A retrospective metagenomics approach to studying Blastocystis

Blastocystis is a common single-celled intestinal parasitic genus, comprising several subtypes. Here, we screened data obtained by metagenomic analysis of faecal DNA for Blastocystis by searching for subtype-specific genes in coabundance gene groups, which are groups of genes that covary across a selection of 316 human faecal samples, hence representing genes originating from a single subtype. The 316 faecal samples were from 236 healthy individuals, 13 patients with Crohn's disease (CD) and 67 patients with ulcerative colitis (UC). The prevalence of Blastocystis was 20.3% in the healthy individuals and 14.9% in patients with UC. Meanwhile, Blastocystis was absent in patients with CD. Individuals with intestinal microbiota dominated by Bacteroides were much less prone to having Blastocystis-positive stool (Matthew's correlation coefficient = -0.25, P <0.0001) than individuals with Ruminococcus- and Prevotella-driven enterotypes. This is the first study to investigate the relationship between Blastocystis and communities of gut bacteria using a metagenomics approach. The study serves as an example of how it is possible to retrospectively investigate microbial eukaryotic communities in the gut using metagenomic datasets targeting the bacterial component of the intestinal microbiome and the interplay between these microbial communities.

General information
State: Published
Organisations: Novo Nordisk Foundation Center for Biosustainability, iLoop, Department of Systems Biology, Center for Biological Sequence Analysis, Statens Serum Institut
Contributors: Andersen, L. O., Bonde, I., Nielsen, H. B., Stensvold, C. R.
Number of pages: 9
Publication date: 2015
Peer-reviewed: Yes
Early online date: 2015

Publication information
Journal: F E M S Microbiology Reviews
Volume: 91
Issue number: 7
Article number: fiv072
ISSN (Print): 0168-6445
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 12.68 SJR 7.063 SNIP 3.444
Web of Science (2017): Impact factor 11.392
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 13.54 SJR 7.779 SNIP 3.916
Web of Science (2016): Impact factor 12.198
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 13.38 SJR 7.689 SNIP 4.216
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 12.9 SJR 7.192 SNIP 4.116
Web of Science (2014): Impact factor 13.244
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 13.78 SJR 7.687 SNIP 4.274
Web of Science (2013): Impact factor 13.806
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 12.18 SJR 6.037 SNIP 3.869
Web of Science (2012): Impact factor 13.231
ISI indexed (2012): ISI indexed yes