PLoS Human Mircobiome Project Collection Manuscript Summaries

Collection Citation:

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Paper 1:

PLoS ONE: A Metagenomic Approach to Characterization of the Vaginal Microbiome Signature in Pregnancy

In parallel with the Human Microbiome Project, this study compared the vaginal bacterial biota in 24 pregnant women to that of 60 non-pregnant women (HMP subjects) using broad-range 16S rRNA-based metagenomics. There are few studies that have examined the vaginal bacterial biota using this robust approach. The authors conclude that there is a unique microbial signature in pregnancy marked by decreased species richness and diversity, and note several operational taxonomic units (OTUs) that are either overrepresented or underrepresented in pregnant women. Given this data, it appears that the vaginal microbial community is distinctly structured in pregnancy, which represents an important finding.

Citation: Aagaard K, Riehle K, Ma J, Segata N, Mistretta T-A, et al. (2012) A Metagenomic Approach to Characterization of the Vaginal Microbiome Signature in Pregnancy. PLoS ONE 7(6): e36466. doi:10.1371/journal.pone.0036466

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Competing Interest Statement: The authors have declared that no competing interests exist.

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FOR A PRESS-ONLY PREVIEW OF THE FULL ARTICLE, VISIT THE FOLLOWING URL:

http://www.plos.org/media/press/2012/pone-07-06-aagaard.pdf

Paper 2:

PLoS ONE: Complex Carbohydrate Utilization by the Healthy Human Microbiome

Do available nutrients direct the colonization by microbes, or do microbes adapt to the nutrients that are available? This study looks at the expression of carbohydrate active enzymes (CAZymes) from microbial populations from several (12) different sites in the human body, and finds evidence to support the idea that the microbes that colonize each site do so because of the sugars available. These authors find there is considerable variation in the presence of enzymes for carbohydrate metabolism from site to site, and propose that local carbohydrate composition may be one of the major driving forces that shapes each of the microbial sub-communities of the human microbiome.

Citation: Cantarel BL, Lombard V, Henrissat B (2012) Complex Carbohydrate Utilization by the Healthy Human Microbiome. PLoS ONE 7(6): e28742. doi:10.1371/journal.pone.0028742

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http://www.plos.org/media/press/2012/pone-07-06-cantarel.pdf

Paper 3:

PLoS ONE: A case study for large-scale human microbiome analysis using JCVI's Metagenomics Reports (METAREP)

This paper describes the newest updates made on already published JCVI's metagenomics open source software, METAREP. The new improvements increase the functionality of the software for more effective querying, browsing and comparison of extremely large volumes of metagenomic annotations derived from multiple samples. It also includes improvements in the data model to allow dynamic weighting of annotations, visualization, and statistical analysis. In several scenarios, the authors demonstrate how the updated version of METAREP can be used to effectively answer questions relating to the human microbiome. Additional information about the software and data is available at www.jcvi.org/hmp-metarep.

Citation: Goll J, Thiagarajan M, Abubucker S, Huttenhower C, Yooseph S, et al. (2012) A Case Study for Large-Scale Human Microbiome Analysis Using JCVI's Metagenomics Reports (METAREP). PLoS ONE 7(6): e29044. doi:10.1371/journal.pone.0029044

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http://www.plos.org/media/press/2012/pone-07-06-goll.pdf

Paper 4:

PLoS ONE: A Core Human Microbiome as Viewed Through 16S rRNA Sequence Clusters

This study examined the richness of microbial communities from multiple sites on the human body, looking at over 200 healthy individuals and 18 different body sites. The authors used hypervariable regions of a ribosomal RNA gene (16S) to understand which bacteria were living on and in the human body. Healthy individuals harbor thousands of different kinds of bacteria. Not surprisingly, different body sites harbor different communities, with skin and vaginal samples having fewer kinds of bacteria than the mouth, and the gut showing the greatest richness. But even for a given body site, different people have very different communities, not only in which bacteria are present but also in how abundant those bacteria are, ranging from dominant to undetectable. For instance, bacteria with the same name found throughout the mouth actually represent multiple subtypes with distinct preferences for different locations in the mouth. Even the enterotypes previously identified in the human gut represent a broad spectrum of communities, blurring distinct categories. Overall, the authors found that while there are a few "core" bacteria found in most healthy people, the closer we look, the more variation we find in the microbiome of healthy humans.

Citation: Huse SM, Ye Y, Zhou Y, Fodor AA (2012) A Core Human Microbiome as Viewed through 16S rRNA Sequence Clusters. PLoS ONE 7(6): e34242. doi:10.1371/journal.pone.0034242

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Competing Interest Statement: The authors have declared that no competing interests exist.

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http://www.plos.org/media/press/2012/pone-07-06-huse.pdf

Paper 5:

PLoS ONE: Host genes related to Paneth cells and xenobiotic metabolism are associated with shifts in human ileum-associated microbial composition

The findings in this study build upon recent human genetic data pointing to the Paneth cell as a key player both in regulating the gut microbiota and in the pathogenesis of Crohn's disease. The research provides data correlating changes in expression of Paneth cell genes and genes involved in xenobiotic metabolism with shifts in the gut microbome, comparing patients with Crohn's disease or Ulcerative colitis with healthy controls. The data are very much in line with the evolving concept of dysbiosis as a major contributing factor in the pathogenesis of inflammatory bowel disease.

Citation: Zhang T, DeSimone RA, Jiao X, Rohlf FJ, Zhu W, et al. (2012) Host Genes Related to Paneth Cells and Xenobiotic Metabolism Are Associated with Shifts in Human Ileum-Associated Microbial Composition. PLoS ONE 7(6): e30044. doi:10.1371/journal.pone.0030044

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Competing Interest Statement: The authors have declared that no competing interests exist.

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http://www.plos.org/media/press/2012/pone-07-06-li.pdf

Paper 6:

PLoS ONE: Inflammatory bowel diseases phenotype, C. difficile and NOD2 genotype are associated with shifts in human ileum associated microbial composition

These authors examine the correlation between host immune expression and microbial composition by comparing patients with inflammatory bowel diseases to healthy controls. They find evidence suggesting that inflammatory bowel diseases phenotype, concomitant clostridia difficile infection and NOD2 genotype, a genetic risk factor for the development of Crohn's disease, affect the composition of the microbes inhabiting the gut lining.

Citation: Li E, Hamm CM, Gulati AS, Sartor RB, Chen H, et al. (2012) Inflammatory Bowel Diseases Phenotype, C. difficile and NOD2 Genotype Are Associated with Shifts in Human Ileum Associated Microbial Composition. PLoS ONE 7(6): e26284. doi:10.1371/journal.pone.0026284

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Competing Interest Statement: The authors have declared that no competing interests exist.

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http://www.plos.org/media/press/2012/pone-07-06-li2.pdf

Paper 7:

PLoS ONE: Analyses of the Microbial Diversity across the Human Microbiome

This manuscript describes the application and development of statistics to describe the diversity of microbial communities associated with the human body. Using 16S rRNA gene sequences that were collected as part of the Human Microbiome Project, the authors identify the long tail in rank abundance curves that are typical to microbial communities and develop a statistic called the Tail Statistic. This statistic is proposed as a means to measure the impact of low-abundance taxa on microbial diversity.

Its application to diversity estimation revealed a greater range of values recovered between individuals versus body habitats, contrasting patterns of diversity within habitats, and that low abundant taxa serve as an important reservoir of genetic diversity in the human microbiome

Citation: Li K, Bihan M, Yooseph S, Methe´ BA (2012) Analyses of the Microbial Diversity across the Human Microbiome. PLoS ONE 7(6): e32118. doi:10.1371/journal.pone.0032118

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http://www.plos.org/media/press/2012/pone-07-06-methe.pdf

Paper 8:

PLoS ONE: Optimizing Read Mapping to Reference Genomes to Determine Composition and Species Prevalence in Microbial Communities

Optimizing Read Mapping to Reference Genomes to Determine Composition and Species Prevalence in Microbial Communities This paper describes the testing of six different sequence alignment tools and optimizes the parameters for aligning metagenomic WGS reads against reference databases to obtain accurate, sensitive and rapid identification of microbial species, as well as their relative abundance in a given sample. This work will be of considerable interest to others working with metagenomic data and provides valuable insight into the effects of next-generation read mapping tools, mapping strategy and database bias on metagenomics studies.

Citation: Martin J, Sykes S, Young S, Kota K, Sanka R, et al. (2012) Optimizing Read Mapping to Reference Genomes to Determine Composition and Species Prevalence in Microbial Communities. PLoS ONE 7(6): e36427. doi:10.1371/journal.pone.0036427

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http://www.plos.org/media/press/2012/pone-07-06-mitreva.pdf

Paper 9:

PLoS ONE: Novel Bacterial Taxa in the Human Microbiome

This manuscript by Wylie et al., reports on the identification of novel, low abundance bacterial taxa in human gut microbiome samples using a combination of 16S rDNA-amplicon and direct metagenomic shotgun sequencing strategies. The authors deploy a stringent combination of filtering steps to distinguish novel taxa from chimeras and other false positives. This revelation is fundamentally important as it portrays the breadth of potential gut species more realistically. The observed findings and methodology will be important to interpreting the data that is emerging from the ongoing Human

Microbiome Project (from gut and other body sites) and will also provide validated targets for culturing strategies aimed at isolating these rare species.

Citation: Wylie KM, Truty RM, Sharpton TJ, Mihindukulasuriya KA, Zhou Y, et al. (2012) Novel Bacterial Taxa in the Human Microbiome. PLoS ONE 7(6): e35294. doi:10.1371/journal.pone.0035294

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http://www.plos.org/media/press/2012/pone-07-06-truty.pdf

Paper 10:

PLoS ONE: Evaluation of 16S rDNA-based community profiling for human microbiome research

This manuscript evaluates the effect of molecular and bioinformatic protocols, sequence technologies and data quality on accurate determination of community composition, taxonomic classification and richness estimation. The HMP data generating centers exhaustively sequenced a defined synthetic community and select clinical samples as they developed and validated the protocols used for the HMP. The data and analysis described provide a useful resource for benchmarking existing and future studies.

Citation: Jumpstart Consortium Human Microbiome Project Data Generation Working Group (2012) Evaluation of 16S rDNA-based community profiling for human microbiome research. PLoS ONE 7(6): e39315. doi: 10.1371/journal.pone.0039315

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Paper 11:

PLoS ONE: Sequence Analysis of the Human Virome in Febrile and Afebrile Children

In the manuscript "Sequence analysis of the human virome in febrile and afebrile children", Wylie et al. provide a comprehensive characterization of viruses detected in nasopharyngeal and plasma samples from children with and without febrile illness. The authors use two high-throughput sequencing platforms with multiple permutations of library preparation to develop a strategy for viral discovery and characterization in what can be very difficult low viral load samples. They find that children with unexplained fever have a greater viral load and diversity than children with without fever, identifying the presence of both expected and unexpected viruses. Overall, this is a novel and important paper for extending the meta-virome and next generation sequencing approaches to defining human pathogen diversity.

Citation: Wylie KM, Mihindukulasuriya KA, Sodergren E, Weinstock GM, Storch GA (2012) Sequence Analysis of the Human Virome in Febrile and Afebrile Children. PLoS ONE 7(6): e27735. doi:10.1371/journal.pone.0027735

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http://www.plos.org/media/press/2012/pone-07-06-wylie.pdf

Paper 12:

PLoS Computational Biology: Metabolic reconstruction for metagenomic data and its application to the human microbiome

The authors describe a pipeline and method for examining the metabolic functions of a microbial community. Rather than analyzing and organizing sequencing data with an aim to identifying the microbes themselves, they focus on the networks of genes that are expressed. They find that different microbial communities at different sites on the body are specialized for different metabolic requirements. This technique will be valuable for understanding how our microbial inhabitants influence human health and development.

Citation: Abubucker S, Segata N, Goll J, Schubert AM, Izard J, et al. (2012) Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome. PLoS Comput Biol 8(6): e1002358. doi:10.1371/journal.pcbi.1002358

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http://www.plos.org/media/press/2012/pcbi-08-06-huttenhower.pdf

Paper 13:

PLoS Genetics: Diverse CRISPRs evolving in human microbiomes

The authors use data from the human microbiome project to investigate the microbes themselves, examining CRISPRs and CRISPR-associated genes, sequences involved in the microbes' own immune defense system. This is a timely and highly relevant study that expands the utility of the vast amounts of data gathered as a part of various microbiome analyses.

Citation: Rho M, Wu Y-W, Tang H, Doak TG, Ye Y (2012) Diverse CRISPRs Evolving in Human Microbiomes. PLoS Genet 8(6): e1002441. doi:10.1371/journal.pgen.1002441

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Paper 14:

PLoS ONE: Reducing the effects of PCR amplification and sequencing artifacts on 16S rRNA-based studies

These authors examine mock microbial samples to find the sources and rates of error in sequencing, and thereby false identification of novel taxons, in large-scale microbiome studies. They provide detailed recommendations for reducing bias and improving interpretation of microbial community data, which will undoubtedly serve as a valuable resource for researchers in this area.

DOI: doi:10.1371/journal.pone.0027310

Citation: Schloss PD, Gevers D, Westcott SL (2011) Reducing the Effects of PCR Amplification and Sequencing Artifacts on 16S rRNA-Based Studies. PLoS ONE 6(12): e27310. doi:10.1371/journal.pone.0027310

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