Supplemental Content

Holmstroem RB, Dahl EK, Helms M et al. Tofacitinib and fecal microbiota transplantation in treating checkpoint inhibitor-induced enterocolitis – case report

Microbiology during the course
Stool cultures, rectal swaps, and mucus were checked at several timepoints during the course:

At admission, day 0:
Bacteria (stool): *Salmonella, Campylobacter, Shigella, Yersinia,* diarrheagenic *Escherichia coli*, and *Clostridioides difficile* – negative
Virus (stool): *Norovirus* – negative

Rechecked, day 13:
Bacteria (stool): *Clostridioides difficile, Escherichia coli, Salmonella, Campylobacter, Shigella*, and *Yersinia* - negative.
Parasites (stool): *Entamoeba histolytica, Giardia intestinalis, and Cryptosporidium* – negative.
Virus (stool): *Norovirus, rotavirus, and adenovirus* - negative

Rechecked, day 22:
Bacteria (stool): *Clostridioides difficile, Escherichia.coli, Cryptosporidium, Salmonella, Campylobacter, Shigella,* and *Yersinia* - negative.
Parasite (stool): *Entamoeba histolytica, Giardia intestinalis, and Gryptosporidium* – negative.
Virus (stool): *Norovirus, Rotavirus, Adenovirus, and Sapovirus* – negative.
Microbiome 18S for fungi, bacteria, and parasites - negative.
Mucus from the duodenum was checked for trophozoites – negative.

Rechecked, day 32:
Bacteria (rectal swap): *Clostridioides difficile*, *Enterotoxigenic Escherichia coli, Salmonella, Campylobacter, Shigella, Aeromonas, Verotoxin-producing Escherichia coli,* and *Yersinia* were negative.
Parasites (stool): *Entamoeba histolytica, Giardia intestinalis, and Cryptosporidium* – negative.
Virus (rectal swap): *Norovirus, Rotavirus, Adenovirus, and Sapovirus* – negative.
Microbiome 18S for bacteria and parasites - negative. Fungi showed Candida albicans – rechecked at day 33+41 - all negative.

Fecal microbiota

In this case report, we collected stool samples for fecal microbiota data before FMT and after every transplantation. In addition, the patient's stool was rechecked several times during the course for bacteria, viruses, and parasites (see above).

Stool samples were sent to the Department of Microbiology and Infection Control, Statens Serum Institut, Copenhagen, Denmark, for fecal microbiota analyses. Here, purified DNA was amplified using four primers targeting ribosomal 16S and 18S in prokaryotes (universal prokaryotic primers 341F/806R) and eukaryotes (primers G3F1/G3R1,G4F3/G4R3, and G6F1/G6R1), respectively. A k-

mer-based mapping software, BION, was used for mapping sequences. A specific evolutionary taxonomic group denoted the definition of a unique taxon. The methodology is described in Krogsgaard LR, et al. 2018.[1]

1 Krogsgaard LR, Andersen LO, Johannesen TB et al. Characteristics of the bacterial microbiome in association with common intestinal parasites in irritable bowel syndrome. Clin Transl Gastroenterol 2018; 9 (6): 161.