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35th International Mammalian Genome Conference: meeting overview

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Abstract

The 35th International Mammalian Genome Conference (IMGC) was held on July 17–20, 2022 in Vancouver, British Columbia; this conference marked the first time the International Mammalian Genome Society (IMGS) hosted a meeting in Canada. Scientists from around the world participated to share advances in genetics and genomics research across mammalian species. A diverse attendance of pre-doctoral and post-doctoral trainees, young investigators, established researchers, clinicians, bioinformaticians, and computational biologists enjoyed a rich scientific program selected from 88 abstracts in the fields of cancer, conservation genetics, developmental biology, epigenetics, human disease modeling, immunology, infectious diseases, systems genetics, translational biology, and technological advances.

Introduction

The 35th International Mammalian Genome Conference (IMGC) was held at the Westin Bayshore Hotel in Vancouver, Canada as a hybrid meeting. Due to the COVID-19 pandemic, the International Mammalian Genome Society (IMGS) Secretariat delayed the conference date twice until an in-person option became possible. The hybrid format enabled attendees to deliver their work via in-person and virtual oral and poster presentations. The 35th IMGC had 79 in-person attendees and 44 virtual attendees from 10 countries. The IMGS awarded 21 scholarships to pre-doctoral and post-doctoral trainees to attend the 35th IMGC.

The IMGS had previously worked with the GSA on a hybrid TAGC meeting in 2020 (Miller and Siracusa 2021). The exceptional contributions of Darla Miller (Chief Operating Officer of the IMGS) in developing the meeting format and coordinating onsite and remote activities made the 35th IMGC a huge success!

Selected highlights of the 35th IMGC

Session themes for oral presentations focused on (1) Evolution, Gene Drive, and Conservation Genetics, (2) Translational and Systems Genetics, (3) Comparative Genomics and Computational Methods, (4) Development, Epigenetics and Stem Cells, (5) Technology and Resources, and (6) Human Disease Models. IMGS meeting participants elegantly highlighted and illustrated how recent advances in mammalian genetic and genomic approaches have improved our ability to decipher complex biological mechanisms and disease processes as well as detailed how to apply this knowledge to develop novel approaches for treating human disease.

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The IMGS trainee symposium

The Trainee Symposium was held on July 17, 2022, just prior to the start of the main meeting. The Trainee Symposium familiarized organizers, trainees, and participants from the mammalian community with the in-person and on-line formats and continued the tradition of mentoring trainees, which is an essential part of the IMGS mission. A total of 12 excellent talks were delivered by IMGS predoctoral students and post-doctoral fellows; three trainees were selected to receive The Lorraine Flaherty Award and present their talks in the main meeting. Marie Bourdon from the Institut Pasteur was presented with the Verne Chapman Young Scientist Award for her platform presentation. IMGS Secretariat members served as judges of the Trainee Symposium and evaluated more than 40 posters by trainees. The winners (Table 1) were presented with their awards at the conference banquet held at Grouse Mountain in North Vancouver, Canada.

Invited speakers

The Verne Chapman Memorial Lecture was given by Monica J. Justice (Program Head of the Genetics and Genome Biology Program at The Hospital for Sick Children in Toronto, Ontario, Canada). Her talk was entitled “Of mice and (wo)men: from tails to treatments” and focused on the exciting progress made using *Mecp2*-null mice in a sensitized genetic screen for suppressor mutations of the Rett phenotype in understanding genetic pathways leading to Rett Syndrome which hold promise for development of novel treatments for this neurological disorder. The keynote invited speaker was Kent Hunter (Senior Investigator in the Laboratory of Cancer Biology and Genetics at the National Cancer Institute, Bethesda, MD, USA). His talk was entitled “Investigating the etiology of cancer metastasis through the lens of meiotic genetics” and concentrated on the discovery of novel pathways and genetic variants in the host that influence susceptibility to breast cancer metastases using the genetically engineered *MMTV-PyMT* mouse, which is an aggressive metastatic model of mammary tumors. The

Table 1 International mammalian genome society award winners for 2022

Awardee	Institute	Title	Mentor
Verne Chapman Young Scientist Award			
Marie Bourdon*	Institut Pasteur	Dissecting genetic susceptibility to Zika virus in the Collaborative Cross	Xavier Montagutelli
Oral Presentation Awards			
H. Matthew Berns*	NHGRI/NIH	Single-cell RNA sequencing of melanocytes isolated from mice with loss of MC1R signaling reveals the importance of TBX3 in pheomelanogenesis	William Pavan
Haley Fortin	The Jackson Laboratory	Trans-regulation of heterochromatin underlies genetic variation in 3D genome contacts in mouse embryonic stem cells	Christopher Baker
Megan Majocha*	NCI/NIH	Deletion of metastasis susceptibility gene RESF1 occurs in primary mammary tumors and metastases of MMTV-PyMT mice	Kent Hunter
Joe Nguyen	NCI/NIH	CRISPR/Cas9 guided multiomics defines a direct inhibitory role for mTOR in Hippo signaling	Beverly Mock
Wasay Mohiuddin Shaikh Qureshi	University of Manchester	pre-mRNA processing factor 8 (Prpf8) dysfunction results in aberrant laterality establishment and cardiac development	Kathryn Hentges
Poster awards			
Sean Gombart	Seattle Children’s Research Institute	Analysis of a spontaneous mutation causing microtia using whole genome sequencing	David Beier
Sam Stroupe	Texas A&M University	Genomic signatures of cattle introgression in historical and modern North American Bison	James Derr
Qinwei Zhuang	McGill University	Phenotypic sex and sex-chromosome complement impact DNA methylome including brain-specific sex-biased CAC methylome	Guillaume Bourque
Outstanding nomenclature on a research poster—ICSGNM**			
Ana Velasquez	Texas A&M University	A daughterless mouse for island conservation	David Threadgill

*Lorraine Flaherty Award for oral presentation in the Trainee Symposium

**ICSGNM, International Committee on Standardized Genetic Nomenclature for Mice

Mary Lyon Lecture was delivered by Julie Mathieu (University of Washington, Seattle, WA, USA). Her talk was entitled "Interplay between metabolism and epigenetics in early development" and described the clever application of CRISPR/Cas9 tools to study these factors as drivers of the determination of cell fates and lineage specification during embryogenesis, highlighting their importance in regenerative medicine.

Evolution, gene drive, and conservation genetics

Although most presentations at the 35th IMGC focused on studies of laboratory mouse strains and variants, the IMGS expanded its focus this year by devoting a whole session to research on Evolution, Gene Drive, and Conservation Genetics. This session included oral and poster presentations about wild mice and their impact in natural settings. It is evident that mice are destructive invasive species on islands; through predation and competition, mice can cause the loss of other species, resulting in reduced biodiversity. Talks presented by J. Royden Saah (North Carolina State University, Raleigh, NC & Island Conservation, Santa Cruz, CA, USA), Luke Gierus (University of Adelaide, Adelaide, Australia), and Kevin Oh (Macquarie University, Sydney, Australia) described methods to try to eradicate these invasive populations, which included population-sensitive gene drives. Modeling projections suggested that it is possible to eliminate mice on an island within 25 years. Such approaches are preferable to the use of anticoagulant treatments to kill mouse populations, because anticoagulants affect other species as well. Controlling access to islands is also key to keeping invasive species from spreading off an island and preventing the introduction of new species to an island. The Genetics Biocontrol of Invasive Rodents (GBIRd) consortium is a partnership of diverse experts from 7 world-renowned universities, government, and not-for-profit organizations advancing gene drive research to protect island communities and prevent island species extinctions (www.geneticbiocontrol.org/).

Advances in technology and resources

This session highlighted resources and platforms for different mammalian models used around the globe. Elizabeth Bryda (University of Missouri, Columbia, MO, USA) gave an introduction to the Rat Resource and Research Center (RRRC); via the official RRRC website (https://www.rrrc.us), investigators can deposit transgenic rat lines and order rat models provided by the RRRC, all with genetic background details available. Jennifer R. Smith (Medical College of Wisconsin, Madison, WI, USA) presented PhenoMiner Tool 2.0 for the Rat Genome Database (https://rgd.mcw.edu), which has a new user interface to facilitate mining of quantitative phenotype measurement data of interest. Hiroshi Kiyonari (RIKEN BioResource Research Center, Japan) introduced the first breakthroughs with CRISPR/Cas9 gene editing of a marsupial, the gray-tailed opossum (*Monodelphis domestica*). Leonard McMillan (UNC Chapel Hill, Chapel Hill, NC, USA) described improved reference genomes for the Collaborative Cross (CC) compiled using pooled sequencing, which will become available to the community as a new CC-Graphical Genome.

Community discussion on rigor and reproducibility

The 35th IMGC provided a unique opportunity to have a community discussion on Rigor and Reproducibility (R&R) in animal model research, with a special focus on laboratory mice. The session was moderated by Fernando Pardo Manuel de Villena (USA) with an international panel of stakeholders who are researchers, journal editors, and technology experts that included: Kuniya Abe (Japan), James Amos-Landgraf (USA), Monica Justice (Canada), Yann Herault (France), Xavier Montagutelli (France), Nathan Nowak (USA), and Michelle Southard-Smith (USA). Among several topics, the panel discussed the importance of R&R for the research community, founders, and the IMGS itself; the model for R&R covered the key role of setting minimum standards for publication and potential ways to enforce these standards. The session was well-attended, highly interactive, and there was almost unanimous consensus on the importance of the topic for the Society. The discussion on whether to focus on easy wins versus comprehensive standards was protracted, as was the call to continue the conversation and include additional partners (e.g., clinicians and veterinarians).

35th IMGC materials are available on-line

The 35th IMGC emphasized the critical role of model organisms in advancing research in genetics and genomics. Consistent with previous meetings (Miller and Siracusa 2021; Moskowitz et al. 2019; Sanchez-Andrade et al. 2018; Tracey et al. 2020), the 35th IMGC showcased how the mammalian community is moving forward with new discoveries and technologies that deepen our understanding of the complex roles of genetic and epigenetic mechanisms that drive development and disease processes, as well as revealed potential targets for therapy. Despite researchers having to adapt to a global pandemic, the incredible accomplishments of scientists, clinicians, and trainees these past two years were evident from the diversity of biological systems and disorders described across sessions. Abstracts and the entire program for the 35th IMGC are freely available on-line at https://www.imgs.org.

The 36th International Mammalian Genome Society Meeting

The 36th IMGC is scheduled for March 28–31, 2023 in Tsukuba City, Japan. The status of the pandemic has led to this meeting being planned in a hybrid format, with in-person and virtual attendance and presentation options (see www.imgc36.org for more information).

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Declarations

Conflict of interest The authors declare that they have no conflict of interest.

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