

Two distinct metacommunities characterize the gut microbiota in Crohn's disease patients - DTU Orbit (09/11/2017)

Two distinct metacommunities characterize the gut microbiota in Crohn's disease patients

The inflammatory intestinal disorder Crohn's disease (CD) has become a health challenge worldwide. The gut microbiota closely interacts with the host immune system, but its functional impact in CD is unclear. Except for studies on a small number of CD patients, analyses of the gut microbiota in CD have used 16S rDNA amplicon sequencing. Here we employed metagenomic shotgun sequencing to provide a detailed characterization of the compositional and functional features of the CD microbiota, comprising also unannotated bacteria, and investigated its modulation by exclusive enteral nutrition (EEN). Based on signature taxa, CD microbiotas clustered into two distinct metacommunities indicating individual variability in CD microbiome structure. Metacommunity-specific functional shifts in CD showed enrichment in producers of the pro-inflammatory hexa-acylated lipopolysaccharide variant and a reduction in the potential to synthesize short chain fatty acids. Disruption of ecological networks was evident in CD, coupled with reduction in growth rates of many bacterial species. Short-term EEN elicited limited impact on the overall composition of the CD microbiota, although functional changes occurred following treatment. The microbiotas in CD patients can be stratified into two distinct metacommunities with the most severely perturbed metacommunity exhibiting functional potentials that deviate markedly from that of the healthy individuals with possible implication in relation to CD pathogenesis.

General information

State: Published

Organisations: Department of Biotechnology and Biomedicine, Disease Systems Immunology, The Sixth Affiliated Hospital of The Sun Yat-sen University, BGI-Shenzhen, The Second Affiliated Hospital of Nanjing Medical University

Authors: He, Q. (Ekstern), Gao, Y. (Ekstern), Jie, Z. (Ekstern), Yu, X. (Ekstern), Laursen, J. M. (Intern), Xiao, L. (Ekstern), Li, Y. (Ekstern), Li, L. (Ekstern), Zhang, F. (Ekstern), Feng, Q. (Ekstern), Li, X. (Ekstern), Yu, J. (Ekstern), Liu, C. (Ekstern), Lan, P. (Ekstern), Yan, T. (Ekstern), Liu, X. (Ekstern), Xu, X. (Ekstern), Yang, H. (Ekstern), Wang, J. (Ekstern), Madsen, L. (Ekstern), Pedersen, S. B. (Intern), Wang, J. (Ekstern), Kristiansen, K. (Ekstern), Jia, H. (Ekstern)

Number of pages: 43

Publication date: 2017

Main Research Area: Technical/natural sciences

Publication information

Journal: GigaScience

Volume: 6

Issue number: 7

ISSN (Print): 2047-217X

Ratings:

Web of Science (2017): Indexed Yes

Scopus rating (2016): CiteScore 4.87 SJR 4.06 SNIP 1.412

Scopus rating (2015): SNIP 1.181 SJR 3.201 CiteScore 8.64

Web of Science (2015): Indexed yes

Scopus rating (2014): SNIP 1.108 SJR 1.493 CiteScore 9.35

Scopus rating (2013): SNIP 0.855 SJR 1.538 CiteScore 3.56

Original language: English

Crohn's disease, Exclusive enteral nutrition, Gut microbe, Metagenomics

DOIs:

10.1093/gigascience/gix050

Source: FindIt

Source-ID: 2371777656

Publication: Research - peer-review › Journal article – Annual report year: 2017