AGBT2026™
AGRICULTURE

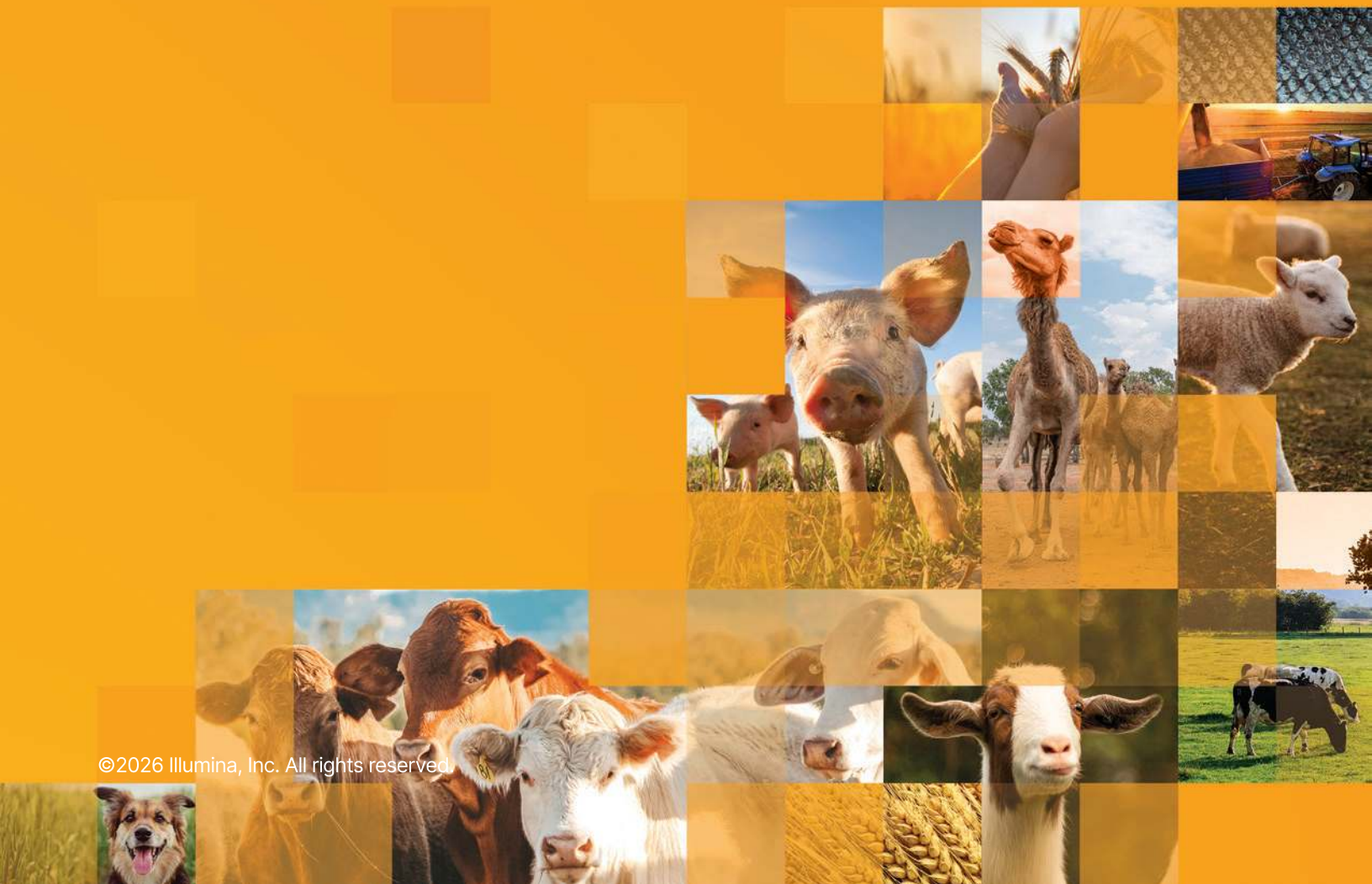
Sheraton Grand at Wild Horse Pass

APRIL 12-15, 2026

illumina

Building a sustainable future through genomic innovation

Visit Illumina at AGBT Ag 2026
Booth 109/111



AGBT 2026™
AGRICULTURE

Sheraton Grand at Wild Horse Pass

APRIL 12-15, 2026

Celebrating the 5th AGBT Agricultural Meeting

Over the next few days, you will engage with leaders across genomics, data science, breeding, policy, funding and technology who are advancing terrestrial and aquatic agriculture around the world.

Together, we will explore how genomics is shaping agriculture in response to a changing planet. Through new research, emerging technologies and cross-sector collaboration, this community is driving the future of food systems and sustainability.

AGBT Agriculture is one of three global meetings organized by The Genome Partnership, a St. Louis-based nonprofit dedicated to advancing research, promoting education and expanding commerce in genome science and technology. For more than 25 years, The Genome Partnership has convened AGBT meetings to foster innovation and collaboration across the genomics community.

Building on this legacy, AGBT Agriculture is designed to bring together leaders across plant, animal and applied genomics to accelerate discovery and real-world impact. The program highlights advances in genome editing, pangenomics and precision breeding, alongside AI-enabled imaging, data analytics and applied genomics across crops, livestock and ecosystems, creating opportunities for meaningful collaboration and new partnerships.

AGBT Agriculture remains committed to supporting students and early-career researchers, helping ensure continued progress and leadership in agricultural genomics.

We are glad you are here and look forward to a productive and engaging meeting.

Wendy Vlieks
President
The Genome Partnership

Scientific Organizing Committee

We are incredibly grateful to our meeting co-chairs, Sarah Hearne and Daniela Lourenco, and the entire Scientific Organizing Committee for the countless hours they have dedicated to making AGBT Agriculture 2026 a content-rich experience.

Over the next several days, we will come together to share advances in agricultural genomics and explore technologies shaping food systems and sustainability, made possible by their leadership and commitment.

Xiaofeng Cao
Principal Investigator, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences

Jack Dekkers
Distinguished Professor, Animal Breeding and Genetics, Department of Animal Science, Iowa State University

Appolinaire Djikeng
Director General, International Livestock Research Institute

Sarah Hearne*
Chief Science and Innovation Officer, CIMMYT

Charlie Johnson
Director, Genomics & Bioinformatics Service, Texas A&M AgriLife

Renee Lafitte
Director, Crops R&D, Gates Foundation

Nathan Lakey
President and Chief Executive Officer, Orion Genomics

Daniela Lourenco*
Associate Professor, Animal Breeding, Genetics, and Genomics, Department of Animal and Dairy Science, University of Georgia

Len Pennacchio
Senior Scientist, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory

Guilherme Rosa
Professor, Quantitative Genetics and Data Science, Department of Animal and Dairy Sciences, University of Wisconsin-Madison

Alison Van Eenennaam
Distinguished Professor of Cooperative Extension, Animal Biotechnology and Genomics, University of California, Davis

Bruce Walsh
Professor, Ecology and Evolutionary Biology, University of Arizona

*Meeting co-chairs

Sponsors

We gratefully acknowledge the generous support provided by the following companies

GOLD

illumina®

BRONZE

TWIST BIOSCIENCE

sptlabtech

cellanome

CONTRIBUTING

AgriGenX

AgriPlex GENOMICS

Ag BioTech INCORPORATED

azora BIOSCIENCES

AIRFoundry
Artificial Intelligence-driven RNA BioFoundry

BD

Breed Bio

Complete GENOMICS

Element Biosciences

labogena DNA analysis

MN MACHEREY-NAGEL

National Association of Plant Breeders NAPB Improving Plants to Improve Lives

NEOGEN®

NEW ENGLAND Biolabs®

NimaGen.

Penn Medicine

Sailgene

seqWell

ThermoFisher SCIENTIFIC

ZYMO RESEARCH
The Beauty of Science is to Make Things Simple®

General Information

Hospitality Desk Hours

- Sunday, April 12: 7:00 a.m. to 7:00 p.m.
- Monday – Wednesday, April 13 to 15: 7:30 a.m. to 7:00 p.m.

The Hospitality Desk is available to assist with general questions, meeting information, and on-site support throughout the meeting.

Name Badges

Name badges are required for meeting security and networking. All attendees must:

- Wear their badge visibly at all times, clipped to the provided lanyard with the name facing outward
- Keep their badge with them throughout the event
- Present their badge for entry to all sessions and events

Badges are non-transferable. Proper badge display helps ensure attendee safety and supports meaningful connections throughout the AGBT Agricultural Meeting.

Transportation

Attendees are responsible for their own airport transfers.

Phoenix Sky Harbor International Airport is approximately 15 miles from Sheraton Grand at Wild Horse Pass. Travel time is typically 20 to 25 minutes, depending on traffic.

Uber, Lyft and taxi services are recommended.

Additional information is available on the Phoenix Sky Harbor Ground Transportation website.

Return transportation will be provided on Thursday, April 16, with departures every hour from 4:00 a.m. to 12:00 noon.

General Information

Social Events

Posters, Pours and Plates Welcome Reception

Monday, April 13, 6:00 to 9:00 p.m., Komatke Ballroom

AGBT Dinner

Tuesday, April 14, 6:30 to 8:00 p.m., Akimel Lawn

Sponsor Social

Tuesday, April 14, beginning at 8:00 p.m., Sponsor Promenade

Farewell Dinner

Wednesday, April 15, 6:00 to 9:00 p.m., Hemapik Lawn

Conference Technology

Official AGBT Mobile App

The AGBT mobile app includes the agenda, speaker details, maps, abstracts and other essential resources.

Access Click2Win to participate in the meeting contest and be entered to win prizes.

Tech Support

- AGBT Hospitality Desk: Akimel Foyer
- Wi-Fi Network: AGBTAg26
- Wi-Fi Password: AGBTAg26

Social Media Engagement

Share your experience and join the conversation using #AGBTAg26.

sptlabtech

Scale Your Science. Not Your Cost Per Sample.

Liquid handling designed for AgBio. Flexible enough for discovery, powerful enough for scale.

AgBio workflows don't follow a single script.

One day it's high-throughput screening across 1536-well plates. The next it's PCR genotyping, NGS library prep, or complex sample matrices from field to lab.

Yet most automation platforms expect your science to adapt to them.

SPT Labtech takes a different approach.

True workflow flexibility, built in:

- Modular systems that evolve with your protocols
- Adaptable deck layouts for changing workflows
- Compatibility with diverse labware and high-density formats (384/1536)

One platform. Multiple applications:

- High-throughput screening (HTS)
- PCR-based genotyping
- NGS library preparation
- Move seamlessly between workflows while maintaining the precision your data demands.

See **automation that adapts** to your science

Visit SPT Labtech at the AGBT-Ag booth and discover flexible automation built for modern AgBio labs.

sptlabtech.com

Agenda

Sunday, April 12

7:00 a.m. – 7:00 p.m.

AGBT Meeting Registration
Akimel Foyer

9:00 a.m. – 7:00 p.m.

Pre-Conference Workshops

9:00 a.m. – 1:00 p.m.

Innovative Approaches and Technologies for Crop Improvement

Description: This workshop explores innovative approaches and technologies designed to enhance crop improvement. Talks will cover diverse research that develops or utilizes emerging methods with the goal of accelerating genetic gain or understanding and manipulating quantitative genetic variation. With this scope, the workshop aims to foster interdisciplinary collaboration between researchers in the fields of quantitative genetics, functional genomics, and molecular biology. The first session of the workshop will examine advanced quantitative tools, including novel statistical approaches to dissect complex genotype-by-environment (GxE) interactions, methods for enhancing multi-trait genomic prediction, and haplotype-based parent selection strategies. The second session bridges these predictive methods with functional applications, exploring how biological knowledge can improve breeding outcomes. Key topics include the application of AI and crop modeling, the integration of novel epi-genomic data (UMR-seq) and the use of targeted genome engineering to optimize complex agronomic traits, such as root architecture. This workshop unifies diverse perspectives to build synergistic strategies for future crop improvement.

Organizers: Jessica Rutkoski, University of Illinois and Lee Hickey, University of Queensland (AU)

Location: Kave 1

1:00 p.m. - 4:00 p.m.

Professional Development Workshop

Description: In this interactive workshop you will experience your own default communication style and those of others. You will gain the ability to read others preferred styles and how you and them can modify your styles to communicate more effectively, meeting ideally somewhere in the middle. This workshop will increase your awareness of a simple framework differentiating four main communication styles called DISC. This is a very common training used in most companies to increase awareness about effective and constructive between team members.

Organizers: Klaus Koehler, former Corteva Agrisciences; Rebecca Lowdon, Bayer Crop Sciences; and Alencar Xavier, Corteva Agrisciences

Location: Deer/Scorpion

Agenda

Sunday, April 12

1:00 p.m. - 5:00 p.m.

Pangenomes and the Genetics of Agricultural Improvement

Description: Reference genomes for crops and livestock allowed us to progress from QTL to specific markers utilized across breeding programs and thus paved the way for genomics-based breeding and genomic prediction. The very recent ability to de novo assemble and annotate multiple genomes within any species, brings us to the pangenome era. Such data can reveal the full scale of variation such as indels and copy-number variation in particular gene models up to presence absence and inversions of larger genomic regions.

The goals of this workshop are to review the current state of the art Ag-related pangenome research, to identify the remaining gaps, and foster community discussion and collaboration to develop innovations and solutions.

Organizers: John McKay, Colorado State University and Nils Stein, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)

Location: Kave 2

5:00 p.m. - 7:00 p.m.

One graph to herd them all, one graph to align them, one graph to include all breeds and in the pangenome bind them

Description: Long-read sequencing and pangenome assembly methods have revolutionized our ability to detect and evaluate genomic variation in agricultural species. By integrating multiple assemblies across many populations and breeds rather than relying on a single linear reference, pangenomes provide a more complete representation of species-level composition and reduce reference bias. As reference models, pangenome graphs can improve mapping rates, variant calling accuracy (particularly for structural variants), and haplotype resolved analyses. This workshop for agricultural researchers will demonstrate the construction and application of pangenomes using the horse as an example. Participants will learn how to leverage containerized workflows to build pangenomes, explore multiple cutting-edge visualization tools, align short reads using the “personalized pangenome” approach, and genotype short and structural variants. Using the equine pangenome as a case study, we will showcase the detection and characterization of previously documented equine structural variants. By the end of the workshop, participants will have gained theoretical insight and practical experience in pangenome construction, visualization, and the identification of biologically relevant variation from pangenome-based point of view.

Organizers: Jonah Cullen, University of Minnesota and Ted Kalbfleisch, University of Kentucky

Location: Kave 2

Agenda

Sunday, April 12

5:00 p.m. - 7:00 p.m.

Innovative Applications of Pangenomes in Agriculture

Description: Despite the explosion of pangenome-related research over the last 12 months, aside from some very notable exceptions, most such papers do little beyond variant counting and applications of standard single-reference methods. This workshop will seek to fill this void by providing a forum for leaders in pangenome applications in agriculture to present recent findings and new approaches.

Organizers: John Lovell, HudsonAlpha and Rachel Rusholme-Picher, Earlham Institute

Location: Kave 2

Monday, April 13

7:30 a.m. – 7:00 p.m.

Meeting Registration / Hospitality Desk
Akimel Foyer

7:30 a.m. – 9:00 a.m.

Breakfast
Komatke Patio

7:30 a.m. – 9:00 a.m.

Women's Networking Event
Akimel Patio

9:00 a.m. – 9:10 a.m.

Opening Remarks: Sarah Hearne, Chief Science and Innovation Officer, CIMMYT, and Daniela Lourenco, Associate Professor, Animal Breeding, Genetics, and Genomics, Department of Animal and Dairy Science, University of Georgia; Co-Chairs of the AGBT Agriculture Scientific Organizing Committee
Akimel Ballroom

Plenary Session I:
Akimel Ballroom

Session Chair: Sarah Hearne, Chief Science and Innovation Officer, CIMMYT, and Co-Chair of the AGBT Agriculture Scientific Organizing Committee

9:10 a.m. – 9:40 a.m.

Heidi Rehm, Harvard, Broad Institute
"Global strategies to solve rare disease"

9:40 a.m. – 10:10 a.m.

Peter Dearden, University of Otago, New Zealand
"The wonder of bees"

10:10 a.m. – 10:25 a.m.

Joshua Stein, International Wheat Genome Sequencing Consortium (Abstract Selected Talk)
"The IWGSC Wheat Diversity Project: foundational genome resources to advance a global food security crop"

10:25 a.m. – 11:00 a.m.

Coffee Break & Exhibits
Sponsored by SPT Labtech
Komatke Ballroom

Agenda

Monday, April 13

Plenary Session II: Akimel Ballroom	**Session Chair:** Jack Dekkers, Distinguished Professor, Animal Breeding and Genetics, Department of Animal Science, Iowa State University, and Organizing Committee Member
11:00 a.m. – 11:30 a.m.	**Andrea Doeschl-Wilson, The Roslin Institute, University of Edinburgh** "Unleashing genetic diversity to combat infectious diseases"
11:30 a.m. – 12:00 p.m.	**Alyx Shigenaga, University of California, Davis** "From genes to grains: engineering rice resilience in a changing climate"
12:00 p.m. – 1:40 p.m.	**AGBT Lunch** Mesquite Terrace and Akimel Ballroom
12:40 p.m. – 1:40 p.m.	**Desserts & Exhibitor Showcase** Exhibit Hall, Komatke Ballroom
Plenary Session III: Akimel Ballroom	**Session Chair:** Nathan Lakey, The Genome Partnership Board and Organizing Committee Member
1:40 p.m. – 2:10 p.m.	**Krishna Niyogi, University of California, Berkeley** "Understanding and altering photoprotection to improve crop productivity"
2:10 p.m. – 2:25 p.m.	**Alencar Xavier, Corteva Agrisciences, Purdue University (Abstract Selected Talk)** "Tricks and extensions for multivariate modeling of genomic and breeding values"
2:25 p.m. – 2:45 p.m.	**Gold Sponsor Talk – Illumina, Andre Eggen, Director Global Agrigenomics** "Genomic innovations for animals and plants: what's next for research and breeding"
2:45 p.m. – 3:30 p.m.	**Coffee Break & Exhibits** Komatke Ballroom
Plenary Session IV: Akimel Ballroom	**Session Chair:** Nathan Lakey, The Genome Partnership Board and Organizing Committee Member
3:30 p.m. – 4:00 p.m.	**Gloria Coruzzi, New York University** "Ratcheting up nitrogen and water use efficiency in crops - an AI inspired approach"
4:00 p.m. – 4:30 p.m.	**Yniv Palti, USDA Agricultural Research Service (REE-ARS)** "Government, academia and industry collaborations to advance selective breeding and genetic research in rainbow trout aquaculture and recreational fisheries"
4:30 p.m. – 5:00 p.m.	**Poster Flash Talks**

Agenda

Monday, April 13

5:00 p.m. – 5:15 p.m.	**Katie Jenike, University of Cambridge (Abstract Selected Talk)** "Haplotype architecture shapes phenotypic diversity across plant and animal pangenomes"
5:15 p.m. – 5:30 p.m.	**Jack Dekkers, Iowa State University (Abstract Selected Talk)** "Stress hormones in hair as genetic indicators of (disease) resilience in pigs"
5:30 p.m. – 5:45 p.m.	**Lucas Borges Dos Santos, University of Illinois at Urbana-Champaign (Abstract Selected Talk)** "Pangenome analysis of nine soybean cyst nematode genomes reveals hidden variation contributing to diversity and adaptation"
5:45 p.m. – 6:00 p.m.	**Charlotte Brault, University of Minnesota (Abstract Selected Talk)** "Advancing Fusarium head blight resistance in wheat: genetic gains and genomic selection strategies"
6:00 p.m. – 9:00 p.m.	**Posters, Pours & Plates: AGBT Agriculture Welcome Reception Sponsored by Twist Bioscience** Komatke Ballroom

Tuesday, April 14

6:30 a.m. – 7:30 a.m.	**Rise and Shine with AGBT (Optional Activity)** Meet at AGBT Hospitality Desk in Akimel Foyer
7:30 a.m. – 7:00 p.m.	**Hospitality / Information Desk** Akimel Foyer
7:30 a.m. – 9:00 a.m.	**Breakfast** Komatke Patio
Plenary Session V: Akimel Ballroom	**Session Chairs:** Daniela Lourenco, Associate Professor, Animal Breeding, Genetics, and Genomics, Department of Animal and Dairy Science, University of Georgia; and Organizing Committee Member. Bruce Walsh, Professor of Ecology and Evolutionary Biology, University of Arizona; and Organizing Committee Member
9:00 a.m. – 9:30 a.m.	**Julie Gray, University of Sheffield** "Stomata and climate resilience"
9:30 a.m. – 10:00 a.m.	**Jeffrey Endelman, University of Wisconsin, Madison** "Quantitative genetics and genomics in potato"
10:00 a.m. – 10:15 a.m.	**Enrique Sanchez Molano, The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh (Abstract Selected Talk)** "From local records to global impact: integrating farmer-led data and genomics in livestock systems for LMICs"

Agenda

Tuesday, April 14

10:15 a.m. – 11:00 a.m.	**Coffee Break & Exhibits** Komatke Ballroom
11:00 a.m. – 11:30 a.m.	**AGBT Next Gen Leadership Awards**
11:30 a.m. – 11:45 a.m.	**Marina Bernardes, University of Georgia (Abstract Selected Talk)** “Fine-tuning Monte Carlo single-step genomic REML for variance components estimation in large datasets”
11:45 a.m. – 12:00 p.m.	**Joseph Guhlin, University of Otago (Abstract Selected Talk)** “D-BLUP: Making genomic BLUP differentiable for end-to-end genomic prediction”
12:00 p.m. - 2:00 p.m.	**AGBT Lunch & Workshop(s)** Mesquite Terrace & Akimel Ballroom
12:20 p.m. - 1:50 p.m.	**Lunch & Learn: Women in Genomics** **Description:** This 90-minute workshop will provide a dynamic forum of panelists including distinguished female scientists and male allies who have built impactful careers in academia, government, and industry. Panelists will discuss a range of topics such as lessons learned from early career experiences that impact their leadership style; overcoming systemic barriers; effective allyship in the workplace; thriving during uncertain economic and political times; shaping the next era of genomic innovation to ensure sustainable food production and global nutritional security; and strategies that enabled them to thrive in their careers. **Organizers:** Olabisi Adebisi, New Mexico State University; Kellye Eversole, Eversole Associates; Deb Hamernik; University of Nebraska-Lincoln; Laura Mathieu, Agroscope & University of Zurich; Charlotte Rambla, Land & Carbon, Inc. **Location:** Akimel Ballroom
Plenary Session VI: Akimel Ballroom	**Session Chair:** Alison Van Eenennaam, Distinguished Professor of Cooperative Extension, Animal Biotechnology and Genomics, University of California, Davis; and Organizing Committee Member
2:00 p.m. – 2:30 p.m.	**Kathy Munkvold, Foundation for Food & Agriculture Research** “Agriculture under pressure: advancing solutions from genome to field through cross-sector collaboration”
2:30 p.m. – 2:40 p.m.	**Bronze 1 Sponsor Talk – Twist Bioscience, Paul Doran, Director of Business Development** "Next level genotyping with Twist"
2:40 p.m. – 2:50 p.m.	**Bronze 2 Sponsor Talk – SPT Labtech**

Agenda

Tuesday, April 14

2:50 p.m. – 3:00 p.m.	**Bronze 3 Sponsor Talk – Cellanome, Gary Schroth, Ph.D., Chief Scientific Officer** "An integrated platform for longitudinal single-cell analysis in plant systems"
3:00 p.m. – 3:40 p.m.	**Coffee Break & Exhibits** Komatke Ballroom
3:40 p.m. – 4:10 p.m.	**Leif Andersson, Uppsala University, Sweden** "How the Atlantic herring became a keystone species in the brackish Baltic Sea"
4:10 p.m. – 4:25 p.m.	**Elinor Karlsson, UMass Chan Medical School (Abstract Selected Talk)** "Translating sequencing innovation into practice: A scalable genotyping platform for working dogs"
4:25 p.m. – 4:40 p.m.	**Talita Estefani Zunino Santana, University of Wisconsin-Madison (Abstract Selected Talk)** "Enviromics-based modeling of genotype-by-environment-by-management interactions for growth, reproductive, and carcass traits in pasture-raised beef cattle"
4:40 p.m. – 4:55 p.m.	**Jicai Jiang, North Carolina State University (Abstract Selected Talk)** "Mapping the functional landscape of complex trait heritability in dairy cattle"
4:55 p.m. – 5:10 p.m.	**David Omar Gonzales Dieguez, CIMMYT/CGIAR (Abstract Selected Talk)** "Turning farmers' fields into selection environments: accelerating CGIAR crop genetic gain through on-farm sparse testing"
5:10 p.m. – 5:25 p.m.	**Nelson Lubanga, Aberystwyth University (Abstract Selected Talk)** "Sparse testing strategies to increase genetic gains in Miscanthus breeding program"
5:25 p.m. – 5:30 p.m.	**Final Remarks for the day**
5:30 p.m. – 6:30 p.m.	**Wine Reception, Posters & Exhibits** Komatke Ballroom
6:30 p.m. – 8:00 p.m.	**AGBT Dinner** Akimel Lawn
Beginning at 8:00 p.m.	**Sponsor Social** Sponsor Promenade

Agenda

Wednesday, April 15

7:30 a.m. – 7:00 p.m.	**Hospitality / Information Desk** Akimel Foyer
7:30 a.m. – 9:00 a.m.	**Breakfast** Komatke Patio
Plenary Session VII: Akimel Ballroom	**Session Chairs:** Guilherme Rosa, Professor of Quantitative Genetics and Data Science in the Department of Animal and Dairy Sciences, University of Wisconsin-Madison; and Organizing Committee Member
9:00 a.m. – 9:30 a.m.	**JoÃo Reboucas Dorea, University of Wisconsin-Madison** “Digital tools and artificial intelligence for scalable phenotyping of novel traits”
9:30 a.m. – 10:00 a.m.	**Kelly Wrighton, Colorado State University** “From sequence to system: unlocking microbiome-enabled agriculture”
10:00 a.m. – 10:15 a.m.	**Timothy Jeffers, New York University, Center for Genomics and Systems Biology (Abstract Selected Talk)** “Bipartite machine learning identifies TF interactions underlying agricultural traits”
10:15 a.m. – 11:00 a.m.	**Coffee Break & Exhibits** Komatke Ballroom
11:00 a.m. – 11:30 a.m.	**Alexander Bucksch, The University of Arizona** “Root phenomics: shaping agriculture from below ground”
11:30 a.m. – 11:45 a.m.	**Guillermo Martinez-Boggio, University of California Davis (Abstract Selected Talk)** “Lifetime Net Merit index and the correlated response on enteric methane emissions”
11:45 a.m. – 12:00 p.m.	**Mohit Verma, Marshall University (Abstract Selected Talk)** “From data to discovery: multi-omics learning platforms for Brassicaceae biofuel crops”
12:00 p.m. - 2:00 p.m.	**AGBT Lunch & Workshop** Mesquite Terrace and Akimel Ballroom

Agenda

Wednesday, April 15

12:20 p.m. - 1:50 p.m.

Lunch & Learn: Animal telomere-to-telomere genomes: new assemblies, new biology, new voices

Description: This workshop will highlight outstanding trainees in advancing telomere-to-telomere (T2T) genome assemblies across diverse animal species, bringing together expertise from genomics, data science, and agricultural biology across multiple institutions. Speakers will showcase new assemblies and analytical strategies while critically examining technical and translational challenges that currently limit adoption of complete genomes in agricultural genomics. The session will identify emerging opportunities at the intersection of long-read sequencing, computational methods, and biological discovery, and will foster discussion of innovative, community-driven approaches to accelerate translation of T2T resources into applications for food, feed, fuel, and fiber production.

Organizers: Brenda Murdoch, University of Idaho and Stephanie McKay, University of Missouri

Plenary Session VIII:
Akimel Ballroom

Session Chair: Renee Lafitte, Director for Crops R&D, Gates Foundation; and Organizing Committee Member

2:00 p.m. – 2:30 p.m.

Noelle Cockett, Utah State University
"The benefits of connecting with the farm animal genomics collective"

2:30 p.m. – 3:00 p.m.

Ian Henderson, University of Cambridge, United Kingdom
"Genetic and epigenetic identity of plant centromeres"

3:00 p.m. – 3:30 p.m.

Coffee Break
Akimel Foyer

3:30 p.m. – 3:45 p.m.

Leo Baumgart, Lawrence Berkeley National Laboratory, DOE Joint Genome Institute (Abstract Selected Talk)
"Mapping the plant gene regulatory landscape: a multi-species atlas of transcription factor binding and single-nucleus transcriptomes"

3:45 p.m. – 4:00 p.m.

Abraham Morales-Cruz, Lawrence Berkeley National Laboratory, DOE Joint Genome Institute (Abstract Selected Talk)
"Conserved regulatory element location shapes cell type-specific gene activity in plants"

4:00 p.m. – 4:15 p.m.

Anindya Bandyopadhyay, CIMMYT (Abstract Selected Talk)
"A high-throughput gene-editing platform for pearl millet flour shelf-life improvement via rancidity mitigation"

Agenda

Wednesday, April 15

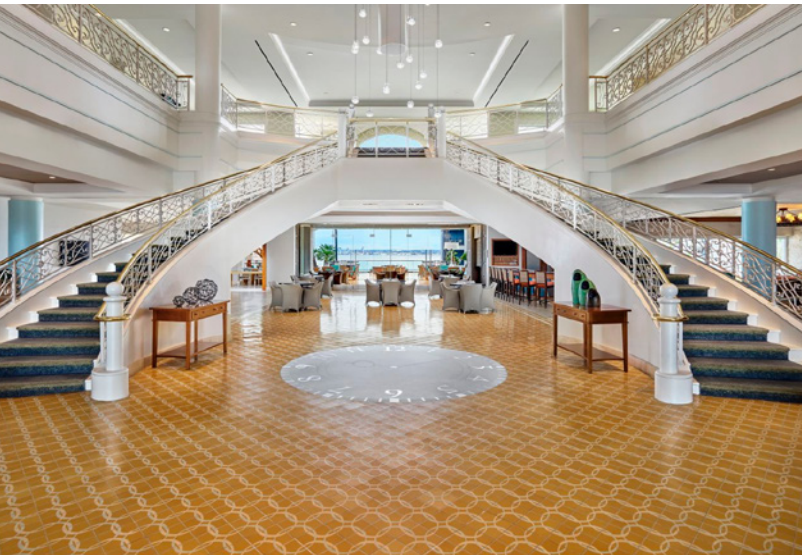
4:15 p.m. – 4:30 p.m.	**Patty Kiesler, National Institute of Standards and Technology (Abstract Selected Talk)** "U.S. Food and Drug Administration (FDA) and U.S. National Institute of Standards and Technology (NIST) collaboration: evaluation of assays and control materials for characterizing animal biotechnology products generated by genome editing"
4:30 p.m. – 5:15 p.m.	**Seeds of Innovation: Navigating IP in Agricultural Genomics** Panel discussion exploring how intellectual property strategies are shaping innovation in genomics for crops, livestock, and microbes, balancing public research, private investment, and global access. **Facilitator:** Sarah Hearne, Chief Science and Innovation Officer, CIMMYT **Panelists:** Neha Kothari, Agricultural Research Service, U.S. Department of Agriculture Karina Najarro, Legal Counsel, Intellectual Assets, CIMMYT Meghan Poon, Morrison Foerster
5:15 p.m. - 5:30 p.m.	**Closing Remarks** Sarah Hearne, Chief Science and Innovation Officer, CIMMYT, and Daniela Lourenco, Associate Professor, Animal Breeding, Genetics, and Genomics, Department of Animal and Dairy Science, University of Georgia; Co-Chairs of the AGBT Agriculture Scientific Organizing Committee
6:00 p.m. - 9:00 p.m.	**AGBT Farewell Dinner** Hemapik Lawn

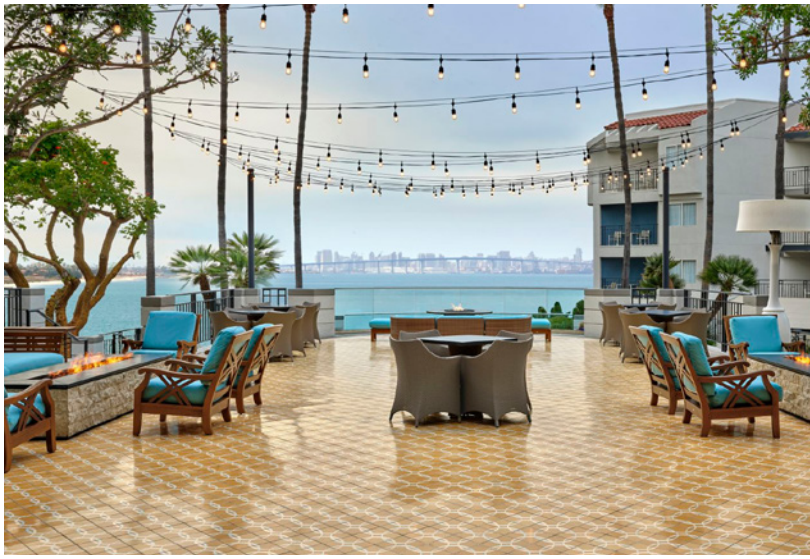
TWIST BIOSCIENCE

AGBT2026™

PRECISION HEALTH

Loews Coronado Bay Resort | San Diego, CA





Save the Date

SEPTEMBER 14-16, 2026

Learn more at www.agbt.org

Scientific Abstracts

POSTER

101

Multi-lineage pangenome graph of rainbow trout reveals large structural variants linked to domestication and adaptive traits

Ali Ali[1], Nada Srour[2], Rafet Al-Tobasei[2], Mohamed Salem[1]

1. University of Maryland, Department of Animal and Avian Sciences, College Park, MD, USA
2. Middle Tennessee State University, Computational and Data Science Program, Murfreesboro, TN, USA

Rainbow trout (*Oncorhynchus mykiss*) is a widely distributed and genetically diverse species, including resident and migratory (steelhead) forms adapted to diverse environments. Despite its ecological and aquacultural importance, the structural genomic basis of traits such as domestication, growth, and stress tolerance remains poorly understood. Genetic association studies have largely focused on SNPs, yet large structural variants (SVs) can have major functional effects and contribute substantially to genetic diversity. Linear single-reference mapping enables SV discovery but is limited by reference bias and reduced sensitivity in structurally complex regions. Pangenome graphs address these limitations by representing multiple assemblies in a unified coordinate system and improving detection of complex and nested SVs. This motivated us to construct a whole-genome, multi-lineage pangenome graph for four *O. mykiss* lineages (Arlee, Swanson, Keithley Creek, Whale Rock) using the reference-free PGGB workflow and characterized graph structure with ODGI. The PGGB graph spans 3.11 Gb (75.3M nodes, 103.9M edges, 128 paths, 203.6M steps), recovers the ~55 Mb chromosome 5 inversion associated with migratory life-history variation, and reveals additional large insertions, deletions, and locally nested variants. We extracted SVs ≥10 kb, intersected SV intervals with annotated gene models, and performed gene-set enrichment analysis to connect SV content to biological function. Additionally, we constructed a whole-genome, multi-lineage pangenome graph with Minigraph-Cactus and mapped paired-end short reads from summer- versus winter-runner ecotypes to compare seasonal groups via SV detection, annotation, and gene enrichment analysis. Together, these results establish a multi-lineage pangenome foundation for rainbow trout and demonstrate a path from graph-based SV representation to functional interpretation and within-lineage comparative analyses relevant to domestication and adaptation.

Connecting the evolutionary and statistical views of epistasis in quantitative trait genomics

POSTER

102

Boris M.E. Alladassi[1,2], Samuel K.T. Owusu-Ansah[3], Geoffrey P. Morris[3], Alexander E. Lipka[1]

1. University of Illinois, Department of Crop Sciences, Urbana, IL, USA
2. University of Illinois, National Center for Supercomputing Applications, Urbana, IL, USA
3. Colorado State University, Department of Soil and Crop Sciences, Fort Collins, CO, USA

The role of epistasis in shaping the genetic architecture of complex traits and influencing evolutionary trajectories in breeding programs remains subject to long-standing debate. This controversy persists in part due to a gap between statistical epistasis, the deviation from additive and dominance expectations commonly modeled in quantitative genetics, and biological epistasis, the molecular and functional interactions of gene products. As a step toward addressing this gap, we developed a statistical framework for quantitative trait genomics that adapts the classical variance decomposition to directly test for three evolutionarily relevant classes of epistasis: magnitude epistasis (ME), sign epistasis (SE), and reciprocal sign epistasis (RSE). First, we constructed a simulation pipeline that combines parental and recombinant haplotype effects to accurately capture distinct genotype–phenotype maps associated with ME, SE, and RSE in both haploid and diploid systems. Next, we developed a permutation-based testing procedure that uses products of intralocus simple effects to classify additive-by-additive (AxA) epistatic interactions into ME, SE, and RSE. Using simulations spanning five genetic architectures, four sample sizes, three AxA epistasis effect sizes, and 1000 replicates, our framework performed well. As expected, uniform distributions of *P*-values were observed under the null and additive architectures. The simulated SE and RSE architectures achieved over 99% true positive rates in detecting AxA interactions, whereas ME produced a lower true positive detection rate of approximately 75%. Importantly, for the simulations that resulted in statistically significant AxA epistasis, our permutation procedure accurately classified all three classes of epistasis in at least 99% of cases. Together, these results illustrate how statistical modeling of physiological epistasis can help unify evolutionary and quantitative genetics perspectives. Our framework provides a step toward integrating functional insights into complex trait dissection and prediction in breeding programs.

Integrating pangenomics and transcriptomics: a new era for yam breeding

POSTER

103

Asrat Amele[1], Paterne A. Agre[1], Nicholas Allsing[2], Leena Triphati[1], Michael Todd[2]

1. International Institute of Tropical Agriculture (IITA), Ibadan, Oyo Nigeria
2. The Salk Institute for Biological Studies, La Jolla, CA, USA

a.amele@cgiar.org

Yam (*Dioscorea* spp.) is a high-value staple crop that supports millions of people in tropical and subtropical regions. Progress in genetic improvement has been slow due to limited genomic resources. To address this, we are adopting new breeding strategies that integrate omics technologies to uncover hidden genetic diversity and accelerate breeding. We first generated high-quality, chromosome-level genome assemblies for six diverse yam genotypes using PacBio HiFi long-read sequencing. Genome sizes ranged from 515 Mb in *D. alata* to 663 Mb in *D. rotundata*, with scaffold N50 values of 20.4 Mb in white Guinea yam and 17.0 Mb in *D. alata*. BUSCO analysis confirmed high completeness, and gene annotation identified over 20,000 protein-coding genes per genome. Transposable elements, especially long terminal repeat (LTR) retrotransposons, accounted for more than 20% of the genomes, reflecting their structural complexity and evolutionary dynamics. Building on this, we recently expanded the yam pangenome to 32 genotypes representing broad genetic diversity. This pangenome captures extensive structural variation, presence–absence variation (PAV), and gene copy-number differences among cultivated and wild yams. Comparative analysis identified structural variants associated with key traits. Notably, polymorphisms associated with sex determination were identified on chromosomes 9, 11, and 20, providing new insights into the genetic basis of dioecy. We also integrated transcriptomic data to study gene expression across different genotypes. Results showed differential regulation of candidate genes involved in plant architecture and tuber formation. By combining long-read assembly, structural genomics, and transcript profiling, this work provides a robust platform for rapid trait discovery and heralds a new era of accelerated yam breeding.

Keywords: Pangenome, PacBio HiFi, Structural variation, Transcriptomics, Yam genomics, Genomic-assisted breeding

POSTER

158

Operational genomics for yam breeding: from variety-tracking markers to genomic selection, pangenomes, and functional discovery

Asrat Amele[1], Leena Tripathi[2], Michael Todd[3], Asrat Asfaw[1]

1. International Institute of Tropical Agriculture (IITA), Ibadan, Oyo, Nigeria
2. International Institute of Tropical Agriculture (IITA), Nairobi, Kenya
3. The Salk Institute for Biological Studies, La Jolla, CA, USA

Yam (*Dioscorea* spp.) is a key staple in the global food system, contributing significantly to food security and rural livelihoods for over 400 million people in the tropics. However, boosting its productivity through genetic improvement has been constrained by complex biology, long breeding cycles, and limited deployable genomic tools. We present an integrated, operational genomics framework that is transforming yam breeding by linking quality-controlled marker systems, genomic selection, and functional genomics into a single breeding pipeline.

We first developed and deployed robust quality-control (QC) SNP markers for variety identification, purity assessment, and breeding-line tracking across multi-location trials. These markers now underpin reliable genotype identity management, a critical foundation for modern yam breeding. Building on this, we established a mid-density genotyping platform, including quality control and trait-linked markers, as the workhorse for genomic selection (GS), enabling prediction of breeding values and optimization of parental selection and crossing decisions through Genomic Prediction of Cross Performance (GPCP) and Optimal Cross Selection (OCS). These tools are routinely used to accelerate early-generation selection and reduce cycle time.

To expand trait discovery beyond standing variation, we developed a multi-species yam pangenome that captures structural variation and presence–absence polymorphisms linked to key breeding traits. Complementary multi-tissue transcriptome profiling (leaf, stem, tuber, flower) revealed regulatory networks controlling growth and tuberization, providing functional validation of genomic predictions.

Using all these genomic resources, such as QC markers, mid-density GS-enabled breeding, and high-resolution pangenome and expression analyses, we demonstrate how genomics can be operationalized to deliver faster, more precise genetic gains in one of Africa's most challenging and impactful crops.

A high-throughput gene-editing platform for pearl millet flour shelf-life improvement via rancidity mitigation

ABSTRACT SELECTED TALK

Anindya Bandyopadhyay[1]*, Mohan Achary[1], Huirong Gao[2], Ning Wang[2], Ping Che[2], Inoussa Drabo[1], Todd jones[2], Laurajean Lewis[1], Nandini Krishnamurthy[2], Pooja Bhatnagar-Mathur[3], Kevin Pixley[1], Sarah Hearne[1]

1. CIMMYT, Biosecurity Laboratory, Genetic Resource Program, Texvoco, Mexico
2. Corteva Agriscience, Johnston, IA, USA
3. FAO-IAEA Plant Breeding and Genetics, Vienna, Austria

*a.bandyopadhyay@cgiar.org

Pearl millet (*Pennisetum glaucum* L.) is a climate-resilient, gluten-free staple that supports more than 90 million people across the arid and semi-arid regions of Sub-Saharan Africa and South Asia. Despite its high nutritional value and low glycemic index, broader commercialization of pearl millet is severely constrained by the rapid onset of flour rancidity following milling. Rancidity is a complex quantitative trait driven by the hydrolytic release of free fatty acids from triacylglycerols by endogenous lipases, followed by oxidative degradation of highly abundant polyunsaturated fatty acids (>78%), leading to the accumulation of odor-active volatile compounds and loss of consumer acceptability.

Here, we report the development of genome-edited pearl millet lines with reduced propensity for flour rancidity by precisely targeting key biochemical drivers of lipid degradation. Using CRISPR-based editing, we disrupted major contributors to rancidification, including fatty acid desaturase 2 (*FAD2*) and selected endogenous lipase genes, with the aim of reducing both substrate availability for oxidation and enzymatic lipid hydrolysis. Edited lines were recovered efficiently in an elite commercial background (IKMB18002) and advanced for trait characterization.

Functional validation of edited lines is underway using accelerated storage assays, combined with gas chromatography–mass spectrometry (GC-MS)–based profiling of free fatty acids and lipid-derived volatile compounds to quantify rancidity progression over time. These analyses are enabling direct assessment of the biochemical and sensory consequences of targeted pathway modification.

Overall, this work reports first ever high throughput gene editing in pearl millet, also demonstrates a mechanistic and targeted strategy to mitigate flour rancidity in pearl millet. The development of non-rancid pearl millet varieties has the potential to substantially extend flour shelf life, unlock new market opportunities, strengthen value chains, and improve the livelihoods of smallholder farmers in dryland regions.

Mapping the plant gene regulatory landscape: a multi-species atlas of transcription factor binding and single-nucleus transcriptomes

ABSTRACT SELECTED TALK

Leo A. Baumgart[1], Sharon I. Greenblum[1], Abraham Morales-Cruz[1], Peng Wang[1], Yu Zhang[1], Lin Yang[2], Cindy Chen[1], David J. Dilworth[1], Alexis C. Garretson[3,4], Nicolas Grosjean[1], Guifen He[1], Emily Savage[1], Yuko Yoshinaga[1], Ian K. Blaby[1], Chris G. Daum[1], Ronan C. O'Malley[1,2]

1. Lawrence Berkeley National Laboratory, Joint Genome Institute, Berkeley, CA, USA
2. University of Chicago, Department of Human Genetics, Chicago, IL, USA
3. The Jackson Laboratory, Bar Harbor, ME, USA
4. Tufts University, Graduate School of Biomedical Sciences, Boston, MA, USA

Transcription factors (TFs) are proteins that bind DNA to control where and when genes are expressed. In plants, dozens of TF families interact with distinct sets of binding sites (TFBSs) that reflect each TF's role in organismal function and species-specific adaptations. However, defining these roles and understanding broader patterns of regulatory evolution remain challenging, as predicted TFBSs may lack a clear impact on transcription, and experimentally derived TF binding maps to date are modest in scale or restricted to model organisms. Here we present a scalable TFBS assay that we leveraged to create an atlas of nearly 3,000 genome-wide binding site maps for 360 TFs in ten species spanning 150 million years of flowering plant evolution. We found that TF orthologs from distant species retain nearly identical binding preferences, while on the same timescales the gain and loss of TFBSs are widespread. Within lineages, however, conserved TFBSs are over-represented and found in regions harboring signatures of functional regulatory elements. Moreover, genes with conserved TFBSs showed striking enrichment for cell-type-specific expression in 14 single-nucleus RNA atlases, providing a robust marker of each TF's activity and developmental role. Finally, we compare distant lineages, illustrating how ancient regulatory modules were recruited and rewired to enable adaptations underlying the evolutionary success of grasses.

Fine-tuning Monte Carlo single-step genomic REML for variance components estimation in large datasets

ABSTRACT SELECTED TALK

Marina Bernardes[1], Matias Bermann[1], Alejandra Álvarez-Munera[1], Ignacy Misztal[1], Daniela Lourenco[1]

1. University of Georgia, Department of Animal and Dairy Science, Athens, GA, USA

As phenotypic and genomic data accumulate, variance components estimation (VCE) becomes challenging due to computational limitations of approaches that rely on sparse matrix inversion, like Expectation Maximization or Average Information REML. However, performing VCE on the same dataset used for genetic evaluation is important, as changes in heritability can impact prediction accuracy. The Monte Carlo single-step Genomic REML (MC-ss-GREML) computes VCE without requiring matrix storage or inversion, offering high computational efficiency and low memory requirements for large datasets and complex models that incorporate pedigree and genomic information. MC-ss-GREML approximates the traces of the first derivatives of the restricted log-likelihood (tr(A^{-1} C^^{uu})) using an average of quadratic forms, through a sampling process. While smaller sample sizes improve computational efficiency, the current convergence criteria for MC-ss-GREML are limited by MC error when the sample size is too small, which can stall the algorithm. The MC error decreases asymptotically as the sample size increases, though this behavior may not hold for smaller samples. Therefore, it is important to select an appropriate number of MC samples to capture the method's inherent behavior. This research aims to develop a method for selecting the optimal number of MC samples to improve convergence, keep computing time reasonable, and determine whether a small increase in the number of samples reduces the MC error. We implemented an adaptive sampling scheme that increased the sample count by five whenever the norm of the scaled first derivatives of the restricted log-likelihood (Δc) fluctuates near convergence. We tested it on a four-trait repeatability model with over 210,000 records, 213,297 animals in the pedigree, and almost 16,000 genotyped animals. Starting with five samples, the algorithm ran until it reached 200. Increasing the number of MC samples did not necessarily improve estimates of tr($A^{-1}C^{uu}$) or convergence, likely because MC-ss-GREML employed a relatively small number of samples. Results indicated that adaptive sampling based solely on Δc did not reduce MC error or improve MC-ss-GREML's convergence behavior. Nevertheless, MC-ss-GREML remains a valuable and scalable framework for VCE in large, complex genomic datasets. Further methodological refinements that explicitly address MC error are expected to enhance its robustness.

Managing powdery mildew diseases in horticultural crops in controlled-environment agriculture

POSTER

104

Krishna Bhattarai[1], V. Hannah Ayala[2], Samantha Knackstadt[2], Jack Ueckert[2], Zhanao Deng[3], Kevin Ong[2]

1. Texas A&M AgriLife Research, Horticultural Sciences, Texas A&M University, Dallas, TX, USA
2. Texas A&M University, Plant Pathology, College Station, TX, USA
3. University of Florida, Environmental Horticulture, Wimauma, FL, USA

Powdery mildew (PM) is a common pathogen affecting a wide range of fruits, vegetables and ornamental crops cultivated under controlled environment agriculture (CEA) systems. Pathogens causing PM are obligatory parasites and show host specific interaction. Therefore, proper characterization of pathogen causing the disease in a crop is critical for management and loss minimization. We have, for the first time, characterized the causal agents involved in PM disease development in lettuce and strawberries in CEA. Morphological study of PM pathogen in lettuce revealed solitary, indistinct hyphal to nipple shaped appressoria, and hyaline and erect conidiophores. Conidiogenesis was *Euoidium*-type and chasmothecia was absent. In strawberry PM pathogen, appressoria were indistinct to nipple-shaped, and conidiophores were erect and catenulate. Conidia were hyaline, ovoid to doliform, containing fibrosin bodies. Chasmothecia were dark brown to black with short, unbranched appendages. Molecular characterization of PM pathogens is commonly done by amplifying internal transcribed spacer (ITS), 28S rDNA, 18S rDNA, β-tubulin, Chintin synthase, EF-1α, RNA-polymerase II subunits. Amplification of ITS and 28S regions using ITS5/ITS4 and ITS1/TW14 and PM28/PM28R resulted in characterization of lettuce PM pathogen as *Golovinomyces bolayi*. Similarly, amplification of ITS region of strawberry PM pathogen characterized it as *Podosphaera aphanis*. Various cultural-, chemical-, biological- and genetic host resistance-based control methods have been used in mitigating crop losses due to PM. Growing resistant varieties, improving air flow and avoiding overhead irrigation are commonly used cultural methods. Burning sulfur is used in non-edible crops whereas frequent applications of chemical fungicides are the most used control method in wide range of crops. Identification of PM resistant genes and their introgression in new cultivars is a sustainable and long-term solution deployed in crops including cucurbits, grapes, roses, and tomato. Using transcriptome sequencing, we identified seven PM resistant candidate genes in *Gerbera hybrida*. These genes can be introgressed in PM-susceptible lines and develop resistant cultivars. Genes in susceptibility gene family, Mildew locus O (MLO) has been mutated in a few crops using CRISPR-genome editing to enhance PM resistance. We have identified four MLO candidate genes in *G. hybrida* that can also be targeted to further increase the resistance durability.

POSTER

105

Connecting the dots: from high-throughput feed phenotyping to genomic dissection of heterosis in maize

Mythri Bikkasani[1], Tosh Garg[1], Surinder Sandhu[1], Krithika Anbazhagan[2], KVSV Prasad[2], Krishna Sundaram[3], Gopikrishna Adapala[4], Yogesh Vikal[1], BS Vivek[5]

1. Punjab Agricultural University, Department of Plant Breeding and Genetics, Ludhiana, Punjab, India
2. International Livestock Research Institute, Hyderabad, Telangana, India
3. International Rice Research Institute, Hyderabad, Telangana, India
4. International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, Telangana, India
5. International Maize and Wheat Improvement Center, Hyderabad, Telangana, India

High-throughput and reliable phenotyping of feed quality traits is essential for integrating genomics into breeding programs targeting livestock-oriented crops. Near-infrared spectroscopy (NIRS) enables rapid assessment of silage quality, but its routine deployment requires robust and regularly updated prediction models. In this study, scalable NIRS-based phenotyping was first established and subsequently integrated with genomic imputation and genome-wide association studies (GWAS) to dissect the genetic architecture of feed-quality traits and heterosis in maize.

A global maize stover NIRS prediction model was applied to 1,600 silage-stage maize samples analyzed using a FOSS XDS Rapid Content Analyser. Validation using 150 wet-chemistry reference samples revealed reduced predictive accuracy for crude protein, necessitating model refinement. The global model was upgraded using reference values for dry matter, ash, and crude protein, achieving high calibration and validation accuracy across five feed-quality traits. In parallel, a silage-stage-specific local model for crude protein was developed, demonstrating strong predictive performance and suitability for breeding applications.

NIRS-derived phenotypes were integrated with genomic data from 42 diverse maize inbred parents representing temperate and sub-tropical germplasm pools. These parents were crossed in structured mating designs to generate 354 hybrids. Hybrid genotypes were reconstructed in silico using parental whole-genome resequencing data, enabling cost-efficient GWAS without direct hybrid sequencing. Single-nucleotide polymorphisms were encoded under additive and over-dominant models and analyzed using mixed linear models incorporating kinship. GWAS identified loci associated with digestibility, fiber composition, and metabolizable energy, including genomic regions co-localizing with known cell wall and lignin biosynthesis genes. Over-dominant models revealed additional loci associated with heterosis indices, highlighting the contribution of non-additive genetic effects.

This integrated phenomics–genomics framework demonstrates a scalable strategy for linking high-throughput feed quality phenotyping with genome-level inference, providing insights into the genetic basis of silage quality and heterosis while enabling genomics-assisted hybrid design.

POSTER

106

Genomic evaluation of rump fat–adjusted residual feed intake in zebu cattle: implications for selection strategies

Larissa Bordin Temp[1], Letícia Pereira[2], Roberto D. Sainz[3], Fernando Bussiman[4], Jorge Hidalgo[4], Daniela Lourenco[4], Fernando Baldi[5]

1. São Paulo State University, Department of Animal Science, Jaboticabal, Sao Paolo, Brasil
2. Sustainable Livestock Research Center, Animal Science Institute, São José do Rio Preto, Sao Paolo, Brazil
3. University of California, Davis, Department of Animal Science, Davis, CA, USA
4. University of Georgia, Department of Animal and Dairy Science, Athens, GA, USA
5. São Paulo University, Departament of Animal Science, Pirassununga, Sao Paolo, Brasil

Feed costs can account for up to 75% of total production expenses, making feed efficiency a critical driver of profitability in beef cattle systems. Residual feed intake (RFI) is widely used to improve feed efficiency, while rump fat thickness (RFT) is an important indicator of carcass quality, energy balance, and reproductive maturity. Understanding the genetic relationships among RFI, RFT, and other performance traits is essential for balanced breeding decisions. In this study, we aimed to: (1) estimate (co)variance components and genetic correlations between RFI—calculated with (RFI_F) and without (RFI_W) adjustment for RFT—and key performance traits using genomic data in Nellore cattle; and (2) evaluate the accuracy, bias, and dispersion of genomic breeding values for both RFI measures predicted using single-step GBLUP (ssGBLUP). We hypothesized that accounting for RFT would explain only a small fraction of RFI variation, resulting in minimal differences in selection responses. Phenotypic data were collected from 9,094 Nellore cattle evaluated in 14 feed efficiency tests conducted between 2011 and 2024. The pedigree included 17,407 animals, of which 5,812 were genotyped. Linear and threshold animal models were applied for continuous and categorical traits. Heritability estimates were low for both RFI_W (0.17) and RFI_F (0.16), and the genetic correlation between them was high (r = 0.98). The modest correlation between RFI and RFT (r = 0.15) suggests little shared genetic basis between feed efficiency and fat deposition. Spearman's correlations of genomic breeding values for RFI_F and RFI_W reached 0.98 in females and 0.95 in males. Genetic correlations of the two RFI measures with growth, reproductive, and carcass traits ranged from –0.33 to 0.35, indicating that selection for RFI is unlikely to adversely affect performance. Prediction accuracy was similar for RFI_F (0.43) and RFI_W (0.44), with only minor differences in bias and dispersion. Although RFI_F captured slightly more genetic variability, this advantage was minimal, and the strong linear association with RFI_W shows that adjusting for RFT provides limited biological or practical benefit. Overall, these results offer valuable guidance for genomic selection strategies in Nellore cattle, demonstrating that feed efficiency can be effectively improved without adjusting RFI for rump fat. This simplification supports faster breeding decisions while preserving balanced genetic gains across key economic traits.

Keywords: Bos taurus indicus, correlation, feed efficiency, ssGBLUP

Pangenome analysis of nine soybean cyst nematode genomes reveals hidden variation contributing to diversity and adaptation

ABSTRACT SELECTED TALK

Lucas Borges dos Santos[1], Kurt C. Showmaker[2], Rick E. Masonbrink[3], Kimberly K.O. Walden[4], João P. Gomes Viana[5], Khee-Man Kwon[6], Alvaro G. Hernandez[4], Zhihai Zhang[7], Christopher J. Fields[4], Thomas R. Maier[8], Andrew J. Severin[3], Thomas J. Baum[8], Melissa G. Mitchum[9], Matthew Hudson[10]

1. University of Illinois at Urbana-Champaign, Urbana, IL, USA
2. Dasomics LLC, Madison, MS, USA
3. Iowa State University, Genome Informatics Facility, Ames, IA, USA
4. University of Illinois at Urbana-Champaign, Roy J. Carver Biotechnology Center, Urbana, IL, USA
5. University of Illinois at Urbana-Champaign, National Center for Supercomputing Applications, Urbana, IL, USA
6. University of Wisconsin-Madison, Department of Plant Pathology, Madison, WI, USA
7. University of Illinois at Urbana-Champaign, DOE Center for Advanced Bioenergy and Bioproducts Innovation (CABBI), Urbana, IL, USA
8. Iowa State University, Department of Plant Pathology, Entomology and Microbiology, Ames, IA, USA
9. University of Georgia, Department of Plant Pathology and Institute of Plant Breeding, Genetics and Genomics, Athens, GA, USA
10. University of Illinois at Urbana-Champaign, Department of Crop Sciences, Urbana, IL, USA

The soybean cyst nematode (SCN) is the most damaging pathogen of soybean, causing over $1.5 billion in yield losses annually in the United States. SCN persists for years in agricultural soils and can rapidly adapt to overcome host resistance, making it difficult for breeders to develop durable and broadly effective soybean cultivars, while its genomic diversity and the mechanisms underlying virulence and host adaptation remain poorly understood. Here we report a pangenome constructed from nine SCN populations of different pathotypes, including eight newly generated high-fidelity genome assemblies.

We detected over 19,000 orthologous gene families and more than 12,000 putative secreted proteins in SCN. Combined, these data indicate substantial diversity across populations. Gene content analysis showed that 35% of gene families were the conserved core, 15% were soft-core, and 48% were accessory. Evidence of rapid evolution was identified in a high portion (40%) of core single-copy genes, most notably inside the protein domains responsible for host recognition and immune modulation. Analysis of gene-family expansion revealed extensive duplication and loss across lineages, suggesting ongoing paralog turnover within SCN populations. Finally, a graph-based pangenome enabled the identification of numerous structural variants within regions under selection.

Our study highlights substantial genetic variation in SCN that is not captured by single-reference analyses. By integrating multiple high-quality assemblies, we show that the SCN genome is highly dynamic, with extensive gene duplication and loss as well as structural variation shaping the differences among nematode populations. Collectively, the SCN pangenome provides a robust resource for studying virulence and adaptation mechanisms in SCN and establishes a genomic foundation for the development of more precise management strategies.

Advancing Fusarium head blight resistance in wheat: genetic gains and genomic selection strategies

ABSTRACT SELECTED TALK

Charlotte Brault[1]*, Emily J. Conley[1], Andrew C. Read[1,2], Harsimardeep S. Gill[1], Sarah Blecha[2], Andrew J. Green[3], Karl D. Glover[4], Jason P. Cook[5], Ruth Dill-Macky[6], Jason Fiedler[7], James Anderson[1]

1. University of Minnesota, Department of Agronomy and Plant Genetics, St. Paul, MN, USA
2. United States Department of Agriculture Agricultural Research Service (USDA-ARS), Plant Science Research Unit, St. Paul, MN, USA
3. North Dakota State University, Department of Plant Sciences, Fargo, ND, USA
4. South Dakota State University, Agronomy, Horticulture, and Plant Science Department, Brookings, SD, USA
5. Montana State University, Plant Sciences and Plant Pathology Department, Bozeman, MT, USA
6. University of Minnesota, Department of Plant Pathology, St. Paul, MN, USA
7. United States Department of Agriculture Agricultural Research Service (USDA-ARS), Edward T. Schafer Agricultural Research Center, Cereal Crops Improvement Research Unit, Fargo, ND, USA

*Corresponding author: Charlotte Brault, cbrault@umn.edu

Public wheat breeding programs (BPs) play a key role in developing cultivars that combine high yield, desirable quality, and resistance to major diseases. In the Northern Great Plains of the United States, Fusarium Head Blight (FHB) remains the most damaging wheat disease, causing significant yield losses and mycotoxin contamination. Breeders have actively sought FHB resistance by using collaborative inoculated nurseries and incorporating quantitative trait loci (QTLs) associated with resistance.

In this work, we evaluated three decades of breeding progress for FHB resistance and evaluated strategies to improve the use of genomic selection (GS) in four public BPs. Using data from a cooperative historical nursery, we measured genetic gains for FHB resistance over the past 30 years and tracked changes in allele frequencies at three major FHB resistance QTLs. We observed substantial progress, including a 0.4% average annual reduction in visually scabby kernels (VSK) and a significant increase in resistance allele frequencies, with up to a 300% increase in the Fhb1 QTL. All three QTLs studied had significant and positive effects on FHB-related traits without harming other agronomic traits. However, genetic gains have plateaued in the last five years, highlighting the need to identify and utilize additional minor-effect loci.

To support continued improvement, we investigated key factors influencing predictive ability in GS. Genomic prediction within each BP's genotypes yielded, most of the time, the highest predictive ability (e.g., r = 0.70 for the North Dakota BP for VSK). Using nursery data to predict BP performance was beneficial only when the BP training set was small (100–200 genotypes). For example, the Montana State BP's VSK predictive ability increased from 0.12 to 0.26 when trained with Montana or nursery data, respectively. Cross-prediction between BPs or pooling all available data rarely increased predictive ability relative to nursery data alone when predicting BPs. These findings demonstrate a critical trade-off between training population size and genetic relatedness and show the usefulness of having such a cooperative nursery. Together, these results provide a roadmap for accelerating FHB resistance improvement and lowering the barrier to deploying GS in public breeding settings.

Translating science into scalable agricultural products

POSTER

107

Richard Brogile[1]

1. AG Forward Advisors, Landenberg, PA, USA

The agricultural technology (AgTech) sector is undergoing rapid and significant changes, driven by advances in genomics, synthetic biology, and artificial intelligence, as well as evolving investment trends. This dynamic environment offers major opportunities for innovators but also brings complex challenges in integrating and adopting new technologies in crop production. Experienced leaders are essential for bridging the gap between innovation and practical implementation. As Principal at AG forward advisors with over 40 years of experience in technology discovery and product development at DuPont Pioneer (now Corteva Agriscience) and Pivot Bio, I work with technology innovators to transform advanced solutions into scalable, real-world tools for growers. Successfully integrating technology in large-scale agriculture and resource-limited smallholder farming systems will be key for the ongoing modernization and resilience of agricultural systems.

Details matter: a guide to low-pass genotyping

POSTER

108

Marcel Brun[1], Joshua Hill[1], Matt Stull[1], Alex Watros[1], Charles D. Johnson[1]

1. Texas A&M AgriLife Genomics and Bioinformatics Service, College Station, TX, USA

For more than three decades, microarray-based and before that RFLP/AFLP genotyping has dominated the genomics selection space, largely due to its favorable economics, but with an inherent limitation: it can only measure pre-defined variants present on the array.

Over the last nearly decade, advances in sequencing have established low-coverage whole-genome sequencing (LowPass) as a viable and widely popular alternative. When applied at scale on high-throughput platforms with low cost per unit of data, LowPass is uniquely suited to meet the demands of large agricultural populations. The remaining challenge lies in complete implementation—developing a consistent, end-to-end workflow that performs reliably at scale.

Most low pass methods have focus on the analysis or libraries prep, but not the whole process. We present a complete LowPass sequencing workflow, spanning DNA extraction, library preparation, pooling, changes to the operation of the sequencer, genotyping, imputation and data delivery, refined over nearly a decade of development. This discussion focuses on the practical decisions that determine performance and cost of each step, such as barcode design for reduced index swapping, the alignment of extraction methods with library preparation, the impact of library construction on read yield and duplication, and the specific sequencing considerations when pooling hundreds of samples.

Beyond the laboratory we examine critical bioinformatics choices, including reference panel construction and imputation strategies. A central theme is the propagation of variation: how minor inconsistencies at any stage can compound to degrade final genotype quality.

Because the integrity of the output depends on the synergy of the entire pipeline, we detail our rigorous quality control (QC) protocols. To illustrate this, we discuss real-world case studies where deviations from requirements such as DNA fragmentation levels, barcode strategies, or library quantification directly impacted read duplication rates, sample assignment, and normalization, respectively.

This robust pipeline has already been applied numerous projects for many different plant and animal species. Having processed thousands of samples and generated hundreds of terabytes of data, it stands as a proven solution for low coverage high-throughput genomic selection.

How different microbiome similarity matrices affects genetic parameters estimation: an example in American Angus beef cattle

POSTER

109

Fernando Bussiman[1], Rebeka M. Costa[1], Andre Garcia[2], Kelli Retallick[2], Daniela Lourenco[1], Jeferson Lourenco[1]

1. University of Georgia, Department of Animal and Dairy Science, Athens, GA, USA
2. Angus Genetics Inc., American Angus Association, Saint Joseph, MO, USA

We investigated integrating ruminal or fecal microbiome data into genomic prediction models for ~900 yearling Angus cattle. Phenotypic and genotypic data were provided by the American Angus Association. Our research focused on four traits: weaning weight (WW), post-weaning gain (PWG), dry matter intake (DMI), and ultrasound backfat thickness (uFAT). Ruminal and fecal samples were collected between June/2022 and January/2023 across seven commercial feed efficiency testing centers in the US. Amplicon sequence variant (ASV) abundances were inferred using DADA2, and taxonomy was assigned using the Greengenes2 v2022.10 database. After rarefying samples to 10,000 reads and filtering ASVs with total abundance <1,200 and prevalence <5%, 1,451 ruminal and 1,388 fecal ASVs remained for further analyses. We compared three microbiome similarity matrices: M_1, based on log transformed abundances, M_2, an exponential kernel based on Euclidean distance, and M_3, a standardized microbial relationship matrix. The perspective of microbiome inclusion was evaluated using three models: GBLUP (additive genetic effects only), MBLUP (microbiome effects only), and GMBLUP (both additive and microbiome effects). Variance components were estimated via single-trait models and AI-REML using blupf90+. Key parameters were estimated included the residual heritability (h_r^2), microbiability (c_m^2), and microbiome heritability (h_m^2), as well as the trait heritability (h^2). M_1 failed to converge for all traits. M_2 tended to inflate microbiability estimates (up to 0.82 for fecal data), specially for DMI and WW. M_3 provided the most stable and biologically consistent results, better reflecting host genetic control over microbial composition. From GBLUP, h^2 estimates were between 0.17 to 0.31. In the GMBLUP model with M_3, ruminal c_m^2 ranged from 0.05 to 0.23, while h_m^2 was between 0.10 and 0.17. Ruminal microbiome showed stronger effects on phenotypic variation than fecal microbiome. The choice of similarity matrix is critical for model interpretation. We generally recommend M_3 for integrating microbiome information in beef cattle genomic evaluations, as it provides a more stable and accurate reflection of host-microbiome interactions.

Transcriptomic profiling of oil palm explants under abiotic stress using RNA-Seq

POSTER

110

Kuang-Lim Chan[1,2], Tatiana V. Tatarinova[3], Wei Yee Wee[2], Eng-Ti Leslie Low[1]

1. Malaysian Palm Oil Board, Advanced Biotechnology and Breeding Centre, Kajang, Selangor, Malaysia
2. Monash University Malaysia, School of Science, Subang Jaya, Selangor, Malaysia
3. University of La Verne, La Verne, CA, USA

Oil palm (*Elaeis guineensis*) is one of the world's most important oil crops, contributing significantly to the global supply of vegetable oils and supporting the economies of major producing countries. However, its productivity is increasingly threatened by abiotic stresses such as heat, drought, and salinity, which are intensifying under climate change. Understanding the molecular mechanisms underlying these stress responses is critical for developing more resilient oil palm varieties. To address this challenge, we applied an integrative RNA-Seq–based informatics workflow to characterise transcriptomic responses of oil palm leaf explants under controlled abiotic stress conditions. Explants were exposed to temperature stress (19 °C, 29 °C control, and 40 °C) for 24, and to osmotic and salt stress using increasing concentrations of mannitol and NaCl for five days, all under dark conditions. High-quality RNA was sequenced using Illumina 150 bp paired-end strand-specific technology. Following quality control and rRNA removal, reads were mapped to the latest *E. guineensis* genome (EG11) using the STAR 2-pass strategy. Transcriptome assembly and merging with StringTie generated a reference dataset comprising 27,664 genes with 66,166 transcripts. Expression quantification was performed with HTSeq, and differential expression analysis was conducted using DESeq2. Significant transcriptional changes were observed in all treatments, with 40 °C heat stress led to 1,986 up- and 859 down-regulated genes. Salt stress at 600 mM NaCl triggered 2,932 up- and 3,415 down-regulated genes, while 600 mM mannitol induced 1,936 up- and 3,620 down-regulated genes. Intersection analysis of DEGs from high osmotic and salt stress (400 mM and 600 mM) identified 1,400 common genes. KEGG pathway enrichment analysis of these shared DEGs revealed significant over-representation of the phenylpropanoid biosynthesis pathway, highlighting its central role in coordinated abiotic stress adaptation. Functional annotation further indicated that this response is largely regulated by NAC and AP2/ERF transcription factors, together with protective protein families such as Dehydrins/LEA. This study demonstrates how informatics-driven transcriptome analysis can generate high-resolution molecular insights to support data-informed strategies aimed at enhancing survival and productivity in oil palm.

Closing the nitrogen gap: microbial nitrogen use as a hidden regulator of crop-available nitrogen

POSTER

111

Christopher E. Chorpenning[1], Laura Mason[1], Alexandra G. Firth[1], Megan B. Machmuller[1], Mikayla A. Borton[2], Eugene F. Kelly[1], Kelly C. Wrighton[1]

1. Colorado State University, Department of Soil and Crop Sciences, Fort Collins, CO, USA
2. Colorado State University, Department of Food Science and Human Nutrition, Fort Collins, CO, USA

Globally, less than half of the nitrogen (N) within crops originates from fertilizer applied the same growing season, highlighting a fundamental disconnect between fertilizer inputs and crop N usage. Despite decades of optimization in fertilizer timing, placement, and formulation, a major challenge in modern agriculture remains improving N use efficiency to boost on-farm profitability and mitigate the deleterious effects of N loss on the environment. A key, yet underutilized, factor of this disconnect is the soil microbiome, which facilitates the transformation of organic N into crop-available forms and mediates pathways that retain or irreversibly lose N from agroecosystems. Here, we adopted a functional microbiome framework to identify how soil microbial N metabolism constrains and enables crop-available N across agroecosystems. We analyzed metagenomic data from hundreds of agricultural soils spanning diverse management and edaphic conditions in the intermountain west, assembling 1,950 medium- and high-quality metagenome-assembled genomes. This approach allowed us to link genes for N transformations to whole microbial genomic content, revealing how suites of co-occurring traits within and across individual organisms shape crop available N. Using a custom annotation pipeline targeting key N transformations, we resolved microbial capacities for organic N depolymerization (e.g., peptidases, chitinases, amidases), inorganic N transformations (e.g., nitrification and denitrification), and N assimilation and retention. Integrating microbiome functional profiles with paired soil chemical, physical, and management data revealed agroecosystems enriched in traits associated with N retention versus N loss pathways. By resolving microbial control points that regulate the transformation of soil N into crop-available forms, this work links soil microbiome genomics to crop N use efficiency. The resulting framework supports predictive, context-aware approaches to fertility management that align microbial function with plant demand.

NLP4Biocuration: advancing FAIR, AI-assisted literature curation across the AgBioData Consortium

POSTER

112

Kapeel Chougule[1], Biocuration Working Group[1]

1. United States Department of Agriculture, Agricultural Research Service (USDA-ARS), Corn Insects and Crop Genetics Research Unit, Ames, IA, USA

The AgBioData NLP4Biocuration Working Group was formed in March 2025 to evaluate, prototype, and coordinate the integration of natural-language-processing (NLP) and large language model (LLM) tools to support scalable, ontology-driven literature curation across agricultural genomics databases. This effort is conducted under the umbrella of the AgBioData Consortium and is supported by the NSF Research Coordination Network award #2126334, a shared community resource initiative that promotes interoperable informatics solutions.

Over the past eight months, working group members performed a coordinated assessment of AI-assisted literature tools, developed shared benchmarking practices, and explored infrastructure options for cross-database deployment. Tools evaluated include BioBERT, Elicit, Textpresso, OntoGPT, and early agentic-AI frameworks, with attention to their utility for named entity recognition, relationship extraction, summarization, and paper prioritization for plant and crop species. Several members implemented pilot pipelines comparing AI-generated literature sets with manually curated datasets, providing practical insights into recall, precision, and model behavior within agriculture-specific contexts. To facilitate shared learning and reproducibility, the group established a structured “tool review” framework and a community repository of test cases, datasets, and documented workflows. A major milestone is the ongoing organization of a Textpresso proof-of-concept deployment tailored for agricultural species. Participating AgBioData resources, including SorghumBase, MaizeGDB, GDR, SoyBase, GrainGenes, and others, are assembling FAIR-compliant gene lists, entity vocabularies, and open-access corpora, and are coordinating with the Alliance of Genome Resources team on compute requirements for a shared AWS-based test environment. In parallel, the group distributed a survey across AgBioData member databases to capture literature volume, workflows, AI adoption, and technical barriers; survey findings are guiding both a manuscript currently in development and continued infrastructure planning. Aligned with FAIR principles, the AgBioData consortium advances sustainable informatics infrastructure. By aligning NLP4Biocuration activities with these principles, the working group is helping establish sustainable informatics infrastructure and analytics-driven methods that benefit the entire agricultural genomics community.

POSTER

114

Novel spin column solution for optimized purification of nucleic acids from heavily inhibited plant and environmental samples for highly accurate sequencing and PCR analysis

Aaron Clausen[1], Ana Barrionuevo[1], Zoe Hermsen[1], Joshua Lee[1]

1. Zymo Research, Irvine, CA, USA

Accurate DNA sequencing analysis is essential for advancing crop genomics and understanding complex environmental microbiomes. However, polymerase chain reaction (PCR) and next-generation sequencing (NGS) performance can be severely compromised by the presence of PCR inhibitors, such as polyphenolic compounds. These inhibitors, including humic and fulvic acids and tannins, are common in plant and soil samples and can co-purify with nucleic acids during extraction. Their presence disrupts enzymatic reactions, reduces amplification efficiency, and often results in costly re-runs or false-negative results. In this study, we evaluated a simple, single-step centrifugation-based spin column system for the removal of common PCR inhibitors from plant and soil samples.

First, DNA was spiked with either humic acid or a PCR inhibitor cocktail containing bile salts, indigo, and hematin, then processed through the inhibitor removal column and inhibitor removal and DNA recovery of the flow-through was quantified using spectrophotometry and fluorometry. Additionally, quantitative PCR was performed to evaluate DNA amplification before and after treatment with the column. Next, performance of this inhibitor removal technology was assessed with DNA extracted from seeds, leaves, roots, stems, and soil using commercially available DNA extraction kits and PCR and NGS. Results showed that the column removed more than 96% of PCR inhibitors present without significant DNA loss. Additionally, quantitative PCR analysis demonstrated that amplification failed or was reduced in untreated samples but fully restored following treatment with the inhibitor removal column. Furthermore, both targeted NGS and whole-genome sequencing was successful using plant DNA treated with this novel spin-column and 16S rRNA sequencing revealed that untreated DNA extracted from soil was too inhibited for identifying bacteria in the soil, whereas column treatment restored bacteria identification.

These results demonstrate that polyphenolic compounds can significantly inhibit PCR amplification and NGS-based analysis, and that this novel PCR inhibitor removal technology effectively removes inhibitors without compromising nucleic acid yield. This PCR inhibitor removal treatment enhances amplification sensitivity, and analytical accuracy, ensuring reliable detection and sequencing even from inhibitor-rich plant and environmental samples. This study underscores the importance of optimizing nucleic acid purification from inhibitor-rich plant and environmental samples to ensure highly accurate downstream analysis.

Stress hormones in hair as genetic indicators of (disease) resilience in pigs

ABSTRACT SELECTED TALK

Fazhir Kayondo[1], Hayder Al-Shanoon[2], Yolande Seddon[2], Dylan Carette[2], Carmen Cole[2], David Janz[2], Frederic Fortin[3], John Harding[2], Michael Dyck[4], Graham Plastow[4], PigGen Canada[5], Jack Dekkers[1]

1. Iowa State University, Department of Animal Science, Ames, IA, USA
2. University of Saskatchewan, Western College of Veterinary Medicine, Saskatoon, Saskatchewan, Canada
3. Centre de Devéloppement du Porc du Québec Inc., Québec City, Canada
4. University of Alberta, Department of Agricultural, Food & Nutritional Science, Edmonton, Alberta, Canada
5. PigGen Canada Research Consortium, Guelph, Canada

The potential of stress hormones in hair as genetic indicator traits for (disease) resilience was investigated. Detailed performance and disease resilience data were collected on 65 batches of healthy Yorkshire*Landrace barrows (n=4068) from 7 companies, by exposing them to a natural polymicrobial disease challenge at ~40 days of age. Hair was collected from the last 15 batches (n=863) just before exposure (H1), as well as its regrowth (H2) 42 days later. Levels of cortisone, cortisol, DHEA, and DHEA-S were determined. Using genotypes on >400K SNPs, heritability estimates were moderate for cortisol in H1 (0.33±0.10) and H2 (0.23±0.09), for cortisone in H2 (0.27±0.10), for DHEA-S in H1 (0.31±0.10), and for DHEA in H2 (0.15±0.09). Estimates for the other combinations were <0.04. For cortisol, a major QTL was identified near the glucocorticoid receptor gene that explained 45% of genetic variance in H1 and 38% in H2. This QTL was not associated with a causative mutation previously identified in this gene for cortisol in blood. Levels of some stress hormones were genetically correlated with some disease resilience traits in H2 and to a lesser degree in H1, but standard errors were large. An extra copy of the minor allele at the major gene (frequency=9%) was also favorably associated with some disease resilience traits. These findings demonstrate that stress hormones in hair from young healthy pigs are potential genetic indicator traits for response to stress and disease resilience. Also, stress hormone levels in hair from older pigs have potential as resilience phenotypes collected on pigs in commercial farms. Supported by Genome Canada, PigGen Canada, RDAR, and USDA-NIFA.

Identifying virulence loci in soybean cyst nematode

POSTER

115

Lauren Docherty[1], Vishnu Ramasubramanian[1], Cory Hirsch[2], Aaron Lorenz[1], Senyu Chen[2,3]

1. University of Minnesota, Department of Agronomy and Plant Genetics, St. Paul, MN, USA
2. University of Minnesota, Department of Plant Pathology, St. Paul, MN, USA
3. University of Minnesota, Southern Research and Outreach Center, Waseca, MN, USA

Soybean (*Glycine max*) is a major crop both globally and in the United States. It is the 4th most grown crop worldwide by acreage, and the U.S. is the 2nd largest producer of soybeans in the world. Soybean cyst nematode (SCN) (*Heterodera glycines*), in turn, is the most damaging pathogen of soybean, causing an estimated $1.2 billion in yield loss each year in North America. The most cost-effective management strategy for SCN is growing resistant cultivars. For over 30 years now, more than 90% of commercial varieties available in North America have relied on a single source of SCN resistance, PI 88788. As a result, many SCN populations have evolved to overcome this resistance. While significant work has been done to identify additional resistance loci in soybean, relatively little is known about loci controlling virulence in SCN. SCN populations are very heterogeneous and individuals are microscopic, making it difficult to extract sufficient DNA for genomic analysis. To overcome these challenges, 178 inbred lines of SCN were developed for this research. These nematodes were originally collected from field samples and inbred using single-cyst descent for at least 10 generations. The genome of each line was sequenced to an average depth of 40x, aligned to the TN7 reference genome, and variants were identified. The lines were also phenotyped for their virulence on six soybean indicator lines with diverse sources of resistance. A phylogenetic tree, principal component analysis, and admixture analysis suggest little population structure among the lines. However, the virulence phenotyping results show significant diversity is present. A genome-wide association analysis was conducted to identify loci associated with virulence on the six tested resistant soybeans. Sixteen variants were identified, and all but one were uniquely associated with a single resistant soybean. The results of this project could be used to develop a molecular test for virulence in SCN populations, allowing for more efficient tracking of virulence shifts across landscapes. They also provide insights into SCN's virulence mechanisms and can inform breeding efforts for more durable soybean resistance.

Development of an optimized hybrid capture system for target enrichment of bovine samples

POSTER

116

Paul Doran[1], Owen Smith[1], Cibelle Nassif[1], Paul Doran[1], Elian Lee[1], Esteban Toro[1], Siyuan Chen[1]

1. Twist Bioscience, Research and Development, South San Francisco, CA, USA

High-throughput next-generation sequencing workflows are required for population-level bovine genomic research to support SNP analysis and discovery for genetic verification, breeding, and microbiome analysis. With the rapid decline in sequencing costs and driven by the superior data quality as well as the ability to use a single platform for both variant discovery and genotyping, sequencing-based methods are increasingly replacing traditional genotyping arrays.

Targeted sequencing is achieved using a DNA probe target enrichment panel that specifically hybridizes to predefined genomic regions of interest. Effective target enrichment requires a hybrid capture solution designed to improve both the uniformity and coverage of the desired targets, of which, blockers play a critical role in this process by preventing non-specific hybridization between target enrichment probes and off-target sequences. By minimizing unwanted probe and target sequence interactions, blockers enhance capture specificity and reduce the amount of sequencing required per sample, ultimately improving data quality and cost efficiency.

In this study, to demonstrate the effectiveness of these bovine-specific target enrichment products, we leveraged Twist's high-throughput, self-normalizing FlexPrep™ library preparation and 96-plex FlexPrep™ target enrichment workflow, which efficiently captured genomic regions corresponding to those represented in current bovine SNP arrays. This study showcases a >30% relative reduction of average %Off-Bait across all 18 bovine species tested when utilizing the Twist Bovine Blocker Solution in place of human CoT-1 for bovine sample target enrichment. The Twist Bovine Blocker Solution used in conjunction with the Twist Genotyping Panel - Bovine 100K allows users to sequence an additional 5% of samples while achieving a given level of coverage in their target enrichment sequencing experiments.

As target enrichment sequencing applications expand, optimized bovine panels and species-specific genomic blockers offer significant potential to support breeding program efficiency, accelerate genetic gain, and advance the precision and sustainability of modern agricultural practices. The Twist Bovine Blocker Solution and Twist Genotyping Panel – Bovine 100k are well-positioned to reduce off-target reads, enabling researchers to lower sequencing costs per sample while maximizing usable data for bovine genetic testing.

Integrating metagenomics with QTL mapping to characterize root rot resistance in common bean

POSTER

117

Shelby Ellison[1], Rebecca Arias[1], Eliot Stanton[2], Douglas Rouse[3], Ken Kmiecik[3]

1. University of Wisconsin-Madison, Department of Plant and Agroecosystem Sciences, Madison, WI, USA
2. University of Wisconsin-Madison, Bioinformatics Resource Center, Madison, WI, USA
3. University of Wisconsin-Madison, Department of Plant Pathology, Madison, WI, USA

Aphanomyces euteiches is a destructive soilborne oomycete that causes root rot in common bean (*Phaseolus vulgaris* L.), leading to significant yield losses in temperate production systems. Resistance is quantitative and difficult to phenotype accurately using visual assessments alone. To improve resolution of host resistance and better capture infection dynamics, we implemented an integrated QTL and metagenomic approach. A recombinant inbred population segregating for resistance was phenotyped using the standard 1–9 root rot severity scale and genotyped using Illumina. In addition to conventional SNP-based QTL mapping, we leveraged unmapped ("junk") reads typically discarded during host alignment. These reads were aligned to microbial reference databases to identify sequences derived from *A. euteiches* and other root-associated microorganisms. Normalized pathogen read counts were used as a quantitative proxy for pathogen load and mapped as an independent phenotype. We compared QTL identified using visual disease scores with those detected using pathogen read abundance to determine whether loci associated with reduced symptom severity also correspond to reduced pathogen count. This dual-phenotyping framework enables direct evaluation of resistance mechanisms affecting colonization versus symptom expression. Beyond *A. euteiches*, metagenomic profiling revealed diverse fungi, oomycetes, and bacteria associated with infected roots. Variation in microbial composition among genotypes suggests potential host genetic effects on the broader root-associated microbiome. These data provide an opportunity to map co-infection phenotypes and explore genetic control of host-microbe and microbe-microbe interactions that may contribute to disease outcomes. By integrating host QTL mapping with sequence-derived pathogen and microbiome signals embedded within genotyping data, this approach expands our capacity to characterize quantitative disease resistance and more precisely define the biological processes underlying field-relevant phenotypes.

Estimating the genetic heterogeneity of residual variance for egg weight using double hierarchical generalized linear models

POSTER

118

Suelen Fernandes Padilha[1], Alejandra Álvarez-Múnera[2], Matias Bermann[2], Vivian Likness[3], Laila Talarico Dias[1], Daniela Lourenco[2]

1. Universidade Federal do Paraná, Programa de Pós-Graduação em Zootecnia, Curitiba, Paraná, Brazil
2. University of Georgia, Department of Animal and Dairy Science, Athens, GA, USA
3. Cobb-Vantress, Inc., AR, USA

In breeding, individuals that exhibit good performance and a uniform response to environmental conditions are desirable. Although animals differ in their sensitivity to environmental changes, residual variance is generally assumed to be homogeneous in traditional genetic evaluations. However, genetic differences in phenotypic stability can be captured by estimating the genetic heterogeneity of residual variance. One common approach for this purpose is the use of Double Hierarchical Generalized Linear Models (DHGLM), which estimate genetic values and variance components for both the mean and the dispersion. Genetic and non-genetic factors may influence the dispersion. This study aimed to investigate the genetic heterogeneity of residual variance for weekly mean egg weight in broiler chickens by estimating variance components for the mean and dispersion using DHGLM. Data from a pure broiler line from Cobb-Vantress were used. The dataset included pedigree information for 5,008 animals and 48,040 records of weekly mean egg weight from 3,231 hens collected over a 28-week laying period. The model included the fixed effects of dam generation and laying week. Random effects included additive genetic, permanent environmental, and residual effects for both mean and dispersion. Variance components and genetic parameters for mean and dispersion were estimated using DHGLMF90, which variance components are estimated using REML via BLUPF90+. The additive genetic variance of the dispersion component for mean egg weight was 0.048 ± 0.012, indicating that part of the animals' stability for this trait may be attributable to the genetic factors. The permanent environmental variance was 0.153 ± 0.012, indicating that non-genetic effects also contributed to phenotypic uniformity. Heritability for weekly mean egg weight was 0.25 ± 0.025. The correlation between additive effects for mean and dispersion was -0.49 ± 0.087. These results suggest that both mean and dispersion could respond to selection, and that the selection for this trait could improve phenotypic uniformity in egg production. In addition, the Genetic Coefficient of Variation on the standard deviation level (GCVSDe) for the dispersion was 0.11, indicating that the genetic standard deviation of weekly mean egg weight can be reduced by 11% in one generation.

Genotyping technologies for plant genome analysis and breeding

POSTER

119

Martin Ganal[1], Joerg Plieske[1], Eva-Grafahren Belau[1], Karolina Greziak[1], Dagmar Kulosa[1], Naser Poursarebani[1], Thomas Gross[1], Lydia Gramzow[1], Heike Molenaar[1], Heike Gnad[1]

1. SGS INSTITUT FRESENIUS GmbH TraitGenetics Section, Am Schwabeplan 1b, D-06466 Seeland/Gatersleben, Germany

Genotyping of large sample numbers using single nucleotide polymorphisms (SNPs) is nowadays an indispensable tool in combination with the use of other Omics technologies in research and plant breeding. Especially for purposes such as the association of genomic regions with specific Omics traits and the determination of breeding values of individual progeny plants, SNP genotyping is still the method of choice since it is in most cases sufficient in terms of resolution, predictive value and costs. This is particularly true for optimized genotyping panels, which can be screened on arrays that are based on marker distribution based on haplotype structure and genetic recombination maps. We have developed such optimized genotyping marker panels for many important crop plants such as maize, wheat, barley, Brassica, soybean, cotton and for many other crop species. Plant breeding has become increasingly complex as the industry must respond more rapidly to the demands of selecting for specific traits. Sequencing-based genotyping using a targeted approach with limited (<1,000) numbers of defined and trait-specific marker sets (targeted Genotyping-by-Sequencing or tGBS) can be performed at low costs. We have evaluated tGBS technologies regarding their data quality in a number of crop species such as sunflower, wheat, barley and maize. The outcome of these studies demonstrates that tGBS is a very cost-efficient technology if one can accept a somewhat higher rate of failed datapoints compared to arrays in inbred material. In highly heterozygous material, tGBS has some issues due to technical features and is less accurate compared to arrays unless one focusses only on validated markers.

Developing genomic tools for climate-resilient underutilized tropical forages to enhance livestock productivity in Sub-Saharan Africa

POSTER

120

Abel Teshome Gari[1], Meki Shehabu Muktar[1], Alemayehu Teressa Negawo[1], Ermias Habte[1], Susanne Barth[2], Aklilu Mekasha[3], Mesfin Dejene[3], Jiyu Zhang[4], Claire Domoney[5], Jose De Vega[6], Chris Stephen Jones[7]

1. International Livestock Research Institute (ILRI), Feeds and Forages Unit, Addis Ababa, Ethiopia
2. Teagasc, Oak Park, Carlow, Ireland
3. Ethiopian Institute of Agricultural Research (EIAR), Holeta Research Center, Holeta, Ethiopia
4. Lanzhou University, College of Pastoral Agriculture Science and Technology, State Key Laboratory of Grassland Agro-ecosystems, Lanzhou, China
5. John Innes Centre, Norwich Research Park, Norwich, United Kingdom
6. Earlham Institute, Norwich Research Park, Norwich, United Kingdom
7. International Livestock Research Institute (ILRI), Feeds and Forages Unit, Nairobi, Kenya

Livestock production in Sub-Saharan Africa (SSA) faces the dual challenges of low productivity and increasing pressure from climate change and the need to reduce greenhouse gas emissions, particularly enteric methane. Improved tropical forage grasses and legumes represents a scalable strategy to enhance feed efficiency, productivity, and methane mitigation in ruminant systems. However, the application of modern genomics in tropical forage breeding has lagged behind that of major food crops, largely due to limited genomic resources and poorly characterized germplasm.

Here, we report the development and application of genomics-enabled breeding tools for a set of underutilized tropical forages conserved in the ILRI Forage genebank. Using genotyping-by-sequencing and whole-genome sequencing, we generated genome-wide marker datasets for key forage species including Napier grass, Rhodes grass, *Urochloa* spp., oat, lablab, and cowpea. Notably, this work reports the first high-quality reference genome assemblies for Napier grass and lablab, providing foundational genomic resources for these species. These datasets were used to characterize genetic diversity, population structure, and linkage disequilibrium, and to identify QTLs through association mapping for desirable traits relevant to climate adaptation and livestock productivity.

Across species, analyses revealed substantial population differentiation and previously uncharacterized genetic diversity, which was reflected in pronounced phenotypic variation observed under field conditions. Field-based characterization of diverse germplasm enabled the identification of high-performing “best-bet” accessions with superior agronomic performance and feed quality, suitable for direct release or for use as parental material in the next cycle of genomics-assisted breeding. Building on this phenotypic diversity, genome-wide association analyses identified quantitative trait loci associated with biomass yield, water-use efficiency, and forage quality traits linked to methane mitigation potential. Together, the resulting marker and phenotypic resources provide a foundation for implementing genomic prediction and selection strategies, with the potential to reduce breeding cycle time and costs in tropical forage improvement programs.

All genomic datasets and analytical outputs are being deposited in the public domain to support broader adoption of genomics-enabled, climate-smart forage breeding across SSA and beyond.

POSTER

121

Huaxi cattle reference genome: integrating structural variation to enhance association mapping and genomic prediction for economic trait

Fei Ge[1], Junya Li[2], Guilherme J.M. Rosa[1]

1. University of Wisconsin-Madison, Department of Animal and Dairy Sciences, Madison, WI, USA
2. Chinese Academy of Agricultual Sciences, Institute of Animal Science, Beijing, China

Constructing a high-quality genome for Huaxi cattle is a critical foundation for exploring the relationships between genetic variation and phenotypic traits. In this study, we *de novo* assembled a chromosome-level genome of Huaxi cattle using 41× PacBio HiFi reads combined with 100x coverage of Hi-C data. The genome size is 3.06 Gb, with a Contig N50 of 99.52 Mb, and 24 chromosomes were fully assembled. Using the *de novo* assembly as a reference, we constructed a reference panel based on whole-genome resequencing (WGS) of 218 Huaxi cattle. This panel was used to perform genotype imputation for 5,193 Huaxi cattle genotyped with Illumina BovineHD BeadChips, achieving an average imputation accuracy of 0.96. We further integrated 20× PacBio HiFi sequencing data from eight individuals to characterize the structural variation (SV) landscape, identifying a total of 119,243 insertions and deletions. We then performed a genome-wide association study (GWAS) using a Mixed Linear Model (MLM) for 46 economically important traits to identify putative functional variants and candidate genes. The phenotypic correlations ranged from −0.323 (lung with trachea and spleen weight) to 0.986 (lean meat and carcass weight). The GWAS revealed 1,258 significant SNPs and 846 SVs at the Bonferroni-corrected threshold, with most overlapping known QTLs for live weight, carcass weight, and average daily gain. Notably, a 1,347 bp deletion in the *NCAPG* gene on chromosome 6 was significantly associated with thigh thickness and hind-leg circumference. Additionally, we performed genomic best linear unbiased prediction (GBLUP) to evaluate genomic estimated breeding values (GEBVs) using four different loci sets: Illumina BovineHD BeadChip, WGS, SVs, and SNPs from the newly assembled Huaxi cattle genome. The heritability of the traits ranged from 0.06 (Stomach weight) to 0.84 (Carcass chest depth). Results from a 5-fold cross-validation showed that incorporating Huaxi cattle–specific loci into the Illumina BovineHD BeadChip increased GBLUP prediction accuracy by 5.4% – 10.4% compared with using the chip alone. Furthermore, using SVs for GBLUP prediction improved accuracy for traits such as shin weight and striploin weight by approximately 4%. In summary, this study enabled the exploration of SVs for fine-mapping functional variants and to enhance genomic prediction. These findings support precision breeding in Huaxi cattle and contribute to the “Global Cattle Pan-Genome Project.”

Turning farmers' fields into selection environments: accelerating CGIAR crop genetic gain through on-farm sparse testing

ABSTRACT SELECTED TALK

David González-Diéguez[1,2], Keith Gardner[2], Gary Atlin[3], Christian Werner[1,2]

1. Consultative Group of International Agricultural Research (CGIAR), Breeding Innovation and Modernization, Texcoco, Mexico
2. International Maize and Wheat Improvement Center (CIMMYT), Texcoco, Mexico
3. Bill & Melinda Gates Foundation, Seattle, WA, USA

Smallholder farms under 2 hectares constitute over 80% of the world's 570 million farms, supporting the livelihoods of impoverished rural communities. They are often characterized by low input use, multiple biotic and abiotic stresses, and diverse management practices. Smallholder farmers represent a substantial fraction of the 690 million people experiencing daily hunger, and their production systems are particularly vulnerable to increasingly erratic weather extremes linked to climate change.

CGIAR is a global agricultural research partnership that delivers improved crop varieties through a network of international agricultural research centers, including CIMMYT (International Maize and Wheat Improvement Center) and CIAT (International Center for Tropical Agriculture). Its staple crop breeding programs target smallholder farmers across diverse target populations of environments (TPE). Yet, evaluations are often conducted at well-managed research stations and trial sites that do not fully capture smallholder conditions. Consequently, genotype performance may translate poorly to farmers' fields, and realized gains on farms can lag behind gains observed under managed conditions.

To better reflect real-world conditions in selection decisions, CGIAR crop programs are expanding on-farm testing across both early and late stages. Using farm-as-incomplete-block (FAIB) designs, small blocks with only a few plots can be embedded within smallholder fields, where fully replicated trials are not feasible alongside subsistence production. In early stages of selection, sparse testing can improve selection accuracy through broader sampling of the TPE while increasing selection intensity by testing more candidates with less replicates. In late stages, with few genotypes left, sparse testing can be effective at increasing broad-sense heritability across the TPE and identifying the most promising candidate varieties.

Drawing on examples across crop breeding programs, including two pilot studies of early-stage on-farm sparse testing in CIMMYT maize and CIAT beans, we outline and evaluate a strategy to shift some testing from managed stations into farmers' fields and increase genetic gain where it matters most.

Toward a single-nuclei atlas of flagship bioenergy crops

POSTER

123

Sharon Greenblum[1], **Peng Wang**[1], **Leo Baumgart**[1]

1. Department of Energy (DOE) Joint Genome Institute, Lawrence Berkeley National Laboratory, Berkeley, CA, USA

Single-cell RNA sequencing (scRNA-seq) has transformed our ability to resolve cellular diversity and developmental trajectories, yet its application to plants remains technically challenging and underrepresented relative to animal systems. Key obstacles include rigid cell walls, high ambient RNA contamination, species-specific protocol requirements, and the lack of scalable, reproducible analysis frameworks. Here, we present an integrated effort at the DOE Joint Genome Institute (JGI) to establish a comprehensive developmental single-nuclei atlas of flagship bioenergy plant species.

Our approach combines optimized nuclei-based single-cell workflows with species multiplexing on the BD Rhapsody microwell platform, enabling efficient processing of diverse plant tissues while reducing costs and providing a reliable measurement of ambient RNA levels. By extracting nuclei from multiple species simultaneously (the “mixed greens” approach), we improve quality control diagnostics, identify empty wells and multiplets, and better characterize tissue-specific background contamination. These experimental advances are paired with reproducible, automated analysis pipelines and clear quality metrics. Initial datasets span key developmental tissues at multiple stages of maturation (roots, leaves, inflorescences) across model species and bioenergy-relevant plants including sorghum, switchgrass, brachypodium, and pennycress. The resulting atlases provide a foundation for cross-species cell type comparison and evolutionary analysis. To address the persistent bottleneck of cell type annotation in new species, we explore the use of existing cross-species mapping and foundation-model approaches, reducing the need for *de novo* training for each organism.

Looking ahead, this initiative will expand to standardized metadata collection, improved data storage and sharing, seamless lab-analysis integration, and robust statistical frameworks for single-cell data, providing the requisite foundation to launch plant snRNA-seq as a community-accessible JGI user product. Together, these efforts aim to accelerate plant functional genomics, enable rational crop and bioenergy trait engineering, and deliver a scalable, reproducible single-cell resource for the global plant research community.

D-BLUP: making genomic BLUP differentiable for end-to-end genomic prediction

ABSTRACT SELECTED TALK

Joseph Guhlin[1], **Peter K. Dearden**[1]

1. University of Otago, Genomics Aotearoa and Department of Biochemistry, Dunedin, New Zealand

Best linear unbiased prediction (BLUP) is foundational for genetic evaluation in agriculture, with SNP, GRM, and combined genomic-pedigree formulations. BLUP tools use fixed solvers to tune variance parameters externally via REML or grid search, creating a boundary between BLUP and machine learning (ML), thereby preventing end-to-end learning and limiting the ability to jointly train BLUP with neural networks.

We present D-BLUP, a differentiable formulation of BLUP that removes this boundary by exposing the mixed-model solve as part of an automatic differentiation graph. Implemented in JAX, D-BLUP treats the BLUP system as a trainable model component, allowing the variance ratio (regularisation) and optionally kernel or marker weights to be optimised directly from the prediction loss via gradient descent, while preserving the structure and interpretability of classical BLUP.

Prior BLUP–ML integrations typically solved BLUP externally or treated BLUP outputs as fixed targets. In contrast, D-BLUP functions as a native machine-learning layer: the solve participates in backpropagation and can be jointly optimised with other differentiable components, including deep networks that learn non-linear covariate effects (demonstrated by jointly training a covariate MLP alongside a BLUP head).

D-BLUP supports SNP-BLUP, GBLUP, and ssBLUP. Both covariance-form and precision-form solves are supported. On public livestock datasets, D-BLUP reproduces standard BLUP breeding values and predictive performance while learning regularisation parameters end-to-end, recovering the same operating regime as conventional grid-based tuning. We further demonstrate weighted extensions in which non-negative block weights learn heterogeneous genomic contributions, with a safe collapse to standard BLUP under strong regularisation.

The implementation targets scale by avoiding explicit $O(n^2)$ materialisation of dense G or H, shifting cost to iterative matrix-free solves, and accelerating key operations with custom GPU kernels on modern accelerators. D-BLUP reframes BLUP from a fixed solver into a differentiable, composable model layer for end-to-end training in next-generation breeding pipelines.

Achieving ultimate accuracy with nanopore sequencing data for plant genotyping

POSTER

125

Courtney Hall[1], Jared Simpson[2,3], Winston Timp[1,4]

1. Johns Hopkins University, Department of Biomedical Engineering, Baltimore, MD, USA
2. Ontario Institute for Cancer Research, Toronto, Ontario, Canada
3. University of Toronto, Department of Molecular Genetics, Toronto, Ontario, Canada
4. Johns Hopkins University, Department of Molecular Biology & Genetics, Baltimore, MD, USA

Single-molecule sequencing from Oxford Nanopore Technologies (ONT) offers the potential to generate real-time results on the small, affordable MinION device, making it a promising option for rapid, field-based plant genotyping. Long ONT reads have proven essential for resolving repetitive regions and assembling complex plant genomes, but are far less used for targeted sequencing assays due to their relatively low accuracy. This is especially problematic when near-identical gene copies must be distinguished based on a handful of single-nucleotide polymorphisms (SNPs) spanning several kilobases, such as MYB transcription factors in octoploid strawberries. Unique molecular identifiers (UMIs), which link PCR-amplified reads back to their original templates for error correction, reduce background noise in ONT reads and enable accurate variant calling even across long, highly similar homeologs. Here we explore the ultimate accuracy of nanopore sequencing using UMI-enabled approaches and assess its potential in plant breeding.

We first show that UMI incorporation and consensus polishing can generate higher single-molecule accuracy than previously thought possible on ONT sequencing platforms. Regions of interest were tagged with dual UMIs, amplified, and sequenced on MinION flow cells. Using our custom computational pipeline, reads were binned by UMI pair and consensus sequences were generated with multiple rounds of polishing to eliminate sequencing errors. This approach reduced the error rate of raw ONT reads over 100-fold, achieving accuracies above 99.998%. To lower per-sample cost without increasing processing time, we extended our workflow to incorporate sample-specific barcodes during amplification of UMI-tagged molecules. This approach provides a scalable solution for profiling tens to hundreds of samples in a single ONT sequencing run.

We then applied our methods to profile MYB transcription factor homeologs in strawberries. Our results demonstrate that this approach preserves long-range haplotype information, capturing rare variants across multi-kilobase regions. The phasing capabilities of our approach proved particularly valuable for resolving highly similar homeologs. With further development of our methods and continued advancements from ONT, we anticipate that UMI nanopore sequencing could provide a rapid, cost-effective solution for marker-assisted breeding in polyploid crops.

Applications of a pangenome-informed genotyping approach in *Sorghum*

POSTER

126

Adam Healey[1], Chloee McLaughlin[1,2], Avril Harder[1], Lillian Padgitt-Cobb[1], David Flowers[1], Jeremy Schmutz[1,3], John Lovell[1,3]

1. HudsonAlpha Institute for Biotechnology, Genome Sequencing Center, Huntsville, AL, USA
2. Colorado State University, Department of Horticulture and Landscape Architecture, Fort Collins, CO, USA
3. Lawrence Berkeley National Laboratory, Department of Energy Joint Genome Institute, Berkeley, CA, USA

Large structural variants (SVs) have been routinely demonstrated to underlie important agricultural and agronomic traits in crops, such as disease resistance in rice or barley, or desirable flavor in tomato. Despite their genomic importance and phenotypic impact, large SVs are often difficult to capture and characterize within populations for multiple reasons: SVs are difficult to detect in single reference genomes and haplotype determination in short-read resequenced data is both conceptually challenging and computationally intensive. Here we present a novel, easily updatable approach for genotyping large structural variants in pan-genomes via haplotype specific markers within regions of interest. Using our pangenome-informed genotyping approach, we identify haplotype structures harboring previously unknown large intergenic INDELs in a ~175kb biosynthetic gene cluster for dhurrin biosynthesis, a locus important for both pest resistance and drought response. We show that haplotype-level variation, as described with our approach, corresponds to both significant differences in dhurrin seed content as well as environmental continent-wide precipitation gradients. Together, our pangenome-informed genotyping approach allows for the characterization of complex genomic variation that is often difficult to detect in whole-genome resequencing data. Most importantly, the marker database containing haplotype information can be updated to include newly sequenced reference genomes, and the genotype information to calculate haplotype blocks is pre-computed genome-wide scale per sequencing library such that any a *priori* region of interest can be queried and haplotyped across the population quickly and with relative ease. This methodology can be extended into other crop systems allowing advances in sequencing technology, genome assembly, annotation and pangenome development to be directly utilized for discovery and trait improvement using existing short-read Illumina resources.

Cat-alyzing feline genomics: a comprehensive imputation reference panel for domestic cats

POSTER

128

Nils Homer[1], Tim Fennell[1], Yossi Farjoun[1], Alison Meynert[1], Zach Norgaard[1], Clint Valentine[1], Michelle White[2], Kasia Bryc[2,3], Elinor Karlsson[1,2,4]

1. Fulcrum Genomics, Somerville, MA, USA
2. The Broad Institute, Cambridge, MA, USA
3. Darwin's Ark Foundation, Edmonds, WA, USA
4. University of Massachusetts (UMass) Chan Medical School, Worcester, MA, USA

Genomic imputation has transformed human and agricultural genomics research, but comparable reference resources remain limited for non-model mammalian species. Domestic cats (Felis catus) represent valuable models for mammalian genetics, sharing >250 hereditary diseases with humans and living in human-relevant environments. In collaboration with Darwin's Ark, the Broad Institute, and UMass Chan Medical School, we developed the first high-resolution imputation reference panel for feline genomics leveraging genomes available through public sequence archives.

We constructed a reference panel from 992 cats: 26 from 7 wildcat species and 966 domestic cats (80% mixed-breed, 20% purebred spanning 44 breeds). Over half were sequenced at the Broad Institute with mean ~38x coverage. Reads were aligned to F.catus_Fca126_mat1.0, variants called using GATK best practices, and haplotypes phased with SHAPEIT5. Outlier samples were removed based on coverage, relatedness, duplicate samples, and missingness thresholds.

The resulting panel contains 99 million variants across 2,000 haplotypes—the largest feline genomic resource to date. We implemented GLIMPSE2-based imputation in a containerized workflow optimized for efficiency and reproducibility. Validation using held-out samples downsampled to 0.2–2X coverage showed imputation accuracy exceeding 98% for common variants, reaching 99.5% with quality filtering, with X chromosome accuracy comparable to autosomes.

To demonstrate biological validity, we imputed variants for 379 domestic cats. GWAS reproduced expected associations including fur length (FGF5), white fur amount (KIT), black nose (ASIP), and tabby pattern (ASIP). Population structure analysis revealed geographic rather than breed-based clustering across North America.

This work establishes the first comprehensive imputation resource for feline genetics, enabling large-scale low-coverage sequencing studies. With over 20,000 cats enrolled in Darwin's Ark and 2,500 DNA sequencing participants, this resource will accelerate discovery of the genetic basis for feline phenotypes while providing a transferable template for agricultural and companion animal genomics.

POSTER

129

From genome to cell: genome-wide mapping and single-cell transcriptomics reveal the genetic basis of chicken feather pigmentation patterning and molecular identities

Pei-Jung Hsin[1], Zheng Li[2], Leif Andersson[2], Brian W. Davis[1]

1. Texas A&M University, Department of Veterinary Pathobiology, College Station, TX, USA
2. Uppsala University, Department of Medical Biochemistry and Microbiology, Uppsala, Sweden

Bird feathers display striking diversity in morphology. The genetic basis of intra-feather pigmentation patterning and how body-region specific feather is established remain unclarified. This study carried out a Mendelian cross between red junglefowl (RJF) and domestic Silver Sebright (SS) chickens to generate F2s with more than 10 feather pattern categories observed. Whole-genome sequencing of over 300 F2s along with F1s and parentals was performed. Five large-effect loci were implicated, including three known pigmentation-related genes (*SOX10*, *GJA5*, and *MC1R*) and two previously undocumented signals on chromosome 1 and chromosome 2. SS-derived *GJA5* alleles, and segregation at *MC1R* and the newly discovered locus on chr. 1, were linked to appearance and completeness of the single-lacing pattern. RJF-derived *SOX10* alleles was related to the increase of the single-lacing thickness, and RJF-derived alleles on chr. 2 further enhanced the eumelanin amount, making the plumage nearly black. Heterozygosity at the five loci led to 1.5-lacing or double-lacing patterns. Other allele combinations produced more complex patterns that have not been defined before. To explore the molecular addresses and the regulatory pathways, single-cell RNA sequencing was done on active feather follicles from four body regions (breast, leg, dorsal, and hackle) in an adult male RJF. Twelve major follicular cell types and body-region specific expression patterns were identified. *HOX* genes were highly and differentially expressed on the anterior-posterior axis in dermal papilla, which is known to be essential for feather regeneration. Pigmentation genes were mostly expressed in melanocytes, except for the *ASIP* gene mainly expressed in dermal papilla, which can be the signal of the dorsoventral identity. Together, this study integrated classical genetics with single-cell transcriptomics to reveal candidate variants and cellular expression programs underlying feather pigmentation patterning and morphologies.

Rapid, high-throughput genotyping solutions for companion animals and crop breeding research

POSTER

130

Stephen Jackson[1], **Dorothy Oliver**[1], **Dongyeop Kim**[1]

1. Thermo Fisher Scientific, Santa Clara, CA, USA

The ability to analyze genomic content is revolutionizing our interactions with non-human organisms. These advances in genotyping can help identify deleterious alleles that can be important in breeding, crop improvement, and veterinary care. Thermo Fisher Scientific has high-throughput genotyping solutions for genome analysis of companion animals, aquaculture and plant crops. In this study, we demonstrate practical workflows for collecting and purifying DNA samples from these samples. Using these samples, we introduce the SwiftArray Assay for genotyping and show how it provides high-quality data in 30 hours. Together, this study demonstrates that aquaculture and crop producers, companion animal breeders, veterinary practices and direct-to-consumer genotyping companies can quickly and accurately obtain genotypic information from non-human organisms.

Bipartite machine learning identifies transcription factor interactions underlying agricultural traits

ABSTRACT SELECTED TALK

Tim L. Jeffers[1], Yitao Long[2], Bingran Shen[2], Amari Hill[1], Amelia Henry[3], Matthew D. Brooks[4,5], Dennis Shasha[2], Gloria M. Coruzzi[1]

1. New York University, Center for Genomics & Systems Biology, New York, NY, USA
2. New York University, Courant Institute of Mathematical Sciences, New York, NY, USA
3. International Rice Research Institute (IRRI), Los Baños, Laguna, Philippines
4. United States Department of Agriculture, Agricultural Research Service (USDA-ARS), Urbana, IL, USA
5. University of Illinois Urbana–Champaign, Urbana, IL, USA

Predicting regulatory networks that can be engineered to improve crop traits remains a major computational challenge, as agricultural phenotypes emerge from complex and hierarchical gene regulation. In this hierarchy, trait outcomes are mediated by interacting genes, while the expression of those genes is itself controlled by interacting transcription factors (TFs). Conventional machine learning of transcriptomic data has not been designed to identify the complex TF interactions that underlie plant traits.

To address this challenge, we developed **Bipartite machine learning (ML)**, a novel computational framework that overcomes limitations of prediction from 'omics data, including dimensionality, redundancy, and feature interdependence (Shen *et al*. 2024). Bipartite ML iterates *(i)* feature reduction to identify minimal gene sets that best predict outcomes, followed by *(ii)* leave-out of those minimal sets to reveal disjoint, equally predictive feature combinations. When run across multiple random seeds, this strategy reveals feature co-occurrence patterns linked to accurate predictions, providing evidence of features that interact to mediate outcomes.

We have implemented Bipartite ML on agricultural data for both gene-to-trait and TF-to-target-gene predictive modelling. By integrating the target genes' trait importance with TF-TF cooccurrence networks, we have ranked interactive TF pairs with the strongest influence over specific phenotypes. We applied this pipeline to field data with sample-matched transcriptome and phenotype data. We ranked TF pairs predicting nitrogen use efficiency and yield across maize accessions (Cheng *et al.* 2021) and synergistic nitrogen and water impacts on stress and yield in rice accessions (Swift et al 2019). We are currently validating the direct impacts of TF pairs on networks through a cell-based interactive TF assay and the impact of TF pairs on field traits by developing co-overexpression lines. In total, Bipartite ML provides a framework for identifying and ranking interactive TF networks influencing complex crop traits, which expedites network bioengineering of improved crop traits.

Quantification of anthocyanins and gene expression in a Texas maize variety

POSTER

131

Hannah Jeffery[1], Jamal Mohammed[1], Ankita Mishra[1], Michael Dzakovich[2], Wenwei Xu[3,4], Timothy Paape[4,5]*

1. Texas A&M AgriLife, Institute for Advancing Health Through Agriculture, College Station, TX, USA
2. Baylor College of Medicine, Department of Pediatrics, United States Department of Agriculture, Agricultural Research Service (USDA-ARS) Children's Nutrition Research Center, Houston, TX, USA
3. Texas A&M University System, Texas Agricultural Research and Extension Center, Lubbock, TX, USA
4. Texas A&M AgriLife, Department of Soil and Crop Sciences, College Station, TX, USA
5. United States Department of Agriculture, Agricultural Research Service (USDA-ARS), Responsive Agriculture Food Systems Research Unit, College Station, TX, USA

*Corresponding author

Anthocyanins are flavonoids that function as both a pigment and a source of antioxidants. In maize (*Zea mays*) and other plant species, the core anthocyanin biosynthesis pathway is well-characterized. However, a more complete understanding of the genomic and environmental factors that regulate anthocyanin biosynthesis is needed to be able to fine tune the genetic architecture of anthocyanin-producing maize in response to environmental variation. This study delivers insights into the gene regulatory pathways that affect the production of 8 classes of anthocyanins and alternative reaction pathway products in maize kernels grown in both field and greenhouse environments using bulk RNA-seq and targeted metabolomics. Anthocyanin content and gene expression levels were compared in a purple maize variety (HiA) with that of a closely related yellow maize variety at 10, 20, and 30 days post-anthesis. Total anthocyanin production was 100 times higher in whole pulverized HiA kernels compared to the yellow kernels in greenhouse conditions. Differential expression analysis showed that nine genes were significantly more expressed in HiA corn than in yellow maize kernels across all the environments. Gene co-expression network analyses were conducted using either 1) the anthocyanin biosynthesis genes with stable expression as bait genes (SimpleTidy Gene CoEx), or 2) anthocyanin concentrations as weights for unsupervised correlation-based gene clustering (WGCNA). The resulting co-expression networks overlapped substantially in terms of gene content, although the supervised clustering method identified slightly more known anthocyanin biosynthesis genes. Gene expression levels in the unsupervised network were the most strongly correlated with acylated cyanidin levels, corresponding to the high cyanidin levels of the HiA kernels. The expression levels of the bait genes were strongly correlated with each other within locations, suggesting that the expression of these genes is under *cis*-regulation.

Haplotype architecture shapes phenotypic diversity across plant and animal pangenomes

ABSTRACT SELECTED TALK

Katharine M. Jenike[1], Nicole Brown[2], Sam Kovaka[2,†], Matthias Benoit[3], Robin Burns[1], Frances Chen[4,5], Tyler Collins[6], Rachel Daniels[4,5], Blaine Fitzgerald[7,8], Iacopo Gentile[7,8], Anat Hendelman[7,8], Rachel Johnston[4,8], Delphine Larivière[9], Betty Y.H. Huang[6], Alex Ostrovsky[2], Srividya Ramakrishnan[2], Katia Renault[4,10], Gina M. Robitaille[7,8], James W. Satterlee[11], Hagai Shohat[7,8], Anton Nekrutenko[9], Elinor K. Karlsson[4,5], Zachary B. Lippman[7,8], Ian R. Henderson[1], Michael C. Schatz[2,6]

1. University of Cambridge, Department of Plant Sciences, Cambridge, United Kingdom
2. Johns Hopkins University, Department of Computer Science, Baltimore, MD, USA
3. Université de Toulouse, LIPME, INRAE, CNRS, Castanet-Tolosan, France
4. Broad Institute of MIT and Harvard, Cambridge, MA, USA
5. UMass Chan Medical School, Genomics and Computational Biology, Worcester, MA, USA
6. Johns Hopkins University, Department of Biology, Baltimore, MD, USA
7. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA
8. Howard Hughes Medical Institute, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA
9. The Pennsylvania State University, Department of Biochemistry and Molecular Biology, University Park, PA, USA
10. Harvard University, Department of Molecular and Cellular Biology, Cambridge, MA, USA
11. University of Wisconsin Madison, Department of Botany, Madison, WI, USA

[†]Present address: Glyphic Biotechnologies, Berkeley, CA, USA

Pangenomes provide a powerful lens into adaptation and phenotypic variation across agriculture, human health, and fundamental biology. Structurally diverse sequences revealed by pangenomes are increasingly recognized as potential contributors to phenotypic diversity, yet understanding how these sequences are organized and relate to traits remains poorly resolved. Despite rapid progress in genome sequencing, methods for analyzing pangenomes are computationally demanding and have shown limited ability to resolve how complex genetic variation is organized into functional units that shape phenotypes.

Addressing this need, we introduce Panagram (https://github.com/kjenike/panagram), an ultrafast reference-free platform for assembling and annotating the haplotype architecture within a pangenome consisting of evolutionarily coherent blocks of shared sequence variation. The core metric of Panagram is the pan-kmer bitmap that quantifies local sequence similarity across samples and enables rapid, on-the-fly clustering and analyses of haplotypic blocks. These capabilities provide a unified framework for association testing, introgression detection, and the flexible discovery of biologically meaningful variation across pangenomes.

We apply Panagram to multiple plant and animal systems using both short and long read sequencing, including all 605 vertebrate genomes from the Zoonomia Project spanning mammalian and avian clades. In Zoonomia, we use Panagram to identify 1163 genes associated with longevity and metabolic function ($p<4.8e6$). Then in *A. thaliana*, we analyze 143 globally diverse genomes across 44 environmental conditions, revealing thousands of haplotypic associations ($p<10e10$) within previously known and newly characterized genes. In *Solanum*, Panagram accurately identifies introgressions in the indigenous crop *S. aethiopicum* underlying widespread exchange of disease-resistance genes and other agronomically important loci. Finally, using six newly assembled domesticated and mixed-breed genomes in *Canis*, Panagram places them within the broader evolutionary context of Zoonomia and uncovers breed-specific haplotype blocks, extensive tracts of nonreference sequence, and lineage-restricted variants associated with morphology and disease. These analyses demonstrate how Panagram unifies haplotype-centered pangenome assembly, visualization, and trait association to illuminate architectures that shape phenotypic variation across plants and animals.

Mapping the functional landscape of complex trait heritability in dairy cattle

ABSTRACT SELECTED TALK

Jicai Jiang[1], Junjian Wang[1], Yahui Gao[2], Sajjad Toghiani[3], Dailu Guan[4], Huaijun Zhou[4], John B. Cole[5], Christian Maltecca[1], Li Ma[2]

1. North Carolina State University, Department of Animal Science, Raleigh, NC, USA
2. University of Maryland, Department of Animal and Avian Sciences, College Park, MD, USA
3. United States Department of Agriculture, Agricultural Research Service (USDA-ARS), Animal Genomics and Improvement Laboratory, Beltsville, MD, USA
4. University of California, Department of Animal Science, Davis, CA, USA
5. Council on Dairy Cattle Breeding, Bowie, MD, USA

Integrating functional annotations into genome-to-phenome studies remains challenging in farm animals. Stratified LD score regression relies on approximations for human populations and fails under strong linkage disequilibrium. Genomic feature BLUP models typically accommodate only two annotation categories at a time, failing to account for confounding effects among multiple annotations. Furthermore, we found that large-effect QTLs distort heritability partitioning in multi-component genomic REML models. Their effects can be incorrectly absorbed by small functional categories, severely inflating variance estimates for these categories.

We developed a unified framework with two complementary approaches. GEMRICH, our newly developed R package, estimates enrichment of causal variants in functional annotations based on statistical fine-mapping of significant association regions. MPH, a fast REML implementation, enables simultaneous heritability partitioning across many functional annotations while modeling fine-mapped lead variants as fixed effects, preventing large-effect QTLs from inflating polygenic variance estimates. This quantifies genetic architecture comprehensively: causal variant enrichment in significant regions and per-SNP heritability enrichment of sub-threshold polygenic effects. Simulation analyses confirmed this strategy eliminates bias in heritability partitioning caused by large-effect QTLs.

We analyzed 38 dairy cattle traits using ~50,000 Holstein bulls with 11 million imputed sequence variants. Analysis across genic regions, evolutionarily constrained elements, cis-eQTLs and cis-sQTLs, chromatin states, and ATAC-seq peaks from over 40 tissues revealed substantial heritability enrichment (e.g., 5–10-fold in coding sequences, ~10-fold in constrained elements, and 2–5-fold in regulatory regions). Tissue-specific analyses revealed particularly strong enrichment in mammary tissue annotations for yield traits, and bone marrow annotations showed broad relevance across diverse dairy traits. Incorporating functional enrichments into genomic prediction improved accuracy over chip-SNP-based GBLUP by 1.17% on average across 36 traits (two traits excluded due to insufficient validation bulls), with gains of up to 3.42% for cow livability, using old–young validation with December 2020 training and December 2021 validation data. To enable broad adoption, we released open-source software tools at github.com/jiang18/gemrich and jiang18.github.io/mph.

Precise gene expression tuning via cis-regulatory element editing in *Sorghum bicolor* for optimizing photosynthesis

POSTER

132

Amala John[1,2], Evan D. Groover[1,2], David Ding[2,3], Flora Z. Wang[1,2], Jianqiang Shen[1,2], Peggy G. Lemaux[1,2], David F. Savage[2,3,4], Krishna K. Niyogi[1,2,4]

1. University of California, Department of Plant and Microbial Biology, Berkeley, CA, USA
2. University of California, Innovative Genomics Institute, Berkeley, CA, USA
3. University of California, Department of Molecular and Cellular Biology, Berkeley, CA, USA
4. University of California, Howard Hughes Medical Institute, Berkeley, CA, USA

Extensive research has uncovered targets for genetic manipulation of crop plants, but the lack of tools to predictably fine-tune gene expression, rather than simply mutate or overexpress genes, limits our ability to optimize complex traits in crops. We use a novel pipeline that circumvents some of the regulatory and technical hurdles of developing transgenic plants and allows us to make precise edits to *cis*-regulatory elements (cREs) to alter gene expression in predictable ways. This method involves screening synthetic promoter mutant libraries in Sorghum protoplasts to determine the regulatory landscape of our target gene by uncovering activating and repressive regions within the 2 kb upstream promoter region. By screening CRISPR-inspired variants of promoters, including insertions, deletions and SNPs, we identify promising mutations to generate via genome editing in Sorghum plants. We aim to optimize photoprotective nonphotochemical quenching (NPQ) mechanisms that regulate photosynthetic light harvesting in plants. NPQ is a promising target because slow NPQ dynamics result in competition between photoprotection and photosynthesis. Several studies have shown that overexpression of *PSBS*, in combination with other genes, improves NPQ kinetics, water use efficiency, carbon assimilation and crop yield. We focus our efforts on generating mutations in a repressive hotspot identified from the promoter library screen in the *SbPSBS* promoter to increase its expression, and subsequently measure gene expression, protein levels and NPQ dynamics. Beyond its relevance in optimizing photosynthetic efficiency, this study demonstrates a scalable pipeline for identifying and editing specific cREs to fine-tune gene expression, providing a generalizable framework for improving plant performance and other traits in crops.

Functional introgression within the horse MHC genes

POSTER

133

Lauren Johnson[1], Ernest Bailey[1], Ted Kalbfleisch[1]

1. University of Kentucky, Maxwell H. Gluck Equine Research Center, Lexington, KY, USA

Introgression is the transfer of genetic material between species through repeated backcrossing of interspecific hybrids with one parental species. These events play a critical role in molecular evolution by enabling the rapid spread of pre-adapted alleles across species boundaries, effectively accelerating adaptation. In this study, we investigate historical introgression in equids as a mechanism contributing to pathogen recognition diversity. To mitigate reference bias, we leveraged multiple equine genome assemblies and analyzed a population of 230 Thoroughbreds using a novel statistical approach. This analysis identified approximately 50 loci within the major histocompatibility complex (MHC) region. The MHC was targeted due to its central role in immune function and pathogen identification, which is essential for species survival. Of the identified loci, 15 exhibited coding consequences, while the remaining variants were intronic, as annotated by Ensembl's Variant Effect Predictor (VEP). The prevalence of intronic variants suggests regulatory effects, while coding variants likely contribute to functional diversity in pathogen recognition. Previous work estimates divergence within the *Equus* genus at approximately 4–5 million years ago (Orlando et al., 2013). However, phylogenetic analyses generated using BEAST2 and published mutation rates (Furukawa et al., 2025; Librado et al., 2024) indicate that introgression events persisted until roughly 1 million years ago. This timing postdates the onset of major chromosomal rearrangements in equids approximately 2 million years ago (Jonsson et al., 2014), suggesting that gene flow occurred despite increasing reproductive barriers. These introgression events were likely mediated by one or more now-extinct *Equus* species. Recent reconstruction of the Grevy's zebra–ass clade provides a potential framework for identifying this extinct facilitator (Cirilli et al., 2021). Given the present-day reproductive isolation between caballine and non-caballine equids, studying historical introgression offers a valuable model for understanding cross-species gene flow and its potential applications in future gene-editing strategies. Introgression within horses, particularly in the Thoroughbred, helps resolve evolutionary relationships and highlights how shared alleles can promote rapid adaptation to emerging pathogens and environmental pressures through changes in gene function or regulation.

POSTER

134

Genomic divergence between circulating and vaccine Rift Valley Fever virus strains and implications for vaccine design

John Juma[1], Samson Konongoi[2], Houriiyah Tegally[3], Rosemary Sang[2], Tulio de Oliviera[3], Alan Christoffels[4], Bernard Bett[1], Samuel Oyola[1]

1. International Livestock Research Institute (ILRI), Health Program, Nairobi, Kenya
2. Kenya Medical Research Institute (KEMRI), Centre for Virus Research, Nairobi, Kenya
3. Stellenbosch University, Centre for Epidemic Response and Innovation (CERI), School of Data Science and Computational Thinking, Stellenbosch, South Africa
4. University of the Western Cape, South African National Bioinformatics Institute (SANBI), Cape Town, South Africa

Rapid evolution of Rift Valley fever virus (RVFV) strains poses a significant challenge to the effectiveness of existing vaccines, underscoring the urgent need for genome-informed vaccine design. Rift Valley fever (RVF) is a climate-sensitive zoonotic disease with substantial epidemic potential and the capacity to establish endemicity in regions previously considered virus-free. RVFV is a single-stranded RNA virus with a tripartite genome comprising large (L), medium (M), and small (S) segments that encode proteins essential for viral replication, infection, and virulence. Although several vaccines are available for livestock, their effectiveness in controlling RVF in endemic settings remains limited, and no licensed vaccines currently exist for human use. In this study, we conducted comprehensive mutational and phylogenetic analyses to characterize genetic differences between circulating RVFV strains and commonly used vaccine isolates. Phylogenetic reconstruction revealed distinct clustering of circulating strains separate from vaccine strains, indicating substantial genomic divergence. Circulating RVFV lineages exhibited extensive mutational accumulation, reflecting high genomic variability. Notably, we observed an elevated frequency of C→T and A→G transitions between circulating strains and the Smithburn, MP-12, and Clone 13 vaccine strains, consistent with potential cytosine deaminase–mediated editing. Mutational profiling identified vaccine-specific amino acid substitutions, including H259Y and G1182R in the glycoproteins, and A172V and I1244M in the RNA-dependent RNA polymerase (RdRp). Shared substitutions among vaccine strains were also detected, including S278N in RdRp and D95, I602V, and V659A in the glycoproteins. Selection pressure analyses revealed evidence of positive (diversifying) selection acting on several key residues. Additionally, we mapped N-glycosylation sites across structural (glycoproteins and nucleoprotein) and non-structural (RdRp) proteins, identifying host-specific N-glycosylated sites at Asn-88 in RdRp and Asn-517 in glycoproteins among human-derived strains. Collectively, these findings provide critical insights into RVFV genomic evolution and vaccine–strain mismatches, offering a robust foundation for the rational design of next-generation vaccines with improved efficacy against circulating RVFV strains, particularly in endemic regions.

Phylogenetic and functional analysis of tiller angle control homeologs in allotetraploid cotton

POSTER

135

Foster Kangben[1], Sonika Kumar[1], Zhigang Li[1], Avinash Sreedasyam[2], Chris Dardick[3], Don Jones[4], Chris Saski[1]

1. Clemson University, Clemson, SC, USA
2. HudsonAlpha Institute for Biotechnology, Huntsville, AL, USA
3. United States Department of Agriculture, Agricultural Research Service (USDA-ARS), Appalachian Fruit Research Station (AFRS), Kearneysville, WV, USA
4. Cotton Incorporated, Cary, NC, USA

Plants can adapt their growth to optimize light capture in competitive environments, with branch angle being a crucial factor influencing plant phenotype and physiology. Decreased branch angles in cereal crops have been shown to enhance productivity in high-density plantings. The Tiller Angle Control (TAC1) gene, known for regulating tiller inclination in rice and corn, has been found to control branch angle in eudicots. Manipulating TAC1 in field crops like cotton offers the potential for improving crop productivity. Gene duplication events of TAC1 specific to the Gossypium lineage were identified, with 6 copies in allotetraploid cottons. Sequence analysis of the TAC1 homeologs in Gossypium hirsutum revealed divergence from other angiosperms with 1-2 copies, suggesting possible neo- or sub-functionalization for the duplicated copies. These TAC1 homeologs exhibited distinct gene expression patterns in various tissues over developmental time, with elevated expression of A11G109300 and D11G112200, specifically in flowers and stems, respectively. CRISPR-mediated loss of these TAC1 homeologous genes resulted in a reduction in branch angle and altered petiole angles and a 5 to 10-fold reduction in TAC1 expression in the mutants, confirming their role in controlling branch and petiole angles. This research provides a promising strategy for genetically engineering branch and petiole angles in commercial cotton varieties, potentially leading to increased productivity.

Cell-type–resolved gene expression signatures to identify and predict persistent PRRSV infection

POSTER

136

Mehak Kapoor[1], Chi Chen[2], Akhila Naru[2], Courtney Hayes[3], Nicole Herndon[3], Crystal Loving[4], Jack Dekkers[1a], Christopher K. Tuggle[1a], Ying Fang[2a]

1. BCB Interdepartmental Program and Iowa State University, Department of Animal Science, Ames, IA, USA
2. University of Illinois at Urbana-Champaign, Department of Pathobiology, Urbana, IL, USA
3. University of Illinois at Urbana-Champaign, Department of Veterinary Clinical Medicine, Urbana, IL, USA
4. United States Department of Agriculture, Agricultural Research Service (USDA-ARS), Ames, IA, USA

[a]Co-corresponding authors

Porcine reproductive and respiratory syndrome virus (PRRSV) poses a unique industry challenge due to immune evasion, causing persistent infection. This study aims to identify cell-type specific molecular markers to improve prediction of PRRSV persistence or extinction, which is observed in a minority of animals. We used single cell RNA sequencing (scRNA) to characterize blood cells collected at 14- and 84-days post-infection (DPI) from pigs challenged with PRRSV. Infected pigs were grouped as having persistently infected (PI) or virus extinction (VE) phenotypes based on viral RNA detection at 84DPI, with control as mock-infected (MI).

Focusing on monocytes hereafter; neighborhood-level differential abundance (DA) at both 14 and 84DPI revealed significant differences between MI compared to both VE and PI phenotypes. In contrast, no significant DA was detected between VE and PI pigs, indicating that early divergence between infected phenotypes is driven by transcriptional programs rather than composition. To assess reliability, we compared scRNA-derived proportions with matched flow cytometry proportions. Strong correlations were observed, with higher concordance at 14DPI than at 84DPI.

Consistent with DA patterns, monocyte transcriptional programs diverged early and evolved over time. At 14DPI, monocytes from VE pigs displayed activation of antiviral and interferon response genes (*OAS2*, *ISG15*, *IFI6*) compared to PI pigs, reflecting a controlled, effective immune response promoting viral clearance. By 84DPI, VE monocytes transitioned towards immune homeostasis, whereas PI monocytes had a profile consistent with sustained inflammation, suggesting that major differences between PI and VE arise from immune resolution that is uniquely activated in VE pigs. To explore unique early and late PRRSV immune responses, we performed comparative enrichment and pathway analyses between PI and VE pigs and found 592 differentially expressed genes (DEGs) that responded only in VE pigs at 14DPI. These unique responses were active in tuning immune signals to resolve inflammation; enabling prioritization of early cell-type–specific candidate monocyte biomarkers associated with viral clearance.

Translating sequencing innovation into practice: a scalable genotyping platform for working dogs

ABSTRACT SELECTED TALK

Elinor Karlsson[1,2], Vista Sohrab[1,2], Kate Megquier[2], Jane Russenberger[3], Madeline Zimmermann[3], Brittney Kenney[1,2], Shauneen O'Neill[3], Eldin Leighton[4], Breno Fragomeni[3], Elinor Karlsson[1,2]

1. UMass Chan Medical School, Genomics and Computational Biology, Worcester, MA, USA
2. Broad Institute of MIT & Harvard, Vertebrate Genomics, Cambridge, MA, USA
3. University of Connecticut, Animal Science, Storrs, CT, USA
4. International Working Dog Registry, San Antonio, TX, USA

Working dogs play critical roles across agriculture, security and defense, assistance work, detection, and as valued companions. Despite expanding demand, the supply of healthy, high-performing, purpose-bred dogs remains far below need, and traditional phenotypic selection has proven insufficient for improving the complex behavioral, health, and performance traits required for working dog success. A major barrier has been the lack of an affordable, scalable genotyping solution that can be integrated into routine breeding workflows while also generating genomic data needed for discovery, genomic evaluation, and future genomic selection.

Here we present a dual-purpose genotyping platform that combines low-pass whole-genome sequencing suitable for high-density genotype imputation with targeted capture, which provides deep sequencing coverage and high-accuracy genotypes, without imputation, at disease- and trait-associated loci used in breeding decisions.

We designed a custom capture panel in collaboration with Twist Bioscience targeting 361 variants, including routinely screened disease variants, aesthetic trait variants, and candidate disease-risk loci. The platform was evaluated in a pilot cohort of 286 dogs spanning multiple breeds and organizations. Using a Twist hybrid capture workflow sequenced on Illumina platforms, 93.6% of targeted sites achieved greater than 150x coverage (mean 289x), while low-pass whole-genome sequencing achieved a mean genome-wide depth of 1.68x, sufficient for high-quality imputation. We validated the accuracy of the targeted sequencing using samples from dogs known to carry variants associated with early onset blindness, copper toxicosis, and exercise induced collapse.

To improve scalability of the combined approach, we evaluated the Element Biosciences Trinity hybrid capture workflow, which performs hybrid capture directly on the sequencing flow cell, simplifying target enrichment and substantially reducing turnaround time. The Trinity workflow achieved mean genome-wide coverage closer to the 1x target (1.1x) and higher mean coverage at targeted loci (353x). Genotype calls between Illumina- and Element-based workflows were 99.9% concordant, demonstrating technical equivalence while enabling a simpler, more scalable workflow. We are now integrating this tool into genetic-testing workflows used by working dog organizations through the International Working Dog Registry and the International Breeding Cooperative.

A near-perfect T2T genome assembly for the Alpine chamois: manual curation, progress, and challenges

POSTER

138

Sarem Khilji[1], Benjamin D. Rosen[2], Gabrielle A. Hartley[3], Nicole Pauloski[3], Rachel J. O'Neill[3], Timothy P.L. Smith[4], Kristen L. Kuhn[4], Stephanie D. McKay[5], Brenda M. Murdoch[1]

1. University of Idaho, Department of Animal, Veterinary, and Food Sciences, Moscow, ID, USA
2. United States Department of Agriculture, Agricultural Research Service (USDA-ARS), Animal Genomics and Improvement Laboratory, Beltsville, MD, USA
3. University of Connecticut, Institute for Systems Genomics, Storrs, CT, USA
4. United States Department of Agriculture, Agricultural Research Service (USDA-ARS), U.S. Meat Animal Research Center, Clay Center, NE, USA
5. University of Missouri, Columbia, Division of Animal Sciences, Columbia, MO, USA

Telomere-to-telomere (T2T) genome assemblies are transforming genomics by resolving repetitive and structurally complex regions that current reference genomes lack. However, high quality T2T assemblies are largely restricted to model organisms and domesticated animals. Closing this gap is especially pressing for wildlife species, where T2T reference genomes could illuminate the genetic basis of adaptation and inform conservation efforts. The Alpine chamois (*Rupicapra rupicapra*) is a wild caprine adapted to extreme mountainous environments across Europe and Asia and has been included as one of the primary species in the ruminant T2T initiative (RT2T).

Our current draft assembly consists of 21 and 17 T2T contigs and a total of 22 and 23 scaffolds across two haplotypes, with 50 and 51 telomeres identified. This brings both haplotypes close to T2T complete across the expected 28 autosomes and the X and Y chromosomes. A total of 14 gaps were initially present across the two haplotype assemblies. Some of these gaps largely arise from challenges associated with phasing without trio data. In the absence of parental information, haplotype separation relies entirely on read-level heterozygosity, which can be insufficient in regions of low diversity or high repeat density, occasionally leading to haplotype switches or collapsed heterozygous loci. These challenges are being addressed through targeted manual curation and careful read-alignment validation, guided by comparisons across multiple assembly versions incorporating different combinations of HiFi, ONT, and Hi-C data, to ensure the most accurate haplotype representation. However, of the 14 gaps, ongoing manual curation has left only eight remaining.

Curation efforts are focused on three critical challenges: filling small sequence gaps by bridging incomplete contig junctions; resolving tangled/repetitive regions, including ribosomal DNA arrays prone to tangling; and correctly assigning telomeric contigs at chromosome ends using repeat motifs. Genome graph visualization and targeted read-alignment inspection help guide each curation step, ensuring structural integrity across complex loci.

This assembly will establish the first near-complete T2T reference assembly for chamois, supporting studies of alpine adaptation, population structure, and comparative genomics across Caprinae, while demonstrating the feasibility of T2T assembly for wildlife species.

ABSTRACT SELECTED TALK

U.S. Food and Drug Administration (FDA) and U.S. National Institute of Standards and Technology (NIST) collaboration: evaluation of assays and control materials for characterizing animal biotechnology products generated by genome editing

Patricia Kiesler[1], Natalia Kolmakova[1], Sierra Miller[1], Ayah Shevchenko[1], Stella S. Lee[2], Ashley L. Cook[2], Alexis L. Norris[2], Mayumi F. Miller[3], Carlo J. Mercado[2], Adam L. Moyer[2], Samantha Maragh[1]

1. National Institute of Standards and Technology (NIST), Biosystems and Biomaterials Division, Gaithersburg, MD, USA
2. U.S. Food and Drug Administration (FDA), Center for Veterinary Medicine, Office of New Animal Product Evaluation, College Park, MD, USA
3. Office of Applied Science, Laurel, MD, USA

Genome editing technology has revolutionized the ability to make targeted changes to an animal's genome (intentional genomic alterations [IGAs]), offering promise for the development of animal biotechnology products that address animal and public health needs. Characterization of these IGAs is an important part of the regulatory process to ensure that the edit to the animal is as intended and to identify any unintended genomic alterations. However, there are currently no validated measurements and standards for characterizing unintended genomic alterations in animals. FDA-CVM has established a collaboration with NIST to generate resources for characterizing both intended and unintended genomic alterations in animal biotechnology products resulting from genome editing. These resources will provide developers and FDA regulators with example characterization approaches that they could use as part of the development and regulatory process for IGAs in animals as well as for validating methods, materials, and data.

NIST qualified commercially available porcine and bovine cell lines as potential control materials by characterizing their DNA sequences at on-target and potential off-target loci before and after CRISPR/Cas9 genome editing. Multiple guides targeting porcine or bovine safe harbor loci were studied, including one newly developed by NIST that targets both species. The off-target analyses performed to characterize unintended alterations include comparisons between off-target loci identified by *in silico* methods (Cas-OFFinder, CCtop, CHOPCHOP, COSMID and CRISPOR), biochemical assays (CHANGE-seq and SITE-Seq), and a cell-based assay (GUIDE-seq-2), and assessment of editing at nominated off-target loci in edited animal cells through rhAmpSeq analyses. Off-target assays exhibited reproducibility, with similar performance demonstrated on animal samples as compared to human samples. Preliminary outcomes of comparative analyses identified off-target sites that were nominated across multiple nomination methods; however, many off-targets were nominated by a single method. The rhAmpSeq analyses identified reproducible off-target editing in edited cells, albeit at low levels. Future work involves expanding off-target analyses to identify reasons that may explain the discordance observed across off-target sites nominated by various methods. Resulting protocols and datasets will be published and made accessible to developers and the general public.

Toward a pangenome annotation of rainbow trout

POSTER

139

Johnny Konvalina[1], Yniv Palti[1], Christine Elsik[2], Gregory Wiens[1], Guangtu Gao[1]

1. United States Department of Agriculture (USDA), Auburn, AL, USA
2. University of Missouri, Columbia, MO, USA

Rainbow trout (Oncorhynchus mykiss) is an important model for salmonid biology and a key species in global aquaculture, yet existing genome annotations are largely based on single reference assemblies and do not capture the full extent of genomic diversity within the species. Here, we present a comprehensive pangenome annotation generated from four current rainbow trout genome assemblies. Each assembly was independently annotated using a unified pipeline integrating EGAPx and BRAKER3, with full-length transcript evidence from PacBio Iso-Seq data to improve gene model accuracy, alternative isoform resolution, and annotation completeness. To assess genome conservation and structural relationships among assemblies, we performed synteny analyses using MCScanX, enabling the identification of conserved gene blocks and assembly-specific rearrangements. The resulting annotations and synteny relationships were integrated into a genome browser with customizable tracks, allowing interactive visualization and comparative exploration across assemblies. This pangenome annotation framework provides an expanded and harmonized view of gene content, structural variation, and transcript diversity in rainbow trout, offering a valuable resource for functional genomics, evolutionary studies, and applied breeding research.

Machine learning reveals predictive features of gene co-expression within topologically associating domains in rice

POSTER

140

Amina Kurbidaeva[1], **Michael Purugganan**[1]

1. New York University, Center for Genomics & Systems Biology, New York, NY, USA

Three-dimensional genome organization through Topologically Associating Domains (TADs) represents a critical yet underexplored regulatory layer in crop genomics. In rice, TADs may compartmentalize co-regulated gene clusters underlying agronomically important traits, including coordinated stress responses, grain quality pathways, and developmental timing programs. Identifying which molecular features govern within-TAD co-expression could enable breeders to predict the regulatory consequences of structural variants that disrupt TAD boundaries, a growing concern as pangenome studies reveal extensive chromosomal rearrangements across rice cultivars. Moreover, understanding co-expression architecture at the TAD scale may inform strategies for synthetic biology and gene stacking, where maintaining coordinated expression of introduced gene cassettes is essential for trait stability across environments.

We systematically assessed whether TAD-level molecular features predict gene co-expression variability in *Oryza sativa* (cv. Nipponbare). Using TADs identified from Micro-C data at 5 kb resolution, we computed the coefficient of variation (CV) of gene expression within each TAD as a co-expression measure. We assembled a comprehensive feature matrix encompassing TAD structural properties, mean expression level, histone modifications (H3K4me3, H3K18ac, H3K27me3, H3K27ac), chromatin accessibility (ATAC-seq), DNA methylation, GC content, evolutionary conservation (PhastCons), regulatory potential (PRO-seq), and genomic variant densities (SNP, SV, TE). Modeling rounds employing regression, classification, and LOESS-based residual regression strategies were conducted with systematic feature ablation across up to 18 algorithms.

Our best classifier (Random Forest, AUC = 0.80) distinguished TADs with high versus low co-expression when expression level and gene count were included. Removing these features collapsed performance to near-chance levels. Critically, LOESS-based residual regression demonstrated that all remaining epigenomic features collectively explained only 1–3% of residual variance, rigorously validated by showing negligible improvement upon re-introducing expression level (ΔR^2 = +0.006).

These findings establish that within-TAD co-expression in rice is predominantly governed by expression level and gene density rather than the chromatin landscape. For crop improvement, this implies that TAD-level chromatin signatures alone are insufficient proxies for predicting co-expression modules. Breeding programs targeting co-regulated gene clusters, particularly for multigenic traits like drought tolerance or nitrogen use efficiency, will require higher-resolution data, including gene-level chromatin profiling, enhancer–promoter contact maps, and single-cell transcriptomics, to decode the regulatory logic governing coordinated expression in crop genomes.

POSTER

141

Scalable Genotyping by Sequencing (GBS) using low-pass whole genome sequencing (lpWGS) and a one-step, TnX™ transposase-based library prep method for genomic selection

Jack Leonard[1], Michelle Rahardja[1], Rebecca Feeley[1], Jenna Couture[1], Yanyan Liu[1], Stella Huang[1], Jack Leonard[1], Maura Costello[1], Joe Mellor[1]

1. seqWell, Inc., Beverly, MA, USA

The use of genomic prediction in agriculture has proven to be an effective strategy for accelerating breeding programs by enabling rapid and cost-efficient assessment of genetic potential. Genome-wide genotypes of sufficient density and accuracy can substitute for extensive phenotypic data collection, significantly shortening selection cycles. Several sequencing-based methods have been adopted to generate genotypes for these applications. Here we present a low-pass whole genome sequencing (lpWGS) workflow optimized for agricultural genomics for high-throughput, low-coverage genotyping in plant species of agricultural relevance.

We evaluated the performance of AgriPrep, a one-step library preparation method, for lpWGS. As a proof of concept, genomic DNA from soybean, rice, and barley was processed using AgriPrep at various input, generating three normalized 6-plex library pools. Libraries were sequenced on an Illumina NovaSeq X Plus (2 × 150 bp), producing >2x coverage. Sequencing reads were aligned to their respective reference genomes. Datasets were downsampled to 0.1x to 2x coverage prior on variant calling and imputation to evaluate performance across coverage depths. Genotype imputation was performed using Gencove analysis platform. The genotype accuracy was calculated.

Our results demonstrate the robustness of AgriPrep for routine low-pass WGS in crop species, providing highly uniform multiplexing performance and accurate genotype imputation. This workflow supports the cost-effective generation of genomic data for large-scale breeding and genomic selection initiatives across diverse plant species.

Sparse testing strategies to increase genetic gains in *Miscanthus* breeding program

ABSTRACT SELECTED TALK

Nelson Lubanga[1], Chris Davey, Iain Donnison[1], Beatrice Ifie[1], Gancho Slavov[1,2], Kerrie Farrar[1], Diego Jarquin[3]

1. Aberystwyth University, Institute of Biological, Environmental and Rural Sciences, Aberystwyth, United Kingdom
2. Oregon State University, Department of Forest Engineering, Resources, and Management, Corvallis, OR, USA
3. University of Florida, Agronomy Department, Gainesville, FL, USA

Miscanthus is a fast-growing perennial grass that can grow across a wide range of environments and provide a sustainable source of ligno-cellulosic biomass. Genotype × environment (G×E) interaction is a major challenge in plant breeding, as it results in differential genotype performance across environments, often leading to changes in their relative rankings. Multi-environment trials (METs) facilitate the assessment of genotype stability through the analysis of G×E. However, field testing in METs is costly, and seed availability may be insufficient to evaluate same genotypes in all target environments. Sparse testing is an approach in which field evaluation of genotypes is unreplicated or partially replicated across environments. In this study, 125 genotypes were selected as the training set, and evaluated for three traits (dry matter, DM; fresh weight, FW; moisture content, MC) across five environments. Three models, M1 (Environment + Genotype), M2 (Environment + Genotype + Genomic), and M3 (Environment + Genotype + Genomic + Genomic × Environment interaction) were tested under two cross-validation (CV) schemes. CV1 predicts the performance of newly developed genotypes, whereas CV2 predicts the performance of genotypes tested in sparse multi-location trials. Additionally, various proportions of non-overlapping (NOL) relative to overlapping (OL) genotypes were randomly selected, and their predictive performance was subsequently evaluated. Our results showed that predictive ability was higher when predicting genotypes under sparse testing (CV2) than when predicting newly developed genotypes (CV1). However, the advantage of incorporating G×E was more pronounced under CV1 than in CV2. Sparse testing can be effectively implemented in the *Miscanthus* breeding program by using completely NOL genotypes across target environments. This enables the assessment of a larger number of genotypes across multiple environments, reducing trial costs while maintaining the selection accuracy. Sparse testing is particularly effective in the early stages of evaluation in *Miscanthus*, where the number of seedlings is limited, allowing for efficient assessment without the need to test every genotype in all environments.

Fiber-seq: a long-read protein footprinting assay for resolving multiomic regulatory architecture

POSTER

143

Keith E. Maier[1], James T. Anderson[1], Connor P. Frasier[1], Allison R. Hickman[1], Sabrina R. Hunt[1], Zu-Wen Sun[1], Martis W. Cowles[1], Andrew Stergachis[2], Bryan J. Venters[1], Michael-Christopher Keogh[1]

1. EpiCypher Inc, Durham, NC, USA
2. University of Washington, Division of Medical Genetics, Department of Medicine, Seattle, WA, USA

Gene regulation arises from coordinated interactions among DNA sequence, chromatin accessibility, DNA methylation, nucleosome positioning, and transcription factor occupancy. These regulatory features are typically measured using separate short-read assays, fragmenting regulatory information and separating co-occurring regulatory features across experiments. This fragmentation obscures how regulatory elements function together along individual DNA molecules and limits reconstruction of long-range cis-regulatory architecture. These limitations are particularly pronounced in complex and repetitive genomes, where regulatory elements frequently occur in structurally challenging regions that are poorly resolved by short-read approaches.

Fiber-seq is a long-read, single-assay multiomic method that preserves regulatory context across individual DNA molecules by integrating chromatin accessibility footprinting with native long-read sequencing. Accessible adenines are enzymatically methylated with Hia5, an N6-adenine methyltransferase, and sequenced alongside endogenous 5mC cytosine methylation using native PacBio or Oxford Nanopore Technologies (ONT) sequencing platforms.

Fiber-seq recapitulates accessibility patterns observed with conventional assays while revealing chromatin architecture that is collapsed in short-read data. By labeling individual accessible bases, Fiber-seq enables direct protein footprinting at a resolution not achievable with fragment-based accessibility assays such as ATAC-seq. Single-molecule profiles reveal heterogeneous protein occupancy across individual DNA molecules, enabling detection of nucleosome positioning, transcription factor binding, and polymerase II recruitment at active promoters.

By distinguishing protected from accessible motifs within motif-dense regions, Fiber-seq enables composite motif analysis that prioritizes candidate regulatory elements and transcription factors for functional validation. These capabilities provide a framework for decoding cis-regulatory grammar and enabling functional interpretation of non-coding variation in complex plant and animal genomes.

Lifetime Net Merit Index and the correlated response on enteric methane emissions

ABSTRACT SELECTED TALK

Guillermo Martinez-Boggio[1], John B. Cole[2], Juan M. Tricarico[3], Kent A. Weigel[4], Francisco Peñagaricano[4]

1. University of California, Department of Animal Science, Davis, CA, USA
2. Council on Dairy Cattle Breeding, Bowie, MD, USA
3. Dary Management Inc., Rosemont, IL, USA
4. University of Wisconsin, Department of Animal and Dairy Sciences, Madison, WI, USA

Genetic selection is a potent tool for achieving lasting gains in environmental sustainability. However, the impact of genetic selection on reducing the environmental footprint of dairy farming is not well documented to stakeholders, consumers, and society. Therefore, there is a critical need to understand what the dairy industry has achieved through selective breeding in reducing the environmental impact of dairy farming. We aim to quantify reductions in methane emissions over the last 50 years using USDA selection indices. We evaluated 12 different selection indices from 1971 to the 2025 Lifetime Net Merit Index (NM$). From them, we calculated response to selection for 24 traits and type composites, as well as three methane-emission traits: methane production (CH4, g/d), residual methane intensity (RMI), and residual methane yield (RMY). The RMI was calculated as CH4 production adjusted for milk energy and metabolic body weight, and the RMY was calculated as CH4 production adjusted for dry matter intake. Correlated responses were calculated as a function of the genetic and phenotypic correlations among the traits in the objective and the criterion, and the index weights using an extension of the breeder's equation. The heritability, genetic and phenotypic correlations for milk, fat, and protein yields, residual feed intake (RFI), and methane traits (CH4, RMI, and RMY) were estimated using a dataset of 1,980 lactating Holstein cows. For traits not available in our dataset, we calculated correlations among gPTAs from CDCB. We observed a consistent decline in the correlated response in CH4 production, from 6.28 in 1971 to 1.26 PTA change/year in 2025. Similarly, we observed a consistent decline in the correlated response in residual methane traits, RMI from 1.36 (1971) to -0.48 PTA change/year (2025), and RMY from 1.30 (1971) to 0.98 PTA change/year (2025). Overall, our results indicate that changes in NM$ over the past five decades, particularly the inclusion of body size and residual feed intake, have led to a marked decrease in the correlated response in CH4 traits. The inclusion of CH4 traits into U.S. selection indices in the near future will undoubtedly further reduce the environmental impact of dairy farming.

Population genomics of East African finger millet identifies genomic regions shaped by extended selection

POSTER

147

Susan Moenga[1], Emmanuel Ejiet[2], Damaris Odeny[1]

1. International Crops Research Institute for the Semi-Arid Tropics, Trait Discovery and Delivery, Nairobi, Kenya
2. Ministry of Agriculture, Animal Industry and Fisheries, Entebbe, Uganda

Finger millet (*Eleusine coracana* (L.) Gaertn.; 2n = 4x = 36) is an allotetraploid cereal domesticated in East Africa and widely cultivated in low-input, stress-prone agro-ecologies. Despite its importance for food security, nutritional quality, and environmental resilience, genome-scale characterization of the crop has lagged behind that of major cereals, limiting the application of population genomics and genomics-assisted breeding approaches. Here, we present a genome-wide analysis of East African finger millet germplasm to characterize population structure, genetic diversity, and signatures of selection relevant to conservation and breeding.

A large, geographically diverse panel of accessions from Kenya, Ethiopia, Tanzania, and Uganda was analyzed using high-density SNP markers. Genome-wide diversity metrics, multivariate ordination, discriminant clustering, linkage disequilibrium analyses, and selection scans were applied to resolve evolutionary structure and identify genomic regions shaped by selection. Pronounced geographic structuring of genetic variation was detected across East Africa, with country-associated genomic signatures and substantial heterogeneity in within-country diversity, particularly in Kenya. Overall population differentiation is low to moderate, consistent with recent divergence and historical gene flow, yet distinct regional gene pools persist, reflecting localized evolutionary trajectories. Patterns of genetic diversity, linkage disequilibrium, and selection are broadly comparable between the two subgenomes, consistent with long-term maintenance of functional allotetraploidy. Genome-wide linkage disequilibrium is extensive over large physical distances, reflective of a predominantly self-pollinating system and domestication-associated bottlenecks with implications for association mapping resolution and the design of genomic selection strategies. Selection scans identify numerous genomic regions exhibiting signatures of selection, including non-randomly distributed selective sweeps spanning broad chromosomal intervals, notably on chromosome 7A, suggesting recurrent selection pressures likely driven by local adaptation and farmer-mediated selection.

Together, these findings establish a robust population genomic framework for East African finger millet, identify genomic regions shaped by extended selection, and delineate genetically distinct populations of high priority for conservation and pre-breeding.

From local records to global impact: integrating farmer-led data and genomics in livestock systems for LMICs

ABSTRACT SELECTED TALK

Enrique Sanchez-Molano[1], Robert Mukiibi[1], Valentina Riggio[1], Joel Ogwang[2], Leonard Kawule[3], Katali Benda[2], Peter Beine[2], Barend M. de Clare Bronsvoort[1], James Prendergast[1], Andrea B. Doeschl-Wilson[1], Adrian Muwonge[1]

1. The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, Midlothian, United Kingdom
2. National Animal Genetic Resources Centre and Data Bank, Entebbe, Uganda
3. Vetline Services Ltd., Kampala, Uganda

Sustainable improvement of livestock in low and middle-income countries (LMICs) depends on breeding strategies that effectively balance increased productivity with resilience, and the preservation of genetic diversity over time. In the absence of centralised recording systems, information gathered through veterinary visits and directly from farmers is often the only source of usable data. Therefore, the development and maintenance of farmer-led databases are essential for capturing and retaining this information, also empowering farmers to participate directly in breeding decisions.

We recently showed the usefulness of such databases by integrating them with genomic data from both crossbred and purebred dairy cattle in Kampala, Uganda. Using high-density SNP genotypes from crossbred, exotic and indigenous animals, we characterised population structure, admixture patterns, genetic diversity, and inbreeding, and linked these genomic insights to disease records collected through a farmer-led digital platform. Ugandan crossbred cattle exhibited high levels of exotic introgression, primarily from Holstein and Jersey breeds, alongside lower levels of homozygosity and inbreeding compared with indigenous or intensively selected exotic populations. While this genetic diversity reflects recent crossbreeding practices aimed at improving productivity, it also implies substantial heterogeneity among animals and potential maladaptation, underscoring the need for informed, locally adapted breeding strategies.

We also explored associations between breed composition and disease occurrence in crossbred animals. Although our statistical power was constrained by limited sample size and unbalanced disease records, we observed clear evidence of survivor bias for East Coast fever, a lethal disease to exotic cattle. Animals with higher levels of exotic ancestry were strongly under-represented among recorded cases, likely because the most susceptible individuals had already been infected and died before sampling. This highlights the need for farmer-led data collection that is both systematic and longitudinal; without it, inferences about disease risk and breed suitability may be misleading, especially in high pressure environments.

In summary, farmer-led databases combined with genomics provide cost-effective tools to improve understanding of genetic susceptibility to disease in imported or admixed livestock populations, strengthening global biosecurity and resilience.

Temporal dynamics of major SNP markers in large broiler chicken populations

POSTER

148

Brenda Moreno[1], Matias Bermann[1], Fernando Bussiman[1], Vivian Likness[2], Daniela Lourenco[1]

1. University of Georgia, Department of Animal and Dairy Science, Athens, GA, USA
2. Cobb-Vantress, Siloam Springs, AR, USA

Genome-wide association studies (GWAS) identify genomic regions linked to traits by detecting associations between genomic markers and phenotypes of interest. Marker effects and the percentage of genetic variance explained aim to identify marker contributions but may overlook estimate uncertainty and lack proper statistical properties for comparison. Thus, p-values are typically used to detect significant marker-trait associations, reflecting linkage disequilibrium with quantitative trait loci (QTL). Detection power for QTL effects can vary across generations due to selection, migration, and drift, or be influenced by trait heritability, population size, and number of genotyped animals. Single-step GWAS (ssGWAS) is computationally demanding, but the Algorithm for Proven and Young (APY) efficiently approximate the inverse of the mixed model equations, using a core set of genotyped animals. This study aimed to evaluate the consistency of significant markers across generations using p-values. Marker effects and the percentage of variance explained were also examined. Finally, the impact of different APY core sizes on the results was assessed. Data from Cobb Vantress Inc. included 1,515,952 broiler chickens, of which 721,041 were genotyped for 46,199 markers. Traits analyzed included body weight (BW), breast meat percentage (BM%), and leg score (LS). A multi-trait model accounted for sex, contemporary group, additive genetic effects, and a maternal permanent environment effect (for BW). Marker effects were backsolved from GEBVs and applied in ssGWAS using four APY core sizes (99%,98%,(99%)/2,(99%)/3) across generations 1-3, 2-4, 3-5, and 4-6. Additionally, marker effects and variance explained were evaluated. The BLUPF90 software suite was used for the analyses. GWAS revealed consistent BW peaks on GGA1, with stable markers across generations, similar patterns were observed for BM% and LS. Larger APY cores maintained mapping resolution, while smaller cores reduced precision. Compared with p-values, marker effect and variance explained approaches revealed diffuse signals, with associations spread across multiple chromosomes and no clearly outstanding marker effect, reflecting limitations that ignore uncertainty. Therefore, major markers were stable across generations and were detected by p-value analyses. Larger APY cores better preserved mapping resolution. Marker effect and variance explained approaches did not identify clear signals over generations, providing limited information compared with p-values.

Cross-population genomic prediction in global breeding networks must account for emergent fitness epistasis

POSTER

149

Ted Monyak[1], Geoffrey Morris[1]

1. Colorado State University, Soil and Crop Sciences, Fort Collins, CO, USA

To develop a stronger capacity to address food security challenges, global networks of crop breeding programs are increasingly leveraging information across diverse germplasm. As genomic selection becomes a widespread breeding strategy, this exchange of genetic materials may be rendered less effective by the difficulty of achieving accurate cross-population genomic prediction. Historically, the introgression of donor breeding lines from one breeding program into another has been limited due to the risk of disrupting the genetic stability of locally-adapted attained traits in the recipient elite population. To characterize this phenomenon and develop insights on how to mitigate it, we used breeding simulations in the context of fitness landscapes to replicate the history of the development of elite breeding populations. We showed how independent adaptive walks of subpopulations towards the same fitness peak are impacted by genetic drift, leading to cryptic genetic heterogeneity among elite genepools. This variation is released when elite lines derived from independent subpopulations are crossed, leading to segregation for major-effect QTL that had been differentially fixed in each of the subpopulations. Further, we demonstrated how undesirable transgressive segregation for attained traits in admixed populations leads to the emergence of fitness epistasis for traits under stabilizing selection. The prevalence of fitness epistasis was significantly associated with the degree of genetic divergence across subpopulations, and with the accuracy of cross-population genomic prediction. These findings suggest that in networks of nascent breeding programs, strategies for effective germplasm exchange must account for epistasis among the oligogenic component of the genetic architecture of locally-adapted traits.

POSTER

150

Connecting genome-resolved microbiomes to plant-relevant functions in agriculture

Laura K. Moore[1], Madeline Scyphers[1], Sophie K. Jurgensen[1], Christopher E. Chorpenning[1], Lady Grant[1], Laura Mason[1], Mikayla A. Borton[2], Kelly C. Wrighton[1]

1. Colorado State University, Soil and Crop Sciences, Fort Collins, CO, USA
2. Colorado State University, Food Science and Human Nutrition, Fort Collins, CO, USA

Crop performance depends not only on plant genetics and fertilizer inputs, but also on the soil microbiome, which regulates nutrient availability, stress buffering, and growth-promoting processes in the rhizosphere. While plant genomics has rapidly advanced trait discovery and prediction, comparable genome-resolved frameworks for agricultural soil microbiomes remain limited, constraining the integration of microbial function into crop improvement and management strategies. Here, we present a genome-resolved agricultural microbiome resource designed to identify microbial functional traits that influence plant-relevant outcomes and soil health. Our emerging database integrates ~3,000 agricultural soil metagenomes and ~10,000 metagenome-assembled genomes (MAGs) from diverse cropping systems across the United States, paired with soil physicochemical measurements, cropping systems, and management histories. Using Distilled and Refined Annotations of Metabolism for Agriculture (DRAM-AG), an agriculture-focused functional genomic annotation platform, we resolve microbial genomic traits involved in fertilizer transformations, phytohormone regulation, stress tolerance, and root-microbe interactions, traits directly relevant to plant nutrient acquisition and growth. We resolve plant growth–promoting functions within members of Proteobacteria, Actinobacteriota, and Firmicutes, uncovering functional roles for numerous previously unnamed genera in agricultural systems. Genome-resolved biogeographic analyses further reveal a set of core microbial taxa and functional traits conserved across agroecosystems, alongside context-responsive lineages whose functions shift with climate, soil type, and management. Together, this work positions the agricultural microbiome as a complementary genomic layer for precision agriculture, enabling data-driven strategies that better align microbial function with plant demand. By enabling trait-based, genome-resolved interrogation of microbial function at scale, this framework supports the integration of microbiome biology into predictive models and decision-support tools for crop improvement and agricultural management.

Conserved regulatory element location shapes cell-type–specific gene activity in plants

ABSTRACT SELECTED TALK

Abraham Morales-Cruz[1], Sharon I. Greenblum[1], Peng Wang[1], Yu Zhang[1], Lin Yang[2], Chris G. Daum[1], Jenifer Johnson[1], Leo A. Baumgart[1], Ronan C. O'Malley[1,2]

1. U.S. Department of Energy, Joint Genome Institute, Lawrence Berkeley National Laboratory, Berkeley, CA, USA
2. University of Chicago, Department of Human Genetics, Chicago, IL, USA

Understanding how transcription factor binding site (TFBS) position influences gene regulation remains a fundamental challenge in plant genomics. Here, we leverage a comprehensive atlas of nearly 3,000 genome-wide TFBS maps across 360 transcription factors in ten plant species to investigate the relationship between TFBS location and cell type-specific gene regulation. We identify deeply conserved positional "neighborhoods" where TF families preferentially bind—patterns that persist across 150 million years of flowering plant evolution. To assess the functional significance of these neighborhoods, we generated a multi-species, multi-tissue single-nucleus ATAC-seq atlas containing over 74,000 nuclei, revealing that different TF neighborhoods associate with distinct chromatin accessibility patterns and cell type specificity. Surprisingly, we find that a TF's preferred binding neighborhood does not correspond to its sites of strongest regulatory impact. Instead, TFBSs in intronic regions, transcription start sites, and 5′ UTRs consistently show the highest influence on cell type-specific gene expression, while TSS-proximal chromatin, despite being highly accessible, is the poorest predictor of cell type-specific expression. Finally, we identify and characterize conserved distal cis-regulatory modules with classical enhancer signatures, including cell type-specific accessibility that correlates with target gene expression and enrichment for developmental functions. Together, our results establish that TFBS location, chromatin context, and regulatory function are governed by complex, conserved principles that extend beyond simple binding site density.

Integrating technology to refine the estimation of social genetic effects in pigs

POSTER

151

Pedro Nuñez[1], Sara Negro[2], Joaquim Casellas[3], Luis Varona[4], Noelia Ibañez Escriche[1]

1. Universitat Politècnica de València, Valencia, Spain
2. Inga Food S.A., Tres Cantos, Spain
3. Universitat Autonoma de Barcelona, Barcelona, Spain
4. Universidad de Zaragoza, Zaragoza, Aragon, Spain

Advances in automated recording systems in pig production provide detailed information on feed intake and social behaviour in group-housed animals. These data create new opportunities to solve a classic problem in the analysis of social genetic effects in pigs. In the classical formulation of social genetic models, the phenotype is expressed as the sum of its direct genetic effect and the social (indirect) genetic effects received from its pen-mates, together with contemporary-group effects: $y = Xb + Zu + Zs + Zc + e$

where u, s, and c represent vectors of direct genetic, social genetic and contemporary-group effects, respectively. A major difficulty in modelling social genetic effects lies in separating them from contemporary-group effects, because both are usually highly collinear. In this study, we constructed an interaction matrix based on information from automatic feeders to describe the intensity of contacts among pen mates. Rather than assigning identical interaction weights to pigs within the same group, we first estimated frequency and intensity of pairwise interactions at the feeder and combined them into a continuous variable, which was then allocated to each pair of animals in the social incidence matrix. This matrix was compared with a conventional binary matrix assuming equal interaction among all individuals in the pen, and both approaches were evaluated against a standard model without social effects.

We analysed feed conversion ratio (FCR) and residual feed intake (RFI) from 1,357 Iberian pigs kept in groups of 12 ± 3 animals, with feeding behavior continuously recorded. Models including social genetic effects explained a larger proportion of total genetic variance. However, the binary interaction structure failed to clearly distinguish contemporary-group effects from indirect genetic effects, resulting in inflated estimates of the social component. By contrast, the intensity-based matrix enabled a clearer separation between contemporary-group and social genetic effects, increasing total genetic variance from 0.15 to 0.40 for FCR and from 0.25 to 0.32 for RFI compared to the classical animal model. These results highlight the value of detailed behavioral records for improving genetic evaluations by providing realistic representations of social interactions among pigs.

POSTER

154

Functional analysis of three resistant genes (3R-gene), Late Blight resistant (LBr) transgenic events over generations in *Solanum tuberosum* (Potato)

Daniel Omote[1,2], Justus Onguso[1], Eric Magembe[2]

1. Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya
2. International Potato Center, Nairobi, Kenya

The cultivation and consumption of potatoes have witnessed a global surge, particularly in developing nations. However, the persistent threat of late blight disease, caused by the pathogen Phytophthora infestans, continues to challenge potato production, resulting in substantial economic losses. To address this, the International Potato Centre (CIP) has developed genetically engineered potato events that incorporate three resistance (3R) genes (Rpi-blb1, Rpi-blb2, and Rpi-vnt1.1) from wild potato relatives. This research proposal outlines a comprehensive study to assess the genetic stability of these 3R gene potato events over multiple generations. Event-specific PCR was used to confirm the presence and integrity of the insertion sites, while the expression of each of the R genes and their corresponding effectors was analysed to evaluate their functionality. The T-DNA copy number was validated by Southern blot to assess the copy number and stability of the integrated genes. This study will generate robust scientific evidence supporting the efficacy and safety of 3R potato events by addressing uncertainties related to the stability and inheritability of genetically engineered traits. The findings will contribute to regulatory submissions, facilitate the approval process, and promote the adoption of these potato varieties. Ultimately, this research endeavours to enhance crop performance, bolster food security, and foster sustainable agricultural practices in regions heavily reliant on potato cultivation.

POSTER

155

Exploiting genomic variability in *Listeria* for the development of molecular diagnostic markers

Viona Osei[1], Emmanuel Kuufire[1], Rejoice Nyarku[1], Kingsley Bentum[1], Tyric James[1], Asmaa Elrefaey[1], Temesgen Samuel[1], Woubit Abebe[1]

1. Tuskegee University, Department of Pathobiology, Tuskegee, AL, USA

Listeria, a genus of gram-positive bacteria, is one of the four major foodborne pathogens with significant global public health implications. Accurate detection methods, including PCR, rely on robust gene-specific targets for species-level identification in food safety applications. This study employed pan-genomic and core-genomic analyses to characterize Listeria spp. and L. monocytogenes serotypes and to identify genetic variations that can inform molecular diagnostics. A total of 33 high-quality genomes representing 13 Listeria species and 15 genomes from 8 L. monocytogenes serotypes were retrieved from NCBI and curated using CheckM. Genomes were annotated and analyzed with the Roary ILP Bacterial Annotation Pipeline (RIBAP). Candidate species-specific targets were extracted from the RIBAP presence/absence matrix, validated via NCBI MegaBLAST, and functionally annotated with the Genome Annotation and Information Analysis (GAIA) platform. Substantial interspecies genomic diversity was observed, with core gene counts decreasing at higher nucleotide identity thresholds: 856, 665, 362, 89, and 16 core genes at 60%, 70%, 80%, 90%, and 95% identity, respectively. At 95% identity, conserved genes such as rpmG2, mnmE, rplP, and rpsS were identified, each linked to essential cellular functions. Accessory gene counts expanded from 10,400 at 60% identity to 25,486 at 95%, underscoring extensive genomic variability. By contrast, L. monocytogenes serotypes displayed reduced genomic variability, with 2,458 core genes at 60% identity and 2,145 at 95%. Several gene-specific targets, many encoding hypothetical proteins, demonstrated strong diagnostic potential with 90% sensitivity and 98–100% specificity. These findings highlight the extensive genomic diversity within the Listeria genus and support the development of improved molecular diagnostics and enhanced surveillance strategies for foodborne pathogens.

Work supported by grants from the National Institute of Food and Agriculture, United States Department of Agriculture (NIFA-USDA): 2021-38821-34710; 2022-67017-36982; 2022-38821-37362.

Quantitative genomic signatures of epistasis to harness transgressive traits in global breeding networks

POSTER

156

Samuel Owusu-Ansah[1], Geoffrey Morris[1]

1. Colorado State University, Soil and Crop Sciences, Fort Collins, CO, USA

Selection in plant breeding relies on transgressive segregation to generate phenotypes beyond the parental range. While this variation can be beneficial for genetic gain, it also poses a challenge for population improvement when the bulk of the progeny shifts towards undesirable phenotypes. Understanding how these extreme scenarios arise is critical for developing breeding strategies that harness transgressive segregation across breeding networks. This work tests the hypothesis that structured populations harbor distinct genomic signatures of epistasis that influence asymmetric transgressive segregation of complex trait phenotypes. We evaluate whether the prevalence of magnitude, sign, and reciprocal sign epistasis explains progeny shifts toward parental extremes in simulations and in empirical data capturing global sorghum diversity. Forward simulations show that genetic backgrounds enriched for these epistatic patterns systematically push progeny toward one parental extreme. Empirical analyses across the 10 families in our sorghum nested association mapping (NAM) population reveal the contribution of these distinct epistatic signatures to extreme phenotype shifts. The findings suggest that asymmetric transgressive segregation is a predictable consequence of specific genomic signatures of epistasis rather than a stochastic breeding outcome. By dissecting these epistatic signatures, the findings provide a conceptual and practical framework for harnessing extreme phenotypes in breeding programs.

The bias wars: a new hope (graph-pangenomes)

POSTER

157

Matteo Paini[1], Jonah Cullen[2], Sam Stroupe[3], Leif Andersson[4,5], Terje Raudsepp[5], Sian Durward-Akhurst[6], Jessica L. Petersen[7], Molly McCue[2], Ted Kalbfleisch[8], Brian W. Davis[3]

1. University of Verona, Department of Biotechnology, Verona, Italy
2. University of Minnesota, Department of Veterinary Population Medicine, Minneapolis, MN, USA
3. Texas A&M University, College of Veterinary Medicine and Biomedical Sciences, Department of Veterinary Pathobiology, College Station, TX, USA
4. Uppsala University, Department of Medical Biochemistry and Microbiology, Uppsala, Sweden
5. Texas A&M University, College of Veterinary Medicine and Biomedical Sciences, Department of Veterinary Integrative Biosciences, College Station, TX, USA
6. University of Minnesota, Department of Veterinary Clinical Sciences, Minneapolis, MN, USA
7. University of Nebraska-Lincoln, Department of Animal Science, Lincoln, NE, USA
8. University of Kentucky, Martin Gatton-College of Agriculture, Food, and Environment, Department of Veterinary Science, Lexington, KY, USA

Bioinformatic analyses using a linear reference genome can lead to biased results, because a single haplotype does not represent the genomic diversity of a population or species. This can cause misalignment of genomic regions that are not representative of one another, termed “reference bias”. In this study, we investigated regional bias in the linear reference genome of *Equus caballus* to see if our recently constructed pangenome-graph improves those regions. To perform this comparison, we aligned publicly available (NCBI) short-read data from a Thoroughbred horse (30X Coverage) to the linear and pangenome references and we assessed read depth, variant density, and non-diploid loci across sliding-window regions. These metrics enabled the identification of biased regions in the linear genome, which were later examined in the pangenome.

The results showed a reduction in the number of biased regions in the pangenome-graph compared to the linear genome. This difference became even more pronounced when we performed the same analysis using publicly available data from an Arabian horse (30X Coverage), with the linear genome exhibiting a higher number of problematic regions. This demonstrates that graph-based references better capture population-level diversity and reduce mapping artifacts associated with reference divergence than linear references. Among the 50 most biased regions identified in the linear genome, 25 were located on Chromosome12, a chromosome known for its high density of paralogous genes. Interestingly, 13 out of these 25 regions overlapped olfactory receptor family genes, which recent graph-pangenome studies have shown to be enriched for CNVs implicated in local adaptation. Furthermore, when projecting the coordinates of the most problematic linear reference regions onto the pangenome-graph, these loci corresponded to parts of the graph characterized by a high density of structural variants. This shows that many bias-prone regions come from structural complexity and that graph representations may handle this variation better.

Overall, our results demonstrate that graph-pangenomes substantially reduce alignment bias compared to linear references, particularly in genetically diverse samples and complex genomic regions. These findings highlight the importance of reference choice in genomic analyses and provide quantitative evidence supporting the adoption of pangenomes can improve mapping accuracy and downstream variant interpretation.

Optimized dairy cattle evaluation using 100,000 markers on the high-throughput Applied Biosystems™ Axiom™ Bovine Genotyping Array

POSTER

159

Ali Pirani[1], Christofer Bertani[1], Dorothy Oliver[1]

1. Thermo Fisher Scientific, Inc., Santa Clara, CA, USA

As the global population grows at an unprecedented pace, meeting the increasing demand for food remains a significant challenge. For over a decade, the bovine dairy industry has leveraged cattle genetics to enhance key production traits, such as milk yield and protein content. This approach has proven essential for improving dairy cattle productivity. The breeding strategy involves genotyping thousands of biallelic SNPs that are evenly distributed across the genome, thereby capturing most relevant quantitative trait loci (QTL) for use in Genomic Selection (GS). Given the need to rapidly analyze a fixed set of markers across thousands of samples, medium-density microarrays, ranging from 25,000 to 100,000 markers, are ideally suited for this purpose.

Thermo Fisher Scientific offers a variety of Applied Biosystems Axiom microarrays for genotyping dairy cattle. For example, the Axiom Bovine Genotyping v3 Array includes 44,000 markers recognized by the Council on Dairy Cattle Breeding (CDCB). The CDCB has also released a larger list of 80,000 markers for use in genetic evaluation.

A 100,000-marker microarray designed to comprehensively interrogate all 80,000 CDCB-relevant markers has been developed by Thermo Fisher Scientific. In addition, this large array includes markers for even genomic coverage, economically important trait associations, sex-linked loci, microsatellite imputation, and parentage verification markers, including those from the International Society for Animal Genetics (ISAG) 200 and ICAR 354 panels. This high-density array also facilitates the monitoring of undesirable genetic trends, such as inbreeding depression, supporting the overall genetic improvement of dairy cattle in commercial breeding programs.

Rapid Ag-biotech enablement via autonomous laboratories

POSTER

162

Keith Robison[1], **Reetika Rawat**[1], **Deeya Burman**[1], **Timothy Harden**[1], **Roberto Lozano**[1]

1. Ginkgo Bioworks, Boston, MA, USA

Autonomous laboratories integrate laboratory instruments with a combination of hardware and software to enable researchers or machine learning agents to run sophisticated laboratory experiments. Ginkgo has built an autonomous laboratory with over 50 scientific instruments based on our Reconfigurable Automation Cart (RAC) technology and offers a Cloud Lab which enables scientists to access these capabilities. The integration of RACs and Autonomous Lab infrastructure marks a transformative shift in plant and animal biotechnology, moving beyond traditional manual benchwork to a fully programmable, AI-driven environment. This study explores how these next-gen laboratories can be leveraged for high-throughput plant genotyping in precision breeding, and seed quality control (QC). A wide variety of cell, molecular and biochemical experiments relevant to Ag-biotech can be operated with our current configuration, including protein engineering and NGS library prep. In collaboration with OpenAI, we have demonstrated the ability of an AI agent to perform optimization of a Cell-Free Protein Synthesis reaction.

A single-cell platform for longitudinal monitoring of protoplast physiology and transcriptomics

POSTER

163

Gary P. Schroth[1]

1. Cellanome, Foster City, CA, USA

Protoplasts are a versatile system for studying cellular differentiation, stress responses, and genetic manipulation. However, conventional bulk assays obscure individual cell behaviors, making it difficult to distinguish whether increased cell numbers reflect enhanced proliferation or improved survival.

To address this, we applied the Cellanome R3200 platform, which integrates imaging, AI-powered cell segmentation, and automated micro-3D printing to capture thousands of individual protoplasts in bio-compatible hydrogel compartments called CellCage™ enclosures (CCEs) within an 8-lane flow cell. CCEs are tunable in shape, size, and permeability, allowing optimization for different cell types. Cells remain alive within CCEs as nutrients and reagents diffuse through the hydrogel, enabling longitudinal live-cell experiments over days. Multiple cellular phenotypes, including proliferation, viability, and morphology, can be quantified via bright-field and fluorescence imaging (up to 4 channels). Cells are then lysed within their compartments for mRNA capture and sequencing, with data matched back to individual CCEs.

In collaboration with Joe Ecker's Lab at The Salk Institute, we profiled protoplasts from Marchantia thallus, Arabidopsis root, and Arabidopsis aerial seedling tissues encapsulated in 120-micron CCEs. Across these tissue types, we recovered thousands of cages per sample, detecting up to 2,000 genes and 5,000 molecular barcodes (MBCs) per cage. Notably, intact protoplasts yielded very high MBC counts, exceeding 60,000 to 110,000 per cell in some instances. UMAP analysis revealed distinct transcriptional clusters within each tissue type, and differential expression analysis identified tissue-specific marker genes.

This workflow also accommodates perturbations such as hormone treatments or CRISPR-mediated editing, with the ability to sequence detect single-guide RNAs in addition to mRNAs from each CCE. By integrating longitudinal imaging with single-cell transcriptomics, this platform enables direct linkage of phenotypic readouts to gene expression without inference across separate experiments, supporting applications in plant cell biology, health, and resilience.

POSTER

164

Resurrection of the plant immune receptor Sr50 to overcome pathogen immune evasion

Kyungyong Seong[1], Wei Wei[1], Sophie C. Sent[3], Brandon Vega[1], Amanda Dee[1], Griselda Ramirez-Bernardino[1], Rakesh Kumar[1], Lorena Parra[1], Isabel ML Saur[3,4], Ksenia Krasileva[1,2]

1. University of California, Berkeley, Department of Plant and Microbial Biology, Berkeley, CA, USA
2. University of California, Berkeley, Innovative Genomics Institute, Berkeley, CA, USA
3. University of Cologne, Institute for Plant Sciences, Cologne, Germany
4. Cluster of Excellence on Plant Sciences (CEPLAS), Cologne, Germany

Plant diseases driven by rapidly evolving pathogens cause major crop losses worldwide. A common strategy for disease control is to introduce immune receptor genes into elite crop varieties, but pathogens frequently mutate to evade recognition, leading to resistance breakdown. This creates a critical need for predictive methods to redesign immune receptors rather than repeatedly searching for new natural resistance genes.

Here, we demonstrate a structure-guided framework to reprogram a wheat immune receptor, Sr50, to recognize a pathogen effector variant that has escaped natural detection. Instead of relying on cryo-EM, we used computational protein structure prediction combined with precision mutagenesis to infer interaction surfaces and guide receptor redesign. We identified a key amino acid substitution that partially restored recognition of the escaped effector, and through expression optimization and structural refinement, generated engineered receptor variants that robustly detect both the original and escaped pathogen proteins in plant systems.

Importantly, the engineered mutations are not found in nature and reveal how combinations of substitutions interact synergistically to reshape protein recognition. The essential mutation we identified also improved the accuracy of AlphaFold-based structural models, enabling predictive interpretation of receptor–effector interactions.

Together, this work establishes a scalable strategy for combining predictive structural modeling and experimental validation to rationally engineer immune receptors. This approach provides a path toward programmable crop immunity, enabling faster responses to pathogen evolution and supporting durable disease resistance in agriculture.

POSTER

165

Scaling agritech innovation: a public–private model for de-risking and commercializing technologies in agriculture

Rahul Singh[1]

1. B.C. Centre for Agritech Innovation, Simon Fraser University, Burnaby, British Columbia, Canada

Global agriculture faces unprecedented pressures from climate volatility, labour shortages, supply chain instability, and rising input costs. At the same time, scientific breakthroughs in genomics, artificial intelligence, automation, controlled environment agriculture, and precision technologies offer transformative potential. The persistent challenge, however, is not discovery—it is scaling science into practice. Canada, for example, ranks among the top 10 globally in innovation inputs—research investment, talent, education, and infrastructure—yet falls closer to 20th–25th in innovation outputs. While we excel at generating knowledge, we struggle to translate it into economic value, such as intellectual property, commercial products, high-tech exports, and scalable enterprises.

This presentation introduces the BC Centre for Agritech Innovation (BCCAI) model as a scalable, public–private framework for accelerating the adoption and commercialization of science-based agritech solutions. Hosted at Simon Fraser University (SFU), BCCAI operates as a de-risking intermediary, connecting researchers, technology developers, farmers, processors, and policymakers through cost-shared pilot projects, validation platforms, and targeted workforce training.

Key elements of the model include: (1) industry-led project selection aligned with market demand; (2) co-investment structures that leverage public funding to attract private capital; (3) demonstration and validation environments that reduce technical and financial risk; (4) regulatory and policy alignment through active government engagement; and (5) ecosystem development through partnerships with Indigenous communities, municipalities, trade associations, and global collaborators.

By lowering barriers to piloting and adoption, the model shortens the pathway from lab to field while strengthening regional competitiveness. Early outcomes demonstrate increased SME engagement, accelerated commercialization timelines, workforce upskilling, and enhanced resilience across the agriculture and agrifood sectors.

The BCCAI approach offers a replicable blueprint for jurisdictions seeking to translate scientific excellence into economic and societal impact.

POSTER

166

Proteomic insights into the molecular mechanisms underlying improved performance in creep-fed beef calves

Nedenia B. Stafuzza[1], Gabriel S.S. David[2], Bianca R. Domingos[2], Letícia S. Pereira[3], Mateus J.I. Abreu[2], Rafael N. Assunção[2], Gustavo R. Siqueira[2,4], Flávio D. Resende[2,4], Daniela Lourenco[1], Claudia C.P. Paz[3]

1. University of Georgia, Department of Animal and Dairy Science, Athens, GA, USA
2. São Paulo State University, Department of Animal Science, Sao Paolo, Jaboticabal, Brazil
3. Sustainable Livestock Research Center, Animal Science Institute, São José do Rio Preto, Sao Paolo, Brazil
4. São Paulo Agency for Agribusiness Technology, Colina, Sao Paolo, Brazil

Creep feeding supplements suckling calves with energy- and protein-rich diets to increase weaning weight and improve performance and meat quality traits. However, the molecular mechanisms driving these effects remain unexplored. This study investigated how creep feeding modulates the proteome of the *Longissimus thoracis* muscle in Nellore calves after weaning and before harvest. Thirty male Nellore calves were assigned into two groups: 15 received creep feeding (5g/kg BW; CF) and 15 received mineral supplementation (NCF) from day 40 to day 240. After weaning (240 days), all animals were grazed with protein supplementation (10g/kg BW/day), followed by ad libitum concentrate during the finishing phase. Before harvesting, the NCF group exhibited lower mean hot carcass weight (321 vs. 335 kg; P=0.01) than the CF group. Muscle samples were collected from both groups after weaning (CFw and NCFw) and before harvest (CFs and NCFs) for proteomic analysis by LC-MS/MS. Proteins with absolute log2-fold change >0.58 (P<0.05) were considered differentially abundant (DAPs) between groups and subjected to functional enrichment analyses using DAVID (P<0.05). Thirty-five DAPs were identified between the CFw and NCFw groups, whereas 71 DAPs were identified between the CFs and NCFs groups. Functional analysis revealed that the DAPs on the weaning acts in important pathways that contributes to the growth and carcass traits, such as bta04723-Retrograde endocannabinoid signaling (food intake and energy balance), bta04926-Relaxin signaling (muscle functions, remodeling, perfusion, vascularization, glucose metabolism, and energy balance), and bta00190-Oxidative phosphorylation (protein synthesis, growth, metabolism, and adaptive signaling). The DAPs at harvesting also contributed to the differences observed between groups, but via distinct molecular mechanisms, including: GO:0009267-Cellular response to starvation (metabolic adaptations, energy conservation, and protein turnover), GO:0071230-Cellular response to amino acid stimulus (protein synthesis, growth, muscle hypertrophy, and homeostasis), R-BTA-8953897-Cellular responses to stimuli (growth, metabolism, immune functions, and stress adaptation), and bta04150-mTOR signaling (protein synthesis, growth, and muscle hypertrophy). In conclusion, creep feeding enhances productive efficiency in Nellore calves through phase-specific molecular mechanisms, promoting lasting improvements in muscle deposition and carcass quality traits.

The IWGSC Wheat Diversity Project: foundational genome resources to advance a global food security crop

ABSTRACT SELECTED TALK

Joshua C. Stein[1], Kellye Eversole[1], C. Robin Buell[2], John P. Hamilton[2], Hélène Rimbert[3], Pauline Lasserre-Zuber[3], Kevin Fengler[4], Victor Llaca[4], Véronique Gautier[3], Frederic Choulet[3], Clément Debiton[3], Sophie Bouchet[3], Moussa Benhamed[5], Leonardo Pereyra-Bistrain[5], Cyrille Saintenac[3], Michael Alaux[6], Catalina Johnson[7], Pierre Sourdille[3]

1. International Wheat Genome Sequencing Consortium (IWGSC), Eau Claire, WI, USA
2. University of Georgia, Department of Crop & Soil Sciences, Athens, GA, USA
3. INRAE-GDEC, Clermont-Ferrand, Rhone-Alpes-Auvergne, France
4. Corteva Agriscience, Johnston, IA, USA
5. Institute of Plant Sciences - Paris-Saclay, Orsay, France
6. URGI, INRAE, Université Paris-Saclay, Versailles, France
7. Colorado Parks and Wildlife, Denver, CO, USA

Genetic diversity is essential for sustaining the future adaptive capacity of agriculture. In bread wheat, most genetic diversity is held within landrace varieties that were locally adapted over thousands of years by traditional farming prior to modern agriculture. While today's high-yielding cultivars contain only a fraction of this available gene pool, landraces remain a key reservoir for adaptive traits that will be essential for meeting future demands for wheat improvement. The IWGSC Wheat Diversity Project addresses the critical need to preserve, discover, and mobilize these genetic resources by sequencing 12 wheat landraces that represent the worldwide diversity of bread wheat. State-of-the-art sequencing, assembly, and annotation methods were applied to these genomes and to a platinum-quality update of the community reference, Chinese Spring, to be released as IWGSC CS RefSeq 3.0. Finally, representation of the wheat pangenome as a Practical Haplotype Graph will provide powerful tools to accelerate future genomics and breeding research. This project is funded by NSF Award #2322957, INRAE, the European Union European Research Council, and the IWGSC.

POSTER

167

A miniaturized high-throughput workflow for low-pass NGS using the Revvity NEXTFLEX Agrigenomics kit

Matthew Stull[1], Marcel Brun[1], Joshua Hill[1], Alex Watros[1], Charles D. Johnson[1]

1. Texas A&M AgriLife Genomics and Bioinformatics Service, College Station, TX, USA

Agrigenomics is increasingly central to global food security, using the genomes of crops and livestock to accelerate breeding and improve agricultural productivity. Over the past decade, low-coverage whole-genome sequencing (LowPass) has emerged as a scalable and cost-effective alternative to traditional genotyping arrays. As sequencing and library preparation costs have declined, however, the primary financial and labor bottleneck in large genotyping projects has shifted toward the library preparation workflow itself. To fully realize the potential of population-scale genomics, library preps must be miniaturized and automated while maintaining consistent performance and data quality. Low-pass sequencing is particularly well suited to this strategy because the reduced sequencing depth lowers the requirement for extreme library complexity. Previously, we demonstrated successful miniaturization to one-tenth reaction volume for the PerkinElmer NEXTFLEX DNA kit using a PerkinElmer Sciclone HT 384 liquid handling system, producing consistent yields and high library success rates at a massive cost savings.

In this work, we show that the same miniaturization strategy can be extended to similar kits, including the recently released Revvity NEXTFLEX Agrigenomics HT kit. Based on the original reagent composition, we selected a one-third reaction volume as a practical balance between robustness, library quality, and reagent cost savings. We describe our approach to volume calibration and process optimization, resulting in a validated workflow that produces libraries with consistent insert size distributions and DNA yields. By controlling input DNA quality and adjusting fragmentation conditions, bead ratios, and PCR cycle numbers, we demonstrate the ability to tune library characteristics to match different sequencing chemistries, read lengths, sequencing depths, and downstream QC requirements.

Our results show that substantial cost reductions can be achieved through automation without compromising library quality or variant detection sensitivity. The miniaturization framework described here is readily transferable to other liquid-handling platforms and library preparation kits. For the Revvity NEXTFLEX Agrigenomics HT kit, the final optimized workflow reduced reagent cost, lowered PCR cycle requirements, and decreased plastic consumption relative to standard protocols while maintaining tight control over library concentration and fragment size distributions.

POSTER

168

PurePrep 0.0: a safe, effective, and environmentally responsible nucleic acid purification method

Jennifer Taylor[1], Dan Street[1]

1. AgriGenX, Bremerton, WA, USA

As the demand for genotyping data continues to increase in the agriculture and aquaculture spaces, labs tasked with generating this data face an increasing need to balance speed with quality in the lab. Protocols need to be cost effective and automatable to process the large amount of samples that come through labs each year. Additionally, managing these labs often requires storage and handling of large amounts of hazardous and flammable waste that can be time consuming and have health and environmental implications. Balancing all these requirements can be challenging.

With the launch of the PurePrep Plant 0.0 and PurePrep Animal 0.0 kits, AgriGenX provides a solution for nucleic acid extraction and purification that balances all these needs in one simple solution. Both kits allow extraction of DNA with yield and quality suitable for a wide range of downstream applications (eg., Single-plex genotyping, arrays, NGS) with none of the hazardous high chaotropic salt, isopropanol, or ethanol waste common to other kits and workflows. The protocol is fast and highly automatable, allowing labs to purify responsibly and quickly. Here we present some initial findings generated using the Plant 0.0 and Animal 0.0 kits.

POSTER

169

Identification of putative long non-coding RNAs of *Stenocereus thurberi* (Sweet Pitaya) exocarp fruit transcriptome through comparative genomics

Heriberto García-Coronado[1,2], Miguel-Ángel Hernández-Oñate[3], Julio-César Tafolla-Arellano[2], Martín-Ernesto Tiznado-Hernández[4]*

1. SECIHTI-Coordinación de Tecnología de Alimentos de Origen Vegetal, Centro de Investigación en Alimentación y Desarrollo A.C. Carretera Gustavo Enrique Astiazarán Rosas No. 46, Hermosillo, Sonora, México
2. Universidad Autónoma Agraria Antonio Narro, Laboratorio de Biotecnología y Biología Molecular, Departamento de Ciencias Básicas, Calzada Antonio Narro 1923, Buenavista, Saltillo, Coahuila, México
3. SECIHTI-Coordinación de Ciencias de los Alimentos, Centro de Investigación en Alimentación y Desarrollo, A.C. Carretera Gustavo Enrique Astiazarán Rosas No. 46, Colonia La Victoria, Hermosillo, Sonora, México
4. Coordinación de Tecnología de Alimentos de Origen Vegetal, Centro de Investigación en Alimentación y Desarrollo A.C. Carretera Gustavo Enrique Astiazarán Rosas No. 46, Hermosillo, Sonora, México

*Corresponding author: tiznado@ciad.mx

Long non-coding RNAs (lncRNAs) are regulatory elements playing a role in several physiological functions in plants. It has been shown that they are involved in the tolerance of plants to drought stress. Sweet pitaya (*Stenocereus thurberi*) is a cactus endemic to the Sonoran Desert that produces a fleshy fruit. With the objective to help in elucidating the role of lncRNA in the adaptation of cactus to the arid environment, a transcriptome of sweet pitaya fruit exocarp was assembled. In this study, 43,391 tentatively lncRNA were identified and aligned to the genomes of the cactus saguaro (*Carnegiea gigantea*) and pitahaya (*Selenicereus undatus*) by blat, blastn, and minimap2 software alignment. In the case of saguaro and pitahaya, 34,047 and 30,293 lncRNAs, respectively, were aligned through the three software used. Out of these lncRNAs, 27,057 aligned in both saguaro and pitahaya genomes, whereas 6,990 lncRNAs aligned only to the saguaro genome. These results further support that the sweet pitaya transcriptome assembly process is robust and the lncRNAs found in sweet pitaya are not artifacts created by the bioinformatic analysis. Furthermore, 18,727 lncRNAs were aligned to the transcriptomes of the cactus *Hylocereus polyrhizus*, *Pachycereus pringlei*, and S*elenicereus undatus*, which suggests that they are homologous to several species of the Cactaceae family and confirms that they are expressed in these plants. The sequence of the sweet pitaya genome at the chromosome level will help to reduce redundancy in the lncRNA set, classify them, establish their position with respect to coding RNA, and predict their regulatory roles. Further expression analysis of these transcripts should be carried out to better elucidate their function in sweet pitaya adaptation to arid environments.

Peresphone: a multi-genome browser for comparative genomics

POSTER

170

Maxim Troukhan[1]

1. Peresphone Software, Agoura Hills, CA, USA

Persephone® is an industrial-scale genome browser built to visualize massive datasets in a smooth animated manner. It overcomes challenges that traditionally limit genome browsers, enabling real-time handling of large volumes of data.

Beyond high-performance visualization, Persephone provides a robust platform for storing thousands of genomes, hundreds of millions of maps, and billions of variants (SNPs, indels, and SV). Organization-wide repositories can be integrated with user data tracks for unified exploration.

Its ability to display multiple maps and align genomic sequences with genetic maps accelerates pan-genomic tasks such as structural variation analysis and sequence assembly validation. Real-time sequence alignment is supported through minimap2 and NCBI BLASTN. Recent improvements include fast visualization of large (up to 200 GB) BAM/CRAM files, enhanced variant data processing, advanced DNA motif search, gene model editing interface, and multiple alignment of DNA and protein sequences.

Persephone is used daily in large corporations and academic institutions and continues to uphold its reputation for stability, power, and versatility.

The free web application is available at https://web.persephonesoft.com.

Using airborne DNA sequencing to monitor sporulation, infection, and relative abundance of cereal rust fungi

POSTER

171

Jade van Wijk[1], Darren Heavens[1], Charlotte Hayes[2], Diane Saunders[3], Paul Nicholson[3], Matt D. Clark[4], Richard M. Leggett[1]

1. Earlham Institute, Norwich, Norfolk, United Kingdom
2. Elsoms Wheat, Lincolnshire, England
3. John Innes Centre, Norwich, England
4. The Natural History Museum, London, England

Wheat provides roughly 20% of caloric intake worldwide, making it vitally important to protect. Some of the biggest threats to wheat include the cereal rusts Puccinia striiformis f. sp. tritici (Pst) and P. triticina (Pt), which cause yellow rust and brown rust respectively. Pst alone is known to cause yield losses of up to 5.5 million tonnes annually (Beddow et al., 2015). The obligate biotrophic nature of these pathogens also makes them impossible to culture and therefore difficult to study pre-infection. Here, we apply AirSeq, a sequencing-based approach for studying environmental bioaerosols, to monitor rust pathogens on wheat farms. This approach can be used to quantify fungal spores in the air before infection occurs, offering early warning of cereal rust infections and providing valuable insights to enable effective integrated pest management strategies (IPM). This environmentally conscious approach to IPM can aid farmers in reducing costs, while supporting sustainable farming practices. Here we present AirSeq surveillance data from 7 commercial UK wheat breeding sites and from a research farm, monitored through regular air collections from Spring to Autumn over several years. DNA was then extracted, nanopore sequenced and the data analysed using MARTi (Metagenomic Analysis in Real-time), as well as mapped to reference genomes in Phi-base. Using this methodology, we demonstrate how air-detected pathogen levels rise in advance of leaf detected infections, through benchmarking these datasets against field disease scoring observations and infected leaf samples. Furthermore, we show the influence the weather has on disease spread through comparisons to meteorological data.

From data to discovery: multi-omics learning platforms for Brassicaceae biofuel crops

ABSTRACT SELECTED TALK

Mohit Verma[1]*, Preethi Sai Induri[2], Yen On Chan[2], Dong Xu[2], Jay J. Thelen[2], Maneesh Lingwan[3], Jiahong Zhou[3], Doug K. Allen[3], Philip D. Bates[4], Alisha Lnu[5], Timothy P. Durreett[5], Ruth Welti[5], Edgar B. Cahoon[6], Trupti Joshi[1,2]

1. Marshall University, Huntington, WV, USA
2. University of Missouri, Columbia, MO, USA
3. Donald Danforth Plant Science Center, St. Louis, MO, USA
4. Washington State University, Pullman, WA, USA
5. Kansas State University, Manhattan, KS, USA
6. University of Nebraska-Lincoln, Lincoln, NE, USA

*Presenter

Scalable, low-carbon biofuels require oilseed feedstocks whose lipid yield, composition, and resilience are governed by predictable, multi-layer regulatory control.

Using an integrative, cross-species multi-omics framework spanning transcriptomics, proteomics, and lipidomics, we have systematically linked molecular regulation to fatty acid outcomes across seed development in *Camelina sativa* and *Thlaspi arvense* (pennycress). Cross-species analyses revealed a conserved Brassicaceae lipid biosynthetic backbone overlaid by pronounced species-specific regulatory programs. Camelina exhibited a broad, distributed transcriptional and proteomic response coupled with flexible lipid remodeling, resulting in diversified C18-dominated lipid profiles indicative of metabolic plasticity. In contrast, pennycress showed a more constrained but higher-amplitude regulatory changes, associated with enrichment of longer-chain lipid species and pathways linked to structural protection and environmental robustness.

Multi-layer correlation and network analyses demonstrated that lipid phenotypes arise from coordinated regulation across pathways and developmental stages rather than from isolated enzymatic control. Regulatory concordance between species was limited despite shared pathway membership, highlighting extensive developmental and regulatory rewiring. These patterns were consistent across wild-type and engineered lines, underscoring the importance of systems-level context in interpreting genetic perturbations.

To support scalable integration and automated interpretation of these datasets, we have established a comprehensive integrative bioinformatics framework enabling unified data access, interactive visualization, multi-omics based learning platform and AI based solutions for discovery. Together, this combined analytical and informatics framework delivers a predictive, cross-species regulatory blueprint that complements ongoing fatty acid synthase optimization efforts and informs rational engineering and domestication of resilient, composition-optimized Brassicaceae oilseed feedstocks aligned with DOE BER sustainability objectives.

Funding Statement: This research was supported by the DOE Office of Science, Office of Biological and Environmental Research (BER), grant no. DE-SC0023142.

Toward systematic engineering of endogenous overexpression in plants via MPRA-guided cis-regulatory element insertion

POSTER

172

Laura Wang[1], Viktoriya Georgieva[1,3], Zeke Lam[2], Madison Williams[3], Evan D. Groover[1,2], Joseph L. Rivera[1,4], Hana Chang[2], Myeong-Je Cho[1], Krishna K. Niyogi[1,2,4,5], David F. Savage[1,3,4]

1. Innovative Genomics Institute, University of California, Berkeley, CA, USA
2. Department of Plant and Microbial Biology, University of California, Berkeley, CA, USA
3. Department of Molecular and Cellular Biology, University of California, Berkeley, CA, USA
4. Howard Hughes Medical Institute, University of California, Berkeley, CA, USA
5. Molecular Biophysics and Integrated Bioimaging Division, Lawrence Berkeley National Laboratory, Berkeley, CA, USA

Transgenic overexpression of photosynthetic targets has led to rapid improvements in plant photosynthesis and productivity. However, regulatory constraints and public perception limit the deployment of genetically modified crops. CRISPR-based promoter mutagenesis offers a transgene-free alternative to modulate endogenous gene expression. However, while knockout and knockdown alleles can be efficiently generated using such an approach, methods for generating hypermorphic alleles remain underdeveloped. Targeted insertion of enhancers and or mutagenesis of repressors have enabled overexpression of endogenous genes, but these methods often lack precision and generalizability, limiting their ability to fine-tune gene expression within complex pathways such as photosynthesis. Here, we describe a plant engineering pipeline integrating a modified mesophyll protoplast–based MPRA system with state-of-the-art prime editing to facilitate identification and targeted generation of candidate hypermorphic alleles via insertion of simple cis-regulatory elements (CREs). Using rice – a model monocot and major crop – we evaluate the strengths and limitations of current MPRA implementations and highlight a more systematic and broadly generalizable promoter-engineering strategy based on insertion of a shortlist of transcription factor binding sites (TFBS) and interrogation of their CRE grammar. With prime-edited stable rice lines carrying TFBS insertions in key photosynthetic genes currently undergoing *in planta* validation, this work offers a foundation for developing elite varieties with optimized photosynthesis and other complex metabolic traits.

POSTER

173

Addressing the DNA extraction bottleneck: a high-throughput, low-cost automated workflow for agrigenomics applications

Alex Watros[1], Matt Stull[1], Marcel Brun[1], Joshua Hill[1], Charles D. Johnson[1]

1. Texas A&M AgriLife Genomics and Bioinformatics Service, College Station, TX, USA

The rapid decline in sequencing and library preparation costs has shifted the primary bottleneck in large-scale agrigenomics projects to genomic DNA (gDNA) isolation. In many studies focused on low-coverage genotyping of small-genome plant species, the cost and labor associated with DNA extraction now exceed the cost of sequencing itself. This shift has important implications for experimental design, throughput, and overall project economics, particularly in breeding and population-scale studies where tens of thousands of samples must be processed efficiently.

Here, we present an optimized high-throughput workflow combining the Omni Bead Ruptor 96 with the Chemagic magnetic bead-based platform. This protocol achieves a significant cost savings while maintaining our own services high gDNA QC requirements. To validate the robustness of this method, we processed 1,479 samples from 12 major crop species across multiple plant families and developmental stages.

Using a standardized 20-second rupture at 29Hz, the protocol yielded remarkably consistent concentrations across 96-well plates. The average yields were 1mg, 14 ng/µL in a 75 µL total volume from 10–20 mg of starting tissue. Even in challenging adult Sorghum samples, the workflow provided a functional average yield of 5.5 ng/µL. Size distribution analysis showed that 75% of the isolated gDNA exceeded 5,000 bp across most species. Furthermore, the Chemagic system's inherent bead-based size selection minimizes fragmented DNA, ensuring high-quality input for downstream sequencing. This workflow allows a single technician to process 288 samples per day, offering a scalable solution for modern low-pass sequencing initiatives.

POSTER

174

Universal rRNA depletion method enables a unified workflow for RNA-Seq in major crops and model plants

Elaine Wolfe[1]

1. Zymo Research, Irvine, CA, USA

Background: RNA sequencing (RNA-Seq) is widely used in plant biology to characterize transcriptomic changes that influence yield, pathogen resistance, stress tolerance, and nutritional quality. A major technical barrier in plant RNA-Seq is the high abundance of ribosomal RNA (rRNA), which reduces informative read depth and increases sequencing costs. Traditional probe-based depletion methods require species-specific design and iterative optimization. A universal and efficient rRNA removal strategy is needed to support reproducible, cost-effective transcriptome profiling across diverse plant species.

Methods: We evaluated a probe-free rRNA depletion method, the RiboFree Universal rRNA Depletion, which removes rRNA-derived cDNA by targeting abundant DNA-RNA hybrids. The method was tested on leaf tissues from *Zea mays* (corn), *Solanum lycopersicum* (tomato), *Triticum aestivum* (wheat), and *Arabidopsis thaliana*. Samples were homogenized in a unique DNA and RNA stabilizer solution to preserve RNA quality immediately after collection. Total RNA was isolated using a robust RNA purification workflow designed to retain both mRNA and small RNA species. The RiboFree rRNA depletion method, integrated with streamlined library preparation, produced libraries ready for sequencing on the Illumina NovaSeq 6000.

Results: Across all species, RiboFree achieved strong depletion performance, reducing rRNA content to < 3 % in tomato, < 5% in wheat, approximately 10% in Arabidopsis, and 15% in corn. The method enabled broad transcriptomic coverage, detecting 22,162 genes in tomato, 51,850 in wheat, 25,162 in Arabidopsis, and 37,959 in corn. These results show that the probe-free approach efficiently removes rRNA from various plant species, including both monocots and dicots, without the need for custom probe sets.

Conclusions: This study establishes RiboFree Universal rRNA Depletion as a “one-for-all” solution for plant transcriptomics. Its probe-free approach simplifies RNA-Seq library preparation and ensures efficient rRNA removal across diverse crops and model species. This approach has the potential to accelerate functional genomics, trait discovery, and large-scale transcriptomic studies in plants.

Going against the grain: developing genomic resources to support finger millet breeding

POSTER

175

Hallie Wright[1], Katrien Devos[2,3,4], Josh Clevenger[1,2]

1. HudsonAlpha Institute for Biotechnology, Huntsville, AL, USA
2. University of Georgia, Institute of Plant Breeding, Genetics and Genomics, Athens, GA, USA
3. University of Georgia, Department of Crop and Soil Sciences, Athens, GA, USA
4. University of Georgia, Department of Plant Biology, Athens, GA, USA

Global food demand is predicted to increase by 61% by the end of the century. Four major crops account for most of the global calories consumed, yet their yields are projected to decline with global warming and environmental changes. One means of sustaining food supply under such challenges is the diversification of food systems by incorporating crops that thrive in challenging climates. Finger millet (*Eleusine coracana* (L.) Gaertn.) is a C4 allotetraploid (2n = 4x = 36, AABB) cereal grown in the arid and semi-arid regions of eastern Africa and India. It can withstand abiotic stresses like heat, drought, and salinity to a higher degree than many crops and can be grown on marginal lands under minimal inputs. It is highly nutritious and rich in calcium and the essential amino acid methionine. Despite its importance, finger millet lags behind major crops in terms of genomic resources available. One high-quality reference assembly and short-read resequencing for only 68 accessions have been made publicly available. The dearth of genomic resources has hampered breeding efforts, and no cultivars have been released using marker-assisted selection (MAS) to-date. To bring finger millet forward in the genomics era, we have generated a HiFi-based long-read, low-pass genotyping resource for over 200 mini-core and diversity accessions to accurately catalogue variation to support pre-breeding genetic characterization and trait mapping. Generating an average read length of 10.3 kb and an average 4x depth of coverage per sample enables us to characterize species-wide diversity and profile haplotypes for global finger millet germplasm. Our aim is to generate a publicly available genotyping resource that harnesses both short (< 50bp) and long (≥ 50bp) genetic variants across a global panel to expedite identifying marker-trait associations and support breeding programs for a crop that has received little attention despite its relevance as a climate-resilient staple.

Climate change adaptation strategies of smallholder farmers in Peru and Ethiopia

POSTER

176

Maria Wurzinger[1], Gustavo Gutierrez[1], Milagros Aguilar[2], Emna Rekik[3,4]

1. Iowa State University, Department of Animal Science, Ames, IA, USA
2. DESCOSUR, Arequipa, Peru
3. ICARDA, Addis Ababa, Ethiopia
4. BOKU University, Vienna, Austria

Smallholder farmers around the world notice the negative effects of a changing climate. They face decreasing rainfall, rising temperatures, and unpredictable start times for the rainy season. These changes are especially difficult for farmers who raise animals on pasture, as implementing adaptation measures is challenging. This paper aims to investigate how llama and alpaca farmers in Peru and sheep farmers in Ethiopia perceive climate change, the strategies they use, and the challenges they face when adopting adaptation measures. Surveys were conducted in both countries: 70 farmers were personally interviewed in Ethiopia, and 407 participated in Ethiopia. The interview data were analysed using SPSS. Farmers in both countries have confirmed that the climate has been changing over the past 20 years, leading to feed shortages, reduced feed quality, and water scarcity. Peruvian and Ethiopian farmers rely entirely on pasture throughout the year; therefore, feed conservation and strategic feeding plans are among the options they explore. In the Peruvian Andes, farmers are experimenting with various water harvesting techniques. In both locations, farmers are also seeking off-farm opportunities to reduce dependence on income from livestock production. Ethiopian farmers also mentioned destocking as a strategy to manage feed shortages. Irrespective of the country, all farmers mentioned several barriers to implementing more measures on their farms. Lack of knowledge, combined with limited access to credit and restricted access to farm inputs, is cited as the top barrier. Although farmers keep livestock in various environments, the challenges they face in adapting to climate change are similar. The findings highlight both shared and context-specific adaptation pathways among smallholder pastoral systems across contrasting agroecological zones. Addressing the identified barriers will require targeted extension services, improved access to credit, and locally appropriate policy support to enhance farmers' adaptive capacity. These insights contribute to a better understanding of livestock-based climate adaptation in vulnerable smallholder systems and can inform future adaptation planning and development interventions.

Tricks and extensions for multivariate modeling of genomic breeding values

ABSTRACT SELECTED TALK

Alencar Xavier[1,2], Daniel Runcie[3], David Habier[2]

1. Corteva Agrisciences, Seed Product Development, Johnston, IA, USA
2. Purdue University, Department of Agronomy, West Lafayette, IN, USA
3. University of California Davis, Department of Plant Sciences, Davis, CA, USA

The integration of multi-environment trial data into genomic prediction is critical for capturing genotype-by-environment (GxE) interactions and tailoring cultivars to a specific target population of environments. Multivariate genomic best linear unbiased prediction (GBLUP) models, solved via Restricted Maximum Likelihood or Bayesian Gibbs Sampling, face significant computational bottlenecks as the number of traits or environments. This study presents a suite of scalable "tricks and extensions" designed to overcome these challenges, enabling the analysis of large datasets in plant breeding. Central to these advancements is the Pseudo-expectation Gauss–Seidel (PEGS) algorithm. PEGS is an iterative solver that combines randomized Gauss–Seidel residual updates for regression coefficients with pseudo-expectation estimators for variance-covariance components. By avoiding large-scale matrix inversions and Kronecker products, PEGS is orders of magnitude faster than traditional solvers. It remains robust under the unbalanced experimental designs common in breeding trials and scales efficiently with increasing numbers of markers, individuals, and environments. Complementing this efficient solver, we present the MegaSEM model that utilizes latent representations to capture complex trait interactions. This approach allows for the simultaneous analysis of thousands of traits or environments in a fraction of the time required by traditional methods. Prediction of new environments is discussed. Benchmarks on simulated scenarios and real-world datasets demonstrate that these parsimonious structures often provide higher accuracy than unstructured models in sparse testing environments by reducing the number of parameters to be estimated. Collectively, these methods provide a computationally feasible toolkit for robust and scalable genomic prediction. By utilizing efficient solvers and dimensionality-reduction tricks, breeders can efficiently leverage correlated information across vast environmental networks to enhance selection accuracy.

ABSTRACT SELECTED TALK

Enviromics-based modeling of genotype-by-environment-by-management interactions for growth, reproductive, and carcass traits in pasture-raised beef cattle

Talita E.Z. Santana[1,2], Renata Veroneze[1], Gilberto R.O. Menezes[3], Guilherme J.M. Rosa[2]

1. Federal University of Vicosa, Department of Animal Science, Vicosa, MG, Brazil
2. University of Wisconsin-Madison, Department of Animal and Dairy Sciences, Madison, WI, USA
3. Brazilian Agricultural Research Corporation, National Center of Research on Beef Cattle, Campo Grande, MS, Brazil

Pasture-raised beef cattle face wide environmental and management variability, which challenges genetic evaluation and selection. We propose an enviromics-based framework to assess genotype-by-environment-by-management (GxExM) interactions in Nellore cattle raised on pasture across Brazil. The dataset integrated animal-level records, including pedigree, genotypes, and phenotypes for yearling weight (YW), scrotal circumference (SC), age at first calving (AFC), ribeye area (REA), backfat thickness (FAT), and marbling score (MARB), along with farm-level descriptors of environment (climate, soil, elevation) and management practices. Management information was collected via electronic surveys and covered 24 practices related to technical assistance, soil management and conservation, feed supplementation, and reproductive strategies. Statistical analyses followed a two-step approach: (1) Environmental and management variables were used to define environmental conditions (EC), and (2) Bi-trait ssGBLUP models were fitted to estimate (co)variance components and breeding values. Genetic correlations and comparisons of genomic estimated breeding values (GEBV) for bulls between ENV1 and ENV2 were used to evaluate GxExM interactions. The lowest genetic correlations were observed for AFC (0.32 ± 0.09), followed by YW (0.39 ± 0.01) and REA (0.65 ± 0.08), which indicates stronger GxExM interactions for these traits, whereas MARB (0.96 ± 0.03), FAT (0.86 ± 0.08), and SC (0.81 ± 0.04) indicate weaker interactions. Spearman's rank correlations between GEBVs of bulls with ≥5 offspring in both ECs further supported these results, showing 0.43, 0.57, and 0.75 for AFC, YW, and REA, respectively. Among bulls with high-accuracy GEBV (≥ 90th percentile), the percentage of top ranked animals was lowest in the top 1% for all traits and increased toward the top 25% rankings. Specifically, values ranged from 10–53% for AFC, 16–55% for YW, and 35–70% for REA, were intermediate for SC (52–80%), and consistently high for FAT (72–88%) and MARB (86–94%). These findings provide strong evidence of GxExM interactions affecting key growth, reproductive, and carcass traits in pasture-raised beef cattle, particularly for AFC, YW, and REA. The integration of farm-level environmental and management factors into genetic evaluations can be critical to improve selection decisions, enhance genetic gains, and foster sustainable and resilient beef cattle production.

Keywords: GxExM interaction, environmental and management factors, genetic evaluation, Nellore cattle

AGBT2027™
GENERAL MEETING

Signia by Hilton Bonnet Creek

MARCH 1-4, 2027

Learn more at www.agbt.org

Index

Index

Index

Thank you to our Bronze Sponsor, Cellanome, for your support of the AGBT Agricultural Meeting.

We appreciate your partnership and commitment to advancing innovation in agricultural genomics.

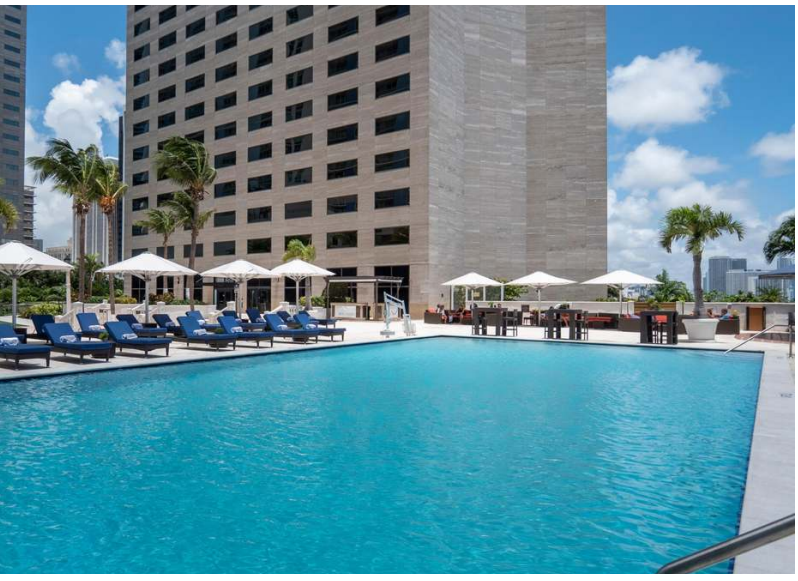
cellanome

AGBT 2027™
AGRICULTURE

SAVE THE DATE

April 4-7, 2027

InterContinental Miami | Miami Florida



Mark your calendar and
learn more: www.agbt.org