Dovetail Genomics, LLC
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.

Genetalks
Genetalks is a gene technology enterprise. It has a complete industrial chain of research and development, production, sales and the third party medical laboratory. With the world-leading BT+IT R&D transformation capability, Genetalks has built medical diagnosis, health management, and genetic big-data platforms. It is the first batch of China national demonstration center of genetic testing, and established Hunan Engineering Center of genomic big data application. In 2016, it won the first prize of gene big data compression and genome high performance computing technologies in Genomics and Cloud Technology Alliance conference (GCTA), and the records still remain in the field.

Guangzhou Biolight Equipment Co., Ltd.
Guangzhou Biolight Equipment Co., Ltd. is located in Guangzhou Higher Education Mega Center, and focus on the development of high efficiency receiving and recognition technology of photon signal, and applying this technology in the fields of life science research, food safety inspection, environmental quality control, medical diagnosis service and so on. It is very few can provide a series of professional photon detection equipment specialized companies in the world, because it integrates research and development, manufacture and service. Since its establishment, it had successfully develop a variety of products with independent intellectual property rights, and access a number of patent certificates. And it was identified the Guangzhou "Science and technology innovation small giant Enterprise" in 2015, and through the first batch of "High-tech Enterprises" in Guangdong Province in 2017.
Hangzhou Houze Bio-Technology Co., Ltd. is a high-tech biological enterprise integrating sales, promotion and after-sales service of scientific instruments, consumables and reagents. The company was established in June 2013. With the excellence of product quality and the development of the marketing team, the market space has gradually expanded, the marketing network covers the whole country, and the high-quality and dedicated service has won the trust and praise of many companies, and has risen rapidly in the field of biological equipment. With the core value of “customer first, service attentively”, the company always takes the customer service and provides comprehensive service as the service tenet, and improves the technical service level in the process of continuous development and improvement. We believe that through our continuous efforts and pursuit, we will be able to achieve mutual benefit and win-win with service providers.

HC Scientific (Chengdu) L.L.C.
HC Scientific (Chengdu) Co. Ltd. is a high-tech company located in Chengdu, China, representing high standard of lab automation design and manufacturing, meeting global high throughput genotyping demands from plant and animal genomic research. The company is now providing the complete system of GeneMatrix, a highly automated platform with related hardware, software and consumables, for China and overseas markets of high throughput genotyping, able to generate up to 30,000 datapoints per workshift at a much more affordable price. The system has been already installed in numerous agricultural breeding labs and well utilized in their daily work.

Illumina China
Illumina - Accelerating plant and animal genomic breakthroughs. A history of progress. A future of promise. Illumina is a leading developer, manufacturer, and marketer of life science tools and integrated systems for large-scale analysis of genetic variation and function. These systems are enabling advances in agriculture that were not even imaginable just a few years ago. With rapid advances in technology taking place, it is mission-critical to offer solutions that are not only innovative, but flexible, and scalable, with industry-leading support and service. Our customers include a broad range of academic, government, aquaculture producers, seed companies and livestock producers around the globe. For further details please visit www.illumina.com.

Kazusa DNA Research Institute
KAZUSA LAB for plant data solutions is now Open! KAZUSA LAB in Kazusa DNA Research Institute provides solutions for digital data generation and analysis via a 3D modeling system, a low-cost environmental sensor system, programs for image analysis and a digital field book system. We also open a beta version of plant genome portal site, Plant GARDEN (https://plantgarden.jp/en/). The system and DB development was supported by JST CREST JST CREST (JPMJCR16O1) and Life Science Database Integration Project (17934006).
LGC, Biosearch Technologies
Biosearch Technologies is the comprehensive genomics portfolio from LGC, providing products and services for genomic analysis that support mission critical applications for agrigenomics. Our integrated tools and technologies enable customers’ achievements whether through oligonucleotides, reagents, enzymes, and instrumentation in addition to extraction, genotyping, targeted GBS, SSR conversion, and NGS services.

Meridian Bioscience, Inc.
Meridian Bioscience, Inc. is a leading large scale manufacturer of:
• Antibodies
• Viral antigens
• Recombinant proteins
• PCR enzymes
• Nucleotides
• Critical assay reagents
Meridian has been providing innovative life science solutions and building trusted partnerships for over 40 years. Meridian’s focus is to offer products and services that help to advance the development of diagnostic assays and vaccine development.
• Commercial scale manufacturing of antigens and antibodies with protein purification expertise
• Full line of immunoassay reagents, including antigens, antibodies and blockers
• Large scale production of reagents for molecular assays
• Technical support with assay development experience
• Dedicated R&D and manufacturing teams
• Robust and mature Quality System
ISO certified

MGI Tech Co., Ltd.
MGI Tech Co., Ltd. (MGI), a subsidiary of BGI Group, is committed to enabling effective and affordable healthcare solutions for all. Based on its proprietary technology, MGI produces sequencing devices, equipment, consumables and reagents to support life science research, medicine and healthcare.

Neogen Bio-Scientific Technology (Shanghai) Co., Ltd
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. With leading commercial genomic laboratories located around the world our facilities are close to our customer base in USA, Canada, Europe, Brazil, China and Australia. Neogen’s Genomics laboratories deliver a consistent service with rapid turnaround times, empowering your decision making in genomic selection, health management and research.
New England Biolabs

Founded in the mid-1970s as a collective of scientists committed to developing innovative products for the life sciences industry, New England Biolabs is now a recognized world leader in the discovery and production of enzymes for molecular biology applications. Created "by scientists for scientists", NEB is renowned for consistently providing exceptional product quality and unsurpassed technical support. For over four decades, NEB has been shaping the landscape of bioscience research by discovering, developing and supporting superior research reagents. From our founding principles – placing the advancement of science and the stewardship of the environment as our highest priorities – to our unique corporate culture, NEB’s philosophy can be distilled down to three core values: passion, humility and being genuine. A supplier-of-choice for scientists across the globe, NEB offers the largest selection of recombinant and native enzymes for genomic research. While restriction enzymes remain part of our core product portfolio, our ever-expanding catalog also includes products related to PCR, gene expression, sample preparation for next generation sequencing, synthetic biology, glycobiology, epigenetics and RNA analysis. Additionally, NEB is focused on strengthening alliances that enable new technologies to reach key market sectors, including molecular diagnostics development.

Nextomics Biosciences Co., Ltd

NextOmics was found in 2011 and owns a young but highly talented team with sophisticated genome sequencing and application experience, 150+ employees, 30+ long reading sequencing machines and terabase-scale supercomputer groups are working for a better genome sequencing service. It is open for all genomic scientists and labs to obtain a golden reference genome for nearly all species with NextOmics. With global collaboration, we have finished hundreds of pilot projects and participated in several influential articles in human, plant, animal, insects, bacteria genome and transcriptome, such as the maize Mol7 Nature Genetics article and the Chinese HX1 genome article, the Arabidopsis methylation article in Development Cell. NextOmics sincerely welcome scientists from all over the world to work with us to climb the huge and complex genome mountain and discover the mystery of the unknown genome knowledge with long read sequencing technology!

NRGene

The genomic company that provides turn-key solutions to leading breeding companies, NRGene leverages advanced algorithms & extensive proprietary databases to empower breeders to achieve stronger and more productive yields in record time. NRGene tools are used by leading agri-biotech companies worldwide, and the most influential academic research teams.

Oxford Nanopore Technologies

Sequencing devices from Oxford Nanopore Technologies enable the accurate assembly of complex, multi-gigabase plant genomes and real-time detection of plant pathogens. Long sequencing reads enhance genome assembly with complete characterisation of complex genomic regions, delivering new insights into plant biology, evolution and breeding strategies. Identify base modifications alongside nucleotide sequence and explore the impact of epigenetics through direct sequencing of native DNA or RNA. A range of nanopore sequencing devices are available — from the portable MinION to the high-throughput PromethION, capable of sequencing extremely large plant genomes or sample numbers, such as transgenic lines and seed collections.
PacBio
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.

PHENOMIX
Phenomix develops tools for automated plant phenotyping systems in greenhouses. We can help you for new full set-up or upgrade of existing automated greenhouses, roots analysis, growth chamber, workbench ... Several imaging stations are available, either in stand alone configuration or to integrate in your automated phenotyping system depending on the type of application or traits to analyse. Phenomix Supervisor will allow you a Smart Automation Management. See our website www.phenomix.fr

PhytoTech Labs, Inc
PhytoTechnology Laboratories® is an ISO 9001:2008 certified company, a global supplier of high-quality, competitively-priced products for commercial and research use in the plant sciences. Including biochemicals, tissue culture media for plants and microbes, molecular biology and microbiology biochemicals and buffers, kits, and laboratory supplies. With more than 1000 products, we have you covered for your plant tissue culture and plant molecular biology research. Most orders are shipped within 24-48 hours of receipt and we offer competitive shipping to customers around the globe. Order online at www.phytotechlab.com for orders anywhere in the world. Or contact us at sales@phytotechlab.com.

Suzhou Vdo Biotech Co., Ltd.
Suzhou VDO Biotech Co., Ltd. is a high-tech enterprise dedicated in innovative microsphere technology and production of a variety of high quality microspheres for various areas. We provide customized OEM production and development for the special needs according to customers’ requirements. We also provide large production batch reserved for individual customers to ensure a long time supply with stable quality. We provide product lines and services including: Magnetic microspheres, Latex microspheres for PET (particle enhanced turbidimetry), Color-dyed and Fluorescence microspheres, Plain latex microspheres with specific sizes, Size standard microspheres (NIST-Traceable), Counting standard microspheres, Flow cytometry microspheres. We are your reliable source for the solution of any microsphere related applications.

Thermo Fisher
Thermo Fisher Scientific offers a comprehensive range of powerful and innovative genotyping and gene-expression profiling solutions for plant and animal genetics research. Our cost-effective solutions enable researchers and breeders to identify, validate, and screen complex genetic traits in both animals and plants—diploid or polyploids. We supply microarray, sequencing, qPCR, and targeted genotyping by sequencing technologies for agrigenomics.
Gentides is customer focused biotech Ltd. on R&D of SNP genotyping technologies, we provide robust and high quality highthroughput SNP genotyping PCR master mix PARMS, we also provide inexpensive, prompt and high quality highthroughput genotyping service for plant& animal researchers or breeders using PARMS.
W001: Advances in Swine Genomics  
Genomic Selection Using Biochip in Swine Breeding  
Lo Ling-Ling, Chinese Culture University, China

W002: Advances in Swine Genomics  
Dynamic Atlas of DNA Methylation during Skeletal Muscle Development in Pigs  
Zhonglin Tang, Agricultural genomics Institute, CAAS, Shenzhen, China

W003: Advances in Swine Genomics  
Gene Co-Association Network Analysis of Conventional Genome Wide Association Study of sow Reproductive Traits in Yorkshire Population  
Md. Rasel Uzzaman, Chungbuk National University, Cheongju, South Korea

W004: Advances in Swine Genomics  
Comprehensive Annotation of Cis Regulatory Elements and 3D Architecture of the Pig Genome  
Yunxiao Zhao, Huazhong Agriculture University, Wuhan, China

W005: Advances in Swine Genomics  
A Novel ABCA12 Mutation Cause Abnormal Lipid Homeostasis in the Skin and Can be Rescued By Aciitlin Treatment  
Xiao Wang, Institute of Zoology Chinese Academy of Sciences, Beijing, China

W006: Crop Informatics  
Genomic Open-Source Breeding Informatics Tool Portal  

Application of high-density genomic information coupled with phenomic data to the breeding of staple crops in the developing world greatly impact the rate of genetic gain delivered in farmers’ fields. This would require streamlining the use of genomic information to accelerate breeding progress in multiple crops. Integrated data management and analysis offer great potential to increase the rate of genetic gain by decreasing generation interval and identifying the best performers for use as parents in the next generation. We have developed data management systems for data loading, storage, quality control, data query, and also downstream informatics, visualization, and genomics-based selection application tools in an one stop-shop marker portal http://asia.gobi.org:8081/gobi-portal/. We open to work with global crop improvement community to collaborate and adopt systems and tools and increase the genetic gains.

W007: Crop Informatics  
Rice Genome Reannotation and the Information Commons for Rice (IC4R)  
Shuhui Song, Beijing Institute of Genomics, Beijing, China

Rice is the most important staple food for a large part of the world's human population and also a key model organism for plant research. Here, we reannotated the rice genome and present Information Commons for Rice (IC4R; http://ic4r.org), a rice knowledgebase featuring adoption of an extensible and sustainable architecture that integrates multiple omics data through community-contributed modules. Each module is developed and maintained by different committed groups, deals with data collection, processing and visualization, and delivers data on-demand via web services. In the current version, IC4R incorporates a variety of rice data through multiple committed modules, including genome-wide expression profiles derived entirely from RNA-Seq data, resequencing-based genomic variations obtained from resequencing of thousands of rice varieties, plant homologous genes covering multiple diverse plant species, post-translational modifications, rice-related literatures and gene annotations contributed by the rice research community. Unlike extant related databases, IC4R is designed for scalability and sustainability and thus also features collaborative integration of rice data and low costs for database update and maintenance. Future directions of IC4R include incorporation of other omics data and association of multiple omics data with agronomically important traits, dedicating to build IC4R into a valuable knowledgebase for both basic and translational researches in rice

W008: Crop Informatics  
Explore Asian Rice Domestication: Issues on Outgroup, Genotype Density and Unwieldy Diversity  
Hajime Ohyanagi, King Abdullah University of Science and Technology, Thuwal, Saudi Arabia

W009: Crop Informatics  
SNP-Seek Database for Rice Genomic Diversity  
Dmytro Chebotarow, International Rice Research Institute, Los Baños, Philippines

We are in the midst of our planet's sixth mass extinction. Australia has a rich biodiversity, with 87 per cent of the world's mammalian species unique to Australia. The DNA Zoo project is a first of its kind collaboration between academic labs and zoos across the world. The purpose of DNA Zoo Australia is to complement the global effort by DNA Zoo and facilitate comprehensive sampling of Australian biodiversity, including vulnerable and threatened species using HIC genomics and supercomputing. DNA Zoo Australia will shape development of evolutionary studies and the understanding of extinction risk for Australian mammal species, and provide critical information for making sound policy and management decisions. DNA Zoo Australia will provide a data legacy for generations to come and will pave the way for conservation studies, species evolution, identify measures that will aid in the protection and understanding of the impact of fast changing climates and habitats.
Natural variation can help us understand how ecological and evolutionary dynamics shape complex traits. Halictid bees or ‘sweat’ bees harbor extraordinary variation in social behavior. In this group, eusociality has evolved independently 2-3 times, and variation among species encapsulates nearly all forms of social structure from solitary to eusocial. To identify the genetic factors associated with the evolution of social behavior in this group, we have generated genomic resources for 19 halictid species that encompass all of the well characterized gains and losses of eusociality within this family. This enables an integrative examination of the link between the proximate mechanisms underlying variation in social behavior and the ecological processes driving their evolution. We searched for signatures of convergent evolution in this group using relative evolutionary rates on both coding and non-coding sequence. In general, we find that the evolution of social behavior is primarily associated with changes in non-coding sequence. These putatively regulatory, non-coding elements are highly enriched for proximity to genes involved in behavior and nervous system functioning, including several previously implicated in social evolution in distantly related taxa.

Annotation of Animal and Plant Genomes

W014: DNA Zoo
DNA Zoo China
Liechun Jiang, Shanghai Tech, Shanghai, China

W015: DNA Zoo
Convergent Evolution of Social Behavior in Sweat Bees
Sarah Kocher, Princeton University, Princeton, NJ

Natural variation can help us understand how ecological and evolutionary dynamics shape complex traits. Halictid bees or ‘sweat’ bees harbor extraordinary variation in social behavior. In this group, eusociality has evolved independently 2-3 times, and variation among species encapsulates nearly all forms of social structure from solitary to eusocial. To identify the genetic factors associated with the evolution of social behavior in this group, we have generated genomic resources for 19 halictid species that encompass all of the well characterized gains and losses of eusociality within this family. This enables an integrative examination of the link between the proximate mechanisms underlying variation in social behavior and the ecological processes driving their evolution. We searched for signatures of convergent evolution in this group using relative evolutionary rates on both coding and non-coding sequence. In general, we find that the evolution of social behavior is primarily associated with changes in non-coding sequence. These putatively regulatory, non-coding elements are highly enriched for proximity to genes involved in behavior and nervous system functioning, including several previously implicated in social evolution in distantly related taxa.

The Gene Networks Involved in Wheat Drought Response

W016: EBI/IWGSC: Annotation of Gene Families in Animal and Plant Genomes
New Opportunities for Efficiently Studying the Complex Glutenin and Gliadin Genes to Aid the Enhancement of Wheat End-Use Traits
Daowen Wang1,2 and Kunpu Zhang1, (1)Institute of Genetics and Developmental Biology, Beijing, China, (2)College of Agronomy, Zhengzhou, China

Wheat (Triticum aestivum L.) is the most widely cultivated staple crop on Earth, and provides about 20% of the food calories and proteins consumed by human. Glutenins, composed of high- and low-molecular weight glutenin subunits (HMW-GSs and LMW-GSs), and gliadins, consisted of alpha-, gamma-, delta- and omega-types, are two major families of storage proteins in wheat seeds. They account for approximately 40% and 50% of the total wheat flour proteins, respectively. Consequently, variations in the quantity and composition of glutenin and gliadin genes have strong impact on the end-use quality and nutritional value of wheat food products, and better understanding and proper manipulation of these genes are critical for developing wheat cultivars with desired end-use traits. However, it has been difficult to precisely and rapidly elucidate the complements of glutenins and gliadin genes, especially those encoding LMW-GSs and various types of gliadins, in desired wheat genotypes. This is because these genes are located in large and complex chromosomal loci, and exhibit strong allelic variations among different wheat genotypes. Copy number changes, single nucleotide polymorphisms and indels of various sizes can all contribute to the allelic variations of glutenin and gliadin genes. Furthermore, there exists transcriptional regulation, which results in differences in mRNA abundance among different glutenin and gliadin genes. Nevertheless, the efficiency in studying glutenin and gliadin genes is expected to rise because of the accumulation of high-quality genomic information for hexaploid wheat, tetraploid wheat and their diploid progenitors since 2017. The availability of rich genomic information, plus the application of complementary functional genomics tools, will stimulate a new phase of molecular studies on glutenin and gliadin genes with the aim to enhance wheat end-use traits. In this presentation, we will report our efforts in dissecting the composition and function of glutenin and gliadin genes in elite Chinese winter wheat cultivars and the application of resultant genetic resources in improving breadmaking quality. We suggest that, although the reference genome sequence information generated for various wheat species is very helpful, genotype-specific efforts are still needed for precisely and efficiently revealing the glutenin and gliadin genes in specific wheat varieties.

The Genetic Basis of Domestication and Improvement in Pear

W017: EBI/IWGSC: Annotation of Gene Families in Animal and Plant Genomes
The Gene Networks Involved in Wheat Drought Response
Sergio Galvez1, Rosa Mierda-Garcia1, Carlos Camino1, Philippa Bornill2, Michael Abrouk1, Ricardo Ramirez-Gonzalez2, Sergii Biyiklioglu3, Gabriel Dorado3, IWGSC4, Francisco Amil-Ruiz5, Hikmet Budak1, Victoria Gonzalez-Dugo2, Pablo Zarco-Tejada1, Rudi Appels6, Cristobal Unu1, Pilar Hernandez2 and IWGSC, (1)Universidad de Malaga, Spain, (2)University of Melbourne, Melbourne, VIC, Australia, (3)University of Birmingham, Birmingham, United Kingdom, (4)Institute of Experimental Botany, Olomouc, Czech Republic, (5)John Innes Centre, Norwich, United Kingdom, (6)College of Agronomy, Zhengzhou, China

Pear is a globally grown fruit, with thousands of cultivars in five domesticated species and dozens of wild species. However, little is known about the evolutionary history of these pear species, and knowledge of the genetic changes that occurred during the domestication and improvement is limited. Recently, we report the genome resequencing of 113 pear accessions from worldwide collections, representing both cultivated and wild pear species. Based on 18,302,883 identified SNPs, we conduct phylogenetics, population structure, gene flow, and selective sweep analyses. Furthermore, we propose a model for the divergence, dissemination, and independent domestication of Asian and European pears. Meanwhile, RNA-seq analysis was used to compare representative sets of wild, landrace, and improved accessions of sand pear (Pyrus pyrifolia) to gain insight into the genetic changes associated with domestication and improvement. The expression diversity of selected genes exhibited reduction from the wild group to the landrace group, but a recovery was observed from the landrace to the improved group, showing a distinctly different pattern with variation of DNA sequence diversity. In addition, separate selective sweep signatures, combined with co-localized QTLs and differentially expressed genes, underline distinct phenotypic fruit traits, including fruit size, flesh texture, sugar, acidity, aroma, and stone cells. Thus, our study reveals the specific pattern of domestication and improvement of perennial trees at the DNA and transcriptome level, which provides substantive and valuable genetic resources that will significantly advance pear improvement and molecular breeding efforts.

The Genetic Basis of Domestication and Improvement in Pear

W018: EBI/IWGSC: Annotation of Gene Families in Animal and Plant Genomes
Annotation of Animal and Plant Genomes
Jane Loveland, EMBL-EBI, Cambridge, United Kingdom and Toby Hunt, EMBL-EBI, Hinxton, United Kingdom

The Genetic Basis of Domestication and Improvement in Pear

W019: Fruit Trees: Genomics and Molecular Genetics
The Genetic Basis of Domestication and Improvement in Pear
Jun Wu, Xiaolong Li and Shaoling Zhang, Nanjing Agricultural University, Nanjing, China

Pear is a globally grown fruit, with thousands of cultivars in five domesticated species and dozens of wild species. However, little is known about the evolutionary history of these pear species, and knowledge of the genetic changes that occurred during the domestication and improvement is limited. Recently, we report the genome resequencing of 113 pear accessions from worldwide collections, representing both cultivated and wild pear species. Based on 18,302,883 identified SNPs, we conduct phylogenetics, population structure, gene flow, and selective sweep analyses. Furthermore, we propose a model for the divergence, dissemination, and independent domestication of Asian and European pears. Meanwhile, RNA-seq analysis was used to compare representative sets of wild, landrace, and improved accessions of sand pear (Pyrus pyrifolia) to gain insight into the genetic changes associated with domestication and improvement. The expression diversity of selected genes exhibited reduction from the wild group to the landrace group, but a recovery was observed from the landrace to the improved group, showing a distinctly different pattern with variation of DNA sequence diversity. In addition, separate selective sweep signatures, combined with co-localized QTLs and differentially expressed genes, underline distinct phenotypic fruit traits, including fruit size, flesh texture, sugar, acidity, aroma, and stone cells. Thus, our study reveals the specific pattern of domestication and improvement of perennial trees at the DNA and transcriptome level, which provides substantive and valuable genetic resources that will significantly advance pear improvement and molecular breeding efforts.
develops a fine-tuning regulatory loop to balance PA and anthocyanin accumulation. This is achieved by competing with MYB activators for binding to Basic Helix Loop Helixes (bHLHs), which are involved in metabolite accumulation at the transcriptional level.

interval, a candidate gene encoding a NAC domain transcription factor, designated BLOOD PpMYB10.1, resulting in anthocyanin pigmentation. Moreover, a R2R3-MYB gene, designated  

PpMYB18  

acts as a negative regulator of anthocyanin and PA accumulation and can be activated by both anthocyanin- and PA-related MYB activators. The PpMYB18 protein competes with MYB activators for binding to basic Helix Loop Helices (bHLHs), which develops a fine-tuning regulatory loop to balance PA and anthocyanin accumulation. This demonstrates a modulating negative feedback loop, which prevents cells from excess accumulation of anthocyanin and PAs, and serves as a model for balancing secondary metabolite accumulation at the transcriptional level.

Fusaric Acid is a Vernaland Molecule of Foc TR4 and Modulates Its Invasion in Banana

Fusarium oxysporum f. sp. cubense (Foc) Tropical race 4 (TR4) had become a great threat for the world banana industry. Fusaric acid (FSA) is a non-specific phytotoxin produced by TR4, and we found that it is a vernaland molecule which spreads ahead of the invading pathogen. Further research revealed that the lack of FSA production in several fsh mutants of TR4 results in less serious symptoms and reduced fungal biomass in banana plants. Banana embryogenic cell suspensions (ECs) treated with FSA exhibited a lower rate of O2 uptake, loss of mitochondrial membrane potential, increased rates of reactive oxygen species (ROS) accumulation, nuclear condensation and cell death. Transcriptomic analysis of FSA-treated ECs confirmed that FSA has the potential to induce plant cell death, possibly by regulating mitochondrial function. Taken together, the results demonstrate that FSA acts as a positive virulence factor for TR4 by accelerating disease in host plants.

W024: Fruit Trees: Genomics and Molecular Genetics

Citrus Genome Sequencing and Its Application

Qi Gao, Huazhong Agricultural University, Wuhan, China

W025: Genetic and Genomic Analysis in Polyplody Species

PAN-Genome Engineering of Nicotiana Benthamiana Highlights the Functional Difference between Laboratory and Other Wild Ecotypes

Hyungtaek Jung, Queensland University of Technology, Brisbane, QLD, Australia

W026: Genetic and Genomic Analysis in Polyplody Species

The Whole Genome of the Sweetpotato Tetraploid Relatives Ipomoea tabacum

Qinghe Cao, Sweetpotato Research Institute, CAAS, Xuzhou, China

Origin and evolution of sweetpotato were puzzle for researchers until now. We just knew Ipomoea trifida (2X, 6X) was the ancestor species of sweetpotato. Little was known about tetraploid plant in genus Ipomoea, especially genome level. Here, we reported the genome of Ipomoea tabacum, which was the most closely related tetraploid species to sweetpotato in Ipomoea Section Batatas. De novo assembly of the long reads from SMRT Sequencing was performed using FALCON and FALCON-Unzip. In order to get enough corrected reads, the longest 78 coverage of sub-reads was firstly selected as seed reads to do error correction. The corrected reads N50 and coverage were 9.3K and 55, respectively. We got an assembly with a contig N50 size of 616.4Kb. The total length of this version is 957.0Mb. Finally, scaffolding was performed by FragScaff with the barcoded sequencing reads, generating a genome with a scaffold N50 size of 1.10 Mb. The total length of this version is 963.07Mb, containing 0.64% Ns. The quality of I. tabacum genome assembly was first assessed using BUSCO. The analysis revealed that 93% of the core eukaryotic genes were detected in I. tabacum genome. To predict protein coding genes in this genome, we used homolog-based prediction, de novo prediction and transcriptome based prediction. A total of 68,400 protein-coding genes were predicted from I. tabacum genome, which is comparable to the number of genes predicted in Nsp323 trifida_v3 (31,426) and in Nsp306 trifida_v3 (32,501). The gene length and CDS sequences in I. tabacum have an average length of 2922.5bp and 1100.68bp, respectively. And the predicted genes have an average of 4.72 exons. A total of 61,176 (95.5%) I. tabacum protein have at least one homologue in database including NR, KEGG, Swiss-Prot and TAIR10 et al.
Uncovering Genetic Regions Controlling Strawberry Fruit Color By Genome-Wide Association Study

Takuya Wada, Masao Tsunobu, Miyuji Mori, Chihara Hiraoka, Hiroto Nagamatsu, Koichiro Oku, Soichiro Naganu, Sachiko Isobe, Hideyuki Suzuki, Katsumi Shimomura, Keita Hirashima and Hideyuki Ikegami, (1)Fukasuka Agriculture and Forestry Research Center, Chikushino, Fukuoka, Japan, (2)Kazusa DNA Research Institute, Kisarazu, Japan, (3)Kazusa DNA Research Institute, Kisharau, Chiba, Japan, (4)Fukuoka Agriculture and Forestry Research Center, Yurukanashi, Japan

Fruit quality related traits, including days to flowering (DTF), fruit weight (FW), fruit firmness (FF), fruit color (FC), soluble solid content (SC), and titratable acidity (TA), of the MAGIC population were evaluated over two years. Out of them, fruit color exhibited the highest correlation coefficient overall and was distributed normally regardless of differences in DTF, FW, FF, SC, and TA. These facts suggested that major genetic factors, which are not influenced by fluctuations in other fruit traits, could control the distribution of FC. This MAGIC population is a promising resource for genome-wide association studies and genomic selection for efficient strawberry breeding.

A genome-wide association study of 13 strawberry fruit quality-related traits was conducted to reveal critical QTLs for the relevant traits. The QTLs for fruit surface color (FSC), fruit surface region, and were mainly located on chromosomes 1, 2, and 7 of the cultivated strawberry genome (Fragaria × ananassa) is an important fruit species both in Japan and worldwide. This allotriploid species has a highly heterozygous octoploid genome. The complexities of the cultivated strawberry genome have prevented researchers from detecting quantitative trait loci (QTLs) for important agronomic traits and developing DNA markers tightly linked to these traits.

In our study, a strawberry Multi-parent Advanced Generation Inter crosses (MAGIC) population, derived from crosses using six founder strawberry cultivars: ‘Fukokka 86’, ‘Kaorinai’, ‘Sachihoko’, ‘06-A-154’, ‘Beri hoppe’, and ‘Ookainai’, was successfully developed. The population was composed of 338 individuals; genome conformation was evaluated by expressed sequence tag-derived simple short repeat (EST-SSR) markers. Cluster analysis and principal component analysis (PCA) based on EST-SSR marker polymorphisms revealed that the MAGIC population was a mosaic of the six founder cultivars and covered the genomic regions of the six founders evenly. Fruit quality related traits, including days to flowering (DTF), fruit weight (FW), fruit firmness (FF), soluble solid content (SC), and titratable acidity (TA), of the MAGIC population were evaluated over two years. Out of them, fruit color exhibited the highest correlation coefficient overall and was distributed normally regardless of differences in DTF, FW, FF, SC, and TA. These facts suggested that major genetic factors, which are not influenced by fluctuations in other fruit traits, could control the distribution of FC. This MAGIC population is a promising resource for genome-wide association studies and genomic selection for efficient strawberry breeding.

A genome-wide association analysis using high-density single nucleotide polymorphism (SNP) is useful in precisely detecting QTLs and genes. In this study, followed by Genotyping-by-Sequencing (GBS) analysis, using selected 22,112 SNPs to map QTL for nutritional, agronomic, and bacterial leaf blight (BLB) resistance traits. Wide variations and normal frequency distributions were observed for most of the traits except anthocyanin content and BLB resistance. The structural and principal component analysis revealed two subgroups. The linkage disequilibrium (LD) analysis showed 74.3% of the marker pairs in complete LD, with an average LD distance of 1000 kb and, interestingly, 36% of the LD pairs were less than 5 kb, indicating high recombination in the panel. In total, 57 QTLs were identified for ten traits, and the phenotypic variance explained (PVE) by these QTLs varied from 9% to 18%. Interestingly, 30 QTLs were co-located with known or functional genes. Some of the important candidate genes for grain Zn (Zn1) and BLB resistance were OsZFP252, OsZn1, OsZn4, OsZn5, OsZn7, OsZn11, and OsZn25. Tetraploidy genome analysis in polyploid species can be a valuable material for a breeding program for nutritious rice. Overall, the QTLs identified in our study can be used for QTL pyramiding as well as genomic selection. Some of the novel QTLs can be further validated by fine mapping and functional characterization. The results show that pigmented rice is a valuable resource for mineral elements and antioxidant compounds.

Genome-Wide Identification of the Genes Linked to Grain Nutritional Traits and Bacterial Leaf Blight Resistance in Colored Rice Population

Joong Hyoun Chin, Sejong University, Seoul, South Korea

We’ve collected 152 colored rice accession globally and evaluated in temperate and tropical condition to identify useful grain nutrition traits and pest resistance. Genome-wide association analysis using high-density single nucleotide polymorphism (SNP) is useful in precisely detecting QTLs and genes. In this study, followed by Genotyping-by-Sequencing (GBS) analysis, using selected 22,112 SNPs to map QTL for nutritional, agronomic, and bacterial leaf blight (BLB) resistance traits. Wide variations and normal frequency distributions were observed for most of the traits except anthocyanin content and BLB resistance. The structural and principal component analysis revealed two subgroups. The linkage disequilibrium (LD) analysis showed 74.3% of the marker pairs in complete LD, with an average LD distance of 1000 kb and, interestingly, 36% of the LD pairs were less than 5 kb, indicating high recombination in the panel. In total, 57 QTLs were identified for ten traits, and the phenotypic variance explained (PVE) by these QTLs varied from 9% to 18%. Interestingly, 30 QTLs were co-located with known or functional genes. Some of the important candidate genes for grain Zn (Zn1) and BLB resistance were OsZFP252, OsZn1, OsZn4, OsZn5, OsZn7, OsZn11, and OsZn25. Tetraploidy genome analysis in polyploid species can be a valuable material for a breeding program for nutritious rice. Overall, the QTLs identified in our study can be used for QTL pyramiding as well as genomic selection. Some of the novel QTLs can be further validated by fine mapping and functional characterization. The results show that pigmented rice is a valuable resource for mineral elements and antioxidant compounds.
W033: Genome-Wide Association Studies and Genomic Selection for Plant and Animal
Longitudinal Genome-Wide Association Analysis Revealed the Genetic Architectures for Dynamic Body Weights in Chickens
Congjiao Sun, China Agricultural University, Beijing, China
Body weight is a complex and important trait for animals. The genetic determinants for body weights should theoretically change with the growth of animal. Here, an experimental population of 1.512 F2 chickens derived from reciprocal crosses between White Leghorn (WL) and Dongxing chickens (DX) was used. The body weights (BW) for individuals at 30 age points from hatching to 72 weeks of age were measured. The optimal Richard model was chosen to describe the weight-age data, and the whole growth process was divided into three stages (Stage 1: 0-7 wks, Stage 2: 8-22 wks, Stage 3: 23-72 wks) at the growth inflection point and age at first egg. Body weights of all age points exhibited high SNP-based heritability estimates (0.36-0.67). According to univariate and regression genome-wide analysis, different loci were screened to significantly associated with each growth stage. Genomic region spanning from 159.8-174.4M on GGA1 was one of the most significant ones, locating at the gene of ATP7B and rs318027552 (GGA1) was one of the most significant ones, locating at the gene of ATP7B and accounted for 4.61-9.05% of the phenotypic variances. The genomic region at GGA4 and GGA27 were related to BW at stage2 and 3 respectively. A total of nine candidate genes were finally screened, and they were related to the biological functions of bone development (RB1, BST1), muscle development (LDB2, LCR1), body size (NCAPG), skeletal muscle development (FOXO1), Copper transport (ATP7B), adipogenesis (NGFR, GIP). Identification of the promising regions as well as potential candidate genes could be helpful to future marker-assisted selection and genomic selection in chickens.

W034: Genome-Wide Association Studies and Genomic Selection for Plant and Animal
A Command-Line-Interface Based User Interactive and Learning-Costless Tool for Genome Wide Association Study and Genomic Selection
Xiaolei Liu, Huazhong Agricultural University, Wuhan, China
The ultimate goals of genetic researches are to identify the genes underlying human diseases and agricultural production traits, and make accurate prediction. Genome Wide Association Study (GWAS) and Genomic Selection (GS) have been developed to achieve the goals. During the last two decades, many statistical methods and software tools of GWAS and GS were developed, such as PLINK, GCTA, BLUPF90, and DMU. The tools incorporated plenty of functions, which requires high learning costs. The genetics researchers always spend a long time reading the user manual and creating complex configure files for data analyzes. To solve this problem, we developed a command-line-interface based tool, which can reduce the learning cost by interacting with users. So far, the tool has been developed to cover the functions of PMVP, JWAS, and HIBLUP softwares, mainly including the functions of (1) construction of relationship matrix and principal components analysis, (2) variance components estimated by Brem, FEMA, H2 Regression, AI-REML, and EM-REML. (3) association tests by general linear model, mixed linear model, and FarmCPU; (4) breeding values and marker effects estimated by both statistical methods under BLUP frame work and Bayesian-alphabet methods. We believe that the abundant functions and user interactive system will facilitate the genetics researches.

W035: Genomics Applied to Tropically Adapted Livestock
The Need for Higher Productivity of Tropically Adapted Livestock
Alfred de Vries, Bill and Melinda Gates Foundation, Seattle, WA

W036: Genomics Applied to Tropically Adapted Livestock
The Unravelling of the Genomics – Environment Interactions in Tropical Chicken
Olivier Hanotte, School of Life Sciences, University of Nottingham, Nottingham, United Kingdom

W037: Genomics Applied to Tropically Adapted Livestock
Decoding Genetic Mechanisms for Adaptation in African Indigenous Sheep
Joram M. Mwacharo, International Centre for Agricultural Research Dry Areas, Addis Ababa, Ethiopia; Ahmed El Belgay, Animal Production Research Institute, Egypt, Egypt; Ayele Abebe, Ethio-Abhar University, Ethiopia, Aylgasm Abbara, University of Nottingham, Nottingham, United Kingdom, Eui-Soo Kim, Acceligen Inc. Animal Ag. Subsidiary of Recombinetics, St. Paul, MN, Barbara Rischkowsky, ICARDA, Addis Ababa, Ethiopia, Max F. Rothschild, Department of Animal Science, Iowa State University, Ames, IA and Olivier Hanotte, LiveGene – CTLGH, ILRI, Addis Ababa, Ethiopia
How animals respond to long-term alterations in temperature and precipitation patterns depends largely on the genetic architecture of traits, such as preferential fat deposition, that mediate local adaptation to current climatic conditions. African indigenous sheep are adapted to diverse environments. However, the genetic basis of this adaptation and associated traits remains poorly investigated. In a genome-wide selection signature analysis using sheep adapted to a hot-arid environment in Egypt, we revealed that multiple genomic regions spanning genes associated with thermotolerance (FGF2, GNA1, PLCB1), body size and development (BMP2, BMPA, GJA1), energy and digestive metabolism (MTH, TPHDI, AODH1A), nervous (GRIA1) and immune response (IL2, IL7, IL12, IL1RI) underpin adaptation to stressful marginal environments. Using comparative genome mapping, we identified a shared selection signature found on caprine and ovine chromosomes 12 and 10 respectively, that spans a conserved syntetic segment to bovine chromosome 12. Eight genes mapped to this common candidate region, providing possible evidence of convergent genome evolution for adaptation to a common environment in ovi-caprines. Investigations involving fat-tail, fat-rump and thin-tail African sheep identified HOX5R1, SPAG8 and PARP3 as likely candidate genes determining tail-length and tail-fat deposition, two adaptation traits in African sheep.

W038: Genomics Applied to Tropically Adapted Livestock
Adaptmap Project: Exploring Worldwide Goat Diversity and Adaptation
Alessandra Stella, National Research Council of Italy, Milano, Italy

W039: Genomics Applied to Tropically Adapted Livestock
The Tropical and Subtropical Adaptation and Genetic Diversity of Chinese Local Cattle Based on the Whole-Genome Data
Ningbo Chen, College of Animal Sci and Technology, NW Ag and Forestry Uni, Yangling, Shannxi, China

W040: Genomics Applied to Tropically Adapted Livestock
Genomic Strategies to Accelerate Breeding for Productive, Tropically Adapted Cattle
Ben J. Hayes, Department of Environment and Primary Industries, Bundoora, Australia

W041: IWGSC - Towards a Functionally Annotated Wheat Genome Reference Sequence
Frequent Intra- and Inter-Species Introrgression Shape the Landscape of Genetic Variation in Bread Wheat
Jiang Yu, CSIRO Animal, Food and Health Sciences, Brisbane, Australia

W042: IWGSC - Towards a Functionally Annotated Wheat Genome Reference Sequence
Enhancing Grain Yield By Improving Floret Fertility in Wheat
Shan Sakuma, Faculty of Agriculture, Tottori University, Tottori, Japan
Floret fertility determines the number of grains per floret. During wheat evolution, floret fertility has been increased and current broad wheat produces three to five grains per spikelet; however, little is known about the genetic basis controlling floret fertility. Here we identify the quantitative trait locus Grain Number Increase 1 (GNI1), encoding a homeodomain leucine zipper class I (HD-Zip I) transcription factor. GNI1 evolved in the Triticeae through gene duplication and functionalization. GNI1 was expressed most abundantly in the apical florus primordia at the distal end of the spikelets and in parts of the rachilla, suggesting that it acts to inhibit apical florus/rachilla growth and development. GNI1 expression decreased during wheat evolution, and as a consequence, more fertile florus and grains per spikelet are being produced. Genetic analysis revealed that the reduced-function allele of GNI1-A1 contributes to increase the number of fertile flours per spikelet. The knockdown of GNI1 in transgenic hexaploid wheat improved fertile floret and grain number. Furthermore, wheat plants carrying the impaired allele increased grain yield under field conditions. Our findings illuminate that gene duplication and functionalization generated evolutionary novelty for floret fertility (i.e. reducing floral numbers) while the mutations towards increased grain production have undergone selection post domestication.
W043: IWGSC - Towards a Functionally Annotated Wheat Genome Reference Sequence

Control of Wheat Leaf Surface Structure Under Limited Water Conditions

Nikolai V. Borisjuk, School of Life Science, Huaqin Normal University, Huaian, China

Limitation of water availability significantly limits crops productivity and the duration of drought periods is increasing due to climate change. Water preservation during the dry periods, which relies on the ability to retain accumulated water reserves, is one of the essential plant drought adaptation mechanisms. The major portion of water lost in plants occurs through leaf surfaces, contributed from stomatal transpiration and cuticle diffusion and the reduction of this loss is a promising strategy toward improving crop's drought tolerance. Therefore, during the recent years leaf cuticle and stomata became a subject of intensive investigations in relation to improve water use efficiency in cereals. This presentation will summarize information gained from the IWGSC project and the experimental data on gene networks controlling stomata development and leaf cuticle structure in wheat. A special attention will be paid to transcription factors and genes related to biosynthesis of aliphatic cuticle components and molecular factors involved in stomata biogenesis. The gene networks will be exemplified based on the characterization of Australian wheat varieties with different levels of drought tolerance which demonstrated considerable variation between genotypes in leaf surface composition and structure. The potential of the gained genomics knowledge for improving crop’s traits will be highlighted by our recent study on overexpression of transcription factor TaSHN1 in wheat.

This genetic intervention resulted in generation of transgenic wheat lines with significantly enhanced drought tolerance without yield reduction, as a consequence of altered cuticle composition and reduced stomata frequency.

W044: IWGSC - Towards a Functionally Annotated Wheat Genome Reference Sequence

Controlling Grain Size in Wheat

Huixian Zhao, Northwest A & F University, Yangling, Shaanxi, China

Wheat is an important staple food crop and the most important cereal crop in China. Wheat grain size is one of the most important agronomic traits and its genetic control is still not fully understood. In this study, we characterized two parental varieties of bread wheat, which are different in their grain size, and sequenced their genomes. We then performed a genome-wide association study (GWAS) to identify the genetic markers associated with grain size. We identified a significant QTL located on chromosome 4B, which contained a gene encoding a transcription factor. This gene was found to be differentially expressed in the parents with different grain sizes, suggesting its potential role in controlling grain size. This study provides new insights into the genetic basis of wheat grain size and opens up new avenues for improving wheat breeding.

W046: IWGSC - Towards a Functionally Annotated Wheat Genome Reference Sequence

The Wheat Cell Atlas (WCA) for a New View of the Wheat Plant

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Over the past 150 years scientists have classified cells by their structures, functions, locations, and, more recently, molecular profiles, but the characterization of cell types and states has remained surprisingly limited. Single cell genomics opens a new era with the possibilities to interrogate every cell of an organism in order to decipher the important biological processes that occur within. This has emerged as a ground-breaking technology that is greatly enhancing our understanding of the complexity of gene expression at a microscopic resolution. Bread wheat is a hexaploid derived from the hybridizations between three distinct diploid species and provides more than 20% of the protein and caloric intake of humans. Our proposed Wheat Cell Atlas (WCA) project aims to define all wheat cell types in terms of their distinctive patterns of gene expression, physiological states, developmental trajectories, and location. The project is open to collaborations and aims to build on the work of the IWGSC to map the wheat genome, by expanding functional attributes of the genome including the transcriptional landscape, epigenetic, and proteomic elements to provide fingerprints for individual cells of tissues.

Through some specific examples we will demonstrate how the WCA can provide a foundation for biological research and translational genomics: a comprehensive reference map of the types and properties of cells in the tissues of the wheat plant and a basis for understanding and defining strategies to improve trait biology for targeted genomics.

W047: Legumes Genomics

Genomic Analysis Identifies Genomic Variation and History of Peanut Breeding

Zheng Zheng, Ziqi Sun, Yuanjin Fang, Feiyuan Qi, Hingyan Huang and Xinyou Zhang, Henan Academy of Agricultural Sciences, Zhengzhou, China

The polyplidization of Arachis hypogaea was estimated to be ~3,500-4,500 years ago, since then, no evidence of natural introgression from wild species were reported due to sterility barriers and ploidy differences which resulted the isolation of cultivated peanut from other Arachis species. Therefore, in the cultivated peanuts, narrow genetic diversity and low genomic polymorphism with lack of variation at molecular level were widely recognized. On the other hand, morphological characteristics were observed in the cultivated peanuts. Based on these characteristic features, peanuts were classified into two subspecies (subsp. hypogaea and subsp. fastigiala), which were further divided to six botanical groups on the basis of different growth habits, seeds/pods morphology and inflorescence characteristics. These morphological differences resulted diversification in peanuts is considered mainly caused by intensive selection pressure during cultivation. However, the population structure of genetic variation between subspecies and botanical groups besides sweeps of selection during domestication and improvement by plant breeding activities in peanuts remain largely elusive. The assembly of peanut genome is very challenging not only because the close relatedness between the A and B subgenomes, but also on account of 64% repetitive sequences contents in the genome. Recently, the International Peanut Genome Initiative (IPG) as well as two other independent groups announced finishing assembly of the cultivated peanut genome sequences makes it possible to explore the genetic basis of diversity and domestication of peanuts via population genomics. To understand genome diversity and evolution in cultivated peanuts, we re-sequenced a population comprised worldwide cultivated peanut accessions. In addition, we identified loci associated with several important agronomical traits for peanut breeding by conducting a genome-wide association study (GWAS).
W048: Legumes Genomics
The Genome of Cultivated Peanut Reveals a Differential A and B Subgenome Evolution after Tetraploidization
Weijian Zhuang, Hua Chen, Chong Zhang, Rajev K. Varshey, Mengyang, Xiyin Wang, Quang Yang, Yue Deng, Dongyang Xie and Teicheng Cai
Fujian Provincial Key Laboratory of Plant Molecular and Cell Biology, Oil Crops Research Institute, Fujian Agriculture and Forestry University, Fuzhou, Fujian, China.
Center of Excellence in Genomics & Systems Biology, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India.
1 Nexomics Biosciences Institute, Wuhan, Hubei, China. Tangshan, Hebei, China.
3 North China University of Science and Technology.
Arachis hypogaea (peanut or groundnut) is a globally important crop of oil and protein. Here, we report a high-quality reference genome sequence for tetraploid peanut. We assembled a genome of 2.54 Gb with 20 chromosomal pseudomolecules, predicted 83,709 protein-coding gene models supported by extensive expression data, and provided insights into the evolution of A. hypogaea after tetraploidization. B subgenome showed more gene expansion (12.46% versus 0.85%) than A subgenome compared with their corresponding ancestors after tetraploidization. A total of 30,596 non-redundant peanut genes were identified including 24,208 homeolog pairs genes which demonstrated widespread differential expression with dominant expression much more frequent among B homeologs. The B subgenome is more similar to A. ipaensis with more anchored contigs (55.8% of assemblies) and shared more (38,417) colinear genes. More A subgenome genes (58.7% of 629) were converted by their B subgenome counterparts. Consequently, peanut A subgenomes underwent more unbalanced structural rearrangements after tetraploidization and in LTR transposable elements expanded only after tetraploidization, but B subgenome mainly derived from A. ipaensis. The results not only explain the prevalence of dysfunctional expression or loss of A subgenome homologs but also deny the sequenced A. duranensis was the A subgenome progenitor.

W049: Legumes Genomics
The Genomes of Cultivated Peanut and Its Suspected Wild Progenitors
Xiaoping Chen, Crops Research Institute, GAAS, Guangzhou, China

W050: Legumes Genomics
Genomic Basis for Environmental Adaptation Revealed By Resources of Lotus Japonicus
Shasei Sato, Graduate School of Life Sciences, Tohoku University, Sendai, Japan
A quarter of a century has passed since Lotus japonicus was proposed as a model legume because of its suitability for molecular genetic studies. Since then, a comprehensive set of genetic resources and tools has been developed, including cDNA clones with expressed sequence tag (EST) information, genomic clones with end-sequence information, a reference genome sequence, reconstituted inbred lines (RILs), published mutant lines, a collection of wild accessions and a large collection of mutant lines tagged with endogenous retrotransposon (LORRET) insertions. Resource centers in Japan and Denmark ensure easy access to data and materials, and the National BioResource Project (NBRP) Lotus and Glycine, the Japanese resource center, renewed its web database, “LegumeBase”, as a kickoff of the phase 4 in 2017. Among these resources, more than 200 wild accessions of L. japonicus have been collected from throughout Japan. To facilitate genome-wide association (GWA) analysis using these material resources, 135 accessions were re-sequenced. Based on the obtained genotype data, the wild accessions of L. japonicus in Japan could be separated into three major sub-populations and these sub-populations thought to have been established on Kyushu Island. To investigate the genetic loci related to local adaptation, we carried out phenotyping of over 100 accessions on Koshimadai field in Miyagi, the northeast region of Japan. The ability to survive cold winters could be considered as a relevant trait during the migration of L. japonicus from South to North, and thus phenotypic data on winter hardness were collected. As a result of GWAS analysis of the over-winter survival rate, we identified two significant signals on chr1 and chr6. Alleles on chr1 were found in all sub-populations with biased proportion, whereas the northern allele on chr6 was identified in a single sub-population. The result suggests that L. japonicus has applied both existed variation and novel mutations for colonization in Japan. Along with the collection of their natural symbionts, the established research materials of wild accessions of L. japonicus could be a good resources for ecological and evolutionary studies. The materials and information resources of wild accessions of L. japonicus are available from LegumeBase (https://www.legumebase.brc.miyazaki-u.ac.jp) and LotusBase (https://lotus.mz.riken.jp).

W051: Legumes Genomics
Monticula Genome Abstract
Dongmei Yin, College of Agronomy, Henan, China

W052: Modern SNP technologies in plants: From tools in laboratory to commercial service
GWAS-Based Search for Significant SNPs and Target Genes for Development of Potato with Genetically Designed Starch Properties
Vadim Khlestin 1,2, Irina Rozanova1, Tatiana Eer1, Lubov Gvozdeva1, Vadim Efimov1 and Elena Khlestkina 1, (1) Institute of Cytology and Genetics, Novosibirsk, Russian Federation, (2) Research Institute of Farm Animal Genetics and Breeding, Saint Petersburg, Russian Federation, (3) Vavilov All-Russian Institute of Plant Genetic Resources, Saint Petersburg, Russian Federation
Starch is one of the most important, renewable and economical organic resource of the humankind. Due to simplicity of potato tuber starch industrial isolation, potato is one of the most important starch sources. Additional benefits of potato starch are its natural purity, high molecular weight, high degree of phosphorylation, resulting into useful industrial properties, like higher starch gel viscosity, freeze/thaw stability, neutral taste and flavor, clearness, more predictable behavior in chemical and biochemical transformations.
There are plenty of publications about comparative studies of starch extracted from different crop species, while imprecise variation of starch properties are not widely investigated.
Starch yield is the only heritable trait assessed in genetic studies and breeding programs. Meanwhile, intraspecific forming of commercially viable seedstock properties may become a beneficial ideology for potato and potato starch production. Genome and marker assisted selection may promote breeding potato varieties with starch specially tuned for certain beneficial ideology for potato and potato starch production. Genome and marker assisted selection may promote breeding potato varieties with starch specially tuned for certain beneficial ideology for potato and potato starch production.

W053: Modern SNP technologies in plants: From tools in laboratory to commercial service
Target SNP-Seq Technology and Its Application in Genetic Analysis of Cucurbits Crvars Varieties
Changlong Wen, Jian Zhang and Jingjing Yang, Beijing Vegetable Research Center (BVRC), Beijing, China
As the third-generation molecular markers, single nucleotide polymorphism (SNPs) are widely used in genotyping and genetic research. Although many SNP-based genotyping platforms are available, the accuracy, flexibility and affordable genotyping cost are still limiting the utility. In this study, we developed a new method called target SNP-seq which harboring stable flanking sequences and unique in these crops were discovered based on varicone information. And the sets of 163, 251 and 151 perfect SNPs were detected and selected from a total of 30,169,204 SNPs in resequencing datasets of 182 cucumber, 400 watermelon and 56 melon accessions, respectively. These perfect SNPs were screened using multiplex PCR of target SNP-seq technology in cucurbits varieties, then the PCR products were constructed as Library and sequenced on Illumina HiSeq X Ten platform. This study analyzed 261 cucumber, 388 watermelon and 201 melon varieties by sequencing perfect SNPs with each SNP coverage more than 2000 times. Genetic diversity and population structure of 850 cucurbits varieties were analyzed. The Chinese cucumber varieties were identified as four subgroups, the north China type, the south China type, the Europe type, the Xishuangbanna type, and the Chinese watermelon varieties were classified as three subgroups, the East Asia type, the America type, the Asia-America type, as well as the Chinese melon varieties were divided into three subgroups the thick-skin type, the thin-skin type and the mixture type. Furthermore, the narrow genetic diversity of cucurbits varieties was observed and the genetic erosion risk in breeding system was confront of community. Finally, the according core set of SNPs in distinguishing cucurbits varieties in China were calculated, and the core cucurbits varieties were identified as backbone varieties in Chinese market. Therefore, this study provided a new method in genotyping SNPs and a perfect SNP discovery protocol were established in genetic research, and in DNA fingerprint analysis of cucurbits crops. The high efficiency and low cost of target SNP-seq has excellent application prospects in promoting plant breeding process in near future.
W054: Modern SNP technologies in plants: From tools in laboratory to commercial service
Development and Application of FcRAN1-Based SNP Marker for Fig Sex Identification
Hidetoshi Iegami1, Kenta Shirasawa2, Hiroshi Yukishii3, Shuichi Himeno3 and Hiroshi Nogata1, (1)Fukuoka Agriculture and Forestry Research Center, Yukuhashi, Japan, (2)Kazusa DNA Research Institute, Kisarazu, Japan, (3)Institute of Fruit Tree and Tea Science, NARO, Higashihiroshima, Japan, (4)Fukuoka Keichiku Agricultural Extension Center, Yukuhashi, Japan

Fig (Ficus carica L.) is a gymnosporous species with bisexual flowers (male caprifs) and unisexual female trees. Fig is a permanent crop, but only female figs are edible. Thus, discriminating the sex phenotype at an early stage is crucial for fig breeding programs. We previously completed a linkage analysis with a SNP-based high-density genetic map, which was established based on restriction site-associated DNA sequencing. A genome-wide association study and a whole-genome ressequencing analysis of our genetic resources identified a fig RAV1-like gene (PrfRAN1). This gene is a prime candidate for the fig sex-determining gene because it can fully explain the sex phenotype. Here, we show the development of a duplex allele-specific marker that exclusively targets FcRAN1 as a primary selection marker prior to high-throughput genotyping. We are currently applying the developed marker in our breeding program to expand the breeding scale. This marker developing method is not restricted by primer design. Moreover, the marker is practically co-dominant and can be easily analyzed with minimal experimental equipments. However, because non-specific amplifications may be problems associated with this method, some experimental solutions for minimizing these potential issues are also discussed.

W055: Modern SNP technologies in plants: From tools in laboratory to commercial service
Climate Adaptation of Prunus mume, Native to China, Associated with Its Chilling Requirements
Xiao Huang, Nanjing Agricultural University, Nanjing, China

Prunus mume Sieb. et Zucc., is an important fruit crop of the subtropical region, originating in China. P. mume blooms earlier than other deciduous fruit trees, but different regions have different blooming periods. The time of anthesis is related to the dormancy period, and a certain amount of chilling can break dormancy. To identify the relationship between chilling requirements and the climate adaptation of P. mume cultivars in China, the nuclear and chloroplast genomes of 19 cultivars from the main cultivation areas of P. mume in China were re-sequenced. The studied accessions were divided into three groups based on their chilling requirements: low, medium and high. Associated with the chilling requirement groups, 21 selective sweep regions based on Specific-Locus Amplified Fragment (SLAF) with SNP were identified, which could provide evidence supporting the model of P. mume domestication originating due to natural selection. Furthermore, we identified a flowering gene, FRIGIDA LIKE 1 (FLR1), seems to affect the chilling requirements and the climate adaptation of P. mume cultivars. This study is a major step toward understanding the climate adaptation of P. mume cultivars in China.

W056: Modern SNP technologies in plants: From tools in laboratory to commercial service
SeqSNP Targeted Genotyping By Sequencing, an Alternative to Array Genotyping in Routine Breeding Programs
Jason Hein, LGC, Biosearch Technologies, Alexandria, MN

Comprehensive assessment of complex traits and genetic selection has up to recently been possible using fixed arrays. SeqSNP, a refined targeted genotyping by sequencing technology has been developed by LGG, Biosearch Technologies. SeqSNP not only provides flexibility in single nucleotide polymorphism (SNP) sequence selection, but also scalability in sample numbers which can be restrictive on fixed arrays. Independently analysed data is presented here, which not only substantiates that the SeqSNP service delivers genotyping data with high concordance to array genotyping, but it also surpasses other sequence based genotyping options in de novo SNP discovery and the analysis of multi-allelic target SNP sequences. The impact of increased accuracy allows cost efficiency and increased confidence in selections made using targeted genotyping by sequencing. SeqSNP is the next stage in sequence based genotyping as services or bespoke kits for all breeding communities.

W057: Modern SNP technologies in plants: From tools in laboratory to commercial service
Plant Genotyping with Application of Amplifluor-like SNP Markers
Satyavady Jatayev1, Lyudmila Zotova2, Gulmirza Khashanova2, Akmaral Baidyusen1, Katso Lethola2, Maryam Aldammas 2 and Yuri Shavruk2, (1)Seifullin Kazakh AgroTechnical University, Nur-Sultan, Kazakhstan, (2)Flinders University, Adelaide, Australia
Various methods exist for the analysis of Single nucleotide polymorphisms (SNP), most of which have been commercialised by companies that offer either reagents and kits or full genotyping services. The Amplifluor (Amplification with Fluorescence) SNP method is based on competitive allele-specific PCR, similar to the principles applied in KASP markers. The use of Fluorescence in SNP genotyping allows for a one-off order that can be used in all further experiments. Allele-specific primers can then be designed and ordered as for regular oligos. The high degree of freedom in the design and adjustment of genotyping can be an attractive prospect for researchers working with Amplifluor-like SNP markers. A diverse range of SNP genotyping studies using self-designed Amplifluor-like markers is presented, showing the analysis of many genes in a number of different plant species. Examples include: Transcription factors TaBRRT and TaMYCT1; and transcriptional regulator TaDVI in wheat; intracellular vesicle trafficking genes, CaRatlC-GTP in chickpea; HsPhoC and Hs-SAP genes encoding phytocrome C and stress-associated proteins in barley, respectively; chitinase gene, HsSP2 and HsSE2, in sugar beet; as well as genetic polymorphism in different species of crested wheatgrass, Agropyron. The analyses of candidate gene expression presented demonstrate the suitability of Amplifluor-like SNP markers for accurate genotyping results. All candidate genes were confirmed in response to the studied stresses and conditions, and, therefore, the developed Amplifluor-like SNP method represents a very useful tool for Marker-assisted selection.

W058: Modulating Plant MicroRNAs by Short tandem Target Mimic (STTM) For Crop Improvement
An Update on the Application of STTM in Crops
Lin Liu, Shenzhen University, Shenzhen, China

Plant microRNAs (miRNA) are endogenous small non-coding RNAs that play key roles in plant development, adaptation to stresses and flexible environments through regulating the expression of their target genes post-translationally. Extensive studies have demonstrated that miRNAs are critical for regulating agronomic traits of important economic crops such as rice, maize and soybean, and have great potential in improving crop traits. The interrogation of miRNA functions requires effective, widely applicable methods to specifically block miRNA miRNA function. Short tandem target mimic (STTM) technology has been developed to specifically deactivate endogenous miRNAs and siRNAs by mimicking small RNA target sites in plants. Here, we applied the STTM technology to maize to investigated functions of conserved monocot specific miRNAs. We optimized the STTM knockdown efficiency by replacing 35S promoter which drives the STTM expression with maize Ubiquitin promoter. Four monocot specific miRNAs were successfully deactivated and their potential functions have been revealed, demonstrating that STTM technology is an effective approach for functional dissection of miRNAs in maize.

Hui Zhang, Shanghai Normal University, Shanghai, China

W059: Modulating Plant MicroRNAs by Short tandem Target Mimic (STTM) For Crop Improvement
A Resource for Inactivation of Micrornas Using Short Tandem Target Mimic Technology in Model and Crop Plants
Guiliang Tang, Michigan Technological University, Houghton, MI

W060: Modulating Plant MicroRNAs by Short tandem Target Mimic (STTM) For Crop Improvement
Climate Adaptation of Prunus mume, Native to China, Associated with Its Chilling Requirements
Xiao Huang, Nanjing Agricultural University, Nanjing, China

Prunus mume Sieb. et Zucc., is an important fruit crop of the subtropical region, originating in China. P. mume blooms earlier than other deciduous fruit trees, but different regions have different blooming periods. The time of anthesis is related to the dormancy period, and a certain amount of chilling can break dormancy. To identify the relationship between chilling requirements and the climate adaptation of P. mume cultivars in China, the nuclear and chloroplast genomes of 19 cultivars from the main cultivation areas of P. mume in China were re-sequenced. The studied accessions were divided into three groups based on their chilling requirements: low, medium and high. Associated with the chilling requirement groups, 21 selective sweep regions based on Specific-Locus Amplified Fragment (SLAF) with SNP were identified, which could provide evidence supporting the model of P. mume domestication originating due to natural selection. Furthermore, we identified a flowering gene, FRIGIDA LIKE 1 (FLR1), seems to affect the chilling requirements and the climate adaptation of P. mume cultivars. This study is a major step toward understanding the climate adaptation of P. mume cultivars in China.
W063: Nitrogen-fixing Root Nodule Symbiosis: Genetics, Evolution, and Engineering for Future Crops

Yu Zhang, Agricultural Genome Institute at Shenzhen, CAAS, Shenzhen, China

Plants play a crucial role in ecosystem, food, nutrition, and medicine; while genome, the basic source code of life, is the fundamental connection in context of biodiversity that helps us better understand and exploit innovative traits in evolution through big data mining, resulting in a huge potential in science as well as in application. Many plant specialized genetic pathways of nitrogenase reductase (Fe protein) and dinitrogenase (XFe protein, where X is equivalent to Mo, V, or Fe, depending on the heteromeric composition of the active site cofactor) catalyze the biological reduction of N₂ into NH₃, i.e., 2NH₃ + nH₂ (n ≥ 1).

W064: Nitrogen-fixing Root Nodule Symbiosis: Genetics, Evolution, and Engineering for Future Crops

Yu Zhang, Agricultural Genome Institute at Shenzhen, CAAS, Shenzhen, China

Using Ovine High-Density 600 K SNP Array

W065: Nitrogen-fixing Root Nodule Symbiosis: Genetics, Evolution, and Engineering for Future Crops

Pathway Discovery in Deep Convergence: Big Data in Phylogenomics for Nitrogen-Fixing Root Nodule Symbiosis

Shifeng Cheng, Agricultural Genomics Institute at Shenzhen, CAAS, Shenzhen, China

Plants play a crucial role in ecosystem, food, nutrition, and medicine; while genome, the basic source code of life, is the fundamental connection in context of biodiversity that helps us better understand and exploit innovative traits in evolution through big data mining, resulting in a huge potential in science as well as in application. Many plant specialized genetic pathways of nitrogenase reductase (Fe protein) and dinitrogenase (XFe protein, where X is equivalent to Mo, V, or Fe, depending on the heteromeric composition of the active site cofactor) catalyze the biological reduction of N₂ into NH₃, i.e., 2NH₃ + nH₂ (n ≥ 1).

W066: Nitrogen-fixing Root Nodule Symbiosis: Genetics, Evolution, and Engineering for Future Crops

Comparative "Omics" of Nitrogen-Fixing Nodulated Plants

Yu Zhang, Agricultural Genome Institute at Shenzhen, CAAS, Shenzhen, China

Using Ovine High-Density 600 K SNP Array

W067: Non-Chinese Young Scientists Working on Animal Genomics Diversity and Association Study of Copy Number Variation in Worldwide Sheep

Plastid Phylogenomic Insights into the Evolution of Legumes

Ting-Shuang Yi, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China

The family Fabaceae (Leguminosae) is the third largest angiosperm family in terms of species richness with c. 770 genera and over 19,500 species. Leguminosae are diverse in habit and ecology, morphology, and biochemistry, and many domesticated legumes have played a major role in the development of agriculture. Approximately 88% of legume species have the ability to make associations with nitrogen fixing bacteria via root nodules and hence are important for sustainable agriculture and ecosystem function. However phylogenetic resolution in the backbone of the Leguminosae remains poor, which has greatly blocked the correct understanding of the nitrorgen fixation in this lineage. Our analyses on plastomes from representative species of major clades of Leguminosae resolved some long-controversial deep relationships, particularly in the subfamilies Caesalpinioideae and Papilionoideae. The robust phylogenetic backbone reconstructed in this study establishes a framework for future studies on classification, evolution and diversification of this important plant family. Based on the newly reconstructed scheme, we used newly developed tool of ARACHIS to reconstruct ancestral plastome architecture of Fabaceae and explored the factors associated with structural variations across those plastomes. We found that the loss of inverted repeats was related to the occurrence of inversion, and that the occurrence of inversions was highly correlated with the substitution rates.
Afar, Begait, Central Highland and Meafure goat populations, respectively. We identified 731 polymorphisms (SNPs) as well as 123,577 insertions and deletions. Specially, 11,137,576, re-sequencing of 44 Ethiopian indigenous goats produced 16 million single-nucleotide.

**LiveGene – CTLGH, ILRI, Addis Ababa, Ethiopia**

**Unique Trypanotolerant Adaptation**

**Whole Genome Sequence Analysis of West African Taurine Reveals Their Functional annotation of genes within candidate regions reveals genes involved in pathways,**

**Non-Chinese Young Scientists Working on Animal Genomics**

**Whole Genome Re-Sequencing Reveals Selection Signatures Associated with Important Traits in Ethiopian Indigenous Goat Populations**

**Haile Berihulay Gebereselassea**

**Whole Genome of the remaining four Ethiopian goat breeds. The comparative population genomic analysis provides useful genetic information associated with important traits. Whole-genome**

**Stress**

**Genomic Characterization and Introgression of Indigenous Cattle Breeds of Pakistan**

**Endashaw T. Assegidaw**

**Genetic background governs animal adaptation to environment. Adapted animals genetically withstand environmental challenges and reproduce. The genetic control of adaptive traits may be revealed following signature of selection analysis. Taking advantage of the diversity of Ethiopian auro-ecologies, we analyzed at autosomal genome level the diversity and genetic control of environmental adaptive traits of four indigenous Ethiopian cattle, representing populations living at high altitude (HA): Bale (3586m) and Semien (3732m), and low altitude (LA), Afar (792m) and Baguria (688m). A total of 36,368,321 SNPs were identified following alignment against the new cattle genome of reference (ARS-UCD1.2). Genome-scale wide for candidate positive signature of selection were analyzed using within population pooled heterozygosity (θp) and between population differentiation (Fst) tests. θp analysis reveals 177, 130, 119 and 96 candidate genes under positive selection in Afar, Baguria, Bale and Semien cattle, respectively, and 191 genes were identified in Fst test contrasting the two LA and HA populations.**

**Master). We achieved ~10 X to ~41 X genome coverage after mapping the clean reads to the bovine reference genome (ARS-UCD1.2) for each of the sequenced animals. A total of 16.56 million single nucleotide polymorphisms (SNPs) and 1.05 million insertions-deletions (indels) were detected across the whole genomes with 3.06 million SNPs and 0.389 million indels to be common and possibly associated with important traits with Begait goat population. After the annotations of functional genes linked with these genomic regions, we found 36 Gene ontology (GO) terms (17 in biological processes, 12 in molecular function and 7 in cellular components) and 6 Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways. Several candidate genes are related to the body growth and milk production traits (ZNF385B, GLYCAM1, PDE1B, and PPP1R14A), reproduction/fertility traits (MCPT1 and STK35), thermotolerance (MAPK1, MAPK13 and MAPK14) and immune response (UCN7, IL12A, and DEFB119). Our investigation contributes to deliver valuable genetic information and paves the way to design conservation strategy, breed management, genetic improvement, and utilization programs.**

**Pakistan. The breeds can be divided into three geographic regions: (1) Indus valley, tropically adapted, milk and dual purpose breeds (Achai and Gabrialli); and (2) Upper Pakistan, high-altitude adapted, milk and dual purpose breeds (Achai and Gabrialli); and (3) Mehrgarh, near the Arabian Sea coast, milk and beef breeds (Red Sindhi, Bhugari and Nari Master). We achieved ~10 X to ~41 X genome coverage after mapping the clean reads to the bovine reference genome (ARS-UCD1.2) for each of the sequenced animals. A total of 16.56 million single nucleotide polymorphisms (SNPs) and 1.05 million insertions-deletions (indels) were detected across the whole genomes with 3.06 million SNPs and 0.389 million indels to be novel. Comparative analyses revealed the diversity and the history of cattle domestication in this region. The SNPs in the coding region showed a close relation between the Indus valley and Mehrgarh regions. Sahiwal, Cholistan, Tharparker, Dajal and Bhugari tend to share the highest number of heat tolerant and immune regulatory genes. Achai and Gabrialli show a separate clad from rest of the breeds, depicting their taurine introgression following migratory routes towards China and Afghanistan borders. The current study elaborates the potential in the indigenous cattle breeds of Pakistan. Our results demonstrate the variation and baseline information for further investigation to prompt rational conservation and sustainable exploitation of economically important traits of cattle in the country.**

**Genomic Mapping Identifies The Causative Gene MC1R For The Coat Color Variation In Chinese Tan Sheep**

**Non-Chinese Young Scientists Working on Animal Genomics**

**Whole Genome Sequence of West African Taurine Reveals Their Unique Trypanotolerant Adaptation**

**Abdul fattah Tijani. LiveGene – CTLGH, ILRI, Addis Ababa, Ethiopia**

**The West African taurine represent a unique group of indigenous African cattle population. They possess the ability to thrive in their local production environment where trypanosomiasis is endemic. In this study, we investigated the signatures of selection across the genome of two trypanotolerant West African taurine breeds (WAT), the shorthorn Murnu and the longhorn N’Dama, using six selection scan tests. Each of the trypanotolerant cattle was compared to two groups of trypanosusceptible cattle populations (African zebu and European taurine). Functional annotation of genes within candidate regions reveals genes involved in pathways, e.g. T cell and B cell activation and Natural Killer Cell mediated cytotoxicity, that are relevant to trypanosomiasis disease progression. The list of common genes between Murnu and N’Dama were investigated further. Our findings identify PTPN6 involved in several of these pathways. Protein-protein network indicates its pivotal role through its interactions with bovine MHC class II genes and other genes, and therefore a possible central role of the gene in the initiation and control of a cascade of biological processes necessary to confer protective immunity linked to trypanotolerance. The importance of PTPN6 is further supported by the presence of an unique WAT haplotype closed to fixation. Our results support that PTPN6 gene is linked to the trypanotolerance status of the WAT calling for further functional investigation of the gene.**

**Kurt-al-Ain Hanif. Pakistan Inst. of Engineering and Applied Sciences, Islamabad, Pakistan and Jian-Lin Han, CAAS-ILRI Joint Lab, Inst. of Anim. Sci., CAAS, Beijing, China**

**Indus valley civilization and Mehrgarh in Pakistan represent one of the oldest civilizations in Asia. The early Neolithic periods and Fertile Crescent gave rise to the first domesticated cattle, which later became the most important livestock in the world. The diverse pattern of cattle demographic history and the genetic diversity under natural and/or human selection in Pakistan need to be addressed. To understand the genetic architecture and variation of such a rich civilization supported by cattle farming, we re-sequenced the complete genomes of 50 animals from 10 geographically isolated and phenotypically distinct representative breeds from all over Pakistan. The breeds can be divided into three geographic regions: (1) Indus valley, tropically adapted, milk and dual purpose breeds (Sahiwal, Cholistan, Tharparker, Dajal and Bhugari); and (2) Upper Pakistan, high-altitude adapted, milk and dual purpose breeds (Achai and Gabrialli); and (3) Mehrgarh, near the Arabian Sea coast, milk and beef breeds (Red Sindhi, Bhugari and Nari Master). We achieved ~10 X to ~41 X genome coverage after mapping the clean reads to the bovine reference genome (ARS-UCD1.2) for each of the sequenced animals. A total of 16.56 million single nucleotide polymorphisms (SNPs) and 1.05 million insertions-deletions (indels) were detected across the whole genomes with 3.06 million SNPs and 0.389 million indels to be novel. Comparative analyses revealed the diversity and the history of cattle domestication in this region. The SNPs in the coding region showed a close relation between the Indus valley and Mehrgarh regions. Sahiwal, Cholistan, Tharparker, Dajal and Bhugari tend to share the highest number of heat tolerant and immune regulatory genes. Achai and Gabrialli show a separate clad from rest of the breeds, depicting their taurine introgression following migratory routes towards China and Afghanistan borders. The current study elaborates the potential in the indigenous cattle breeds of Pakistan. Our results demonstrate the variation and baseline information for further investigation to prompt rational conservation and sustainable exploitation of economically important traits of cattle in the country.**

**Genomic Mapping Identifies The Causative Gene MC1R For The Coat Color Variation In Chinese Tan Sheep**

**Gebremedhin Gebreselassie Hidaru, Institute of Animal Science, Beijing, China**

**Non-Chinese Young Scientists Working on Animal Genomics**

**Whole Genome Sequence Analysis of West African Taurine Reveals Their Unique Trypanotolerant Adaptation**

**W070:**

**W069:**

**W068:**
W073: Poultry Genomics and Biotechnology
Chicken Gene Editing and Model Development
Jae Yong Han, Seoul National University, Seoul, South Korea
Avian species, especially chickens, have been recognized as ideal animal models due to their unique embryogenesis, although there are distinct characteristics compared to human species physiologically and genetically. Various genome editing techniques have been used to develop model chickens and the simplicity and versatility of clustered regularly interspaced short palindromic repeats (CRISPR) and CRISPR-associated protein 9 (Cas9) technology has led to a widespread application of genome editing tools in avian species as in other species. Here, we applied the novel genome editing system by applying CRISPR/Cas9 and non-homologous end joining (NHEJ) pathway, which has previously not been applied to avian species before. Based on the genome editing strategy, we developed the novel germ cell tracing chicken model by gene tagging into the chicken germ cell-specific gene to analyze germ cells at whole developmental stages in chickens. And, we also developed a sexing chicken model by targeted gene disruption of sex determination factor gene, which play a major role in male sex determination. This chicken model can be used to broaden knowledge of the molecular mechanism governing sex determination in avian species. Collectively, we expect that the simple and efficient genome editing method will facilitate the production of genome-edited chickens for diverse purposes by gene tagging, targeted gene insertion and targeted gene disruption.

W074: Poultry Genomics and Biotechnology
circFOXO3 Acts As a Kern in Regulating Global DNA Methylation By Sponging Mir-29-3p
Qinghua Nie, South China Agricultural University, Guangzhou, China

W076: Poultry Genomics and Biotechnology
Gene Expression Network Comparison Identifies Conserved Network Modules for Chicken Adipogenesis
Zhi-Qiang Du, Northeast Agricultural University, Harbin, China
Excessive fat deposition in chickens could adversely affect the production efficiency, and meat product processing and quality, causing economic losses to the industry. However, the molecular underpinning of the complex adiposity trait remains elusive. In the current study we employed the weighted gene co-expression network analysis (WGCNA) method on four transcriptome profiling datasets from our and French chicken lines under divergent selection for abdominal fat content, to delve further into the gene regulatory networks underlying adipose tissue growth and development. After functional enrichment analysis, 9 network modules were discovered to be of importance, involved in lipid metabolism, PPAR and insulin signaling pathways, containing hub genes related to adipogenesis, cell cycle, inflammation and protein synthesis. Furthermore, common sub-modules of similar functionality for chicken fat deposition were identified after functional annotation and comparison of network modules. Thus, common molecular pathways could be underlying the growth and development of adipose tissues even in different chicken lines. Our findings provide novel insights into the genetic basis of complex traits, which could help animal breeding practices, and further investigation into human obesity and related metabolic diseases.

W077: Ruminants Genomics
Recent Advances in Yak Genomics
Jian-Lin Han, CAAS-ILRI Joint Lab, Inst. of Anim. Sci., CAAS, Beijing, China

W075: Poultry Genomics and Biotechnology
Functional Analysis of PIWI Protein and piRNAs during Chicken Spermatogenesis
Guohua Chang, Yangzhou University, Yangzhou, Jiangsu, China, Yangzhou, China
Germ cells are responsible for the generation of genetic information, and their genomic characteristics, expression and regulation patterns are essential for individual and species maintenance. In this study, we analyzed the function of Piwi and piRNAs in spermatogenesis from several side like: the profile of small RNAs in the germ cells of different stages of spermatogenesis was analyzed, the profile of piRNAs which combine with PIWI protein, the relationship between piRNAs and target genes, the function of Piwi in meiosis and the effect of spermatogenesis to chicken after knockout Piwi and found that chicken piRNAs do bind to PDH1 proteins and participate in the regulation of chicken spermatogenesis and proliferation and differentiation of stem cells. Through bioinformatics analyses and functional verification, we found that piRNA-19128 involves in the process of spermatogenesis in the meiosis by targeting RIT and inhibiting its transcription. Finally, we constructed piwi1-knockout chicken using CRISPR/Cas9 and found that the knockout Piwil1 in chicken had no influence on the body weight but sperm quality, which including decreased sperm viability and activity, unobvious cloudiness, and lower volume of sperm. In summary, the Piwil1 was involved in spermatogenesis and play an important role in poultry. This study provides the theory for biological function in poultry and the improvement of poultry fecundity, and also add new information for the study of epigenetic regulation mechanism of germ cell and spermatogenesis.

W078: Ruminants Genomics
Comparison of Long Non-Coding RNA Expression Profiles of Cattle and Buffalo Differing in Muscle Characteristics
Hui Li, Kongwei Huang, Pengcheng Wang and Qingyou Liu, Guangxi University, Nanning, China
Buffalo meat is of good quality because it is lean and tender, which can confer significant cardiovascular benefits. However, the regulatory mechanisms of IncRNA underlying differences in meat quality are largely unknown. The chemical-physical characteristics results revealed that under the same breeding and management, the muscle quality of buffalo can be equivalent to that of cattle, but there are significant differences in shear force and muscle fiber structure. Then we examined IncRNA expression profiles of cattle and buffalo skeletal muscle to provide first insights into their potential involvement in buffalo myogenesis. Total RNAs from longissimus thoracis muscles of buffalo and cattle were used to construct libraries for Illumina next-generation sequencing using the Ribo-Zero RNA sequencing method. Here we profile the expression of IncRNA in cattle and buffalo skeletal muscle tissue, and detect 16,236 IncRNA candidates with 865 up-regulated IncRNAs, while 1,296 down-regulated IncRNAs when comparing buffalo to cattle muscle tissue. We constructed co-expression and cell networks, and found IncRNA MST84.469303.0, MST84.469303.4, and MST84.203758.46 could be as competitive endogenous RNA (ceRNA) containing potential binding sites for miR-1-206 and miR-133a. Tissue expression analysis showed that MST84.469303.0, MST84.469303.4, and MST84.203758.46 were highly and specifically expressed in muscle tissue. Our study may serve as a starting point for in-depth investigations into the roles played by several of those IncRNAs during buffalo myogenesis.

W079: Ruminants Genomics
Whole-Genome Resequencing Reveals Selection Signatures for Body Size in Chinese Buffalo
Yi Zhang, College of Anim. & Tech., China Agricultural University, Beijing, China

W080: Ruminants Genomics
Whole-Genome Sequencing Reveals the Genetic Mechanisms Underlying the High-Altitude Adaptation in Tibetan Horses
XueXue Liu, Institute of Animal Science, CAAS, Beijing, China

W081: Ruminants Genomics
Strong Signatures of Selection in Three Korean Cattle Breeds Exposed to Different Selective Pressures
Kwan-Suk Kim, Chungbuk National University, Cheongju, South Korea
Admixture

Taehyung Kwon
Li-juan Qiu

Li-juan Qiu, Institute of Crop Science, CAAS, Beijing, China

Landraces often contain genetic diversity that has been lost in modern cultivar, including alleles that confer enhanced local adaptation. Here we show the comprehensive identification of loci associated for flowering time using GWAS approach in soybean landraces. iGBS was used to genotype 9,358 diverse landraces representing the genetic diversity of soybean and 97 accessions of the wild progenitor of cultivated soybean, Glycine soja. Based on 99,085 high quality SNPs, landraces were classified into three populations which exhibit geographical genetic differentiation. Using phenotypic data collected at two locations separated by 30 degrees of latitude, 17 SNPs associated with flowering time were identified; and 13 of these co-localize with previously identified flowering time genes or QTLs. Allele frequency and Fst analyses showed significant population differentiation for the 17 flowering time TASs among the three populations of landraces. Of the 17 TASs, six experienced selection during both domestication and subsequent landrace diversification and adaptation; three underwent selection only during domestication; six underwent selection only during landrace diversification and adaptation; and two did not exhibit signals of selection. Using passport data associated with the collection sites of the landraces, 27 SNPs associated with adaptation to three bioclimatic variables (temperature, day length, and precipitation) were identified. A series of candidate flowering genes were detected within the linkage disequilibrium (LD) blocks surrounding 12 bioclimatic TASs. Nine of these TASs exhibit significant differences in flowering time between alleles within one or more of the three individual sub-populations. Signals of selection during domestication and/or subsequent landrace diversification and adaptation were detected at 38 of the 44 flowering and bioclimatic TASs. Hence, this study lays the groundwork to begin breeding for novel environments predicted to arise following global climate change.

Soybean Functional Genomics

W084: Soybean Functional Genomics
TBA
Jisheng Zhang, iGBS, Chinese Academy of Sciences, China

W086: Soybean Functional Genomics
Fine Mapping of Soybean Important Agronomic Trait QTLs with CSSL Population
Qingshan Chen, Agriculture-Northeast Agricultural University, Harbin, China

Soybean is an important source of oil and protein for people consumption in China. A chromosome segment substitution lines (CSSLs) covering the whole genome of wild parent ZYD00006 was constructed by cross and backcross of ZYD00006 (donor parent) with cultivar Suinong 14 (recipient parent). The bin map have been constructed based on genome re-sequencing which was performed at 3.3Mb, and get the candidate genes for further research. For the quality trait, we fine mapped a QTL into 3.3Mb, and get the candidate genes for further research. For the quality trait, we fine mapped a QTL into 852Kb, and get the candidate genes. For the extreme materials in quality phenotype, transcriptome sequencing was performed to establish a regulatory networks. Meta-analysis was also conducted to integrate recent 30 years soybean protein and oil content QTLs. Meta-QTL and transcriptome data were analyzed together to construct the co-expression networks; seven candidate genes were verified by combining analysis. Furthermore, we selected some elite lines for test trials and production trials, some of them showed good performance in field. The CSSLs can provide theoretical basis and molecular breeding for high quality and yield breeding of soybean.

W087: Soybean Functional Genomics
Application of High-Throughput CRISPR-Cas9 for Multiplex Mutagenesis in Soybean
Yuefeng Guan, Fujian Agricultural and Forestry University, Fuzhou, China

Various mutant resources have been generated for the genetic study and crop improvement of soybean [Glycine max (L.) Merr. ]; however, the output is limited by the paleopolyploid genome of this species. CRISPR-Cas9 could generate multiplex mutants in several ways, shedding light to overcoming the gene redundancy problem in crops. Nevertheless, it remains questionable whether CRISPR-Cas9 could be used as a high-throughput screening tool in crops with low transformation efficiencies, including in soybean. We have developed an optimized procedure for high-throughput CRISPR-Cas9 in soybean, which included vector construction, sgRNA assessment in hairy roots, pooled transformation, sgRNA identification, and gene editing verification. As demonstration, we constructed 70 CRISPR-Cas9 vectors to target 102 soybean genes and subjected 16 batches to pooled transformation of CRISPR sublibraries. A population consisting of 407 T0 lines was obtained with 100% sgRNA coverage and 49.15% average mutation frequency. The occurrence of mutations in the T1 progeny could be further increased, despite the presence of mosaicism in T0 transgenic plants. Utilizing this platform, we characterized a series of single, double or triple mutants for genes potentially involved in nodulation or seed quality traits. Our study generates a resource of multiplex CRISPR mutants for soybean, and provides an advanced solution for genetic screening in crops with complex genome.

W088: Sugar Beet
Analysis of the IncRNA Related to Vernalization in Sugar Beet
Dayou Cheng, Harbin Institute of Technology, Harbin, China

W089: Sugar Beet
Preliminary Study on the Physiology and Molecular Mechanisms of Alkali Tolerance in Sugar Beet
Gui Geng, Heilongjiang University, Harbin, China

W090: Sugar Beet
The Role of BZR Transcription Factors in the Growth of Sugar Beet
Wei Wang, Inner Mongolia Agricultural University, Huhhot, China
**W091:** Sugar Beet

Function and Expression Pattern of Multiple Transcription Factors in Response to Salt Stress in *Beta vulgaris*

Jie Cui, Harbin Institute of Technology, Harbin, China

Salinity is a major environmental factor that affects the growth, productivity and geographical distribution of crops. The induction of salt-stress transcription factors (TFs) plays a crucial role in response to salt stress at the transcriptional level in plants. Large families of TFs, such as WRKY, AP2/ERF, MYB, BHLH, and NAC, are integral in linking salt-sensing pathways mediating plant salt-stress tolerance responses. Our study analyzed the expression pattern of these transcription factors under salt stress in beta vulgaris and suggested a presumptive regulatory network of salt-responsive by bioinformatics in Beta vulgaris. This data will provide some insights into the TFs-mediated regulatory pathways in salt-stress responses and improve the understanding of the salt-stress response of *B. vulgaris*.

**W092:** Sugar Beet

Establishing a Sugar Beet Core Germplasm Collections for Molecular Breeding

XiaoDong Li

Universtiy of Wisconsin, Madison, WI, (7)School of Integrative Plant Science, Cornell University, (8)Biology, IST, IST, University of Trieste, Italy, (9)Laboratory, Charleston, SC, (17)Department of Horticulture, Michigan State University, East Lansing, MI, (12)Agricultural Research Organization, ARO, Ramat Yishay, Israel, (13)Boyce Thompson Institute, Cornell University, (14)Department of Crop Sciences, University of Illinois, Urbana, IL, (15)Newe Yaar Research Center, ARO, Ramat Yishay, Israel

In order to facilitate low-cost and high-throughput genotyping for CGAAR centers and Partner institutes including National Agricultural Research Systems (NARS), a research initiative was established as “High Throughput Genotyping Project (HTGP)” led by CRISAT with support from IERR and CIMMYT through Excellence in Breeding (EiB) Platform. This project is funded by Bill and Melinda Gates Foundation (BMGF) to offer low-cost access to world-class genotyping services for CGAAR institutes and NARS partners. Through the HTGP service agreement, more than 40 public institutions globally (16 species) listed as key users for the SNPLine genotyping platform.

Primary objective of the project is to broker access of the latest genotyping platform to a wide user group at a reduced cost ($1.50 to $2.00 per sample) via sample aggregation. HTGP platform offers SNPs genotyping services in rice, wheat, maize, some millets, legumes and other crops, which are readily deployable in the breeding programmes. It also offers value added services, i.e. capacity building in high throughput sampling, digitization, barcoding and data interpretation support at no cost to partners. It helps in generation of economical, faster and quality SNP data for all genomics-related activities.

The initiative also ensures that the latest molecular advances across the community brought under a single shared platform to facilitate effective and high impact collaboration. Lowering the genotyping cost will enable CGAAR, NARS and other public sector breeders to utilize marker-based selection in forward breeding and routine QC application in breeding pipeline to expedite the delivery of improved breeding products to farmers globally.

**W096:** Transforming Breeding through Integrated Data Management and Analysis

Maize Genomic Selection Use Case and Galaxy Analysis Pipeline

Xuecai Zhang, CIMMYT, Texcoco, Mexico

The greatest areas of need to accelerate genetic gain in the existing 70+ CGIAR breeding programs in developing world for greater impact on food and nutrition security, climate change adaptation and development. (http://www.excellenceinbreeding.org/)

The platform, used in an international pan-genome project. Molecular breeding tools including a 299-training modules are commissioned based on the greatest areas of need to accelerate genetic gain in the existing 70+ CGIAR breeding programs globally. EiB team members are currently located across multiple continents and all EiB shared services are accessible globally.

**W097:** Transforming Breeding through Integrated Data Management and Analysis

Cucurbit Genomics Database (CuGenDB): A Central Portal for Comparative and Functional Genomics of Cucurbit Crops

Yi Zheng1, Shan Wu1, Yang Bai1, Honghe Sun1, Chen Jiao1, Shaogui Guo2, Kun Zhao1, Jose Blanca1, Zhonghui Zhang3, Sarwen Huang4, Yong Xu5, Yiqun Weng6, Michael Marzouk7, Umesh K. Reddy8, Kaori Ando9, James D. McCleary10, Arthur A. Schaffer11, Joseph Burger12, Yaakov (Kobi) Tadmor1, Nutit Katr12, Xuemei Yang13, Ying Li14, James J. Giovannello15, Kai-Shuo Ling16, Patrick Wechter17, Ann Son Levi18, Rebecca Grumet19 and Zhangjun Fei20, (1)Boyce Thompson Institute, Cornell University, Ithaca, NY, (2)Beijing Academy of Agriculture and Forestry Sciences, Beijing, China, (3)COMAV-UPV, Valencia, Spain, (4)Chinese Academy of Agricultural Sciences, Beijing, China, (5)Ibaraki Institute of Technology, Ibaraki, Japan, (6)University of Wisconsin, Madison, WI, (7)School of Integrative Plant Science, Cornell University, Ithaca, NY, (8)Department of Biology, West Virginia State University, Institute, WV, (9)/SDA-ARS, Crop Improvement and Protection Research, Salinas, CA, (10)/Volcani Research Institute, ARO, Bet Dagan, Israel, (11)(New)Eyre Research Center, ARO, Ramat Yishay, Israel, (12)Agricultural Research Organization, ARO, Ramat Yishay, Israel, (13)Boyce Thompson Institute for Plant Science, Ithaca, NY, (14)/SDA-ARS, U.S. Vegetable Laboratory, Charleston, SC, (15)/SDA-ARS, Charleston, SC, (16)/SDA-ARS, U.S. Vegetable Laboratory, Charleston, SC, (17)Department of Horticulture, Michigan State University, East Lansing, MI

The Cucurbitaceae family (cucurbits) includes several economically important crops, such as melon, cucumber, watermelon, pumpkin, squash and gourds. During the past several years, genomic and genetic data have been rapidly accumulated for cucurbits. To store, mine, analyze, integrate and disseminate these large-scale datasets and to provide a central portal for the cucurbit research and breeding community, we have developed the Cucurbit Genomics Database (CuGenDB). http://cucurbitgenomics.org/ using the Espanol tools. The database currently contains all available genomic and expression sequence tag (EST) sequences, genetic maps, and transcriptome profiles for cucurbit species, as well as sequence annotations, biochemical pathways and comparative genomic analysis results such as synteny blocks and homologous gene pairs between different cucurbit species. A set of analysis and visualization tools and user-friendly query interfaces have been implemented in the database to facilitate the usage of these large-scale data by the community. In particular, two new tools have been developed in the database: a ‘SyntenyViewer’ view genome synteny between different cucurbit species and an ‘RNA-Seq’ module to analyze and visualize gene expression profiles. Both tools have been packaged as Tripal extension modules that can be adopted in other genomics databases developed using the Tripal system.

**W098:** Translational Genomics

Leveraging Genomic Resources to Secure Quality and Climate-Resilient Vegetable Cowpea Breeding

Pei Xu, Zhejiang Academy of Agricultural Sciences, Hangzhou, China

Cowpea (*Vigna unguiculata* L. Walp) is an important grain, fodder and vegetable legume around the world. Two main divisions of cultivated cowpeas are the subspecies *sudanensis* used primarily for dry grain and *senegensis*, which is also known as yard-long bean for long and succulent pods used as a vegetable. In the past decade, tremendous genomic resources have been developed for cowpea, including the cowpea consensus map, Select consortium array and, more recently, a reference genome for *spp.* *sudanensis*. While these tools have been very useful in dissecting genetic architecture of many traits, genomic resources for subspecies *senegensis* would be valuable for better understanding the genetic basis of vegetable end-use traits (e.g. pod length, softness) and biotic/abiotic stresses more common in humid areas (e.g. rust, flooding). Using long-read sequencing and Hi-C technologies we recently assembled the genomes of three vegetable cowpea accessions, which included the super long-podded landrace 'G98', the multiple disease-resistant landrace 'ZN016', and 'ZJ282', a commercial cultivar. The contig and scaffold N50 values of up to 10 Mb and 37 Mb, respectively, demonstrate the quality of these assemblies. Genome sequences of ZN016 and ZJ282 are being used in an international pan-genome project. Molecular breeding tools including a 299-accession GWAS panel and a KASP marker library have also been developed, bringing insights into the domestication history of pod length and allowing the fine mapping of a novel rust resistance gene in vegetable cowpeas.

**W099:** Translational Genomics

Transcriptome Analysis of Genes Involving in Zn2+ Response during Peanut Seed Germination

Weichang Yu, College of Life Sciences, Shenzhen University, Shenzhen, China

Peanuts (*Arachis hypogaea* L.) are a significant legume crop. The greatest areas of need to accelerate genetic gain in the existing 70+ CGIAR breeding programs in developing world for greater impact on food and nutrition security, climate change adaptation and development. (http://www.excellenceinbreeding.org/)

We report a transcriptome analysis of genes involved in the *Zn*2+ response during peanut seed germination. Using RNA-Seq, the expression patterns of 5466 genes involved in the *Zn*2+ response during peanut seed germination were determined. Gene ontology (GO) analysis showed that genes involved in the *Zn*2+ response were mainly enriched in GO terms related to ion ion transmembrane transport, metal ion binding, and antioxidation. The expression patterns of 82 genes related to the *Zn*2+ response were validated by real-time PCR. This study provides a valuable resource for investigating the genetic basis of the *Zn*2+ response during peanut seed germination.
W102: Translational Genomics
A High Resolution Gene Expression Atlas in Chickpea: Implications in Crop Improvement
Himabindu Kudapa, ICRISAT, Hyderabad, India

W103: Wheat Genomics, Genetic Diversity, Evolution and Domestication History
A Total Diversity Map for Polyploidy Crop: What It Looks like?
Shifeng Cheng, Agricultural Genomics Institute at Shenzhen, CAAS, Shenzhen, China
Understanding and utilizing the population genomic diversity is the fundamental basis of breeding practices for crops. However, until recently, it has been a big challenge for decades to decode the genome sequences as well as to build the genomic and genetic diversity across populations for polyploidy crops, partly due to the limitation of sequencing technologies and the highly homoeologous and repetitive characterizations of the genomes. Nowadays, the genome sequences of many polyploidy crops have been routinely generated using a combinatorial strategy using the most cutting-edge technologies, enabling us to define a “total genetic/genomic diversity map” even for the complex polyploidy plants, like the cultivated wheat, sugarcane, oilseed, peanut, cotton and so on. Besides of the SNP-based information and analysis, large-scale genomic variations would affect the most on both the evolution/domestication processes and the traits of agricultural interests, including a pangenome generated by either an iterative short-read mapping strategy or assembly-based comparison, gene presence and absence variations, gene copy number variations and structural variations. Aim for a total diversity would provide information from haplotype phasing, chromosome recombination, introgression of new genes and sequences, as well as high resolution for gene discovery in association study.

W104: Wheat Genomics, Genetic Diversity, Evolution and Domestication History
Genome-Wide Sequence Analysis of Wild and Cultivated Emmer
Song Wei, Northwest A&F University, Yangling, Shaanxi, China
Emmer wheat, one of the earliest cultivated crops, is of great value to the birth of bread wheat, agriculture and human civilization. In this study, we used wild emmer wheat and cultivated emmer wheat from the center of origin and other areas of the world for genome-wide sequence analysis combined with population genetics and evolutionary genomics methods to identify and analyze SNP and CNV loci genomic level.

W105: Wheat Genomics, Genetic Diversity, Evolution and Domestication History
The Genome of Triticum urartu and Its Comparative Analysis
Hong-Qing Ling1, Xiaoli Shi1, Bin Ma1, Lingli Dong1, Aimin Zhang1, Daowen Wang1, Chengzhong Liang2 and Xiaoli Shi, (1)Institute of Genetics and Developmental Biology, CAS, Beijing, China
Triticum urartu, a wild diploid wheat, is the progenitor of the wheat A genome. For studying the evolution and domestication of wheat, we have been working on the genome sequencing of T. urartu since 2009. First, we generated the draft genome of T. urartu using the whole-genome shotgun sequencing strategy on the Illumina Hiseqation (2000) platform (Ling et al., 2013, Nature 496: 87-90). Subsequently, we produced a high-quality genome sequence of T. urartu using BAC-by-BAC sequencing strategy combining single molecule real-time sequencing and next-generation mapping technologies (Ling et al., 2018, Nature 557: 424-428). The assembled contig sequences were 4.79 Gb with an N50 of 344 kb and scaffold sequences were 4.86 Gb with an N50 of 3.67 Mb. With a high density single nucleotide polymorphism genetic map, 4.67 Gb (95.9%) of the scaffold sequences were successfully anchored on T. urartu chromosomes, constructing seven chromosome-scale pseudomolecules. By comparing collinear segments between T. urartu and its grass relatives, we proposed an evolution model of T. urartu chromosomes, and found that T. urartu and Brachypodium were independently evolved from the grass ancestor with 12 chromosomes. Furthermore, we also found that the ancient genome duplications, which well maintained in rice, sorghum and Brachypodium, were strongly corrupted in T. urartu because of extensive amplifications of transposable elements and widespread gene loss.

In conclusion, we successfully generated a reference genome of the wheat A subgenome progenitor T. urartu. The assembly provides a valuable resource for studying genome evolution and genetic variation in wheat and related grasses, and promises to facilitate the discovery of genes that could be useful for wheat improvement.

W106: Wheat Genomics, Genetic Diversity, Evolution and Domestication History
Map-Based Cloning of FHB1 Revealed Unique Mutation of a Well-Conserved Gene Resulting in Resistance to Wheat Fusarium Head Blight
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Head or ear blight caused by Fusarium spp. fungi can devastate staple cereal crops, particularly wheat. Deployment of resistant cultivars is currently the best control measure, but lack of understanding of resistance mechanisms has greatly hindered the breeding efforts. In the FHB-resistant germplasm Wangshuibai, we previously identified a major QTL on chromosome 3BS conferring resistance to spread within spike, the type II resistance. To clone this gene, NIL isogenic lines of this QTL and the Sumai3 FHB1 QTL, developed utilizing FHB-susceptible lines Binninj and Lonsdale, were utilized in secondary segregation population construction. Using recombinants identified in these populations, both QTL were fine mapped. In the constructed BAC physical map, they were confined to a common 26.8 kb interval containing only three ORFs. Sequence-based analysis demonstrated that Wangshuibai and Sumai 3 contain an identical FHB1 resistance gene in the target interval. The FHB1 candidate was determined based on sequence comparison and transcriptional profiling analysis, and was confirmed through haplotyping and transgenic studies. This gene is conserved among plants, but a unique mutation of the 3BS homolog causes shift of its start codon, consequently, results in the function in FHB resistance.

W107: Wheat Genomics, Genetic Diversity, Evolution and Domestication History
Genetic Instability in a Synthetic Tetraploid Wheat (AADD) Revealed By Genome Resequencing
Bao Liu, Northeast Normal University, Jilin, China
P0001: Aquaculture
Integrated WG, RNA and BS-Seq Uncovers Mechanisms of Genomic Regulation and Epigenomic Modification of Sexual Size Dimorphism in Fish
Haping Wang1, Shaokui Yi2, Zhigang Shen3 and Hong Yao4, (1)The Ohio State University, Columbus, OH, (2)The Ohio State University, OH
Sexual size dimorphism (SSD) has been the most common phenotypic dimorphism across taxa. Theory has long suggested that the development of SSD is facilitated by chromosomies, since sex chromosomes are the only portions of the genome that differ between two sexes. However, our recent studies showed that hormonal-induced neo-males with female genotype (XX♂) and normal males (XY♂) exhibited no SSD in yellow perch, where females naturally grow significantly faster and larger than males. Why are phenotypic traits correlated with phenotypic sex instead of genetic (chromosomes) sex of an organism?

P0002: Brassicas, Arabidopsis, and related
A CACTA-like Transposable Element in the Upstream Region of BnaA9.CYP78A9 Acts as an Enhancer to Increase Silique Length and Seed Weight in Rapesed
Liliu Shi1, Jurong Song1, Chaosheng Guo1, Bo Wang2, Zhiling Guan1, Pu Yang1, Xin Chen1, Qinghua Zhang1, Graham J. King1, Jing Wang1 and Kede Liu1, (1)Huazhong Agricultural University, China, (2)Huazhong Agricultural University, Wuhan, China, and Epigenomic Modification of Sexual Size Dimorphism in Fish

P0003: Cattle
Identification of Active Enhancers Associated with Bovine Myoblast Differentiation
Honglin Jiang1, Robert Settlage2 and Xinyan Leng1, (1)VirginiaTech, Blacksburg, VA, (2)Virginia Tech, VA
The objective of this work was to identify regulatory DNA elements and transcription factors that control gene expression during bovine skeletal muscle differentiation. The main approach was using ChIP-seq to identify genomic regions with H3K27ac modification (i.e., active enhancers) in undifferentiated and differentiating bovine myoblasts. We isolated satellite cells, which are myogenic progenitor cells in adult animals, from Angus crossbred steers, and cultured them in growth medium as undifferentiated myoblasts for 10 days and subsequently in differentiation medium as differentiating myoblasts for 2 days. ChIP-seq libraries were constructed from DNA precipitated with an H3K27ac antibody and input DNA. Sequencing the libraries and mapping the sequence reads generated approximately 5, 6, and 10 million uniquely mapped sequence reads from input DNA, H3K27ac antibody-precipitated DNA from undifferentiated myoblasts, and H3K27ac antibody-precipitated DNA from differentiating myoblasts, respectively. Analyzing the uniquely mapped sequences using MACS revealed 57,705 and 69,039 H3K27ac-marked genomic regions in undifferentiated and differentiating myoblasts, respectively. Of these regions, 15,223 were unique to undifferentiated myoblasts and 26,559 to differentiating myoblasts. Both undifferentiated and differentiating myoblasts, H3K27ac-marked genomic regions were associated with greater gene expression. The expression level of BnaA9.CYP78A9 elevates the expression level, suggesting that the CACTA-like TE acts as an enhancer to stimulate the high gene expression and silique elongation. Marker and sequence analysis revealed that the TE in B. napus had recently been introgressed from B. rapa by interspecific hybridization. The insertion of the TE is consistently associated with long-silique and large-seeds in both B. napus and B. rapa collections. However, the frequency of the CACTA-like TE in rapseed varieties is still very low, suggesting that this allele has not been widely used in rapseed breeding program and would be invaluable for yield improvement in rapseed breeding.

P0004: Cattle
Investigation on the Single Nucleotide Polymorphisms (SNPs) Panel for Parentage Testing and Deciphering Their Usage across Different Cattle Breeds
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Reliable genotyping information is essential for accurate genetic evaluation and accelerated genetic improvement of cattle breeds. The genotyping of SNP is becoming an increasingly favoured tool for parentage verification. The International Society for Animal Genetics (ISAG) proposed a panel of single nucleotide polymorphisms (SNPs) for parentage testing in cattle (a core panel of 100 SNPs and an additional list of 100 SNPs). However, there has been a continuous concern of this SNPs panel for its adequate performance. We aimed our study to investigate the ISAG SNP markers in different tissue as well as ezbio cattle breeds from Asia and Africa region. A total of five hundred and eighty six (586) animals were genotyped with the high-density bovine 80K Bead Chip. We identified 187 SNPs and were common from the core (90) and additional (97) list of the ISAG panels. With the core panel of SNPs the average minor allele frequency (MAF) varied from 0.03 to 0.06 in two Bangladesh and 0.07 to 0.17 in eight Ethiopian zebu populations. The average MAF of Nellore cattle was 0.12. On the other hand, the MAF of the tame cattle (Chausius, Holstein, Angus and Jersey) varied from 0.21 to 0.34. The number of fixed (MAF=0) markers were varied from 16.67 to 22.2% in two Bangladesh and 4.4 to 11.1% in eight Ethiopian zebu populations. About 2.2% SNPs were fixed in Nellore cattle. On the other hand, almost all tame cattle had MAF ranged between 0.06 and above. After merging the core and additional panel we still found 9.09 to 11.7% SNPs were specifically fixed to two Bangladesh zebu and 1.2 to 5.3% SNPs specifically fixed to eight Ethiopian zebu populations. Our study suggests that there must need reconfigurations for the inclusion of many cattle breeds to find a suitable panel and/or development of region specific SNPs panel for the parentage detection of cattle breeds.
P0005: Rice
Rice Genome Reannotation and the Information Commons for Rice (IC4R)
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Rice is the most important staple food for a large part of the world's human population and also a key model organism for plant research. Here, we reannotated the rice genome and present Information Commons for Rice (IC4R; http://ic4r.org), a rice knowledgebase featuring adoption of an extensible and sustainable architecture that integrates multiple omics data through community-contributed modules. Each module is developed and maintained by different committed groups, deals with data collection, processing and visualization, and delivers data on-demand via web services. In the current version, IC4R incorporates a variety of rice data through multiple committed modules, including genome-wide expression profiles derived entirely from RNA-Seq data, resequencing-based genomic variations obtained from resequencing data of thousands of rice varieties, plant homologous genes covering multiple diverse plant species, post-translational modifications, rice-related literatures and gene annotations contributed by the rice research community. Unlike extant related databases, IC4R is designed for scalability and sustainability and thus also features collaborative integration of rice data and low costs for database update and maintenance. Future directions of IC4R include incorporation of other omics data and association of multiple omics data with agronomically important traits, dedicating to build IC4R into a valuable knowledgebase for both basic and translational researches in rice.

P0008: Equine
Whole-Genome Sequencing Reveals the Genetic Mechanisms Underlying the High-Altitude Adaptation in Tibetan Horses
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Chinese horse breeds had experienced a very long history of breeding, with good adaptation to extreme environments. We tried to detect the genome-wide selective signatures towards the high-altitude adaptation of Tibetan horse. Tibetan horse populations have evolved mechanisms that allow them to survive and perform as the major transporter for local farmers at the altitude of 4500 m on the Qinghai-Tibetan Plateau. We performed whole genome resequencing of about 138 horses from all around China, including Tibetan horses (65), lowland horses (61), Przewalski(5) and Thoroughbreds(7). A composite of multiple signals from fixation index (Fst), ZHp (Heterozygosity), pi-ratio (nucleotide diversity), and Tajima’s D-test revealed the top candidate region for the altitude adaptation reside the gene of EPAS1, which has been identified in many species, including human, goat, sheep and yak. We found two significant SNPs in EPAS1 (HIF2a) gene. Interestingly, the overexpression of these two EPAS1 mutants in A549 cells showed significantly increased activities than the wild type protein. In large horse populations (N = 948) these two EPAS1 SNPs showed even more remarkable genetic differentiation between Tibetan breeds and lowland horses. By measuring the blood samples on spot, we found significant physiological difference between Tibetan (N = 88) and lowland (N = 85) horses, including lower HMG level and HCT but higher MCHC in Tibetan horse. We also found the metabolic difference between Tibetan and lowland horses, including higher LDH and higher α-HBDH, suggesting a greater capacity for anaerobic lactate production in Tibetan horses. These results suggest that mutations in EPAS1 gene contribute to a hematological and metabolic basis in Tibetan horses, implying a quite similar adaptive mechanism of the Sherpa (Horescraft et al., 2017, PNAS). Therefore, we tested the downstream target of EPAS1 gene, such as VEGFA, EDN, VHL, EGLN, and EPO after the overexpression of two EPAS1 mutants separately in A549 cells. Both two mutations lead to up-regulation of all these five targets. Our study suggests that the two missense EPAS1 mutations represent key evolutionary changes underlying the adaptation to high-altitude hypoxia in Tibetan horses.

Key words: Tibetan horse, hypoxia adaptation, EPAS1, genomic selection signatures, metabolic basis

P0009: Forest Trees
Tissue Differential Expression of Diterpene Synthesis Related Genes in P. elliottii and P. densiflora
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Pine oleoresin is one of the useful natural resources which consists of varieties of isoprenoids. In naval stores industry, the oleoresin is gathered from pine stem through variable tapping methods and would be further purified to targeted compounds, mainly such as monoterpens, sesquiterpenes and diterpenes. In plants, those isoprenoids are derived from prenyl diphosphate (prenyl-PP) precursors which is synthesized by two independent metabolic pathways: the mevalonate (MVA) pathway in the cytoplasm and the 2-C-methyl-d-erythritol 4-phosphate (MEP) pathway in plastids. However, the specific use of the above two metabolic pathways in certain tissues and its oleoresin secretion mechanism in pine trees have not been fully understood. Here, we present the new insight on the MVA and MEP pathway usage based on tissue types by analyzing the differentially expressed genes (DEG) data from pine needle, phloem and secondary xylem, respectively. Our DEG data suggest that the MEP pathway is strongly activated in the leaf tissue more than the MVA. On the other hand, the MVA pathway is the main biosynthetic pathway for prenyl-PP production in woody tissues. In addition, the genes related to diterpene synthesis, which produce the major component of pine resin, are far active in leaf tissue. We have not yet determined the biological switches, such as transcription factors and RNA interaction molecules, which would be responsible for this tissue-dependent pathway usage. Therefore, further DEG data and enzymatic analysis of isoprenoid metabolic pathway are necessary.

P0010: Fruit Species
Climate Adaptation of Prunus mume, Native to China, Associated with Its Chilling Requirements
Ting Shi, Xiao Huang, Shahid Iqbal and Zhihong Gao, Nanjing Agricultural University, Nanjing, China

Prunus mume Sieb. et Zucc., is an important fruit crop of the subtropical region, originating in China. P. mume blooms earlier than other deciduous fruit trees, but different regions have different blooming periods. The time of anthesis is related to the dormancy period, and a certain amount of chilling can break dormancy. To identify the relationship between chilling requirements and the climate adaptation of P. mume cultivars in China, the nuclear and chloroplast genomes of 19 cultivars from the main cultivation areas of P. mume in China were resequenced. The average depth of coverage was 34X-76X and a total of 388,134 SNPs were located within the coding regions of the gene (CDs). Additionally, the 19 cultivar accessions were divided into three groups based on their chilling requirements: low, mid, and high. Associated with the chilling requirement groups, 21 selected sweep regions were identified, which could provide evidence supporting the model of P. mume domestication originating due to natural selection. Furthermore, we identified a flowering gene, FRIGIDA LIKE 3 (FRgL1), seems to affect the chilling requirements and the climate adaptation of P. mume cultivars. This study is a major step toward understanding the climate adaptation of P. mume cultivars in China.
P0011: Fruit Species

Single-Step Genomic Prediction of Fruit-Quality Traits Using Phenotypic Records of Non-Genotyped Relatives in Citrus

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The potential of genomic selection (GS) is now being evaluated for fruit breeding. GS models are usually constructed based on information from both the genotype and phenotype of population. However, information from phenotyped but non-genotyped relatives can also be used to construct GS models, and this additional information can improve their accuracy. In the present study, we evaluated the single-step genomic best linear unbiased prediction (sGBLUP), which is a genomic prediction method that combines the kinship information from genotyped and non-genotyped relatives into a single relationship matrix for a mixed model to apply GS. We evaluated three fruit-quality traits including fruit weight, sugar content, and acid content of 1,935 citrus individuals, of which 483 had 2,354 genome-wide single nucleotide polymorphisms. These data were used to construct sGBLUP models, and their performance was compared with that of genomic BLUP (GBLUP) and conventional BLUP (ABLUP) method, assuming that selection was carried out at the juvenile stage in the genotyped individuals and that selection was after phenotypic evaluation in the non-genotyped individuals. The prediction accuracy of sGBLUP for genotyped individuals was similar or higher than that of GBLUP method, especially for sugar content. The prediction accuracy of sGBLUP for non-genotyped individuals was also slightly higher than that of ABLUP method. These results demonstrate the potential of sGBLUP for fruit breeding, including citrus.

P0012: Fruit Species

Cucurbit Genomics Database (CuGenDB): A Central Portal for Comparative and Functional Genomics of Cucurbit Crops


The Cucurbitaceae family (cucurbit) includes several economically important crops, such as melon, cucumber, watermelon, pumpkins, squash and gourds. During the past several years, genomic and genetic data have been rapidly accumulated for cucurbits. To store, mine, analyze, integrate and disseminate these large-scale datasets and to provide a central portal for the cucurbit research and breeding community, we have developed the Cucurbit Genomics Database (CuGenDB; http://cucurbitgenomics.org) using the Triplip toolkit. The database currently contains all available genome and expressed sequence tag (EST) sequences, genetic maps, and transcriptome profiles for cucurbit species, as well as sequence annotations, biochemical pathways and comparative genomic analysis results such as synteny blocks and homologous gene pairs between different cucurbit species. A set of analysis and visualization tools and user-friendly query interfaces have been implemented in the database to facilitate the usage of these large-scale data by the community. In particular, two new tools have been developed in the database, a ‘SyntenyViewer’ to view genome synteny between different cucurbit species and an ‘rRNA-Seq’ module to analyze and visualize gene expression profiles. Both tools have been packed as Tripal extension modules that can be adopted in other genomes databases developed using the Tripal system.

P0013: Gene Editing/CRISPR

CRISPR Engineering to Knockdown Begomovirus (CLCuV) and Its Insect Vector Bemisia Tabaci

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Cotton leaf curl virus (CLCuV) a Begomovirus causes significant economic damage to cotton crop specially in sub-continent. The CLCuV devastated the Pakistan cotton industry in the early 1990s where it resulted in estimated yield reduction of 30-35% and still causes a yearly loss of USD 660 Million. Begomoviruses are obligately transmitted by an insect vector like the Whitefly gut Rep-region of the Alpha-satellite DNA, the C1-region of the Beta-satellite and the Whitefly gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut gut
P0016: Insects
A High-Quality De Novo Genome Assembly from a Single Mosquito Using PacBio Sequencing
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A high-quality reference genome is an essential tool for studies of plant and animal genomics. PacBio Single Molecule, Real-Time (SMRT) Sequencing generates long reads with uniform coverage and high consensus accuracy, making it a powerful technology for de novo genome assembly. While PacBio is the core technology for many large genome initiatives, relatively high DNA input requirements (3 µg for standard library protocol) have placed PacBio out of reach for many projects on small, noninbred organisms that may have lower DNA content. Here we present high-quality de novo genome assemblies from single invertebrate individuals for two different species: the Anopheles coluzzii mosquito and the Schistosoma mansoni parasitic flatworm. A modified SMRTbell library construction protocol without DNA shearing and size selection was used to generate a SMRTbell library from just 150 ng of starting genomic DNA. The libraries were run on the Sequel System with chemistry v3.0 and software v6.0, generating a range of 21-32 Gb of sequence per SMRT Cell with 20-hour movies (10-12 Gb for 10-hour movies), and followed by diploid de novo genome assembly with FALCON-Unzip. The resulting assemblies had high contiguity (contig N50s over 3 Mb for both species) and completeness (as determined by conserved BUSCO gene analysis). We were also able to resolve maternal and paternal haplotypes for 1/3 of the genome in both cases. By sequencing and assembling material from a single diploid individual, only two haplotypes are present, simplifying the assembly process compared to samples from multiple pooled individuals. This new low-input approach puts PacBio-based assemblies in reach for small, highly heterozygous organisms that comprise much of the diversity of life. The method presented here can be applied to samples with starting DNA amounts around 150 ng per 250 Mb – 600 Mb genome size.

P0017: Insects
Draft Genome of the Edible Insect, Whiter-Spotted Flower Chafer (Protaetia brevitartis)
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Whiter-spotted flower chafer (Protaetia brevitartis) is a phytophagous beetle, which belongs to Scarabaeidae family. The larvae of this beetle is important in human diet and they have been served as material for health products and food for protein source. In spite of the valuable features of P. brevitartis, no genomic information has been available and related research has still been limited. Here, we report the first whole genome assembly and transcriptome analysis of the P. brevitartis using the Pacific Biosciences (PacBio) long-read sequencing platform. The newly assembled P. brevitartis genome is approximately 805 Mb in length consisted of 9,605 contigs with a contig N50 of 109 kb. For annotation, a total of 18,487 protein-coding genes were predicted. Of them, 94.79%were annotated against non-redundant protein database at GenBank. For differential expression analysis between larvae and adult stages, we identified 819 and 1,570 transcripts with significantly higher expression in larva and adult P. brevitartis respectively. The availability of information from genomic and transcriptomic analyses from our study is expected to facilitate the study of the edible insect, P. brevitartis.

P0018: Legumes, Soybean, Common Bean, and related
Fourth Phase National Bioresource Project (NBRP) in Japan –“Legumebase” for Lotus and Glycine Plant Research in Japan
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The purpose of the National BioResource Project (NBRP) in Japan is to collect, conserve and distribute biological materials that form the basis of life science research. It consists of 30 biological resources, including animals, plants, microorganisms, DNA resources and an information center. The NBRP has entered the 4th phase from April 2017 and established a new system collaborate with University of Miyazaki and Tohoku University. We will rebuild and expand fundamental information on collected resources and provision of height quality resources to users via web database, “Legumebase” (https://www.legumebase.brc.miyazaki-u.ac.jp/). Lotus japonicus is a perennial legume that grows naturally throughout Japan. It is widely used as a model legume because of its small genome size and short life cycle and availability of transformation. On the other hand, soybean (Glycine max) is the most important legume crop worldwide, for its useful component protein, oil and secondary metabolite, and the research community has accumulated a large amount of basic research and valuable bioresources. NBRP Lotus and Glycine support legume research and development through collection, storage and distribution of these bioresources. In here, we introduce the outline and usage of NBRP Lotus and Glycine BioResources.

P0019: Legumes, Soybean, Common Bean, and related
Automatic Omnidirectional Image Photographing System and 3D Model Construction System for Plant
Atsushi Hayashi¹, Nobuo Kochi¹,², Kunihiro Kodama¹, Takanari Tanabata¹ and Sachiko Isobe¹, (¹)Kazusa DNA Research Institute, Kisarazu, Chiba, Japan, (²)Chuo University, Tokyo, Japan
Photogrammetry measurement in plants is difficult especially for leaf occlusion because of lack of feature points. We have developed automatic omnidirectional image photographing system with turntable and 3D model construction system for plant. The developed photographing system is basically consisted with commercial products. The photos are automatically taken with simply process by using an operation system developed by us. Cameras are positioned to reduce leaf occlusion. Sticks with random patterns are placed around turntable to increase feature points for support of camera alignment on 3D model construction system.
When rotation angle of the turntable is decreased, more photos are taken and leaf occlusions is reduced. On the other hand, camera estimation error increases and point clouds on a stem are missing. The constructed 3D model system improves camera alignment and point cloud building process and increase its robustness even in the case of small rotation angle.
**P0020: Legumes, Soybean, Common Bean, and related**

**Protein Content and OIL Quality Assessment of Soybean Cultivars in South Africa**

Alina Mofokeng and Paul Rantso, Agricultural Research Council-Grain Crops, Potchefstroom, South Africa

Soybean is one of the most important leguminous crops grown globally for food and feed. It is a good source of protein and nutrients. Studies of genetic diversity are invaluable for efficient utilization, conservation and management of germplasm collections. The objective of the study was to assess genetic diversity present among the soybean genotypes using protein and oil quality traits. Ninety-eight soybean accessions were planted in Potchefstroom and Brits in the North West Province of South Africa in 2016-17 growing season. The experiments were laid out in an alpha lattice design replicated twice. The nutritional quality traits were measured using near infrared spectrophotometer (DA 72500). Data were analysed using analysis of variance and means were separated by least significance difference. The Principal Component analysis was done in GenStat 18th version. The principal component analysis revealed three major PCs contributing 98.5%, 1.1% and 0.2% with the total variation of 99.8%. The ANOVA revealed highly significant differences among the genotypes for oil, stearic acid, ash, fibre, moisture content and protein content. The oil content ranged between 2.08% and 29.73% whereas protein content ranged between 1.85% and 35.62%. The accessions Essex, Hampton 266 A, Viozie, and Soja (pautena) Vaschadaka had the highest oil content. Moziana, 99/05, PI 170889(R56-49), F 82-7145 had the highest protein content. Linoleic and linolenic acids were high in genotype PR 162 -18. There was vast genetic diversity among the soybean genotypes evaluated. The presence of genetic diversity will aid breeders in selections and hybridization programmes for crop quality improvement.

**P0021: Legumes, Soybean, Common Bean, and related**

**Wild Soybean SnRK1 Kinase Regulates an Ethylene-Responsive Transcription Factor to Generate Stress Resistance in Plants**

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Plant SnRK kinases are well-known to regulate tolerance to environmental stresses. From a wild soybean cDNA library, we identified a GsSnRK1 binding protein designated as GsERF7. GsERF7 gene dominantly expressed in wild soybean roots and demonstrated high responses to ethylene, salt, alkaline, GsSnRK1 interacted and were co-localized with GsERF7 in nucleus, and phosphorylated GsERF7 at S36 residue. Moreover, GsERF7 phosphorylation by GsSnRK1 is required for its translocation from cytoplasm to nucleus and transcriptional activity. To investigate the physiological functions, we co-expressed GsERF7 and GsSnRK1 in hair roots of soybean cotyledons mediated by Agrobacterium rhizogenes. All the transgenic roots showed similar growth on normal medium. However, the roots carrying GsERF7 and GsSnRK1(wt) demonstrated stronger growth than the ones carrying GsERF7 and GsSnRK1(K49M) on the media containing NaCl or NaHCO3, suggesting that the kinase activity of GsSnRK1 is indispensable for GsERF7 to regulate plant tolerance to abiotic stresses. Moreover, RT-qPCR determined the altered the transcription levels of representative abiotic stress-responsive and hormone-synthetic genes. These results will aid our further understanding of the mechanism of how SnRK1 kinase plays a cardinal role in regulating plant stress resistances through activating the biological functions of downstream factors.

**P0022: Legumes, Soybean, Common Bean, and related**

**Screening of Cowpea Genotypes for Canning Ability in South Africa**

Magdalene Mohlala1, Alina Mofokeng2, Lucy Molatadi1, Lebogang Angelo Madumbiya1 and Thuli Mthombeni1, (1)University of Limpopo, Sovenga, South Africa, (2)Agricultural Research Council-Grain Crops, Potchefstroom, South Africa, (3)University of Limpopo, Sovenga, South Africa, (4)Agricultural Research Council, Potchefstroom, South Africa

Cowpea (Vigna unguiculata) is a pulse crop containing high protein, vitamins and minerals. It is consumed as a high-quality plant protein source in many parts of the world. Hence, referred to as “poor man’s meat” due to the high levels of protein found in the seeds and leaves. However, there are limited efforts for prolonging its shelf life in a form of seed canning in South Africa. The objective of the study was to screen cowpea for canning ability using canning quality traits. The ARC-GC in-house method was used for canning. One-hundred grams of seed samples were soaked in a 30°C water bath for 30 minutes and then blanched at 88°C for 30 minutes. Bean weight after soaking was recorded as Ingo mass. Soaked beans were canned in a tomato puree canning medium and heat sterilised at 121.1 °C for 30 minutes. Cans were left to stabilise for 14 days before opening. Bean splitting and visual appearance were evaluated subjectively on a scale from 1 to 10. Mass of washed beans was recorded as drained mass. Completely broken splits bean and loose skins were considered as splits and expressed as a percentage of drained mass. The texture of the canned beans were determined by using the Stable Micro Systems Texture Analyser, which calculates the amount of force required to compress the beans and the force was recorded. Water uptake ranged from 58 to 139.9%, splits ranged between 0% and 3.75%, and the force ranged between 1257.6 and 1275.9 N. Out of 90 cowpea genotypes, only 11 genotypes were spoiled and had bad odour. Among the 79 remainders, seven genotypes had less water uptake as compared to others. RV446, OLOYIN, Glenda, Pan311, RV555 and RV411 had the highest water uptake. RV416, RV 411, OLERU, TVU5138, 97K-44935, and RV465, had an excellent appearance without cracks or loose skins and even colour. RV 411, Oloyin, RV446, TVU5138, 97K-44935, RV 441, RV 10 and RV 512 were the genotypes with high water uptake, good visual appearance and without splits. These genotypes were recommended for canning.

**P0023: Legumes, Soybean, Common Bean, and related**

**Identification, Molecular Characterization and Expression of Genes Involved in the Nodulation of Chickpea (Cicer arietinum L.)**

Phoebe N. Calica, Ateneo De Davao University, Davao, Philippines

Chickpea (Cicer arietinum) is the second most widely grown legume in the world. Climate change along with the incidence of fungal diseases is affecting the production and yield. The nodulation and associated nitrogen fixation ability of chickpea are critical parameters for crop yield and sustainability. The nodulation ability of legumes is controlled by an internal autoregulation of nodulation (AON) mechanism. Comparative genomic approaches were used in this study to identify the central components in the AON pathway of chickpea. This includes identifying of CaNARK, which encodes a LRR receptor kinase that acts to regulate root nodule numbers. Furthermore, CLE peptide genes (CaRs1, CaRIs2 and CaNIC1), CaRN1, CaRO2, CaRDN3, CaRN41, CaRN42, CaRN43 and CaRN44 were identified. CLE and other nodulation genes found were orthologs with Medicago truncatula nodulation genes. Expression of all nodulation genes was confirmed by inoculating Cicer arietinum plants with Mesorhizobium cicer.
P0024: Legumes, Soybean, Common Bean, and related
Genome of an Allotetraploid Wild Peanut Arachis Monticola
Dongmei Yin, College of Agronomy, Henan, China
Arachis monticola (2n = 4x = 40) is the only allotetraploid wild peanut within the Arachis genus and section, with an AABB-type genome of ~2.7 Gb in size. The AA-type subgenome is derived from diploid wild peanut Arachis duranensis, and the BB-type subgenome is derived from diploid wild peanut Arachis ipaensis. A. monticola is regarded either as the direct progenitor of the cultivated peanut or as an introgressive derivative between the cultivated peanut and wild species. The large polyploidy genome structure and enormous nearly identical regions of the genome make the assembly of chromosomal pseudomolecules very challenging. Here we report the first reference quality assembly of the A.monticola genome, using a series of advanced technologies. The final whole genome of A.monticola is ~2.62 Gb and has a contig N50 and scaffold N50 of 106.66 Kb and 124.92 Mb, respectively. The vast majority (91.83%) of the assembled sequence was anchored onto the 20 pseudo-chromosomes, and 96.07% of assemblies were accurately separated into AA- and BB-subgenomes. We demonstrated the efficiency of the current state of the strategy for de novo assembly of the highly complex allotetraploid species, wild peanut (A.monticola), based on whole-genome shotgun sequencing, single molecule real-time sequencing, high-throughput chromosome conformation capture technology, and BioNano optical genome maps. Reconstruction of peanut genomes demonstrated a monophyletic origin of allotetraploid peanut subgenomes. The tetraploids underwent asymmetric subgenome evolution, including homoeologous exchanges, homoeolog expression bias, gene family expansion, and structural variation (SV), leading to subgenome functional divergence during peanut domestication. These genomic resources are uniquely valuable for studying polyploid genome evolution, crop domestication, and genome-assisted improvement of peanut production and evolution within the Arachis genus and among legume crops.

P0025: Methods: Bioinformatics
Plant Omics Databases: Plant Omics Data Center (PODC), CATChUP and TOMATOMICS
Shizuka Koshimizu1, Shin Okhi1, Maasa Kanno1, Misa Saito1, Misao Senboku1, Hajime Ohyama2, Eiji Nambara1, Koh Aoki2 and Kentaro Yano1, (1)School of Agriculture, Meiji University, Kawasaki, Japan, (2)King Abdullah University of Science and Technology, Thuwal, Saudi Arabia, (3)University of Toronto, Toronto, ON, Canada, (4)Otsuka Prefecture University, Sakai, Japan
Here, we introduce three databases “Plant Omics Data Center” (PODC), http://bioinf.mind.meiji.ac.jp/podc/), CATChUP (http://plantomics.mind.meiji.ac.jp/CATChUP/) and TOMATOMICS (http://bioinf.mind.meiji.ac.jp/tomatomics/). The current version of PODC contains omics information on 11 plant species; Arabidopsis thaliana, Glycine max, Medicago truncatula, Nicotiana tabacum, Oryza sativa, Physcomitrella patens, Solanum lycopersicum, Solanum tuberosum, Sordaria macrospora, Fritillaria imperialis, Zea mays. RNA-Seq datasets were collected from the Sequence Read Archive (SRA) in NCBI. The samples (RMs) were manually categorized and assigned with Plant Ontology and Plant Environmental Ontology terms according to the descriptions of the experimental conditions of each sample. After calculation of gene expression levels in each sample, a large-scale expression matrix through all samples (RNA-Seq datasets) was obtained in each species. The similarity or reciprocity of expression profiles between two transcripts were evaluated by correspondence analysis with the expression matrix. The relationships of genes were graphically shown by gene expression networks (GENs) in PODC. To compare GENs among different species, orthologues were identified and employed to integrate GENs of all species. Finally, we assigned knowledge-based functional annotations to about 30,000 genes by natural language processing techniques and manual curation of literature. Synonyms of gene and protein names were also manually collected from literature. Recently, the information of the cis elements and transcription factors for around 30,000 transcripts, obtained by manual curation of literature, was combined in PODC. By using PODC, the omics information and knowledge-based annotations are freely accessible. In addition, users can construct gene expression networks by using transcripts of interest. Some spatiotemporally expressed genes play a role as a master regulator of biological processes such as growth and stress response. A database CATChUP provides the information of spatiotemporally expressed genes mined in eight plant species. With a developed statistical method, we comprehensively evaluated transcripts using large-scale RNA sequencing (RNA-Seq) data stored in the SRA. As a result, approximately 70,000 transcripts were extracted as candidates of spatiotemporally expressed genes. The CATChUP database assists us in identifying genes specifically expressed under particular conditions with powerful search functions and an intuitive graphical user interface.

P0026: Methods: Bioinformatics
Development of Plant a Genome Portal Site, Plant Garden
Daikiro Harada1, Hisako Ichihara2, Akihiko Nakaya2, Andrea Ghelfi1, Manabu Yamada1, Mitsuyo Kohara2, Hideki Hirakawa2, Satoshi Tabata3 and Sachiko Isohe1,
(1)Kazusa DNA Research Institute, Kisarazu, Chiba, Japan, (2)Graduate School of Medicine, Osaka University, Suita, Osaka, Japan
In recent years, genome analysis can be performed more inexpensively and efficiently with the development of sequencing technologies. De novo whole genome assembly has become common in non-model species. Currently (April 2019), more than 380 plant genomes have been deciphered, and it is considered that the numbers of assembled genomes will keep increasing in future. In addition, resequencing is commonly performed in plant species which reference genomes have already been constructed. Not only quantity, the accuracy of genome sequences is also improved year by year. The explosive increase of genome sequences data requires portal websites that completely covers the plant genomes. There are a few portal websites are available for plant genomes such as Phytozome (http://phytozome.jgi.doe.gov/pz/portal.html) and Ensembl (https://asia.ensembl.org/index.html). However, these are more for experts and sometimes difficult to beginners. Therefore we are developing a non-expert friendly plant genome integration database, Plant GARDEN (https://plantgarden.jp/en/). The database includes assembled genomes, genes, DNA markers and trait related loci information. Gene sequence similarities across plant species is also available in the DB. The English beta version is opened in June 2019 for nine plant species. Currently, only limited information is available, however, Plant GARDEN is aimed to include most of plant genome information in future. This work is supported by the JST Life Science Database Integration Project (I7934006).

P0027: Methods: Bioinformatics
Complementarity-Based Selection Strategy for Genomic Selection
Megan Wellner, Saba Meoinizadeh, Guiping Hu and Lizhi Wang, Iowa State University, Ames, IA
Genomic selection is a technique that breeders use to select plant or animal individuals to mate and produce new generations of species. The conventional selection approach was to select individuals that are either observed or predicted to be the best based on the assumption that parents with better phenotypes will produce better children. A major limitation of this approach is its focus on the short-term genetic gains at the cost of genetic diversity and long-term growth potential. Recently, several new genomic selection approaches were proposed to maximize the long-term potential. Along this research direction, we propose a new approach, the complementarity-based selection strategy, to improve the tradeoff between short-term genetic gain and long-term potential. This approach was inspired by how two genders of wild animals take different roles in fighting for food and caring for their offspring. Our selection approach selects individuals with the highest short-term achievement as male, and then select individuals that are the most complementary to the male as their female partners to emphasize the probability to produce outstanding offspring in the long term. The male and female roles refer to the motivating analogy of mating choices in wild animals. They do not refer to the sex of the plant individuals that are selected in the complementarity-based selection strategy. We present simulation results that compare the performance of the new approach against the state-of-the-art approaches in the literature.
Methods: Bioinformatics
Multi-Trait Genomic Selection for Crop Improvement
Saba Moeinizade1, Guiping Hu1, Liithi Wang2 and Patrick S. Schnable2, (1)Iowa State University, Ames, IA, (2)Department of Agronomy, Iowa State University, Ames, IA
Plant breeders make selection decisions based on multiple traits, such as yield, plant height, flowering time, and disease resistance. A commonly used approach in multi-trait genomic selection is index selection, which assigns subjectively defined weights to all traits. Multi-objective optimization has also been used to identify the Pareto frontier of selection decisions, which represents different trade-offs across multiple traits. We propose a new approach, which maximizes some traits while keeping others within desirable ranges. Optimal selection decisions are made using a new version of the look-ahead selection algorithm, which was recently proposed for single trait genomic selection and demonstrated superior performance with respect to other state-of-the-art selection methods. We demonstrate the effectiveness of this new approach using case studies with realistic data sets.

Methods: Bioinformatics
Advancing GWAS Models and Tools to Dissecting Environmental and Genetic Causes of Complex Plant Traits
Wenchao Zhang1, Xinbin Dai1, Bongsong Kim1, Shizhong Xu2 and Patrick X. Zhao1, (1)Noble Research Institute, Ardmore, OK, (2)Dept. of Botany & Plant Sciences, University of California, Riverside, CA
The success in identifying causal variants, such as single nucleotide polymorphisms (SNPs) conferring complex genetic traits or diseases, the genome-wide association study (GWAS) approach has revolutionized quantitative genetics and disease biology of Humans. The GWAS approach also has been applied, and shown great promise in plant research, crop sciences, modern plant genetic engineering and breeding. However, the use of conventional GWAS and genomic selection based on GWAS markers in plant research, genetic engineering and crop improvement poses several significant limitations. Conventional statistical genetic models only measure the additive effects, no epistatic effects and gene-environment interaction effects are considered, by the underline statistical genetic models, typically the linear mixed models (LMMs); yet complex plant traits, such as yield, tolerance to abiotic and biotic stresses, are often quantitative in nature, and complex in etiology, with multiple environmental and genetic causes that are governed by individual genes (G), gene-gene interactions (GxG) and gene-environment interactions (GxE). The analysis of complex plant trait thus demands accurately dissecting these genetic causal effects that are consistently associated with the observed phenotypes.

We present a trio of genotype-phenotype association analysis tools, namely 1) GWASPRO (https://bioinfo.noble.org/GWASPRO), which adopts a simple LMM for the analysis of additive genetic effects (referred as one-dimensional mapping or 1D GWAS here) and is specially optimized for the analysis of “big data” generated from large-scale genome-wide association studies (GWASs); 2) PEPPIS (https://bioinfo.noble.org/PEPPIS_OTLM), which adopts a full polygenetic linear mixed model to analyze the additive (1D GWAS), dominance effects (1D GWAS) and epistatic effects such as additive x additive, additive x dominance, dominance x dominance x dominance (referred as two-dimensional mapping or 2D GWAS here) effects in GWASs and quantitative trait loci mapping; and 3) PATOWAS (https://bioinfo.noble.org/PATOWAS), which further extends the 2D GWAS LMMs for broader association studies, i.e. the LMMs can not only be applied to GWASs, but also transcriptomics-wide association studies (TWASs) and metabolomics-wide association studies (MWASs). Furthermore, to facilitate the analyses of large-scale GWASs with ‘big omics’ data, we also developed a series of data pre-process tools, including a SNP marker binning tool for data dimensional reduction and a graphic processing unit (GPU)-empowered Kimshp matrix computing tool for 1D and 2D GWAS analyses. We demonstrated the high performance of our developed LMMs and tools, and their successful applications in plant genotype-phenotype association discoveries and complex trait analyses.

A Statistical Pipeline for Genetic Analysis in Multiparental Populations
Chaozhi Zheng, Martin P. Boer and Fred A. van Eeuwijk, Wageningen University & Research - Biometrics, Wageningen, Netherlands
Many multiparental populations have been recently produced to increase genetic diversity and quantitative trait loci (QTL) detection resolution, and low coverage genotyping by sequencing (GBS) technology has become cost effective tool for QTL mapping in these populations. The poster describes a statistical pipeline RABBIT (Reconstruct Ancestral Block Hit by bit) for genetic analysis in diploid experimental crosses. The pipeline includes three main functions: magicReconstruct is to calculate posterior identical by decent probabilities that can be used in explanatory variables to increase QTL detection power, where the required parental genotypes can be phased and imputed by magicImpute and the required genetic map can be constructed by magicMap. The pipeline builds on our previously developed hidden Markov model framework, hidden states being the ancestral origins along two homologous chromosomes within an offspring. The pipeline can be applied to both bi- and multi-parental populations, despite that genotypic data are homozygous or heterozygous. Furthermore, it can integrate with genotype calling to account for the uncertainties due to few number of reads in GBS data. We evaluate the RABBIT pipeline by extensive simulations and real mapping populations such as the Arabidopsis multi-parental advanced generation intercrosses (MAGICC) and the apple cross pollinated (CP). Not only is RABBIT the only software capable of accommodating all of these designs, it is more accurate and robust than commonly used packages. The RABBIT software is freely available at https://github.com/chaozhi/RABBIT.

References

The European Variation Archive: Genetic Archiving and Accessioning for All Species
Baron Koyliss, Cristina Yenyze Gonzalez, Andrea Silva, Jose Miguel Mat-Lopez, Kirill Tsukanov, Sundararaman Venkataraman and Thomas Keane, (EMBL) - The European Bioinformatics Institute, Cambridge, United Kingdom
Introduction: The European Variation Archive (EVA, https://www.ebi.ac.uk/eva) is a primary open repository for archiving, accessing, and distributing genome variation including single nucleotide variants, short insertions and deletions, and larger structural variants in any species. Materials and Methods: Since launching in 2014, the EVA peers with NCBI-based database dbSNP to form a worldwide network for exchanging and brokering of variation data. From 2017, issuing and maintaining variant accessions is divided by species: the EVA is responsible for non-human species and dbSNP for human. Other services include standard variant annotation, calculation of population statistics, and an intuitive browser to view and download queried variants in either Variant Call Format (VCF) or Conna-Separated Value (CSV) files. In addition, a comprehensive REST-API is available to query/export data that supports the hg19 streaming protocol defined by the Global Alliance for Genomics and Health (GA4GH). The EVA also contributes to maintaining the VCF, implementing a validation suite https://github.com/chivo/variation/ to ensure correctness of all the submissions made to the archive.

Results: The EVA has archived more than 770 million unique variants across 546 studies and 51 species. 288 million identifiers have also been imported to dbSNP, and 330 million new identifiers have been issued. The API is also species-agnostic and is extensively used by translational resources including Ensemble, Ensembl Genomes, Open Targets, WheatSP and the 1000 Sheep Genomes Project.

Conclusion: A key function of the EVA as a long term data archive is to provide standardised stable identifiers so that studies and discovered variants can be referenced in publications, cross-linked between databases, and integrated with successive reference genome builds. With these goals, the EVA will continue to act as a primary repository for variation data from any species.
Long-read sequencing techniques provide us an efficient and convenient way to obtain large contiguous genomes. However, the error-prone reads at the same time bring a final draft assembly that contains plenty of errors of which the frameshift-introducing indels are particularly problematic for downstream analyses, including, for example, 1) gene annotation: such errors in protein coding regions altered, and often truncated, protein predictions; 2) scaffolding: the optical mapping based methods count on accurate sequence to identify the enzyme recognition site, while both 10 x Genomics and Hi-C rely on correct mapping of short reads. Pilon, the most widely-used polishing tool, applies for genome improvement using short reads and was developed to correct small-scale assemblies for organisms of small genome size. Although it has been successfully applied in large eukaryotic genomes, the process consumes considerable time and thus requires excessive computational resources. Here, we introduce NextPolish, an integrated tool programmed in C and Python, which can improve long-read assemblies by virtue of an algorithm based on K-mer score chain and K-mer count. We benchmark NextPolish against Pilon v1.23 using long-read assemblies of Arabidopsis thaliana and Homo sapiens and show that it can deliver more accurate genome correction with a speed boost of 20-50 times.
SoEM: A Novel PCR-Free Biodiversity Assessment Method Based on Small-Organelles Enriched Metagenomics

Jihoon Jo and Chunggo Park, Chonnam National University, Gwangju, South Korea

DNA metabarcoding is currently used for large-scale taxonomic identification to understand the community composition in various marine ecosystems. However, before being widely used in this emerging field, this experimental and analytic approach still has several technical challenges to overcome, such as polymerase chain reaction (PCR) bias, and lack of well-established metabarcoding markers, a task which is difficult but not impossible to achieve. In this study, we present an adapted PCR-free small-organelles enriched metagenomics (SoEM) method for marine biodiversity assessment. To avoid PCR bias and random artefacts, we extracted target DNA sequences without PCR amplification from marine environmental samples enriched with small organelles including mitochondria and plastids because their genome sequences provide a valuable source of molecular markers for phylogenetic analysis. To experimentally enrich small organelles, we performed subcellular fractionation using a novel chromosome identification system by selecting specific regions on every chromosome and producing complimentary stretches of labeled oligonucleotides for binding to these distinct regions. These oligos generated distinct fluorescent in situ hybridization (FISH) signals that can be used as a bar code or banding patterns to uniquely label individual chromosomes, from both diploid and polyploid species. The technique was proven with both maize as well as potato species. In experiments with the potato FISH probes, it was shown the same bar codes can be used to identify the 12 homologous chromosomes among distantly related Solanum species, including tomato and eggplant. In maize, the probes demonstrated ability to identify homologous chromosomes in somatic root tip metaphase cells as well as in interphase nuclei. We believe these techniques can be applied to a wide range of plant and animal species for analyzing rearrangements and chromosomal relationships.

Cost Effective Marker Assessment in O. Sativa

We developed a panel covering the 2,015 single nucleotide polymorphisms previously identified as markers for polymorphism detection in O. Sativa. Here, we will demonstrate the application of this panel to cost-effectively enrich defined SNP markers in a highly specific and uniform manner prior to next-generation sequencing.

Methods: High-throughput Methods

Application of a Novel, Targeted Sequencing-Based Genotyping Approach for Cost Effective Marker Assessment in O. Sativa

Cynthia L. Hendrickson1, Amy B. Emerman1, Kruti M. Patel1, Sarah K. Bowman1, Scott M. Adams1, Brendan S. Desmond1, Jonathon S. Dunn1, Susan E. Corbett1, Charles D. Elfie2, Evan Mauceli1, Andrew Barry1 and Theodore B Davis1, (1)Directed Genomics, Ipswich, MA, (2)New England Biolabs, Ipswich, MA

Decreases in sequencing costs have increased the availability of public SNP databases while necessitating development of targeted genotyping assays for use in marker assisted genomic selection for a variety of crop species. The NEBNext Direct Genotyping Solution is a novel, hybridization-based target enrichment approach that has been optimized for use in genotyping applications to increase the number of assays that can be performed in a single reaction, while providing sequencing coverage depth suitable for SNP identification. The approach enables high-levels of multiplexing of both isolates and markers, allowing enrichment of hundreds of thousands of SNP targets in a single hybridization reaction, and the protocol is easily completed in a single day. We developed a panel covering the 2,015 single nucleotide polymorphisms previously identified as markers for polymorphism detection in O. Sativa. Here, we will demonstrate the application of this panel to cost-effectively enrich defined SNP markers in a highly specific and uniform manner prior to next-generation sequencing.

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Application of a Novel, Targeted Sequencing-Based Genotyping Approach for Cost Effective Marker Assessment in O. Sativa

Cynthia L. Hendrickson1, Amy B. Emerman1, Kruti M. Patel1, Sarah K. Bowman1, Scott M. Adams1, Brendan S. Desmond1, Jonathon S. Dunn1, Susan E. Corbett1, Charles D. Elfie2, Evan Mauceli1, Andrew Barry1 and Theodore B Davis1, (1)Directed Genomics, Ipswich, MA, (2)New England Biolabs, Ipswich, MA

Decreases in sequencing costs have increased the availability of public SNP databases while necessitating development of targeted genotyping assays for use in marker assisted genomic selection for a variety of crop species. The NEBNext Direct Genotyping Solution is a novel, hybridization-based target enrichment approach that has been optimized for use in genotyping applications to increase the number of assays that can be performed in a single reaction, while providing sequencing coverage depth suitable for SNP identification. The approach enables high-levels of multiplexing of both isolates and markers, allowing enrichment of hundreds of thousands of SNP targets in a single hybridization reaction, and the protocol is easily completed in a single day. We developed a panel covering the 2,015 single nucleotide polymorphisms previously identified as markers for polymorphism detection in O. Sativa. Here, we will demonstrate the application of this panel to cost-effectively enrich defined SNP markers in a highly specific and uniform manner prior to next-generation sequencing.
P0040: Methods: Other Genome Methodology
A Novel Method for Isolating High-Quality UHMW DNA from 10 Mg of Freshly Frozen or Liquid-Preserved Animal and Human Tissue Including Solid Tumors
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High-quality UHMW DNA is key to success in optical mapping of long genomic DNA using Bionano Genomics Saphyr® system for de novo genome assembly and structural variation detection. Ideally, ~100 mg of tissue is frozen immediately upon collection using liquid nitrogen or dry ice, and stored at -80°C before DNA isolation. Practically, tissue amounts may be limited and collection often occurs at sites where low temperature preservation for storage and shipping may be unavailable.
Here we present a novel method to isolate UHMW DNA from 10 mg of either freshly frozen or room temperature preserved animal and human tissue for subsequent enzymatic labeling using direct labeling and staining (DLS) to generate Bionano maps. With a TissueRapporter, 10 mg tissue is homogenized followed by a three-step purification process before embedding the purified nuclei in agarose gel plugs. This process takes less than 3 hours for a batch of 6 samples. Using this method, we have successfully isolated high quality UHMW DNA from various tissue types of rat and human including solid tumors. The method is very attractive compared to other protocols because: 1) tissue preservation, shipping and handling can be done at room temperature, 2) uses very small amount of tissue - possible application for rare samples and human tissue biopsy tests, and 3) the length and quality of the resulting single molecules generate high quality optical maps for genome finishing and IV calling.

P0041: Methods: Sequencing
SeqSNP Targeted Genotyping By Sequencing, an Alternative to Array Genotyping in Routine Breeding Programs
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Comprehensive assessment of complex traits and genomic selection has led to recently only being possible using fixed arrays. SeqSNP, a refined targeted genotyping by sequencing technology has been developed by LGC, Biosearch Technologies. SeqSNP not only provides flexibility in single nucleotide polymorphism (SNP) sequence selection, but also scalability in sample numbers which can be restrictive on fixed arrays. Independently analysed data is presented here, which not only substantiates that the SeqSNP service delivers genotyping data with high concordance to array genotyping, but it also surpasses other sequence based genotyping options in de novo SNP discovery and the analysis of multi-allelic target SNP sequences. The impact of increased accuracy allows cost efficiency and increased confidence in selections made using targeted genotyping by sequencing. SeqSNP is the next stage in sequence based genotyping as services or bespoke kits for all breeding communities.

P0042: Methods: Sequencing
Magnetic Microspheres (beads) for NGS Library Construction
Daisy Feng, Suzhou Vds Biotech Co., Ltd., Suzhou, China

1. CLEANNGS: DNA And RNA Clean-Up For Next Generation Sequencing Library Construction
The CleanNGS kit offers a highly efficient magnetic bead based clean-up system for the purification of both DNA and RNA for next-generation sequencing workflows. CleanNGS provides maximum flexibility allowing for left, right or double-ended size selection by readily adjusting the sample to CleanNGS volume ratios.

Features:
- Designed for both DNA and RNA purification
- Ideal for (double-ended) size selection for Next-Generation Sequencing
- Efficient removal of unincorporated dNTPs, primers, primer dimers and other contaminants
- No centrifugation or filtration

2. Magnetic Microspheres (Beads) for Nucleic Acid Purification
This series of superparamagnetic silica nanoparticles are designed for nucleic acid purification (NAP) with high recovery rate and efficiency. These silica-based beads have a core-shell structure consisting of a magnetic core and a layer of inorganic silica shell, with large numbers of distinct groups on the surface. They are available as aqueous suspensions, ready to use after a short vortex. The nucleic acids can be rapidly isolated from a biological samples by mixing the magnetic silica beads with chaotropic salts, such as guanidine hydrochloride or guanidine-isothiocyanate, without centrifugation and organic extraction steps. These products enable laboratories to automatically and safely process tens of thousands of samples per day.

Features:
- Superparamagnetic beads, excellent redispersibility
- Variety of selection of particle sizes and large amount of surface functional groups
- Rapid magnetic response for fast purifications
- Rapid magnetic response for fast purifications
- High specific surface area for enhanced binding capacity
- Low non-specific binding for easy elution
- Large-droplet production for lowering iso-variation, achieving highly reproducible results

3. Oligo(2) Magnetic Microspheres for Purification of mRNA
This series of magnetic microspheres can isolate highly purified intact mRNA from eukaryotic total RNA or directly from crude extracts of cells, animal and plant tissues. The isolated mRNA can be used directly in most downstream applications, such as RT-PCR, solid-phase cDNA library construction, primer extension, in vitro translation experiments, RACE, northern analysis, gene expression analysis and so on. The isolation occurs through the hybridization of covalently coupled oligo(2) sequences bound to the surface of the microspheres to the poly(A) region present in most eukaryotic mRNA. After annealing, the ssDNA is placed on a magnet to concentrate the microspheres with their bound mRNA at the side of the tube. The supernatant containing unbound contaminants is discarded.

Binding Capacities:
Up to 10µg mRNA can be isolated per 10µl (1 mg) of microspheres, depending on the tissue or cell type and the expression level of the mRNA.

P0043: Methods: Markers
High-Density Genetic Map Construction Using Specific-Locus Amplified Fragment (SLAF) Sequencing in Pyrus L.
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Pear (Pyrus L.) is one of the most important fruits in the world. Construction of a reliable and dense genetic map is crucial for marker-assisted breeding (MAS). A high-density genetic map using 288 F1 progenies produced by sand pear (P. pyriforlia) cultivar ‘Cuiguan’ × pea pear (P. calleryana) were constructed by SLAF markers. A total of 738.46 M paired-end reads were generated with an average GC content of 39.98%. Totals of 879,487 SLAF markers and 7,882,618 SNPs were detected and 3,988,503 markers might be used in the genetic mapping.

Finally, 11,052 markers were chosen in the genetic map construction which spanned 2,144.07cM in 17 linkage groups. The results will take an important step towards the identification of QTLs related to horticultural characters and MAS in Pyrus.
P0045: Other Category

The Awareness of Taxonomic Misidentification Using DNA Barcodes on a Public Database

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The National Center for Biotechnology Information (NCBI, http://www.ncbi.nlm.nih.gov) provides analysis and resources for various biological data through the NCBI web site (NCBI Resource Coordinators., 2013). The non-redundant nucleotide (nt) database which is one of resources maintained by NCBI is used universally when researchers need to identify certain species by DNA barcode sequence. However, there are multitude inconsistencies such as different sequence lengths, bases and regions, although they represent same genetic element. Because their registers are derived from various and different laboratory works with a range of technologies and assumptions without any assessment process (Chen et al., 2016). To assign this problem, we designed to explore how many DNA barcode sequences within the database show high identity each other even though those are different species. Firstly, in the database, each barcode sequence was sorted in descending order by the number of those. And total four barcode sequences (Cytochrome c oxidase subunit I, Internal transcribed spacer, Ribulose-bisphosphate carboxylase, Elongation factor Tu 1) which are representatives in each subcellular organelle (i.e. nucleus, mitochondria and chloroplast) were selected. Second, each reciprocal BLAST search would be proceeded within each barcode sequence group. Then the number of case of identical barcode sequences but different species would be counted in each BLAST result. We expect that there may be instances of indicating as same species for different species by same barcode region. If those cases would be existed, we can argue that we need to have cautions with species identification using public database.
P0048: Other Category

Publishing Genomes in Gigascience Database (GigaDB)

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GigaDB (http://gigadb.org) is the curated data-hosting platform linked to the journal Gigascience: an online open-access, open-data journal that publishes 'big-data' studies across the life sciences. Our curators directly engage with GigaScience article authors to make the raw and intermediary data, computational tools and data processing pipelines described in the papers available and, where possible, executable on an informatics platform. By making both the data and processes involved in the analysis freely accessible we can maximize their reuse potential. To date, GigaDB comprises over 1700 datasets from multiple disciplines in the life sciences including: genomic, proteomic, metagenomic, neuroimaging and many more. Here we present a selection of the features that are pertinent to genomic datasets that have recently been added through widgets in the individual dataset pages; JBrowse (genome browsers), Sample map-browser, and protocols.io. For those datasets that have content available in these formats users can access them directly within the dataset page. The sample map browser (http://gigadb.org/site/mapbrowser) allows users to explore samples across any dataset by geographic location. The JBrowse genome assembly viewer is available as a widget for datasets that provide chromosome level assemblies with comprehensive annotations, e.g. DOI:10.5524/100580

available in these formats users can access them directly within the dataset page.

The JBrowse genome assembly viewer is available as a widget for datasets that provide chromosome level assemblies with comprehensive annotations, e.g. DOI:10.5524/100580. The sample map browser (http://gigadb.org/site/mapbrowser) allows users to explore samples across any dataset by geographic location. The JBrowse genome assembly viewer is available as a widget for datasets that provide chromosome level assemblies with comprehensive annotations, e.g. DOI:10.5524/100580. Gigadb is addressing data visualization, transparency and reproducibility of research with the integration of the above tools, making it easier for reviewers, readers and users to view and access big data.

P0049: Other Plant Species

Characterization of Complete Chloroplast Genome Sequences of Chrysanthemum zawadskii and Chrysanthemum boreale

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Chloroplast (cp) genome sequence has been served as a valuable source for understanding evolutionary history and developing molecular markers. We assembled cp genome sequences of Chrysanthemum zawadskii, an herb plant used as medicine in the treatment of dyspepsia, and Chrysanthemum boreale, a similar plant as an economically motivated adulteration. The cp genome sequences of C. zawadskii and C. boreale were analyzed to investigate phylogenetic relationships and discover potential molecular markers for its authentication. We developed the four DNA markers based on the cp genome sequences in this research. The molecular markers including Insertion/Deletion (InDel) could be able to discriminate these two species around genic-intergenic regions of atpB-rbcL, petA-psbJ, pufB-psbL, and rpl33 loci. The cp genomes identified in this study would help as useful tools for fundamental molecular understanding and future authentication of Chrysanthemum species.

We highly appreciate Medical Herb Garden of College of Pharmacy in Seoul National University, Korea, for providing us plant materials. This research was supported by a grant (17162MDFS065) from Ministry of Food and Drug Safety, Korea, in 2019.

P0050: Other Plant Species

Analysis of the IncRNA Related to Vernalization in Sugar Beet

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Beet (Beta vulgaris) is a biennial herb which belongs to the Polygonaceae family. It is main sugar crop except for sugar cane. In order to induce bolting and flowering sugar beet requires a prolonged exposure to low temperatures, a phenomenon called vernalization. Vernalization is an important factor affecting the transition of plants from vegetative growth stage to reproductive growth stage. Vernalization is affected and regulated by many factors, and long ncRNA (lncRNA) may be one of them. LncRNA is non-coding RNAs (ncRNAs) which don’t have protein coding potential. According to the size of transcripts, ncRNAs can be divided into two categories. ncRNA with more than 200 nucleotides is considered to be lncRNA, while short ncRNA is less than 200 nucleotides. The function of short ncRNAs have been well studied, while the molecular mechanisms of IncRNAs are still not very clear. Studies have shown that IncRNA is involved in X chromosome silencing, genomic imprinting, chromatin modification, transcriptional activation, transcriptional interference, nuclear transport and other important regulatory processes, and these regulatory effects of IncRNA have also begun to attract extensive attention.

In this study, the differentially expressed IncRNA during the vernalization of sugar beet were identified by high-throughput sequencing, and the function of IncRNA in vernalization were explored. A total of 7421 differentially expressed IncRNAs were identified, of which 292 were significantly different, and 723 of these 292 IncRNA trans-acting target genes were predicted. Through bioinformatics analysis, these target genes were found mainly involved in ATP binding, protein binding, nucleus, translation activity, transfer phosphorus-containing groups, catalytic activity and integral component of membrane. Among them, four target genes involved in flower development are related to vernalization.

P0051: Other Plant Species

The Whole Genome of the Sweetpotato Tetraploid Relatives Ipomoea tabascana

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Origin and evolution of sweetpotato were puzzle for researchers until now. We just knew Ipomoea trifida (2X, 6X) was the ancestor species of sweetpotato. Little was known about tetraploid plant in genus Ipomoea, especially genome level. Here, we reported the genome of Ipomoea tabascana, which was the most closely related tetraploid species to sweetpotato in Ipomoea Section Batusis. De novo assembly of the long reads from SMRT Sequencing was performed using FALCON and FALCON-Unzip. In order to get enough corrected reads, the longest 78 coverage of sub-reads was firstly selected as seed reads to do error correction. The corrected reads N50 and coverage were 9.8K and 55, respectively. We get an assembly with a contig N50 size of 616.43kb. The total length of this version is 957.00Mb. Finally, scaffolding was performed by FragScaff with the barcoded sequencing reads, generating a genome with a scaffold N50 size of 1.10 Mb. The total length of this version is 963.07Mb, containing 0.64% Ns. The quality of I. tabascana genome assembly was first assessed using BUSCO. The analysis revealed that 93% of the core eukaryotic genes were detected in I. tabascana genome. To predict protein coding genes in this genome, we used homolog-based prediction, de novo prediction and transcriptome based prediction. A total of 68,400 protein-coding genes were predicted from I. tabascana genome, which is comparable to the number of genes predicted in NSP323_triloba_v3 (31,426) and in NSP306_trifida_v3 (32,301). The gene length and CDS sequences in I. tabascana have an average length of 2922.5bp and 1100.68bp, respectively. And the predicted genes have an average of 4.72 exons. A total of 61,176 (95.5%) I. tabascana proteins have at least one homolog in database including NR, KEGG, Swiss-Prot and TAIR10 et al.
Genome Center (Project No. PJ01349002), Rural Development Administration, Republic of Korea.

Acknowledgement: This work was supported by a grant from the National Agricultural Research and Extension Services, Jinan, South Korea, (4)National Institute of Agricultural Sciences, RDA, Jeonju, South Korea

Schisandra chinensis (Omija) is a fruit-bearing vine, and its purple-red berries are described as having five tastes. In particular, the seeds contain lignans, having beneficial effects on health. To obtain transcriptomic data that offers a more comprehensive view of fruit development in S. chinensis, we generated genome-wide transcriptome data from different tissues using PacBio Isoform sequencing (Iso-Seq) technology. A total of 132,856 assembled transcripts were generated with an average length of 1.9 kb and high assembly completeness. Of those unigenes, 71.6% were predicted to be complete full-length (FL) ORFs and exhibited a high gene annotation rate. Furthermore, we successfully identified unique full-length genes involved in polyphenol synthesis. Based on these unigenes, we have identified the expression change of genes from different ripening stages of fruit, thus extrapolating regulatory networks genes, especially regulators, related to polyphenol synthesis. In conclusion, our results suggest that long-read, full-length or partial-unigene data with high-quality assemblies are invaluable especially regulators, related to polyphenol synthesis. In conclusion, our results suggest that long-read, full-length or partial-unigene data with high-quality assemblies are invaluable resources as transcriptomic references in S. chinensis and can be used for comparative analyses for fruit development in closely related medicinal plants.

Pyo Hong

QTLs) were detected from Ici mapping v4.0. using composite interval mapping method. and phenotypic (sourness traits data), a total of 14 QTLs (5 pH and 9 titratable acidity (TA) revealed that Melon (Cucumis melo L.) is one of the vital species of Cucurbitaceae family. The consumption of melon fruit takes place at mature and immature stages for different purposes. Among the molecular markers, single nucleotide polymorphism (SNP) markers are mostly used in genetic diversity and gene/QTL localization due to its abundance. The 2nd generation sequencing technology (High-throughput) has facilitated the genotyping of mapping populations for identification of candidate genomic regions of important horticultural traits. Here, we report a genetic linkage map using the whole genome sequencing based SNPs detection and CAPS markers development for QTL analysis of fruit sourness associated traits in melon. From the sequencing analysis of two parental lines (M4-7 as P1 and MR-1 as P2), a total of 2,671,701 SNPs and 7740 CAPS loci were derived. The F2, mapping population was used for final genetic map, which comprised of 12 LGs and 130 SNP-CAPS markers with 1764.63 cM distance in length and 13.57 cM average b/w flanking markers. Normal distribution frequency of sourness related traits was found in F2, segregated population. By combining the genotype and phenotypic (sourness traits data), a total of 14 QTLs with pH and 9 titratable acidity (TA) QTLs were detected from F2 mapping using composite interval mapping method. High-throughput sequencing tech. was successfully used for speedy construction of genetic linkage map in F2 population and also to detect the QTL for sourness traits in melon. The present study will be helpful for marker assisted selection (MAS) in breeding programs.
**P0056: Other Species**

Large-Scale Gene Duplications in the Dinoflagellate Lineage

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Dinoflagellates are one of the ecologically important algal groups in the ocean, contributing to marine primary production and coral reef building. They showed many unique biological and physiological features such as the absence of nucleus, endosymbiosis, complex life cycle and bioluminescence. Among these characteristics, they have the most striking genomic feature which is immense and widely varied nucleic genomes size, extending 1 to 270 giga bp (Gb). Large cellular DNA content is mainly known as a result of accumulation of transposable elements (TE), whole genome duplication (WGD), and retention of duplicate genes. Paleopolyploidy is the result of WGD or massive gene duplication occurred at least several million years ago, also is well-known for plant and some animal genome evolution, but little is known in the dinoflagellate phylum. Until recently, genome capable of detecting paleopolyploidy in dinoflagellate lineage have rarely been published. However, previous studies showed that ancient WGDs can detect through age distributions of duplicated genes analyzed using transcriptome data in plants and insects. Here, we used recently published genome/transcriptomes and newly sequenced transcriptomes data from forty dinoflagellates and two organisms to investigate the ancient gene duplication event of dinoflagellates. We performed comparative genomic and phylogenetic analyses to detect ancient gene duplication and to reconstruct their relationships, respectively. Using age distributions of duplicate genes and a phylogenetic tree, we found evidences for at least one round dinoflagellate-wide massive gene duplications (polyploidy or aneuploidy). Interestingly, these bursts of gene duplication were more frequently observed at the Gonoyucleates, Prorontzea, and Gymnoziales, including species previously reported to have large genomes (~ 55 to 165 Gb). Our finding provides evidences that ancient massive gene duplications could contribute to genome size complexity during dinoflagellate evolution.

**Acknowledgement:**

This work was financially supported by the Key Program of Applied Technology Research in Guangdong Province (No. 2016B020233007), the Engineering Centre of Chicken Commercial Breeding in Guangdong Province - 2017-1649 and Guangdong Provincial Key Laboratory of Animal Molecular Design and Precise Breeding (1632018XMZ0001041554).

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**P0057: Poultry**

RNA-Seq of Time Serial Cock Comb and Testis to Investigate the Developmental Process and Genetic Basis of Cock Sexual Maturity

Xiao Jian, Hua Xiang, Hui Lu, Yuyong Hong, Siyu Chen, Huiming Kang, Hui Yu, Shuwen Tan, Daoshu Zeng and Jianhua Wu, Foshan University, Foshan, China

Chicken sexual maturity, marking the beginning of reproductive activities, is an important economic trait but still lack of study on the genetic basis. Here we compared the high and dwarf cockscomb and testis using transcriptome data in tissue samples from time series of 56, 79 and 112-day-old. The aim of this study is to determine the genetic regulation mechanism of precocious puberty in roosters. The revealed different developmental processes for both comb and testicle between the high and dwarf cockscomb groups at day 56, 79 and 112 (P<0.05). And the cockscomb height and testicular index were significantly correlated for both groups (P<0.05) during these days. A total of 258, 222 and 185 differentially expressed genes (DEGs) were found in cockscomb between the high and dwarf cockscomb groups, while 2030, 44 and 65 in testis at day 56, 79 and 112, respectively. Genes including vasoactive intestinal peptide, vasoactive intestinal peptide receptor-1, fibroblast growth factor-18, fibroblast growth factor receptor-1, tubulin polymerization promoting protein family member-5, wt family member, wnt and adenylylcyclase genes were suggested to affect the development of cockscomb and testis. The GO analyses showed the different development processes of cockscomb and testis were mainly involved in the functions of protein extracellular matrix, extracellular space, extracellular domain and extracellular. And a number of lipid metabolism pathways including apelin signaling pathway, retinol metabolism, ECM receptor interaction and PPAR signaling were involved in the development of chicken cockscomb and testis. The aldehyde dehydrogenase 1 family member A1 gene was enrolled into several GO terms and KEGG pathways both in cockscomb and testis at different ages, suggesting the potential genetic regulation to chicken sexual maturity.

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**P0058: Poultry**

The Regulation of IncRNA Expression Profile to the Early- and Late-Feathering in Qingyuan Partridge Chickens

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Long non-coding RNAs (lncRNAs) might be important in feather development and feathering patterns, but very few studies on IncRNA have been conducted in chickens. Here, IncRNA expression profiles in wing skin tissues were compared among early-, late- and no feathering chickens at birth. By combining analyses with our previous miRNA and mRNA dataset, this work aimed to elucidate the regulatory mechanism networks and the bioprocess of follicle development and the formation of different feathering phenotypes. As a result, the early-feathering chickens had 776 differentially expressed IncRNAs to no feathering ones, and 443 differentially expressed IncRNAs to the late feathering chickens. Meanwhile, only 45 IncRNAs were differentially expressed between late- and no feathering chickens. Functional analysis revealed that the targets of altered IncRNAs were involved in multiple biological processes related to feather growth and development, such as embryonic hindlimb morphogenesis, and so on. The integrated analyses of IncRNAs, miRNAs and mRNA identified a total of 16 pairs of negative interactions and 17 pairs of positive interactions in the process of feather formation. Particularly, the IncRNA XLLOC_045182 might inhibit early and late feather formation and feather phenotype via FKH1. The LncRNA 10705243 might negatively regulate the biological processes of feather growth and development via gga-miR-35-3p, the LncRNA 10705261 might restrict feather development via regulating SHHI expression. The results also revealed that XLLOC_235660 might have a positive effect on feather development via FGF10. Correspondence author: okhuali@fosu.edu.cn

Acknowledgement: This work was financially supported by the Key Program of Applied Technology Research in Guangdong Province (No. 2016B020233007), the Engineering Centre of Chicken Commercial Breeding in Guangdong Province - 2017-1649 and Guangdong Provincial Key Laboratory of Animal Molecular Design and Precise Breeding (1632018XMZ0001041554).

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**P0059: Poultry**

Identification of Loci and Genes for Growth and Feed Efficiency Traits in Broilers Using Genome-Wide Association Analyses

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Background:

Feed cost accounts for about 70% of total costs in poultry production. Residual feed intake (RFI) is defined as the variation between the observed and expected feed intake during the measurement period. RFI was calculated based on regression of average daily feed intake (ADFI) on metabolic body weight at mid-test (MBW) and average daily gain (ADG). The genetic mechanisms controlling RFI and growth in fast-growing chicken (broiler) were still largely unknown. The objective of this study was to perform a genome-wide association study (GWAS) to identify candidate loci and genes associated with growth and feed efficiency traits in broilers.

**Methods:**

A total of 3365 fast-growing broilers from a purebred line II were measured for body weight at day 28 (BW28), BW at day 42 (BW42), ADFI and ABW. All broilers were genotyped using the customized chicken 55K SNP array (Inking No. 1). After performing quality control, 41242 variants and 3314 birds were used for further analyses. Phenotypic and genetic (co)variances of growth and feed efficiency traits were estimated by using the genomic relationship matrix G in ASReml-v3.0 package. GWAS was carried out by using a single-SNP based univariate linear mixed model in GEMMA. In addition, we investigated five associated regions on GGA16 and GGA1 using the fast Family-Based SKAT and SKAT-O (FBRSKAT) implemented in R package FREDSAT. Candidate genes for feed efficiency traits were assessed in the liver, breast muscle, leg muscle and abdominal fat from hypothalamus tissues of high (HRFI) and low RFI (LRFI) groups using qPCR.

**Results:**

The heritability of growth and feed efficiency traits were from low to moderate (0.12-0.21). A total of 12 genome-wide significant SNPs and 22 suggestively significant SNPs were found by GWAS analysis. One region (GGA16: 2.3-2.7 Mb) was associated with BW28 and BW42, respectively; the most significant SNP, AX_101003762, accounted for 6.94% of the genetic variance for BW28. One region on GGA3 (GGA3: 91.27-92.43 Mb) was found to be associated with ADFI and EPAM68 and NSU3 were the described genes in that region. The TME/M4768879 near significant SNP, AX_172668794, was only significantly associated with RFI. In the liver, breast muscle, leg muscle and abdominal fat, the relative expression of NSUN3 and TME/M4768879 was significantly different between HRFI and LRFI groups (P<0.01 or 0.05). The expression of EPAM68 was only detected in the hypothalamus and significantly different these groups (P<0.05).

**Conclusions:**

The heritability of growth and feed efficiency traits are estimated as low to moderate (0.12-0.21). A total of 12 genome-wide significant SNPs and 22 suggestively significant SNPs were found. Three significant QTL regions and genes associated with BW28 and BW42 (GGA16: 2.3-4.25 Mb) and feed efficiency traits were revealed (GGA1: 91.27-92.43 Mb and GGA3: 91.27-92.43 Mb). These results thus facilitate the discovery of causative variants and genes for growth and feed efficiency traits in broiler.
P0060: Rice
Providing Opportunities Testing Wide-Adaptable Stress-Tolerant Rice Varieties Under F-Deficient and Drought Conditions
Jae-Hyuk Han, Sejong University, Seoul, South Korea
Rice is a staple food for more than 50% of the world’s population. The effect of the climate change to the field crop such as rice would cause serious problems in food security in temperate regions as well as in tropical regions. The recent main issues on climate change in Korea is drought in early spring and less predictable rainfall in autumn, causing mostly quality loss. "Pup1" is not only a P-deficient tolerant but also is effective for good establishment in early growth stage in less water condition. We have developed BC2F7 QTL pyramiding breeding materials into MS11 (a japonica rice variety adaptable to tropical regions), utilizing Pup1 and DTF41, respectively. Background genotyping of the breeding lines showed more than 80% of genomic similarity of them to MS11. They showed mostly similar under normal growth condition to MS11 in the overall plant type and yield capacity. Under drought and abiotic stress conditions, the developed varieties showed tolerance in grain yield and fertility. A molecular breeding approaches utilizing abiotic stress QTLs using MS11 might provide the opportunities on testing the lines in various climate conditions.

P0061: Rice
Genome-Wide Identification of the Genes Linked to Grain Nutritional Traits and Bacterial Leaf Blight Resistance in Colored Rice Population
Joong Hyoun Chin, Sejong University, Seoul, South Korea
We’ve collected 152 colored rice accession globally and evaluated in temperate and tropical conditions to identify useful grain nutrition traits and pest resistance. Genome-wide association analysis using high-density single nucleotide polymorphism (SNP) is useful in precisely detecting QTLs and genes. In this study, followed by Genotyping-by-Sequentialing (GBS) analysis, using selected 22,112 SNPs to map QTLs for nutritional, agronomic, and bacterial leaf blight (BLB) resistance traits. Wide variations and normal frequency distributions were observed for most of the traits except anthocyanin content and BLB resistance. The structural and principal component analysis revealed two subgroups. The linkage disequilibrium (LD) analysis showed 74.3% of the marker pairs in complete LD, with an average LD distance of 1000 kb and, interestingly, 36% of the LD pairs were less than 5 Kb, indicating high recombination in the panel. In total, 57 QTLs were identified for ten traits, and the phenotypic variance explained (PVE) by these QTLs varied from 9% to 18%. Interestingly, 30 QTLs were co-located with known or functional genes. Some of the important candidate genes for grain Zinc (Zn) and BLB resistance were OsHMA9, OsMAPK6, OsNRAMP7, OsMAIN6.1, and OsZFP252, and Xa1, Xa3, xa5, xa13, and xa26, respectively. Red rice genotype, Sayllebon, which is high in both Zn and anthocyanin content, could be a valuable material for a breeding program for nutritious rice. Overall, the QTLs identified in our study can be used for QTL pyramiding as well as genomic selection. Some of the novel QTLs can be further validated by fine mapping and functional characterization. The results show that pigmented rice is a valuable resource for mineral elements and antioxidant compounds.

P0062: Rice
A Systemic View of Carbohydrate Metabolism in Rice to Facilitate Productivity
Woo-Jong Hong, KyungHee University, Yongin, South Korea, Yu-Jin Kim, KyungHee University, South Korea and Ki-Hong Jung, Kyung Hee University, Yongin, Korea, Republic of (South)
Rice (Oryza sativa L.), a model monocot plant, is also a staple crop in Asia and Africa. Due to global climate change and rapid population growth in these areas, increasing crop yield has become a more vital issue. Carbohydrate metabolism is an important biochemical process related to developmental growth, abiotic stress response, biotic stress response, and yield-related traits. Source-sink communication of carbohydrates is especially essential for yield increase. To understand whole carbon metabolism pathways and find related clues for enhancing yield, we systematically dissected genes in whole carbohydrate metabolism pathways in rice using various meta-transcriptome data such as anatomy, abiotic stress, and hormone treatment. We identified 760 carbohydrate genes from the MapMan and Kyoto Encyclopedia of Genes and Genomes (KEGG) databases and split them into 11 clusters of different anatomical expression profiles. Analysis of the overview of functionally characterized genes in Rice Qline (ORQO) database revealed that source activity and eating quality are the most well-known functions associated with carbohydrate metabolism in rice. In addition, we investigated the correlations of these genes with abiotic stress and hormone treatment. Finally, we proposed a model of carbohydrate metabolism for improving productivity associated with gene clusters in terms of anatomy, abiotic stress, and hormone treatment. We expect this systemic insight about carbohydrate metabolism to be useful to improve rice yield.

P0063: Sheep
Genome-Wide Insights of Ethiopian Indigenous Sheep Populations Reveal the Population Structure Adheres to Tail Morphology Than Phylogeography
Agraw Amane Abde, Addis Ababa University, Addis Ababa, Ethiopia, Addis Ababa, Ethiopia
Ethiopia is endowed with a huge traditional sheep population spread across diverse ecology and production system. Here, we investigated genome-wide genetic diversity and population structure of 8 Ethiopian sheep populations using the Illumina Ovine 50K SNP HapChip genotyping data. The study populations were Washera, Farta, Wollo, Menz, Horro, Arsi-Bale, Adile and Black Head Somali. A total of 156 blood samples were collected. Genomic DNA was extracted using Quick-DNATM Miniprep plus kit following the procedures of Biological Fluid and Tissue protocol. Populations from East Africa, North Africa, South Africa, Middle East and Asia were included addressing continentally and globally, the genetic relationships and infer population structure of Ethiopian sheep populations. Mean genetic diversity of Ethiopian sheep populations ranged from 0.352±0.14 for Horro to 0.379±0.14 for Arsi-Bale sheep while estimates of genetic differentiation among populations ranged from 0.004 to 0.074. Population structure and PCA analysis clustered the 8 Ethiopian sheep populations according to their tail phenotype. Four genetic backgrounds were found within Ethiopian sheep populations with different proportions. The short fat-tailed sheep did not represent a monophyletic group rather they showed similar patterns of two genetic backgrounds. Ethiopian fat-tailed sheep shared a common genetic background with the Kenyan fat-tailed sheep. Low genetic background of Asian thin-tailed sheep was detected in Africa fat-tailed and fat-tailed sheep populations. It indicates an independent introduction of thin-tailed sheep from fat-tailed and fat-tailed sheep into Africa. The genetic diversity and population structure analysis revealed clear signature of admixture among Ethiopian sheep populations. Overall, the population structure of Ethiopian sheep populations follows a clear pattern of the tail morphology than their phylogeography.
**P0064: Sheep**

Genomic Mapping Identifies Causative Mutation in MC1R Gene to Affect Coat Color Variation in Chinese Tan Sheep

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Coat color is one of the most important economic traits in livestock to be used in breed characterization and other applications. Chinese indigenous sheep breeds have diverse coat color phenotypes. The aim of this study was to perform a genome-wide association study (GWAS) to identify the variants responsible for coat color variation and investigate their biological effect in Chinese Tan sheep. A total of 94 white and colored Chinese Tan sheep were genotyped using the Illumina Ovine 60k SNP BeadChip. After quality control, 377,998 variants were used for GWAS analysis. We identified five top SNPs located in a region spanning 14,213-14,242 Mb on chromosome 14 to be associated with coat color phenotypes. The two most strongly associated SNPs (rs409851164 and rs409851063) were located in a region flanking 14:226-14:231/Mb with P-values of 7.32×10^-17 and 2.37×10^-12, respectively. The closest candidate to one of the most strongly associated SNP (rs409851063) is MC1R/Melanocortin 1 Receptor gene located in 14,231,363-14,232,541bp. One non-synonymous substitution c.313G>A (Asp105Asn) and three synonymous substitutions were identified in the MC1R gene of colored sheep. RT-PCR of different phenotypes showed that MC1R expression in colored sheep carrying the misense substitution was approximately two times that in white sheep. Our finding helps for a deeper understanding of the genetic bases of coat color variation and causative variants in sheep.

**Keywords:** Genomic mapping, Causative gene, Coat color, Gene expression

**P0065: Sheep**

Whole-Genome Sequencing of Fine Wool Sheep Revealed Population Genetics and Adaptation to High Altitude

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Sheep (Ovis aries) have played an important role in human society and have spread almost globally as one of the first animals ever domesticated, following human migrations. In order to meet the needs of human survival, sheep were reared mainly for meat, especially as the main meat of minority areas initially. With the improvement of people’s living standards and the continuous enrichment of material needs, fine wool sheep have emerged later, specialization for secondary products, such as wool. Fine Wool Sheep are renowned for their ability to produce the natural fiber wool which is an important agricultural commodity used in clothing and textiles. The wool traits of fine wool sheep have always been focused on artificial selection in breeding. However, the high-altitude adaptability is always natural selection during many years, due to the extreme differentiation of the ecological environment in which they live. For example, some fine wool sheep live in desert grassland plateaus and other high-altitude pastoral areas, while others live in low-altitude agricultural areas or desert regions, and so on. Thus it is important to understand the genetic basis of well-adapted local livestock breeds in extreme environments to develop appropriate breeding programs under scenarios of future climate change. Sheep became adapted to a wide range of agroecological conditions and sensitive to climate change. Thus, fine wool sheep provide an excellent model to gain novel insights into genetic mechanisms underlying the rapid adaptations of livestock to extreme environments within a short period of time.

We resequenced the whole genomes of 120 fine wool sheep to resequencing depth of 8 samples selected for each breeding was 30×, others was 5×, including the set of samples represented four fine wool sheep breeds of different genetic and geographic origins from habitats in different altitude environments in China. Based on the obtained information of SNP, CNV, Indel and SV, PCA analysis was carried out, the phylogenetic tree and the population genetic structure and other genetic diversity analysis were constructed, and the population variation map of Chinese fine-wool sheep was drawn in the first time. GWAS analysis was carried out for 21 traits such as wool traits, growth traits, reproductive traits, horn, adaptation, and other relevant candidate loci and domestication trait. A total of 85 candidate genes were chosen by the regional gene functional annotation and analysis, enrichment of mining candidate genes related to the target environment and domestication traits. Through different ways of grouping (e.g. horn vs. nohorn, high altitude vs. low altitude, etc.), the genomes of sheep from different high altitude environments with those from different ecotopes were aligned, the genetic variation in genomic regions that show evidence of selection were explored further. Methods such as G0, Pathway, Fst, Pi and tmid0 are responsible for the rapid adaptations and horn of sheep to the high altitude plateaus, to elucidate the population genetics and adaptation to high altitude. Additionally, a comprehensive analysis of the genomic diversity, population structure and demographic history of these animals was performed based on genomic data.

**P0066: Student Competition**

Is Phylotranscriptomics As Reliable As Phylogenetics?

Seongmin Cheon1, Jianzhi Zhang2 and Chungoo Park3, (1)Chonnam National University, Gwangju, South Korea, (2)University of Michigan, Ann Arbor, MI

Phylogenomics, the study of phylogenetic relationships among taxa based on their genome sequences, has emerged as the preferred phylogenetic method because of the wealth of phylogenetic information contained in genome sequences. Genome sequencing, however, can be prohibitively expensive, especially for taxa with huge genomes. Consequently, the less costly phylotranscriptomics has seen an increased use in recent years. Phylotranscriptomics reconstruct phylogenies using DNA sequences derived from transcriptomes, which are often orders of magnitude smaller than genomes. However, in the absence of corresponding genome sequences, comparative analyses of transcriptomes can be challenging and it is unclear whether phylotranscriptomics is as reliable as phylogenomics. Here we respectively compare the phylogenomic and phylotranscriptomic trees of 22 mammals and 15 plants that have both transcriptomes and genome sequences, comparative analyses of transcriptomes can be challenging and it is unclear whether the same tissue is used across species. These findings validate and brighten the prospect of phylotranscriptomics and illustrate the criticality of reliable ortholog detection in such practices.

**P0067: Student Competition**

Evolutionary Signatures of the Mitochondria – Nucleus Conflict in African Cattle Admixture

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The mitochondria - nucleus conflict is a major barrier to cross-species hybridization affecting the fitness of hybrid progenies. Despite the admixed zebu-taurine nature of the majority of African cattle, only taurine mitochondrion haplotypes are found on the continent. Here, we proposed and investigated two evolutionary hypotheses as the bases of this observation, sex-biased asymmetries in zebu-taurine hybridization and selection pressure driven by the mito-nuclear discordance. We firstly reconstructed the phylogenetic trees based on mitochondrial DNA (mtDNA) and nuclear DNA (nucDNA), using public data and 162 African indigenous cattle whole genome sequences. It confirms the discordance of tree topologies between mtDNA and nucDNA. We then simulated the zebu-taurine population admixture processes to test the taureine mitochondrial haplotype fixation hypothesis, under different male – female ratios and demographic scenarios. Finally, we screened candidate selection signatures between African and Asian zebu. We identified non-synonymous mutations in known mito-nuclear interacting candidates that are involved in the regulation of cellular metabolism and aerobic respiration. These include NDUFPS1 playing a central role in oxidative phosphorylation pathway. In addition, we also spotted several non-synonymous mutations in various neurotransmitter synapse signaling and circadian entrainment pathways, illustrating the impact of mito-nuclear discordance on organismal functions cooperating with mitochondrion. Our results indicate that the combination of selection pressure and demographic events were likely the main driving forces of evolution behind the only presence of taureine mtDNA in admixed African cattle population. We believe that our findings provide a new stepping stone toward the full understanding of the evolution of cattle population and their adaptation to the African continent.
Effect of H3K4me3 on the Function of Ovary Granulosa Cells in Sows

Xiaofeng Zhou, Yingting He, Xiaolong Yuan and Jia-Qi Li, South China Agricultural University, Guangzhou, China

Ovary is the site of follicular development and ovulation. Its normal development is crucial for maintaining the reproductive ability of females. Follicular development is closely related to the growth, proliferation and apoptosis of granulosa cells, and is precisely regulated by a series of genes. Histone methylation, as an important gene regulation mechanism, can change the binding ability of histones to DNA, thereby regulating the expression level of genes. In this study, the growth and development of porcine granulosa cells (pGCs) was used as a cell model for exploring the development of follicles in vivo. The trimethylation of lysine No. 4 on histone H3 (H3K4me3) was used as the entry point to investigate the effect of H3K4me3 on the function of pGCs.

To explore the mechanism of H3K4me3 affecting follicular development in sows, this study used H3K4me3 inhibitors (BCL-121) and agonists (PBIT) to treat pGCs. The effects of H3K4me3 on proliferation, apoptosis and cycle of pGCs were studied by using EdU, CCK-8, Annexin V-FITC, Caspase3/7 and Western Blot. Subsequently, the mice were injected with BCL-121 and PBIT, drugs in vivo to investigate the effect of the drug on the concentration of blood gonadotropin in the mice. In this study, we found that H3K4me3 has different contents in large, medium and small follicles. H3K4me3 can promote the proliferation of pGCs, inhibit the apoptosis of pGCs, reduce the proportion of pGCs arrested in G0/G1 phase, promote the secretion of E2 by pGCs. Compared with the control group, BCL-121 reduced the level of GnRH in the blood of mice at 42 days of age, and decreased the levels of LH and FSH in the blood of mice at 35 and 42 days of age. PBIT can increase the level of GnRH in the blood at 42 days of age, and decreased the levels of LH and FSH in the blood of mice at 35 and 42 days of age. PBIT can increase the level of GnRH in the blood at 42 days of age, and decreased the levels of LH and FSH in the blood of mice at 35 and 42 days of age. PBIT can increase the level of GnRH in the blood at 42 days of age, and decreased the levels of LH and FSH in the blood of mice at 35 and 42 days of age. PBIT can increase the level of GnRH in the blood at 42 days of age, and decreased the levels of LH and FSH in the blood of mice at 35 and 42 days of age.

In conclusion, this study found that H3K4me3 can promote the proliferation of pGCs, inhibit the apoptosis of pGCs, reduce the proportion of pGCs arrested in G0/G1 phase, promote the secretion of E2 by pGCs, and increase the content of sex hormones in mice. These results will provide a theoretical reference for further exploration of the mechanism of histone methylation on the development of ovarian follicles.

Keywords: Porcine, WGCNA, GWAS, Birth Weight
P0072: Swine
A Comprehensive Map of Cis-Regulatory Elements in the Pig Genome By the Encode Project
Yunxia Zhao, Hua Zhong Agriculture University, Wuhan, China
The continuous development of pig genome studies provide a valuable resource for further improvement of this important species in the livestock industry and biology research. But functional annotation of genomic sequences, especially the identification of cis-regulatory elements, is largely uncharacterized in pig genome. To break through this problem, we identified the cis-regulatory elements of pig genome by taking a similar approach adopted by the ENCODE and Roadmap Epigenomics projects. We carried out RNAseq and ChIP-seq for H3K27ac and H3K4me3 to comprehensively identify genome sequence and characterized function of cis-regulatory elements of pig genome in skeletal muscle, spleen, heart, kidney, liver, backfat, lung, thymus, small intestine (duodenum), cerebrum and cerebellum from Enshi Black, Meishan, Duroc and Large White pigs. In total, 47,612 putative promoters and 146,399 potential enhancers were identified, among them, 15,758 enhancers showed tissue specific characteristic. We also designed high-throughput chromosome conformation capture (Hi-C) experiment to further explore the three dimension (3D) structure of pig genome. Here, 2,305 topologically-associated domains (TAD) were identified in muscle tissue respectively. On bias of the difference cross pig breeds on economic traits, 8,863 significantly differential expressed genes were identified in muscle, fat, spleen, liver and heart cross four breeds pigs. Then enhancer and their target genes were predict according to Spearman correlation coefficients (SCCs) at cutoff of R>0.5 as well in the same TAD. We found the fold change of enhancers which associated up-regulated expression genes and down-regulated gene was significantly different (P<0.001) and up-regulated genes associated with more positive fold changes enhancers (mean fold change=0.72545) relative to down-regulated genes (mean fold change=−1.27425). As same as enhancers, active promoters of DEGs, showed the similar pattern. These results indicated that gene expression difference of breeds are linked with difference enrichment of enhancers and active promoters.

P0074: Tomato, Potato, Pepper, and related
Regulation of Primary Metabolite Profile in Postharvest Tomato By Exogenous Abscisic Acid during Ripening
Xiaoya Tao and Tiejin Ying, Zhejiang University, Hangzhou, China
Phytohormone abscisic acid (ABA) plays an important role in tomato ripening. However, the regulation of primary metabolites by ABA during tomato ripening is still obscure. In the present research, fruit were infiltrated with ABA (1.0 mM) and deionized water (control), and were kept in darkness for 15 days, and the effects of exogenous ABA on the relative contents of sugars, organic acids, amino acids and the expressions of key genes related with sugar and organic acid metabolisms were analyzed. The results showed that exogenous ABA accelerated tomato ripening, accompanying with the enhanced change of fruit colour and firmness, the higher levels of respiration rate and ethylene production. Meanwhile, it also enhanced the relative levels of some primary metabolites, such as glucose, lysine and fructose, citric acid, citramalic acid, ascorbic acid and gluconic acid, as well as serine, pyroglutamic acid, GABA, glutamic acid, asparagine and glutamine. Additionally, the expressions of most key genes were stimulated by exogenous ABA during tomato ripening. These results indicate ABA is systematically involved in the regulation of primary metabolites and the expression of related genes, which may be a useful regulation target to improve tomato taste and flavor.

P0075: Tomato, Potato, Pepper, and related
A Comparative Synteny Analysis Tool for Target-Gene SNP Marker Discovery: Connecting Genomics Data to Breeding in Solanaceae
Junkyoung Choe1, Ji-Eun Kim2, Bong-Woo Lee1, Jeong-Hee Lee2, Moon Nam1, Youn-II Park1 and Sung-Hwan Je1, (1)SEEDERS Inc., Daejeon, South Korea, (2)Chungnam National University, Daejeon, South Korea
It is necessary for molecular breeders to overcome the difficulties in applying abundant genomic information to crop breeding. Candidate orthologs would be discovered more efficiently in less-studied crops if the information gained from studies of related crops were used. We developed a comparative analysis tool and web-based genome viewer to identify orthologous genes based synteny as well as sequence similarity between tomato, pepper and potato. The tool has a step-by-step interface with multiple viewing levels to support the easy and accurate exploration of functional orthologs. Furthermore, it provides access to single nucleotide-polymerization markers from the massive genetic resource pool in order to accelerate the development of molecular markers for candidate orthologs in the Solanaceae. This tool provides a bridge between genome data and breeding by supporting effective marker development, data utilization and communication.

Database URL: http://tgsol.seeders.co.kr/tgsol
Acknowledgement: This work was supported by a grant from the Next-Generation BioGreen 21 Program (No. PJ01100301, PJ01313203), Rural Development Administration, Republic of Korea.


**P0076: Tomato, Potato, Pepper, and related**

Global Multi-Environment Phenotyping and Genome-Wide Association Mapping in a Tetraploid Potato Diversity Panel for Tuber Bulking Maturity

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Most commercially cultivated potato varieties are tetraploid (2n=4x=48), consisting mostly of the Solanum tuberosum Group tuberosum genome with variable levels of introgressions from wild species and cultivated landrace groups. Tetraploid potato has high levels of heterozygosity, as well as complex genetics analysis arising from outcrossing autotriploidy. To that end, genes affect agronomic and cultivated landrace groups. Tetraploid potato has high levels of heterozygosity, as well as complex genetics analysis arising from outcrossing autotriploidy. To that end, genes affect agronomic performance, or traits ranks unknown. Most traits are quantitative, controlled by many alleles of small effect. Hence, accurate detection of the quantitative traits in genetic materials at CIP is paramount to a better understanding of the regulation of these traits, and their application in breeding programs around the globe. Despite a limited number of genetic markers for traits being available for detection in a Tetraploid Potato Diversity Panel for Tuber Bulking Maturity

**P0077: Wheat, Barley, Oat, and related**

Genetic and Environmental Variation in Yield and Root Development in Winter Wheat Using a Semi-Field Phenotyping System

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Continuing climate change increases probability of plant crops experiencing drought during growth and deeper roots can help plants to uptake potential resource in deep soil and ensure the plants having better growth.

The objective was to explore the genetic and environmental variation in yield and root traits of winter wheat measured in a semi-field root phenotyping facility. Both phenotypic and genotypic data were available for 84 winter wheat lines which were planted in two beds with 150 rows located at north and south, respectively. In each row, wet and drought treatments were applied by varying the distance to underground watering system. Root data were collected based on the pictures taken from a minirhizotron below each row. The total length of visible roots in each row was analyzed.

The statistical model used for yield included fixed effects of bed-location-treatment, random effects of additive genomic effects, residual line effects, row error, spatial effects and residual error. For root depth, the fixed effects of camera were also included, while the random effects of row error were excluded since there was only one record for each row. Results showed that the coefficients of genetic variation were 16 for yield and 13 for root length. For both traits, spatial effects maintained relatively large variation, which were 14 for yield and 27 for root length.

In conclusion, it is possible to obtain accurate records of yield in the semi field facility. More accurate root records will allow breeders to include this trait in their breeding programs.

**P0078: wheat, barley, oat, and related**

Wheat Exome Capture Panel Designed with the IWGSC Bread Wheat Reference Genome Assembly

Matthew Hymes and Jake Enk. Arbor Biosciences, Ann Arbor, MI

The International Wheat Genome Sequencing Consortium (IWGSC) recently released the best-resolved wheat genome sequence and associated annotations ever generated. Thanks to the fully contiguous chromosomal scaffolds reconstructed via directly sequencing each sub-genomic homeolog, the sequence and locations of each coding region of the Chinese Spring cultivar are now accessible, enabling unprecedented opportunities in wheat crop improvement. In close collaboration with the IWGSC, Arbor Biosciences developed an exome targeted sequencing kit that captures more than 95% of the exons identified in the reference sequence’s early-bulking pattern in each of the four different locations. The average tube weight (of a marketable tuber) of these ten genotypes ranged from 126.79 to 208.65 g across the harvest times. The marketable tubers of these outstanding genotypes were smaller at the first harvest in all experiments but still over 90 g, indicating that they had reached a marketable size at the early harvest stage, and can be considered early bulking genotypes in their respective environments.

Associations analysis identified discrete significance for traits AYP, AWMT, and WMT, albeit marginal. Some of these markers are in regions previously identified for tuber yield and the number-of-tubers per plant. Two markers on chromosome 9, detected in the Kunming dataset, are in a region linked to late bulk growth and deeper roots can help plants to uptake potential resource in deep soil and ensure the plants having better growth.

In conclusion, it is possible to obtain accurate records of yield in the semi field facility. More accurate root records will allow breeders to include this trait in their breeding programs.
Methods: Markers

A Universal Pipeline for Mobile mRNA Detection in Heterografting Systems and New Insights into Watermelon - Bottle Gourd Grafting Advantages

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Chilling stress seriously restricts watermelon industry. Heterograft has long been widely employed to enhance chilling tolerance of watermelon. Large-scale mRNAs movement of heterograft is well established, but the number of mobile mRNAs varied widely. In this study, using a watermelon-bottle gourd heterografts, we developed a universal pipeline for mobile mRNA detection in heterografting systems and collected an exhaustive profile of mobile mRNAs in commercial watermelon-bottle gourd heterografts which were confirmed by experimental evidence. In our investigations, we found effective mobile mRNAs were induced by cold stress and mRNAs mobility showed no correlation to their abundances in source tissues. Furthermore, our results bring insight into how watermelon scion and bottle gourd rootstock interact at the molecular level to confer heterografting advantages under chilling stress. Our results would not only provide several candidate genes for further functional characterization, but also provide a more profound overview of the molecular mechanism of how scion and rootstock interact with each other to resistant chilling stress.
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