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Scientists Characterize Effects of Transplanted Fecal Microbiota:
Longitudinal study examines patients treated for recurrent Clostridium difficile infections

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Scientists at the Institute for Genome Sciences at the University of Maryland School of Medicine and physicians at Sinai Hospital, Baltimore, MD, have found that restoring the normal, helpful bacteria of the gut and intestines may treat patients suffering from recurrent *Clostridium difficile* infections. Transplanting fecal matter of healthy donors into patients with recurrent *C. difficile* infection (RCDI) appears to restore normal bacterial composition and resolve infection. The study findings appear in the November 26th issue of *PLOS ONE*.

C. difficile, one of the most common hospital-acquired infections, is responsible for a large fraction of antibiotic-associated diarrhea. The rate of RCDI after standard antibiotic therapy is about 20 percent, and is even higher in patients who receive additional antibiotic regimens. Morbidity and mortality due to RCDI, as well as associated healthcare costs, have been increasing in the recent years, and are linked to approximately 14,000 deaths annually and an estimated cost of \$800 million in the United States.

Patients with RCDI exhibit less diversity of beneficial gut bacteria, which may contribute to disease. Fecal microbiota transplantation (FMT) has recently gained attention as a viable treatment option for patients with RCDI because it aims to restore a normal, functional intestinal bacterial mix in the patient. FMT has been highly successful in treating RCDI. However, how FMT works is still not understood and long-term effects of FMT on the patient's microbiota have not been studied. The goal of this research study was to describe the immediate and long-term effects of FMT on the microbiome of patients with RCDI by applying a simultaneous sampling strategy of post-FMT patients and healthy donors as a control.

The investigators examined a large population of FMT patients and donors, which were sampled at multiple time points up to one year after the treatment at Sinai Hospital of Baltimore. Analyzing patients and donors over an extended period of time gave the investigators insights into how the microbiota continues to evolve long after FMT and the patients become asymptomatic for RCDI.

“New genomic tools and bioinformatic analysis methods are allowing us to better study the subtle changes of the microbiota in patients after FMT. This is especially important as we are only beginning to get an idea of whether FMT will permanently change the patient microbiota,” says W. Florian Fricke, Ph.D., Assistant Professor of Microbiology and Immunology at the Institute for Genome Sciences (IGS) at the University of Maryland School of Medicine and one of the lead authors of the paper. “Better insight into the microbiota events associated with the disease and FMT-induced recovery could lead to better treatments with a controlled,

manufactured microbiota instead of fecal material, which might also prove to be relevant as a treatment option for other microbiota-associated diseases in the future.”

“The key clinical question is related to the reoccurrence of *C. difficile* infection in a subgroup of patients. The long-term follow up of these patients is critical for genomic studies which will help us identify seminal changes in the bacterial microbiota of these patients,” said Sudhir K. Dutta, M.D., MACG, FACN, FACP, director of the Division of Gastroenterology, Sinai Hospital of Baltimore. “Insight into these microbial changes will hopefully identify biomarkers of susceptibility through this infection in this subgroup of patients.”

The patient cohort clinical analysis was conducted by Dr. Dutta and his gastroenterology department at Sinai Hospital, and included thorough individual case metadata. Dr. Fricke led the genomic and bioinformatics analysis at the Institute for Genome Sciences.

“This study helps underscore the importance of the microbiome in maintaining health and demonstrates that good bacteria play an integral role in immune defenses against disease,” says E. Albert Reece, M.D., Ph.D., M.B.A., Vice President for Medical Affairs at the University of Maryland and the John Z. and Akiko K. Bowers Distinguished Professor and Dean of the University of Maryland School of Medicine. “These findings also provide a potential therapeutic model for other diseases that have been linked to changes in the human intestinal microbiota, such as obesity and diabetes.”

The project was supported by a grant from the Weinberg Foundation, the Friedman and Friedman Group and private donors. The paper can be found at:
<http://dx.plos.org/10.1371/journal.pone.0081330>

About the Institute for Genome Sciences

The Institute for Genome Sciences (IGS) is an international research center at the University of Maryland School of Medicine. Comprised of an interdisciplinary, multidepartment team of investigators, the Institute uses the powerful tools of genomics and bioinformatics to understand genome function in health and disease, to study molecular and cellular networks in a variety of model systems, and to generate data and bioinformatics resources of value to the international scientific community. www.igs.umaryland.edu

About Sinai Hospital

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