signal there was a problem has arguably harmed [his] students."

In a brief phone call, Pruitt, who has attributed the discovered problems to "data management" errors rather than misconduct, said he couldn't comment because he considers McMaster's investigation ongoing.

Over the past 15 years, Pruitt's star rose quickly—in 2018 he was named a Canada 150 Research Chair—with innovative findings on the behaviors of spiders and other animals. Many colleagues took advantage of Pruitt's offers to share field data on animals—information he said he or his lab members had collected. He has more than 170 research papers, according to Google Scholar.

In late 2019, behavioral ecologist Kate Laskowski at the University of California, Davis, was alerted to data problems, such as measurements that seemed to repeat themselves, in a paper she co-authored with Pruitt. She found issues with two more such papers, all of which were eventually retracted, and blogged about her experience.

Other Pruitt collaborators reviewed data from him, and additional papers were called into question. Many in the field found Pruitt's limited explanations lacking. "The extent of the problems is hard to reconcile with accidents," Daniel Bolnick, editor-in-chief of *The American Naturalist*, told *Science* in 2020. But public debate quieted after Pruitt hired a lawyer who sent letters to journal editors and co-authors advising against further retractions or public comments until any university investigations were complete.

Pruitt's Ph.D. adviser and mentor, Susan Riechert, now a UTK emeritus behavioral ecologist, had alerted the school's office of scientific integrity to the concerns about Pruitt's work, but she and others at the university say they had heard nothing further on the matter until DiRienzo tweeted on 11 November about the change in status for Pruitt's thesis. (A UTK spokesperson says: "The university is prohibited from disclosing student information, including the presence or absence of a research integrity investigation.")

A McMaster spokesperson declined to detail what happens next in its "process" but did say the Canada 150 Research Chairs funders had been contacted. Pruitt's position is tenured, and he may have an appeal process if found to have committed scientific misconduct or other fireable offenses. Many ecologists are anxious to learn what the McMaster probe found. "I think it's very important that science does get an answer and I wish that McMaster would be as open as they can possibly be," says Jeremy Fox of the University of Calgary, who has been involved in the scrutiny of Pruitt's data. ■

BIOMEDICINE

200,000 whole genomes made available for biomedical studies

UK Biobank offers easy access to genomic database for researchers around the world

By **Jocelyn Kaiser**

In the largest single release of whole genomes ever, the UK Biobank (UKBB) last week unveiled to scientists the entire DNA sequences of 200,000 mostly European people who are part of the long-term British health study.

The trove of genomes, each linked to anonymized medical information, will allow biomedical scientists to scour the full 3 billion base pairs of human DNA for insights into the interplay of genes and health that could not be gleaned from partial sequences or scans of genome markers. "It is thrilling to see the release of this long-awaited resource," says Stephen Glatt, a psychiatric geneticist at the State University of New York Upstate Medical University.

Other biobanks are also compiling vast numbers of whole genomes, 100,000 or more in some cases (see table, below), and the U.S. efforts have deliberately recruited much more ancestrally diverse participants. But UKBB stands out because it offers easy access to the genomic information, according to some of the more than 20,000 researchers in 90 countries approved to use the data.

"In terms of availability and data quality, [UKBB] surpasses all others," says physician and statistician Omar Yaxmehen Bello-Chavolla of the National Institute for Geriatrics in Mexico City.

Having enrolled 500,000 middle-age and elderly participants from 2006 to 2010, UKBB is one of the largest genetics research databases in the world. It proved its worth even before releasing whole genomes. Studies of specific DNA markers that vary among participants have revealed hundreds of new disease risk genes.

Since 2019 researchers have also been probing participants' exomes, the 2% of the whole genome sequence (WGS) that encodes proteins; the exomes from nearly all participants became available in the past 2 months. Exome studies are yielding risk genes that are very rare.

But whole genomes will make it possible to explore the influence of noncoding DNA, which controls when genes are turned off or on, and of gene rearrangements, as well as missing, repeated, or extra stretches of DNA in genes. Such changes play a role in diseases such as Huntington disease.

Iceland's deCODE genetics, now a subsidiary of Amgen, sequenced most of the 200,000 whole genomes released by UKBB, as part of an industry consortium that is helping cover the £200 million costs of the sequencing. The companies, eager to find drug targets, got a 9-month head start on using the WGS data. DeCODE reported initial findings this week in a bioRxiv preprint, among them variants in noncoding regions that influence height and the onset of puberty in girls.

Although researchers tapping into UKBB once had to download massive data sets onto their own computers, they can now log into a secure cloud-based computing environment. That will make it easier to collaborate and integrate different types of clinical and genetic data, UKBB says.

Bello-Chavolla's team expects to probe the newly released genomes and related health data for clues to metabolic diseases and aging, then follow up with studies of those genes in Mexicans. "This type of data availability is crucial for researchers in low- and middle-income countries," he says. ■

The whole truth

A number of efforts are releasing many thousands of whole genomes, with varying degrees of access, to accelerate biomedical research.

BIOBANK	COMPLETED WHOLE GENOMES	RELEASE INFORMATION
UK Biobank	200,000	300,000 more in early 2023
Trans-Omics for Precision Medicine	161,000	National Institutes of Health (NIH) requires project-specific consent
Million Veteran Program	125,000	Non–Veterans Affairs researchers get access in 2022
100,000 Genomes Project	120,000	Researchers must join Genomics England collaboration
All of Us	90,000	NIH expects to release by early 2022

200,000 whole genomes made available for biomedical studies

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