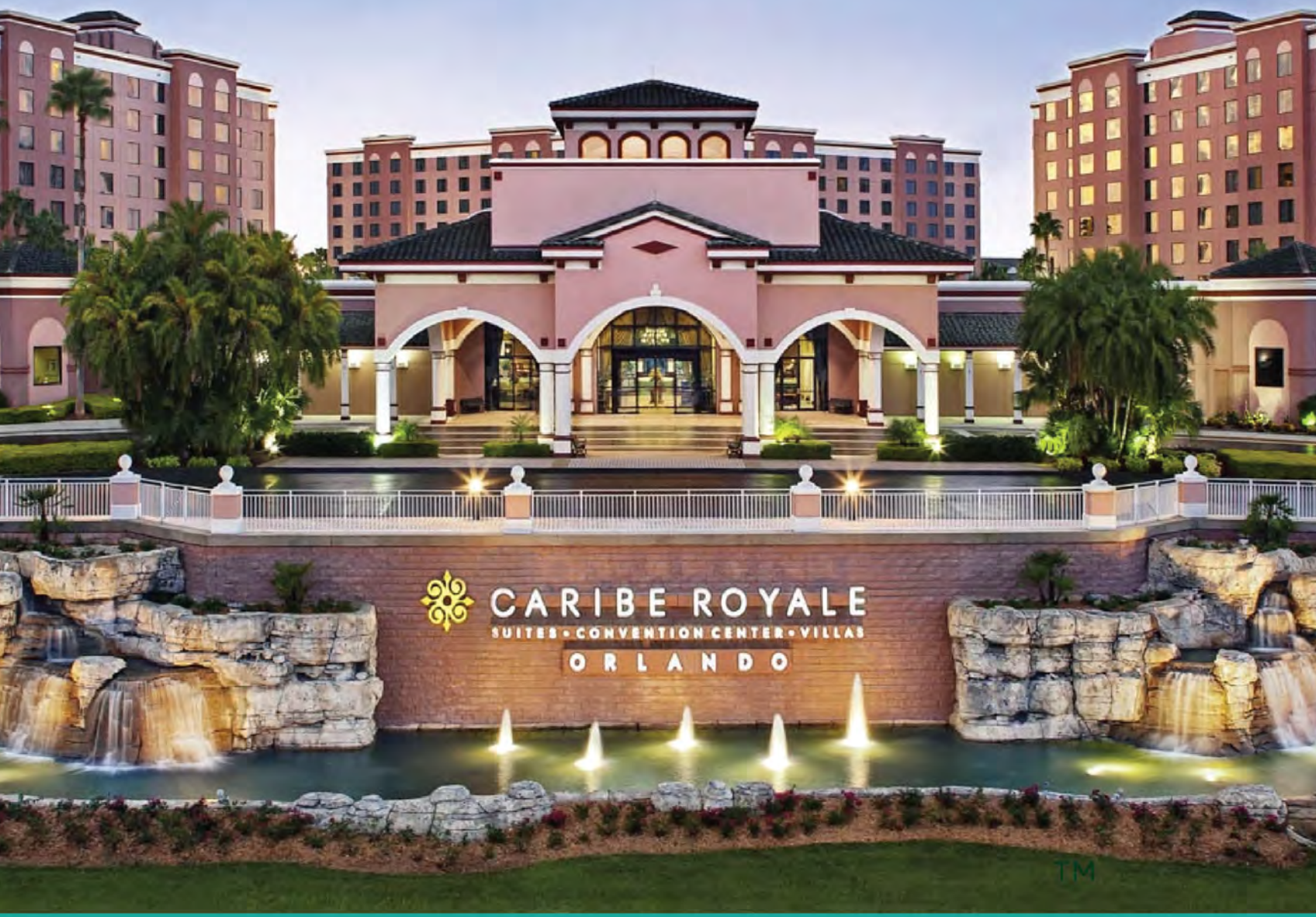
AGBT2025™

AGRICULTURE



March 31 - April 2, 2025 • Orlando, FL

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AGBT2025™ AGRICULTURE

Welcome to the 4th Annual AGBT Agriculture Meeting

Over the next few days, you'll engage with leading genome researchers, data scientists, breeders, policy influencers, funders and technology innovators from around the world who are working to transform terrestrial and aquatic agriculture.

Together, we will explore how genomics and agriculture intersect to address the challenges of a changing planet. Through groundbreaking research, innovative technologies, and collaborative discussions, we strive to shape the future of food 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 25 years, The Genome Partnership has proudly organized AGBT meetings, fostering innovation and collaboration across the genomics community.

Building on AGBT's legacy, this meeting brings together agriculture's brightest minds to drive innovation. AGBT Agriculture is designed to foster meaningful conversations and drive high-impact discoveries through cross-disciplinary collaboration, cutting-edge innovation and focused networking opportunities. With sessions highlighting advancements in CRISPR, single-cell genomics, precision breeding and discussions on informatics, data analytics and genome optimization, this meeting serves as a hub for transformative ideas and solutions.

Additionally, AGBT Agriculture remains committed to investing in the next generation by supporting students and early-career researchers, ensuring the future of agricultural genomics continues to thrive.

We're thrilled to have you here and look forward to an inspiring and influential meeting.

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 2025 a content-rich experience.

Over the next several days, we will gather to collaborate, share the latest scientific discoveries, and discuss new technological breakthroughs—thanks in large part to the hard work of our organizing committee.

Scientific Organizing Committee

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

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

Appolinaire Djikeng
Director General, International Livestock Research Institute (ILRI); Senior Director, CGIAR Livestock-Based Systems

Sarah Hearne*
Chief Science and Innovation Officer, CIMMYT

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

Renee Lafitte
Director for Crops R&D, Gates Foundation

Nathan Lakey
President and Chief Executive Officer, Orion Genomics

Daniela Lourenco*
Associate Professor, Animal and Dairy Science, University of Georgia

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

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

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

**Meeting co-chairs*

AGBT2025™
AGRICULTURAL MEETING

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General Information

Hospitality Desk Hours

Sunday, March 30: 7:00 a.m. – 7:00 p.m.
Monday through Wednesday: 7:30 a.m. – 7:00 p.m.

Name Badges

Badges are essential for conference security and networking. All attendees must:

- Always wear badges visibly, clipped to the provided lanyard with the name facing outward
- Keep badges with you throughout the event
- Present badges for entry to meeting sessions and events

Important: Badges are non-transferable. A proper badge display ensures attendee safety and facilitates valuable connections during our AGBT Agricultural Meeting.

Transportation

Attendees are responsible for their own airport transfers. Orlando International Airport (MCO) is approximately 16 miles from the Caribe Royale Orlando, with a travel time of 20–25 minutes depending on traffic. We recommend arranging transportation in advance using one of the following options:

- Uber, Lyft, Mears or taxi services
- Private shuttle services or local providers

Social Events

- **Posters, Pours & Plates "Welcome Reception"**: Monday, March 31, 5:30 p.m. - 8:30 p.m. - Caribbean Ballrooms IV-VII
- **Sponsor Social & Click2Win**: Tuesday, April 1, beginning at 8 p.m., Boca Foyer. The grand prize will be awarded at the end of Wednesday's plenary session. (This prize is non-transferable.)
- **Farewell Dinner**: Wednesday, April 2, 6–9 p.m., Stadium Club. Show off your team spirit—wear your favorite fan gear to dinner and represent your team in style!

Conference Technology

Official AGBT Mobile App

Enhance your conference experience with our comprehensive mobile app, designed to keep you connected throughout the meeting.

- **App Features:** Comprehensive conference tools – Interactive agenda, detailed speaker and abstract information, and networking features. Seamless event navigation – Interactive venue map and real-time schedule updates.

Access to Click2Win – Participate in our contest for a chance to win prizes. Download instructions:

- Download app from the AGBT email link
- iOS: Scan QR code or visit App Store
- Android: Scan QR code or visit Google Play
- Alternative: Scan QR code at the registration desk or ask for assistance

Social Media Engagement

Stay connected and share your AGBT experience! We've put together some social posts and images to help you easily share that you're attending AGBT Ag—whether you're announcing your participation or posting live from the meeting, we've got you covered! You can access these posts and images here.

Conference Hashtag: #AGBTAg2025

- Handles to Tag: X - @AGBT | LinkedIn - @AGBT Advances in Genome Biology and Technology | Facebook - @Advances in Genome Biology and Technology - AGBT

Tech Support:

- AGBT Hospitality Desk: Caribbean Foyer East
- Wi-Fi Network: AGBT Ag Meeting
- Wi-Fi Password: AGBTAg2025

Share your experience, engage with the community and be part of the conversation!

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Agenda

Sunday, March 30

7:00 a.m. – 7:00 p.m.

AGBT Meeting Registration
Caribbean Foyer East

9:00 a.m. – 9:00 p.m.

Pre-Conference Workshops

9:00 a.m. – 4:15 p.m.

AG2PI Single Cell Workshop
Moderator: Chris Tuggle, Iowa State University
Speakers: Jennifer Clarke, Sharon Greenblum, Wes Warren, Irene Papatheodorou, Fiona McCarthy
Single-cell (SC) genomics offers the opportunity to understand how gene expression contributes to important agricultural phenotypes at a cellular and molecular level, providing new opportunities for precision agriculture. To adapt such SC analysis approaches to improve genotype to phenotype prediction in agriculture, the agricultural community must collectively develop resources, such as harmonized sample and process records and workflows, to achieve the integrated analyses required. The goal of this workshop is to develop a community of agricultural researchers and data resource experts to address this challenge. The impact of a successful workshop will be the ability to effectively interpret and apply SC genomics knowledge to understand the contributions of cell types to complex agricultural phenotypes.
Hibiscus

7:00 p.m. – 9:00 p.m.

The Horse Pangenome Project: Introduction to Agricultural Pangenomics with Practical Applications
Organizers: Jonah Cullen, Sam Stroupe, Sian Durward-Akhurst, Jessica Petersen, Molly McCue, Brian Davis, Ted Kalbfleisch:
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.

(Continue to page 9)

(Continued from page 8)

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 analyses
Hibiscus

Monday, March 31

Scientific Program

6:30 a.m. – 7:30 a.m.
Rise and Shine with AGBT (Optional Activity)
Caribbean Foyer East

7:30 a.m. – 7:00 p.m.
Meeting Registration / Hospitality Desk
Caribbean Foyer East

7:30 a.m. – 9:00 a.m.
Breakfast
Boca 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
Caribbean Ballrooms I-III

Plenary Session I:
Global Opportunities and Challenges for Agriculture
Session Chair: Sarah Hearne, Chief Science and Innovation Officer, CIMMYT, and Co-Chair of the AGBT Agriculture Scientific Organizing Committee
Caribbean Ballrooms I-III

9:10 a.m. – 9:40 a.m.
Dr. Molly Jahn, Professor, University of Wisconsin-Madison
"The future of food"

9:40 a.m. – 10:10 a.m.
Laura Boykin Okalebo, Senior Tech Business Development Manager - Research Computing Solutions with AWS (Amazon Web Services) and a TED Senior Fellow
"Real time portable genomics for food security"

10:10 a.m. – 10:22 a.m.	**Major Sponsor Talk - Twist Bioscience** **Paul Doran, Director of Business Development** "FlexPrep drives the shift from arrays to sequencing for any plant or animal"
10:22 a.m. – 11:00 a.m.	**Coffee Break & Exhibits** Caribbean Ballrooms IV-VII
Plenary Session II:	**Applying the Science I** **Session Chair:** Nathan Lakey, President and Chief Executive Officer, Orion Genomics; The Genome Partnership Board and Organizing Committee Member Caribbean Ballrooms I-III
11:00 a.m. – 11:30 a.m.	**Dr. Suzanne Rowe, Principal Scientist, AgResearch Ltd.** "Updating the toolbox: measuring the biological impacts of breeding for low methane emitting ruminants, and the identification of new molecular phenotypes"
11:30 a.m. – 12:00 p.m.	**Roger Hellens, Chief Technology Officer, Kiwifruit Breeding Centre Limited** "The Kiwifruit Breeding Center: breeding more kiwifruit, better and faster"
12:00 p.m. – 2:00 p.m.	**AGBT Lunch & Workshop(s)** Porte-Cochere
12:20 p.m. – 1:50 p.m.	**CRISPR based gene editing technology development for Agriculture Workshop & Lunch** **Moderator:** Anindya Bandyopadhyay, CIMMYT **Speakers:** Blake Wiedenheft, Markita Landry, Alain Tisser, Tim Kelliher Discovery of CRISPR based gene editing system usher in new possibilities in engineering traits for Agricultural crops and Livestock. Novel trait development, with unprecedented accuracy, has become easier and faster by the application of CRISPR tools. Participants will learn about the latest advancements in the field of CRISPR based gene editing, especially about the next generation CRISPR based tools with wider applicability for precise knockin, RNA editing, germplasm independent editing and engineering of RNA viruses. Talks and discussion will also cover new approaches of trait development in livestock, insect resistance in crops and different beneficial trait development approaches for Global South using CRISPR system-based gene editing Caribbean Ballrooms I-III

Plenary Session III:	**Applying the Science II** **Session Chair:** Alison Van Eenennaam , Distinguished Professor of Cooperative Extension, Animal Biotechnology and Genomics, University of California, Davis, and Organizing Committee Member Caribbean Ballrooms I-III
2:00 p.m. – 2:15 p.m.	**Saif Agha, The Roslin Institute, University of Edinburgh (Abstract Selected Talk)** "New insights into pig social interactions through social network analysis of digital phenotypes"
2:15 p.m. – 2:30 p.m.	**Kelly Balmant, University of Florida (Abstract Selected Talk)** "Elucidating the single-cell transcriptomic landscape of maize leaf senescence"
2:30 p.m. – 2:45 p.m.	**Janeen Braynen, Cold Spring Harbor Laboratory (Abstract Selected Talk)** "Understanding nitrogen adaptation in maize and sorghum through gene networks"
2:45 p.m. – 3:45 p.m.	**Coffee Break & Exhibits** Caribbean Ballrooms IV-VII
Plenary Session IV:	**Re-evolving the Genome** **Session Chair:** Charlie Johnson, Director Genomics & Bioinformatics Service, Texas A&M AgriLife, and Organizing Committee Member Caribbean Ballrooms I-III
3:45 p.m. – 4:15 p.m.	**Bishal Tamang, Research Scientist, University of Illinois** "Optimizing photosynthesis for atmospheric change"
4:15 p.m. – 4:30 p.m.	**Eula Carrara, University of Georgia (Abstract Selected Talk)** "Large-scale single-step GWAS for dairy cattle in the US"
4:30 p.m. – 4:45 p.m.	**Ziming Chen, University of Queensland (Abstract Selected Talk)** "Characterize DNA methylation variation of Escherichia coli under different growth phases using nanopore sequencing"

4:45 p.m. – 5:00 p.m.	**Isidore Houaga, The Roslin Institute, University of Edinburgh (Abstract Selected Talk)** "Building high quality genome assemblies of African cattle breeds using PacBio HiFi"
5:00 p.m. – 5:30 p.m.	**Poster Flash Talks**
5:30 p.m. – 8:30 p.m.	**Posters, Pours & Plates "Welcome Reception"** Caribbean Ballrooms IV-VII
Tuesday, April 1	**(Morning)**
7:30 a.m. – 7:00 p.m.	**Hospitality / Information Desk** Caribbean Foyer East
7:30 a.m. – 9:00 a.m.	**Breakfast** Boca Patio
Plenary Session V:	**Informatics and Data Analytics** **Session Chair:** Daniela Lourenco, Associate Professor, Animal Breeding, Genetics, and Genomics, Department of Animal and Dairy Science, University of Georgia; Co-Chair of the AGBT Agriculture Scientific Organizing Committee Caribbean Ballrooms I-III
9:00 a.m. – 9:30 a.m.	**Dr. Guilherme Rosa, Professor of Quantitative Genetics and Data Science - Department of Animal and Dairy Sciences, University of Wisconsin-Madison** "Enhancing cattle selection and management with big data and omics technologies"
9:30 a.m. – 10:00 a.m.	**Dr. Zulma Vitezica, Institut National Polytechnique de Toulouse, INPT, Animal Genetics** "Non-additive genetic effects, What else?"
10:00 a.m. – 10:15 a.m.	**Jonathan Cahn, Postdoctoral Researcher, Cold Spring Harbor Laboratory (Abstract Selected Talk)** "MaizeCODE: Enhancers and enhancer RNAs shaped maize domestication"

10:15 a.m. – 11:00 a.m.	**Coffee Break & Exhibits** Caribbean Ballroom IV-VII
11:00 a.m. – 11:15 a.m.	**Mina Shumaly, Iowa State University (Abstract Selected Talk)** "Biologically informed machine vision for gait pattern analysis yields novel locomotion phenotypes in pigs"
11:15 a.m. – 11:30 a.m.	**Caleb Stull, University of Missouri (Abstract Selected Talk)** "Evaluation of cross-species single-cell references for automated cell type annotation"
11:30 a.m. – 12:00 p.m.	**AGBT Next Gen Leadership Awards**
12:00 p.m. – 2:00 p.m.	**AGBT Lunch & Workshop(s)** Porte-Cochere
12:20 p.m. – 1:50 p.m.	**Application of gene editing for trait development in Agriculture Workshop and Lunch** **Moderator:** Anindya Bandyopadhyay, CIMMYT **Speakers:** Shuangxia Jin, Leena Tripathi, Alison Van Eenennaam, Bishal Tamang Discovery of CRISPR based gene editing system usher in new possibilities in engineering traits for Agricultural crops and Livestock. Novel trait development, with unprecedented accuracy, has become easier and faster by the application of CRISPR tools. Participants will learn about the latest advancements in the field of CRISPR based gene editing, especially about the next generation CRISPR based tools with wider applicability for precise knockin, RNA editing, germplasm independent editing and engineering of RNA viruses. Talks and discussion will also cover new approaches of trait development in livestock, insect resistance in crops and different beneficial trait development approaches for Global South using CRISPR system-based gene editing Caribbean Ballrooms I-III

Plenary Session VI:	**Transdisciplinary Technologies** **Session Chair:** Appolinaire Djikeng, Director General, International Livestock Research Institute (ILRI), and Organizing Committee Member Caribbean Ballrooms I-III
2:00 p.m. – 2:30 p.m.	**Dr. Gertje Petersen, CEO, FutureBees NZ; Director, LAVES Institute for Agricuture** "The buzziness on bees - How genomics can advance honeybee breeding and conservation efforts"
2:30 p.m. – 2:45 p.m.	**Vanda Marosi, Technical University of Munich, Helmholtz Munich (Abstract Selected Talk)** “Barley pan-transcriptome comparative correlation network analysis reveals ortholog divergence”
2:45 p.m. – 2:57 p.m.	**Major Sponsor Talk: Element Biosciences** **Brian Coullahan, Regional Market Development, Element Biosciences** Natively Integrating Hybrid Selection Technology into the Sequencing Process to Create a Novel Low-pass Plus Capture Genotyping Workflow
2:57 p.m. – 3:40 p.m.	**Dessert & Coffee with Sponsors** Boca Foyer
3:40 p.m. – 4:10 p.m.	**Blake C. Meyers, Ph.D., Editor-in-Chief of The Plant Cell, Director of the UC Davis Genome Center Distinguished Professor, Dept. of Plant Sciences University of California, Davis** "Phased, secondary siRNAs in plant reproduction and other pathways"
4:10 p.m. – 4:25 p.m.	**Chiara Gini, North Carolina State University (Abstract Selected Talk)** "Microbiome response of lactating sows of different genetic background to heat stress: implications for productivity and health"
4:25 p.m. – 4:40 p.m.	**Pedro Ramos, Angus Genetics Inc. (Abstract Selected Talk)** “Genomic Evaluation for Functional Longevity in North American Angus Cattle Using Longitudinal Models”
4:40 p.m. – 4:55 p.m.	**Troy Rowan, University of Tennessee (Abstract Selected Talk)** “Dissecting the molecular basis heterosis in beef cattle”

4:55 p.m. – 5:10 p.m.	**Brenda Murdoch, University of Idaho (Abstract Selected Talk)** "Chromosomal conformation difference in mammalian tissues"
5:10 p.m. – 5:20 p.m.	**Closing Remarks**
5:20 p.m. – 6:30 p.m.	**Wine Reception & Exhibits** Caribbean Ballrooms IV-VII
6:30 p.m. – 8:00 p.m.	**Dinner** The Grove
Beginning at 8:00 p.m.	**Sponsor Social** Boca Foyer

Wednesday, April 2

7:30 a.m. – 7:00 p.m.	**Hospitality / Information Desk** Caribbean Foyer East
7:30 a.m. – 9:00 a.m.	**Breakfast** Boca Patio
Plenary Session VII:	**Quantitative and Molecular Genetics** **Session Chair:** Jack Dekkers, Distinguished Professor, Animal Breeding and Genetics, Department of Animal Science, Iowa State University, and Organizing Committee Member Caribbean Ballrooms I-III
9:00 a.m. – 9:30 a.m.	**Jennie Pryce, Professor, Research Director, Agriculture Victoria Research and La Trobe University, Melbourne Australia** "From genes to green: reducing dairy methane emissions through genomic selection"
9:30 a.m. – 10:00 a.m.	**Dr. Antonio (Toni) Reverter-Gomez, Senior Principal Research Scientist, Animal Genomics, CSIRO Agriculture and Food** "Advanced genomic tools aiding the commercial beef cattle sector: A case study from Australia"
10:00 a.m. – 10:15 a.m.	**Shunichiro Tomura, University of Queensland (Abstract Selected Talk)** "Developing ensembles of genomic prediction models to accelerate crop breeding"

10:15 a.m. – 10:30 a.m.	**Hélène Wilmot, University of Georgia (Abstract Selected Talk)** “Optimizing breed or line assignment based on genomic information: best practices for accurate results”
10:30 a.m. – 11:00 a.m.	**Coffee Break & Exhibits** Caribbean Ballrooms IV-VII
11:00 a.m. – 11:30 a.m.	**José Manuel Yáñez, Professor, University of Chile** "Advancing sustainable aquaculture: Genomic innovations for enhanced production and genetic resilience"
11:30 a.m. – 11:45 a.m.	**Hagai Shohat, Cold Spring Harbor Laboratory (Abstract Selected Talk)** “Contingencies among flowering regulators drove parallel domestication of Solanum crops”
11:45 a.m. – 12:00 p.m.	**Angela Canovas, University of Guelph (Abstract Selected Talk)** “A multi-OMICs integration approach to breed healthier and more sustainable livestock”
12:00 p.m. – 2:00 p.m.	**AGBT Lunch** Porte-Cochere
Plenary Session VIII:	**From the Cutting Edge-New Ideas and Opportunities** **Session Chair:** Renee Lafitte, Deputy Director for Crops R&D, Bill and Melinda Gates Foundation, and Organizing Committee Member Caribbean Ballrooms I-III
2:00 p.m. – 2:30 p.m.	**Irene Papatheodorou, Head of Data Science at the Earlham Institute** "Insights form cross-species comparisons of cell atlases”
2:30 p.m. – 3:00 p.m.	**Charlie Underwood, Professor of Plant Genome Engineering, Radboud University, Nijmegen, the Netherlands, Guest Group Leader Max Planck Institute for Plant Breeding Research, Cologne, Germany** “Polyploid genome design: next generation hybrid breeding”

3:00 p.m. – 3:30 p.m.	**Coffee Break** Caribbean Foyer
3:30 p.m. – 3:45 p.m.	**Marcio Resende, University of Florida (Abstract Selected Talk)** "Using bayesian factor analytic models and environmental predictors for variety recommendation in potatoes"
3:45 p.m. – 4:00 p.m.	**Adam Healey, HudsonAlpha Institute for Biotechnology (Abstract Selected Talk)** "Exploring sorghum's genomic diversity: Pangenomics for adaptation and breeding innovation"
4:00 p.m. – 4:15 p.m.	**Catalin Voiniciuc, University of Florida (Abstract Selected Talk)** "Automation and bioengineering of plant-based polymers for a circular bioeconomy"
4:15 p.m. – 4:45 p.m.	"Taking agricultural innovation from lab to launch: Entrepreneurial insights on scaling scientific discoveries" **(Abstract Selected Panel)** **Panelists include:** Chris Eiben, Founder and CEO, GigaCrop; Kerryann Kocher, CEO, Vytelle; and Bryan Witherbee, President and CEO, Agragene **Facilitator:** Renee Lafitte, Director for Crops R&D, Gates Foundation, and Organizing Committee Member
4:45 p.m. – 5:00 p.m.	**Closing Comments & Click2Win! Winners Announced** 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.	**Farewell Dinner** Stadium Club

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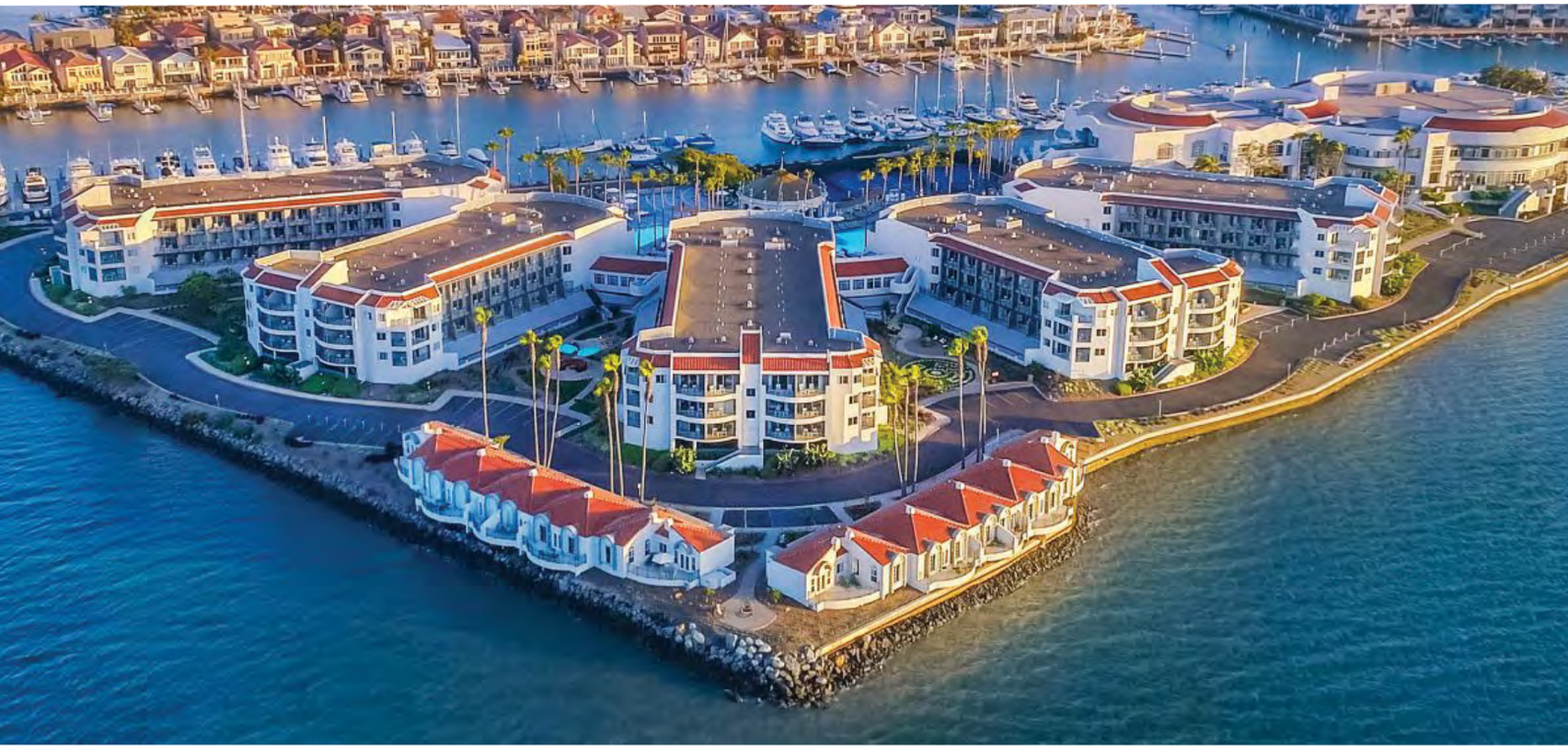

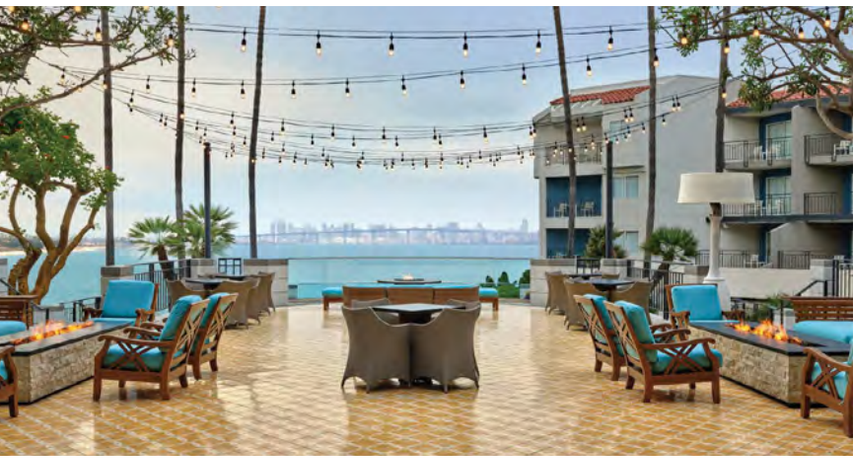

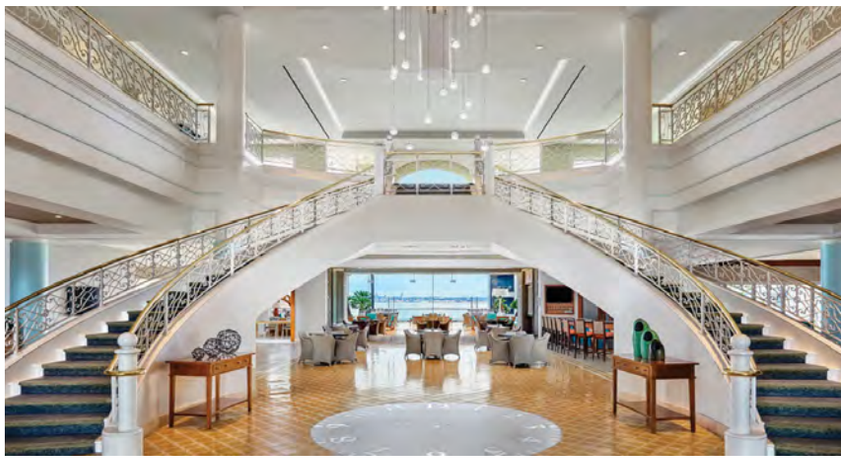

SEPTEMBER 8 – 10, 2025

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CALL FOR ABSTRACTS & REGISTRATION OPENS MAY 13, 2025

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Abstract Table of Contents

page

Applying the Science - Scaling Science Innovation for Use

Unlocking genetic potential within an Agaricus bisporus diversity panel

Nolan Bornowski[1]

1 Amycel/Spawn Mate, Biotechnical Research Laboratory, Royal Oaks, CA

The button mushroom, Agaricus bisporus (J.E. Lange) Imbach, is the most commercially relevant mushroom in the United States, accounting for over 90% of total mushroom production. Despite a long history of button mushroom, deliberate genetic improvement of this crop (i.e. breeding progress) has only occurred within the last 50 years due to biological and technical challenges. Fortunately, mushroom scientists have embraced modern methods that harness sequence data to uncover and utilize genetic diversity within breeding programs. Since most mushroom strains on the market are derived from a handful of clonal lineages, assessing and expanding the germplasm base is critical to make genetic gains and put an end to monoculture. Here, we have sequenced and analyzed a panel of wild and commercial mushroom strains to characterize genetic diversity for use in a button mushroom breeding program. Commercial strains clustered separately from wild strains due to deliberate breeding and/or historical admixture. Although some wild strains were extremely similar to each other, representative wild strains have potential as new parents to infuse useful genetic variation and break free of the industry monoculture.

Founders and futures: genomic monitoring of reintroduced lions in Mozambique

Caitlin J. Curry[1], Willem Briers-Louw[2,3], David Gaynor[4]

1 San Diego Zoo Wildlife Alliance, Conservation Genetics, Escondido, CA
2 Zambeze Delta Conservation Foundation, Marromeu, Sofala, Mozambique
3 Stellenbosch University, Stellenbosch, South Africa
4 University of Pretoria, Mammal Research Institute, Pretoria, South Africa

African lions were extirpated from much of central Mozambique during the Civil War (1974–1994). In 2018, lions from private reserves in South Africa were reintroduced to a 10,000 km² expanse of rehabilitated, contiguous conservation land known as the Zambezi Delta. A comprehensive understanding of the genetics of a founding population, though rarely available, is crucial for effective reintroduction management to mitigate founder effects—negative consequences associated with establishing a population from a small number of individuals from a larger population. Using whole-genome sequencing of 21 of the 27 reintroduced lions, we evaluated the genetic health and viability of the founding population, laying the groundwork for ongoing genomic monitoring and strategies to mitigate founder effects. Runs of homozygosity ranged widely (0.013–0.513), but the founders exhibited low overall kinship (-0.4) and heterozygosity levels consistent with other lion populations (mean HO=0.262). Principal components analysis identified four clusters strongly influenced by shared demographic history and we identified fixed private alleles unique to each source location. This genetic structure will benefit future generations by increasing genetic diversity as individuals from different source locations interbreed. Tracking the integration of these fixed private alleles across generations will provide valuable insights into the genetic consequences of the lion social system and its implications for conservation. These findings will guide conservation policy and management in the Zambezi Delta, aiming to prevent genetic erosion and enhance population viability.

Optimizing the delivery of CRISPR/Cas9 ribonucleoproteins for efficient genome editing in bovine embryos

Xiaofeng Du[1], Alex Quinn[1], Laercio Porto-Neto[1]

1 Commonwealth Scientific and Industrial Research Organisation, Agriculture & Food, Brisbane, Queensland, Australia

Genome editing applications in livestock to enhance traits or create new biomedical research models have proven to be both feasible and valuable. However, the lack of efficient approaches for the delivery of CRISPR molecules into zygotes has been a technical hurdle for large-scale applications of gene editing in livestock. Herein, we aimed to optimize the delivery of CRISPR components into zygotes to assist in establishing a streamlined and efficient workflow for generating gene-edited bovine embryos. Using Bos taurus prolactin receptor (PRLR) as the target gene, we evaluated three transfection approaches for delivery of Cas9-sgRNA ribonucleoproteins into bovine zygotes: lipofection with Lipofectamine CRISPRMAX, or electroporation using either the Neon or NEPA21 electroporation systems. PCR genotyping of individual embryos showed that CRISPRMAX transfection generated up to 30% PRLR-edited blastocysts, without affecting the embryo cleavage (93%) and blastocyst rate (39%) relative to non-transfected controls. For both NEPA21 and Neon electroporation, we found higher pulse voltage, pulse length and number of pulses resulted in enhanced gene editing efficiency but compromised embryo cleavage and blastocyst rates. NEPA21 electroporation with a commercial electroporation enhancer reagent produced up to 47.6% transfected embryos with PRLR deletion, but with decreased embryo cleavage (62%) and blastocyst (18%) rates. In addition, we found that combining NEPA21 electroporation with CRISPRMAX lipofection enhanced the gene editing efficiency to 50%, with 64% embryo cleavage rate and 18% blastocyst rate. For Neon electroporation, voltage was within the range 550-700 V for 1 pulse of 10-20 ms. PCR assays and Sanger sequencing analysis demonstrated that 65.2% blastocysts from Neon electroporated groups (50% cleavage rate and 10% blastocyst rate) possessed the PRLR deletion (700 V for 1 pulse of 20 ms). Additional studies may be necessary to further optimize electroporation parameters to achieve an optimal balance between embryo viability and gene editing efficiency. These outcomes will provide valuable insights for improving gene editing workflows for bovines and could help to promote and accelerate the widespread implementation of genome editing technology in livestock.

Genome British Columbia: 25 years of investing in agriculture, agrifood, and beyond

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Genome BC was founded in 2000 and is a not-for-profit funding organization supporting omics research, innovation and commercialization to grow globally competitive life sciences sectors and deliver sustainable benefits for British Columbia (BC), Canada and beyond. Our work expands across sectors such as forestry, fisheries and aquaculture, agriculture, mining, energy and environment as well as human health. We have leveraged our strategic programs and projects to manage a cumulative portfolio of nearly $1.3B in over 525 research projects, technology platforms and innovation initiatives. In addition, Genome BC works to integrate genomics into society by supporting genomics-related social science research and providing opportunities to learn more about life sciences for educators, students, and the public. We also developed an Indigenous Peoples Engagement Framework to empower Indigenous innovation through partnerships that deliver solutions to the most pressing challenges as identified by Indigenous peoples. Owing to our province's diverse climate and landscape, BC produces a wide range of commodities including greenhouse and indoor growing, field and horticultural crops and livestock. The agriculture sector contributes over $2 billion to the province's GDP and is an important source of income for many communities. Since inception, Genome BC has invested over $22 million in 60 agricultural genomic projects and attracted close to $88 million in co-investment. This poster provides an overview of our investments in the agriculture sector which address challenges across commodities, support resilient food systems and strengthen food security, especially in the face of unpredictable climate events. Our investments benefit producers, processors and consumers and help to meet the demand for healthy food produced through sustainable practices that support the environment.

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Optimizing cost-effective gene expression phenotyping approaches in cattle using 3' mRNA sequencing

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Background Genetic and genomic selection programs require large numbers of phenotypes observed for animals in shared environments. Direct measurements of phenotypes like meat quality, methane emission, and disease susceptibility are difficult and expensive to measure at scale but are critically important to livestock production. Our work leans on our understanding of the "Central Dogma" of molecular genetics to leverage molecular intermediates as cheaply-measured proxies of organism-level phenotypes. The rapidly declining cost of next-generation sequencing presents opportunities for population-level molecular phenotyping. While the cost of whole transcriptome sequencing has declined recently, its required sequencing depth still makes it an expensive choice for wide-scale molecular phenotyping. We aim to optimize 3' mRNA sequencing (3' mRNA-Seq) approaches for collecting cost-effective proxy molecular phenotypes for cattle from easy-to-collect tissue samples (i.e., whole blood). We used matched 3' mRNA-Seq samples for 15 Holstein male calves in a heat stress trail to identify the 1) best library preparation kit (Takara SMART-Seq v4 3' DE and Lexogen QuantSeq) and 2) optimal sequencing depth (0.5 to 20 million reads/sample) to capture gene expression phenotypes most cost-effectively.

Results Takara SMART-Seq v4 3' DE outperformed Lexogen QuantSeq libraries across all metrics: number of quality reads, expressed genes, informative genes, differentially expressed genes, and 3' biased intragenic variants. Serial downsampling analyses identified that as few as 8.0 million reads per sample could effectively capture most of the between-sample variation in gene expression. However, progressively more reads did provide marginal increases in recall across metrics. These 3' mRNA-Seq reads can also capture animal genotypes that could be used as the basis for downstream imputation. The 10 million read downsampled groups called an average of 104,386 SNPs and 20,131 INDELs, many of which segregate at moderate minor allele frequencies in the population.

Conclusion This work demonstrates that 3' mRNA-Seq with Takara SMART-Seq v4 3' DE can provide an incredibly cost-effective (<$25/sample) approach to quantifying molecular phenotypes (gene expression) while discovering sufficient variation for use in genotype imputation. Ongoing work is evaluating the accuracy of imputation and the ability of much larger datasets to predict individual animal phenotypes.

Integrative approaches to conservation and genomic insights of Cylicomorpha solmsii (Urb.) Urb: a step toward sustainable restoration planning

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Cylicomorpha solmsii (Urb.) Urb, a dioecious tropical tree in the Caricaceae family, endemic to Cameroon, holds significant potential for bioenergy production and pharmaceutical applications. Unfortunately, this potent economic reservoir to date remains unexploited, non-domesticated, and non-commercialized. Moreover, C. solmsii is a threatened IUCN red-list species that is gradually becoming extinct for agricultural purposes, wood exploitation, and growing urbanization. This study aims to prioritize sustainable restoration efforts by integrating ecological, morphological, and genomic approaches. Results reveal that its seeds germinate exclusively under light, exhibiting physiological embryonic dormancy. Morphological analysis confirmed C. solmsii as dioecious, with incomplete unisexual flower whorls. Fruit production occurred year-round, though with varying intensity. We further explored the molecular basis of C. solmsii's sex determination system using bioinformatics approaches. De novo assembly of female and male genomes using PacBio HiFi and Illumina NovaSeq 6000 data revealed genome sizes of 1.09 Gb (female) and 1.06 Gb (male) in nine pseudo-chromosomes. Gene annotation identified 39,429 gene models, with repeats comprising 63.80% of the genome. An XY heterogametic sex determination system was identified, with 193 Y-linked contigs and the SDR region spanning ~49.15 Mb and 172 X-linked counterparts totaling ~53.00 Mb. Analysis of 30 X/Y gene pairs revealed evolutionary strata with divergence times ranging from 0.53 to 11.39 million years, supporting the hypothesis of a recent origin of sex chromosomes in Caricaceae. Population genomic analysis of 20 individuals revealed genetic differentiation (Fst = 0.14) and distinct nucleotide diversity patterns ($\pi = 3.64 \times 10^{-5}$ for X; 1.10×10^{-4} for Y). Tajima's D values indicated a bottleneck in the X-haplotype (-0.17) and high heterozygosity in the Y-haplotype (1.09). Two candidate sex-determining genes, SVP-like and EREBP13, were identified, suggesting conserved roles in carpel suppression and stamen promotion. These findings advance our understanding of dioecy evolution and sex chromosome emergence in C. solmsii, providing critical insights for its conservation and genetic research.

Integrated approach to genotyping with NGS and imputation analysis

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Low-pass whole genome sequencing (LP-WGS) offers a cost-effective approach to sequencing entire genomes at coverages ranging from 0.1x to 10x. This technique, followed by imputation, is becoming the preferred method for genotyping among plant and animal breeders. LP-WGS can capture a much broader spectrum of genetic variation compared to SNP arrays and is not limited by a fixed content, speeding up the selection process and improving the reliability of predictions. However, the high computational demands associated with processing and imputing LP-WGS data make it less accessible for many research programs and breeding initiatives.

Using rice as an example, we present LP-WGS data obtained using the Revvity solutions for homogenization, DNA extraction, and our new NEXTFLEX® HT Agrigenomics Low-Pass WGS Kit, followed up by analysis and imputation with CURIO™ Genomics Platform. An integrated approach for library preparation and imputation analysis of plant and animal genomes, resolving many of the challenges associated to imputation accuracy and computational demand.

For research use only. Not for use in diagnostic procedures.

Adoption of different omics to adapt alfalfa to southeastern USA

Pablo Sipowicz, Ayush Sharma, Mario Andrade, Aditya Singh & Esteban Rios

Adapting alfalfa (Medicago sativa L. subsp. sativa) to southeastern United States is challenging. Stand persistence is highly reduced, as plant survival is heavily impacted by extreme weather conditions and disease pressure. Also, genetic gain for dry matter yield (DMY) has remained stagnant in recent decades in alfalfa. Prediction breeding has been proposed as an effective framework to increase genetic gain for complex traits. Genomic prediction models have routinely been developed for alfalfa breeding programs. More recently, phenomic prediction has been proposed as an effective tool for breeders and has shown promising results in other crops. The objectives of this study were to compare prediction models for persistence and DMY using genomic and/or phenomic predictors under different management practices. Two trials were established at Citra, FL with 139 half-sib families and five commercial checks under different nitrogen fertilization management practices in a randomized complete block design with two replications. Phenotypic data for DMY and persistence were recorded for nine and seven harvests, respectively, between 2021 and 2023. Genomic prediction models (GP) were developed using the best linear unbiased prediction (GBLUP) approach using genotypic data from 2,305 markers from the DArTag 3K panel. Phenomic prediction models (PP) were developed using a similar approach by creating a relationship matrix from reflectance data of 273 wavelengths (PBLUP approach) acquired by unmanned aerial vehicle flights. For DMY, PP outperformed GP when performing predictions within harvest and fertilization management achieving maximum predictive ability of 0.71 compared to 0.46 respectively. When predicting across harvests or management practice predictive ability for PP models decreased and their performance was similar or reversed, relative to GP, depending on the harvest or management practice considered. For persistence, GP models achieved moderate predictive ability (0.33) while PP models varied depending on the harvest in which reflectance was captured (ranging from 0.22-0.55). Our results suggest that phenomic prediction shows promise to be incorporated in alfalfa breeding programs but is influenced by fertilization management and the timepoint of reflectance data collection.

From FASTQ to Fork - Omics Assisted Product Development

Switching from arrays to sequence-based genotyping in cattle breeding operation

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As sequencing costs continue to drop dramatically, sequencing-based approaches are in the process of replacing costly genotyping arrays. This shift to sequencing is driven by better data, lower cost, and the capability to run a single platform for both discovery and genotyping. This simplification of lab capabilities has profound implications for breeding program efficiency, genetic gain, and the sustainability and precision of agricultural practices. On the other hand, breeders have trusted array data for a long time, and its use is fully integrated into their breeding and discovery operations. Therefore, any sequencing-based approach to genotyping must provide breeders with the same level of confidence in the results while also allowing them to continue to leverage their wealth of legacy array data. Here we present an example of a 25,000-head cow-calf operation that has made the switch working in collaboration with Curio Genomics and Twist Bioscience. First, we mapped the existing array data from the 70k bovine array into the CURIO™ agrigenomics data analysis platform. Next, we leveraged Twist's new HTP FlexPrep library prep and multiplex capture to target genomic regions previously captured by arrays. Finally, using CURIO, we evaluated the concordance of results from arrays and targeted sequencing in the same animals. The results were 99.9% concordant with each other providing the confidence to complete the switch from arrays to sequencing both increasing efficiency and accelerating best practice development.

From the Cutting Edge - New Ideas and Opportunities

Improving pipeline efficiencies in Agrobacterium-mediated transformation of maize through the use of BULKEDIT Agrobacterium cultures

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The Wisconsin Crop Innovation Center has recently, through discovery of the developmental gene WOX2A, improved maize transformation of the agronomically relevant inbred LH244 to an efficiency in excess of 100%. This level of efficiency suggested that it might be possible to combine multiple constructs within an independent experiment, but in order for the output to be practicable, the resulting T0 plants have to be deconvoluted to understand which plants received which T-DNA molecule. To address this challenge, a total of 40 DIRECTCLONE MAIZEEDIT binary vectors, each containing one unique guide RNA were assembled. Three independent, equimolar mixtures containing either 12, 13, or 16 plasmids (with the MAIZEOE control binary allowing for non-destructive monitoring of the process included in both the second and third mixes) were used to prepare BULKEDIT Agrobacterium stocks via electroporation of the Thy- auxotrophic mutant of Agrobacterium tumefaciens strain LBA4404, which also carried the WCIC Helper Plasmid 3 (WH3). Importantly, the recovery broth from the electroporation cuvette was directly subcultured into bulk liquid culture, bypassing solid phase culture to minimize enrichment of any single construct. Each BULKEDIT mix was used to inoculate immature embryos from the elite maize inbred line, LH244. A total of 371 plantlets were recovered from tissue culture with a distribution of 132, 143, and 96 individuals from mix 1, 2 and 3, respectively. Sequencing of T0 genomic DNA allowed for identification of which individuals received which guide RNA and confirmed that 324 plantlets had single T-DNA insertions. Chi-square tests indicated that mixes 1 and 2 had equal representation of their guides at a 99% significance level, while mix 3 showed unequal representation. Overall, these results suggest that the BULK approach to pool multiple binary plasmids into a single Agrobacterium culture is a promising approach to improve plant transformation pipeline efficiency. Future work will focus on analysis of the gene editing outcomes in the existing plants and generating new BULKEDIT mixes for further testing.

Natively integrating hybrid selection technology into the sequencing process to create a novel low-pass plus capture genotyping workflow

From the Cutting Edge - New Ideas and Opportunities

POSTER 303

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Modern agricultural breeding programs increasingly rely on genotyping data as a fundamental component of genomic selection models. These programs often generate high-density genotype information (ranging from tens to hundreds of thousands of genotypes per sample) from key members of a population. Common methods for acquiring this data include whole exome/hybrid capture enrichment, genotyping arrays, and, more recently, low-pass whole genome sequencing, each with distinct advantages and limitations. As the cost of next-generation sequencing continues to decrease, the shift from legacy microarray methods has become more widespread. However, broader adoption of hybrid capture methods has been hindered due to increased workflow complexity. Similarly, adoption of low-pass whole genome sequencing has many operational benefits but often misses direct observation of high-power, trait-linked markers. In this study, we present Trinity™ as a solution that overcomes the limitations of both standalone methods. Trinity is a novel targeted sequencing approach that simplifies the hybrid capture process by automating post-hybridization steps directly on the sequencer, resulting in highly uniform and consistent coverage of targeted genomic regions. In our experiment, we obtained a mean target coverage of 24x with over 94% of the targets having >10x coverage for a 43k target peanut panel. Furthermore, in a second experiment we demonstrate the ability to incorporate user-defined low-pass genome coverage within the same sequencing run and using the same libraries, enabling accurate imputation across the entire genome. In this second experiment, we obtained ~1.5x average WGS coverage with a mean target coverage of 40-50x for the 43k target peanut panel. By reducing total library preparation time from over 20 hours to 5 hours, and combining targeted enrichment with whole genome sequencing, the Trinity hybrid capture workflow can offer an efficient, scalable and comprehensive alternative to traditional genotyping arrays at a lower overall cost.

Targeted reduction of repetitive sequences to lower whole-genome sequencing costs for crop breeding

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Key food crops are costly to sequence due to large genome sizes, repetitive sequences, and varying ploidy levels. Reducing whole-genome sequencing (WGS) costs is therefore critical to making plant genome sequencing more accessible for breeding programs. We have developed an innovative technology to selectively eliminate unwanted repetitive sequences from WGS libraries using the Argonaute protein from Thermus thermophilus (TtAgo). Unlike nucleases such as Cas9, TtAgo offers an important advantage; it can generate its own DNA guides from double-stranded DNA (dsDNA) through a process known as 'chopping,' removing the need for complex guide design. Our method has successfully depleted 10% of the cucumber genome and 4% of the papaya genome using 77 short dsDNA probes, with reproducible results under standardized experimental conditions. We are currently optimizing our technology, aiming to deplete ~50% of the maize genome, while increasing the proportion of sequences covering genes and other regulatory elements. It is our goal to extend this to all genomes, even beyond plants, which significantly reduces the costs of WGS while retaining most of the genome's genetic diversity.

The technology presented in this abstract is protected by a patent application owned by Genetwister IP B.V.

Global Opportunities and Challenges for Agriculture

Harnessing the polyploid genomes of Australian wild millets to strengthen food systems

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Australian native millets, such as Echinochloa turneriana (channel millet) and Panicum decompositum (native millet), hold great promise for addressing global food security challenges. They thrive in saline and arid environments, thanks to their resilience and efficient C4 photosynthetic pathway, making them particularly valuable for agriculture in drought-prone regions. With the growing urgency of climate change and food insecurity, the conservation and utilisation of Crop Wild Relatives (CWRs) have become paramount. These CWRs provide crucial genetic resources that can be harnessed to develop 'climate-smart' crops. Millets, both domesticated and wild, have long played an essential role in indigenous diets across the world, with Australian wild millets offering unique genetic contributions to global breeding programs. We now report the sequencing of the genomes of Echinochloa turneriana and Panicum decompositum, along with the resequencing of other millets, to uncover genetic diversity, evolutionary relationships, and key traits that could expedite domestication. A high-quality reference assembly and haplotype-resolved genome of E. turneriana have been constructed, revealing its allododecaploid nature (AABBCCGGHHII; 2n=108) with a base chromosome number of x=9. The genome contains six distinct subgenomes and a total size of 2.77 Gb. Long terminal repeat (LTR) analysis identified SG5 as the oldest and most stable subgenome, reflecting its evolutionary persistence. The assembly exhibits an N50 value of 42 Mb, coupled with 99.6% BUSCO completeness, underscoring its structural and functional integrity. This genomic characterisation enhances our understanding of the complex genetic architecture of polyploid species and provides a model for identifying domestication genes. By integrating genomics and biotechnology, the de-novo domestication of Australian millets offers a unique opportunity to diversify Australian farming systems, ensuring environmental and economic sustainability while developing climate-resilient crops with superior traits.

Exploring NLRome diversity in melon: unlocking resources for association studies and resistance breeding

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Growing disease-resistant plant varieties is the best way to avoid yield and quality loss during pathogen infection while ensuring sustainable agriculture. However, the challenge is identifying and introducing alleles conferring resistance into elite backgrounds. Traditionally, mainly monogenic resistance, simpler but less durable, has been introduced in crops. Integrating polygenic resistance is challenging but promises lasting protection. Among plant resistance genes, the Nucleotide-binding-site-Leucine-rich-Repeat (NLR) family stands as the most important, playing a central role in the so-called effector triggered immunity. However, their role in quantitative resistance remains unclear. Additionally, the NLR family is highly variable, meaning reference genomes capture only a fraction of the species' NLR diversity. Thus, sequencing a large number of genotypes is essential for a complete understanding.

In melon, as in many other plant species, the specific link between NLR genotypes and phenotypes remains largely unexplored. This is due to challenges in sequencing, assembling, and annotating NLRs, which are often arranged in complex and repetitive clusters. Moreover, large-scale phenotyping presents significant challenges. We defined an approach for NLR resistance association. On the one hand, we constructed a diversity panel of more than 200 melon accessions coming from very diverse origins, and presenting a different degree of resistance to a dozen of pests and pathogens. On the other hand, we evaluated and implemented Nanopore adaptive sampling (NAS), a targeted sequencing method, for the long-reads sequencing and assembly of the melon NLRome. When classical Genome Wide Association Studies provided evidence of NLR linkage with the studied resistance, we used the NLRome data for refinement and candidate NLR identification. To develop and test our analysis procedure, we first worked on resistance to Fusarium wilt and aphids, traits known to be associated with NLR genes. We used matrices of presence or absence of k-mers or NLR genes derived from NAS data, as well as a pangenome graph. Quality of results were highly promising, allowing to identify new alleles of resistance. In the next phase of the project, we will extend this approach to 11 phenotyped diseases, paving the way for the creation of the first-ever complete and comprehensive melon NLRome atlas.

Building high-quality comparative genomic resources for invert-repeat lacking clade-legumes to fuel base-level modeling of functionality

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Each species represents an evolutionary solution to survival on earth and an opportunity to understand and model biological processes. With regard to improving the productivity and sustainability of food production, relatives of crop species capture valuable diversity that can be compared to understand and predict biological form and function. As part of the Genome Canada PEAce (Pea Climate Efficient) project, and the Canadian GRDI (Genome Research and Development Initiative) GenARCC (Genomic Adaptation and Resilience to Climate Change) we are assembling and annotating dozens of cool season legumes belonging to the invert-repeat lacking clade (IRLC). Here we report on genome assembly progress for these projects including the development of a high-throughput and robust high-molecular weight DNA extraction protocol suitable for both PacBio HiFi and ultralong Nanopore sequencing across many species. Further we describe the benefits to contiguity of combining Nanopore and PacBio HiFi data in this clade rich in oversized retroelements and how we are leveraging differences in gene expression in this clade to train gene expression models.

CRISPR/Cas9 activation and overexpression of MusaVicilin gene for disease resistance in banana

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Banana Xanthomonas wilt disease caused by Xanthomonas campestris pv. musacearum (Xvm) is a major banana production constraint in East and Central African nations. Limitations in classical breeding have prompted the exploration of precise molecular genetic tools like genetic modification and genome editing. All cultivated banana varieties are susceptible to Xcm; the only resistant variety is the progenitor species Musa balbisiana. In our previous study, there was a 5-fold up-regulation of MusaVicilin gene in the BXW-resistant progenitor species Musa balbisiana, compared to BXW-susceptible banana genotype Pisang Awak, when challenged with Xvm, suggesting involvement of the gene in plant defense. To further exploit the efficacy of the MusaVicilin gene against Xvm, we investigated the suitability of overexpression of MusaVicilin antimicrobial protein gene with a plasmid vector containing the full length of the gene, and CRISPR activated (CRISPa) the promoter region of MusaVicilin gene in BXW-susceptible banana cultivar Sukali Ndiizi for resistance against BXW. Disease resistance and gene expression analysis demonstrated significant differences between transgenic events generated by the two transformation strategies. The transgenic banana events overexpressing MusaVicilin gene exhibited enhanced resistance to BXW disease compared to non-transgenic control plants. Therefore, banana transgenic events overexpressing MusaVicilin antimicrobial protein gene have potential to provide resistance against Xanthomonas bacterium. Our main purpose is to generate transgenic banana with a stack genes construct which includes, this antimicrobial protein gene with other R genes or receptor genes to provide enhance resistance against this deadly disease. Further, these banana events need to be tested in the confined field trial for BXW resistance and agronomic performance.

Maladaptation in cereal crop landraces following a soot-producing climate catastrophe

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Extreme and sudden changes to climate would threaten plant populations that are adapted to historical local climates, while also the intraspecific diversity present in crop landraces (traditional varieties) may aid in increasing agricultural resilience under changing climates. Soot-producing global catastrophes such as nuclear war, super-volcano eruption, or asteroid strike, although rare, pose a serious threat to human survival. Light-absorbing aerosols would sharply reduce temperature and solar radiation reaching the earth's surface, decreasing crop productivity including for locally adapted traditional crop varieties, i.e. landraces. Here, we test post-catastrophic climate impacts on barley, maize, rice, and sorghum, four crops with extensive landrace cultivation, under a range of nuclear war scenarios that differ in the amount of soot injected into the climate model. We used a crop growth model to estimate gradients of environmental stressors that drive local adaptation. We then fit genotype environment associations using high density genomic markers with gradient forest offset (GF offset) methods and predicted maladaptation through time. As a validation, we found that our GF models successfully predicted local adaptation of maize landraces in multiple common gardens across Mexico. We found strong concordance between GF offset and disruptions in climate, and landraces were predicted to be the most maladapted across space and time where soot-induced climate change was the greatest. We further used our GF models to identify landrace varieties best matched to specific post-catastrophic conditions, indicating potential substitutions for agricultural resilience. We found the best landrace genotype was often far away or in another nation, though countries with more climatic diversity had better within-country substitutions. Our results highlight that a soot-producing catastrophe would result in the global maladaptation of landraces and suggest that current landrace adaptive diversity is insufficient for agricultural resilience in the case of the scenarios with the greatest change to climate.

Building plant breeding capacity in the United States: a new graduate program launched at the University of Florida

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Recent studies have highlighted the diminishing number of skilled and experienced plant breeders in the United States (Gepts and Hancock, 2006; Coe et al., 2020). This shortage poses a significant risk to global food systems and our ability to feed a growing population. To address this challenge, the Plant Breeding Working Group (PBWG) at the Institute of Food and Agricultural Sciences (UF/IFAS), University of Florida (UF), established the Plant Breeding Graduate Program (PBGP) with the goal of training the next generation of plant breeders. As Florida's land-grant institution, UF/IFAS is a leader in cultivar development and licensing, with over 30 plant breeding faculty members strategically located across the state. Since the first cohort of PhD students joined the PBGP in 2021, the program has grown rapidly to 40 students working on a diverse range of crops and breeding systems. Several of our students are presenting posters/talks at AGBT-Agricultural Meeting 2025. The program is designed to produce well-rounded plant breeding professionals ready to take on roles in academia, industry, non-profits, and other sectors. The curriculum blends traditional and modern breeding methods, including quantitative genetics, field evaluations, molecular techniques, and advanced phenotyping technologies. Florida's unique and challenging climate offers an ideal setting for breeding specialty crops, such as berries, citrus, vegetables, forages, and turfgrass, that are difficult to produce in other parts of the U.S. As demand for these crops increases, UF/IFAS strives to be the premier institution for training graduate students in specialty crop breeding. The program benefits from cutting-edge facilities, strong industry partnerships, and robust research support, making UF/IFAS an attractive destination for aspiring plant breeders. Up to five fully funded graduate assistantships are available to competitive applicants through the PBGP program every year (https://programs.ifas.ufl.edu/plant-breeding/financial-support/). Besides, UF/IFAS's collaboration with the Florida Foundation Seed Producers ensures that breeding innovations are licensed globally, with 70% of royalty revenues reinvested directly into the breeding programs and the PBGP, further supporting the university's mission to develop new plant varieties and train the next generation of plant breeders.

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Informatics and Data Analytics

Unraveling molecular and cellular insights in soybean-AMF symbiosis

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Beneficial microbes like arbuscular mycorrhizal fungi (AMF) present an opportunity for sustainable enhancements to nutrient uptake in legume crops. AMF-plant symbiosis increases nutrient and water accessibility through their hyphal-arbuscule networks, as well as resistance to drought and salinity stress. However, the complexity of signal perception, metabolic-flux, nutrient absorption and translocation at the sub-cellular level is elusive in soybean. In this study, we have employed single nucleus sequencing technology utilizing five distinct time points of AMF colonization to create a comprehensive atlas combining both structural and temporal gene expression. Comparative analyses have offered insights into cell-type specific changes in pathways such as organelle development, nutrient uptake, and senescence over time. Investigation so far has identified novel symbiosis-induced genes significant for establishing and maintaining cooperative relationships, as well as providing further evidence for previously established symbiosis related genes. Previously unstudied soybean specific genes have been chosen for functional validation experiments to further identify and characterize genes essential for soybean-AMF symbiosis. This resource provides valuable information for optimizing symbiotic relationships in agricultural practices, as well as a framework for genetic discovery in a non-model crop species.

Mutations in several key genes influences equine disorders of sexual development

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Disorders of sex development (DSDs) are clinically heterogeneous conditions affecting sex determination, sexual differentiation, gonadal development, and reproduction. Many cases and forms of DSDs have been described in horses, though knowledge about the genomics of equine DSDs is sparse and no causative genes or risk factors are known for most. Here we initiated systematic research on the genomics of three select, recurrently observed, chromosomally normal equine DSDs: 64,XX mares with X-monosomy-like gonadal dysgenesis; 64,XY SRY- positive female-like horses, and 64,XX intersex horses. Whole genome short-read Illumina data has been generated for 91 and long-read PacBio HiFi data for 18 DSD horses. The first stage of analysis used short-read data-based variant VCF files of all DSD cases and ~200 control horses to inspect a set of ~80 candidate genes for mutations of high and moderate effect and for homozygosity for alternate alleles with < 1% frequency. Missense, nonsense, frameshift or indel mutations were found in 15 sex development key genes in 25 DSD cases, whereas mutations in five genes (AR, FRAS1, FREM2, NR0B1, STAG3) were found in two or more cases and one case had two missense mutations in TACR3. Notably, seven 64,XY female-like horses had seven different mutations in the androgen receptor gene resulting in androgen insensitivity syndrome. Genomic findings were aligned with endocrine profiles for anti-Müllerian hormone and testosterone that were obtained for 60 DSD cases. Data analysis continues with hypothesis free genome-wide candidate variant discovery against a variant database of ~1500 horse genomes and with structural variant discovery from the long-read data. The findings will contribute to the development of improved molecular and endocrine diagnostics of horse DSDs and advance the knowledge about the genetic regulation of sex development in horses and other mammals.

Association between rumen metagenomics and performance phenotypes in young bulls

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Studies using 16S rRNA sequencing have revealed insights into microbiota composition and its associations with host phenotypic traits and animal performance. This study investigated the fecal microbiota of 475 young Nelore bulls (aged 18–30 months), with samples collected over four different years, from 2019 to 2022. Fecal samples were collected, and DNA was extracted using the Quick-DNA™ Fecal/Soil Microbe Miniprep Kit. Amplicons from 16S rRNA were sequenced on an Illumina NovaSeq platform (2 × 250 bp). Quality-filtered reads (>Q25) were processed with QIIME 2 and the DADA2 package to generate amplicon sequence variants (ASVs), annotated using the SILVA v.138.1 database. The resulting ASV tables for bacteria and archaea were rarefied and used to determine alpha (ASV count, Shannon-Wiener index) and beta diversity (Unweighted UniFrac distance). Features with a prevalence of ⩾5% were retained and normalized using the Centered Log-Ratio (CLR) transformation. The normalized ASV table was used to evaluate associations with phenotypic traits using linear mixed models (LMMs) in the lme4qtl package, with a genomic relationship matrix as a random effect. We identified 1268 bacterial and 75 archaeal ASVs post-filtering. Alpha diversity analysis revealed significant intra-year diversity for both bacterial and archaeal populations. When comparing the Shannon diversity index ($p \leqslant 0.05$, Wilcoxon test), significant differences in bacterial diversity were observed across all years, except between 2019 and 2021. For archaeal diversity, significant differences were found between most years, except for 2019–2020 and 2021–2022. Beta diversity analysis showed no bacterial sample segregation across years, except for 2022, which formed a distinct cluster. No archaeal sample segregation was observed. In bacterial ASVs analyses at the genus level, significant associations were observed with Loin Eye Area (LEA) and Average Metabolic Live Weight (AMLW), with specific ASVs associated with high and low values of the traits. In archaeal ASVs analyses at the genus level, significant associations were also identified with LEA and AMLW (both high and low values), and with Expected Dry Matter Intake (EDMI), ASVs were associated with low trait values. Further Genome-Wide Association Analyses will be conducted, along with estimates of heritability and genetic predictions incorporating microbiome parameters.

Multi-objective optimization-based feature selection accurately deconvolutes whole-blood RNA-seq into 11 specific cell types

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We are interested in improving disease resilience (DR) in pigs using blood phenotyping. Blood samples are practical, but blood is very complex and many factors including the cell composition of the sample can confuse the interpretation of the results. Thus, new methods to measure disease resistance using blood are needed. We propose that by measuring the genes expressed in every cell component of blood we can estimate the specific transcriptomes of each major cell type in a mixed sample and test for cell-type specific eQTL associated with DR as well as cell type abundance and expression associated with DR. To do this on a large scale, we need to deconvolute low-cost whole blood RNAseq data into individual cell types, by establishing marker genes that can predict the proportion of each cell type in whole blood.

We have used seven independent PBMC single-cell RNAseq datasets to determine the transcriptome of all major mononuclear cell types. Using AutogeneS on 5000 highly variable genes from the scRNAseq data, we created a gene expression matrix (GEM) of 400 signature genes that was optimized to best separate the individual cell transcriptomes for every pseudobulk sample. This GEM was validated using leave-one-out training and testing methods with the original scRNAseq data, resulting in Pearson correlation coefficients (PCC) with known composition within the test samples of up to 91%, although low-abundance cell types were overestimated, except for cDCs, which were accurately predicted.

To refine this approach in deconvolution of whole blood RNAseq data, we have also integrated unpublished polymorphonuclear cells (PMNs, an abundant leukocyte in blood which is separate from PBMC) RNAseq data with the PBMC scRNAseq data to create an improved GEM (GEM2). We are currently testing this GEM2 for deconvolution in two ways: (a) by testing against a set of 47 samples for which we have cell composition estimates from flow cytometry data and (b) testing against known combinations (synthetic/simulated datasets) of cell types created from sorted cell transcriptomes. Initial results show that GEM2 has good performance with PMNs and NK cells, showing a PCC 0.77 and 0.74, whereas major overprediction was seen in pDCs (-0.43) and B cells (0.28), suggesting the need to refine the training dataset by addition of sorted cell transcriptomes or single cell datasets that provide improved representation of minor cell types.

Unlocking genomic diversity through comparative and pan-genome analysis for crop research communities

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Advancing crop research and improvement depends on equipping agricultural scientists and plant breeders with the tools and data needed to develop resilient, high-yielding crop varieties. Integrated genomic datasets and functional annotations from diverse plant genomes, analyzed through comparative genomics, enable researchers to uncover genetic insights. To support these efforts, the Gramene Plants database (https://www.gramene.org) provides access to biological information from over 150 plant genomes, including major crops and model species, empowering breeders to leverage genomic discoveries across the plant kingdom. Gramene further strengthens the research community by fostering collaboration, ensuring robust gene annotations and functional curation, and adhering to FAIR principles through computational innovations and community-driven data stewardship. Recent expansions to Gramene include pan-genome resources for maize, rice, sorghum, and grapevine. These crop-focused platforms enable researchers to explore core and accessory genomes; uncovering structural variants, presence-absence variations (PAVs), and genome-specific features critical for breeding programs and evolutionary studies. Integrating Reference SNP cluster IDs (rsIDs), unique identifiers for genetic variation, into the pan-genome sites allows us to link traits to rsIDs mapped to multiple genomes. Gramene also offers advanced tools for analyzing gene structure, expression, homology, and pathways within the Ensembl genome browser. Collaborations with platforms such as the EMBL-EBI Expression Atlas, Bio-Analytic Resources (BAR), and the CLIMTools suite further expand Gramene's capabilities for agricultural research. The addition of eFP Browsers from BAR enables visualization of gene expression in crops like maize, Arabidopsis, soybean, and sorghum, while the CLIMTools suite supports genotype-environment (GxE) association studies. By integrating over 400 climate descriptors from satellite data, CLIMTools facilitates genome-wide association analyses, providing actionable insights for breeding programs. These advancements underscore Gramene's commitment to agricultural innovation and solidify its role as a cornerstone for agricultural genomics and collaborative breakthroughs.

Exploring the evolution of plant regulatory elements using multiDAP

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Transcription Factor (TF) binding sites play a pivotal role in gene regulation networks of plant growth, development, and environmental responsiveness, and thus hold key insights into basic organismal biology. Identifying TF binding sequence, location, structure and determining their contribution to gene regulation is essential for understanding gene regulation in plants. However, the considerable sequence divergence surrounding TF binding sites in plants makes direct sequence alignments difficult, if not impossible, making it challenging to examine the evolution of regulatory elements. Here, we explore features from TF binding sites generated by multiDAP to study the evolution of promoters across four Brassicaceae species. Previous studies, including our own, have demonstrated that different TF families have unique features including preferred distributions of binding sites relative to gene starts. We were interested to further explore these preferred location patterns across species, specifically considering that the more conserved binding sites showed evidence of enrichment for functional regulatory elements. We observed diverse binding patterns across TFs with some families showing strong preference for binding sites within the promoter or just downstream of the gene start. We thus leveraged multiDAP features to create a scoring method that uses genomic windows and TF binding sites for a given gene that can then be compared across species. Using this promoter scoring method we identified the closest orthologs across species based on the similarity of their promoters. Further exploration of a large number of gene comparisons will provide insights into the evolution of promoter within orthologous groups, including new or altered functions of regulatory sequences, as well as the ability to detect expressologs within and between species.

Enabling FAIR single-cell RNAseq data management with COPO

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We present our work into standards and tooling for validating and depositing single-cell RNAseq data and metadata using the brokering tool COPO. Research data management is a crucial part of the scientific method, facilitating data reuse, integration and the discovery of novel biological insights via machine learning applications. There are however, significant gaps appearing as new technologies are invented. The magnitude change in resolution offered by single cell technologies offers an unprecedented insight into biological function, such as understanding gene expression and regulation in crops, studying pathogen interaction at the cellular level, or identifying stress resistant cell types. Yet without excellent metadata and tools to manage it, the full value of single-cell technologies cannot be realised. This necessitates the implementation of the FAIR principles, key to which is high quality metadata. Currently only limited standards and tooling exist for the description of single-cell transcriptomic data. Through thorough and fastidious consultation with various research groups working with single cell RNAseq technologies, and integration with existing standards, we have developed a template metadata standard, which can be used to describe such experiments. Our brokering platform, COPO, implements this standard to easily validate and disseminate such data and metadata to public repositories. This has many benefits to the researcher and community at large. Standardised metadata makes associated data discoverable, using known keywords and field names. This standardisation also allows data to be found, shared and integrated across different platforms, repositories or tools. This in turn can foster collaboration between disparate and diverse disciplines and groups. Good labelling and provenance of data ensures that those who produced it are properly credited for their work. By brokering data and metadata using COPO, protocols are reproducible, their results findable, and crucially, their data and metadata interoperable. This interoperability transforms such data from experimental output, into high quality machine learning training data. Our work therefore bridges critical gaps in managing single-cell RNAseq data by developing standards and tools within the COPO platform. By implementing FAIR-aligned metadata, we ensure data is discoverable, interoperable, and reproducible, fostering collaboration and maximizing research impact.

Precision Genetic Technologies

Cell-type characterization of bovine bulk RNA-seq using scRNA-seq as reference

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Single cell RNA-seq (scRNA-seq) provides high-resolution gene expression at the cellular level, but the high cost of scRNA-seq library preparation and practical difficulties in sample handling prevent its adoption for large numbers of samples. In contrast, the bulk RNAseq assay is much more affordable, but the expression includes a composite of cell types and each gene expressed in bulk RNAseq might include a single or multiple cell types. In this context, computational deconvolution provides a cost-effective approach to identify the composite expression of different cell types in bulk tissue samples by inferring the cell types from a scRNA-seq dataset. For a given tissue, an ideal deconvolution approach would be to prepare a scRNA-seq assay with a small sample dataset, characterize the cell types, and use it as a reference to deconvolute cell types in bulk tissues with a large number of cells. In the present study, we used two bovine liver scRNA-seq data as reference sets to deconvolute the bovine bulk RNA-seq data extracted from 88 liver tissue samples to characterize cell types based on gene expression. We performed the deconvolution using two different tools, Bisque and Omicverse. Bisque uses gene-specific transformations of bulk expression and accounts for biases in single-cell sequencing protocols. It is robust to increasing variation between reference profile generation and bulk expression. OmicVerse uses a specialized algorithm, BulkTrajBlend, to account for "omissions" in single-cell data and a graph neural network-based algorithm to deconvolute single-cell data from bulk RNA-seq. We performed cell type characterization using these two tools and compared the cell clusters produced by these methods. This preliminary study provided a preview of the cell clusters generated in bovine bulk RNA-seq data and the opportunity to refine the parameters for future studies with larger sample sizes.

High-throughput assembly of long, complex DNA by mating bacteria

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DNA constructs longer than 5kb are valuable in plant and animal engineering for a variety of applications including gene stacking in transgenic crops, pathway engineering, and expressing large genes or gene clusters. Existing in vitro based technologies have difficulty assembling highly complex DNA and have limited throughput. To scale engineering of long complex DNA, we report here a novel in vivo DNA assembly technology platform that combines bacterial conjugation, in vivo DNA cutting, and in vivo homologous recombination to seamlessly stitch blocks of DNA together by mating E. coli in large arrays or pools. For long DNA, this workflow is simpler, cheaper, and higher throughput than current in vitro based DNA assembly approaches such as Gibson Assembly and Golden Gate Assembly that require DNA to be moved in and out of cells at different procedural steps. We perform over 5,000 assemblies with two to 13 DNA blocks that range from 240 bp to 8 kb to generate constructs as long as 23 kb at relatively high throughput and fidelity. Most assembly errors are deletions between long interspersed repeats. However, these errors can be overcome by performing multiple replicates: additional cost and hands-on time for assembly and sequence verification for additional replicates are nominal. We show the platform can be used to build directed combinatorial libraries in arrays or pools, and that DNA blocks onboarded into the platform can be repurposed and reused with any other DNA block in high throughput without a PCR step. Because of these features, the platform has the potential to accelerate design-build-test-learn cycles of DNA products.

CRISPR editing of bovine IGF2 and MSTN to enhance productivity

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The CRISPR/Cas9 system has been shown to improve specificity and efficacy of genome modification in livestock. There are two genes where molecular variation in different species has shown significant effects on increased lean growth and reduced adiposity: insulin-like growth factor 2 (IGF2) and myostatin (MSTN). In pigs, a G-to-A substitution in intron 3 of IGF2 (g.3072G>A) disrupts a binding site of the transcriptional repressor ZBED6 increasing postnatal IGF2 expression resulting in increased lean muscle yield and intramuscular fat deposition while decreasing backfat. In other livestock species, numerous MSTN loss-of-function (LOF) mutations have been reported. MSTN is a known early regulator of myoblast differentiation, resulting in muscle hyperplasia and the "double-muscled" phenotype. Animals of this phenotype have significantly increased skeletal muscle mass, improved feed conversion, and decreased fat deposition. These mutations can act synergistically as demonstrated by a mouse line possessing both mutations. Within this line, wild-type (WT) mice have an average body weight of 19.64 ± 1.89 grams at 11 weeks of age. In comparison, mice with the IGF2 overexpression, MSTN LOF, and combination of both mutations have average body weights of 23.54 ± 2.31 grams, 26.14 ± 2.35 grams, and 31.43 ± 2.39 grams, respectively ($p<0.0001$). Based on these results in mice we have initiated editing of both genes in cattle. Two male fetal fibroblast cell lines were generated from day 75 fetuses from high genetic merit Angus matings. Four CRISPR guide RNAs (gRNA) have been designed for both genes, and ribonuclear protein complexes were electroporated into each cell line. Numerous individual targeted modifications were confirmed through sequencing, and a combination of gRNAs are being used to target both genes simultaneously. Successfully modified cell lines will undergo somatic cell nuclear transfer to produce live animals.

Keywords: CRISPR/Cas9, myostatin, insulin-like growth factor 2

AgriSeqTM ULTRA: A fast, simple, high-throughput workflow for targeted genotyping-by-sequencing of aquaculture samples

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Targeted genotyping-by-sequencing (GBS) is a robust agrigenomics tool that is used to identify SNPs for breeding selection or trait identification. High-throughput targeted GBS applications rely on rapid, high-accuracy sequencing results of thousands of markers per day with minimal labor and laboratory inputs. The AgriSeq™ ULTRA targeted GBS kit is the next generation of AgriSeq™ library prep products. The updated protocol's partial-combinatorial dual barcodes allow for processing of up to 3,072 uniquely barcoded sample libraries, while reducing the amount of barcode material needed to only 4 plates and 8 tubes. Up to 3,072 libraries can then be sequenced on a single Ion 550™ chip, with two chips sequenced per day, allowing processing of a total of up to 6,144 samples daily per Ion GeneStudio™ S5 System. Updates to the Torrent Suite analysis software and the addition of the AgriSeqVariantCallerLiteTM plugin allow full data processing in approximately 24 hours or less, allowing for reduced wait time between sequencing and acquiring results. AgriSeq™ ULTRA is compatible with aquaculture sample types, such as pleopods and fin punches. Reliable genotype calls are generated with both purified nucleic acids and direct lysates due to our novel AgriSeqTM Anti-Inhibitor Solution, which negates effects of PCR inhibitors carried over from crude extraction and allows highly inhibited samples to be used for targeted GBS library preparation. Here we illustrate how AgriSeq™ ULTRA successfully generates data from pleopods and fin punch lysates extracted using the AgriSeq™ Genomic DNA Extraction Kit.

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Gene editing for a stronger tef: engineering lodging resistance with CRISPR

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Tef (Eragrostis tef) is an ancient grain cultivated on approximately 3.2 million hectares by over 6 million farmers in Ethiopia. It serves as a staple food and an important forage crop. This nutrient-rich grain is naturally gluten free, has a low glycemic index, and is an excellent source of calcium, iron and Magnesium. In the United States, tef is grown both for its grain and as a high-quality forage and fodder crop. Despite its nutritional and agricultural significance, tef's average grain yield remains low, typically below 2 tons per hectare, primarily due to lodging, the bending or collapse of stems, which results in a 25 to 30 percent yield reduction. In modern cereal breeding, dwarfing genes have played a pivotal role in improving lodging resistance. For example, mutations in the REDUCED HEIGHT1 (RHT1) gene in wheat and the SEMIDWARF1 (SD-1) gene in rice, both key regulators of gibberellin signaling and biosynthesis, enabled the development of semidwarf varieties, fueling the Green Revolution of the 1960s and 1970s. Similarly, in sorghum, the DWARFING3 (DW3) gene, which encodes an auxin efflux transporter, and DW1, involved in brassinosteroid signaling, have been widely utilized to reduce lodging and improve mechanical harvesting. To address lodging in tef, CRISPR Cas9 gene editing was used to target orthologs of SD-1, DW1, and DW3. Mutations were introduced individually and in various combinations, leading to the development of multiple semidwarf tef lines. These lines were subsequently evaluated under field conditions in St. Charles, MO, where they exhibited significant improvements in lodging resistance. Among the seven edited lines tested, single (sd-1), double (sd-1/dw3), and triple (sd-1/dw1/dw3) knockout lines demonstrated enhanced structural stability and reduced susceptibility to lodging. This study represents the first successful application of targeted gene editing to improve lodging resistance in tef, offering a promising strategy to enhance crop resilience and productivity. These findings underscore the potential of gene editing technologies for tef improvement. The newly developed semidwarf lines are now being integrated with additional yield and quality enhancing traits to develop improved varieties that can contribute to increased food production and nutritional security.

Quantitative and Molecular Genetics

Genomic prediction and high-throughput phenotyping applied to alfalfa (Medicago sativa L.) breeding for yield improvement

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Alfalfa (Medicago sativa L., 2n=4x) is the most important leguminous forage crop due its high nutritive value and biomass production. Historically, breeding efforts for dry matter yield (DMY) has been carried out at the family level using phenotypic recurrent selection, and this method has shown low genetic gains for DMY. High-throughput phenotyping (HTP) and genomic prediction (GP) applied in plant breeding can lead to higher genetic gain for complex traits. Here, two alfalfa breeding populations (AGP_17 and AGP_19) consisting of full- and half-sib families and commercial checks were evaluated for DMY across multiple harvests in two separate trials. Both populations were bulked genotyped via targeted sequencing using the DArTag 3K panel. Broad-sense heritability for DMY ranged from 0.18 to 0.28 in AGP_17 and 0.19 to 0.64 in AGP_19 across several harvests. The within-harvest predictive ability (PA) of the GBLUP model for DMY ranged from 0.26 to 0.40 in AGP_17, and -0.06 to 0.26 in AGP_19. We also tested if using aerial measurements of normalized difference vegetation index (NDVI) as secondary traits in GP models could increase PA for DMY. On average, PA increased by 74% across harvests when NDVI was used as a secondary trait in bivariate models with DMY. These findings highlight the potential of GP and HTP in accelerating genetic gains for DMY in alfalfa breeding programs.

Integration of phenomic and genomic predictions in cowpea breeding with single-kernel NIRS

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Accurate trait prediction is crucial for accelerating genetic gains in crop breeding. Cowpea (Vigna unguiculata [L.] Walp) is a vital legume crop for food security in many developing regions due to its high nutritional value and adaptability to harsh environments. Phenomic selection (PS) has shown promise in predicting complex traits using spectral data. While some Near-Infrared Spectroscopy (NIRS) methods require laborious seed grinding, which is time-consuming and destructive, single-kernel NIRS provides a rapid, non-destructive alternative that enables high-throughput phenotyping with minimal sample preparation. This study evaluates the predictive ability of PS, genomic selection (GS), and their combination (G+P) for key agronomic traits in cowpea using 253 diverse accessions, including 243 from the UCR Minicore collection and 10 checks. Genomic prediction was based on 46,878 SNP markers generated through genotyping with Cowpea iSelect Consortium Array, while single kernel NIRS generated spectral data, which was normalized and converted into a phenomic relationship matrix for phenomic prediction. PS consistently outperformed GS for most traits, with accuracies ranging from 0.28 (pod number) to 0.87 (100-seed weight), while GS accuracies ranged from 0.20 to 0.65. The combined model (G+P) achieved the highest predictive ability, exceeding 0.84 for seed-related traits. These results show the potential of PS as a viable, cost-effective alternative for improving genetic gains and its ability to complement GS, particularly for complex traits. Future work will validate these predictions across multiple environments and explore additional modeling approaches to improve reliability and applicability in cowpea improvement.

DHGLMF90: a software for genetic heterogeneity of residual variance estimation using double hierarchical generalized linear models

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In animal breeding research and applications, there is an increasing interest in selecting uniform animals expressing a consistent response to the environment. This could be achieved by modeling heteroskedastic residuals when estimating breeding values using a hierarchical model that includes a mean and a dispersion component. The latter could be influenced by both genetic and non-genetic factors. Bayesian methods can estimate heteroskedastic residuals through the Metropolis-Hastings algorithm, which is slow and inefficient. In contrast, Double Hierarchical Generalized Linear Models (DHGLM) provide a faster counterpart to Bayesian methods. We aimed to develop a software named DHGLMF90 to implement DHGLM using an efficient algorithm to accurately estimate heterogeneous residual variances and breeding values for large datasets. We improved the reweighted least squares algorithm (IRWLS) to enhance convergence properties compared to previous implementations. IRWLS iteratively estimates variance components and leverages a bivariate model that includes the mean and dispersion components of the hierarchical model. DHGLMF90 uses BLUPF90+ to estimate variance components using REML. The software was tested using a single-trait model with both simulated and real datasets, the latter from previous studies. The methodology was further extended to a multiple-trait model and tested on simulated data. Additionally, simulations for both single- and multiple-trait scenarios were replicated to ensure a comprehensive evaluation of DHGLMF90 performance. Results indicated that DHGLMF90 achieved convergence by an order of magnitude faster than Bayesian methods, without significant differences in the estimates of the parameters. The feasibility of the multiple-trait scenario was proven. Future developments will focus on integrating genomic information.

Pangenome-enabled trait discovery and marker development for carotenoid biofortification in Sorghum bicolor

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Sorghum (Sorghum bicolor [L.] moench), the second most cultivated cereal crop in sub-Saharan Africa, accumulates low levels of provitamin A (PVA) carotenoids in the grain. Carotenoids can potentially be increased through breeding to alleviate vitamin A deficiency (VAD). A major challenge in carotenoid breeding is that selection of favorable lines for crossing is slow, as it relies on quantitating carotenoids in mature grain post-harvest. A more rapid, indirect selection can be achieved by exploiting the allelic variation in key carotenoid biosynthesis genes to develop genetic markers associated with PVA carotenoids. Pangenomes – the entire set of genes from a species – have emerged as a useful tool to mine for genetic variation within species. Several candidate genes associated with variation in carotenoid concentration in sorghum grain have been identified through forward genetic approaches and are potential targets for use in marker-assisted selection. We hypothesized that the pangenome is a useful tool to mine allelic variation in the candidate genes that can be exploited to develop KASP markers, which are an effective tool for carotenoid selection in sorghum breeding programs. To test this, we used a pan-genome data set to identify gene variants in candidate genes and developed fourteen KASP markers targeting the variants identified. A population of 100 diverse sorghum lines was genotyped with the markers, and two of these – snpSB00803, a 'TA' indel in B-isomerase, and snpSB00804, an 'AC' indel in lycopene-B-cyclase – significantly associated with carotenoid content. This study demonstrates the value and application of the pangenome, and the potential of KASP markers to enhance provitamin A breeding through marker assisted selection. Further validation of these markers in a breeding program is warranted.

Keywords: Sorghum, carotenoids, pan-genome, KASP-marker, biofortification

Heritability estimation and hypothesis testing for complex models and very large datasets

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Likelihood inferences such as heritability estimation with restricted maximum likelihood (REML) or hypothesis testing are widely used in animal and plant breeding and genetics in various computations, including breeding values estimation and genome-wide association studies. Due to memory usage and extremely long computational times, performing likelihood inferences is impossible for large datasets, especially with genomic information. The main computational bottlenecks of likelihood inferences are the calculation of the log-determinant and the trace of a matrix product. This study aimed to derive and present methods to approximate the log-determinant and trace of the matrix product when genomic information is used, hence, making likelihood inferences for very large datasets possible. We proposed to approximate the log-determinant and trace using Monte Carlo sampling. For the log-determinant, this implied using notions of complex calculus and contour integrals. For the trace, the approximation involved the data simulation and fitting a surrogate linear model in a procedure known as Monte Carlo REML. We tested our proposed approximations using beef cattle, dairy cattle, chicken, and pig datasets. The approximation of the log-determinant was 2 to 500 times faster than its exact calculation. The timing difference between exact and approximated log-determinant increased with the size of the data. For example, for the largest dataset, the exact calculation took 19 days, whereas its approximation took one hour. The average absolute difference between the approximated and the exact value was 10-3. We used the beef dataset to assess how the numerical approximations affect the likelihood calculation and heritability estimation. The exact and approximated log-likelihood showed maximums at the same heritability value. The estimation of variance components using a derivative-free method coupled with the approximation of the log-determinant yielded the same results as Average Information REML. The approximated likelihood was also used as a convergence criterion for Monte Carlo REML, making the iterations stop earlier without significant changes in the estimates. Our proposed approaches lifted the computing time and memory limitations for likelihood inferences in large datasets. Therefore, approximated frequentist inferences are now possible for virtually any animal or plant breeding dataset.

Quantifying phenotypic and genetic variation for cow fertility phenotypes in American Simmental cattle using total herd reporting data

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Reproduction plays a major role in the production efficiency of livestock species. However, cow-centric reproductive traits tend to be lowly heritable and are not expressed until later in an animal's lifetime, making phenotypic selection alone inefficient at generating genetic gain. Genetic progress can be accelerated by focusing selection on the predicted genetic component of reproductive traits using Expected Progeny Differences. We used the American Simmental Association's performance and Total Herd Enrollment data, made up of 533,155 calving records from 303,158 females (132,403 cows and 170,755 heifers), 33,732 of which are genotyped, to explore three continuous and two discrete phenotypes focused on quantifying early and sustained fertility in beef cows. We analyzed calving date (cow's calving date relative to the start of the calving season), calving interval (days between calves), first calving interval (calving interval observation between the first and second calving record for a female), heifer pregnancy (did the animal calve as a 2-year-old), and discrete early calving (did animal calve in the first 30 days of the calving season) as distinct, but correlated measures of fertility. This dataset provides insight into population-wide trends related to cow attrition, calving season lengths, and phenotypic variation in fertility. We used pedigree and genomic restricted maximum likelihood (REML) to estimate these five phenotypes' genetic, permanent environment, and temporary environment variance components. Pedigree estimated heritabilities were 0.06 ±0.010079 for calving date, 0.04 ±0.003699 for calving interval, 0.07 ±0.014758 for discrete early calving, 0.05 ±0.013841 for first calving interval, and 0.22 ±0.039218 for heifer pregnancy, consistent with other fertility traits across beef and dairy cattle. The incorporation of genomics increased the heritability estimate for heifer pregnancy (0.24 ±0.037215) and decreased the estimate for first calving interval (0.04 ±0.009604). Positive phenotypic and genetic correlations were found among these phenotypes (rG = 0.01-0.96). Low genetic correlations were found among these traits with both weaning and yearling weights (rG = -0.09-0.24). These results call for further work in optimizing genetic predictions and exploration of the genetic architecture of early and sustained cow fertility through genome-wide studies.

Iron deprivation affects aboveground cell wall biosynthesis in Populus and the role of PtrbHLH011

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Growing bioenergy crops like poplars on marginal land is appealing to minimize competition for arable land. However, this is hampered by a lack of insight into secondary cell wall (SCW) changes caused by environmental stresses. Iron (Fe) deficiency is widespread and detrimental to plants. Here, we report that Fe deprivation increases SCW biosynthesis of poplar stem via the gene regulatory network involving the transcription factor PtrbHLH011, whose expression is downregulated by Fe deprivation. PtrbHLH011 is a potent repressor of SCW biosynthesis, whose overexpression resulted in a reduction of stem SCW by over 65%. Furthermore, PtrbHLH011 overexpression induced foliar disease symptoms caused by reduced iron and flavonoid accumulations. By constructing PtrbHLH011-controlled GRN, we discovered that PtrbHLH011 binds to the AAAGACA sequence and represses essential genes for SCW biosynthesis, flavonoid biosynthesis, and iron homeostasis. Our results suggest that PtrbHLH011 functions as a co-regulator for the rapid activation of systematic Fe deficiency responses.

Genome-wide association studies of puberty and fertility traits in US beef heifers

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Reproductive failure contributes to significant losses annually within the beef cattle industry, and the lowly-heritable nature of traits related to reproduction has made facilitating genetic progress challenging. Selection tools, such as the Heifer Pregnancy expected progeny difference (EPD), have been implemented to identify females more likely to become pregnant within a normal breeding season. However, there is a clear need for the development of selection tools based on quantitative measures of traits directly measuring puberty and fertility, rather than relying on simple binary measures. Further, dissecting the genetic underpinnings of complex traits related to female reproduction would enable the industry to more accurately predict and select for reproductive success. To identify QTL influencing puberty and fertility, we will perform a series of genome-wide association studies using 50K SNP genotypes imputed to 850K density on over 16,000 animals of Angus, Red Angus, Hereford, and Bos indicus-cross descent. Phenotypic records of reproductive tract score (RTS), pelvic width, pelvic height, pelvic area, and days to conception (number of days in a breeding season it took a heifer to become pregnant) were collected on 13,743 animals. First, we will analyze breeds individually in GCTA using a linear mixed model approach. Multivariate GWAS of all 5 traits will be conducted in GEMMA to increase our power to identify QTL. We will then combine breeds into a pooled dataset and fit univariate and multivariate GWAS mixed models as previously described. Next, we will examine differences in variances between genotype classes to identify variance QTLs (vQTLs), which indicate genotype-by-environment and genotype-by-genotype interactions. Lastly, a robust meta-analysis will be conducted by combining p-values from breed-specific GWAS models, further increasing our power to detect QTL. These findings will enhance our understanding of reproductive biology and enable more effective selection by offering insights into the genetic architecture of puberty and fertility.

Single-step genomic analysis of a combined terminal sire and maternal Australian sheep analysis

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The Australian sheep industry utilises a range of sheep breeds in their breeding programs, with non-Merino (fine wool) sheep currently split into two single-step genomic evaluations, a maternal analysis (for breeds based on their mothering abilities) and a terminal analysis (for breeds based on their growth and carcase performance). Some breeds however do not fit cleanly into this definition, e.g. shedding breeds. For this reason, these analyses are being merged, increasing the diversity of breeds analysed together. This presents the opportunity to re-evaluate the most appropriate method for aligning the pedigree and genomic information in single-step genomic across breed BLUP models and re-examine if changing from a breed-adjusted GRM would provide more accurate predictions. The combined analysis consists of 4.8 million pedigree animals, over 23 traits with 13.8 million observations and 246,000 genotypes. The predictive ability of five models was compared via forward cross-validation. These models included a pedigree model, a pedigree model with metafounders, a single-step genomic model using a single set of allele frequencies, a breed-adjusted GRM and metafounders assuming 0.5 for the allele frequencies. These cross-validation analyses were compared via LR validation metrics. The correlation between the whole and part estimated breeding values showed that the metafounder models (pedigree = 0.891 and single-step = 0.912) produced slightly more accurate predictions compared to their non-metafounder counterparts (pedigree = 0.877, regular GRM = 0.901, breed adjusted GRM = 0.894). This pattern was also present in the LR regression slopes of the models, where the metafounder models (pedigree = 0.981 and single-step = 0.964) observed less dispersion bias compared to the non-metafounder models (pedigree = 0.971, regular GRM = 0.958, breed adjusted GRM = 0.957). In terms of the mean breeding value bias, the traditional pedigree model had the lowest estimated bias at 0.009, followed by the metafounder pedigree model (0.023), the genomic metafounder model (0.029) the regular GRM (0.059) and finally the breed-adjusted GRM (0.067). With the metafounder model showing the best predictive ability, this model is currently being incorporated into the new combined LAMBPLAN analysis.

Functional impact of putatively identified introgressed alleles within the horse genome

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Introgression is the transfer of genetic material between two different species via repeated back crossing of the interspecific hybrid and one of the parent species. These are important events to understand in the study of molecular evolutionary relationships between species as introgression is nature's way to fast track evolution by spreading pre-adapted alleles. Previous studies have found 3,275 loci among contemporary horses with signals of introgression. These transfers were likely hundreds of thousands to millions of years ago from a non-caballine equid species that may be extinct. There was no pattern within the data to suggest a statistically significant relationship between effect type and allele. However, the 76 loci are part of the immune system did have a statistically significant relationship between the effect type and allele. This provides insight why the haplotypes are still seen in modern horse populations. Methylation signatures using the 5-methylcytosine signals provided by PacBio Hifi Long Reads, were also investigated, but also had no overlap based on which cytosine was methylated and the variants of the introgressed haplotype. However, the whole haplotype is currently being investigated rather than the individual variants. There are two problems with the current dataset of introgressed regions: reference bias and small sample population as a control. To combat this, we are currently mapping 230 Thoroughbred horses to the Shire and Arabian reference genomes. Due to the current reproductive barrier between caballines and non-caballines, studying this gene flow between species will allow us to use introgression as a model for gene editing. Introgression within horses, specifically the well-known thoroughbred, will help us piece together evolutionary relationships as the shared alleles allow for rapid adaptation to their new environment by changing gene function.

Investigating the genomic basis of B-Hydroxybutyrate in postpartum Holstein cows

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B-Hydroxybutyrate (BHB) blood concentration (mmol/L) is a widely recognized diagnostic indicator for clinical and subclinical ketosis. A bivariate animal model for transformed BHB (TBHB) and single test-day milk yield (SMY) was applied separately to primiparous and multiparous Holstein cows using weighted single-step GWAS to identify candidate genomic regions for TBHB, based on the additive genetic variance explained by 500kb SNP windows. Measurements for BHB and SMY were collected at an average of 7 (SD = 2.3) and 17 (SD = 7.8) days in milk (DIM). Pedigree information extending back five generations, records from 3,624 primiparous and 6,478 multiparous cows, and SNPs from1,153 primiparous and 2,024 multiparous cows genotyped with the Illumina 777K SNP array were considered for analyses. The TBHB trait was calculated as BHB0.07and BHB0.11 for primiparous and multiparous cows, determined using the Box-Cox Power Transformation. After quality control, 578,487 SNPs were retained for variance components and marker effect estimation using the BLUPF90 family of programs. For primiparous cows, TBHB was modeled with fixed effects for herd-year-season and linear and quadratic DIM at BHB measurement, while SMY included herd-year-season and linear and quadratic DIM at SMY measurement. For multiparous cows, lactation number was added as a fixed effect for both traits. Both bivariate models included additive genetic and residual random effects. Heritability estimates of TBHB were 0.06 (0.03) and 0.03 (0.02), and the genetic correlations between TBHB and SMY were 0.46 and -0.02 for primiparous and multiparous cows. Although no SNP explained more than one percent of the additive genetic variance of TBHB in multiparous cows, 20 SNPs on BTA4 exceeded this threshold in primiparous cows. These results provided insights into the genetic architecture of BHB blood concentration and its genetic relationship with milk yield, contributing for research and breeding strategies to enhance postpartum metabolic health in Holstein cows.

Genome-to-phenome approach for understanding pork belly traits and muscle formation characteristics

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Pork belly consists of various muscles and fat. However, most genomic studies have primarily focused on the loin muscle, which is a key economic trait. In a previous study, key transcription factors related to the adipogenesis pathway in pork belly were identified. However, that study was limited to a specific section of pork belly, restricting comprehensive analysis. In this study, we identified genes associated with the entire pork belly and its component muscles using data from 543 Yorkshire pigs and SNP chip analysis via a Genome-to-Phenome approach. A total of 276 SNPs were significantly associated with whole pork belly traits, component muscles, and lean meat production ability. Based on these results, standardized beta values were calculated, confirming positive associations with common traits. Additionally, in silico validation revealed enrichment of genes involved in adipogenesis and energy metabolism pathways. Taken together, genes related to adipogenesis and energy metabolism could serve as valuable markers for improving pork belly.

Influence of genetic selection on viral-responsive regulatory element diversity and phenotypic outcomes in Holsteins

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The US Holstein population has undergone genetic selection predominately for increased milk production traits for nearly a century, most intensely over the past decade through genomic testing, resulting in the most productive and profitable dairy cattle ever. However, despite recent efforts to enhance other traits, the focused rapid improvement in production traits has increased genetic homozygosity in the population and reduced disease-resistant allele frequency. This trend heightens the susceptibility of herds to pathogens and elevates the risk of high prevalence of chronic disease or acute outbreaks of emerging disease that can threaten population survival and incur significant economic harm to dairy producers. Bovine Leukemia Virus (BLV) is one such chronic disease in which roughly 1 in 2 adult American dairy cattle are infected with. The strikingly high prevalence of BLV in the US highlights the concomitant effects of declining genetic diversity and the virus's capacity to hijack immune regulation, drive proliferation of immature B cells, and weakening immune defenses, amplifying susceptibility to infection and disease progression. As the bovine genomic field continues to construct resources that describe population-level genomic diversity through Pangenome initiatives, we seek to understand how changes in important regulatory elements that are responsive to viral infection affect immune phenotypes. Leveraging chromatin accessibility and protein-DNA interaction data, we have developed a DNA hybrid capture-sequencing approach that combines skim-sequencing to obtain genomic data from distinct populations of animals. This study applies this custom DNA bait capture library to a population of elite genomic sires as well as the unselected 1964 population of Holsteins from the University of Minnesota, St. Paul. Our recent findings support our hypothesis that contemporary animals have reduced heterozygosity and allelic diversity at viral response elements. Moreover, these genetic insights are being leveraged to explore connections between BLV disease status, viral dynamics, and production outcomes across hundreds of offspring from dozens of sires in numerous herds throughout the Midwest United States. Our goal is to unravel the genetic inheritance patterns of regulatory elements that influence divergent BLV disease outcomes, enabling the potential for genetic selection of disease resistant genomic variants to improve bovine health and productivity.

Accuracy of indirect predictions for indicine cattle breeds based on a multi-breed genomic evaluation

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Indirect predictions (IP) are used for young genotyped animals without phenotypes or from commercial herds, often excluded from official evaluations to avoid reducing accuracy and increasing bias in genomic breeding values (GEBV). In Brazil, limited information exists for breeds like Brahman, Guzerat, and Tabapua. Using a larger reference population could improve genomic selection accuracy for these breeds as in the case of multi-breed in conjunct with the Metafounders (MF), which can model distinct genetic bases across breeds. Furthermore, individual accuracies (ACC) for IP, though rarely reported, are important for selection decisions. This study aimed to estimate individual IP accuracies based on the error covariance (PEC) of SNP effects, derived from the PEC of GEBV in ssGBLUP, for young genotyped Nellore, Brahman, Guzerat, and Tabapua animals in multi-breed populations, with or without MF. MF acts as pseudo-individuals representing base population animals. Records from four breeding programs of the National Association of Breeders and Researchers (ANCP—Ribeirão Preto, SP, Brazil) were used, including pedigree (4.2M), phenotypes (329K), and genotypes (62K). Traits analyzed were adjusted weight at 450 days (W450) and scrotal circumference at 365 days (SC365). Single-breed and multi-breed analyses were conducted. IP were derived as the sum of SNP effects weighted by gene content using four reference populations: single-breed ssGBLUP, multi-breed ssGBLUP with and without MF. IP accuracies were calculated from the SNP PEC matrix (Cgg) as the square root of one minus the PEV of the individual divided by the genetic variance. Validation included genotyped animals born after 2020 with phenotypes for all traits. Pearson correlations assessed IP accuracy quality, comparing ACCGEBV and ACCIP. Correlations between ACCGEBV and ACCIP for validation animals were consistently high, with the highest correlations always achieved in the multi-breed scenario with MF. For W450, the correlations with MF were 0.87, 0.52, 0.74 and 0.55 while for SC365 were 0.61, 0.28, 0.47 and 0.57, for Nellore, Brahman, Guzerat and Tabapua, respectively. The regression coefficients closest to 1.00 were achieved also with the multi-breed evaluations. Results suggest that IP can be effectively used for young genotyped animals excluded from multi-breed evaluations, especially with the use of MF. However, some correlations were moderate, suggesting that while IP can be useful, its accuracy may depend on the breed, the model used, and the availability of both genotypic and phenotypic data.

Genetic trends of harvest weight in a Channel catfish breeding program in the United States

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Delta Select is a breeding program of Channel catfish, it started in 2006 and implemented genomic selection in 2015, using single-step genomic BLUP (ssGBLUP). We compared pedigree BLUP and ssGBLUP genetic trends, to identify the effective starting point of genomic selection, and the contribution of male/female and genotyped/non-genotyped animals to the genetic gain using partition of genetic trends. The USDA-ARS WARU provided harvest weight records of 54,026 animals from 2008 to 2023, of which 12,279 were genotyped using 53,976 single nucleotide polymorphisms (SNPs). Variance components were estimated using pedigree information REML. Then, breeding values were estimated using pedigree BLUP (EBV) and ssGBLUP (GEBV). The additive genetic effect, common family environment effect, and residual were random; the contemporary group effect (year-pond-sex) and age nested within sex were treated as fixed. Genetic trends were estimated using EBV and GEBV from parents born from 2000 to 2020, being 980 sires and 1384 dams (289 sires and 360 dams genotyped and 691 sires and 1024 dams non-genotyped). The genetic gain by year BLUP and ssGBLUP was 6.6g and 7.7g. Under ssGBLUP, the difference between males' and females' contributions was greater than in BLUP. The contribution of sires in ssGBLUP (BLUP) genetic trends increased from 50% (50%) in 2006 to 69% (57%) in 2020. Effectively, the starting point of genomic selection was 2014, when the difference between GEBV and EBV was, on average, greater than 13 g. At this point, the percentage of genotyped animals was bigger than 20%, reaching 27.4% in 2020, and the contribution of genotyped animals was 46.4% of the genetic trend. The greatest contribution to the genetic trends was from genotyped sires (38.3%) and non-genotyped dams (26.3%). Overall, genomic selection has a positive impact and is helping accelerate the rates of genetic gain in the USDA-ARS WARU breeding program.

Development of a computational interface for the analysis of mixed models: exploring genotype-by-harvest interactions (GHI) in multi-harvest trials

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Linear mixed models (LMMs) have important features, allowing the evaluation of interaction effects and dealing with heterogeneity and dependency among model components. This approach enhances the estimation of genotype-by-harvest interactions (GHI) in analyzing multi-harvest trials (MHT). Proper modeling of GHI improves the efficiency of selecting superior genotypes in breeding programs for perennial and semi-perennial plants. Therefore, the goals of this project are to (i) develop a user-friendly interface within the DesignGen app for analyzing phenotypic data using LMMs, and (ii) demonstrate the selection of an optimal variance-covariance (VCOV) structure for GHI analysis in MHT through the app's interface. DesignGen is an app developed by the Statistical Genetics Lab, and I am adding new features to it. This app and the new interface were coded within the R environment using packages such as Shiny, Golem, and Sommer. This interface was tested with MHT data consisting of dry leaf matter measurements from 23 Megathyrsus maximus genotypes, evaluated in a completely randomized block design with up to 14 harvests in Campo Grande, MS. From the selected model, its interface was used to elect the optimal VCOV structure based on the Akaike (AIC) and Bayesian information criteria (BIC), and execution times for running models were measured using the `system.time()` function to compare the interface's performance with direct R environment usage. The results demonstrated the interface's efficiency, providing execution times comparable to those of the R environment. The selected model confirmed the presence of GHI in the forage data, with a Kronecker product of an identity and an unstructured matrix for the covariance matrix of random effects and a diagonal matrix for the covariance matrix of residuals providing the best fit (AIC -566.16 and BIC -488.31). The interface also provided other essential information for interpreting the analysis, such as the variance components, best linear unbiased predictions, graphical visualizations of interactions, and downloadable analysis results. Therefore, this tool enables the construction and interpretation of LMMs through an accessible interface, helping breeders use advanced modeling techniques in their programs. The complete code is freely available in a GitHub repository, ensuring transparency and reproducibility.

Molecular and genetic characterization of DGAT1 gene in Sudanese dairy cattle Kenana and Butana

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The aim of the study was the characterization of DGAT1 variants in Sudanese dairy cattle breeds. In this study, we examined 94 Kenana and 91 Butana dairy cattle from two regions of Sudan. We genotyped the DGAT1 sequence variant AJ318490.1:g.10433/10434 AA>GC that leads to the Lysine – Alanine substitution at position 232 (K232A) in the protein and the VNTR polymorphism in the promoter region. Genotyping was performed by allele specific PCR and PCR fragment lengths determination, respectively. In both breeds, the DGAT1 Lysine variant (232K) that is associated with high fat and protein content as well as high fat yield in other breeds is the high frequent allele. The frequencies of the 232K allele were 96.3% and 84.6% in Kenana and Butana breeds, respectively. At the DGAT1 promoter VNTR locus, four alleles containing four to seven repeats of the 18 bp motif were found in both breeds. The highest frequent allele was the VNTR allele 3 containing five repeats with 60.4 % and 57.5 % in Kenana and Butana breeds, respectively. In conclusion, the two examined Sudanese dairy cattle breeds do not differ in allele frequencies at the DGAT1 locus.

Recursive modeling to evaluate host genetic and gut microbial influences on feed efficiency in Iberian pigs

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The gut microbiome plays a pivotal role in the performance and health of swine by providing essential nutrients and supporting the immune system. Recent studies have demonstrated that the gut microbiome can explain part of the variation observed in growth, health, and meat quality. Feed efficiency is a critical aspect of swine production, as feed cost constitutes more than 60% of total production costs. This study aimed to assess the relationships between the host genome, the gut microbiome, and feed efficiency in Iberian pigs raised under intensive conditions. The objectives of this study were twofold: first, to infer the mediation effects of the gut microbiome on feed efficiency, and second, to estimate the direct and total heritability of feed efficiency.

The data set included feed conversion ratio (FCR) and residual feed intake (RFI) on 587 Iberian pigs and 16S rRNA gut microbial abundance on 151 Iberian pigs from a nucleus of selection. To disentangle the mediating effect of the microbiome on feed efficiency, we reparametrized variance components from standard bivariate mixed models into recursive models. In our models, the host genome has direct effects on both the phenotype (G-->P) and the gut microbiome (G-->M). In addition, there is an indirect effect of the host genome on the phenotype mediated by the microbiome (G-->M-->P).

Our analysis identified 14 taxa with significant effects on FCR and 16 with relevant effects on RFI. We then categorized the gut microbiome into groups with the potential for practical application in pig farming. Gut microbes with relevant causal effects and low heritability can be manipulated by management interventions, while those with relevant causal effects and moderate heritability can be targeted through selective breeding. The findings of this study suggest that incorporating microbiome data into the scientific framework can lead to a reduction in total heritability for both FCR and RFI. This study offers novel insights into the association between the gut microbiome and feed efficiency, proposing an innovative approach to targeting microbes that can be influenced through selective breeding or external interventions.

Estimating genetic parameters and predicting puberty and fertility traits in multi-breed beef heifer cattle

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Puberty and fertility are critical traits with significant impact on profitability in the cattle industry. These traits are complex as they are influenced by several factors and are difficult to predict. However, technological advancement has allowed for the development of powerful tools like genomic prediction – a genetic tool which produces accurate predictions for lowly heritable traits like puberty and fertility in cattle. Genomic prediction produces estimated breeding values (EBV) for selecting genetically superior animals for any desired trait. Unlike in the dairy cattle industry, relatively less attention has been focused on improving puberty and fertility traits in beef cattle using genomic prediction. Existing preliminary data from our research group had established a relationship between puberty and fertility traits in beef cattle and indicated that there are similar alleles controlling these traits. Moreso, results from our preliminary predictions showed promising potential for traits like Days Open and Days to Conception in Red Angus. Days Open and Days to Conception are considered novel traits in the U.S. beef industry. Days Open is the days of the breeding season a heifer remained open while Days to Conception is the number of days in the breeding season it took a heifer to get pregnant (missing observation if the heifer did not conceive). In this current study, we considered traits such as Days Open, Days to Conception, Pelvic Height, Pelvic Width and Reproductive Tract Score in a multi-breed (Angus, Red Angus, Hereford, and Bos indicus cross) panel of beef cattle. For genetic evaluation and genomic prediction, we aim to leverage a large dataset (13,781 animals, 5 traits, pedigree records and 800k imputed Single Nucleotide Polymorphism [SNP] data) to pursue the following: (1) estimate variance components and correlation between traits, and (2) compare prediction accuracies from univariate and multivariate models using the single-step Genomic Best Linear Unbiased Prediction (ssGBLUP) method. The LR Method will be used in 3-fold cross validation for assessing model accuracies for all the models. We expect low to moderately high heritability across the traits as well as prediction accuracies comparable or better than current heifer pregnancy predictions.

Genomic background of swine inflammation and necrosis syndrome and skin damage

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Lesions and injuries to the extremities of the pig's body (such as the tail, ears, etc.) are commonly associated with biting. Lesion signs identified at birth and in 3-d-old piglets suggest that injuries might be caused not only by biting but, also, by Swine Inflammation and Necrosis Syndrome (SINS), which can occur without any action from other pigs. This study investigated the genetic background of SINS and Damage (DMG) in different body parts. We analyzed about 7k females born from February 2022 to June 2023 on three farms in the Netherlands. We scored SINS (no SINS=1, and SINS=2) at birth on the ears, tail, and teats. The tail was docked after phenotyping. We defined TOTALSINS as the number of affected parts. The same animals were scored for DMG on the ears and tail more than once during the rearing phase (no DMG=4, slight DMG=5, severe DMG=6, and very severe DMG=7), resulting in around 28k DMG records. Single-trait animal models with 23k SNPs from 4,947 genotyped animals and pedigree information were used for variance components estimation. Farm-year-month at birth and line-technician interactions were considered in both models as fixed effects, besides we considered birth weight (linear and quadratic) for SINS and age at scoring for DMG as covariables. As random effects, we had animal, maternal, and litter for SINS, and farm-year-month at scoring, animal and permanent environment for DMG. Direct and (maternal) heritabilities for SINS were equal to 0.04±0.02 (0.03±0.02) for ear, 0.05±0.02 (0.01±0.02) for tail, and 0.10±0.03 (0.06±0.03) for TOTALSINS. Direct heritability for DMG was equal to 0.09±0.01 and 0.07±0.01 for ear and tail, respectively. Except for the maternal heritability for the tail, all heritabilities found here were non-zero, which indicates that there is genetic variability for the traits and that it is possible to apply selection. TOTALSINS is highly correlated with different body parts (>0.7), being a good index for SINS. We hypothesize that TOTALSINS is also genetically correlated with Damage. Investigations are being done to determine whether there is a genetic correlation between SINS and DMG and its magnitude.

Keywords: Genetic correlation, SINS

Enhancing breeding efficiency: assessing the impact of the SimpleMating algorithm for long-term genetic gain and diversity

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The ability to design crosses that maximize genetic gain while maintaining genetic diversity is crucial for long-term breeding success. In this study, we evaluate strategies for optimizing cross-selection in both clonal- and line-development recurrent selection breeding programs using the recently developed SimpleMating algorithm and compare it with programs/algorithms developed for cross-optimization. Breeding programs were simulated in AlphaSimR, incorporating a burn-in phase followed by 20 years of breeding. We tested different trait architectures—varying in heritability, QTL number, and genetic control (additive vs. additive + dominance)—as well as different marker densities and multi-trait scenarios. The effectiveness of various selection strategies, including optimal cross-selection (OCS), optimum contribution selection (OContSel), total cross-genetic value (CTGV), mid-parental value, usefulness, and a benchmark truncation genomic selection scenario, were compared based on genetic gain, inbreeding levels, and conversion efficiency under different inbreeding constraints using both marker- and pedigree-based relationship matrices. Our results indicate that in line-development breeding programs, the SimpleMating algorithm, particularly under OCS using usefulness, consistently outperformed OContSel and mid-parental value in terms of genetic gain while effectively controlling inbreeding. In clonal breeding programs, CTGV-based optimization yielded the highest long-term genetic gain, surpassing usefulness-based cross-selection, which accounted for additive and dominance effects. Importantly, scenarios that incorporated the SimpleMating algorithm to constrain coancestry exhibited lower inbreeding levels, demonstrating the algorithm's ability to balance genetic diversity and selection intensity. Additionally, conversion efficiency was highest in line-development breeding programs using SimpleMating, highlighting its potential for balancing long-term genetic gain and diversity. While usefulness-based selection proved highly effective for line breeding, its impact on clonal breeding was limited, suggesting that alternative strategies may be more beneficial. These findings underscore the importance of tailored selection approaches for different breeding systems. Given the increasing emphasis on genomic selection and rapid breeding cycles, tools like SimpleMating offer a valuable, efficient, and user-friendly framework to enhance breeding decisions.

Decreasing computing time of approximated reliabilities of GEBV in ssGBLUP using different core sizes for APY

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Single-step GBLUP (ssGBLUP) with the Algorithm for Proven and Young (APY) is used to compute GEBV in livestock populations with extensive genomic data. Calculating GEBV reliabilities is computationally expensive with many genotyped animals because it requires inverting the left-hand side of the mixed model equations. The ACCF90GS2 software from the BLUPF90 suite approximates such reliabilities by considering the sparse structure of the APY inverse of the genomic relationship matrix. The bottleneck of the algorithm is a matrix multiplication that has a quadratic cost with the number of core animals. This study aimed to decrease the computing time for approximating GEBV reliabilities in ssGBLUP by reducing the size of the core set in APY without affecting the quality of the approximations. Reliabilities were approximated for two single-trait models with categorical traits. Tests involved commercial dairy cattle datasets comprising 4.5M animals in the pedigree, 1.6M genotypes, and 1.5M records for calf respiratory disease in Holsteins (h2 = 0.042) and 427K animals in the pedigree, 107K genotypes, and 128K records for cystic ovaries in Jerseys (h2 = 0.054). Core sets of varying sizes (25K, 20K, 15K, 10K, and 5K) were tested. Reliabilities obtained with a core set size of 25K were used as a comparison benchmark. Level and dispersion bias were evaluated based on intercept and slope of the regression of reliabilities with 25k core on the other core sizes. For Holsteins, correlations between approximated reliabilities obtained with different core sizes ranged from 0.96 to 0.99, intercepts ranged from 0.02 to 0.30, and slopes from 0.72 to 0.97. Computing times varied from 11.1 to 456.8 minutes for 5K and 25K core sizes, respectively. Results for Jerseys showed less variability among core sizes. Computing times ranged from 0.76 to 7.44 minutes. Decreasing the core size reduced computing time up to 40 times compared to the benchmark time. Having fewer genotyped animals in the APY core is a reasonable approach to obtain GEBV reliability faster; however, changes in the approximated reliabilities occur and are trait-dependent.

Keywords: Accuracy, computing cost, genomics

Characterizing environmental factors influencing beef cattle performance for precision breeding of resilience

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In the U.S., beef cattle are raised in diverse environments with varying management practices and climatic conditions, leading to potential genotype-by-environment interaction (GxE). Under GxE, animal's performance is determined by the combined effects of its genetic make-up (genotype) and environment, rather than the sum of these independent effects. The GXE can cause animals with different genetics to perform differently across environments, resulting in re-ranking of selection candidates. A comprehensive characterization of farm and environmental conditions is crucial for studying GxE. This “enviromics” approach provides insights for precision breeding and optimized management of beef cattle. The objective of this study was to identify environmental factors that significantly affect animal performance across herds and evaluate their use in predicting herd performance. The dataset included 1.92 million weaning weight (WW) records from 5,600 Angus herds, with a mean ± standard deviation (SD) of 305.10 ± 94.6 kg. Environmental data such as Köppen-Geiger climate classification (CLI), soil classification (SOIL), and elevation (ELE) were collected based on the geographical locations of the farms. The first step of the analysis involved obtaining herd-year solutions (HYS) for WW using a linear mixed model from genetic evaluation of Angus cattle. The model included herd-year as a fixed effect, and contemporary group, additive genetic, maternal genetic, and maternal permanent environment as random effects. Genetic parameters for WW were estimated using restricted maximum likelihood (REML), with direct and maternal heritability estimates of 33.0% and 11.0%, respectively. Next, the enviromics variables were used to explore the environmental factors that significantly contributed to HYS variance. The results showed that CLI, ELE, and SOIL explained about 14.8%, 9.0%, and 7.1% of the HYS variance, respectively. Finally, a partial least squares (PLS) model was used to assess the predictive ability of these enviromics variables, yielding a predictive correlation of 0.324 and a mean squared error of prediction (MSEP) of 56.3 kg2. This study highlights the potential of the enviromics approach to characterize GxE in beef cattle, supporting precision breeding and forecasting animal performance under varying conditions. We are currently conducting farm-level surveys to explore how different farm management practices influence animal performance.

Developing a software for statistical analysis of groups of experiments in randomized complete

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Brazil has recently achieved leadership in maize export. It stands out for being the most produced grain in the world, with a wide array of applications, including its use in food, industry and mainly to produce feed for animal use. Therefore, evaluating different varieties under different conditions is essential for crop improvement and maximizing production, providing insights into genotype-by-environment interactions (GEI). In plant breeding, most experiments analyze the interactions between multiple factors to find the most adapted cultivars for each environment using factorial treatment arrangements. Additionally, it is replicated at different locations to assess the consistency of the genotype's performance. Attached to it, the predominant use of “completely randomized block” design is noteworthy due to its ability to control experimental variability in field trials, increasing the accuracy of superior genotype estimates. Thus, the availability of efficient computational resources to process data is essential for researchers to estimate and interpret the desired genetic parameters. In this context, this project focused on developing software to perform statistical analysis for randomized block designs with factorial arrangements, including different environment trials. The study goal was to facilitate the breeders' access to phenotypic data analysis and interpretation, without deep knowledge of programming language, enabling accurate decision-making. As an example, the app tested data provided by the Brazilian Agricultural Research Corporation (Embrapa) Maize & Sorghum, analyzing 156 hybrids of Zea mays evaluated in two seasons and different tropical cities in Brazil. This project demonstrated that the development and implementation of “DesignGen” app capabilities had satisfactory performance, allowing for effective statistical analysis, representing significant advancements in maize breeding programs, allowing selection of superior genotypes more efficiently.

Approximating reliabilities of indirect predictions using SNP effects from large ssGBLUP evaluations

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Reliability is a commonly used metric for assessing breeding values. However, calculating true reliabilities, i.e., from the inverse of the mixed model equations (MME), is computationally intensive for large populations; thus, approximations are often used. Additionally, when individuals have indirect predictions (IP) based on SNP effects, they are not included in the MME; therefore, reliabilities cannot be computed using traditional methods. We aimed to approximate the reliabilities of IP when SNP effects are computed from large, genotyped populations. We then compared two methods for approximating reliabilities: 1) based on the prediction error covariance (PEC) of SNP effects for core animals by back solving from the PEV of genomic estimated breeding values, using single-step GBLUP (ssGBLUP) with the Algorithm for Proven and Young (APY), and 2) using benchmark reliability by calculating PEC in a ssGBLUP model using a block sparse inversion of inverse of the genomic relationship matrix with APY. Data provided by the Council on Dairy Cattle Breeding consisted of 98,938,654 milk yield (MY) records from various breeds, 49,585,192 animals in the pedigree, and 1,877,704 genotyped animals. Reliabilities were calculated using either a multi-breed or a single-breed approach. For validation, males and females born from 2019 to 2021 had their pedigree, phenotypic, and progeny information removed. Reliabilities of indirect predictions were regressed on reliabilities from the analysis including genotypes for validation animals, and the regression coefficients were used to assess the quality of the approximations. In the multibreed analysis, Holstein (HO) regression coefficients were 0.91 for both males and females. For Jersey (JE), the coefficients were -0.14 and 0.63 for males and females, respectively; for Brown Swiss (BS), 1.11 and 0.99 for males and females, respectively. In the single-breed analysis, correlations between the two approximations increased in both JE (from 0.40 in multibreed to 0.99 in single-breed) and BS (from 0.80 in multibreed to 0.93 in single-breed). In this study, we showed that it is possible to approximate reliabilities based on the PEC of SNP effects of core animals in single-breed models. When using multibreed models, dominant breeds affect the reliabilities, indicating that a within-breed approximation of reliabilities is required.

Predictivity and variance components in estimating genetic parameters: impact of genomic selection for growth and carcass on foot structure

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The objective was to evaluate the impact of genomic selection for production traits on foot structure in Angus. Variance component estimation (VCE; Bayesian approach as implemented in gibbsf90+) with partial or no genotypes, and a new predictivity method using all genotypes, were used to examine changes over time in genetic parameters. The traits were Claw Set (CS), Foot Angle (FA), Birth Weight (BW), Weaning Weight (WW), Post Weaning Gain (PWG), and the ultrasound traits: Scan Weight (ScanWT), Fat Thickness (uFAT), and Rib Eye Area (uREA). Genetic parameters through VCE over 5-year intervals and using genotypes were obtained. From 2011-2015 to 2019-2022, changes in heritability were observed for CS (0.12 ± 0.01 to 0.16 ± 0.01), FA (0.18 ± 0.02 to 0.14 ± 0.01), and uFAT (0.32 ± 0.01 to 0.38 ± 0.01). Changes in genetic correlations were found for CS-ScanWT (0.12 ± 0.06 to 0.0 ± 0.03), FA-WW (0.03 to -0.15), and FA-PWG (-0.10 to 0.00). In the last interval, the genetic correlations were between -0.15 and 0.06. For the predictivity method, estimates from two 2-year slices showed that most growth and ultrasound carcass traits heritabilities were lower than those from the last VCE interval (e.g., BW: 0.34 vs. 0.26). In comparison heritabilities estimated through predictivity were higher for CS (0.16 vs 0.30) and FA (0.14 vs 0.21). Genetic correlations through predictivity ranged from -0.16 to 0.12. The predictivity method provides updated genetic parameters for young animals, while VCE estimates are for the base population. Our results indicate that heritability estimates in recent generations for strongly selected traits have decreased compared to older generations. However, genetic correlations between foot structure and production traits have consistently remained close to zero, likely due to the differential selection between these traits. While no strong antagonistic correlations were found, selecting multiple traits is crucial to maintain conformation while improving production. Since the population structure continually changes due to genetic or environmental factors, updating the genetic parameters is vital for achieving expected genetic gains.

Sex-specific gene expression differences in developing bovine blastocysts

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Following embryonic genome activation, developing embryos undergo a cascade of gene expression events that lead to a diversity of downstream phenotype differences further on in development. We found that developing male and female embryos have starkly different patterns of gene expression across both sex chromosome and autosomal genes. We used a dataset of 306 blastocyst transcriptomes from an Angus (Bos taurus) x Brahman (Bos indicus) diallel-like cross to understand how sex differences drive differential gene expression at an early developmental stage. We generated an average of 26 million reads per blastocyst. Reads were trimmed and filtered with Trimmomatic, then aligned to the ARS-UCD 2.0 Bos taurus reference genome via the STAR alignment software. We identified embryo sex by calculating the percentage of reads that mapped to the Y-chromosome, drawing a threshold at <3% for females and >7% for males. Our dataset contained 140 female, 156 male, and 10 unidentified embryos. A Principal Component Analysis showed that embryo sex was the largest driver of differential gene expression, accounting for over 18% of the total variation explained, even when Y chromosome genes were excluded from analysis. This was a larger driver of gene expression than sub-species. We used DESeq2 to identify differentially expressed genes between male and female embryos, resulting in 1,165 genes with log2 fold changes >1 and FDR-corrected p-values <0.05. Only 26 of these genes showed higher expression in male embryos compared with female embryos despite there being no significant difference in developmental rate or embryo quality between the sexes. Numerous genes related to sex differentiation and X chromosome-inactivation were differentially expressed, such as XIST (X inactive specific transcript) and multiple MAGE family members. Of the sex-specific DEGs, 358 (~30%) reside on the X-chromosome. Other autosomal DEGs identified have been previously identified by other studies to be involved in sex-determination or gametogenesis. Functional classes identified were related to known X chromosome-linked phenotypes, immune response, and cell-cell signaling. Ongoing work is identifying sub-species-by-sex interactions that manifest in gene expression differences, as well as mapping sex-specific expression QTL.

Genomic evaluation for functional longevity in North American Angus cattle using longitudinal models

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Cow's Longevity plays a major role in the overall profitability of the beef cattle industry, reflecting the female's ability to remain productive in the herd over time. In this context, longitudinal models as random regression models (RRM) are the preferred method as they account for genetic and environmental effects over time. Traditionally, RRM longevity evaluations use binary phenotypes; however, redefining the phenotype as the number of calves could enhance variability, better identify cows with consistent reproductive performance, and penalize irregular calving patterns. This study aimed to: (1) propose genomic evaluations for a novel functional longevity (FL) definition via RRM; (2) compare model fit using Legendre polynomials (LP) of varying orders; (3) evaluate the FL genetic parameters behavior implication for selection strategies. The dataset included records from 2 million Angus cows and 1.6 million genotyped animals, provided by the American and Canadian Angus Associations. FL was defined as the cumulative number of calvings, measured annually from 2 to 10 years of age. Genetic parameters were estimated with Gibbs sampling without genomic information, and genomic breeding values (GEBV) were estimated using RRM under single-step GBLUP with LP. Models were compared via sire GEBV rankings across ages using Spearman correlations and the percentage of individuals in common (top 1%). The best fit was observed with a third-order LP and homogeneous residual variance. Heritabilities ranged from 0.04 to 0.11. Genetic correlations between ages were positive and high, with minimal fluctuations. The GEBV rank correlations were consistent across ages, with Spearman correlations following the same pattern as the genetic correlations. The percentage of commonly selected individuals between adjacent years was high. However, the percentage decreased as the gap between ages increased, dropping to 53% between ages 3 and 10. In conclusion, the new functional longevity definition using third-order LPs is a feasible alternative for genomic evaluations. Heritability estimates of FL indicate sufficient additive genetic variance to allow a moderate response to selection. Based on genetic correlations and ranking comparisons, age 6 is the optimal age to maximize genetic progress for functional longevity in Angus cattle.

Chromosome-scale assembly of wheat cultivar Sumai 3, the major germplasm source for Fusarium head blight resistance

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Fusarium Head Blight (FHB), also known as scab, is a devastating disease that severely impacts global wheat production. The wheat cultivar Sumai 3, renowned for its resistance to FHB, has played a pivotal role in breeding programs; however, its genome has not been fully resolved at the chromosome scale. Here, we present a high-quality chromosome-scale assembly of the Sumai 3 genome, generated using PacBio HiFi reads and chromosome conformation capture (HiC). The assembly yielded a genome size of 14.6 Gb with a longest contig of 245.2 Mb and a contig N50 of 41.90 Mb. The assembly demonstrated 99.7% BUSCO completeness, with 832 contigs. We identified 104,620 high-confidence protein-coding genes. The assembled genome consisted of 92.67% repetitive DNA sequences. Our analyses included centromeric and subtelomeric regions, tandem repeat and long terminal repeat density, high and non-coding gene density, and GC content across the genome represented in a circos plot, providing a comprehensive view of Sumai 3's structural and functional landscape. Co-linearity analysis showed that Sumai 3 is mostly co-linear with the Chinese Spring v2.1 genome, indicating high conservation in gene order. The region's gene content largely overlaps with annotations for Chinese Spring v2.1, although we discovered two genes at approximately 157.7 kb, including additional copy of a terpene synthase, suggesting a similarity between Sumai 3's 3B and Chinese Spring's 3D in FHB-related gene content. Differential gene expression (DGE) in the Fhb1 region shows up-regulation of genes PFT, Sin, and PAP highlighting genes potentially involved in FHB resistance. This work advances our understanding of Sumai 3's genomic landscape, aiding in breeding strategies for FHB resistance in wheat.

Transdisciplinary Tech

Elucidating the influence of drought on endophytic bacterial diversity in roots of common bean (Phaseolus vulgaris L.) using PCR-based techniques

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Due to its nutrient richness, the common bean (Phaseolus vulgaris L.) is a staple legume in many regions worldwide. Common bean is often subject to environmental stresses across these regions, including drought. Some genotypes have proven tolerance to drought stress, partially due to the presence of symbiotic microorganisms within the roots known as endophytes. This study aims to classify endophytic populations in the roots of drought-tolerant and drought-sensitive common bean genotypes subjected to drought stress. The composition of microbial communities associated with these genotypes may exhibit variations in response to drought stress experienced by the genotypes. To isolate endophytes, the genotypes underwent surface sterilization and were subsequently cultured in nutrient agar using 2-3 cm root segments. After 4 days, microbial growth proximal to the roots was subcultured to isolate individual colonies. Genomic DNA was extracted from these pure cultures and verified using PCR with universal 16S rRNA primers. The DNA samples were sent for Sanger sequencing, and a phylogenetic tree was constructed to elucidate the evolutionary relationships among different bacterial species. Six samples were selected from the Sanger sequencing results to undergo whole genome sequencing and in vitro biochemical testing protocols that measure drought stress tolerance ability, salt tolerance ability, indole acetic acid (IAA) production and 1-aminocyclopropane-1-carboxylate (ACC) deaminase production. The sequencing data revealed that a substantial proportion of the endophytes identified in the study had previously been associated with drought stress, as indicated in prior research. Furthermore, the biochemical testing identified endophyte populations that could possibly provide growth-promoting properties to plants and confer resistance to abiotic stresses. This research contributes to the advancement of endophyte characterization and sheds light on their specific roles in enhancing plant tolerance to abiotic stress, while expanding the potential utility of employing particular endophytes to enhance a plant's tolerance mechanisms to abiotic stresses.

Unlocking Innovations From Basic Science

Mycobacterium bovis infection in cattle is well-predicted using gene-based and composite features from peripheral blood transcriptomics data

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Mycobacterium bovis is the principle causative agent of bovine tuberculosis (bTB), a disease significantly impacting animal health in countries such as Ireland where bTB is endemic. In Ireland, the diagnostic tests employed for bTB diagnosis are the in vivo field-based single intradermal comparative tuberculin test (SICTT) and an ancillary laboratory-based in vitro interferon-γ release assay (IGRA) test. The sensitivity for the SICTT and IGRA tests are estimated to be 75% and 90%, respectively for confirmed bTB cases. The suboptimal sensitivity of both tests culminates in many M. bovis infected animals being misclassified as non-infected, facilitating disease persistence and impeding bTB control and eradication. Efforts have been made to identify blood-based transcriptional biosignatures of M. bovis infection and bTB disease based on differentially expressed genes. However, few studies have applied machine learning (ML) techniques to such data, in contrast to human TB where blood-based ML algorithms have shown powerful discrimination between non-infected and M. tuberculosis infected patients. Here, we analysed peripheral-blood transcriptomic data from 63 control and 60 confirmed M. bovis infected cattle and implemented an elastic net binary logistic regression classifier using as input; 1) normalised genes; 2) inferred principal components (PCs); 3) independent components (ICs) and; 4) rank variables from non-negative matrix factorization (NMF). We observed that a 169 gene signature performed well, achieving a 10-fold cross validation accuracy of 89% on training data, which generalised well to unseen data, obtaining an accuracy of 89%. Methods using low-dimensional representations performed similarly, with PCs, ICs, and NMF factors achieving an accuracy of 86%, 83% and 89% respectively on unseen data. Comparing all models using a receiver operating characteristic (ROC) curve on the unseen data, the 169 gene signature achieved the highest area under the curve at 0.972 compared to 0.948 for the dimensionality reduction methods. Overall, our results suggest that gene-based features from RNA-seq, in combination with a simple ML classifier represents a powerful approach to discriminate between control non-infected and M. bovis infected cattle. Future work will involve rigorously evaluating other ML methods that can capture non-linear relationships to improve classification performance.

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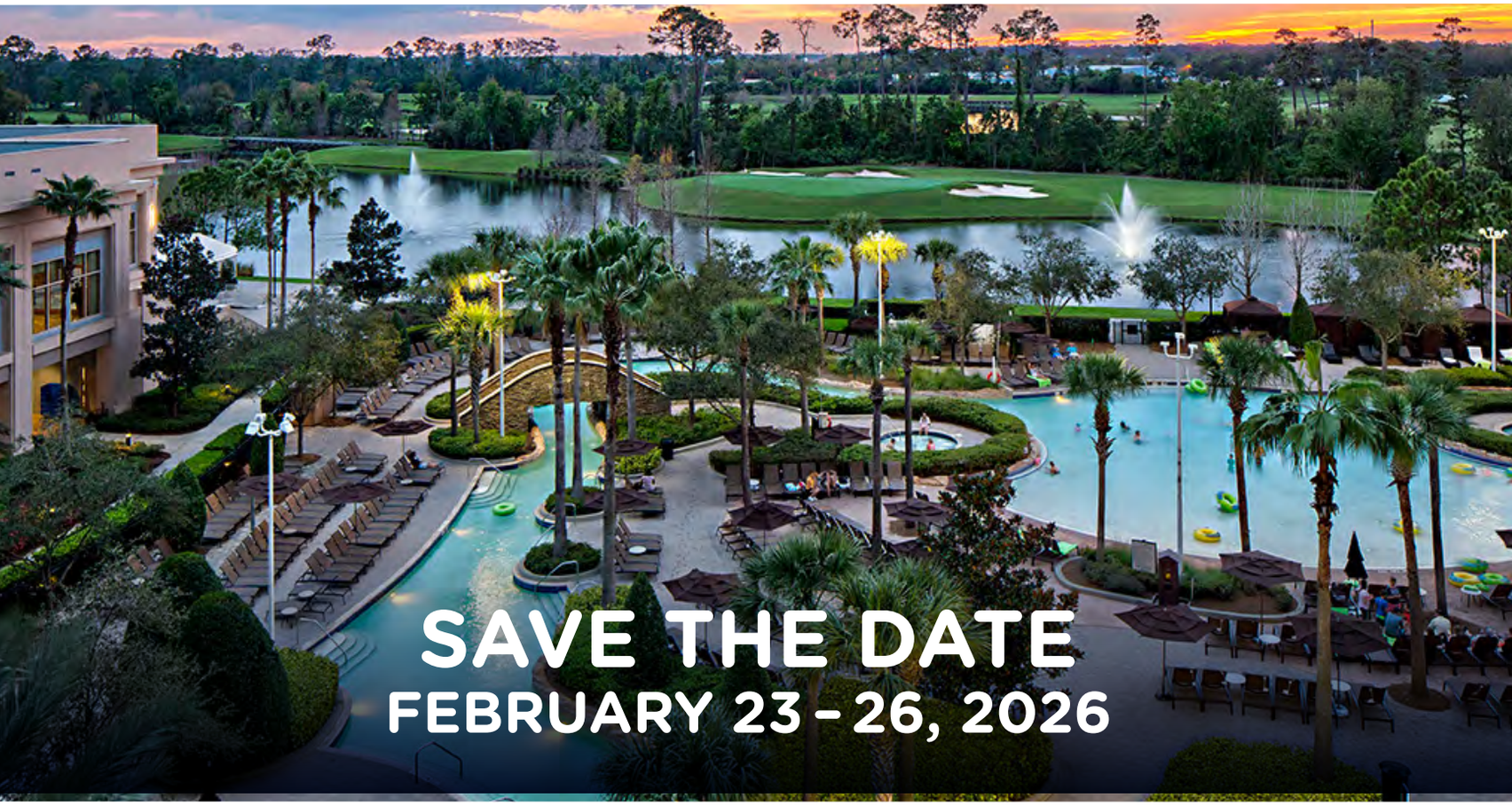
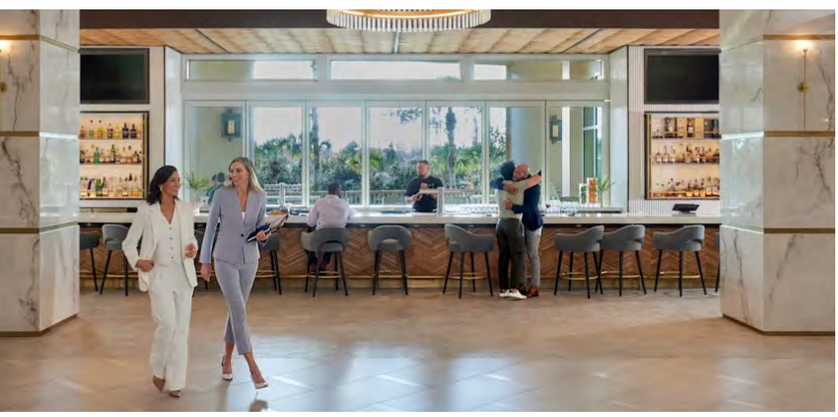
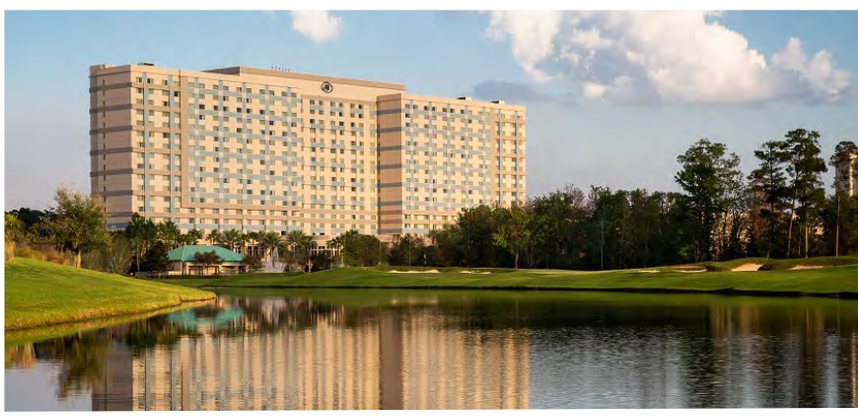
GENERAL MEETING







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Index

	Last Name	First Name	Organization / Company	Page(s)
K	Kapoor	Muskan	Iowa State University	46
	Konkin	David	National Research Council Canada (NRC)	38
	Kumari	Sunita	Cold Spring Harbor Laboratory	47
L	Ladeira	Giovanni	University of Florida	67
	Lavoie	Jennifer	Thermo Fisher Scientific	54
	Lee	Seung Hoon	Chung-Ang University	68
	Lohr	Chaelynne	CentralStar Cooperative	69
	Londoño-Gil	Marisol	Universidade Estadual Paulista UNESP	70
	Lopes de Oliveira	Carlos	University of Georgia	71
M	Macharia	Sarah	International Institute of tropical Agriculture(IITA)	39
	Massaro da Silveira	Pedro Henrique	"Luiz de Queiroz" College of Agriculture - University of São Paulo	72
	McLaughlin	Chloee	HudsonAlpha Institute for Biotechnology	40
	Merga	Ibsa	Donald Danforth Plant Science Center	55
	Mian	Sahr	Genome British Columbia	24
	Mohamed	Ruwaa	University of Tennessee	25
	Mohammed Ali	Safa	Aneelain University	73
	Morales-Cruz	Abraham	Joint Genome Institute (LBNL)	48
N	Na-ah	Raissa	Washington State University	26
	Nijland	Bart	Genetwister Technologies B.V.	34
	Nuñez	Pedro	Universitat Politécnica de Valencia	74
O	Obermoeller	Dawn	Revvity	27
	O'Grady	John Francis	UCD School of Agriculture and Food Science, University College Dublin	89
	Olaoye	Dotun	University of Missouri	64, 75
	Oliveira Garcia	Arielly	University of Georgia	76
P	Peixoto	Marco	University of Florida	77
	Porto Neto	Laercio	Commonwealth Scientific and Industrial Research Organisation	23
Q	Quinn	Shawn	Curio Genomics	27, 30

	Last Name	First Name	Organization / Company	Page(s)
R	Rios	Esteban	University of Florida	28, 41
S	Sanchez-Sierra	Sergio Nicolás	University of Georgia	78
	Shaw	Felix	Earlham Institute	49
	Sigdel	Anil	UW-Madison	79
	Sipowicz	Pablo	University of Florida	28
	Siu	Anson	University of Wisconsin-Madison	32
	Souza Krupek	Raissa	Luiz de Queiroz College of Agriculture - University of São Paulo	80
T	Tabet	Joe Menwer	University of Georgia	81
U	Ulmer	James	University of Tennessee Knoxville	83
V	Vital Brasil Ramos	Pedro	Angus Genetics Inc.	84
Z	Zhao	Junhua	Element Biosciences	33

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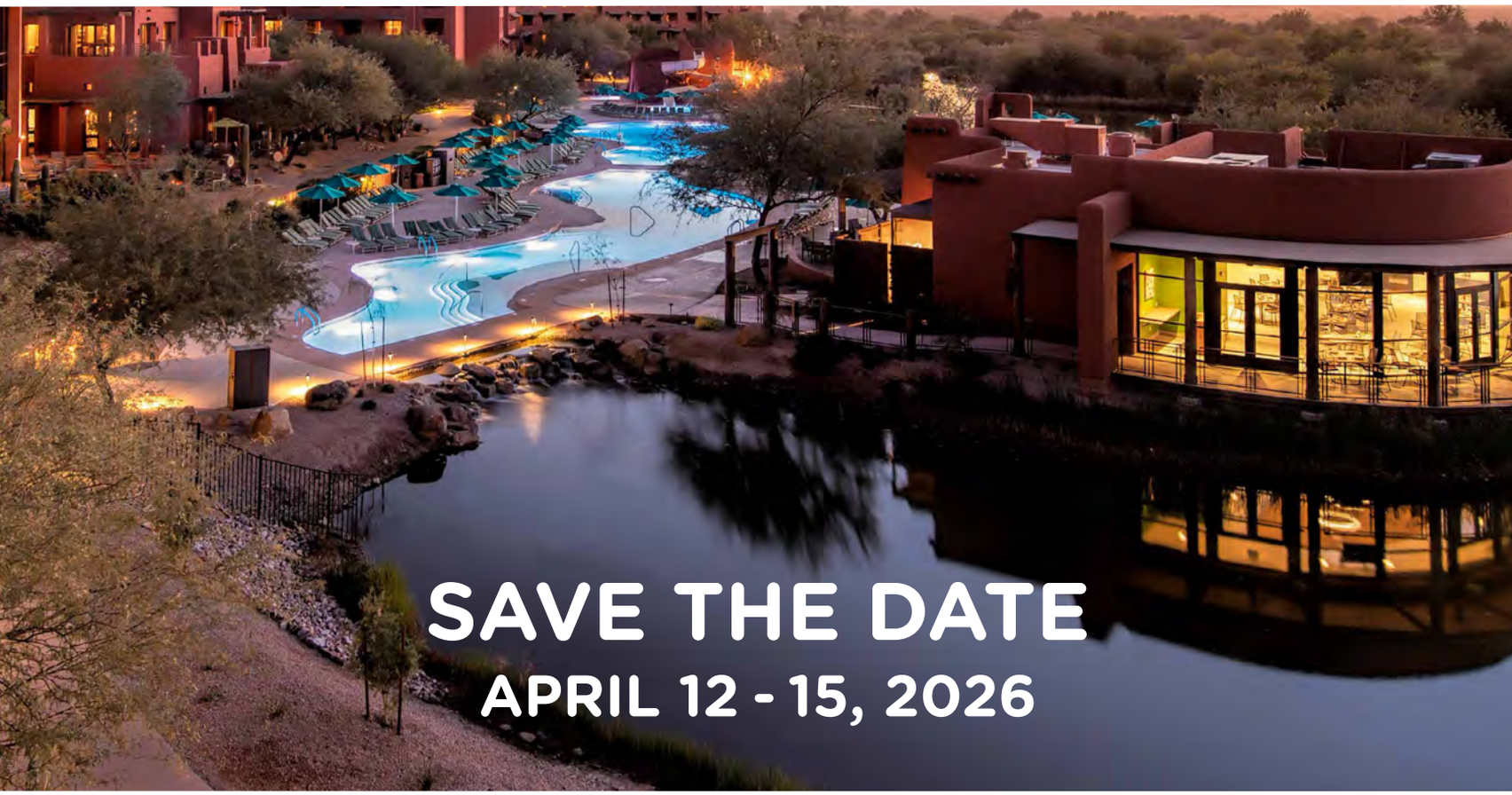

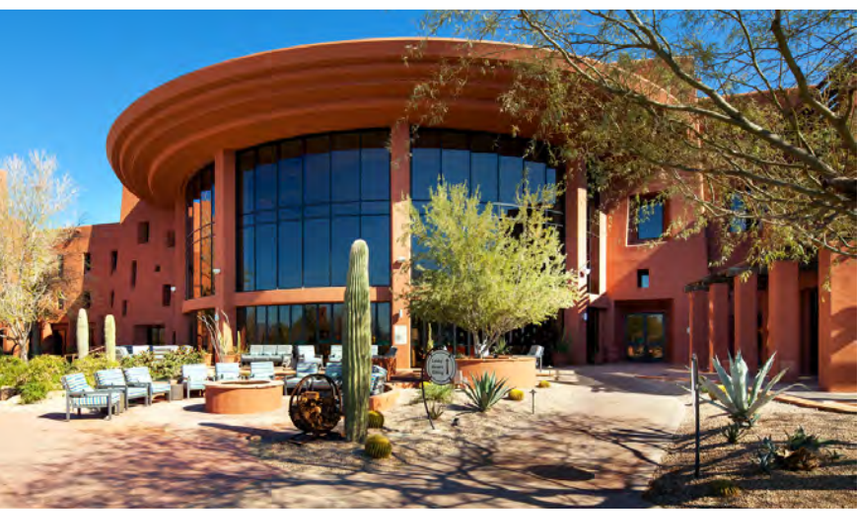

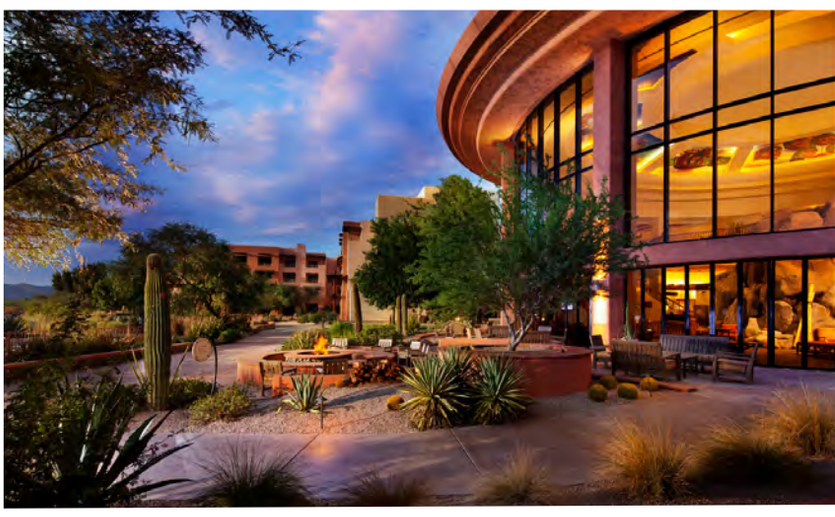

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