IGS

INSTITUTE FOR GENOME SCIENCES

Insider

2023 - Volume 1

UNIVERSITY of MARYLAND
SCHOOL OF MEDICINE
INSTITUTE FOR GENOME SCIENCES

670 WEST BALTIMORE STREET
BALTIMORE MD 21201
WWW.IGS.UMARYLAND.EDU
410.706.1481

Director's Corner

Dear All:

Welcome to the debut issue of our redesigned newsletter: The IGS Insider. We have exciting stories about our Institute for Genome Sciences, our faculty, our technology, our students, and our research.

The biggest story in this issue is a reflection on the 15th Anniversary of IGS, which we celebrated in October 2022. We have assembled photos from the event, as well as an overview of the history and discoveries that put IGS on the map! As the saying goes, "We've come a long way!"

In our revamped look, we are introducing several new sections that you will be able to look forward to in each newsletter:

- **Student Spotlight:** This features students at all levels who have done research in or have been mentored by our IGS faculty and staff.
- **Under the Microscope:** Here, we give you a user-friendly synopsis of our published research with a link to the full paper for those of you who want to dig deeper.
- **Maryland Genomics' Memos**: Look here for updates on our equipment and services to help in your research and clinical care.
- **Three Cheers:** We will highlight the promotions, awards, special recognition, and accolades enjoyed by our faculty and staff.
- **Save The Date:** Check this out for our IGS upcoming seminars, workshops, conferences, deadlines – and other events we think you might enjoy.

Of course, we will continue to bring you all the exciting news and innovations coming out of IGS. Thanks for joining us on these new pages as we move into our 16th year! Enjoy!

Jacques Ravel, PhD

Jacques Ravel, PhD
Acting Director, Institute for Genome Sciences, Professor, Microbiology and Immunology, University of Maryland School of Medicine

IGS Celebrates Its 15th Anniversary

The Institute for Genome Sciences (IGS) at the University of Maryland School of Medicine (UMSOM) celebrated its 15th Anniversary in October 2022 with talks from renowned scientists, recognition from university and political leaders, and the creation of the first-ever timeline of IGS' significant achievements.

Although IGS became part of UMSOM in 2007, the celebration's theme, *When Did It All Begin?* recognized the broader achievements made in the fields of Microbiology and Genomics – and the profound history of Microbial Genomics that began at The Institute of Genomic Research (TIGR) under the leadership of Claire Fraser, PhD, who founded and has led IGS through its first 15 years.

"Thirty years ago, the idea of a research institute focused almost exclusively on genomics was unproven," says Dr. Fraser. "TIGR's success—as the pioneer of high-throughput DNA sequencing—laid the foundation for IGS when we moved to UMSOM with 60 staff and 15 senior scientists."

The Anniversary Celebration included an overview video of Dr. Fraser and IGS' achievements that can be viewed **here**. Bruce Jarrell, MD, FACS, President of the University of Maryland-Baltimore, spoke about the importance of IGS to UMB and presented Dr. Fraser with a proclamation from Maryland Governor Larry Hogan in recognition of the milestone. Baltimore Mayor Brandon Scott also sent a certificate recognizing IGS' anniversary that Mark Gladwin, MD, Dean, University of Maryland School of Medicine, Vice President for Medical Affairs, University of Maryland, Baltimore, and the John Z. and Akiko K.

UMB President Bruce Jarrell, MD, FACS, presents Claire Fraser, PhD, with a proclamation from then-Maryland Governor Larry Hogan to recognize the 15th Anniversary of IGS

IGS leaders Owen White, PhD, Jacques Ravel, PhD, and Claire Fraser, PhD stand with UMSOM Dean Mark Gladwin who presented them with a certificate from Baltimore Mayor Brandon Scott to celebrate the 15th Anniversary of IGS.

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Bowers Distinguished Professor, presented to IGS leaders Dr. Fraser, Jacques Ravel, PhD, Acting Director of IGS, and Owen White, PhD, Associate Director of IGS.

Two "Distinguished Investigators" from the National Institutes of Health delivered the "Frontiers in Genomics" keynotes: Charles Rotimi, PhD, MPH, MS, Scientific Director of the National Human Genome Research Institute (NHGRI), and Yasmine Belkaid, Director of the National Institute of Allergy and Infectious Diseases (NIAID).

Dr. Rotimi's talk, "Implications of Non-Random Distribution of Genomic Variations for Human Identity and Disease Distribution" can be watched **here**.

He concluded with his favorite quote from an editorial in Nature Biotechnology, "Using genetics to define racial groups is like slicing soup. You can cut wherever you want, but the soup stays mixed."

Dr. Belkaid spoke on the "Microbiome Control of Host Immunity," and asked that her talk not be recorded since it contained unpublished work. In a nutshell, her research explores the influences on the immune system's balance, including microbiota, diet, environment, and pathogens.

In addition, two IGS researchers spoke: Seth Ament, PhD, on "Convergent Effects of Nature and Nurture on the Developing Cerebellum in Risk for Psychiatric Disorders," and Joana Carneiro da Silva, PhD, on "At the Junction of Evolutionary Genomics and Vaccinology."

Participants in the day also enjoyed lunch and a vendor fair from event sponsors: Dell, New England BioLabs, PGDx, 10x Genomics, Illumina, Nanostring, PacBio, and Cambridge Computer.

Charles Rotimi, PhD

Yasmine Belkaid, PhD

> **"Using genetics to define racial groups is like slicing soup. You can cut wherever you want, but the soup stays mixed.**

Seth Ament, PhD
Associate Professor, Department of Psychiatry, University of Maryland School of Medicine, Institute for Genome Sciences

Joana Carneiro da Silva, PhD
Professor, Department of Microbiology and Immunology, University of Maryland School of Medicine, Institute for Genome Sciences

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IGS HISTORY

1992

The Institute for Genomic Research (TIGR) based in Rockville, MD, is founded, and Claire Fraser joins as Vice President for Research.

1995

Craig Venter, Hamilton Smith, Claire Fraser, Owen White, and team complete the first genome sequence of a free-living organism, *Haemophilus influenzae*, which causes respiratory tract infections and meningitis in young children. This accomplishment demonstrated the utility of whole genome shotgun sequencing (WGS) and launched the field of microbial genomics.

The complete sequence of the *Mycoplasma genitalium* genome was reported at the end of 1995 by a group of TIGR investigators led by Claire Fraser.

1996

A team of TIGR investigators including Claire Fraser and Owen White complete the first genome sequence of *Methanococcus jannaschi*, a member of the archaeal domain of life. This provides the first look into the biology of this group of single celled organisms that are distinct from bacteria and eukaryotes.

The first complete genome sequence of a eukaryote – the yeast *Saccharomyces cerevisiae* – was reported by an international consortium of investigators that included Hervé Tettelin.

1998

Claire Fraser becomes the President of The Institute for Genomic Research (TIGR). By then, TIGR researchers have completed seven of the 16 microbial sequences completed to date.

2000

TIGR scientists contribute to sequencing the genome of the fruit fly, *Drosophila melanogaster*.

2001

Scientists finish the first draft of the Human Genome. Claire Fraser and others at TIGR contribute to this research.

2002

The TIGR team starts working with the FBI on the genomics forensic investigations anthrax letters attack of 2001. The first whole-genome sequence of Bacillus anthracis isolated from a victim is published in Science. It will serve as a key reference to the FBI investigation.

2006

In a collaboration with David Relman of Stanford and Jeffrey Gordon of Washington University, Claire Fraser and TIGR colleagues publish the first description of the human gut microbiota using a metagenomics approach.

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2007

Claire Fraser comes to University of Maryland School of Medicine to begin the Institute for Genome Sciences (IGS). IGS begins with 60 employees and 15 senior scientists.

Genomics Resource Center at IGS (now Maryland Genomics), led by Luke Tallon and Lisa Sadzewicz, brings the first next- generation sequencer to the University of Maryland, Baltimore with the acquisition of two 454 GS FLX instruments.

NIH establishes the Human Microbiome Project (HMP) with the mission of generating resources to characterize the human microbiome and analyze of its role in human health and disease. IGS receives funding for multiple HMP Demonstration Projects and the Data Analysis and Coordination Center for the HMP, under the leadership of Owen White.

Claire Fraser receives HMP funding to study the role of gut microbiome in inflammatory bowel disease (IBD), while Jacques Ravel initiates work on the role of the vaginal microbiome in bacterial vaginosis.

Ex-TIGR scientists (several now at IGS) publish the first genome of a human vaginal parasite, *Trichomonas vaginalis.*

IGS' Julie Dunning Hotopp's research on bacterial genomes integrated into animal genomes is named one of the top 100 science discoveries of the year by *Discover* Magazine.

2009

Jacques Ravel receives its first Sexually Transmitted Infections Collaborative Research Center grant (U19) to study the role of the vaginal microbiome in chlamydial infections.

2010

Genomics Resource Center at IGS (now Maryland Genomics) becomes one of the first sequencing centers to adopt the first commercially viable long-read sequencing technologies, the Pacific Biosciences RS.

IGS undertakes a large phylogenetic study of the cholera bacterium to help Haiti trace the source of the 2010 outbreak.

2011

IGS researchers publish foundational research establishing the concept of community state types in the vaginal microbiota.

2014

IGS receives a second five-year renewal from the National Institute of Allergy and Infectious Diseases (NIAID) to continue its Genome Center for Infectious Diseases (GCID). In this round of funding there is a major shift to using transcriptomics in infectious disease research with a focus on disease outcomes. With this grant, IGS scientists also will study microbiome-pathogen interactions, fungal evolution, as well as why Plasmodium falciparum – the parasite that causes the most deadly type of malaria – is becoming resistant to the drug artemisinin.

2017

IGS receives funding to create the Neuroscience Multi-Omics (NeMO) Archive as part of the NIH BRAIN initiative. NeMO houses all sequence-based data generated in the BRAIN initiative starting with data from the Brain Initiative Cell Census Network.

2019

Maryland Genomics acquires its first Illumina NovaSeq 6000, the highest-throughput sequencer in the world, enabling human genome sequencing for less than $1,000.

The American Association for Advancement of Science elects Claire Fraser to a three-year term: one year as President-elect; one year as President; and one year as Chair of the AAAS Board of Directors.

IGS receives a third $17.5 million NIH grant renewal to continue the IGS Genome Center for Infectious Diseases. The new center uses a variety of omics-based approaches to study poly-microbial infections and their impact on human health.

2020

IGS's Maryland Genomics partners with the University of Maryland Pathology Associates and the State of Maryland to launch the state's first and largest high-throughput Covid-19 testing laboratory. They have tested more than 1.5 million samples and sequenced more than 17,000 samples in support of the SARS-Cov-2 surveillance program.

2021

Jacques Ravel receives a new Collaborative Research Center grant to establish Structure, Immunity and Microbiome: Human 3D biomimetics cervicovaginal models for Sexually Transmitted Infections (SIM-STI).

2022

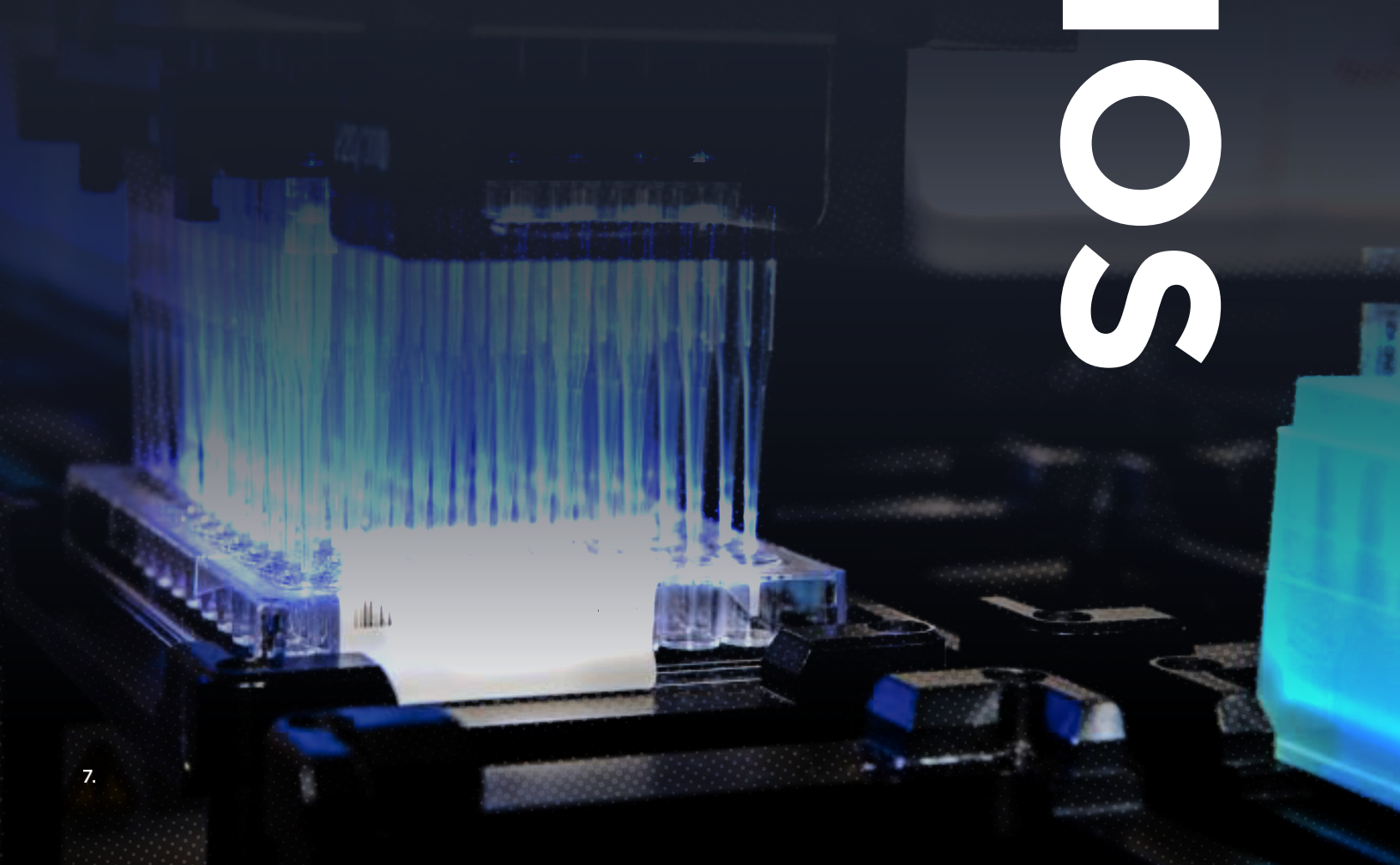
The genome sequences of over 200,000 bacterial isolates have been completed and deposited in public databases using the method pioneered by TIGR in 1995.

IGS CELEBRATES ITS 15TH ANNIVERSARY AS PART OF UNIVERSITY OF MARYLAND SCHOOL OF MEDICINE

MARYLAND GENOMICS

MEMOS

Look here for updates on our equipment and services to help in your research and clinical care.



Streamlined Core Services with Expanded Leading-Edge Technology

Although it's hard to find many silver linings from the COVID-19 Pandemic, the creation of Maryland Genomics is one of the best things to come out of the upheaval of the past few years. Maryland Genomics is the integration and transformation of three previous Institute for Genome Sciences' (IGS) service cores plus a new clinical laboratory into one state-of-the-art operation.

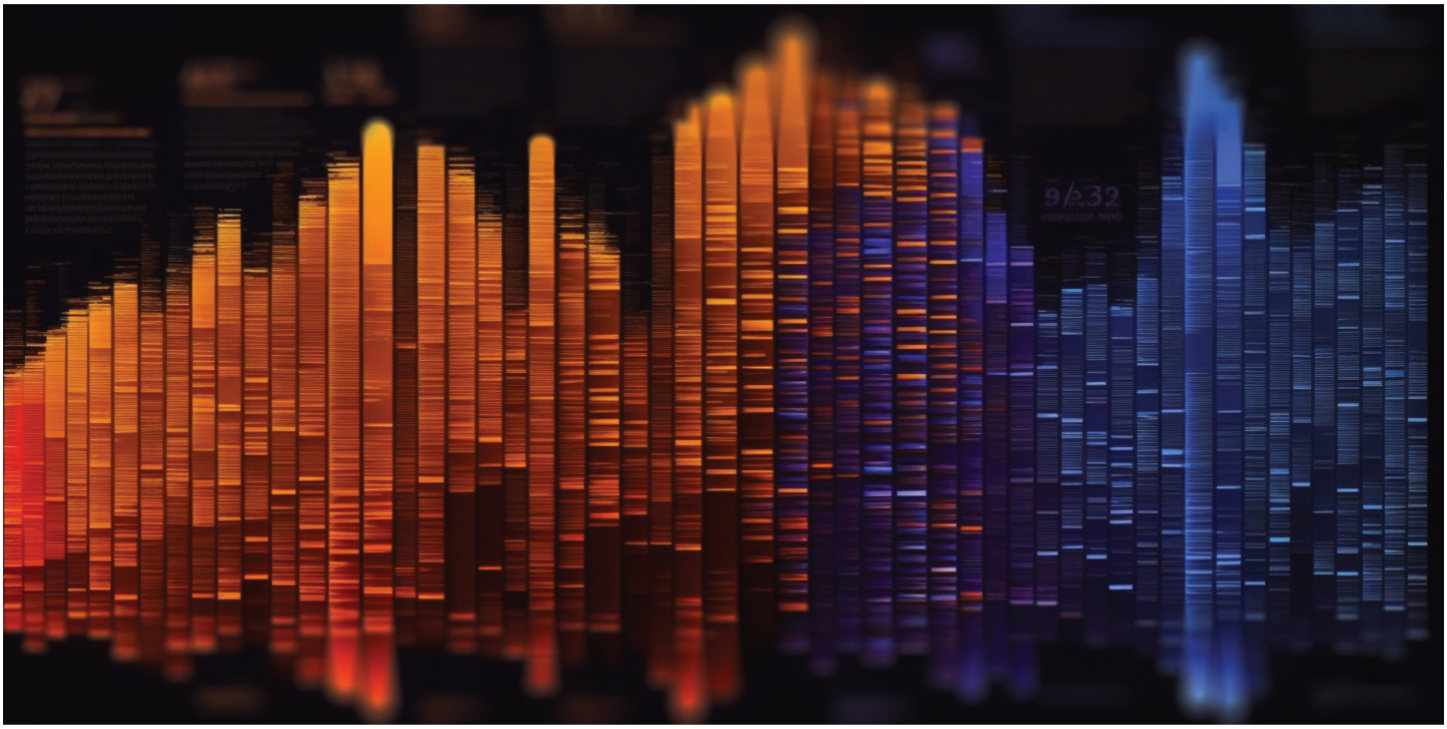
"When the pandemic hit, we needed to quickly transform our laboratory to do COVID-19 testing for the state," says Mike Humphrys, Technical Director of Maryland Genomics. "This meant integrating laboratory and computational infrastructure, cross-training of staff members, and adding new services that combined the expertise of multiple IGS cores."

In April 2020, IGS received $2.5 million from the state of Maryland to launch Maryland's first high-throughput COVID-19 testing laboratory. It ran around the clock providing testing for more than one hundred institutions throughout the state, including nursing homes, universities, and urgent cares. Overall, it tested about two million samples and sequenced the genomes of 17,000 viruses to watch for emerging variants.

"IGS now has the state-of-the art multipurpose technology for large-scale testing capable of processing 40,000 viral samples per day," says Luke Tallon, Scientific Director of Maryland Genomics. "That means that we're ready to respond quickly and do surveillance of any future outbreaks."

As the pandemic waned, the team evaluated their revamped structure and decided it only made sense to combine the services of the former Genomics Resource Center (GRC); Microbiome Service Laboratory (MSL); and Informatics Resource Center (IRC). That—plus the addition of a new CLIA-certified clinical genomics laboratory, the Maryland Genomics Translational & Diagnostics Laboratory (MGTDL)—created the new Maryland Genomics.

MGTDL will bring precision medicine to patients within the University of Maryland Medical System. Physicians now will have a broader selection of clinical genomic and molecular diagnostic testing for their patients. With testing done locally, it could lead to a quicker diagnosis and improved patient care.



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Access to MGTDL's services will not be limited to clinicians. The availability of clinical testing for researchers will enable the translation of novel insights to the clinic, as well as allow scientists to discover ways to better target diseases seen more frequently in local populations.

"Clinical genomic testing can be a huge benefit to patients," says Ramaswamy Iyer, PhD, Director of Clinical Genomics at Maryland Genomics. "Patients receive more accurate disease diagnosis, allowing for tailored treatments that can reduce side-effects and improve quality of life."

With streamlined services, Maryland Genomics will continue to grow and expand services for research and clinical clients both on and off the UMB campus. This includes providing efficient project and grant planning, as well as bioinformatic analysis.

"Any service that people received from us before is still available, along with access to even more assistance and exciting technology," says Lisa Sadzewicz, PhD, Administrative Director of Maryland Genomics. "Our newest acquisitions include the Illumina NextSeq 550 DX for clinical sequencing assays and the new PacBio Revio which will increase long-read sequencing throughput up to 15 times, while also significantly reducing the cost."

There's even more breakthrough technology coming soon to Maryland Genomics, including Spatial Transcriptomics and new short-read sequencers.

Stay tuned.

Who can work with Maryland Genomics?

Everyone! We strive to bring the increasing power and decreasing cost of sequencing and analysis to a continually expanding research community. We provide services to a wide range of researchers – from basic scientists to clinicians to computer scientists. Prior experience with high-throughput technologies is not required. And, you can be located anywhere in the world!

What can I expect?

We work with researchers from both the public and private sector, and our projects span the globe. No matter your experience or expertise, we can guide you through every phase of the process. Each project begins with a complimentary consultation with our scientists and project managers. We use this consultation to learn more about your project goals, and to advise you on project design, platform selection, cost, and timelines. From there, we conduct regular project status and update meetings to ensure the project completes on time and on budget.

Is my project too small? Too large?

No! We routinely work with projects that range from a single sample to multi-year projects with thousands of samples. On average, we have more than 30 active ongoing projects and process more than 50,000 samples per year.

Connect with Maryland Genomics:

MarylandGenomics.org

Under the Microscope

A look at IGS featured research

1 Discovery: IGS Researchers Create the First Extensive Brain Cell Data Repository

Lead Researchers:
Seth Ament, PhD & Owen White, PhD

Published in: *Nucleic Acids Research*

Neuroscience researchers now have access to 50 million brain cells to better understand how the brain develops and functions or changes with disease or trauma. Institute for Genome Science (IGS) researchers—led by **Owen White, PhD**, and **Seth Ament, PhD**—unveiled a "one-stop shop" for brain cell data called the Neuroscience Multi-Omic Archive (**NeMO Archive**). This archive is now available to neuroscience researchers to transform their understanding of the complex workings of the brain.

The expectation is that these cell-type atlases will have a transformative impact on neuroscience research more broadly, including for studies that focus on how each cell type changes in conditions such as Alzheimer's disease, Parkinson's disease, schizophrenia, or substance abuse disorders.


Seth Ament, PhD

"The NeMO Archive is the most comprehensive repository for genomic data on cellular diversity in the human and mouse brain," said Dr. Ament, IGS Scientist and Associate Professor of Psychiatry at the University of Maryland School of Medicine. "Once our consortium finishes analyzing the data, I believe we will have a more rigorous understanding of the cell types of the brain than any previous study or resource."

The ultimate goal is to create comprehensive maps for the diversity of cells in the mammalian brain, providing precise descriptions for thousands of distinct cell types in more than 100 brain regions. The archive will become a centralized resource that is easy for the neuroscience community to find and use. It currently contains transcriptomic, epigenomic, and spatial transcriptomic data from more than 50 million brain cells.


Owen White, PhD

"The data housed in the NeMO Archive is easily accessible to researchers at **nemoarchive.org**," said Owen White, PhD, Professor of Epidemiology and Public Health at UMSOM, Associate Director of IGS, and a lead author on the paper. "Our team developed several user-friendly interface tools to make its use simple, including a searchable web portal, a cloud-computing interface for large-scale data processing, and the ability to download data from the cloud to a local visualization and analysis platform called NeMO Analytics available at **nemoanalytics.org**."

Other IGS faculty who were co-authors on the study include Michelle Giglio, PhD, Associate Professor, Medicine, UMSOM; Associate Director of Analysis, IGS; Ronna Hertzano, MD, PhD, Professor, Otorhinolaryngology, Head & Neck Surgery, UMSOM; Affiliate Faculty, IGS; and Anup A. Mahurkar, MIM, Director of Software Engineering and Information Technology, IGS. The work for the NeMO Archive is supported by an original $6.4 million grant from the National Institute of Mental Health covering 2017 to 2022 and has recently been renewed with an additional $8.5 million to extend the project through 2027.

2 Discovery: IGS Study Finds a New Way to Optimize Treatment Success for Fecal Transplants

Lead Researcher: W. Florian Fricke, PhD

Published in: *Cell Reports Medicine*

Fecal transplants have been successful in treating serious diarrheal infections but have often failed when tried with other diseases. Up until now, no one could predict why these treatments sometimes failed to help restore healthy bacteria in the colon. Now, an Institute for Genome Sciences (IGS) affiliate researcher has discovered important clues that could lead to more personalized approaches to optimize treatment success.

Fecal microbial transplantation is a procedure in which fecal matter, or stool, is collected from a healthy donor and placed into the gastrointestinal tract of a patient. It has been well studied as a cure for serious diarrheal infections, such as *C. difficile* infection, and is being tested for many other conditions, including obesity. In fecal transplants, doctors hope that the good microbes from the donor will multiply and rid the gut of bacteria causing the disease in the patient.

Despite numerous studies, little has been known about the mechanisms that make the transplants work—or fail, in some cases. The latest finding may prove to be a model that could be used to make fecal transplants more successful, so that researchers and clinicians can discover if they help a particular condition, like obesity, or gastrointestinal disease, such as irritable bowel syndrome.

"It's important to view the gut microbiome as an ecosystem," said lead author **W. Florian Fricke, PhD,** Adjunct Assistant Professor of Microbiology and Immunology at UMSOM and an affiliate scientist at IGS. He is also a Professor at the University of Hohenheim in Stuttgart, Germany. "We set out to better understand the microbiome's assembly process within that ecosystem. In other words, we would like to identify what mechanism allows the donor's microbiota strains to grow and overtake the patient's strains to create a balanced and healthy gut."

The goal of a fecal transplant is "engraftment" of the donor's microbiota into the patient, which means the donor microbiota strains replace the patient's own microbiota strains. This generally has worked well as a cure for a *C. difficile* infection, where one strain of bacteria causes severe diarrhea, but it has had far less success for other gastrointestinal conditions. Clinical trials using fecal transplants to treat inflammatory bowel disease, ulcerative colitis, cancer, or obesity have brought disappointing results.

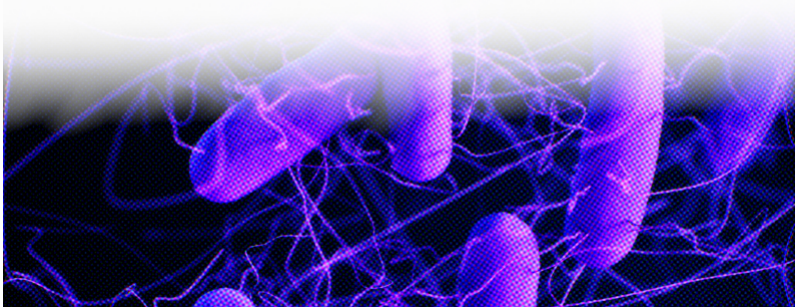
To discover why, Dr. Fricke and his colleagues examined data from 14 fecal transplant trials that included more than 250 patients. They used metagenomics—a process that sequences all genes and genomes from a mixed community at once—to determine the origin of the strains in each patient following transplant. They wanted to see whether patients incorporated the donor strains into their microbiome.

W. Florian Fricke, PhD

"What we discovered is that the success of a fecal transplant depends on the content and imbalance of the recipient's gut microbes before receiving the transplant," Dr. Fricke said. "The more disrupted the patient's gut is, the better it engrafts the donor's microbiota. The good news is that we can clinically replicate that imbalance with a combination of antibiotics and washing out the colon prior to transplant."

The lack of a disruption maybe a key reason that fecal transplants have not worked, as well in curing other specific diseases like it has in treating *C. difficile*, said Dr. Fricke. Another finding is that the microbiota transferred from a donor needs to be carefully matched to a patient. Donor strains should be selected for their strength to keep harmful bacteria in check and their ability to compete against and overtake any strains that may remain inside the patient.

This study was supported by funding from the German Research Foundation, the Austrian Science Fund, a Science Foundation Ireland Centre grant, and a Science Foundation Ireland professorship. Researchers from the University of Hohenheim, Medical University of Graz, University of Sydney, and the University College Cork also co-authored this study.



3 Discovery: The Probiotic Strains of *Bifidobacterium breve* Seem to Strengthen the Gut in Preemies

Lead Researcher: Bing Ma, PhD

Published In: *mBio*

Human breastmilk has long been considered "liquid gold" among clinicians treating premature infants in a newborn intensive care unit (NICU). Breastmilk-fed "preemies" are healthier, on average, than those fed formula. Why is that true, however, has remained a mystery.

Bing Ma, PhD

New research from the Institute for Genome Sciences (IGS) found it is not just the content of breastmilk that makes the difference. It is also the way the babies' microbiome digests it.

The research, led by **Bing Ma, PhD**, Assistant Professor of Microbiology and Immunology at UMSOM and a researcher at IGS, discovered a strain of the *Bifidobacterium breve* bacteria or *B. breve* in the gut microbiome of breastfed babies who received higher volumes of breastmilk than their counterparts. Those preemies had better nutrient absorption because they developed an intact intestinal wall, one week after birth. *B. breve* was much less prevalent in both formula-fed babies and breastfed babies with "leaky gut."

Babies with leaky gut do not develop an adequate intestinal barrier to protect against bacteria and digested food from getting into the bloodstream. For the first time, the team also found that the way *B. breve* metabolizes breastmilk keeps breastfed babies healthier and allows them to gain weight by strengthening their underdeveloped intestinal barrier.

An immature or "leaky" gut can lead to necrotizing enterocolitis (NEC), which is the third leading cause of newborn death in United States and worldwide. In fact, NEC impacts up to 10 percent of premature babies with a devasting mortality rate as high as 50 percent.

"Our discovery could lead to promising and practical clinical interventions to strengthen the babies' gut microbiome and, therefore, increase survival rates of the most vulnerable preemies," said Dr. Ma.

Bifidobacterium in the gut microbiome has long been known to have health benefits. It includes a diverse set of species and strains that have very different properties. Some species are only found in adults; some are mostly in adolescence. One species, *Bifidobacterium infanti*s, has been seen predominantly in full-term infants.

The researchers followed 113 premature babies who were born between 24 and 32 weeks' gestation. This study found *B. breve* only in preemies who had improved gut barrier function within one week after birth. Dr. Ma and her colleagues discovered that *B. breve* is genetically equipped to digest nutrients within its cell rather than the more typical external digestion process in which bacteria secrete digestive enzymes onto nutrients to break them down.

At the most basic level, the gut microbiome in these breastfed preemies with more *B. breve* metabolizes carbohydrates differently than it does formula in a way that allows *B. breve* to deliver its benefits and limit the growth of other non-beneficial bacteria. The researchers say they hypothesize that this process of metabolism then strengthens and matures the intestinal barrier faster, protecting fragile newborns from disease.

"We now know that it is not the breastmilk alone that helps preemies develop their intestinal barrier faster," Dr. Ma said. "We will need to find the best way to prophylactically administer *B. breve* early in life, rather than rely on transmission from breastmilk or even the mother's gut or vaginal microbiota during the birthing process. This is especially critical in formula-fed preemies."

Dr. Ma said that more studies are needed to determine if the *B. breve* originated in the breastmilk, gut, mother's vagina, or even environment.

Authors from the Institute for Genome Sciences include Dr. Ma; Michael France, PhD, Post-Doc Fellow; Elias McComb, BS, Research Technician; Lindsay Rutt, MS, Laboratory Research Manager; Pawel Gajer, PhD, Research Associate, Microbiology and Immunology; Li Fu, BS, Laboratory Research Specialist; Hongqiu Yang, PhD, Microbiome Service Laboratory; Mike Humphrys, MS, Microbiome Service Laboratory Director; Luke J. Tallon, BA, Executive Scientific Director, Maryland Genomics; Lisa Sadzewicz, PhD, Executive Director, Maryland Genomics Administration; and Jacques Ravel, PhD, Professor of Microbiology and Immunology, Associate Director, Genomics, and Acting Director, IGS.

4 Discovery: The Largest Known Bacteria-to-Animal Gene Transfer in a Fruit Fly

Lead Researcher: Julie Dunning Hotopp, PhD

Published in: *Current Biology*

A fruit fly genome is not a just made up of fruit fly DNA – at least for one fruit fly species. New research from the Institute for Genome Sciences (IGS) shows that one fruit fly species contains whole genomes of a kind of bacteria, making this finding the largest bacteria-to-animal transfer of genetic material ever discovered. The new research also sheds light on how this happens.

For the research, **Julie Dunning Hotopp, PhD**, Professor of Microbiology and Immunology at UMSOM and IGS and colleagues, used new genetic long-read sequencing technology to show how genes from the bacteria *Wolbachia* incorporated themselves into the fly genome up to 8,000 years ago.

Julie Dunning Hotopp, PhD

The researchers say their findings show that unlike Darwin's finches or Mendel's peas, genetic variation isn't always small, incremental, and predictable.

Scientist Barbara McClintock first identified "jumping genes" in the 1940s like those that can move around within or transfer into other species genomes. However, researchers continue to discover their significance in evolution and health.

"We did not have the technology previously to unequivocally demonstrate these genomes-inside-genomes especially with such an extensive lateral gene transfer from the bacteria to the fly," explained Dr. Dunning Hotopp. "We used state-of-the-art long-read genetic sequencing to make this important discovery."

In the past, researchers had to break DNA into short pieces to sequence it. Then they needed to assemble them, like a jigsaw puzzle, to look at a gene or section of the genome. Long-read sequencing, however, allows for sequences more than 100,000 DNA letters long, turning a million-piece jigsaw puzzle into one made for toddlers.

In addition to the long reads, the researchers validated junctions between integrated bacterial genes and the host fruit fly genome. To determine if the bacterial genes were functional and not just DNA fossils, the researchers sequenced the RNA from fruit flies specifically looking for copies of RNA that were created from templates of the inserted bacterial DNA. They showed the bacterial genes were encoded into RNA and were edited and rearranged into newly modified sequences indicating that the genetic material is functional.

An analysis of these unique sequences revealed that the bacterial DNA integrated into the fruit fly genome in the last 8,000 years –exclusively within chromosome 4—expanding the chromosome size by making up about 20 percent of chromosome 4. Whole bacterial genome integration supports a DNA-based rather than an RNA-based mechanism of integration. Dr. Dunning Hotopp and colleagues found a full bacterial genome of the common bacteria *Wolbachia* transferred into the genome of the fruit fly *Drosophila ananassae*. They also found a nearly complete second genome and much more with almost 10 copies of some bacterial genome regions.

"There always have been some skeptics about lateral gene transfer, but our research clearly demonstrates for the first time the mechanism of integration of *Wolbachia* DNA into this fruit fly's genome," Dr. Dunning Hotopp said.

Other authors currently at IGS include: Eric Tvedte, PhD, Postdoc Fellow; Mark Gasser, PhD, NextGen Sequence Platform Specialist; Luke J. Tallon, BA, Executive Scientific Director, Maryland Genomics; Lisa Sadzewicz, PhD, Executive Director, Maryland Genomics Administration; Robin Bromley, BA, Lab Research Superviso;, Xuechu Zhao, PhD, Lab Research Specialist; Matthew Chung, PhD, Postdoc Fellow; John Mattick, PhD, Postdoc Fellow; and Benjamin Sparklin, BS, Lab Research Specialist.

5 Discovery: Genomic Research Shows Testing Malaria Vaccines in the Clinic is as Rigorous as Natural Exposure in the Field

Lead Researcher: Joana Carneiro da Silva, PhD

Published in: *Nature Communications*

Malaria is the deadliest mosquito-borne parasitic infection of humans. In 2021, after a century of research, the World Health Organization (WHO) approved the world's first malaria vaccine. That vaccine reduces the incidence of malaria infections in young children aged 5-17 months by only 30 percent, meaning that it remains critical to continue developing and testing more effective vaccines.

WHO's goal is to find a vaccine that prevents infection as well as cases of severe malaria. However, testing vaccines in the field is challenging and requires large number of volunteers and long periods of follow-up. This process increases the expense and reduces the number of trials that researchers can perform.

Now, scientists at the University of Maryland School of Medicine's Institute for Genome Sciences (IGS) and Center for Vaccine Development (CVD) and their collaborators report a new way to test vaccines that may be as rigorous and stringent as exposure to naturally circulating strains of malaria.

Their method has two key aspects. First, they expose vaccinated volunteers to malaria in a controlled clinical environment. Secondly, for this testing, they use a strain of malaria that is genetically very different from the one used in the vaccine, as well as from strains in the geographic region to which the vaccine is intended.

This technique allows scientists to test how well the vaccine works in small numbers of volunteers under controlled settings and in a rapid fashion and predicts how well the vaccine may perform in the field. This lets researchers select the best vaccines for larger studies in the field. This method will increase the efficiency of vaccine testing and should accelerate malaria vaccine development.

"The standard for many investigators has been to test vaccines with a strain similar to the one used in the vaccine's development," explained the study's lead author, **Joana Carneiro da Silva, PhD**, Professor of Microbiology and Immunology at UMSOM and scientist at IGS. "Using a strain that is both genetically distant from the one in the vaccine—as well as from the strains circulating in the area where malaria is rampant, and where the vaccine will be used—is a more stringent way to test vaccine effectiveness."

Joana Carneiro da Silva, PhD

Researchers are studying the effectiveness of a vaccine (PfSPZ Vaccine) made by the company Sanaria, Inc, based in Rockville, Maryland. This vaccine uses the West African parasite strain known as *PfNF54*. One objective is to use this vaccine to protect individuals with little or no previous exposure to malaria, including those living or traveling in Africa. The long-term goal is to use the vaccine in mass vaccination programs to eliminate malaria from specific regions in Africa.

For the study, researchers infected mosquitoes with a Brazilian malarial strain and then exposed U.S. volunteers who had been vaccinated with the Sanaria vaccine (as well as those who received a placebo) to the bites of infected mosquitos in a controlled clinical setting. They also vaccinated research participants in Mali with the same dose of the vaccine to compare observed vaccine efficacy in the field with that in the clinic. Through genomic sequencing, researchers had shown that the Brazilian strain differed greatly from 700 strains previously collected from across Africa, including the one used to make the vaccine.

The researchers looked at about 200 volunteers in four trials – two in the United States and two in Mali. In all four, they observed how many people became infected with malaria, as well as how long it took for them to become infected, comparing clinic to field. At the end of six months, they found the vaccine was just as effective in both populations.

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In addition, previous comparisons had shown that those volunteers who had never been exposed to malaria developed more antibodies than those in the field, proving that it would work well in first-time travelers to the area.

The World Health Organization estimates that in 2020, 241 million cases and 627,000 deaths worldwide were due to malaria, including 2,000 cases diagnosed in the United States from travelers and immigrants who were exposed elsewhere. The variety of malarial strains globally makes vaccine development particularly difficult.

"Given the diversity of malaria strains worldwide, this research demonstrates that the Brazilian strain is as diverse as any strain detected in Africa," said **Kirsten E. Lyke, MD**, Professor of Medicine and Director of the Malaria Vaccine and Challenge Unit at the CVD and an author of the paper.

Dr. da Silva noted this new model can be used in the future in selecting challenge strains to test the efficacy of vaccines against other parasitic diseases, using carefully controlled clinical settings to compare against field studies.

The research team included two scientists from IGS: Ankit Dwivedi, PhD, Bioinformatics Analyst and Kara A. Moser, PhD, previous doctoral student. It also included scientists from: Sanaria Inc.; the Naval Medical Research Center; University of Tübingen in Germany; the Malaria Research and Training Center in Bamako, Mali; and the Laboratory of Malaria Immunology and Vaccinology at NIAID, NIH.

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6 Discovery: Mothers' HIV Status, Breastfeeding, and the Infant Gut Microbiome Can Impact Infant Health for the Long Term

Lead Researcher: Claire Fraser, PhD

Published in: *Microbiome*

Babies born to women with HIV often have poorer health and under-developed growth in the early months of life than infants born to women without the infection — even if those babies don't contract HIV during birth, according to a new study by researchers at the University of Maryland School of Medicine (UMSOM)'s Institute for Genome Sciences (IGS) and Institute of Human Virology (IHV). The study also provides new insights into why these health issues often continue throughout the babies' lives.

Science has come far in preventing HIV transmission from mother to baby, thanks to the standard use of antiretroviral therapy (ART) for HIV-positive pregnant women. However, babies of HIV-positive mothers still struggle with slower growth and adverse health outcomes.

In the study scientists found a complex interaction of factors shaped babies' development and health. These included maternal HIV status, infants' gut microbiota, the length of time that mothers breastfed, and the breastmilk composition.

For 18 months, study leaders **Claire Fraser, PhD**, the Dean's Endowed Professor of Medicine at UMSOM and Director of IGS, and **Man Charurat, PhD, MHS**, Professor of Medicine at UMSOM and the Division Director of Epidemiology & Prevention at UMSOM's Institute of Human Virology, along with colleagues followed a group of 272 Nigerian babies born to mothers with and without HIV. All mothers with HIV in this study were being treated with ART, and none transmitted the virus to their newborns.

Surprisingly, the researchers found no significant differences between the gut and vaginal microbiomes of the mothers with and without HIV, as well as no difference in the gut microbiomes of the babies at birth. Infants born to mothers with HIV exhibited lower weight-to-age Z-scores (WAZ) at birth in comparison to infants born to uninfected mothers. The Z-score measures the distance away from a particular data point. These differences persisted throughout the 18-month study and were further exacerbated in infants who were not breastfed.

The World Health Organization recommends that HIV-positive mothers breastfeed exclusively for six months and continue to nurse, along with solid food, for up to two years. The Fraser/Charurat team discovered that by six months, 99 percent of mothers without HIV were still breastfeeding, but only 39 percent of

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mothers with HIV were breastfeeding. The numbers became even more discrepant at nine months: 95% of mothers without HIV still breastfed their infants, and only 17% mothers with HIV were still breastfeeding.

"We've long known that the composition of the gut microbiome in infants impacts their overall health, growth, and development. That composition is strongly influenced by what the babies eat early in life," Dr. Fraser said.

Scientists know that the gastrointestinal tracts of healthy breastfed infants are filled with the bacteria *Bifidobacterium*. The loss of this – or invasion of other types of bacteria – can predispose an infant to metabolic and autoimmune diseases throughout life.

"We wondered whether the lack of breastfeeding in infants of HIV-positive mothers during the first weeks and months postpartum was associated with a lower abundance of *Bifidobacterium* strains in infants' gut microbiome and, in fact, we found significantly less of these bacteria in non-breastfed babies," Dr. Fraser explained. "We also thought that lower amount might impact a baby's weight, and, again, low *Bifidobacterium* led to lower infant weight."

Is it how long a baby receives breastmilk or is it the content that makes a difference?

"It seems that it is both," Dr. Fraser said. "There's a difference in growth between babies of mothers with HIV who breastfed longer and those who stopped early on. We discovered that the presence of ART in breastmilk correlated with a lower abundance of *Bifidobacterium* in the infant gut microbiome as well."

Researchers don't know whether the ART drug metabolites directly impact Bifidobacterium levels.

"It seems that breastfeeding helps close the gap between the babies in the two different groups," Dr. Fraser explained. "It may mean that breastmilk containing ART metabolites may be less than ideal – perhaps ART is directly toxic to some of the gut microbes."

Dr. Fraser said, the use of Bifidobacterium probiotic supplement may be one way to help strengthen the gut — and ultimately reduce disease — in babies born to mothers with HIV. A stronger gut, then, could reduce ongoing poor growth and mortality among those infants. The team will take a deeper dive into other factors, such as available food choices in the area, which could influence their findings.

The research team included two other authors from IGS: Sylvia Grant-Beurman, PhD, and Olivia A. Martin, MD.

Claire Fraser, PhD
Dean E. Albert Reece Endowed Professor, Director, Institute for Genome Sciences, Professor of Medicine and Microbiology and Immunology, University of Maryland School of Medicine

Student Spotlight

Marielisa Cabrera Sánchez

Marielisa Cabrera Sánchez may only be in medical school, but she's already been recognized by the American Medical Association (AMA) for her stellar research. Out of 1100 competitive research projects submitted to the AMA's 2021 Research Challenge, Marielisa—a student at the University of Puerto Rico School of Medicine—won the top prize for her paper: Genomic Adaptation of Moraxella Catarrhalis During Persistence in the Airways of Chronic Obstructive Pulmonary Disease Patients.

Hervé Tettelin, PhD, Professor of Microbiology & Immunology at the University of Maryland School of Medicine (UMSOM) and a scientist at the Institute for Genome Sciences (IGS), mentored Marielisa remotely during a virtual summer internship funded by an NIH T35 training grant titled "Training the Next Generation of Physician Scientists." Marielisa's other mentor was Timothy Murphy, MD, Senior Associate Dean for Clinical and Translational Research at the University of Buffalo's Jacobs School of Medicine and Biomedical Sciences, the PI on the T35.

"Marielisa really embraced the challenge of genomics and large-scale data bioinformatics with ease and remarkable dedication, making novel discoveries that set the path for potential new therapeutics against COPD," Dr. Tettelin says. "These results—combined with her exemplary data integration and presentation skills—created a paper that distinguished itself among the competition."

The research identified the mechanisms that alter bacterial surface proteins in Chronic Obstructive Pulmonary Disease (COPD), which could help determine antigens that may be better targets for therapeutics and vaccines.

Of the 1100 original submissions, the AMA invited 800 students to submit posters, selected 50 semi-finalists for short talks, and then invited five finalists to the ultimate event. The judges highlighted the sophistication of Marielisa's research, her understanding of the genomic tools, and the quality of her mentoring, as reasons her paper took the top spot.

Maddy Alizadeh

From the time she was a teenager, Maddy Alizadeh knew she wanted to do medical research. Two things pointed her in the direction of genomics and microbiome science – and that, in turn, led her to the lab of **Jacques Ravel, PhD**, Acting Director of the Institute for Genome Sciences.

"First, I read about George Church and personalized genomics at 14, and it hit me that I wanted to do medical research that was meaningful and would be impactful for patients," Maddy says. "Secondly, I fell in love with the gut microbiome after reading about it in college."

For the past two years she has worked in the Ravel Lab on understanding the microbiome's role in complications of Inflammatory Bowel Disease (IBD). With that research, she won a Crohn's and Colitis Congress 2023 "Young Investigators Award" giving her free attendance to the organization's annual conference.

Maddy presented a poster of her award-winning research *Predictors of Developing Multiple Extra-Intestinal Manifestations of Inflammatory Bowel Disease* at the conference held in Denver in January.

Her research characterized which IBD patients were at high risk of developing multiple non-intestinal complications—known medically as Extraintestinal Manifestations (EIMs).

By retrospectively reviewing clinical and demographic data from more than 1200 IBD patients, she found that women and patients with Crohn's Disease (a type of IBD) were most likely to develop multiple EIMs. In addition, any patients with eye complications were most likely to have at least one other EIM.

Maddy is in the fifth year of the MD/PhD program at the University of Maryland School of Medicine (UMSOM). In addition to Dr. Ravel, she also is mentored by Ray Cross, MD, UMSOM Professor and Director of the IBD Program and Codirector of the Digestive Health Center at the University of Maryland Medical Center.

Continued on pg. 19

Student Spotlight

This past summer, IGS hosted seven interns who worked on their own research projects. In alphabetical order:

Nora Badrzadeh from the University of Nevada, Las Vegas, worked on the Neuroscience Multi-Omic (NeMO) project with Victor Felix, continuing the work through the fall. (Read more about NeMO in our Under the Microscope on **pg. 11** section in this newsletter.)

Chakshu Ghandi from Johns Hopkins University worked for Joana Carneiro da Silva, PhD, improving a Single Nucleotide Polymorphism identification pipeline for the malaria-causing parasite *Plasmodium falciparum* and on the development of a graphical user interface for the pipeline.

James Hsia from Howard University worked with Daria Gaykalova, PhD, studying the integration of the human papilloma virus (HPV) genome into a host in head and neck squamous cell cancer.

Charlotte Ravel from the University of Maryland, College Park worked with Michelle Shardell, PhD, studying vaginal microenvironment biomarkers and the genitourinary syndrome of menopause.

Anirudh Saxena from the University of Maryland, College Park worked with Daria Gaykalova, PhD, looking for biomarkers in lung cancer and head and neck squamous cell cancer.

Tyonna Tyson from Hampton University worked with Julie Dunning Hotopp, PhD, generating transcriptomic data using Oxford Nanopore Sequencing that will be used to develop a bioinformatics tool for improved prokaryotic differential expression analyses.

Diana Wasson from the University of Maryland, College Park worked with Chamindi Seneviratne, MD, studying the role of tRNA in substance use disorders and their potential as biomarkers of substance misuse.

New Affiliate Faculty Member

Iqbal Hazma, PhD

Welcome Iqbal Hamza, PhD, IGS' Affiliate Faculty Member

Iqbal Hamza, PhD, Professor in the Department of Pediatrics at the University of Maryland School of Medicine (UMSOM), has been named an Affiliate Faculty Member in the Institute for Genome Sciences (IGS). He joins four other investigators who currently hold this role.

Within Pediatrics, Dr. Hamza works in the Center for Blood Oxygen Transport and Hemostasis. His research focuses on identifying the genes and pathways responsible for heme transport and trafficking in eukaryotes. Heme is found in hemoglobin—the red pigment in the blood that is responsible for binding oxygen in the bloodstream—as well as other blood proteins.

In 2008, using the roundworm *C. elegans*, Dr. Hamza's lab identified the first eukaryotic heme importer/transporter (HRG-1) which is conserved in zebrafish and humans and published the study in ***Nature***. More recently, his lab uncovered how organs communicate with each other, published in ***Nature Cell Biology***.

"Dr. Hamza's work on the genetic underpinnings of heme transport adds an important dimension to our work within IGS," says Jacques Ravel, PhD, Acting Director of IGS and a Professor of Microbiology and Immunology at UMSOM. "We're looking forward to future collaborations with him focused on improving health by better understanding how blood and organs function in health and disease."

Hear Dr. Hamza on March 29

Iqbal Hamza, PhD, Professor, University of Maryland School of Medicine, Department of Pediatrics, Center for Blood Oxygen Transport and Hemostasis, will speak on *"Notes from the Underground: Lessons from Bloodless Worms"*

HSFIII, Lecture Room 1010, 11 am to noon

How to Become an IGS Affiliate Faculty Member

Becoming an IGS Affiliate Faculty member is open to University of Maryland faculty who will promote the basic research, collaboration, and teaching missions of the Institute for Genome Sciences. Appointments are evaluated for renewal every three years.

To apply to become an Affiliate Faculty Member, please read the full requirements and fill out this **application.** Applications are reviewed by a committee that makes recommendations to the IGS Director.

IGS Affiliate Faculty Member Ronna Hertzano to Lead New Branch at the NIH

Ronna Hertzano, MD, PhD, Professor of Otorhinolaryngology-Head & Neck Surgery, at the University of Maryland School of Medicine (UMSOM) and an Affiliate Faculty Member at the Institute for Genome Sciences (IGS) has been appointed to head a new branch at the National Institutes of Health focusing on neurological and genetic conditions that cause hearing loss. Dr. Hertzano has been appointed as Chief of the newly established Neurotology Branch in The National Institute on Deafness and Other Communication Disorders (NIDCD).

Ronna Hertzano, MD, PhD

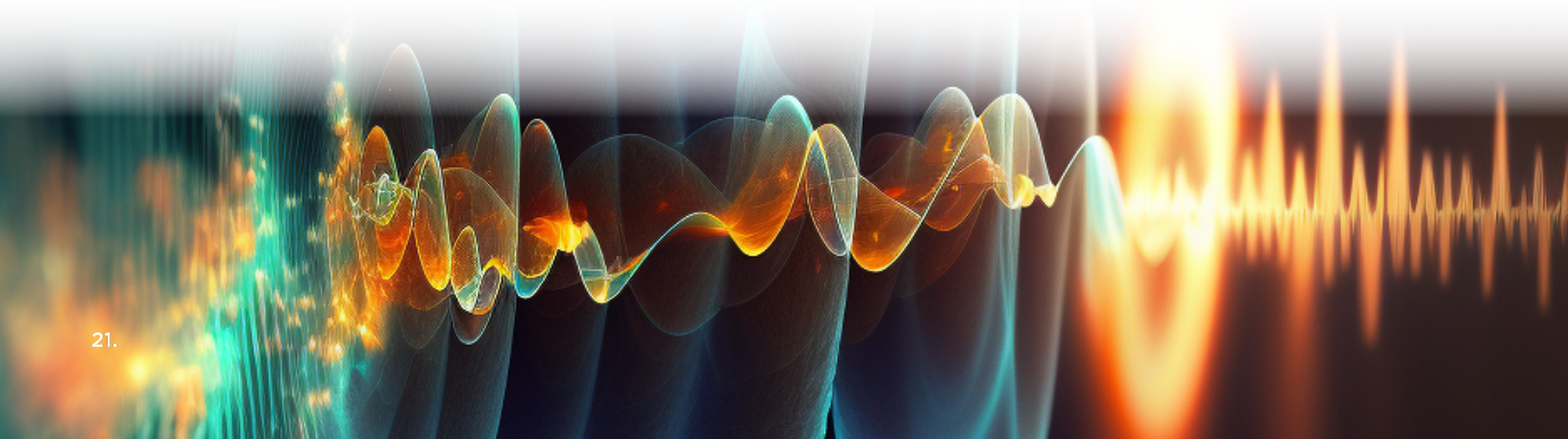
She also will continue as a Clinical Professor at UMSOM and as an affiliate faculty member at IGS. She plans to maintain her surgical practice and clinical duties at the University of Maryland Medical Center on a part time basis. She started her position at NIDCD on Feb. 13, 2023.

Neurotology is the study of neurological issues within the ear, which can cause balance issues, some forms of deafness, and ringing in the ear (tinnitus). Dr. Hertzano will oversee the branch's intramural clinical trials to identify promising new therapeutic strategies including medicines, gene therapies, and surgical procedures.

"Our molecular understanding of hearing loss has reached a new threshold, and now we are able to create interventions to treat hearing loss in a new way, beyond hearing aids or cochlear implants," Dr. Hertzano says. "I am honored and thrilled to head a new branch position at NIDCD to encourage new translational research with the potential to yield exciting new advances in the field."

Her research focuses on the molecular basis of age-related and noise-induced hearing loss. She studies the genes involved in hair cell development in the ear and has found in mouse models certain genetic mutations that lead to the early degeneration of hair cells and subsequent hearing loss. She also developed the innovative genomic data portal for scientists to share and analyze gene expression data, called gEAR (gene Expression Analysis Resource).

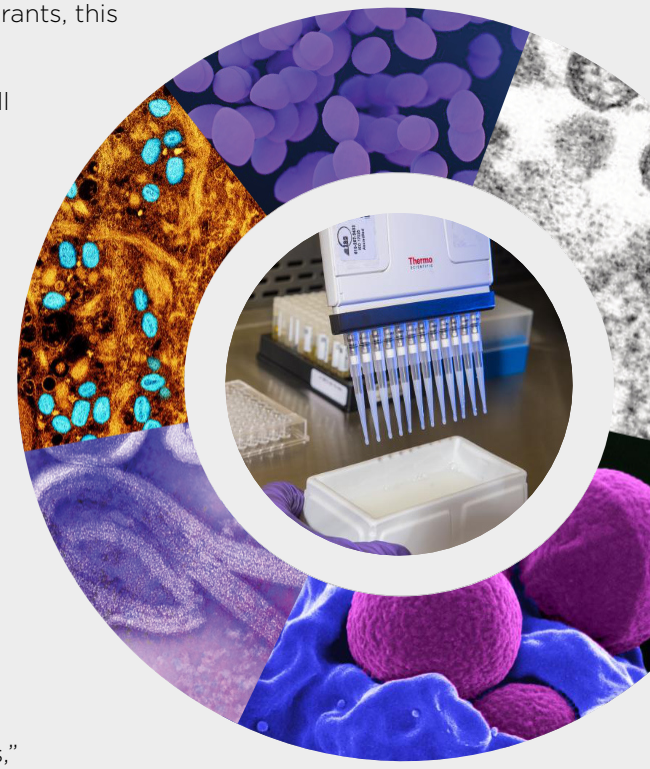
"Dr. Hertzano is an extraordinary clinician-scientist whose research has had an outsized impact on our understanding of the mechanisms of noise-induced hearing loss, and whose compassionate care of her patients is an inspiration," says **Claire Fraser, PhD**, the Dean E. Albert Reece Endowed Professor; Director of IGS; and Professor of Medicine and Microbiology and Immunology at UMSOM, who served as one of Dr. Hertzano's mentors.



IGS Receives a $1.9 Million T32 Training Grant – A First for IGS

From the common flu and COVID-19 pandemics and bacterial infections that are resistant to antibiotics to neglected disease of countries near the equator, infectious diseases sicken and kill hundreds of millions of people globally each year. Although they have been around since the beginning of time, the continual evolution of infectious diseases requires more in-depth genomic research than ever before.

That need for highly skilled infectious disease researchers is the impetus behind the Institute for Genome Sciences (IGS) new T32 training grant: Systems-Level Research in Microbial Pathogenesis. While IGS faculty often train students and fellows on T32 grants, this training grant is the first to be led by investigators within IGS.



The $1.9 million grant was awarded to develop a training program that will examine the interactions between the pathogens, the hosts, and the microbiomes in infectious diseases. It was awarded to the leadership team of **Julie Dunning Hotopp, PhD**, Nicholas Carbonetti, PhD, and **David Rasko, PhD**. Drs. Dunning Hotopp and Rasko are scientists at the Institute for Genome Sciences (IGS) while all three are Professors of Microbiology and Immunology at the University of Maryland School of Medicine (UMSOM).

"One of our main goals is to develop a robust pipeline for diverse scientists to learn new approaches and technologies used in infectious disease research," says Dr. Dunning Hotopp. "Our trainees will receive academic mentoring and professional development from our highly experienced faculty working in this area."

A key aspect of the new training program is the "systems-level" approach that applies to both the type of research the trainees will undertake and the style of education they will receive. Systems level means that it's necessary to understand how the parts of a whole interact, interconnect, interrelate, and often influence each other.

"Infectious disease is a broad field of study; however, the trainees in this program will take an interdisciplinary approach to microbial pathogenesis," Dr. Rasko explains. "They will learn to use systems-level approaches to examine the pathogenesis of parasites, fungi, bacteria, and viruses using genomic and bioinformatic tools to probe difficult research questions."

Trainees also will learn through multiple pathways—from taking traditional classroom courses to hands-on lab experiences, giving presentations, attending meetings and conferences, and receiving mentorship, as well as becoming a mentor to younger students. This will allow trainees to have a hand in helping the next generation of scientists from populations typically underrepresented in science.

The new trainees will benefit not just from IGS faculty but from faculty throughout UMSOM, including the Center for Vaccine Development, as well as from the Schools of Pharmacy and Dentistry. Predoctoral trainees will be selected from UMSOM's MD/PhD and DDS/PhD programs, as well as the Graduate Program in Life Sciences that includes the Genome Biology Track run by IGS faculty. Postdoctoral trainees will be selected through recruitment of fellows to one of the three University of Maryland, Baltimore schools collaborating on the grant. The first cohort of three postdoctoral trainees and three predoctoral trainees include students from all three schools and includes one MD/PhD trainee.

For more information on becoming a pre- or post-doctoral fellow in the program, contact Julie Dunning Hotopp: **JDHotopp@som.umaryland.edu**.

Three Cheers!

Celebrating our IGS Colleagues Promotions, Awards, and Accolades!

Promotions

Congratulations to **Michelle Shardell, PhD**, who has been promoted to Professor with tenure in Epidemiology and Public Health, and **David Serre, PhD**, who has been promoted from Associate to Professor with tenure in Microbiology and Immunology.

IGS' Tim O'Connor Named Co-Leader of UMSOM's Program in Health Equity and Population Health

Institute for Genome Sciences' researcher **Tim O'Connor, PhD**, has long studied population genetics of under-represented populations. Now, Dr. O'Connor, also an Associate Professor in the Department of Medicine at the University of Maryland School of Medicine (UMSOM) will take on a broader role in the field by co-leading—with **Laundette Jones, PhD, MPH**, Associate Professor of Epidemiology and Public Health at UMSOM—an initiative geared at educating scientists and clinicians to make research more equitable.

The Program in Health Equity and Population Health at University of Maryland School of Medicine (UMSOM) has a mission to advance health equity and population health through transdisciplinary research, education, and service.

The program's three main goals are:

- Research: Identify and research factors contributing to health inequities and work to find solutions.
- Education: Educate students, health professionals, and policymakers about health equity issues
- Take Action: Address the healthcare needs of communities that partner in research by translating the work into clinical practices and community programs to better the population's health, and disseminate the research and programming to others who can work to improve health.

For more information on how Drs. O'Connor and Jones can help you make your research more equitable, email: **TOConnor@som.umaryland.edu** or **LPJones@som.umaryland.edu**.

Jacques Ravel's Research Featured in Book Vagina Obscura

"Like eating a Reese's Cup, there's no wrong way to have a vagina," writes author Rachel E. Gross in her new book, Vagina Obscura, An Anatomical Voyage. "But we're learning that there may be a wrong way to have a vaginal microbiome—or at least bacteria within a microbiome that can impact women's health," says Jacques Ravel, PhD, Acting Director of the Institute for Genome Sciences (IGS) at the University of Maryland School of Medicine.

That's why Gross turned to Dr. Ravel for his expertise in vaginal microbiome research for the book. He is featured in the book's fourth chapter, Protection (Vaginal Microbiome).

As a recognized leader in microbiome research, Dr. Ravel has "looked at thousands of women's vaginal microbiomes under the microscope," Gross writes.

At IGS, Dr. Ravel and colleagues have been studying the issues related to the vaginal microbiome – including stubborn infections, sexually transmitted diseases, preterm birth, infant development following vaginal birth, and menopause – for more than 18 years. And, he says, there is so much more yet to learn.

"We just don't know enough to say that any of them are not good, or better, than others," Dr. Ravel says in the book.

In addition to his role at IGS, Dr. Ravel also is founder of LUCA Biologics, which is developing live biotherapeutics medicine to treat urinary tract infections in women.

And, speaking of Dr. Ravel...

According to the analytics company, Clarivate, he is among of the top one percent of scientists worldwide to be cited across multiple disciplines – and the only one at the University of Maryland, Baltimore to hold this distinction.

Emerging Leaders

IGS faculty members Tim O'Connor & Vonetta Edwards and Staff members Riham Keryakos and Robin Bromley were among the 10th cohort in the University of Maryland, Baltimore's Emerging Leader Program in 2022.

Robin Bromley, Vonetta L. Edwards, PhD, Timothy D. O'Connor, PhD, Riham Keryakos

Save the Date

March 16

Jessica Prodger, PhD, Assistant Professor, Departments of Microbiology & Immunology and Epidemiology & Biostatistics; Co-Director, Global Health Systems MMASc Program, Schulich School of Medicine & Dentistry, Western University

"The Penile Microbiome: An Underappreciated Determinant of Health"

HSFIII, Lecture Room 1010, 11 am to noon

March 29

Iqbal Hamza, PhD, Professor, University of Maryland School of Medicine, Department of Pediatrics, Center for Blood Oxygen Transport and Hemostasis

"Notes from the Underground: Lessons from Bloodless Worms"

HSFIII, Lecture Room 1010, 11 am to noon

March 30

Sander Markx, MD, Assistant Professor of Clinical Psychiatry, Columbia University, New York

IGS Seminar Series Information

HSF III, Lecture Room 1010, 11 am to noon

April 13

Manoj Duraisingh, PhD, John LaPorte Given Professor, Harvard School of Public Health, Associate Member, Broad Institute of MIT and Harvard, Team Leader, MESA-International Center for Excellence in Malaria Research

IGS Seminar Series Information

HSFIII, Lecture Room 1010, 11 am to noon

April 25

DNA DAY – 2023 marks the 70th anniversary of the discovery of the double helix and the 20th anniversary of the completion of the human genome sequence, as well as the first DNA Day!

20 YEARS | National DNA DAY APRIL 25

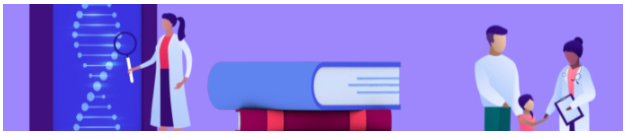
Celebrating Genomics Through Awareness

May 23-25

Introduction to R and Data Visualization for Bioinformatics Workshop. In person in Building HSF III at the University of Maryland School of Medicine.

June 5-9

Healthcare Professionals Genomic Education Week



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3. Aggor, F. E., M. Bertolini, C. Zhou, T. C. Taylor, D. A. Abbott, J. Musgrove, V. M. Bruno, T. W. Hand and S. L. Gaffen (2022). **"A gut-oral microbiome-driven axis controls oropharyngeal candidiasis through retinoic acid."** JCI Insight 7(18).

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