IGS

INSTITUTE FOR GENOME SCIENCES

UNIVERSITY of MARYLAND
School of Medicine
INSTITUTE FOR GENOME SCIENCES

Greetings Colleagues,

We continue to settle in to our space in the School of Medicine's Health Sciences Facility III (HSF III) and are so pleased to be back on campus. As we begin a new academic year, I would like to acknowledge the outstanding collective accomplishments of IGS faculty members who successfully competed for $6.9 million in new funding in FY18 that, together with existing awards, resulted in a 21% increase in our annual research budget to more than $17.4 million.

Not only have their funding levels been impressive, but our investigators are also pushing the boundaries of genomic research through their collaborations with SOM colleagues, as well as the national and international scientific community. Our Institute's investigators focus on a dynamic mix of high impact translational research with large-scale projects that build resources for an international scientific community.

A few of the new projects are profiled in this issue:

* Dr. Hervé Tettelin's research on the *Haemophilus influenzae* bacterium involved in Chronic Obstructive Pulmonary Disease (COPD) with his colleague, Dr. Timothy Murphy, at the University of Buffalo, is providing valuable insights for vaccine researchers **(pg 3)**

* Dr. Chamindi Seneviratne has been awarded an RO1 studying treatments for alcohol use disorders with the application of genomic tools **(pg 4)**, an innovative interdisciplinary application

* Dr. Lynn Schriml continues her leadership role with gene ontology with a new U41 grant to establish standard terms for diseases to help ensure that future researchers are using the same terminology for the same conditions **(pg 7)**

* The team led by Dr. Owen White has been awarded funding for an innovative NIH Data Commons Pilot Phase Consortium (DCPPC) which will have significant impact for storing datasets, computational resources and associated tools for analysis **(pg 8)**

* Dr. Ravel's work on establishing the Vaginal Microbiome Research Consortium with new funding from the Bill & Melinda Gates Foundation (BMGF) **(pg 9)**

It certainly seems that our collaborations are accelerating now that we are back on campus. It's hard to document the value of simply running into colleagues more frequently; often, the most serendipitous conversations lead to real and innovative projects. The leadership of our three cores — large-scale sequencing from the GRC, computational informatics from the IRC and the microbiome analysis from MSL — are always open to brainstorming with investigators here at UMB about how these services can be used, and even ways to incorporate the services into grant applications.

Please do come by to visit us at our new location — check our schedule of seminars, programs or request a behind-the-scenes tour. We'd be happy to show you around.

Please don't hesitate to contact any of us at IGS to discuss your needs and concerns.

Claire M. Fraser, PhD
- Dean's Endowed Professor in the School of Medicine
- Professor of Medicine, Microbiology and Immunology Director
- Institute for Genome Sciences University of Maryland School of Medicine

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With Big Data, IGS Researchers Identify New Targets for Lung Disease Treatments

Institute for Genome Sciences Investigators Target Bacteria Involved In Chronic Obstructive Pulmonary Disease

Every year, approximately 12 million adults in the U.S. are diagnosed with Chronic Obstructive Pulmonary Disease (COPD), and 120,000 die from it. For people with COPD, the pathogen *Haemophilus influenzae* can be particularly dangerous.

The microbe can reside in their lungs and wreak havoc within already weakened organs. Identifying the genetic variations of this microbe is vital to treating these patients effectively.

Hervé Tettelin, PhD, an IGS researcher collaborated with colleagues at the University of Buffalo and Yale University to better understand how the bacterium adapts quickly, which may open new avenues for therapy for COPD patients. The new findings, which relied on genomic analysis, may be useful for people who have other diseases such as ear infections or pneumonia, since this microbe can cause these diseases as well.

He collaborated with Timothy Murphy, MD, senior associate dean for clinical and translational research and professor at the University at Buffalo Jacobs School of Medicine and Melinda Pettigrew, PhD, senior associate dean for academic affairs and a professor of epidemiology at the Yale School of Public Health. Dr. Murphy has collected thousands of *H. influenzae* strains from COPD patients for over 20 years.

The research was published March 22 in the *Proceedings of the National Academy of Sciences*.

"The question we asked was why are certain strains of the bacterium so much more dangerous than others. We discovered a genetic pattern, which helps explain why certain strains are so virulent," said Hervé Tettelin, PhD, associate professor of Microbiology and Immunology and the Institute for Genome Sciences (IGS) at UMSOM. "This offers key clues about what this microbe does to evolve in the lungs of people with COPD, and it may open exciting new avenues for treatments and vaccines for the future." Dr. Tettelin oversaw the genomic data mining with the isolates.

The level of lethality depends in part on which genes get turned on, and which are turned off. Certain patterns allow the bacteria to adapt more efficiently to the lungs, allowing it to cause more damage.

With data mining, the researchers detected certain patterns of genetic activation or inactivation. With this information, the researchers say they may be able to develop new treatments and new vaccines. "We now have a much better understanding of how certain strains of the bacterium adapt to the lungs," said Dr. Murphy.

The team studied the genomic isolates from distinct time periods: what the isolates look like when *H. influenzae* is acquired by a patient, and how they look when they are about to be cleared out of the lungs. The researchers learned that there is evidence of adaptation. *H. influenzae* can vary its genome and the proteins it uses to interact with the host.

Hervé Tettelin, PhD
Associate Professor
Microbiology and Immunology

Interestingly, much of the variation appears to be random. In the bacterium, a subset of genes are randomly turning off and on constantly. Some of these mutations are useful to the bacteria, while some are not. Essentially, the bacterium undergoes a constant state of evolution.

These findings are important for vaccine researchers. This kind of data mining helps researchers more precisely identify better vaccine candidates, which could lead to better treatments for COPD patients.

James Munro, PhD, Bioinformatics Analyst at IGS, and Adonis D'Mello, a graduate student in molecular medicine, also contributed to the research.

Using Genomic Tools to Examine the Placebo Effects in the Treatment of Alcoholism

Dr. Seneviratne Awarded RO1 Studying Treatments for Alcohol Use Disorders

Investigators researching psychiatric studies involving drugs and alcohol have noted that the placebo effects in these studies can be as high as 50 percent. Large placebo effects complicate detection of quantifiable treatment effects for investigational medications, especially for the modestly effective psychiatric drugs. Placebo response arise from a complex interaction of patient, clinical trial staff, and treatment environment factors. Because the placebo response is intricate and variable among individuals, it is challenging to identify these individuals prior to enrollment in a clinical trial.

Chamindi Seneviratne, MD, an Assistant Professor in Psychiatry at UMSOM and at IGS, is particularly interested in examining the placebo effect in alcohol use dependency (AUD) studies, and applying genomic tools to study genetic predictors for certain behaviors. In February 2018, she was awarded a five year RO1 grant through the National Institute of Alcohol Abuse and Alcoholism (NIAAA), part of the NIH, as the lead Principal Investigator for this study.

She is working with Bankole Johnson, Professor and Chair of the Department of Psychiatry as the co-Principal Investigator (MPI). Lisa Sadzewicz, PhD, and Luke Tallon, co-directors of the Genomics Resource Center (GRC), are performing the genomic sequencing. Timothy O'Connor, PhD, and Anup Mahurkar, Director of the Informatics Resource Center, are analyzing the genomics data. Melanie Bennett, PhD, is a co-investigator and supplying samples from her research/clinical trials.

Chamindi Seneviratne, MD
Assistant Professor in Psychiatry

Previous double-blind AUD studies have demonstrated that drinking behaviors vary from complete abstinence to daily heavy drinking during treatment with a placebo. The two extreme groups that react in almost diametric opposition are sizeable, but, as one would expect, smaller compared to the large middle group with a variation of drinking behavior.

Dr. Seneviratne wondered whether the varying drinking patterns in response to placebo treatment was genetically determined, and she and her colleagues could not find comprehensive genomic studies conducted to assess genetic variation in relation to outcomes of AUD treatment of placebo response. Genomic analyses require large sample sizes that are not easy to gather in small to medium scale clinical trials conducted with treatment seeking individuals with an AUD or other drug use disorder.

She and her collaborators designed this RO1 study, leveraging the resources from six completed and two ongoing NIAAA funded phase II AUD treatment trials.

As the first study to characterize genomics of placebo response in phase II AUD trials, findings will provide a wealth of information for future translational research and personalized medicine. Harnessing the placebo response and knowing how to optimize it, will allow investigators to improve overall outcomes, determine who is in need of additional treatment, and characterize the therapeutic index (efficacy/side effects) for particular subgroups with AUD.

"If we can identify gene expression patterns unique to extreme response groups, in the future we can design a more complex study looking at the psychological mechanisms of placebo effect," said Dr. Seneviratne. "Rather than looking at the genetic risk for developing a disease, in this project, we are focused on exploring genomics of treatment response."

"Most of the responses in alcohol clinical studies are related to the placebo response. Thus, greater characterization of this population will facilitate more widespread treatment for alcohol use disorder," said Professor Johnson.

The study has the potential to advance personalized treatment of alcohol use disorder, which is a global health problem that ranks third in preventable causes of death in the United States.

IGS, STEM and Educational Outreach

A Busy Spring and Summer for IGS' Educational and Outreach Programs

Michelle Gwinn Giglio, PhD, Associate Professor, Medicine (Endocrinology) is the IGS Academic and Outreach coordinator. Under her leadership, the IGS outreach program provides a variety of events targeted to different ages of students, from middle school to young adults.

In June, Dr. Giglio and a team of volunteers, hosted a week of the Continuing Umbrella of Research Experiences (CURE) Scholars Summer program. Launched at UMB in 2015, CURE is an innovative program that provides both STEM activities and mentorship to students interested in science, research, or health care careers. Students begin the program in 6th grade and UMB has partnered with several local Baltimore middle schools to recruit scholars. Dr. Giglio has been involved with the program since it began at UMB and for the third year in a row has hosted the children for "IGS Camp CURE" – a week of biology-centered activities on campus during the last week of June.

Dr. Giglio teaches the CURE Scholars during their first summer in the program. During their time at IGS, the children learn

about DNA, cells, and ecology through interactive models, hands-on learning, and videos. One of their favorite activities was learning about cell structure by acting out the roles of organelles.

This spring, Dr. Giglio initiated a new outreach program called the Maryland Microbiome Project. While the CURE program involves Baltimore City students, the Microbiome project is directed toward high school students all around Maryland. In 2018, the program hosted four events

focusing on the importance of microbial communities to the environment and human health, as well as the use of DNA analysis to explore these microbiomes. Groups of students from two Baltimore City high schools, Dunbar High School (part of the P-Tech program of UMB and Johns Hopkins) and the Renaissance Academy High School (part of the UMB School of Social Work's Promise Heights Initiative), each visited IGS this past April for a day full of microbiome science. The students learned about DNA and bacteria with hands-on DNA extractions and microbiome sampling simulations. Students also went out in the field to sample soil from around our campus and from Herring Run Park. These samples have undergone sequencing analysis in the new IGS core,

the Microbiome Service Laboratory, and examination of this data will provide additional activities for students in the program next year.

"Students are often interested in science but don't have a good sense of what scientists do. They think of scientists locked away in labs doing esoteric experiments. I hope this example of environmental microbiome science can show them that as scientists they can get out there and explore our world on a fundamental level and learn information that has real importance to our environment and human health." Dr. Giglio said.

Dr. Giglio has forged partnerships with other University of Maryland System campuses

to extend this outreach to other geographic regions within Maryland. The other two Maryland Microbiome Project events took place at those campus locations. IGS partnered with the Terp Young Scholars program at the University of Maryland College Park (UMCP) which hosts high school students in summer residential programs. Dr. Giglio worked with Virginia Weeks who led the Environmental Biology course as part of this program. Students in this program span the globe, coming from as far away as Alaska and China. Dr. Giglio visited UMCP to lead a full day of activities, including a program where students sampled soil from around the UMCP campus.

Further, IGS partnered with the Regional Math/Science Center (RMSC) at Frostburg State University. This is a summer residential program for Maryland high school students focusing on target schools from Allegany County, Frederick County, Washington County, and Baltimore City. Dr. Giglio worked with Rita Hegeman to plan an event in Western Maryland. As part of the RMSC program, students visited Dan's Mountain State Park in Allegany County. Dr. Giglio joined the students there for a

half-day event where the students learned about metagenomics and sampled soil and water within the park. All of the samples collected by the students have undergone sequencing.

"Not only do we want the students to have an enriching STEM experience, we also hope that over time we will build a body of data about microbiome compositions around Maryland and how they might change over the course of many years that will yield valuable scientific results." said Dr. Giglio.

IGS continues to develop its educational outreach program for middle school, high school and college students.

Michelle Giglio, PhD
Associate Professor

MORE INFORMATION

⊙ http://www.igs.umaryland.edu/education/outreach.php
⊙ http://www.medschool.umaryland.edu/profiles/Giglio-Michelle/

New Classification and Names of Genetic Diseases, Cancers and Other Diseases Will Help Biomedical Researchers

Lynn M. Schriml, PhD, Associate Professor of Epidemiology and Public Health UM School of Medicine and the Institute for Genome Sciences, has been a leader in genome ontology, the process of standardizing terminology for diseases and key scientific terms. Dr. Schriml is the principal investigator on a recently funded, $3,395,191 five-year NIH U41 Genomic Resource grant that was awarded by the National Human Genome Research Institute (NHGRI), entitled the "Human Disease Ontology" project.

She will work with UM co-Investigators Michelle Giglio, PhD, Associate Professor of Medicine, Institute for Genome Sciences; Linda Jeng, MD, PhD, Associate Professor of Medicine; Carol L. Greene, MD, Professor of Pediatrics; Cynthia F. Bearer, MD, PhD, FAAP, Cobey Professor and Director of Neonatology and Professor of Pediatrics; Melanie L. Leu, MD, Assistant Professor of Pediatrics, and Richard Lichenstein, MD, Professor of Pediatrics.

These researchers are mining through medical journals, databases and other authoritative sources to establish standard terms for diseases as a way to help future researchers better understand a wide range of diseases like cancer. The work involves a time-intensive manual curation process, examining the breadth of information, naming systems and levels of evidence in order to integrate information and bridge data across resources.

The project team will augment the content of the Human Disease Ontology, advance the classification of complex genetic diseases, reclassify human cancers by cell of origin and tissue type and produce

(*From left*) Lynn Schriml, PhD, Katharine A. Bisordi, MS, MGC, Carol L. Greene, MD, Anu Pujar, James Munro, PhD (Additional team members not in the photo: Becky Tauber, Michelle Giglio, PhD, Rich Lichenstein, MD, Cynthia F. Bearer, MD, PhD, FAAP)

alternative disease classification views based on environmental exposures. "We work to identify and integrate the most current information about a disease," said Dr. Schriml.

Dr. Schriml's Human Disease Ontology project will provide alternate cellular, molecular and environmental mechanistic profiles and terms of many human diseases. "As more data is gathered, we work with research groups to figure out if it is a new disease or a novel sub-type," said Dr. Schriml. When a community updates their classification of an area of disease, e.g. immune disease, Dr. Schriml and her team integrate the new information, updating previous classification systems and coordinating these changes across pertinent biomedical databases.

Dr. Schriml's team is excited to develop, as part of this work, a novel differential diagnosis disease ontology. Exploring ontological representations for heterogeneous disorders will provide insight on the etiology of complex diseases.

"We are helping researchers navigate the changing landscape of disease knowledge."

– Dr. Lynn Schriml

MORE INFORMATION

→ http://www.medschool.umaryland.edu/profiles/Schriml-Lynn/
→ http://www.disease-ontology.org
→ Nature Biotechnology Paper MISAG and MIMAG

The Informatics Resource Center Awarded Funding for Innovative NIH Data Sharing Space

The NIH Data Commons Pilot Phase Consortium (DCPPC) is a new initiative that was launched in October 2017. Under the direction of principal investigator Dr. Owen White, Professor of Epidemiology and Public Health UM School of Medicine and Associate Director for Bioinformatics, Institute for Genome Sciences, the IGS Informatics Resource Center (IRC) has been awarded funding as part of this consortium.

A data commons is a shared virtual space containing datasets, computational resources, and associated tools for analysis. The NIH plans to create a data commons housed within commercial cloud resources including the Google Cloud Platform, Microsoft Azure, and Amazon Web Services.

This commons will contain data from NIH-funded projects, such as the Trans-Omics for Precision Medicine (TOP-Med), Genotype-Tissue Expression (GTex) and the Model Organism Databases. It

Members of the Data Commons Pilot Phase

will also provide robust, user-friendly analysis pipelines in a cloud-based platform for use by the research community. The DCPPC is the initial phase of this effort and will establish the infrastructure and protocols for the project. Ultimately this resource will provide a storage and computing environment that will facilitate the ability of researchers to store, share, access and carry out analysis on data from NIH-funded projects, resulting in new hypothesis generation and discovery.

Since the kick-off meeting in December 2017, the DCPPC members have been working together to develop a roadmap for this pilot phase, which the NIH expects to span four years. The group is charged with establishing processes and metrics to maximize the "FAIR"ness of the data where FAIR refers to Findable, Accessible, Interoperable, and Reusable. In addition, the DCPPC intends that users of all levels, from novice to bioinformatics experts, will be able to interact effectively with the Data Commons. A final, and extremely important, aspect of the project is ensuring the security of data through state-of-the-art authentication and authorization protocols.

The IGS IRC has several roles on the project. Dr. Owen White is co-leading the overall coordination of the pilot phase. He is a key contributor to the construction of the road map and establishing milestones. In addition, the IRC will be responsible for harmonization of metadata through the use of community and consortium standards encoded in a common data model. Finally, the IRC will produce an overall project portal that will facilitate the ability of researchers to access data and carry out analyses in the cloud.

MORE INFORMATION

➲ NIH Data Commons Pilot Phase Consortium (DCPPC)
➲ The IRC - http://www.igs.umaryland.edu/resources

Gates Foundation - The Vaginal Microbiome Research Consortium

In March 2018, Jacques Ravel, PhD, Associate Director, Genomics and Professor, Microbiology & Immunology, was awarded a Bill & Melinda Gates Foundation (BMGF) grant.

The goal of the project is to develop the framework for a clinical intervention aimed at maintaining and restoring vaginal health, and ultimately, to reduce the burden of sexually transmitted infections, including HIV, as well as prematurity and other adverse pregnancy outcomes.

The interdisciplinary and multi-institutional team are using evidence-based approaches. Collaborators include investigators at Stanford University and Harvard University, working with Dr. Ravel here at the University of Maryland School of Medicine. Patient samples have been collected from women at these institutions, as well as from women in South Africa.

The goal of the study is to identify correlates of stability and resilience in the vaginal microbiota, and leverage these features to devise a framework for an intervention to maintain and restore vaginal health. This will be accomplished in two phases: 1) to characterize the vaginal microbiota of pregnant (Stanford) and non-pregnant (UMB) women who experienced varied levels of stability and resilience using multi-omics approaches, including 16S rRNA gene sequencing compositional survey, metagenomics, metabolomics, and immunological evaluation. The consortium will work together on data integration and interpretation. For the second phase of the project, the group will use the information from phase 1 to develop a framework for a clinical intervention to maintain/
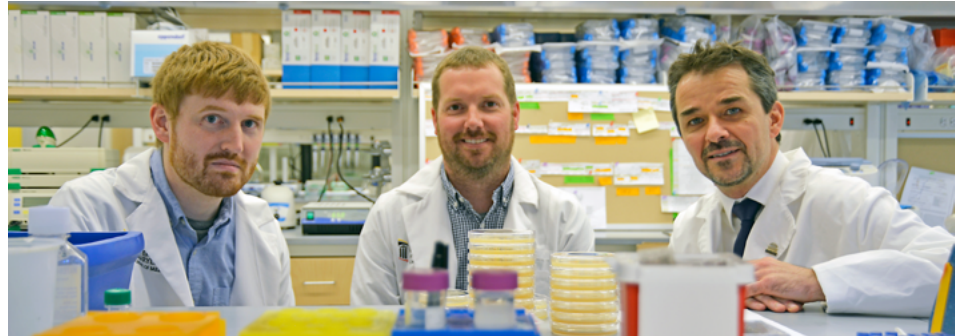
(*From left*) Michael France, PhD, Mike Humphrys, Jacques Ravel, PhD

restore vaginal health. This consortium of experts in vaginal and women's health, microbial genomics, chemical biology and mucosal immunology will work to develop a more complete understanding of the composition, function and ecology of the vaginal microbial ecosystem in order to design microbiota-directed interventions that treat or prevent disease and adverse outcomes.

"This project is truly focused on translating basic science into novel products that will impact women's lives and not only in the US, but in economically burdened countries where access to health care is not readily available. The Bill and Melinda Gates Foundation record in these settings speaks for itself, and we are confident that working with the BMGF on this project will positively improve women's lives," says Dr. Ravel.

Dr. Jacques Ravel, Bill Gates

UMB Innovations Impress Congressional Delegation
By Jena Frick

Staffers from Maryland's U.S. congressional delegation got a sneak peek at Health Sciences Facility Three (HSF III), the newest research facility of the University of Maryland School of Medicine (UMSOM). The cutting-edge facility was just the first stop on a tour meant to introduce the delegation to all of the new innovations and initiatives happening at the University of Maryland, Baltimore (UMB).

The day-long tour began in the pristine lobby of HSF III and a visit to IGS. UMB President, Jay Perman, MD, greeted members of the congressional delegation with warm handshakes and a few words about how imperative UMB's research is to solving global health problems, creating advanced medical practices, and, most importantly, saving lives.

Using state-of-the-art laboratories, researchers from both UMB and the University of Maryland College Park have been able to collaborate on ground-breaking research in genomic sciences, genomic medicine, and child health and brain development.

"We designed an open-lab type of setting," said Jacques Ravel, PhD, Associate Director of IGS. "We want to physically encourage the sharing of ideas and collaboration among professionals because that is how new innovations are discovered."

The delegation also visited the Genomic Research Center (GRC) to hear an overview on high through-put sequencing given by Luke Tallon, co-director of the GRC. They also visited Seth Ament's lab. Dr. Ament's research involves the application of genomics to a better understanding of psychiatric disorders, many of which are hereditary.

"It's always important to get [congressional] staff on campus to see what we have going on," says Jeff Grossi, JD, Senior Government Affairs Specialist. "It allows better opportunities to build relationships, and more than anything, it reinforces the need for continued federal investment in academic research and investment in higher education at the graduate level."
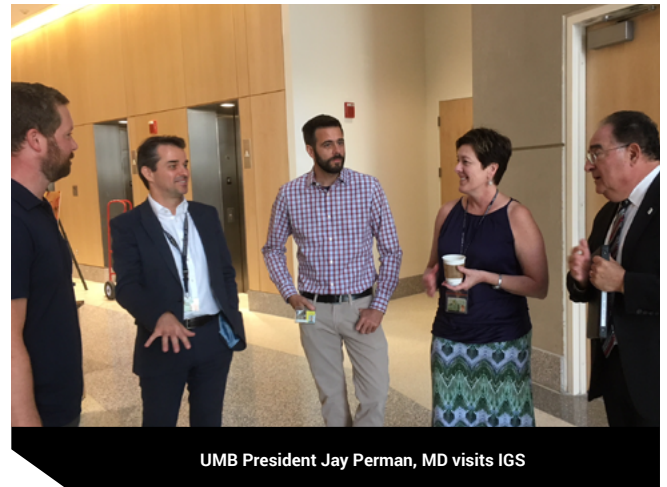
UMB President Jay Perman, MD visits IGS

Congressional delegates visit the Ament Lab

Dr. Seth Ament explains his research to congressional delegates

Q&A

IGS' New Core: Microbiome Services Laboratory

This year, IGS launched its third core – the Microbiome Services Laboratory (MSL) – which provides a range of wet-lab microbiome computational analyses for investigators at UMB and world-wide. About 40% of MSL's business has been with IGS and UMB investigators and the rest of its business comes from global collaborators. MSL works closely and seamlessly with the other two IGS cores – the GRC (Genomic Resource Center) and IRC (Informatics Resource Center) to provide comprehensive high throughput sequencing and analysis.

Jacques Ravel, PhD, Professor, Microbiology & Immunology, Associate Director, Genomics, is a globally recognized expert in the human microbiome. The MSL developed through analysis services that he and his team provided for colleagues. Mike Humphrys, who has been Dr. Ravel's laboratory manager for the past three years, is the MSL Program Director.

Q: What are the range of microbiome analysis services that MSL provides?

We have a complete range of "a la carte" services because our clients have different levels of experiences and needs. Some clients have a good understanding of what they are ordering and have done microbiome work before. In these cases, we send the data back to the clients and they do their own analysis. More commonly, though, we consult with the clients on study design and questions and perform the data analyses. Typically, we receive primary biological samples and process them from DNA extraction to sequencing, as well as detailed analysis and modeling.

Our pioneering work in this field brings confidence and added value to our services. This allows us to provide advice to our clients about experimental design and how to set up studies to best test the hypothesis they are researching. This might include advice about how many samples to include for disease and non-disease states, and what kind of analysis/modeling they would need for that research. We strive to match their needs to our capabilities.

Q: Tell us more about the advice you can give investigators?

Microbiome data informatics and analysis can be overwhelming. **You are transforming samples into gigabytes of data.** The MSL offers a way to smooth that process for investigators and give them data that is more easily interpretable, without having to do extensive informatics.

We offer and prefer consultation during study design, or even during grant proposal writing . We help investigators with the best way to structure and design their experiment to maximize the value of microbiome data. Our experience allows us to make sure that certain critical factors are considered in the

final study design or analysis, such as the inclusion of appropriate controls. These considerations can be vital to the success of the experiments, and clients value our extensive experience with microbiome analysis design.

Q: How does MSL fit in with the other two cores at IGS?

MSL is part of a continuum of services with the Genomic Resource Center (GRC) and the Informatics Resource Center (IRC) which have been a part of IGS since the Institute launched in 2007. This is a seamless process for clients – when we talk to clients about the services they may want, we suggest or guide them about which services might give them the information they want and generally we make it very simple for them.

Johanna Holm, Awarded NIH Postdoctoral Ruth L. Kirschstein National Research Service Award

Dr. Johanna Holm, a postdoctoral fellow in Dr. Ravel's Laboratory, was awarded an NIH Postdoctoral Ruth L. Kirschstein National Research Service Award in December 2017. The purpose of the Ruth L. Kirschstein National Research Service Award (NRSA) Individual Postdoctoral Fellowship is to support research training of highly promising postdoctoral candidates who have the potential to become productive, independent investigators in scientific health-related research fields relevant to the missions of the participating NIH Institutes and Centers.

Johanna's awarded research focuses on the vaginal microbiome and determining biomarkers of susceptibility or resistance to incident sexually transmitted infections (STIs). Specific aims of this research are to (1) conduct a metagenomic analysis to determine associations of vaginal microbial functional genes and gene pathways with incident STI risk, (2) conduct genome reconstruction analyses to characterize genomic strains of *Lactobacillus* species from vaginal metagenomes and determine their associations with STI, and (3) assess the interactions between human pro-inflammatory responses and the vaginal microbiome in risk for incident STI. Johanna is being mentored by Dr. Jacques Ravel and Dr. Rebecca Brotman at IGS and by Dr. Khalil Ghanem at Johns Hopkins University.

Johanna Holm, PhD

Gut Bacteria, Nutrition and Your Health

Tens of trillions of microorganisms inhabit the human digestive tract, and researchers are finding increasing evidence that they play an important role in many aspects of our health, not just how we digest our food. Nutrition is an often misunderstood topic, yet it is an essential element of an individual's overall health.

On July 16, Dr. Claire Fraser, director of IGS and a leading researcher on the gut microbiome, and Caroline Meehan, a registered dietitian at the University of Maryland Medical Center, were featured guests on Maryland Public Television's Direct Connection with host Jeff Salkin. Dr. Fraser and Meehan discussed the differences between good and bad bacteria and how nutrition plays a key role in weight management, interactions with prescription medicines and managing cholesterol, heart disease, and diabetes.

(From left) Caroline Meehan, Dr. Claire M. Fraser of IGS, Jeff Salkin

Celebrating 10 Years As Director of IGS

In recognition of Claire Fraser's 10 years' as director of IGS and in celebration of IGS' move to its new location in HSF III, IGS employees surprised her with a plaque celebrating her leadership.

Dr. Owen White presents Dr. Claire Fraser with a glass plaque

Welcome New Post-Docs

Fahimeh Mirakhori, PhD – Ament Laboratory
Stem cell engineering and *in vitro* disease modeling

Enrique Tortuero, PhD – Hotopp Laboratory
Evolutionary biology and bioinformatics, horizontal gene transfer between bacteria and tumoral cells

Eric Tvedte, PhD – Hotopp Laboratory
Evolutionary genomics and bioinformatics

Michael France, PhD – Ravel Laboratory
Genomic and ecological drivers of community stability in the vaginal microbiome

"Beyond the Finish Line"

Vonetta Edwards, PhD, Lab Research Supervisor in the Ravel Laboratory, received the 2018 "Beyond the Finish Line" award from St. Ignatius Parish in Baltimore this spring. The award was presented to Dr. Edwards in recognition of her volunteer work on behalf of refugee and immigrant families in Baltimore.

Vonetta Edwards, PhD

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