

RGC COLLABORATIONS (30 ACTIVE)

The Regeneron Genetics Center's collaborations combine our genetics knowledge and sequencing capabilities with patient-consented genetic samples and deidentified clinical data to elucidate, on a large scale, genetic factors that cause or influence a range of human diseases. These agreements marry healthcare provider and academic expertise with translational follow up, in essence making data actionable.

We are seeking additional collaborations with leading health-care providers, academic researchers and government researchers who can contribute patient-consented samples, from volunteers, with well-annotated and deidentified clinical data. For more information, please contact rgc@regeneron.com.

Our current collaborations include:



BAYLOR COLLEGE OF MEDICINE

Regeneron is collaborating with Baylor College of Medicine (BCM) and the Human Genome Sequencing Center (HGSC) to study the genetic basis of Mendelian diseases in a unique collaboration of large-scale sequencing projects and functional genomics capabilities. The collaboration is conducting in-depth functional biology, leveraging Regeneron's VelociGene® technology, a genomic modification platform for creating genetically humanized models, to study gene function and mechanisms for candidate Mendelian disease genes discovered by BCM. The BCM-HGSC program has sequenced thousands of subjects as part of its Mendelian diseases program, resulting in the identification of disease causing mutations in hundreds of known and novel genes.

BOSTON CHILDREN'S HOSPITAL

The RGC is working with investigators at Boston Children's Hospital to identify mono-genetic variants that underlie very-early onset inflammatory bowel disease (VEO-IBD). Dr. Scott Snapper has been a pioneer in the study of the cellular and molecular mechanisms of mucosal immunity and host-microbial cross regulation, and their roles in gastrointestinal health and disease. Together investigators in the VEO-IBD consortium, including Dr. Aleixo Muise, have provided much of our basic understanding of the genetics of this disease condition. The collaboration will use whole exome sequencing and functional genomic techniques to identify novel causative protein-coding genetic variants in ~800 individuals with very-early onset inflammatory bowel disease and family members without the disease.

CHILDREN'S NATIONAL MEDICAL CENTER

The RGC is working with investigators at the Children's National Medical Center to identify the genetic basis of undiagnosed genetic diseases. Dr. Marshall Summar and colleagues have deep expertise in the diagnosis and management of genetic disease and run the largest clinical genetics service in the United States, serving over 8,000 new patients per year, of which ~2,000 remain undiagnosed following initial clinical evaluation. Initial studies will use whole exome sequencing and functional genomic techniques, including VelociGene® and other technologies, to understand the genetic causes of disease in previously undiagnosed children and adults with likely genetic disorders.

CLINIC FOR SPECIAL CHILDREN

Together with the Clinic for Special Children (CSC), the RGC is studying the genetic basis of rare pediatric disorders in the Amish and Mennonite populations. The collaboration is conducting whole exome sequencing and genetic analysis of several hundred trios and multiplex families per year, consented for genetics research through CSC. CSC has a strong history of genetic discovery: they have identified approximately eight new disease-causing mutations per year and presently care for patients representing approximately 150 different Mendelian diseases. It is the goal of the collaboration to continue to uncover many new disease-causing mutations underlying a broad range of conditions and disorders.

COLUMBIA UNIVERSITY MEDICAL CENTER

The RGC and Columbia University Medical Center are studying the genetic basis of familial forms of various diseases, including inherited cardiometabolic diseases, cancer predisposition and rare diseases. The collaboration spans exome sequencing and Mendelian disease gene discovery through functional genomics leveraging induced pluripotent stem cell technology and genetically humanized models of disease. Columbia's principal investigators, Drs. Wendy Chung and Rudy Leibel, have made seminal contributions to understanding the genetic and mechanistic basis of several inherited forms of diseases and have developed extensive resources for family based genetics studies. The collaboration has completed exome sequencing and genetic analysis of hundreds of families who have consented and enrolled in studies at Columbia University Medical Center.



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DUKE UNIVERSITY

The RGC is collaborating with the Duke Molecular Physiology Institute (DMPI) and the Duke Center for Applied Genomics & Precision Medicine (DCAGPM) to study the genetics of cardiovascular diseases and metabolism in the CATHGEN cohort using whole exome sequencing. The DMPI and DCAGPM have been leaders in cardiovascular disease genomics and metabolomics research. Among other questions, the collaboration plans to leverage the unique registries and biorepositories developed at Duke to explore the genetic determinants of extreme phenotypes (protective and resilience genes) in the context of cardiometabolic diseases.

ECOGENE 21

Ecogene-21 is a patient-centered non-profit organization conducting clinical and translational research of rare and extreme diseases as well as common conditions in the French Canadian population. Dr. Daniel Gaudet is a world-renowned geneticist who has made seminal contributions to the fields of genetic lipid disorders, metabolic syndrome and associated risks, and numerous clinical studies and academic projects involving the development of new innovative therapeutics. The RGC is collaborating with Dr. Gaudet and colleagues in various sequencing projects, initially including a study of modifier genes in familial hypercholesterolemia and other genetic lipid disorders and a survey of the population genetics and genetic architecture of the French Canadian founder population.

FEINSTEIN INSTITUTE

The RGC is collaborating with investigators at the Feinstein Institute to use whole exome sequencing to uncover the genetic cause of autoimmune disease. The collaboration will study over 400 multiplex families from the Multiple Autoimmune Disease Genetics Consortium (MADGC) and 800 families with rheumatoid arthritis (RA) from the North American Rheumatoid Arthritis Consortium (NARAC). Dr. Peter Gregersen has led several major consortia that have furthered our understanding of the genetic basis of autoimmune diseases such as RA, myasthenia gravis and myositis. Initial efforts will focus on understanding the genetic causes of autoimmune diseases in multiplex families harboring multiple autoimmune diseases (RA, systemic lupus erythematosus, autoimmune thyroid disease, inflammatory bowel disease, psoriasis, type 1 diabetes, multiple sclerosis), as well as sibling recurrence of RA.

GEISINGER HEALTH SYSTEMS

In 2014, Regeneron and Geisinger launched a large-scale initiative to sequence 100,000 consented participants, linking genomic data to de-identified electronic medical record (EMR) data to enable large-scale gene discovery at an unprecedented scale. Having sequenced nearly 50,000 participants by June of 2015, the collaboration has increased its long-term goal to sequencing 250,000 participants consented in Geisinger's MyCode project. The Geisinger Health System is one of the pre-eminent integrated health systems in the country serving nearly three million people in central Pennsylvania. Geisinger has long been a leader in EMR based analytics and research, being one of the first health systems to adopt EMRs in the country and a leader in clinical, genomic and epidemiological research through its involvement in the HMO Research Network, the eMERGE Consortium and numerous other research programs.

THE HOSPITAL FOR SICK CHILDREN

The RGC and the Hospital for Sick Children (SickKids) are collaborating to study the genetic determinants of infantile and pediatric onset cases of inflammatory bowel disease (IBD) through exome sequencing and analysis of thousands of families seen at SickKids and other institutions. Dr. Aleixo Muise and SickKids have established one of the leading IBD clinical and research centers in the world and have led the interNational Early Onset Paediatric IBD Cohort Study (NEOPICS), a SickKids' based initiative that brings together international pediatric gastroenterologists and scientists from around the world.

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INTERNATIONAL PSC GENOME PROJECT: MAYO CLINIC, UNIVERSITY OF KIEL, AND CURABLE

The RGC is collaborating with Curable, a non-profit research accelerator, Mayo Clinic, and the University of Kiel to conduct the International PSC Genome Project. The RGC aims to sequence 5,000 or more primary sclerosing cholangitis (PSC) patients as part of this project; Mayo Clinic and University of Kiel have contributed DNA samples from nearly 2,500 consented PSC patients and many more including primary biliary cirrhosis, healthy volunteers and inflammatory bowel disease (which is strongly associated with and has a high co-occurrence rate in PSC patients) to begin this project. Dr. Konstantinos Lazaridis is a leading clinician and researcher in this field and his Genomic Hepatobiology Laboratory at Mayo Clinic focuses on elucidating the genetic predisposition and the genetic-environmental interaction that contribute to the development and outcomes of chronic cholestatic liver diseases. This project will be the largest sequencing study in PSC to date and aims to identify functional variants of large effects on risk or protection from disease that may lead to actionable insights in genomic medicine and new therapeutic opportunities in PSC.

LOS ANGELES BIOMEDICAL RESEARCH INSTITUTE

The RGC is collaborating with Los Angeles Biomedical Research Institute at Harbor-UCLA and investigators in Taiwan (Taichung Veterans General Hospital, Triservices General Hospital and National Taiwan University Hospital) to conduct whole exome sequencing of Taiwanese individuals to elucidate the genetic basis of diabetes, cardiovascular disease and related traits in East Asians. The TAICHI (TAIwan metaboCHIp) study includes over 14,000 participants with acute and chronic presentations of these diseases, and TAICHI investigators in Taichung and Taipei have provided major contributions to the understanding of cardiometabolic disease traits. The collaboration will initially explore targeted analyses of genes of interest for cardiovascular and diabetes disease risk, and will also look at agnostic association studies to explore the genetic diversity of the Taiwanese population and identify genes underlying a broad range of disease-related traits.

LUND UNIVERSITY

The RGC is collaborating with Lund University in large-scale cardiovascular disease genetics studies. Dr. Olle Melander and Lund University designed and led the Malmo Diet and Cancer Study (MDCS), which includes over 28,000 participants, with a median follow-up of 14 years and extensive cardiometabolic phenotyping. The collaboration will use whole exome sequencing to initially explore targeted analyses of genes of interest for associations with cardiovascular disease risk and cardiometabolic traits, and will expand to other research opportunities afforded by the generation of a comprehensive exome sequence and phenotypic data set.

LUND UNIVERSITY AND HELSINKI UNIVERSITY

The RGC is collaborating with Dr. Leif Group, Lund University, and University of Helsinki to identify novel functional variants conferring risk or protection from type 2 diabetes through sequencing in the Botnia study. Dr. Group initiated the Botnia Study at the west coast of Finland, one of the world's largest family studies in type 2 diabetes. His research group has been involved in many of the genetic discoveries in type 2 diabetes during the past 15 years, including one of the first whole genome association studies for type 2 diabetes. The collaboration will sequence samples from thousands of Finnish and Swedish families with a high degree of familial aggregation of type 2 diabetes and extensive phenotyping across numerous cardiometabolic measurements and traits.

MARIONEGRI INSTITUTE

The RGC is collaborating with investigators at the Mario Negri Institute to study the genetic basis of inherited rare renal disorders. Dr. Giuseppe Remuzzi and colleagues have contributed to our fundamental understanding of the pathophysiology of hemolytic uremic syndrome and other causes of chronic kidney disease. Initial studies will utilize whole exome sequencing to understand the genetic basis of atypical hemolytic uremic syndrome, immunoglobulin-associated membranoproliferative glomerulonephritis and C3 glomerulopathy in individuals in whom known genetic factors have not been identified.

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NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASES (NIAID)

Primary immunodeficiencies are Mendelian diseases, which present usually at an early age. The genetic etiology for many of them is still unknown representing an attractive opportunity to identify genes important for immune system function as well as potential targets for novel therapeutics. This collaboration with Dr. Michael Lenardo's group at NIAID, National Institutes of Health, seeks to identify novel genes and pathways involved in uncharacterized immune dysregulation disorders, including primary immunodeficiencies, autoimmune disorders and severe atopic disease. As an international referral center for these rare diseases, DNA from probands and family members will be sequenced at the RGC and we will seek to identify causative genes. The teams will also work together to perform functional characterization of novel genes using cell-based (e.g., iPS cells from patients) and animal models.

NATIONAL INSTITUTE OF DIABETES AND DIGESTIVE AND KIDNEY DISEASES (NIDDK)

American Indians have extremely high rates of type 2 diabetes mellitus, diabetic nephropathy, and obesity, yet large-scale sequencing efforts to identify disease loci have not included individuals from this ethnic group. Therefore, coding variants that are unique or enriched in American Indians, which may identify new therapeutic targets for type 2 diabetes, diabetic nephropathy or obesity, remain largely unknown. This research project therefore will bring together the extraordinary clinical data on these conditions in American Indians with extensive genetics capabilities of Regeneron Genetics Center LLC (Regeneron). The NIDDK and Regeneron will analyze the clinical data with genetic sequence data to be generated by Regeneron with the goal of attaining better understanding of the genetic contributions to these conditions with the ultimate goal of finding better means to prevent and treat them.

NATIONAL INSTITUTE OF MENTAL HEALTH

The RGC and Dr. Francis McMahon's research program at the National Institute of Mental Health will evaluate the allelic architecture of several distinct Anabaptist founder populations including Amish from Holmes County, OH and Goshen, IN, Swiss-German Mennonites, and Dutch-German "Russian" Mennonites. Through drift, we expect some alleles of medical interest to be enriched in these populations thus enabling novel gene discovery. Initial studies will focus on bipolar disease, which Dr. McMahon has characterized extensively in these Anabaptist sects.

NHGRI UNDIAGNOSED DISEASES PROGRAM

Regeneron is collaborating with the National Institutes of Health Undiagnosed Diseases Program (UDP) to study the genetic basis of rare undiagnosed diseases evaluated at the NIH UDP. The collaboration is leveraging large sequencing databases at the NIH UDP and RGC capabilities to expand upon previous discoveries, and is conducting in depth functional biology, leveraging VelociGene® and other technologies to study gene function and mechanisms.

RAMBAM HEALTH CARE CAMPUS

The RGC is working with The Genetics Institute at Rambam Health Care Campus in Haifa, Israel to identify novel genes for undiagnosed disorders with Mendelian inheritance. Each year, the Rambam group evaluates hundreds of probands and families with rare undiagnosed diseases across a range of Middle-eastern ethnicities such as Ashkenazi Jewish, Iraqi Jewish, Muslim Arab and Druze. Due to founder effects and consanguinity, these rare undiagnosed diseases are more common in these populations and thus provide a unique opportunity to identify novel genes for a variety of medically relevant disorders such as neurodegenerative and metabolic syndromes, kidney, heart, endocrine, gastrointestinal, immunological and bone/skeletal diseases.

SCHNEIDER CHILDREN'S MEDICAL CENTER

The Schneider Children's Medical Center of Israel and Beilinson Hospital, Rabin Medical Center, is the largest children's hospital in Israel. This collaboration will sequence approximately 1,000 Israeli probands and family members with rare undiagnosed Mendelian disorders, including renal, endocrine, epilepsy, immunological and autoimmune, pulmonary, neurological, eye and hematological diseases. Patients will come from various founder ethnic groups such as Arab Muslims, Arab Christians, Bedouins, Druze and Jews of various origins, in which drift consanguinity enhance opportunities for novel gene discovery.

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UNIVERSITY HOSPITAL AND UNIVERSITY OF COPENHAGEN

The RGC is collaborating with Drs. Anne Tybjærg-Hansen and Børge G. Nordestgaard in genetic epidemiology studies and gene discovery projects across numerous diseases and traits of clinical importance. Drs. Tybjærg-Hansen and Nordestgaard initiated and lead several large cohort studies, including the Copenhagen General Population Study (GPCS), Copenhagen City Heart Study (CHS) and other disease specific cohorts, in total representing over 120,000 participants. Through these studies, the investigators have studied the genetics and epidemiology of all-cause mortality and various multifactorial diseases, including ischemic heart disease, ischemic stroke, cancer, chronic obstructive pulmonary disease, diabetes, obesity, gallstone disease, nonalcoholic fatty liver disease, dementia, aging signs, depression, schizophrenia, rheumatoid arthritis and others. Initial studies for the collaboration focus on lipids and atherosclerotic cardiovascular disease, gallstones and others.

UNIVERSITY OF CALIFORNIA AT SAN FRANCISCO

The RGC is collaborating with investigators at the University of California in San Francisco to use targeted sequencing to identify the genetic basis of autism spectrum disorder (ASD). Dr. Matthew State and colleagues have been leaders in the field of neuropsychiatric genetics, and have contributed to our fundamental understanding of the genetic basis of ASDs. The collaboration aims to further understand the basis of these diseases by using targeted sequencing of probable and high confidence ASD genes in ~17,000 individuals to uncover rare genetic variations that may contribute to risk for these diseases.

UNIVERSITY OF CONNECTICUT

The RGC and investigators at the University of Connecticut are using whole exome sequencing to study the genetic basis of keloids in Nigerians. Dr. Ernst Reichenberger and the University of Connecticut have established a robust research program for this disease in individuals of African descent that spans families to large populations. Initial studies will focus on the discovery of highly penetrant genetic variants underlying keloids in over 100 large Yoruba families, with follow-up studies aimed at uncovering the genetic factors predisposing to keloids in Yoruba cases and controls from the general population.

UNIVERSITY OF IOWA

The RGC is collaborating with investigators at the University of Iowa to study the genetic basis of inherited eye diseases using whole exome sequencing. Dr. John Fingert and colleagues at the University of Iowa have contributed major findings to the field of ocular disease genetics, from quantitative features of glaucoma to the genetic basis of optic nerve diseases leading to blindness. The collaboration will initially focus on the genetic basis of pigment dispersion syndrome and pigmentary glaucoma in families.

UNIVERSITY OF MARYLAND AND AMISH RESEARCH CLINIC

The Lancaster Old Order Amish are a founder population in whom the present-day population descended from approximately 300-400 individuals. This unique ancestral history has led to a distinct genetic architecture in which some rare disease-related genetic variants have become enriched in the present-day population through genetic drift. Thus, the Amish are highly desirable for novel gene discovery. The RGC is collaborating with colleagues at the University of Maryland to study a variety of complex diseases and traits including cardiovascular disease, hyperlipidemia, diabetes, osteoporosis and bone health, pulmonary function, longevity, general wellness and pharmacogenetics. DNA samples from as many as 8,000 Old Order Amish research participants will be exome sequenced to discover novel genotype-phenotype associations. In addition, modifier genes will be sought for cholesterol levels in subjects with Familial Defective Apolipoprotein B (R3500Q), which is markedly enriched in the Amish. Future studies will focus on genotype-targeted recruitment and deep phenotyping to unveil mechanisms underlying disease and related traits.

UNIVERSITY OF PENNSYLVANIA

The RGC and investigators at the University of Pennsylvania are working together to understand the genetic basis of cardiometabolic and other diseases using whole exome sequencing. Dr. Dan Rader and colleagues at the University of Pennsylvania have been at the forefront of genetic and translational studies of cardiometabolic disease, including lipid and lipoprotein metabolism, atherosclerosis and fatty liver disease. Initial studies will focus on cardiometabolic phenotypes extracted from electronic health records of over 11,000 participants in the Penn Biobank study, including coronary artery disease, diabetes and variability in laboratory traits.

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UNIVERSITY OF PENNSYLVANIA AND THE CENTER FOR NON-COMMUNICABLE DISEASES (CNCD)

The RGC is collaborating with investigators at the University of Pennsylvania and the Center for Non-Communicable Diseases where ongoing recruitment in Pakistani will provide DNA samples for exome sequencing of up to 40,000 patients with a number of disorders including coronary artery disease, type 2 diabetes, stroke, heart failure and chronic kidney disease. High rates of consanguinity in this population provides an unprecedented opportunity to identify individuals homozygous for rare loss-of-function variants causative of these and other diseases. A subset of the research volunteers have had extensive blood proteomic and metabolomics profiling, providing further opportunity to understand how genetic regulation of circulating proteins, many of which are amenable to therapeutic targeting with antibodies, contribute to disease.

UNIVERSITY OF TEXAS SOUTHWESTERN

The RGC is collaborating with investigators at the University of Texas Southwestern Medical Center to conduct whole exome sequencing of the entire Dallas Heart Study (DHS) cohort to identify genes that contribute to metabolic and other diseases. The DHS is a richly phenotyped, multi-ethnic, population-based sample of Dallas County consisting of approximately 5,000 adult men and women. The DHS has contributed to major genetic discoveries in the fields of lipids, fatty liver disease and other metabolic traits. The overall goal of the collaboration is to identify DNA sequence variants that confer protection from or susceptibility to metabolic diseases such as coronary heart disease, heart failure, fatty liver disease and numerous other traits represented in thousands of phenotypes measured in the DHS.

UNIVERSITY OF UTAH

The RGC and the University of Utah are studying the genetic basis of familial forms of various diseases leveraging the unique capabilities of the University of Utah and the ability to study large kindreds with aggregation of disease. The University of Utah Department of Human Genetics has been a leader in the field, contributing major genetic discoveries in cancer predisposition and other diseases, as well as to the development of advanced methods in genetic epidemiology and genome informatics. The collaboration will include large-scale sequencing and analysis of various cohorts, initially including lung diseases and rheumatologic disorders.