Mission

Studies have linked an imbalance of the gut and the oral microbial communities with diabetes, obesity and immune-mediated disease. Given the role of inflammation in the development of cancer and chronic diseases, it is not surprising that links are being discovered that point to a significant role for gut and oral microbes in Cancer, HIV/AIDS, liver disease, allergy, arthritis and inflammatory bowel disease (IBD), among others.

The **mission** of the Microbiome/Bioinformatic/Gnotobiotic Animal Core is to provide state of the art technology for the identification and functional analysis of the complex microbial communities that have been shown to have a major impact on host metabolism and homeostasis.

Microbiome

To identify the microbes that make up complex communities (**microbiome**), **Dr. Casey Morrow's** laboratory collects and processes samples for DNA. Dr. Morrow's laboratory uses PCR with bar coded primers specific for the 16S rDNA region for amplification. The bar coded PCR products are sequenced using NextGen sequencing (GallX platform) by the **UAB CCC/CFAR Microarray core (Dr. Michael Crowley).**

Bioinformatics

The collection, management, analysis, integration, and reporting of microbiome sequence data are the responsibility of the Bioinformatics Core under the direction of
Dr. Elliot Lefkowitz.
The combined resources of the Molecular and Genetic Bioinformatics Facility (MGBF) of the UAB Center for AIDS Research and the Biomedical Informatics Component (BMI) of the UAB Center for Clinical and Translational Science, support the microbiome core. Together, the MGBF and BMI have provided a broad range of informatics services to UAB investigators for over 20 years. These services include provision of consultation and collaborative assistance on the collection and analysis of data derived from basic biomedical research (Bioinformatics) to clinical, outcomes, public health, and health services research (Clinical and Health Informatics). The available expertise includes the analysis of data derived from next generation

deep-sequencing technologies including whole genome and targeted DNA and RNA transcript sequencing. The Bioinformatics Core leverages this expertise to provide the full range of analytical resources necessary to support the analysis and understanding of data obtained from microbiome experiments.

For information derived from next generation sequencing technologies, including microbiome and metagenomic analysis, the core supports a variety of analytical and visualization tools. These tools include the Galaxy analytical framework (http://galaxyproject.org/) for both the storage and analysis of data; the Broad Integrated Genomics Viewer (IGV-http://www.broadinstitute.org/igv/) for visualization of assembled genomic sequences; and the QIIME tool suite (http://qiime.org/) for the analysis of microbiome sequence data. Our goal is not just to send the investigator a spreadsheet of the results of some analytical program, but to assist each investigator in better understanding the biological meaning of their data, allowing them to use that understanding to support publications, grants, and future research.

Gnotobiotic Animal Core

Understanding the role of the complex microbial communities in health and disease requires investigation of the interactions among genes of the microbiota and host. Essential to such research is the ability to manipulate and define the microbiota, i.e., develop defined-flora and “humanized” animal models, which requires gnotobiotic technology. Transplantation of human microbiomes into gnotobiotic mice, and generation and study of gnotobiotic mice with defined microbiota provides a means to study disease links and health implications of differences identified from the microbiome analysis.

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