Baylor College of Medicine

DEPARTMENT OF MOLECULAR & HUMAN GENETICS

ANNUAL REPORT 2020

Transforming Medicine Through the Practice and Science of Genetics

Message from the Chair

I am delighted to welcome you to our 2020 Annual Report. As we begin a new year, I'd like to briefly reflect on last year's accomplishments.

In spite of the challenges of the COVID-19 pandemic, the Department of Molecular and Human Genetics at Baylor College of Medicine continues to excel in all aspects of its mission to transform medicine with the practice and science of genetics and genomics.

The Department remains a top-ranked genetics department. Among other U.S. genetics departments, it has consistently ranked first in total awarded NIH funding and total number of NIH grants.

We are leaders in the diagnostic testing arena with our joint venture with H.U. Group Holdings, Inc., Baylor Genetics. This jointly governed laboratory supports the academic mission and innovation of the department while promising to extend the impact of genetic diagnostic testing worldwide including, most recently, for infectious diseases.

We continue to support our partnership with the Chinese University of Hong Kong Center for Medical Genetics, where our faculty is delivering the department's clinical, training and research missions to a global venue.

In addition, new and continuing consortia with the National Institutes of Health and industry are leading to new gene discoveries and advancements in the implementation of genetics and genomics. These consortia include the All of Us program, the Undiagnosed Diseases Network, the Center for Mendelian Genomics, the Knockout Mouse Phenotyping Program, the Rare Diseases Clinical Research Network and the newly established Center for Precision Medicine Models.

As we take measure of the past year, let us also look forward. The future holds much promise due to the talent and dedication of our renowned faculty, trainees and staff. I consider myself privileged to be a part of this exciting and vital effort.

Warm regards,

Brendan Lee, M.D., Ph.D.
Robert and Janice McNair Endowed Chair
Professor and Chairman
Department of Molecular and Human Genetics

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We have more than **515 FACULTY, TRAINEES AND STAFF** who occupy **115,000 SQUARE FEET OF SPACE**. Faculty includes:

- **5** members of the National Academy of Medicine
- **3** Howard Hughes Medical Institute Investigators
- **7** Fellows of the American Association for the Advancement of Science
- **3** members of the National Academy of Sciences
- **3** members of the American Academy of Arts and Sciences

Making History

History of the Department of Molecular and Human Genetics at Baylor College of Medicine





Research in genetics began at Baylor College of Medicine in 1971 when Dr. C. Thomas Caskey, professor of molecular and human genetics, and, soon thereafter, Dr. Arthur Beaudet, were recruited from the NIH to lead Baylor's entry into that field. Operating initially within the Departments of Internal Medicine and Pediatrics, the pair created a clinical training program in 1976 to educate and train a group of top investigators in genomics and biomedical research.

As the research team grew in size, scope and ambition, a centralized organization was needed to fuse together the disparate lines of effort. For that reason, in 1985, the Institute of Molecular Genetics was created, thereby placing Baylor on the map as a genetics powerhouse. By leveraging its ability to recruit the best and brightest physicians and scientists in the field, the Institute grew substantially and in 1994, the decision was made to make the Institute a full department.

The Department's success reached new heights with the creation of the Human Genome Sequencing Center in 1996. The Center, led by Dr. Richard Gibbs, the Wofford Cain Chair and Professor of Molecular and Human Genetics at Baylor, was one of three sites (out of six pilot programs) to complete the Human Genome Project. In 2000, scientists triumphantly announced they had deciphered the human genome—the blueprint for human life.

In recent years, the Department has successfully provided comprehensive clinical care to patients worldwide. By assembling the largest clinical genetics program in the country, Baylor offers patients timely and expert assistance, as well as unparalleled treatment and counseling options through 14 specialized clinics.

In addition, the Department has expanded its reach to provide diagnostic genetic testing services to the broader medical genetics community through its laboratory, Baylor Genetics, a joint venture with H.U. Group Holdings. Baylor Genetics offers an expansive menu of genetic tests and provides leading service to practitioners worldwide.

The past almost 50 years have been an exciting time of growth and change. Initially focused on medical and pediatric genetics, the Department has since expanded its reach into diverse areas that include functional genomics, genome sequencing, cancer genetics and more. In the process, it has become the preeminent genetics department in the country, if not the world.

Department Leadership

Brendan Lee, M.D., Ph.D.
Robert and Janice McNair Endowed Chair in Molecular and Human Genetics

Laura Rosales, Ed.D., M.B.A.
Administrator

Carlos Bacino, M.D.
Vice Chair, Clinical Affairs

Christine Eng, M.D.
Vice Chair, Diagnostic Laboratory Affairs

Gad Shaulsky, Ph.D.
Vice Chair, Educational Affairs (Graduate Education)

Lorraine Potocki, M.D.
Vice Chair for Educational Affairs (Undergraduate Medical Education)

V. Reid Sutton, M.D.
Vice Chair for Educational Affairs (Graduate Medical Education)

Daniel Riconda, M.S., CGC
Vice Chair for Educational Affairs (Genetic Counseling Program)

Kim C. Worley, Ph.D.
Vice Chair for Research Affairs - Basic and Translational

Sandesh C. Sreenath Nagamani, M.B.B.S., M.D.
Vice Chair for Research Affairs - Clinical

Shashikant Kulkarni, M.S., Ph.D., F.A.C.M.G.
Vice Chair for Research Affairs (Baylor Genetics)

Debra Murray, Ph.D.,
Co-Director, Office of Community Engagement and Diversity

Susan Fernbach, R.N., B.S.N.,
Co-Director, Office of Community Engagement and Diversity

Genomics teams partner to provide COVID-19 testing for Houston area

Since the outbreak of the COVID-19 pandemic, researchers at Baylor College of Medicine's Human Genome Sequencing Center and Alkek Center for Metagenomics and Microbiome Research have come together to serve the need for COVID-19 testing in the Houston area by combining the expertise of each group's laboratories. Baylor has partnered with local public health departments to provide polymerase chain reaction (PCR) testing for more than 135,000 COVID-19 samples, and researchers are working to detect variant strains through sequencing.

"We are pleased to work with the outstanding local government groups in this critical public health effort," said Dr. Richard Gibbs, director of the Human Genome Sequencing Center and Wofford Cain Chair and professor of molecular and human genetics at Baylor. "We are proud of the tireless determination and expertise of our centers and college staff that enabled the rapid development of this robust testing capacity to serve the greater Houston community."

Baylor is one of the testing providers for Harris County Public Health. The county provides testing for the general public and individuals living in traditionally high-risk congregate settings such as nursing homes.

Samples collected at testing sites are sent to the Alkek Center for Metagenomics and Microbiome Research to be prepared for testing. After arriving at the lab, each sample is decontaminated and put in a liquid solution that helps isolate the virus. Technicians then extract the genomic material of the virus (RNA) from the sample. That RNA is then sent to the Human Genome Sequencing Center to undergo quantitative reverse transcription PCR (RT-qPCR) testing. This process works by looking for specific sequences that are unique to the virus's genome.

If the sample's RNA sequence matches that of the virus, the sample is positive. Each sample must test positive three times to be considered a positive case of COVID-19. A trained interpreter will provide a final review, confirming a positive or negative case. Each report is signed by respiratory virus expert and Medical Director of the Alkek Center for Metagenomics and Microbiome Research lab, Dr. Pedro Piedra.

On average, results are returned to the tested person within 48 hours. Each test kit is equipped with a bar code that allows the test to be tracked digitally, speeding up the process of informing the tested person and county health officials.

"Widespread testing capacity is a critical component for this pandemic response. Whether we are identifying new cases or are performing surveillance, the only way to effectively allocate resources is with a response that includes testing," said Dr. Joseph Petrosino, chair of the department of molecular virology and microbiology and director of the Alkek Center for Metagenomics and Microbiome Research at Baylor.

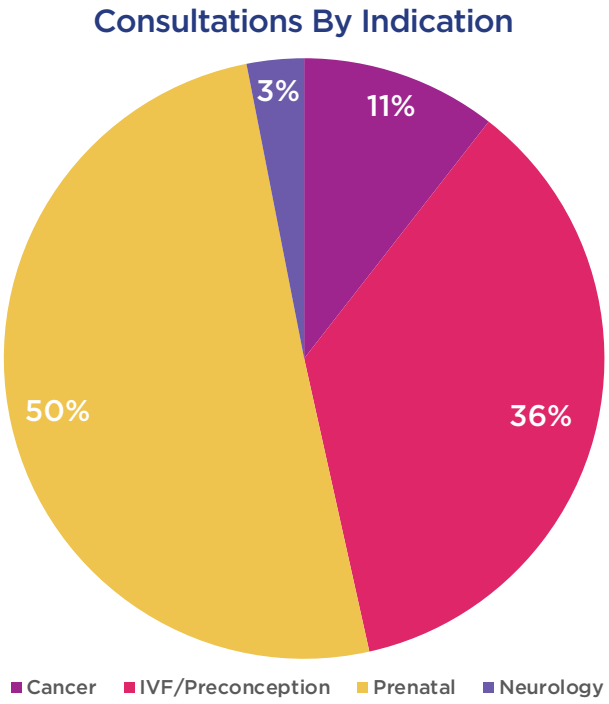
"We knew we had all the pieces to stand up a testing center fast – large scale clinical sequencing, experts in virology and molecular biology, and a secure way to return results to patients," said Ginger Metcalf, Human Genome Sequencing Center Director of Project Development. "We are also fortunate to have such great partners at Harris County Public Health, who have done an amazing job of gathering, tracking and delivering samples, especially for the most at-risk members of our community."

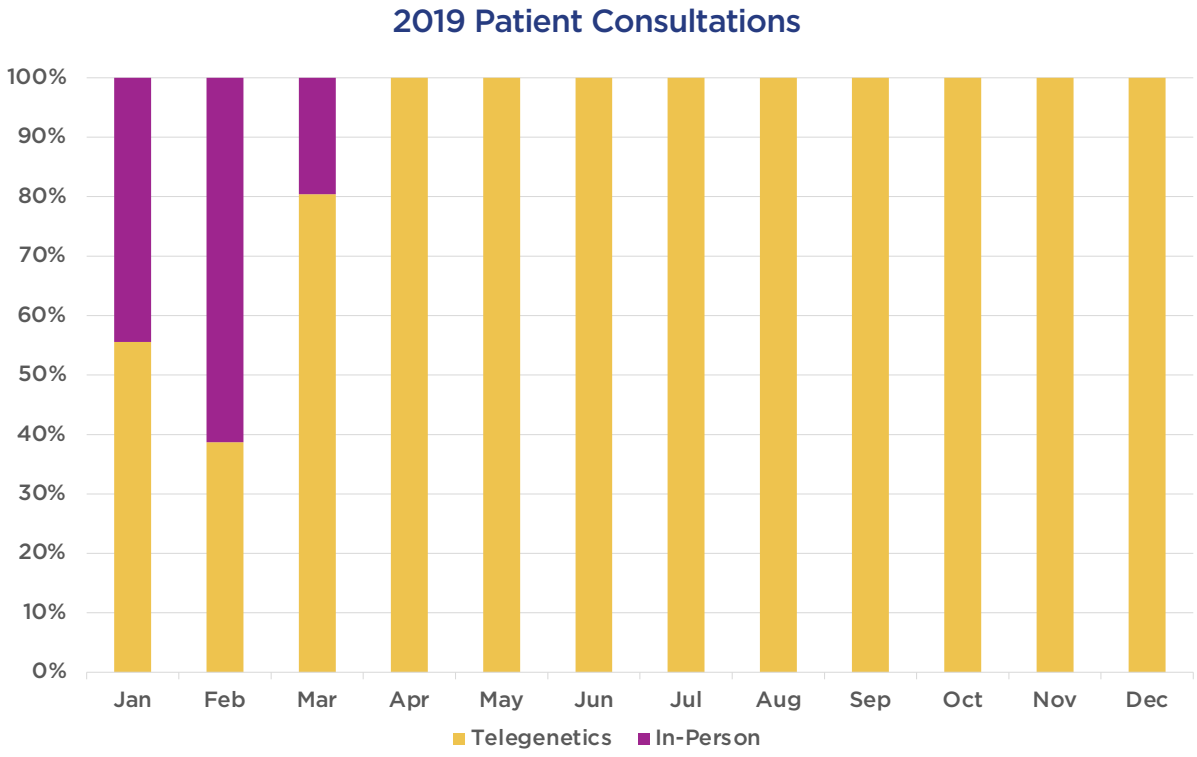
The Consultagene Clinic

The Consultagene Clinic completed its second year of operation in 2020. The Clinic was able to transition seamlessly to all virtual visits in response to the COVID-19 pandemic, with minimal impact to patient volumes. A total of 689 patients were scheduled through Consultagene Clinic this year, as compared to the 642 patients that were seen for genetic counseling in our inaugural year.

In January 2020, the clinic started to accept neurology referrals for indications of family history of Alzheimer's disease, Parkinson's disease, atypical dementia, parkinsonian conditions, ALS and cerebellar ataxia. This year, the majority of patients (50%) were seen for a prenatal indication while an additional third (36%) were seen for an IVF/Preconception consultation, and 11% were seen for cancer counseling.

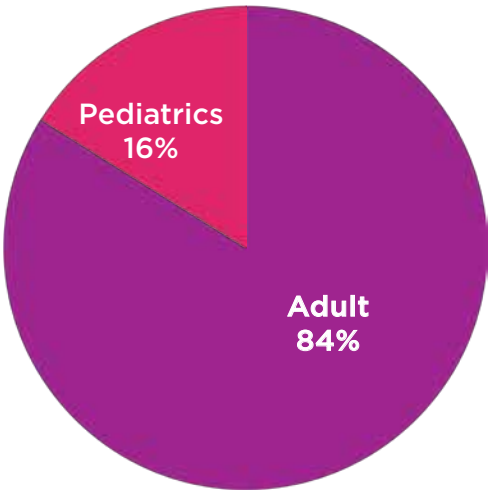
Since July 2019, patients seen in the clinic have been provided access to the Consultagene platform, allowing patients to watch educational videos, explore online resources, message with their provider and access documentation from their consultations. From the start of November 2019, patients have been surveyed to gauge their Consultagene Clinic experience. All survey participants indicated that the genetic counseling met or exceeded their expectations and all of the patients who had telegenetic counseling agreed or strongly agreed that the consultation was equivalent to an in-person visit with a healthcare provider.

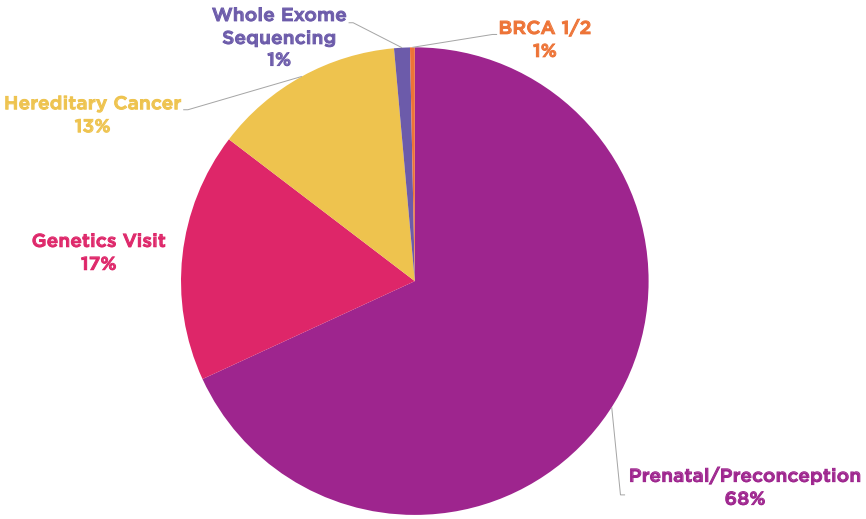




Consultagene By The Numbers

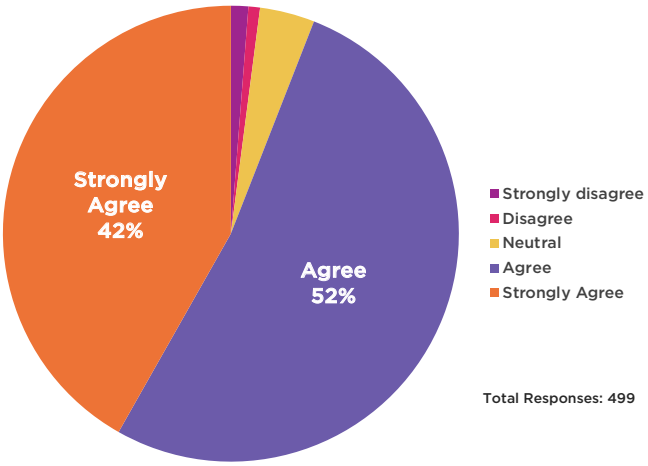
In 2020, there were a total of 918 referrals made to Consultagene.



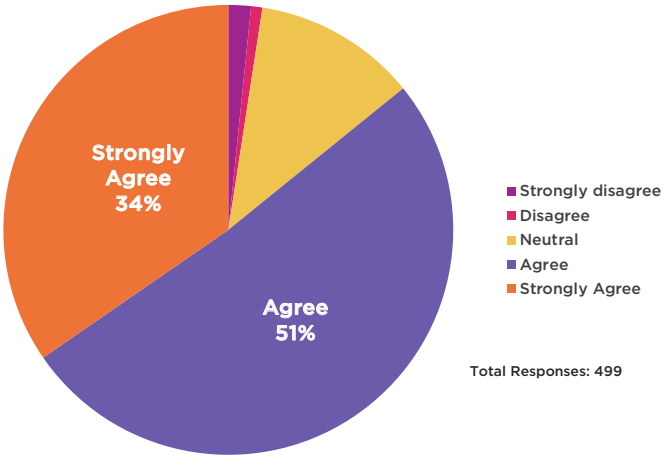


During a patient's journey in Consultagene, the patient is assigned videos to watch as part of the education designed to inform the patient about the indication. Patients were also asked to answer surveys that evaluated the effectiveness those videos.

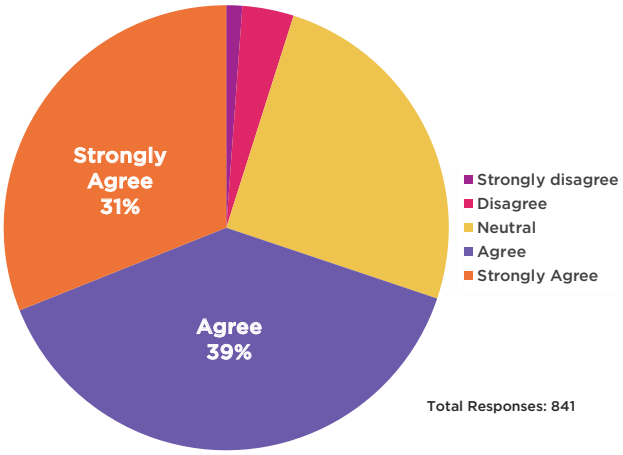
Videos were easy to understand



Videos were informative and helpful



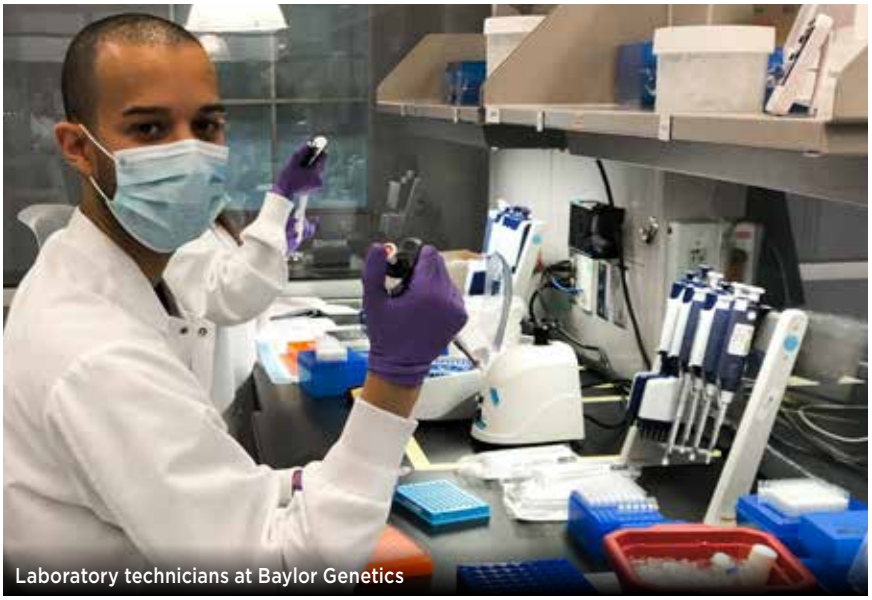
Better Understanding of Indication After Watching the Assigned Videos



Baylor Genetics provides COVID-19 testing for Houston

In response to the global COVID-19 pandemic, Baylor Genetics, a pioneer in genetic testing and precision medicine, launched its official test for COVID-19 on June 16, 2020. To help prevent the spread of COVID-19 in Houston, Texas, Baylor Genetics partnered with the Houston Health Department and Rice University to provide quality, high-throughput testing for COVID-19.

The partnership with the City of Houston entails quick and efficient testing, which helps the city monitor outbreaks and provide valuable data for steps needed to prevent the spread of the virus in Houston communities. The partnership with Rice allowed the university to resume in-person classes for the fall semester.


Laboratory technicians at Baylor Genetics

While Baylor Genetics' main focus has been genetic testing of inherited disorders and cancer, the diagnostic company was quickly able to validate a test for COVID-19 in its high-complexity CLIA-certified, CAP-accredited laboratory. Baylor Genetics has one of the highest sensitivity (true positive) and specificity (true negative) rates for identifying an active coronavirus infection for its COVID-19 test.

"At Baylor Genetics, we are committed to improving healthcare globally and locally – no matter if that involves testing for genetic disorders or testing for infectious diseases," said Dr. Christine Eng, chief medical officer and chief quality officer at Baylor Genetics and professor of molecular and human genetics at Baylor College of Medicine. "With our state-of-the-art molecular processes, our COVID-19 test is poised to help thousands determine if they are infected with SARS-CoV-2. Our goal is to give patients in Houston fast and reliable results, so they can receive the treatment they need."

In October, Baylor Genetics launched an accessible and reliable at-home collection kit for COVID-19. With the launch of the at-home test, individuals nationwide will be able to order a test kit to determine if they are currently infected with COVID-19 within 48 hours or less.

"As we gain more experience with measures to control the spread of SARS-CoV-2, readily accessible and rapid, reliable testing is at the forefront of effective tools that should be utilized. It is important to remove as many obstacles as possible for individuals to access testing," Eng said. "We at Baylor Genetics have developed a convenient and reliable COVID-19 testing process that will provide individuals with the information they need to keep themselves and their families as safe as possible."

In November, Baylor Genetics launched the latest combination test for the novel coronavirus, SARS-CoV-2, and Influenza A and B. While these respiratory viruses have similar symptoms, their treatments are different. For COVID-19, potential treatment and vaccine options are emerging. For the flu, antiviral medications can help address symptoms and potentially shorten the time an individual is sick. Therefore, it is crucial for individuals to be able to confirm which virus they may be infected with to take the proper next steps to restore their health.

Research and Discovery

Research in the Department of Molecular and Human Genetics at Baylor College of Medicine has led to important discoveries that increase understanding of disease and guide potential new treatments. Here are four recent studies that are representative of the groundbreaking research in the department.

Sequencing African genomes illuminates health and migration history

Historically, knowledge of baseline genetic data for African populations has been sparse. To remedy this, the Human Heredity and Health in Africa (H3Africa) Consortium, a collaborative effort supported by the National Institutes of Health, led a global research project to sequence genomes from regions and countries across Africa. The research, including work from Baylor College of Medicine and published in the journal *Nature*, paves the way for more broadly representative and relevant studies ranging from basic through clinical genetics.


Dr. Neil Hanchard

The Human Genome Sequencing Center at Baylor College of Medicine worked with the H3Africa consortium and local African governments to acquire consented samples from 13 countries across the continent and generate high-coverage whole genome sequence data on 314 individuals representing 50 ethnolinguistic groups. This allowed the researchers to examine rare genetic variants in an accurate and quantifiable way, in addition to the common variants that have been the focus of most of the previous genetic studies in Africans.

"We found an impressive breadth of genomic diversity among these genomes, and each ethnolinguistic group had unique genetic variants," said Dr. Neil Hanchard, assistant professor of molecular and human genetics at Baylor and senior author on the study. "There was a great deal of variation among people in the same region of Africa, and even among those from the same country. This reflects the deep history and rich genomic diversity across Africa, from which we can learn much about population history, environmental adaptation and susceptibility to diseases."

The research showed more than 3 million novel variants in the genomes sequenced. Beyond the sheer amount of variation within and among the groups studied, the researchers were able to use the data to examine historic patterns and pinpoint migration events that were previously unknown. The researchers found more than 100 areas of the genome with evidence of being under natural selection. A sizable proportion of these regions were associated with genes related to immunity.

New approach to diagnosing genetic diseases using RNA sequencing increases yield

In the world of rare genetic diseases, exome and genome sequencing are two powerful tools used to make a diagnosis. A recent addition to the toolkit, RNA sequencing, has been demonstrated to help researchers narrow down disease candidate variants identified first on exome and genome sequencing. A Baylor study published in the *Journal of Clinical Investigation* finds that starting genetic analysis with RNA sequencing can increase diagnostic yield even further.

Baylor has been a leader in developing clinical applications of exome and genome sequencing, a technique that is now being used in clinics worldwide. Researchers at the Undiagnosed Diseases Network (UDN) have successfully used exome and genome sequencing to increase the diagnostic rate of rare genetic diseases to about 35%.

"That's impressive because these cases have already had such an extensive workup already," said Dr. Brendan Lee, corresponding author of the study and professor and chair of molecular and human genetics at Baylor. "The 35% diagnostic rate is great, but unfortunately that means there's still 65% that remain undiagnosed."

Exome and genome sequencing do have limits. Only about 1 or 2 percent of the genome is coding, meaning it is translated into RNA and proteins. Researchers are limited in their ability to interpret genetic changes in the noncoding regions of the genome.

To assist in interpretation of exome and genome sequencing, the UDN has increasingly turned to RNA sequencing. While exome and genome sequencing identify genetic changes in the DNA, RNA sequencing can reveal the effects of those changes, for example if a gene has lower expression than expected. RNA sequencing can also tell us about the effects of noncoding changes, something that is very important as we transition from exome to genome sequencing.


Dr. David Murdock

RNA sequencing has been used as a secondary tool to help prioritize disease gene candidates identified with exome and genome sequencing, and it has been shown to increase diagnostic yield to variable degrees. The Baylor team wanted to try a different approach with the UDN cases. Using a novel pipeline developed with collaborators in Germany, they started with the RNA sequencing to first identify unique differences in gene expression and splicing. Researchers could then trace the problem back to a corresponding genetic change in the exome and genome sequencing data.

"This strategy really flips the way we normally approach a case, looking at the end result in the RNA and working backwards to find the cause in the exome or genome. It allows biology to tell us where to look to make a diagnosis," said Dr. David Murdock, lead author of the study and assistant professor of molecular and human genetics at Baylor.

"We found this RNA sequencing first approach was extremely powerful," Lee said. "It was able to very rapidly point at the gene we should look at. Moreover, it did so in cases in which we would not have been able to identify the disease gene candidate using exome and genome sequencing alone. If we had used the old way and generated a priority candidate list, these gene mutations would not have even been in the priority list."

The team found that exome and genome sequencing sometimes missed small deletions in genes. However, the RNA sequencing data showed that these deletions could dramatically affect gene expression. RNA sequencing also picked up changes in expression and splicing caused by variants in noncoding regions that would not have been flagged in regular exome and genome sequencing.

The Baylor study found that beginning with RNA sequencing could increase the diagnostic yield 17% from the traditional exome and genome sequencing approach, bringing their overall diagnosis rate to roughly 50%. As part of the study, researchers analyzed both skin cells and blood cells and found that skin cells were more informative in diagnosis because of their homogenous nature and better gene expression.

"I see RNA sequencing with this approach as eventually becoming standard practice, especially as we move more from exome to genome sequencing. It allows us to diagnose so many more patients and gives families the answer they've been seeking," Murdock said.

This work was supported by the NIH and the BCM Intellectual and Developmental Disabilities Research Center from the Eunice Kennedy Shriver National Institute of Child Health & Human Development.

New molecular roadmap boosts fight against endometrial cancer

A study published in *Cell* provides an unprecedented look at the dozens of molecular steps that occur to bring about endometrial cancer, or uterine cancer. The research offers insights about how physicians might be able to better identify which patients will need aggressive treatment and offers clues about why a common treatment is not effective with some patients.


Dr. Bing Zhang

Dr. Bing Zhang, professor in the Lester and Sue Smith Breast Center and the Department of Molecular and Human Genetics at Baylor, is one of five corresponding authors.

"This work contributes to the personalized medicine we need to deliver for patients who have

endometrial cancer," said Zhang, a member of the Dan L Duncan Comprehensive Cancer Center, a Cancer Prevention & Research Institute of Texas (CPRIT) Scholar and a McNair Scholar at Baylor. "Such work will help us to know which patients will benefit most from which therapies."

Scientists developed a promising new way to identify tumors that currently are classified as not aggressive but which turn out to be just as invasive as a serous tumor, a type of ovarian tumor that grows quickly and is more likely than other tumors to kill patients. The team explored how the activity levels of certain proteins clearly differentiate aggressive from less-aggressive tumors.

Researchers also discovered that non-coding molecules known as circular RNAs seem to be involved in "endothelial-mesenchymal transition," or EMT, a transformation that cells undergo when they gain the ability to spread, which makes endometrial cancer deadly.

HeartCare study tests genetic risk of cardiovascular disease

Human Genome Sequencing Center researchers are working with Baylor cardiologists to determine patients' genetic risk factors for cardiovascular disease, the leading cause of death for men and women in the United States. As part of the HeartCare study, participants went through genetic testing to identify genes that influence risk for cardiovascular disease and related conditions.

"Genomics has the potential to drive precision medicine. Some cardiovascular risk factors can be predicted or detected through genomic methods, making treatment options specific to each person," said Dr. Richard Gibbs, Wofford Cain Chair and professor of molecular and human genetics and director of the Human Genome Sequencing Center. "This program provides the perfect opportunity to introduce genomics into the adult clinical care system. It can potentially shift the paradigm from reactive care to risk prediction."

HeartCare analyzed 158 genes and tested for genetic risk of aortic aneurysms, cardiomyopathies, arrhythmias, high cholesterol and medication sensitivity, among other conditions. Results were returned to the physician, who reviewed the findings and made a care plan if any changes were needed. Genetic counseling services were available for participants who tested positive for a risk gene.

More than 700 participants were enrolled in the study. Some participants have seen results that may impact their clinical care. That includes changes to diet, exercise and lifestyle or further genetic testing for family members.

"So often in cardiovascular disease, we look at the symptoms and make a probable diagnosis. Now we have the ability to tell people exactly what they have," said Dr. Christie Ballantyne, professor of medicine and chief of the sections of cardiology and cardiovascular research at Baylor. "It's remarkable the impact genetics can make in cardiovascular care."

This study was funded by the St. Luke's Foundation.

Research Administration

For the year 2020, a total of 428 grant proposals were submitted to Baylor's Office of Research by the Department of Molecular and Human Genetics with 316 funded, resulting in a total of over $116 million in competing and noncompeting awards passing through the department.

The department has established its first, full-service research administration team to provide enhanced pre-award and post-award services to the department. The team consists of highly experienced research administrators whose roles consist primarily of assisting faculty with grant proposal submissions, award transfers, prior-approvals and compliance regulations. Team members consist of Sherri Weaver, Betty Fernandini, Shibali Patra and Courtney Gomez along with Sharon Sudduth and Elizabeth Barrera performing purchasing and other administrative duties for the team's assigned faculty. Prior to the end of the year, Sherri Weaver, Betty Fernandini and Shibali Patra received their Certified Research Administrator (CRA) designations, furthering the knowledge and credentials of this new team.

Grant Awards Continue to Drive Progress

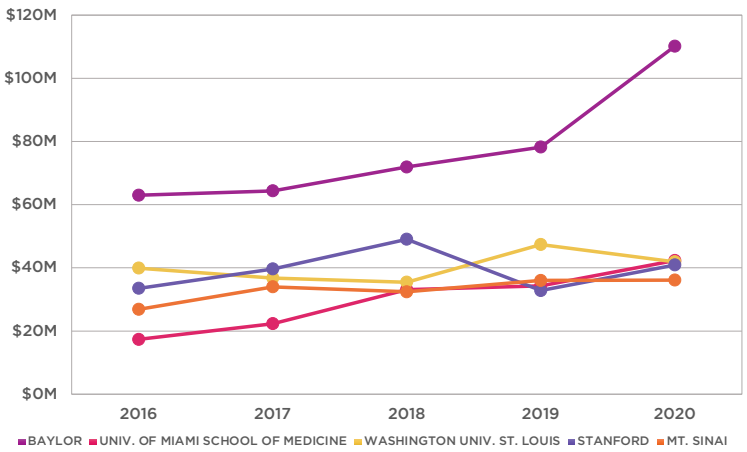
The Department of Molecular and Human Genetics continues to be ranked No. 1 in NIH funding

The National Institutes of Health is the primary governmental agency responsible for biomedical and health-related research in the United States. A department's ability to consistently obtain NIH grants, which are awarded through a competitive peer review process, demonstrates the strength of its research and training programs. On that basis alone, the Department of Molecular and Human Genetics at Baylor College of Medicine continues to distinguish itself.

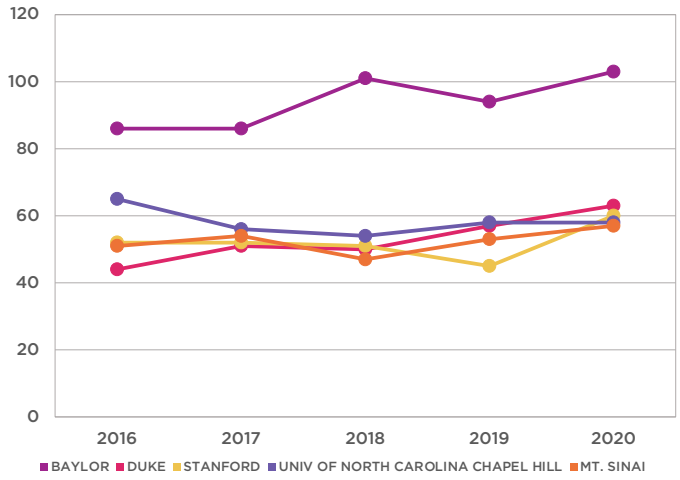
For ten years running, the Department remains the No. 1 ranked U.S. genetics department, as measured by the number of NIH-awarded grants and total funding received. For 2020, the amount in funding dollars from NIH awards totaled more than $110 million (source Blue Ridge rankings).

The Department is excited to receive this funding, and has put this support to excellent use. Through the funding of the Undiagnosed Disease Network Center, the Center for Mendelian Genomics, the Knockout Mouse Project and many other investigator-initiated grants, the Department is finding answers to science's most pressing questions. In the process, the Department is improving the well-being of patients across the world.

NIH Funding to Leading Genetics Departments



NIH Grants Awarded to Leading Genetics Departments



Other Grants/Awards

The Department is proud to receive generous funding from many agencies and foundations, some of which are listed below:

The Howard Hughes Medical Institute
The Robert and Janice McNair Foundation
The Cancer Prevention and Research Institute of Texas
The Welch Foundation
The Simons Foundation
THe Huffington Foundation
The Doris Duke Foundation
The American Heart Assocation
Autism Speaks

NIH-funded center to model rare genetic disease

Baylor College of Medicine received a five-year, $9.94 million grant from the National Institutes of Health for the new Center for Precision Medicine Models to facilitate the study of rare genetic diseases. The center will use precision animal models of a patient's or group of patients' specific genetic variation and study why the change causes disease and how the disease can be treated.

Clinical exome sequencing and whole genome sequencing have led to major advances in diagnosing patients with suspected genetic disease. However, the clinical significance of those genetic variants often remains unclear.


Dr. Jason Heaney

"Our center is connecting the dots between discovery of a change in your genetics and how to treat the associated disease. We may be able to find therapies or lifestyle interventions that can help people manage their disease and improve quality of life," said Dr. Jason Heaney, lead principal investigator of the center and associate professor of molecular and human genetics at Baylor.

The center will take nominations for genetic variants to model from patients, patient groups, clinicians, researchers and NIH-funded consortiums like the Undiagnosed Diseases Network and the Centers for Mendelian Genomics. An accepted disease-causing genetic variant must previously be identified in order to be considered for modeling.

After a case is submitted, the center's clinical and bioinformatics teams will independently assess the genetic variant for likelihood of causing disease. Next, the modeling team will decide if a precision model organism can be produced for that particular genetic change and whether appropriate resources are available within the center to study the disease. A final decision about whether to select the case will be made based on likely clinical benefit to the patient.

"Everything that we plan to do has the overall goal of benefitting the individual with a rare disease in the clinic," Heaney said. "If we can find a therapeutic that makes a tremendous payoff for even just one patient, we will do it."

Although the entire process may take a couple of years to complete, researchers will collaborate with clinicians and patients throughout the process to optimize models and return findings for integration into clinical care or possible clinical trials. The center also aims to provide pre-clinical research data for pharmaceutical companies developing therapeutics for rare diseases.

"The award recognizes the department and institution's worldwide leadership in personalized genomic medicine," said Dr. Brendan Lee, co-principal investigator of the center and chair of the Department of Molecular and Human Genetics at Baylor.

"The traditional 'bedside-to-bench' genetics paradigm has recently become challenged by the high volume of genetic variants revealed by clinical genome sequencing. The center will help alleviate the variant interpretation bottleneck, accelerate discovery and bring the benefit back to the patient." said Dr. Aleksandar Milosavljevic, co-principal investigator of the center, the Henry and Emma Meyer Professor in Molecular and Human Genetics and director of the program in quantitative and computational biosciences at Baylor.

Other Baylor faculty members working with the center include Drs. Lindsay Burrage, David Murdock, Sandesh Nagamani, Jennifer Posey, Hugo Bellen, Michael Wangler, Jeff Rogers, Mary Dickinson, Matthew Roth, Zhandong Liu, Neil Hanchard, Uma Ramamurthy, John Seavitt and Shinya Yamamoto and Jill Mokry.

Research Centers

Baylor College of Medicine is home to one of the largest biomedical research programs in the nation. The Department of Molecular and Human Genetics is proud to work hand-in-hand with the following research centers, each of which focuses on specialized areas of medical research. These centers are led by primary faculty of the Department and, together, advance the current boundaries of scientific knowledge.

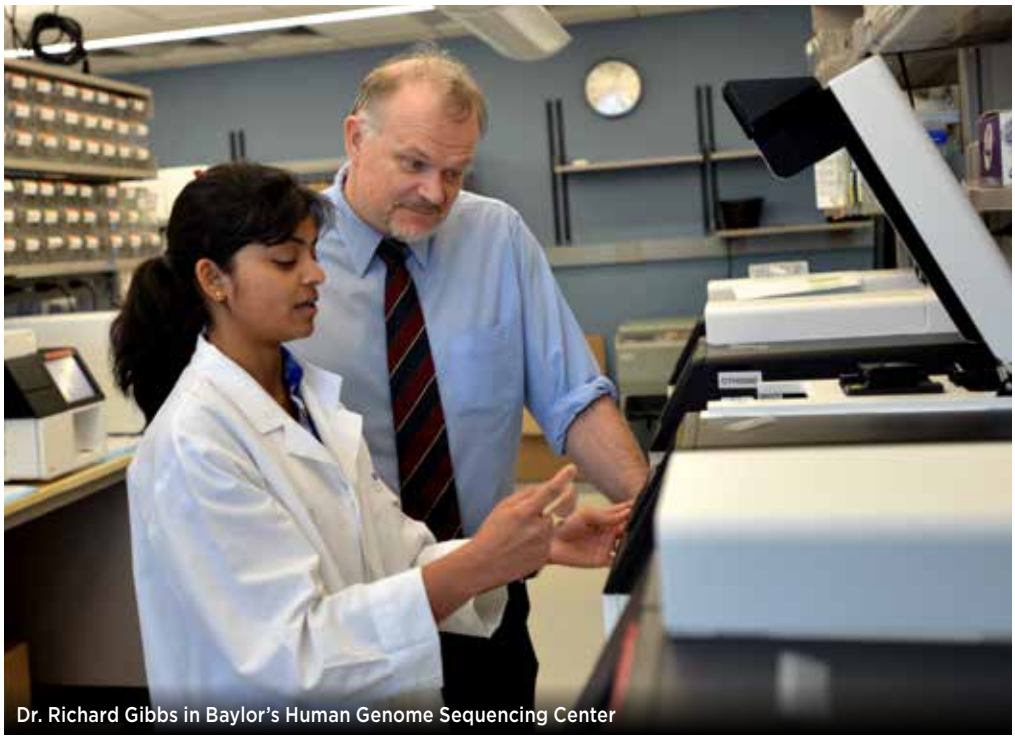
Human Genome Sequencing Center

The Baylor College of Medicine Human Genome Sequencing Center (Baylor HGSC), led by Dr. Richard Gibbs, has been operational for more than 20 years. Originally established in 1996 to participate in, and eventually help complete, the Human Genome Project, the HGSC has grown and achieved international recognition as a large-scale DNA sequencing and analysis center. Currently a Center for Complex Disease Genomics supported by the NIH and the National Human Genome Research Institute (NHGRI), the Baylor HGSC has since expanded its research focus into new and exciting areas.

The Baylor HGSC employs more than 180 staff and occupies more than 36,000 square feet of space in the Margaret M. and Albert B. Alkek Building at Baylor College of Medicine located in the heart of the Texas Medical Center, the world's largest medical complex.

The major activity of the Baylor HGSC is high-throughput DNA sequence generation and the accompanying analysis. The center currently operates multiple sequencing platforms: Illumina, Pacific Biosciences, Oxford Nanopore, and Sanger. The sequence data generated by these machines is analyzed in a complex bioinformatics pipeline, and the data are deposited regularly in the public databases at the National Center for Biotechnology Information (NCBI) or cloud partners for secure data sharing. This ensures that the worldwide research community has timely access to the data.

A major focus of the Baylor HGSC is the deciphering of the genetic architecture of common complex diseases. These include cardiovascular disease, neurodegeneration and cancer predisposition – all major causes of adult death with strong heritable components. Understanding the genetic architecture of these disorders is the key to identifying gene changes that directly cause the diseases in order to direct therapeutic strategies. This pathway from "bench to bedside" is the foundation of the new national initiative in Precision Medicine.


Dr. Richard Gibbs in Baylor's Human Genome Sequencing Center

In direct response to this new era, the Baylor HGSC has launched the HGSC Clinical Lab (HGSC-CL), which has a complete infrastructure to support large-scale sequencing and genomics projects. With its sophisticated informatics core and pipeline and state-of-the-art technology development core, the CAP accredited/CLIA certified HGSC-CL

can deliver clinical test grade data for returning results to diagnosing physicians.

In addition to studying genetic datasets, the Baylor HGSC places great emphasis on integrating other omic data into genetic analyses.

In support of this effort, the Baylor HGSC routinely generates RNA-Seq data to look at expression patterns across samples and time points. Additionally, the Baylor HGSC regularly evaluates metabolomic and methylation profiles across samples. The Baylor HGSC also works in close partnership with the Alkek Center for Metagenomics and Microbiome Research (CMMR) to assess how the microbiome impacts human health.

Developing new technologies and applications is a major objective for the Baylor HGSC. These development steps, which produce laboratory innovations and enhancement to analyses, are made possible by a dedicated R&D team. The Baylor HGSC regularly serves as a beta test site for new technologies and provides feedback to companies on performance. This arrangement allows the Baylor HGSC to have early access to the latest improvements available.

Jan and Dan Duncan Neurological Research Institute (NRI) at Texas Children's Hospital

Jan and Dan Duncan Neurological Research Institute

The Jan and Dan Duncan Neurological Research Institute (NRI) at Texas Children's Hospital celebrated its 10th anniversary in December 2020. The Department of Molecular and Human Genetics faculty and trainees have played a major role in the NRI's success, enhancing our understanding of neurological disorders and training the next generation of investigators. The NRI is directed by Dr. Huda Zoghbi, Ralph D. Feigin, M.D. Endowed Chair and professor in pediatrics, molecular and human genetics, neurology and neuroscience at Baylor College of Medicine.

In December of 2010, the Duncan NRI opened and was the first facility of its kind in the United States with a multidisciplinary research approach dedicated to pediatric brain disorders. Since then, NRI researchers have published more than 1,000 scientific studies in top-tier journals, discovered 72 disease-causing genetic mutations, completed one successful clinical trial for an intractable epilepsy, and have six additional clinical trials in development. The reach of these discoveries extends beyond the pediatric world, impacting critical understanding of a wide spectrum of neurological and psychiatric diseases including Alzheimer's, Parkinson's, bipolar disorder, eating disorders and addiction.

The NRI fosters a one-of-a-kind research environment uniquely designed to impact the future

of neurological disease. About 30 investigators from around the world and their research teams, all experts in diverse disciplines – such as genetics, neurobiology, physics, mathematics, bioinformatics and engineering – work in specially designed "collaboratories." These open labs facilitate the free exchange of ideas, information and resources.

Everything the Duncan NRI has accomplished in the last decade would not have been possible without a generous philanthropic community, starting with Cynthia and Anthony Petrello and then Jan Ellis Duncan, who, with her late husband, Dan, made a $50 million transformational gift in 2007. Ten years later, Jan Ellis Duncan and the Petrellos remain committed to the Duncan NRI's mission in honor of the 300+ million children around the world with neurological diseases.

Computational and Integrative Biomedical Research Center

The Computational and Integrative Biomedical Research (CIBR) Center is directed by Dr. Olivier Lichtarge, Cullen Chair and Professor of Molecular and Human Genetics at Baylor.

The CIBR Center is comprised of over 100 affiliate faculty members from different Houston institutions. The CIBR Center helps the College bridge the translational gap from data to models, and from models to drug discovery and personalized therapy by fostering collaborations among scientists and developing original quantitative approaches to biological and clinical problems.

To assist students and faculty, the CIBR Center provides the resources to help address the broad range of analytical problems posed by the complexity of high throughput biological datasets. The Center organizes the Current Topics in Computational Biomedicine Course where students keep abreast of active quantitative research among the CIBR faculty. To date, the Current Topics course has hosted over 160 seminars and approximately 40 journal clubs.

In addition to the Current Topics course, The CIBR Center coordinates workshops and access to cluster computing for its faculty members. The Center also provides site licenses to scientific software (Mathworks MATLAB and Wolfram Mathematica) and regular consultation on data organization and analysis through its Data Clinics (16 sessions per year).

Huffington Center on Aging

Recognized as one of the premier aging centers in the world, the Roy M. and Phyllis Gough Huffington Center on Aging, led by Dr. Hui Zheng, Huffington Foundation Endowed Chair in Aging and professor of molecular and human genetics, neuroscience and molecular and cellular biology, is committed to addressing the needs of an aging population through basic and clinical science research.

The center facilitates and coordinates interdepartmental research and initiates its own research studies that includes cell and molecular biology of aging, adrenal cell biology, DHEA, aging of the skin, the aging cardiovascular system, healthcare outcomes research and ethical issues in acute and long-term care settings.

The center began the year 2020 by hosting the Huffington Distinguished Lecture featuring Dr. David Sabatini, a professor of biology at the Massachusetts Institute of Technology and a member of the Whitehead Institute for Biomedical Research.

Despite the challenges and uncertainties brought by the COVID-19 pandemic, the Center was successful in recruiting new faculty. Dr. Hongjie Li was recruited from Stanford University and started in January 2021 with a primary appointment in the Department of Molecular and Human Genetics. Li did his postdoc work with Dr. Liqun Luo at Stanford working on neuronal wiring in *Drosophila*. He is the recipient of a NIH Pathway to Independence Award from the National Institute of Aging and a CPRIT Scholar award.

Of the various grants the center received, Dr. Zheng and Dr. Jin Wang, CPRIT Scholar and associate professor of pharmacology and chemical biology, were awarded a five-year cooperative agreement drug development grant from the NIA aimed at developing small molecule inhibitors targeting neuroinflammation as potential Alzheimer's disease therapy.

Intellectual and Developmental Disabilities Research Center

The Intellectual and Developmental Disabilities Research Center (IDDRC) at Baylor, led by Dr. Huda Zoghbi with assistance from Dr. David Nelson, the Cullen Foundation Professor of Molecular and Human Genetics at Baylor, and Dr. Rodney Samaco,

an assistant professor of molecular and human genetics at Baylor, is one of 14 centers across the country funded by the Eunice Kennedy Shriver National Institute of Child Health and Human Development. The core facilities of the center support some 75 investigators engaged in basic, translational and clinical studies of intellectual and developmental disabilities (IDDs). NIH funding was renewed in 2020, supporting cores and a research project aimed at solving challenges facing clinical trials in IDD research. The Center has been continuously funded since 1988.

The IDDRC's Core Facilities play a pivotal role in advancing basic science discoveries 'at the bench' into preclinical and eventual clinical trials in humans. Facilities include the Clinical Translational Research Core, the Cell and Tissue Pathogenesis Core, the Molecular and Expression Analysis Core, the Circuit Analysis and Modulation Core and the Preclinical and Clinical Outcomes Core.

Since 2014, investigators supported by the IDDRC published over 1,600 papers, with 20% in high impact journals. Numerous studies reported discovery of genes and mutations involved in intellectual disability, autism, epilepsy and other developmental disabilities as well as mechanistic studies of previously known genes. Basic understanding of neural cells and circuits has provided pathways for preclinical studies and design of interventions for treating IDDs, and the IDDRC-supported Signature Project helmed by Dr. Mirjana Maletic-Savatic, assistant professor of molecular and human genetics, and Dr. Matthew McGinley, assistant professor of molecular and human genetics, will further our understanding and treatment of gene dosage-dependent disorders in the coming years.

Center for Skeletal Medicine and Biology

The Center for Skeletal Medicine and Biology (CSMB), co-directed by Dr. Brendan Lee, professor and chair of molecular and human genetics at Baylor, and Dr. Florent Elefteriou, professor of molecular and human genetics and orthopedic surgery at Baylor, seeks to improve the understanding, prevention and treatment of congenital and degenerative diseases of the skeleton, including skeletal dysplasias, osteoporosis, osteoarthritis, low back pain and bone cancers.

The CSMB at Baylor leverages the Rolanette and Berdon Lawrence Bone Disease Program of Texas, a contractual collaboration of Baylor College of Medicine, the University of Texas MD Anderson Cancer Center and the University of Texas Health Science Center at Houston, to cultivate teamwork between clinicians, clinical researchers and basic scientists of the Texas Medical Center. The center offers Baylor investigators a number of specialized tools for musculoskeletal investigations and provides avenues for faculty interested in musculoskeletal research to interact and share expertise. In 2020, the Center's development of a helper-dependent adenoviral gene therapy for osteoarthritis is being tested in the first ever in human clinical trial of such an approach under a license agreement to Flexion Therapeutics (ClinicalTrials.Gov NCT04119687).

Brian Dawson in the MicroCT Laboratory

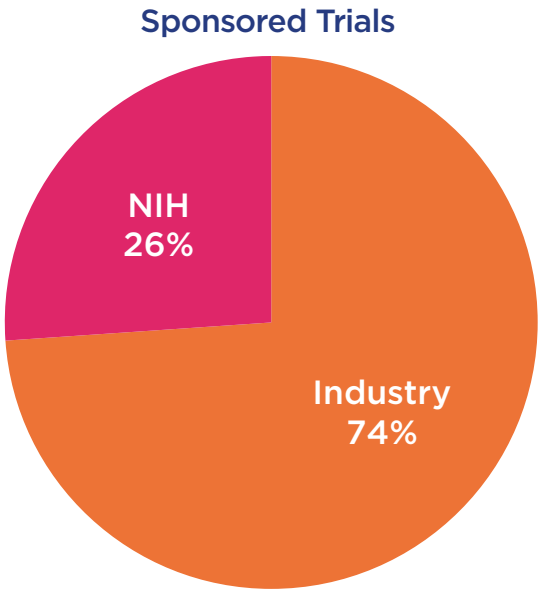
Clinical Research

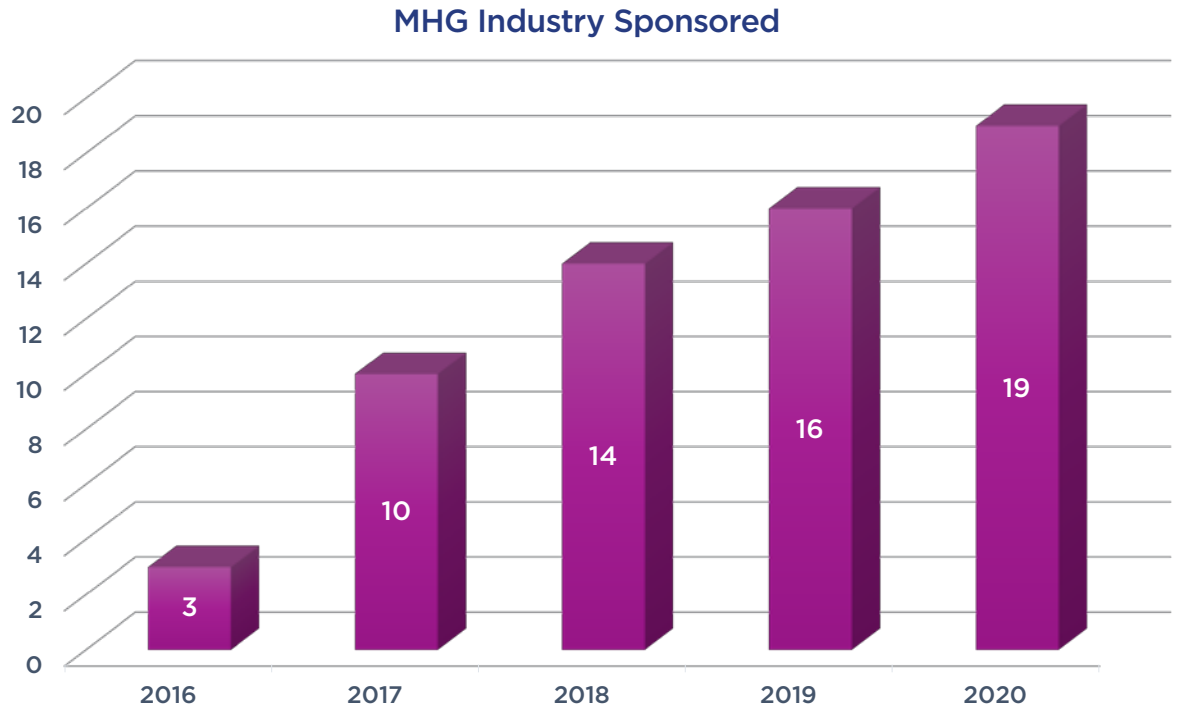
The Clinical Research Division of the Department of Molecular and Human Genetics at Baylor College of Medicine facilitates the implementation and conduct of many clinical studies in rare disorders.

Our department's clinical research consists of studies that aid in the discovery of new genes as causes for human diseases and genetic traits, natural history studies, proof-of-concept studies that help translate research findings from the bench to bedside, and clinical trials of novel therapies for genetic disorders.

In 2020, the division had more than 40 ongoing studies that included investigator-initiated studies where department faculty are sponsors, industry sponsored studies and studies that are conducted within the context of large, multicenter consortia and networks.

We are a primary or a lead site for many consortia of the NIH Rare Diseases Clinical Research Network including Urea Cycle Disorders Consortium, Brittle Bone Disorders Consortium, North American Mitochondrial Disease Consortium, and Frontiers in Congenital Disorders of Glycosylation. Both of Baylor's sites for the NIH Undiagnosed Diseases Network and the Baylor-Hopkins Center for Mendelian Genomics are housed within the department.





Genetics Clinics

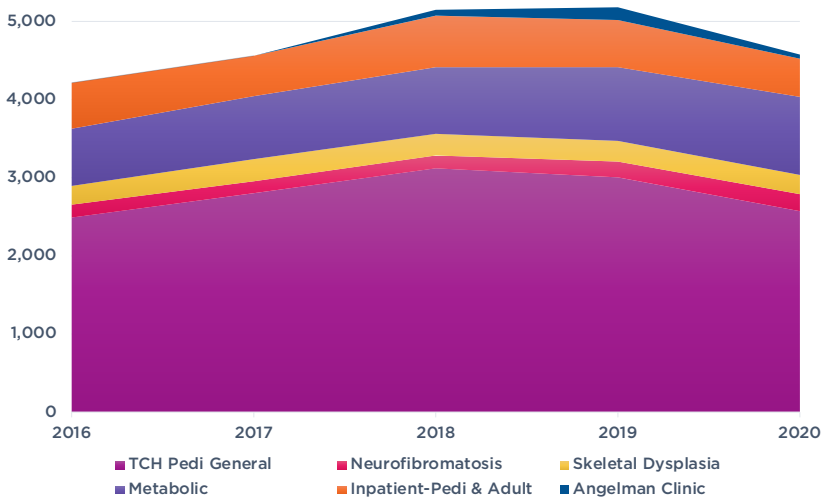
Improving Patients' Lives with Unmatched Clinical Services

Baylor College of Medicine's clinical genetics program is the largest program of its kind in the country, with clinics spanning across multiple genetics-based disciplines. The clinical program takes a collaborative approach that provides patients with the highest quality, individualized care available. Clinical activities take place across several sites.

Pediatric Genetics

Our pediatric genetics service provides genetic counseling and inpatient and outpatient care to complex and/or critically ill at Texas Children's Hospital and several other hospitals within the Texas Medical Center and beyond, including the Texas Children's Hospital West Campus and Texas Children's Hospital The Woodlands. Physicians at the Texas Children's Genetics Clinic see more than 5,000 families each year.

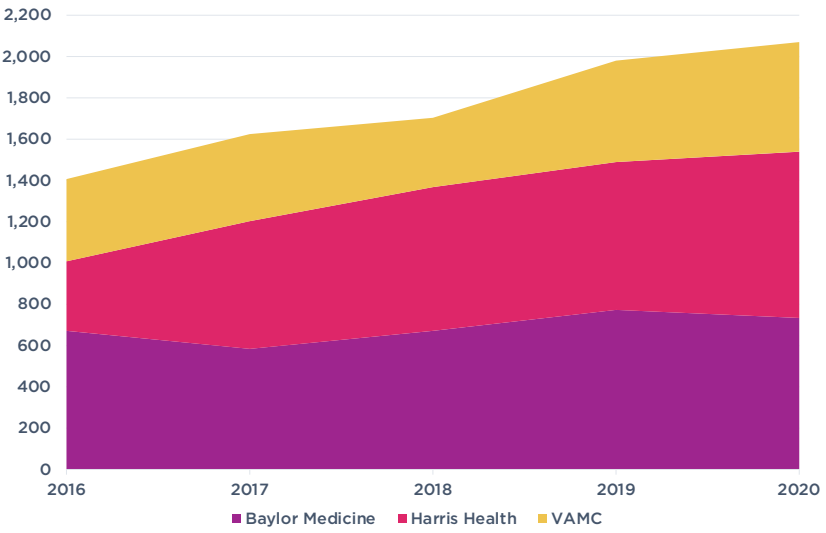
Clinical Genetics Patient Volume (Pediatric)



Specialty clinics within the Texas Children's Genetics Clinic include the metabolic, neurofibromatosis, skeletal dysplasia and cancer genetics clinics. We also have multidisciplinary team clinics that include the Angelman Syndrome Clinic, the Center for Genetic Disorders of Obesity, and the Gender Medicine Program. Genetics physicians and counselors from Baylor also staff joint clinics with other departments, such as otolaryngology (otogenetics), neurology (neurogenetics/tuberous sclerosis) and plastic surgery (craniofacial/craniosynostosis clinics).

As a result of the rapid advances in therapies for metabolic and skeletal diseases, the Metabolic Genetics and the Skeletal Dysplasia clinics now have over 200 patients on chronic enzyme replacement and/or infusion therapies.

Clinical Genetics Patient Volume (Adult)



Adult Genetics

Our adult genetics service is one of the largest in the country providing inpatient and outpatient care and genetic counseling exclusively for adult patients at three different locations: Baylor Medicine at the McNair Campus, the Harris Health System's Smith Clinic, and the Michael E. DeBakey Veterans Affairs Medical Center. The service also sees patients virtually though the Consultagene Clinic. We see patients for a wide variety of indications

including, but not limited to, intellectual disability, neurological conditions, cardiovascular conditions, connective tissue disorders and personal or family history of cancer.

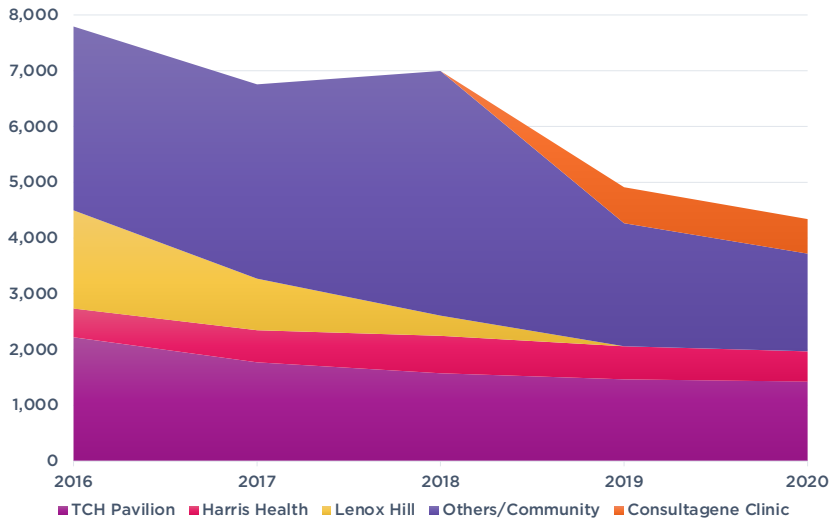
In addition to the general genetics clinics, we also have a specialized Ehlers-Danlos Syndrome Clinic, a Metabolic and Genetic Disorders of the Bone Clinic and a Cardiomyopathy Clinic.

Prenatal Genetics

As the largest of its kind in the U.S., the Baylor Prenatal and Reproductive Genetics Clinic at Texas Children's Pavilion for Women, and its five associated Texas Children's community maternal-fetal medicine clinics, is comprised of physicians and genetic counselors that specialize in prenatal and reproductive genetic risk assessment and the latest genetic testing technologies. Through its partnership with the department and the Texas Children's Fetal Center, the clinic offers world-renowned clinical and research expertise in prenatal and reproductive genetic screening and diagnostic testing and counseling.

Prenatal and reproductive genetic counseling is also available virtually at the Consultagene Clinic.

Clinical Genetics Patient Volume (Prenatal)



Graduate Program

Rigorous Training is Essential for Tomorrow's Genetic Discoveries

The Genetics & Genomics Graduate Program provides outstanding educational opportunities for students who wish to pursue a career in the broad and exciting field of genetics. The inaugural class of the program matriculated in 2019. We started the 2020-2021 academic year with 106 students enrolled in the program.


Dr. Gad Shaulsky in his laboratory

Students are trained by first-class researchers in an unmatched collaborative environment. "Collaborations between different types of researchers prepare our trainees for the challenges of modern biomedical research," said Dr. Gad Shaulsky, professor of molecular and human genetics and the director of the program. "These collaborations are greatly facilitated by easy access to large genome sequencing and diagnostic datasets that are not available to graduate students elsewhere."

In addition to their work in genetics, graduate students receive rigorous training in modern biology, bioinformatics, DNA replication and repair and other diverse fields. They also participate in cutting-edge research and publish their work in the most respected peer-reviewed scientific journals in the world.

Awards and Special Recognition for Genomics & Graduate Program Students

Varduhi Petrosyan was recognized by the Baylor College of Medicine School of Biomedical Sciences as an Outstanding Teaching Assistant in a Quantitative & Computational Biosciences Graduate Program

Stephanie Coffin, Nhung Pham, and Thomas Ravenscroft were recognized by the Baylor College of Medicine School of Biomedical Sciences as an Outstanding Teaching Assistant by the Genetics and Genomics Graduate Program Program

Grant Mangleburg received an F30 Fellowship from the National Institute of Neurological Disorders and Strokes

Moez Dawood, Shelley Gibson, Hamin Lee, Morgan Stephens, Nicole Wang, and Adam Weinstein were recipients of 2020 John J. Trentin Scholarship Awards

Genetic Counseling Program

Promoting excellence in the practice of genetic counseling

Under the School of Health Professions, the Baylor College of Medicine Genetic Counseling Program was established with the financial and logistical support of the Department of Molecular and Human Genetics.

The 22-month master of science degree program was accredited in 2018 by the Accreditation Council for Genetic Counseling. The program provides students a transformative education in genomic medicine and the practice of genetic counseling. The outstanding clinical, laboratory and research faculty empowers graduates to be empathic professionals with effective critical thinking skills. Clinical rotations include a variety of genetics clinics at Baylor Medicine at McNair Campus, Texas Children's Hospital, the Michael E. DeBakey VA Medical Center, Texas Children's Pavilion for Women and the Children's Hospital of San Antonio, among others. The program currently has a total of 17 trainees and plans to welcome another 9 in July of 2021.

In June of 2020, the program graduated its inaugural class. The program has proven itself with 100 percent of its graduates passing the Accreditation Council for Genetic Counseling certification exam.

"The program has been even more rewarding than I expected. With so many clinical sites in the TMC, we have the opportunity to take what we learn in the classroom right into the clinic, where we serve a diverse patient population," said Hannah Helber, program alumna.

Genetic Counseling Program Class of 2020

Yoheved Gerstein
Alyssa Grygiel
Hannah Helber
Stacey Edwards
Emily Magness
Rachel Thomas
Heather Lucas
Farah Ammouri

Residency Programs and Clinical Laboratory Fellowships

Throughout the evolution of the Department of Molecular and Human Genetics, there has been a strong emphasis on training and education. Our residency and clinical lab fellowship programs began in 1987, and we have had hundreds of trainees graduate from our programs. There has been no higher priority in the department. The growth and development of the department and clinical enterprises are inextricably linked to the excellence of the trainees and our training programs.

Residency Programs

The Medical Genetics and Genomics Residency Programs at Baylor College of Medicine are designed to prepare individuals for an academic career by providing an integrated experience in both clinical and experimental genetics. Training activities in clinical genetics and research are coordinated through the Department of Molecular and Human Genetics. The programs prepare trainees to care for both pediatric and adult patients with cytogenetic, biochemical and developmental diseases. Residents also gain laboratory experience in a chosen area of medical genetics and genomics. After the completion of all programs, trainees are eligible for American Board of Medical Genetics and Genomics certification.

Our programs enjoy preeminence in the genetics community. They are approved by the Accreditation Council for Graduate Medical Education and supported by a training grant from the National Institute of General Medical Sciences.

Residency programs we offer:

- Medical Genetics and Genomics
- Pediatrics/Medical Genetics and Genomics
- Internal Medicine/Medical Genetics and Genomics
- Maternal-Fetal Medicine/Medical Genetics and Genomics Fellowship

Medical Biochemical Genetics Fellowship

This one-year training program provides additional training in the diagnosis and management of inborn errors of metabolism. Medical Biochemical Genetics fellows benefit from Baylor's vast laboratory and clinical genetics programs.

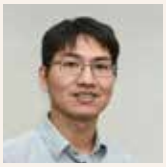
Clinical Laboratory Fellowship Programs

Genetics fellows train at Baylor College of Medicine's genetics diagnostic laboratory, Baylor Genetics, for 24 months. After that period, they are eligible for board certification by the American Board of Medical Genetics and Genomics.

Fellowships are offered in the following areas:

- **Laboratory Genetics and Genomics** is a newly-designed specialty that incorporates training in both molecular and cytogenetic techniques and interpretations into a single program.
- **Clinical Biochemical Genetics** is a specialty where trainees learn existing techniques practiced in the Biochemical Genetics Laboratory and practice writing interpretations for all tests performed in the laboratory.

2020 Graduating Class of Residents and Fellows



Chun-An Chen, Ph.D.
Laboratory Genetics and Genomics Fellowship

Hanyin Cheng, Ph.D.
Laboratory Genetics and Genomics Fellowship

Kevin Glinton, M.D., Ph.D.
Medical Biochemical Genetics Fellowship

Yehoshua "Josh" Manor, M.D.
Pediatric/Medical Genetics Residency

Nichole Owen, Ph.D.
Laboratory Genetics and Genomics Fellowship

Linda Rossetti, M.D.
Pediatric/Medical Genetics Residency

Brian Shayota, M.D., M.P.H.
Medical Biochemical Genetics Fellowship

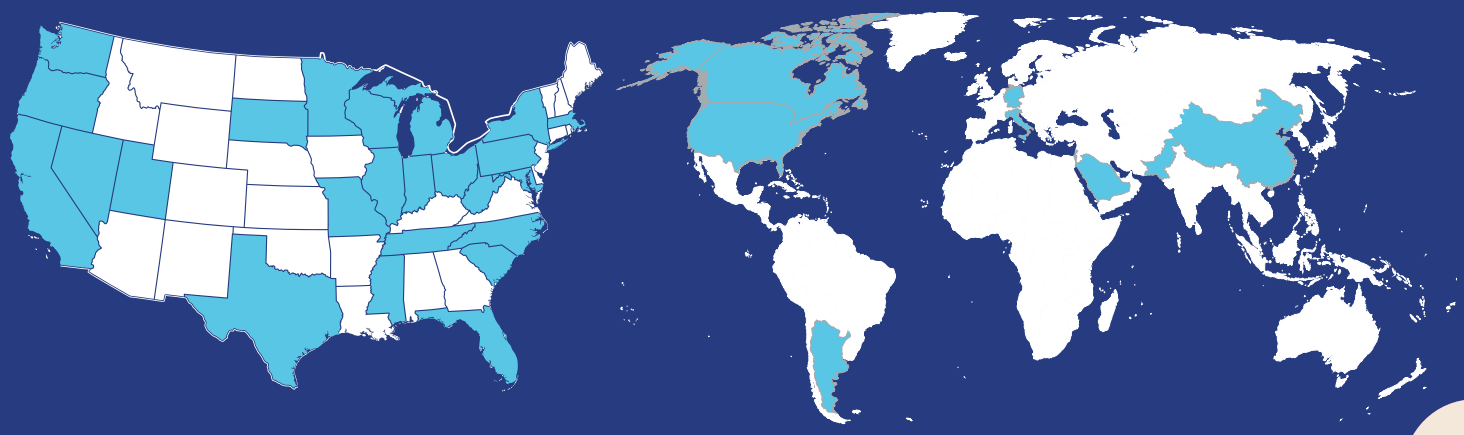
MHG Trainee Awards

Rebecca Markovitz, M.D., Ph.D.
Clinical Resident Award

Monika Weisz Hubshman, M.D., Ph.D.
Clinical Resident Award

Liesbeth Vossaert, Ph.D.
Laboratory Fellow Award

Locations of Former Medical Genetics Trainees



Community Engagement and Diversity

The Department of Molecular and Human Genetics's **Office of Community Engagement and Diversity** is now co-directed by Susan Fernbach, an assistant professor of molecular and human genetics, and Dr. Debra Murray, an assistant professor of molecular and human genetics. The MHG Diversity and Inclusion committee has grown to include the department's administrator, Laura Rosales, Ed.D., M.B.A., Dr. Graeme Mardon, the James R. Davis Chair in Pathology and Immunology and professor of molecular and human genetics, neuroscience and ophthalmology, and Dr. Chaya Murali, an assistant professor of molecular and human genetics.

Department faculty participating the Let's Learn About One Another Series

With a major contribution from Murray, the office built an expansive internal virtual library for the department that centers on diversity and inclusion. The library contains articles and statistics on systemic issues of health and educational equity and other resources.

Evenings with Genetics is a free community seminar series hosted by the department and Texas Children's Hospital. The series features a genetics faculty speaker paired with faculty from another specialty area plus a parent expert speaker at each seminar. The pandemic forced the series to convert to a webinar format, expanding its reach both nationally and globally. The in-person seminars and webinars held this year were attended by over 320 attendees consisting of family members, caregivers, healthcare providers and students. Topics that were covered included genetics of obesity, Turner Syndrome, genetics of cancer, Ehlers-Danlos Syndrome, non-invasive prenatal genetics and Tuberous Sclerosis Complex. To celebrate Rare Disease Day in February, an indoor event was held at Texas Children's, and the office collaborated on a separate outdoor event with the Texas Rare Action Network of the National Organization for Rare Disorders. In April, a **Children's Story Read Along** video series was hosted on our website to help ease the quarantine for children with special needs. This series, spearheaded by Dr. Sarah Elsea, professor of molecular and human genetics, included videos of about 30 children's books read by department faculty, staff, their families and friends, which included students from the Emery Weiner School in Houston. In July, the **From Stress to Strength** program was held as a webinar series with parallel tracks in English and Spanish, led by faculty and trainees from the department, Baylor Medicine Transition Medicine Clinic, the Menninger Department of Psychiatry and Behavioral Sciences and parent co-facilitators.

In collaboration with the UT Texas Center for Disability Studies and the Texas Department of State Health Services, **statewide genetic outreach** included a genetic conference held in El Paso in February with 50 attendees. Beginning in May webinars were held for healthcare providers, and the combined attendance for all five webinars was just shy of 500. We also recorded four other webinars in English and Spanish for community members.

The 2nd annual **Careers in Genetics and Genomics Lunch and Learn** with Baylor summer interns pivoted to a 3-webinar format for underrepresented high school and college students. The series featured medical geneticists, basic scientists, genetic counselors and trainee speakers and had a total of 72 attendees.

The **Let's Learn About One Another** series began this summer with six seminars about the African American experience. The series had a total of 45 attendees. In an effort to promote an inclusive culture, the series continued with short 15-minute interactive presentations (Understanding Climate Surveys, Identity, What is Systemic Racism) at the MHG Administration meeting, which is attended virtually every month by 30 administrative personnel in the department.

Faculty Awards and Recognitions

Bellen elected to National Academy of Sciences


Dr. Hugo Bellen

Dr. Hugo J. Bellen, professor of molecular and human genetics and neuroscience at Baylor and Howard Hughes Medical Institute investigator, has been elected to the prestigious National Academy of Sciences in recognition of distinguished and continuing achievements in original research.

He is one of 120 members elected this year to the National Academy of Sciences, a private, nonprofit institution. The group provides science, engineering and health policy advice to the federal government and other organizations.

In addition, Bellen is among 276 artists, scholars, scientists and leaders in the public, non-profit, and private sectors elected to the American Academy of Arts and Sciences for the class of 2020.

Bellen is one of the world's premier researchers in *Drosophila*, or fruit fly, genetics. His group has made major contributions to the understanding of nervous system development, synaptic transmission and mechanisms of neurodegeneration.

His current research focuses on the discovery of new rare human disease genes and elucidating the pathogenic mechanisms of neurodevelopmental and neurodegenerative diseases using fruit flies, in collaboration with human geneticists worldwide. His lab is the home of the Model Organism Screening Center for the Undiagnosed Diseases Network of the National Institutes of Health. He was also elected to serve as Vice President of the Genetics Society of America in 2020 and President of the Society in 2021.

Rosenberg honored with NIH Director's Pioneer Award


Dr. Susan Rosenberg

Dr. Susan Rosenberg has been awarded the National Institutes of Health Director's Pioneer Award, her second time winning the prestigious honor. She will develop new research on using proteins to prevent and slow DNA damage, protecting against cancer, Alzheimer's disease and aging-related diseases. She joins only four researchers who have received a second Pioneer Award since the program's inception in 2004.

"The hypothesis is that there are a small number of proteins that, if you had just a bit more of them, you could prevent DNA damage. We call this group of protective proteins the protectome," said Rosenberg, Ben F. Love Chair in Cancer Research and professor in molecular and human genetics, biochemistry and molecular biology, and molecular virology and microbiology at Baylor.

Rosenberg will work to discover "molecular-shield" proteins in *E. coli*. She will use this work as a basis to identify similar proteins in humans and to determine if those proteins can be harnessed, without harming other cell functions, for protection of cells from internal problems that lead to DNA damage. If it can be accomplished safely, Rosenberg hopes to develop therapeutics that would boost protectome proteins in cells and prevent DNA decay. She compares the idea to taking aspirin.

"People took it for years very successfully before anyone knew exactly what it did. But it fixes a lot of problems," said Rosenberg, leader of the Mechanisms in Cancer Evolution Program at the Dan L Duncan Comprehensive Cancer Center. "There may be proteins in all cells that are something like the aspirins of the cell. We hope to find them."

The research is based on the idea that cells behave in observable ways—a phenotype—that can be understood and treated, even without knowing the underlying genetic cause in every case. Rosenberg wants to develop a simple blood test that can detect the entropy phenotype in cells and determine whether a person is likely to be at risk for diseases caused by DNA damage. At-risk individuals could then be pointed to more preventative care and screenings.

Zoghbi awarded prestigious Lundbeck Brain Prize

Dr. Huda Zoghbi, professor and Howard Hughes Medical Institute Investigator at Baylor and director of the Jan and Dan Duncan Neurological Research Institute at Texas Children's Hospital, has been awarded what is considered one of the world's most

prestigious prizes in brain research, the Lundbeck Foundation Brain Prize.

Zoghbi is awarded along with Sir Adrian Bird from the University of Edinburgh, United Kingdom. Both are honored for their work in Rett syndrome that has led to a better understanding of the disorder and brought researchers closer to a treatment.

The Brain Prize, which includes research funding, is given once a year in recognition of a researcher's unprecedented contribution to international brain research. The recipient is nominated by their peers and decided on by a panel of the world's top neurological researchers.

Zogbhi's groundbreaking contributions to this research includes identifying the genetic mutation that causes Rett Syndrome, a developmental disease that strikes children, mostly girls, around 1 year old. They begin to regress, showing social withdrawal, loss of hand use and compulsive wringing of the hands, seizures and a variety of neurobehavioral symptoms. Children never recover and will remain developmentally disabled for the rest of their life.


Dr. Huda Zoghbi

The discovery of the Rett syndrome gene provided a straightforward diagnostic genetic test, allowing early and accurate diagnosis of the syndrome. It also revealed that mutations in MECP2 can cause a host of other neuropsychiatric features ranging from autism to juvenile onset schizophrenia. Further, it provided evidence that an autism spectrum disorder or an intellectual disability disorder can be genetic even if it is not inherited.

Her discovery opened up a new area of research on the role of epigenetics in neuropsychiatric phenotypes. Epigenetics is the study of changes in organisms caused by modification of gene expression rather than the genetic code. Zoghbi's use of an antisense oligonucleotide to lower MECP2 levels provides a potential therapeutic strategy for the MECP2 duplication syndrome and inspires similar studies for other duplication disorders.

Zoghbi was also named a 2020 Clarivate Citation Laureate. Clarivate Citation Laureates are researchers whose work is deemed to be 'of Nobel class,' as demonstrated by analysis carried out by the Institute for Scientific Information (ISI).

Yun named Pew-Stewart Scholar for Cancer Research

Dr. Jihye Yun, assistant professor of molecular and human genetics, member of the Dan L Duncan Comprehensive Cancer Center at Baylor and Cancer Prevention and Research Institute of Texas Scholar, is one of five early career scientists named to the 2020 class of the Pew-Stewart Scholars Program for Cancer Research. Yun's work focuses on decoding the molecular connection between sugary drinks and the development of colorectal cancer.

The Pew-Stewart Scholars Program for Cancer Research, presented by the Pew Charitable Trusts and Margaret Stewart Trust, supports cancer researchers working toward a cure for the complex disease. The five early career scholars who make up the 2020 class each receive a four-year grant to advance innovative research into the development, diagnosis and treatment of cancer.


Dr. Jihye Yun

Yun's previous research in this area has been published in the journal *Science*. She and her team found that consuming a daily modest amount of high-fructose corn syrup – the equivalent of people drinking about 12 ounces of a sugar-sweetened beverage daily – accelerates the growth of intestinal tumors in mouse models of the disease, independently of obesity.

Next, Yun and her team will work to identify the molecular mechanisms by which sugary drinks facilitate colon tumorigenesis. They will focus on how sugary drinks can alter gut bacteria and how this altered gut bacteria, in turn, can contribute to colon cancer development. Ultimately, Yun wants to identify sugar-specific bacteria or metabolites, which can serve as new targets for prevention and treatment for colon cancer patients.

Chao awarded Philip R. Dodge Young Investigator Award

Dr. Hsiao-Tuan Chao, assistant professor of pediatrics - neurology, molecular and human genetics and neuroscience at Baylor and researcher at the Dan and Jan Duncan Neurological Research Institute (NRI) at Texas Children's Hospital, was awarded the highly competitive 2020 Philip R. Dodge Young Investigator Award by the Child Neurology Society.

The Dodge award honors physician-scientists who are active members of the Child Neurology Society and who have made great strides in neuroscience research and advance the field of child neurology for the benefit of patients and their families.


Dr. Hsiao-Tuan Chao

Chao, a McNair Scholar, studies the genetic and neural mechanisms underlying neurodevelopmental and psychiatric disorders such as intellectual disability, epilepsy and autism. Her lab at the NRI integrates mechanistic studies of well-defined single gene disorders in fruit flies and mice with human genetics to decipher how genetic alterations perturb neuronal signaling in the brain.

Funding from the 2020 Philip R. Dodge Young Investigator Award will support her work focused on deciphering the molecular and cellular mechanisms governing excitatory and inhibitory neuronal signaling and understand the associated neural circuit alterations to disease. Chao's research will broaden our understanding of the transcriptional regulation of neural circuits and advance therapeutic strategies for neurodevelopmental and psychiatric disorders.

Burrage honored with the Young Investigator Award by The Society for Pediatric Research


Dr. Lindsay Burrage

Dr. Lindsay C. Burrage, assistant professor of molecular and human genetics, received the Society for Pediatric Research (SPR) 2020 Young Investigator Award. The prestigious Young Investigator Award was established by the SPR in 1983. The award recognizes a rising star with outstanding scientific research accomplishments that help to unravel the mysteries of childhood development or disease.

As a physician-scientist and clinical biochemical geneticist, Burrage has a long-standing interest in the pathophysiology of inborn errors of metabolism and their utility as models for more common disorders. She has a particular interest in the urea cycle disorders (UCDs). Burrage leads a clinical and laboratory-based program investigating long-term complications and new therapies for these disorders.

Burrage initiated and completed a study of human recombinant arginase therapy for lowering plasma arginine levels in neonatal and adult mouse models for arginase deficiency, a UCD associated with intellectual disability, seizures and spastic diplegia. This study led to the first clinical trial for a therapeutic agent specifically for individuals with arginase deficiency. She is currently an investigator in the UCD consortium of the NIH Rare Diseases Clinical Research Network. In this consortium, she leads a major project investigating novel biomarkers for liver disease in individuals with UCDs.

Also this year, Burrage was recognized by Baylor College of Medicine with a Norton Rose Fulbright Faculty Excellence Award for Teaching and Evaluation.

PROMOTIONS

Professor, tenured

Florent Elefteriou

Assistant Professor, non-tenure

Olga Dudchenko
Devon Fitzgerald
Kevin Glinton
Yanghong Gu
Jennifer Halliday
Andrew Jackson
Ning Liu
Chaya Murali

Instructor

Maria de Haro
Oguz Kanca
Pamela Luna
Nichole Owen
Junhyoung Park

More Awards and Recognitions for MHG Faculty

Dr. Joshua Shulman, associate professor of molecular and human genetics, neurology and neuroscience was selected by the American Neurological Association (ANA) for the 2020 Derek Denny-Brown Young Neurological Scholar Award.

Dr. Shweta Dhar, associate professor of molecular and human genetics, was elected to American College of Medical Genetics Board of Directors as Clinical Director for a six-year term beginning in 2021. Dr. Dhar was also a recipient of a 2020 Women of Excellence Award from Baylor College of Medicine.

Dr. Hamed Jafar-Nejad, associate professor of molecular and human genetics, was appointed to the nominations committee at the Society for Glycobiology.

Dr. Rodney Samaco, assistant professor of molecular and human genetics received Lab of the Year from the LouLou Foundation for his outstanding work on CDKL5 deficiency.

Dr. Gad Shaulsky, professor of molecular and human genetics was recognized by Baylor College of Medicine with the Barbara & Corbin J. Robertson, Jr. Presidential Award for Excellence in Education.

Susan Fernbach, B.S.N., assistant professor of molecular and human genetics was a recipient of Baylor College of Medicine's Clark Faculty Service Award.

Department Faculty Awards

Best Metabolic Attending
Dr. William Craigen

Best Pediatric Attending
Dr. Seema Lalani

Best Adult Attending
Dr. Jennifer Posey

Best Clinical Educator
Dr. Lindsay Burrage

Best Clinical Research Mentors
Dr. Brendan Lee
Dr. Allison Bertuch
Dr. Reid Sutton

Best Subspecialty Attendings
Dr. Allison Bertuch
Dr. Lisa Emrick

Best Genetic Counselor
Sandra Darilek, M.S., C.G.C.

Baylor Genetics Laboratory Service Awards
Dr. Linyan Meng
Dr. Qin Sun

Outstanding Graduate Teaching Awards
Dr. Andrew Groves
Dr. Daryl Scott

Kenneth Scott Graduate Mentor Award
Dr. Andrew Groves

2020 Rolanette and Berdon Lawrence Family Achievement Awardees
Dr. Shinya Yamamato
Patrick Hunt
Judi Coleman
Dr. Oguz Kanca

“Bad Project” highlighted in Forbes

In December 2020, Dr. Hui Zheng Lab’s “Bad Project (A Lady Gaga Parody)” made Forbes’ list of 10 Best Science Parody Music Videos. The video parody set to Lady Gaga’s Bad Romance won first prize in the video-live skit competition held at the 2011 department scientific retreat. It was subsequently released on YouTube where it became a viral sensation in the scientific community and has amassed over 4.7 million views.

https://www.youtube.com/watch?v=Fl4L4M8m4d0

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