Experimental Approaches for Defining Functional Roles of Microbes in the Human Gut

The complex and intimate relationship between humans and their gut microbial communities is becoming less obscure, due in part to large-scale gut microbial genome-sequencing projects and culture-independent surveys of the composition and gene content of these communities. These studies build upon, and are complemented by, experimental efforts to define underlying mechanisms of host-microbe interactions in simplified model systems. This review highlights the intersection of these approaches. Experimental studies now leverage the advances in high-throughput DNA sequencing that have driven the explosion of microbial genome and community profiling projects, and the loss-of-function and gain-of-function strategies long employed in model organisms are now being extended to microbial genes, species, and communities from the human gut. These developments promise to deepen our understanding of human gut host–microbiota relationships and are readily applicable to other host-associated and free-living microbial communities.

General information
Publication status: Published
Organisations: Department of Systems Biology, Drug Resistance and Community Dynamics, Novo Nordisk Foundation Center for Biosustainability, Bacterial Cell Factories, CFB - Core Flow, Washington University School of Medicine, Yale School of Medicine
Contributors: Dantas, G., Sommer, M., Degnan, P. H., Goodman, A. L.
Pages: 459-475
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Annual Review of Microbiology
Volume: 67
ISSN (Print): 0066-4227
Ratings:
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 15.77 SJR 9.988 SNIP 3.845
Web of Science (2013): Impact factor 13.018
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Original language: English
Keywords: Microbiome, Flora, Metageonomics, Gain-of-function, Loss-of-function
DOIs: 10.1146/annurev-micro-092412-155642
Source: dtu
Source-ID: u:9790
Research output: Contribution to journal › Journal article – Annual report year: 2013 › Research › peer-review