Mammalian Genome (2020) 31:69–76
https://doi.org/10.1007/s00335-020-09830-8

33rd international mammalian genome conference: meeting highlights

Lauren J. Tracey[1] · Kelsey E. Noll[2] · Xavier Montagutelli[3]

Received: 15 January 2020 / Accepted: 22 February 2020 / Published online: 2 March 2020

Abstract
Scientists from 12 countries met at the International Mammalian Genome Conference (IMGC) to share advances in mammalian genetics and genomics research. The event was held in Strasbourg, France and represents the city's second time hosting the IMGC. A diverse attendance of pre-doctoral and post-doctoral trainees, young investigators, established researchers, clinicians, bioinformaticians, and computational biologists enjoyed a rich scientific program of 63 oral presentations, 65 posters, and 5 workshops in the fields of epigenetics, system genetics, developmental biology, cancer, human disease modeling, technical advances, and bioinformatics. This report presents selected highlights of this meeting which illustrate how recent advances in mammalian genetic approaches have improved our ability to decipher complex biological mechanisms.

Introduction

Over 170 researchers from around the world gathered in the beautiful Alsatian city of Strasbourg, France to participate in the 33rd annual IMGC from September 25 to 28, 2019. Organized by the International Mammalian Genome Society (IMGS), this conference built off the success of IMGC 2018 in Puerto Rico (Moskowitz et al. 2019), IMGC 2017 in Germany (Sanchez-Andrade et al. 2018), and previous IMGCs since 1986 (www.imgs.org/?run=home.history). Local organizers Yann Herault and Xavier Montagutelli coordinated the meeting at the Institute of Genetics, Molecular and Cellular Biology (IGMCB), which shares a campus with the France's mouse phenotyping center, Institut Clinique de la Souris, a partner of the International Mouse Phenotyping Consortium (IMPC).

✉ Xavier Montagutelli
xavier.montagutelli@pasteur.fr

Kelsey E. Noll
kenoll@email.unc.edu

[1] Department of Molecular Genetics, University of Toronto & Genetics and Genome Biology Program, The Hospital for Sick Children, Toronto, Canada

[2] Department of Microbiology and Immunology, The University of North Carolina at Chapel Hill, Chapel Hill, NC, USA

[3] Mouse Genetics Laboratory, Institut Pasteur, Paris, France

The meeting began with cutting-edge workshops offered to attendees by specialists in emerging technologies, resources and data analytics (Table 1). Throughout the main meeting, young scientists and field-leading experts shared their recent discoveries through oral and poster sessions in Development, Epigenetics and Stem Cells; Human Disease Models of Neurobehavior, Infection and Immunology, Metabolism and Blood; Cancer and Environmental Factors; Comparative Genomics; and Computational Methods and Evolution. Numerous technical advances and database resources were highlighted which serve as important tools for mammalian geneticists (Table 2). The conference concluded with a gala dinner and awards ceremony at Brasserie Artisanale, where participants enjoyed dishes and beverages from the Alsace region.

This review is intended to highlight some of the most exciting advances presented at IMGC 2019 for the broader genetics research community. A complete set of abstracts from IMGC 2019 can be found at www.imgs.org under the History tab.

Outstanding trainees

The IMGS has a long-standing commitment to support trainees through travel fellowships, a mentoring lunch, and a half-day trainee symposium. Sixteen trainees were selected to give oral presentations at this symposium, with the 5 most outstanding talks being chosen to present again in the main meeting.

Table 1 IMGC 2019 workshops

Topic	Facilitators	Home institution
Easi-CRISPR	Channabasavaiah Gurumurthy	University of Nebraska
MGI's GeneWeaver	Joel Richardson & Jason Bubier	The Jackson Laboratory
GRCm39 in Ensembl	Andrew Berry, Emily Perry & Tayebeh Rezaie	European Bioinformatics Institute; NCBI
Next generation sequencing	Thomas Keane	European Bioinformatics Institute
IMPC	Ann-Marie Mallon	MRC Harwell Institute

Consistent with their dedication to trainee development, the IMGS and its partners sponsored poster and oral awards recognizing exceptional research presentations (Table 3).

Serena Dai won the Verne Chapman Young Scientist Award, given to the trainee with the most outstanding oral presentation. She presented an elegant example using the highly conserved PDX1 protein in the fat sand rat, *Psammomys obesus*. Sand rat PDX1 shares only 15/60 amino acids with other rodent species due to high GC content, which she showed alters protein stability through mutation of key ubiquitination sites. Dai provided evidence that the sand rat evolved to acquire a new ubiquitination site, demonstrating a tug-of-war between natural selection and strong GC skew. At a functional level, sand rat PDX1 appears to be less efficient at activating insulin in pancreatic beta-cells compared to mouse PDX1. A similar pattern of sequence divergence was observed in other sand rat genes involved in diabetes and obesity, which could explain why sand rats develop obesity and diabetes when fed a normal chow diet.

Two trainees, Aaron May-Zhang and Quentin Kimmerlin, won both the Lorraine Flaherty and IMGS Outstanding Oral Presentations awards. May-Zhang conducted a cross-species comparison of RNA-seq data derived from enteric neurons of mouse and human. In situ Hybridization Chain Reaction with key marker genes confirmed the presence of discrete subtypes of enteric neurons in both species, showcasing the power of these datasets. Kimmerlin's study focused on platelet formation from megakaryocytes, specifically the role of a unique microtubule discoid structure known as the platelet marginal band in development and disease. Mice carrying knockout alleles of two microtubule components, α4a tubulin and β1 tubulin, show a severe bleeding phenotype and significant defects in both platelet number and structure. Expression levels of the primary platelet surface receptors appeared normal, and ongoing work aims to better link structural abnormalities with functional platelet defects.

Verne chapman memorial lecture

The Verne Chapman Memorial Lecture was established in the name of a founding member of the IMGS, Dr. Verne Chapman. Verne's legacy within the mammalian genetics community was built on important scientific achievements, community building and leadership, generosity with research tools and ideas, and mentoring the next generation of scientists. The 2019 Verne Chapman lecture was presented by Rudi Balling, who could personally attest to the special way in which Verne brought together those with a love for genetics.

Balling's research focuses on understanding the underlying mechanisms of complex diseases, particularly in a pre-disease state before the chronic condition has fully manifested. Specifically, his work looks at the cellular cascade of events that precedes Parkinson's disease, which causes severe neurodegeneration. Intriguingly, Parkinson's disease pathology shows many parallels with diabetes, particularly with respect to impaired energy metabolism. Patients with diabetes have a significantly higher risk of developing Parkinson's, and diabetic drugs have been shown to have neuroprotective effects in Parkinson's patients. The computational analysis of existing data developed by Balling and others made a key contribution to Parkinson's disease research and to the finding of an impaired energy supply. Balling demonstrated that in Parkinson's patients with a mutation in a familial PD-gene, the activity of pyruvate dehydrogenase, a key enzyme regulating the switch between glycolysis and the TCA cycle, is affected. As a result of this hypo-energetic state, neurons might be forced to break down neurotransmitters as substrates to be fed into the TCA cycle. Based on this hypothesis, Balling suggested that Parkinson's disease could be considered "the diabetes of the brain", and linked the continuing rise in diabetes and obesity with an increase in neuropsychiatric disorders over time.

Mary lyon award

The Mary Lyon Award recognizes early-stage, tenure-track independent female researchers. It is given in honor of Dr. Mary Lyon who contributed to the field of mammalian genetics not only through her prolific and ground-breaking research but also through her involvement as a community member and mentor, and as a founding member of the IMGS. This year's Mary Lyon Award winners were

Table 2 Mammalian genetics databases, resources and tools

Resource	Acronym	URL address
Alliance of genome resources		www.alliancegenome.org
Collaborative Cross (UNC Systems Genetics)	CC	www.csbio.unc.edu/CCstatus/index.py
Database for the exchangeable gene Trap clones	EGTC	egtc.jp/action/main/index
Diversity outbred database	DODB	www.jax.org/research-and-faculty/genetic-diversity-initiative/tools-data/diversity-outbred-database
Functional annotation of the mammalian genome	FANTOM	fantom.gsc.riken.jp
Gene eXpression database	GXD	www.informatics.jax.org/expression.shtml
GeneWeaver		www.geneweaver.org
Human-mouse: disease connection	HMDC	www.informatics.jax.org/humandisease.shtml
International mouse phenotyping consortium	IMPC	www.mousephenotype.org
Infrafrontier (mouse disease models)		www.infrafrontier.eu
MouseBook		www.mousebook.org
Mouse Encyclopedia of DNA elements	ENCODE	www.mouseencode.org
Mouse genome informatics	MGI	www.informatics.jax.org
MouseMine		www.mousemine.org/mousemine/begin.do
Mouse phenome database	MPD	phenome.jax.org
Mouse tumor biology database	MTB	www.tumor.informatics.jax.org
NHGRI-EBI catalog of published GWAS		www.ebi.ac.uk/gwas
Rat genome database	RGD	www.rgd.mcw.edu
Sanger mouse resources portal		www.sanger.ac.uk/science/collaboration/mouse-resource-portal
Sanger mouse genomes project		www.sanger.ac.uk/science/data/mouse-genomes-project
Multi-species genome browsers		
Ensembl genome browser	ENSEMBL	www.ensembl.org
National Center for biotechnology information	NCBI	www.ncbi.nlm.nih.gov/genome
UCSC genome bioinformatics		www.genome.ucsc.edu
Nomenclature guidelines		
HUGO gene nomenclature committee	HGNC	www.genenames.org
Mouse nomenclature home page		www.informatics.jax.org/mgihome/nomen
Rat nomenclature guidelines		www.rgd.mcw.edu/nomen/nomen.shtml
Repositories		
Canadian mouse mutant repository	CMMR	www.cmmr.ca
European mouse mutant archive	EMMA	www.emmanet.org
European mouse mutant cell repository	EuMMCR	www.eummcr.org
International mouse strain resource	IMSR	www.findmice.org
JAX mice database	JAX	www.jax.org
Mutant mouse resource & research centers	MMRRC	www.mmrrc.org
NIH knockout mouse phenotyping program	KOMP2	www.commonfund.nih.gov/komp2
NCI mouse repository at frederick national laboratory		frederick.cancer.gov/science/technology/mouserepository
Mouse mutant resource at JAX	MMR	www.jax.org/research-and-faculty/resources/mouse-mutant-resource
Rat resource and research center	RRRC	www.rrrc.us
UC Davis KOMP repository	KOMP	www.komp.org

Melissa Wilson and Binnaz Yalcin, who gave highlighted oral presentations.

Melissa Wilson delivered an engaging talk on sex-biased genome evolution, with a focus on pregnancy and immune function. She described her pregnancy compensation hypothesis, which posits that immunity evolved in a sex-specific manner to facilitate survival in the context of pregnancy. Wilson discussed the role of industrialization, specifically the decrease in both parity and pathogen burden in modern civilization, in exacerbating sex differences in disease risk.

Binnaz Yalcin used a forward genetics approach to study the genetics of mammalian brain morphogenesis. In collaboration with the Sanger Institute, Yalcin's group utilized

Table 3 IMGC 2019 awardees

Awardee	Institute	Title	Award & Sponsor
Yichen (Serena) Dai	University of Oxford, UK	Weird gene in a weird mammal: a highly divergent pancreatic duodenal homeobox 1 (*Pdx1*) gene in the fat sand rat	Verne Chapman Young Scientist Award (IMGS) OOP Lorraine Flaherty Award (IMGS)
Blake Caldwell	University of Pennsylvania, USA	TET2-mediated active DNA demethylation promotes iPSC generation in a MEF reprogramming model	OOP(GSA)
Sophie Hill	University of Michigan, USA	Anti-sense oligonucleotide therapy delays seizure onset and extends survival in a mouse model of SCN8A encephalopathy	OOP(GSA)
Quentin Kimmerlin	Université de Strasbourg, France	The a4a- and b1-tubulin isotypes work together to sustain efficient platelet biogenesis and hemostasis	OOP (IMGS) OOP Lorraine Flaherty Award (IMGS)
Imtissal Krayem	Institute of Molecular Genetics of the Czech Academy of Sciences, Czech Republic	Strong Epistasis in Genetics of Leishmaniasis—search for genes and mechanisms	OOP Lorraine Flaherty Award (IMGS)
Aaron May-Zhang	Vanderbilt University, USA	Identification of discrete subtypes of enteric neurons in humans using cross-species comparison of RNA-Seq data	OOP (IMGS) OOP Lorraine Flaherty Award (IMGS)
Vi Tang	University of Michigan, USA	SAR1A rescues the hypocholesterolemia resulting from hepatic *Sar1b* deletion in mice	OOP Lorraine Flaherty Award (IMGS)
Céleste Chidiac	Institut de Génétique et de Biologie Moléculaire et Cellulaire, France	Development and characterization of pain-related sodium channel CRISPR-Cas mouse model for mutant *Scn10a*	ORP (IMGS)
Jessica Mayeux	The Scripps Research Institute	Modeling spontaneous systemic autoimmunity using the collaborative cross mouse	ORP (IMGS)
Maria del Mar Muniz	Institut de Génétique et de Biologie Moléculaire et Cellulaire, France	Network analysis of the brain dysfunction observed in down syndrome models	ORP (IMGS)
Juan Aimee	University of Pennsylvania, USA	The Study of the Neuroepigenetic Regulation of Imprinted Gene *Grb10*	ORP (Springer-Verlag)
Liu Haoyi	Université de Strasbourg, France	Characterization of the *Atp 2b1*$^{Tg(Thy1\text{-}CHMP2B*)1Rene}$ (*CHMP2B*^{intron5}) Knock-in mice: a new model of amyotrophic lateral sclerosis (ALS) and frontotemporal dementia (FTD)	ORP (Springer-Verlag)
Adelaide Tovar	University of North Carolina at Chapel Hill, USA	Identification of genetic loci associated with susceptibility to lung injury caused by the air pollutant ozone	ORP (Springer-Verlag)
Helen Long	MRC Harwell Institute	Exploring genes, phenotypes and pathways across the 3D genome	ORP (Genome Research)
Justin Kulchycki	Oakland University, USA	Identifying the Genomic Switch for Cell Type-Specific *B4galnt2* Expression in Mice	ORP (ICSGNM)

OOP outstanding oral presentation, *ORP* outstanding research poster, *IMGS* International Mammalian Genome Society, *GSA* Genetics Society of America *ICSGNM* International Committee on Standardized Genetic Nomenclature for Mice

a histological pipeline to identify genes that disrupt brain morphology. After screening 1500 mutant mouse lines, Yalcin identified approximately 200 genes of interest, many of which share functionally similar roles in different areas of brain development. A subset of the human orthologs of these genes have known importance in cognitive function, while > 80% are newly implicated and could be tied to human cases with no molecular diagnosis. Yalcin's work provides an important resource for both the mouse and human genetics and neuroscience communities.

Invited speakers

The IMGS invited three additional outstanding speakers to share their latest research. Alexandre Reymond described two vignettes from studying Chromosome 16p11.2, a rapidly evolving region of the human genome commonly associated with mirroring neuropsychiatric phenotypes. GWAS studies had also linked this region to age of menarche but have been unable to determine a causative gene. To this end, Reymond used mouse and zebrafish models carrying duplications and deletions within the corresponding region to identify causative genes. Further, he presented work on a gene flanking these duplication/deletion breakpoints, *BOLA2*, which is normally found in humans at > 2 copies. He found that lower copy numbers of *BOLA2* are associated with anemia, suggesting an evolutionary advantage that favored the increased dosage of this region.

Christine Disteche spoke on the regulation of X Chromosome inactivation, describing findings regarding the role of lncRNAs in controlling the 3D structure, heterochromatic features, and localization of the inactive X Chromosome. Using an allelic hybrid mouse system designed to skew X inactivation, Disteche identified genes that escape X inactivation in a cell- and tissue-specific manner. She also highlighted the role of two lncRNAs, cis-acting *Dxz4* and trans-acting *Firre,* and described the different mechanisms by which they regulate the structure and function of the inactive X. Notably, these functions are maintained with ectopic expression of human transgenes, supporting a conserved role for these elements across species.

Marisa Bartolomei presented her research on the epigenetic regulation of imprinted gene clusters. Utilizing gene targeting and genome editing in both cell lines and mice, she investigated the role of specific epigenetic regulators in germline imprinting mechanisms. Her talk highlighted two clusters of imprinted genes, one containing the *H19/IGF2* locus and the other containing the *GRB10* locus, which are unusual, in that they are regulated by CTCF binding rather than by lncRNAs. The *H19/IGF2* locus is associated with Beckwith-Wiedemann Syndrome, whereas the *GRB10* locus has a complex tissue-specific imprinted expression pattern with multiple functions.

Development, epigenetics and stem cells

A number of talks focused on epigenetic mechanisms impacting stem cell biology. Fufa Temesgen's study took an epigenomics approach to better understand retinal development and disease. Using ATAC-seq and RNA-seq from human-induced pluripotent stem cells (iPSCs) differentiated into retinal pigment epithelium, she mapped key regulatory regions genome-wide and identified specific transcription factor motifs enriched at these sites. Importantly, by performing whole-genome sequencing on families with macular dysplasia, she linked a hereditary translocation in a gene desert region with important putative enhancers active during retinal development, underscoring the importance of these regulatory regions in health and disease. Blake Caldwell presented his work using iPSCs to study the role of DNA methylation in reprogramming, which is dependent on TET active DNA demethylases. He showed that iPSC reprogramming efficiency is highly dependent on TET2 catalytic activity, with overexpression of TET2 leading to enhanced reprogramming, while expression of a catalytically dead version of TET2 has the opposite effect. These studies directly implicate TET2′s role in actively promoting Base Excision Repair in iPSC derivation, particularly at reprogramming-specific promoters and enhancers.

Laura Reinholdt discussed a systems genetics approach to understanding the genetic factors underlying variability between murine embryonic stem cell (mESC) lines. ATAC-seq and RNA-seq were used to profile chromatin accessibility and gene expression in 185 mESC lines from the genetically heterogeneous Diversity Outbred (DO) mouse population. Genetic mapping identified 11 clusters of co-localized distant QTL, suggesting broadly important regulatory factors. Mediation analysis identified *Lifr* expression as the intermediate factor for one of these clusters tied to gene expression of pluripotency factors, and a single enhancer variant upstream of *Lifr* was validated to be causal using reciprocal allele swaps. Expanding Reinholdt's work on genetic regulation of ground state pluripotency in DO-derived mESCs, Steve Munger discussed transcriptional analysis of neural progenitor cells (NPCs) differentiated from mESCs. Combined with the transcriptional analysis of the mESCs, Munger showed how transcriptional variation in the differentiated NPCs was affected not only by the genetic variation but also by the transcriptional variation of the progenitor cells at ground state. Genetic mapping identified eQTL that were both shared with mESCs and specific to NPCs. While local variants tended to have effects in both cell types, distant trans-regulatory variants were generally

cell type specific. Mediation analysis showed that transcriptional variation in differentiated NPCs can be driven by transcriptional variation in progenitor mESCs.

Petko Petkov studies the meiosis-specific protein PRDM9, which trimethylates lysine residues of Histone 3 to mark DNA hotspots for meiotic recombination. A yeast two-hybrid assay identified EWSR1 as a PRDM9 protein interactor, and Petkov showed that mice with an *Ewsr1* conditional knockout in testes are sterile, showing decreased number and effectiveness of H3K4me3-marked hotspots. Further, he found that EWSR1 interacts physically with meiosis-specific cohesin REC8. His model suggests that EWSR1 provides a physical connection between PRDM9 and REC8, effectively linking hotspots and the chromosomal axis for double-strand break initiation during meiosis.

Infectious diseases and immunology

Two speakers took aim at genetic determinants of host susceptibility to infection. Lisa Gralinski took a genetic mapping approach to identify host factors regulating differential SARS coronavirus susceptibility in two closely related substrains, BALB/cJ and BALB/cByJ. Analysis of the early immune response in these strains suggested that aberrant signaling is likely driving these different disease outcomes. In the reduced complexity F2 intercross, two QTL were mapped for weight loss and shown to act additively, with resistance being recessive for both. To reduce the pool of candidates within the loci, Gralinski is utilizing approaches that include screening of additional BALB/c substrains for susceptibility and performing fine mapping via PCR. Jean Jaubert discussed an extreme susceptibility phenotype to *Salmonella* bacteria observed in Collaborative Cross CC042/GeniUnc (CC042) mice, which show very high bacterial loads and mortality. CC042 mice have a number of distinct immunological features, including reduced splenocytes and thymocytes. An F2 intercross between CC042 and C57BL/6N was performed to map the genetic loci underlying susceptibility, and two independent QTL on Chromosome 7 were identified. One of these QTL was attributed to a CC042-specific private mutation resulting in complete loss of function of the *Itgal* gene, the effect of which was confirmed by quantitative complementation.

James Amos-Landgraf presented a study of microbial colonization in the Apc^{Min} mouse model of colon cancer. Previous complex colonization studies suggested that abundance of *Bilophila* species was correlated with increased adenoma burden. Amos-Landgraf directly assessed the role of this species using the human isolate, *Bilophila wadsworthia.* After delivery to Apc^{Min} mice by gavage, the *Bilophila* isolate stably colonized and caused a shift in the gut microbial community. Contrary to expectations from the complex community colonization study, *B. wadsworthia*-colonized mice showed lower tumor burdens, which may be due to immune-mediated suppression.

Focusing on another immunological system, Dan Skelly presented his work which aims to better understand the immune component to visceral white adipose tissue (WAT), a tissue heavily implicated in type II diabetes and cardiovascular disease. Using single cell RNA-seq on WAT from mice fed a normal or high-fat diet, Skelly identified > 20 discernable cell types, with the most striking differences between the diets coming from the macrophage compartment. His work suggests a mechanism for WAT-associated macrophages' contributions to pathogenesis, and will serve as a platform for comparing genetically diverse mouse strains with varying susceptibilities to these diseases.

Comparative genomics, technical advances and resources

An abundance of updates were presented on advances in comparative genomics, data analyses and mammalian genetics resources (Table 2). Speakers emphasized the importance of quality control measures, constant improvements, and communication of shared resources.

Judith Blake discussed challenges associated with annotating pseudogenes in the modern era of genetic sequencing and engineering technologies. She described unitary pseudogenes, which code for a protein in one species but not in other species, and polymorphic pseudogenes, which are protein-coding in some but not all strains of the same species. To facilitate functional genomic investigation, the goal is to clarify and refine genome feature classifications across platforms. Blake delivered an update on the current status of the classification system and highlighted specific complex annotation cases.

Using the 16 de novo genome assemblies produced for commonly used inbred strains, Thomas Keane's laboratory identified the most highly divergent regions between these strains. The majority of the coding genes found within these regions have unknown functions, while the one third of genes with known functions are enriched for genes involved in immune processes and pathogen defense. Further, Keane is using long-read sequencing strategies to resolve gaps in reference genomes at highly divergent regions, and demonstrated the ability to achieve a more complete representation of these complex regions, ultimately improving reference genome reliability.

Guillaume Pavlovic described the IMPC's efforts to increase scientific reproducibility within their knockout strains by analyzing the gut microbiome, which can have significant effects on mouse phenotypes. He found that for wild-type C57BL/6N mice, gut microbiota were stable

for > 2 years, despite being housed at different institutes, and saw no correlation between composition and any deviation from normal phenotype. With this strain now set as a reference microbiome, the IMPC plans to use this baseline to analyze their knockout strains with 16S metagenomics and identify both large and subtle changes in composition.

INFRAFRONTIER, a consortium of leading European research institutes responsible for generating, phenotyping, archiving and distributing mouse models in partnership with the IMPC held a panel discussion on sustainability of mouse informatics resources. The presentation by panelists Carol Bult, Anne Kwitek, Kent Lloyd, Terry Meehan, and Michael Raess emphasized the contribution of mammalian data providers, data aggregators and bioinformatics resources across the world. Discussions focused on promoting responsible and reproducible research that is readily accessible, as well as the importance of nomenclature standardization and ongoing resource sustainability. Complementary to this panel, Carol Bult presented an overview of The Alliance of Genome Resources (the Alliance), a comprehensive tool that provides integrated genomic and phenotypic data across the major model organisms. The goals of the Alliance are (1) to have a common mechanism to access data from model organism databases and the Gene Ontology Consortium and (2) to maintain a sustainable modular infrastructure for genome resources to reduce development and maintenance costs. For individual genes, comparative gene expression can be compared through development and anatomy across model organisms. Further, comparative disease associations can be analyzed harmoniously between species, which has historically been challenging for researchers due to each model organism database annotating genes and phenotypes differently. The Alliance hopes that by unifying common tools for data curation, access and analysis will both advance research at a quicker pace and allow for long-term sustainability as these resources expand.

Spotlight on rat genetics

The rat community was well represented at this year's conference. Presenters highlighted development of rat resources, models, and tools to facilitate the utility of these rodents in research.

Shur-Jen Wang provided an overview of the Rat Genome Database, which provides a platform to improve model selection. The database includes a quantitative phenotype tool that provides expected ranges for a phenotype of interest across strain groups, drawing from published literature and other deposited data and resources. This tool can also be used to link phenotypic variation to damaging genomic variants, which are shown in parallel.

Leah Solberg-Woods presented multiple QTL mapping methods to identify genes underlying metabolic traits using heterogeneous stock (HS) outbred rats. Physiological traits, such as body fat and insulin levels, were measured across the entire mapping population, while transcriptional analysis of liver and adipose tissue was conducted in a subset of rats. Mapping used both SNP- and haplotype-based methods, and a subset of QTL were identified by both approaches. eQTL mapping was followed by mediation analysis, which identified *Krtcap3* as a candidate gene within a pleiotropic QTL that affected fat pad size and fasting triglycerides. Preliminary studies demonstrated that CRISPR knockout of *Krtcap3* leads to increased body weight, supporting a role for this gene in regulating metabolic traits. *Krtcap3* is also present in a human locus mapped for waist–hip ratio, suggesting translational relevance of this gene.

Thomas Saunders presented the use of CRISPR/Cas9 to create transgenic rats carrying Cre recombinase at two loci for neurological receptors. Cre transgenes were inserted preceding the termination codons and following a self-cleaving peptide sequence, which was included to preserve receptor function. Successful targeting and function of the Cre and receptors were validated, and rat behavior was normal, thus providing useful Cre-expressing rat models for future neurological studies.

Wojtek Auerbach discussed the generation of rat embryonic stem cells (rESCs) from multiple rat strains. Using BAC-based genome targeting combined with CRISPR/Cas9, it was possible to make large targeted modifications in rESCs with high efficiency. This technique was used to create humanized loci spanning > 1 Mb, further improving the utility of these cell lines for translational research.

Conclusions and looking ahead

As with previous meetings, the IMGC 2019 was the forum of choice for researchers to exchange their latest results on mammalian genetics, epigenetics and genomics. The development of new or improved technologies in genetic manipulation, transcriptomic analyses, and data sharing resources is providing new opportunities to decipher the complexity of various developmental and disease phenotypes, and to investigate fundamental biological questions. This feat was convincingly showcased by the diversity of biological systems and diseases described by presenters.

In 2020, the IMGS will hold its meeting as part of The Allied Genetics Conference (TAGC) from April 22 to 26 in Washington D.C., which will bring mouse and rat geneticists together with yeast, *C. elegans*, *Drosophila*, *Xenopus*, zebrafish and PEQG (Population, Evolutionary and Quantitative Genetics) communities to emphasize the critical role of model organisms in genetics and genomics advances.

Updates on TAGC 2020 can be found at www.imgs.org and genetics-gsa.org/tagc-2020/.

Acknowledgements The 33rd IMGC was organized by IGMBC and the IMGS. The Scientific Organizers were Yann Herault and Xavier Montagutelli. Joelle Pensavalle, Myriam Rebetz (IGMBC), and Darla Miller (IMGS) provided invaluable logistical support. The IMGS would like to thank Secretariat members, Linda Siracusa (President), Fernando Pardo-Manuel de Villena (Vice President), Martin Hrabê de Angelis (Past-President), Kuniye Abe, Ruth Arkell, Elizabeth Bryda, Junyue Cao, Laura Reinholdt, Michelle Southard-Smith, and Lauren Tracey for their assistance in planning the conference and their service to the Society. The IMGS would also like to thank the members of the Nominations and Elections Committee, comprising James Amos-Landgraf, David Aylor, Elena de la Casa Esperon, Marty Ferris, and Viive Howell for their service. This meeting was supported in part by generous financial contributions from the University of Strasbourg, Biology Open, Charles River, GeneSeek (Neogen), Geranimaux 2.0, INFRAFRONTIER, The International Society for Transgenic Technologies (ISTT), The Jackson Laboratory, TECAN, Techniplast, and TransnetYX. Sponsors for this year's presentation awards included the IMGS, Cambridge Journals, Genome Research, The Genetics Society of America, and Springer. Funding for student scholarships was made possible by NIH grant 2R13HG002394 from NHGRI, NIEHS and NICHD. The IMGS would like to extend special thanks to Monica McAndrews (The Jackson Laboratory) for reviewing and correcting nomenclature in all meeting abstracts as well as in this manuscript.

Compliance with ethical standards

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

References

Moskowitz J, Tracey LJ, Widmayer S, Dumont B (2019) Meeting report: 32nd International Mammalian Genome Conference. Mamm Genome 30(3–4):43–53

Sanchez-Andrade G, Moskowitz J, Howe S, Gunn TM (2018) Meeting report: 31st International Mammalian Genome Conference, Mammalian Genetics and Genomics: from molecular mechanisms to translational applications. Mamm Genome 29(5–6):299–309