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1                   **Roles of the gut virome and mycobiome in faecal microbiota**  
2                   **transplantation**

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## 26 **Summary**

27 Faecal microbiota transplantation (FMT) is an innovative approach to treat  
28 diseases associated with a gut dysbiosis, by transferring a healthy stool  
29 microbiota to a diseased recipient. Beyond the bacteriome, the human gut  
30 also harbours diverse communities of viruses and fungi, collectively known  
31 as the virome and the mycobiome. The impact of these latter two microbiome  
32 components on success of FMT therapy has not been appreciated until very  
33 recently. We herein review the current literature on the effects of the gut  
34 virome and mycobiome in the FMT treatment of various diseases. We  
35 discuss both the beneficial effects and health concerns of the viral and fungal  
36 transfer during FMT. We particularly highlight the roles of bacteriophages  
37 (bacterial viruses) and *Candida* species (fungi) in FMT efficacy. We also  
38 summarise the intricate relationships between the gut virome, mycobiome,  
39 bacteriome, and host immunity, underlying FMT. Future efforts should be  
40 devoted to understanding the versatile roles as well as the therapeutic  
41 mechanisms of specific and/or combination of viral and fungal lineages in  
42 different diseases. Harnessing the gut virome, mycobiome, and bacteriome in  
43 combination and precision hold a promising prospect in future FMT- and  
44 microbiota-based therapies.

45

## 46 Introduction

47 A large number of diseases are characterized by compositional and  
48 functional changes in the gut microbiota. Faecal microbiota transplantation  
49 (FMT) is a gut microbiota restoration treatment, performed through oral, intra-  
50 intestinal or intra-colonic administration of donor faecal matter containing  
51 natural microbial consortia. It is well established that the bacterial microbiome  
52 (bacteriome) plays a prominent role in the pathogenesis of gastrointestinal  
53 tract (GI) diseases and affects the outcome of therapies.<sup>1,2</sup> Apart from  
54 bacteriome, the human gut contains diverse and largely under-explored  
55 communities of viruses and fungi.<sup>3,4</sup> Recent evidence suggests that the gut  
56 virome and mycobiome not only constitute a significant fraction of the total  
57 microbiome, but also work in synergy with the bacteriome to modulate host  
58 immunity and physiology.<sup>5,6</sup> Evidence on the roles of gut virome and  
59 mycobiome in FMT outcome is also accumulating.<sup>7-9</sup>

60

61 FMT has garnered substantial clinical and translational research interests.<sup>10,11</sup>  
62 It has broad applications across different diseases, both intra- and extra-  
63 intestinal diseases, including *Clostridioides difficile* infection (CDI), recurrent  
64 CDI (rCDI), inflammatory bowel diseases (IBD), graft versus host disease  
65 (GvHD), irritable bowel syndrome (IBS), obesity and diabetes.<sup>8-10,12-14</sup> While  
66 FMT was previously found comparable with the treatment of probiotics in  
67 efficacy when treating various diseases, it was recently demonstrated that  
68 autologous FMT, but not a multi-strain probiotic product, was effective in  
69 post-antibiotic restoration of microbiome in mice.<sup>15,16</sup> This is likely due to the  
70 fact that FMT transfers a complete and complex consortium of host-adapted  
71 microbial species, including bacteria, bacteriophages, fungi, as well as their  
72 metabolites, as opposed to a greatly simplified multi-strain bacteriotherapy.  
73 The efficacy of FMT has long been ascribed to the transfer of bacteria.<sup>10,11</sup>  
74 Compared to that, the roles of virome and mycobiome are relatively less  
75 studied and are yet to be fully emphasized.<sup>2,6,17-19</sup>

76

77 In this review, we aim to summarise relevant clinical, translational, and basic  
78 research evidence in the field to enhance the community's understanding of  
79 the roles of gut virome and mycobiome in FMT, to inform better clinical  
80 practice by incorporating the viral and fungal components of the gut  
81 microbiome into FMT regime, and in a broader context, to guide future  
82 development of microbiota-based therapies. We will discuss the roles of gut  
83 virome and mycobiome in FMT in conjunction with their functional  
84 importance, donor-recipient effect, as well as safety concerns, and highlight  
85 how they potentially impact treatment efficacy and host immunity during FMT.

86

## 87 Roles of gut virome in FMT

### 88 The human gut virome

89 The human gut virome is primarily comprised of prokaryotic viruses (mostly  
90 bacteriophages infecting bacteria, collectively known as 'phageome') and  
91 eukaryotic viruses (infecting humans), with bacteriophages of the order  
92 *Caudovirales* (tailed icosahedral viruses with dsDNA genomes) and the  
93 family *Microviridae* (small icosahedral viruses with ssDNA genomes) being  
94 most abundant (figure 1a).<sup>3,20–22</sup> Bacteriophages in the human GI tract have  
95 both temperate and lytic lifecycles, driving the bacteriome composition by  
96 prophage integration and lytic predation respectively.<sup>3,23</sup> Healthy human gut  
97 virome is dominated by temperate bacteriophages, while it shifts from  
98 temperate to lytic replication during host inflammation and stress.<sup>3,24</sup> Given  
99 the predominance of bacteriophages over eukaryotic viruses in the gut  
100 virome and its direct roles in regulating bacteriome composition and function,  
101 most gut virome research in humans has been focusing on the phageome.  
102 While a minority of eukaryotic viruses can cause serious infections, emerging  
103 data on a large diversity of gut-resident eukaryotic viruses show that they are  
104 somewhat capable of recapitulating the beneficial effects of commensal  
105 bacteria through different mechanisms involving host immunity.<sup>25,26</sup>  
106 Eukaryotic viruses can ameliorate gut inflammation in mice via viral RNA  
107 sensing by host Toll-like Receptors (TLRs)-3 and 7 and its downstream IFN-  
108  $\beta$  secretion, and antiviral treatment led to more severe colitis in dextran

109 sulfate sodium (DSS)-treated mice.<sup>27</sup> A recent study in mice also shows that  
 110 enteric eukaryotic viruses evoke broad and enduring host immune responses  
 111 resembling those elicited by the commensal bacteria.<sup>28</sup> These data suggest  
 112 that gut viruses play an important role in host immunity and homeostasis.

113

114 Gut viruses overall constitute a more diverse genetic entity than the gut  
 115 bacteria, with virus to microbe ratio (VMR) ranging from 1:1 to 10:1 in the  
 116 gut.<sup>29,30</sup> Human gut virome is highly diverse and immensely affected by  
 117 geography, ethnicity, diet, lifestyle and age (figure 1a, together accounting for  
 118 ~30% of gut virome variations).<sup>31,32</sup> Gut virome dysbiosis has been implicated  
 119 in the pathogenesis of a diversity of GI and extra-GI diseases, such as  
 120 IBD<sup>21,33</sup>, IBS<sup>34</sup>, CDI<sup>7,35</sup>, GvHD<sup>12,36</sup>, obesity and diabetes<sup>37,38</sup>, and FMT have  
 121 demonstrated a varying degree of success in treating these diseases.<sup>7,12,14,39–</sup>  
 122 <sup>42</sup> One commonly observed feature of the gut virome alterations in GI  
 123 inflammation-related diseases, including in CDI and IBD, is expansion of  
 124 *Caudovirales*, which was significantly decreased after FMT.<sup>7,21,33,35,43</sup> In a  
 125 DSS-induced colitis model of a mouse colony without colonisation of *E. coli*,  
 126 cocktail of *Enterobacteriaceae* bacteriophages, belonging to *Caudovirales*,  
 127 exacerbated intestinal inflammation and did not induce lysis of any  
 128 endogenous microbes.<sup>43</sup> This study corroborated that *Enterobacteriaceae*  
 129 phages alone were sufficient to elicit inflammatory responses without  
 130 engagement of *Enterobacteriaceae* or its constituent LPS. These data  
 131 highlight the importance of *Caudovirales* bacteriophages in gut homeostasis  
 132 and inflammation and that *Caudovirales* can be manipulated by FMT.

133

134

### 135 **Translational studies investigating FMT and virome**

136 Transfer and engraftment of viruses, along with bacteria, during naïve FMT  
 137 correlated with treatment outcome in difference diseases, including CDI, IBD,  
 138 GvHD following hematopoietic stem cell transplant (HSCT).<sup>7,12,44–47</sup> In a  
 139 seminal study conducted by Ott et al, the authors showed that sterile faecal  
 140 filtrate (containing viruses, as well as various metabolites and polymers, but

not bacteria) was sufficient for successful remission in patients with CDI<sup>48</sup>. Following that, a number of studies further emphasised the importance of gut viruses, beyond bacteria, in FMT therapies.<sup>7,14,48,49</sup> In recent years, a handful of sterile faecal filtrate and faecal viral transplantation (FVT) studies have emerged investigating the role of gut virome in disease therapeutics, including obesity, type 2 diabetes (T2D), necrotizing enterocolitis (NEC), small intestinal bacterial growth, and post-antibiotic microbiome dysbiosis.<sup>14,49–51</sup>

149

#### 150 ***FMT in CDI***

The efficacy of FMT in treating CDI is 90%, which is the most promising compared to its applications in other diseases.<sup>52–56</sup> In our pilot FMT study on patients with CDI (n=9; FMT was conducted via nasoduodenal infusion of donor stool from a healthy household individual to each patient), we found that the gut virome of CDI was characterized by a significant elevation in *Caudovirales* bacteriophages and a reduced virome diversity compared to healthy individuals.<sup>7</sup> After FMT, patients showed substantial viral transmission from donor to recipient.<sup>7</sup> Patients who were cured from CDI exhibited much higher engraftment rates of *Caudovirales* taxa derived from the FMT donor, than those who were not responsive to FMT.<sup>7</sup> Recently, a study on rCDI (n=9) showed that after FMT, the coding genes repertoire of the patients' gut virome was more similar to that of the donors' compared to their pre-FMT profiles, including KO (Kyoto encyclopedia genes and genomes Orthology) terms associated with viral replication, iron transporters, ssDNA phage assembly, and antimicrobial peptide resistance, paralleling the changes in their host bacteria after FMT.<sup>35</sup> This data indicates a potential functionality change in the gut virome of recipient along with the compositional changes in viral taxa after FMT. Concordantly, several studies reported that recipient viromes resembled those of their donors and remained stable after FMT.<sup>7,46,47</sup> Among these studies, one with longer follow-up showed that patients with CDI (n=14) showed a post-FMT gut virome profile similar to that of their donors for up to 1 year after FMT.<sup>47</sup>

173

174 **FMT in IBD**

175 The efficacy of FMT in treating IBD varies from ulcerative colitis (UC) to  
176 Crohn's disease (CD). A systematic analysis documented 53 studies that the  
177 overall FMT efficacy is around 36% in UC, 50.5% in CD and 21.5% in  
178 patients with pouchitis.<sup>57</sup> In patients with IBD, the faecal virome displayed  
179 increased richness of *Caudovirales* bacteriophages along with a decreased  
180 bacterial diversity (n=174; patients were from Cambridge, UK; Chicago, Los  
181 Angeles, and Boston, in USA).<sup>21</sup> At the intestinal mucosal level, patients with  
182 UC (n=91; three China cohorts) showed that the rectal tissues consistently  
183 had an expansion of *Caudovirales* bacteriophages compared with healthy  
184 individuals.<sup>33</sup> Phages of *Escherichia* and *Enterobacteria*, belonging to the  
185 order *Caudovirales*, were experimentally demonstrated to aggravate  
186 intestinal inflammation and colitis as a consequence of overproduction of  
187 IFN- $\gamma$  via TLR-9 signalling in the murine host<sup>43</sup>. These data together suggest  
188 that certain *Caudovirales* taxa play a crucial role in the disease course of  
189 IBD. However, the role of the phageome (particularly *Caudovirales*  
190 bacteriophages) in FMT therapies of IBD has not been thoroughly  
191 investigated to date, which warrants in-depth research.

192

193 An increased eukaryotic virome richness was also observed in faeces of  
194 patients with UC.<sup>44</sup> One pilot FMT study in UC patients (n=9) found that UC  
195 individuals who successfully responded to FMT contained a significantly  
196 lower eukaryotic virome richness (both before and after FMT) compared to  
197 non-responders.<sup>44</sup> This study indicates that a low baseline eukaryotic viral  
198 richness might be important for a successful FMT in UC, albeit the  
199 mechanism is lacking. Overall, the role of viral engraftment and virome  
200 alterations in FMT therapies targeting IBD is still in its infancy and represents  
201 an area of particular interest.

202



### 203 ***FMT in GvHD***

204 Limited studies have found some effectiveness of FMT in treating GvHD,  
 205 though the overall efficacy is lacking.<sup>12,58</sup> Patients with GvHD following HSCT  
 206 manifested significant GI symptoms and showed a persistent dominance of  
 207 eukaryotic viruses (anelloviruses, herpesviruses, papillomaviruses and  
 208 polyomaviruses) in the gut.<sup>36</sup> Among them, picobirnaviruses were determined  
 209 as a predictive marker for the development of severe GvHD.<sup>36</sup> In a single  
 210 case study, a GvHD patient was treated with 4 episodes of FMT.<sup>12</sup> Following  
 211 treatment, an increase in faecal virome diversity was observed, accompanied  
 212 by expansion of *Caudovirales* bacteriophages and shrinkage in the  
 213 eukaryotic Torque teno viruses.<sup>12</sup> Consistent with FMT effects on virome  
 214 reported in CDI, the transfer of *Caudovirales* bacteriophages also underpins  
 215 a positive treatment outcome in GvHD.<sup>7,12</sup> Future research with expanded  
 216 sample sizes is needed to convincingly address the therapeutic effect of FMT  
 217 and virome modulations in GvHD.<sup>58,59</sup>

218

### 219 ***Faecal viral transplantation (FVT) in other disease indications***

220 As viruses are co-transferred alongside bacteria during naïve FMT, the role  
 221 of viruses is fastidious to tease apart from that of bacteria in treating disease.  
 222 Two pilot case series studies (n=5 and 4) explored the effect of sterile faecal  
 223 filtrate in treating CDI, a refined FMT protocol where the bacteria were filtered  
 224 out.<sup>48,60</sup> This study showed that sterile faecal filtrate restored normal stool  
 225 habits and eliminated symptoms of CDI, suggesting a possible role of  
 226 bacteriophages and viruses (as a prominent component of sterile faecal  
 227 filtrate) in the therapeutic mechanism of FMT. However, caution should be  
 228 taken when interpreting these studies considering that the biological effect of  
 229 sterile faecal filtrate is not solely attributed to the viral microbiota *per se*,  
 230 where the metabolites, digested micro-nutrients, extracellular active  
 231 ingredients (such as viral envelope, bacterial cell wall components and  
 232 antimicrobial peptides) are also present in sterile faecal filtrate.

233

234 Following that, more studies have employed a further refined protocol, FVT,  
 235 to specifically investigate the effect of faecal viruses in treating diseases,  
 236 where faecal virus-like particle (VLP) are isolated, purified, and enriched.<sup>14,49–</sup>  
 237 <sup>51</sup> In a piglet model of preterm infants, Brunse et al. showed that orally  
 238 administrated FVT successfully prevented the development of necrotising  
 239 enterocolitis (NEC) in all preterm piglets that received FVT, whereas FMT did  
 240 not perform better than the control arm, indicating that a gut virome transfer  
 241 and modification might be critical in preventing the development of NEC.<sup>50</sup>  
 242 Following antibiotic-mediated disruption of the bacteriome in human patients,  
 243 rapid restoration of the depleted microbiota might confer significant health  
 244 benefits.<sup>49</sup> Probiotics were shown to be not only ineffective in post-antibiotic  
 245 restoration of the gut microbiome, but sometimes even leading to impaired  
 246 microbiome recovery<sup>15,16</sup>. In contrast to that, a study investigated the effect of  
 247 autologous FVT (harvested prior to antibiotics perturbation) in mice reported  
 248 a better gut bacteriome recovery after antibiotic perturbation, compared to  
 249 the control treatment.<sup>49</sup> More recently, a study reported the effect of FVT in  
 250 treatment of type 2 diabetes and obesity in mice.<sup>14</sup> Obese mice treated with  
 251 FVT showed improvement in glucose tolerance and reduced further weight  
 252 gain caused by high-fat diet.<sup>14</sup> In these mice, FVT was found to impact not  
 253 only the virome but also the bacteriome, due to the transfer of  
 254 bacteriophages.<sup>14</sup> In addition, FVT can reduce high-fat diet-induced small  
 255 intestinal bacterial overgrowth.<sup>51</sup> Taken together, these findings emphasise  
 256 the critical role of virome transfer in successful FMT therapies of various  
 257 human diseases.

258

## 259 **Donor and recipient effect**

260 In our prior FMT-CDI study, we found that donor-recipient pairs with a higher  
 261 faecal viral richness of *Caudovirales* in donor than recipient was predictive of  
 262 a better clinical outcome in CDI.<sup>7</sup> This result at the same time was coupled  
 263 with changes in the bacteriome, where FMT-driven *Caudovirales* transfer  
 264 was positively correlated to the bacterial richness and diversity in the  
 265 responders.<sup>7</sup> Due to the co-transfer nature of virome and bacteriome during  
 266 FMT, it precludes us separating the effect of virome and that of bacteriome in

267 influencing FMT outcome in this setting. Albeit, it highlights the importance of  
268 donor virome composition and significance of appropriate donor-recipient  
269 pairing for the efficacy of FMT. Consistently, another study found that donors  
270 with a high faecal bacteriophage  $\alpha$ -diversity and a low bacteriophage  
271 abundance were associated with a successful FMT in CDI.<sup>45</sup>

272

273 By adopting a single-cell viral tagging (VT) approach, researchers  
274 investigated whether individual phages isolated from one subject's faeces  
275 could interact with bacteria isolated from a different subject, as a proxy for  
276 FMT.<sup>61,62</sup> They found that a high level of cross-reactivity between  
277 bacteriophages and bacteria from different human subjects, which however  
278 varied across donor-recipient pairs, highlighting a significant donor-recipient  
279 pairing effect on FMT/FVT outcomes.<sup>62</sup> Therefore, by modelling a bacteria–  
280 bacteriophage interaction network between the donor and recipient microbial  
281 communities, based on single-cell VT results, it may become possible to  
282 identify optimal donor-recipient pairs and to predict the outcomes of FMT.

283

## 284 **Safety concerns of virome transfer in FMT**

285 While data suggests that viral transfer during FMT is an important beneficial  
286 factor for the success of therapy, undesirable viral transmissions constitute a  
287 serious safety concern, especially when transplanting into an  
288 immunocompromised recipient. One report showed that norovirus was  
289 transmitted to 2 out of 13 CDI patients via FMT procedure, who later  
290 developed a post-FMT norovirus gastroenteritis.<sup>63</sup> This report claimed that  
291 viral contamination and transfer during the FMT procedure by a procedure-  
292 involved employee who had previously developed norovirus-like symptoms  
293 might be a cause to the observed post-FMT norovirus gastroenteritis.<sup>63</sup> A  
294 number of pathogenic eukaryotic viruses can potentially be present in the  
295 human gut, including papillomaviruses, herpesviruses, hepatitis viruses,  
296 bocaviruses, enteroviruses, rotaviruses, and sapoviruses.<sup>64</sup> To prevent  
297 potential transfer of pathogenic eukaryotic viruses during FMT, a thorough  
298 faecal virome screening of the donor should be performed to ensure the

299 safety of faecal transplant. Despite such concerns, FVT seems to be  
300 generally safer than FMT due to the removal of intact bacteria, in particular  
301 obligate and opportunistic bacterial pathogens, prior to transplantation. FVT  
302 can also avoid transfer of certain gut commensals with unwanted properties,  
303 which under certain conditions can interact with host physiology exacerbating  
304 disease. Overall, FMT in general has been found to be safe provided that the  
305 donor screening is done adequately as instructed in international guidelines.  
306 Most, if not all, unfortunate cases have been due to sloppy and highly  
307 unacceptable donor screening.

308

309 Bacteriophages targeting gut bacteria can have cascade effects on bystander  
310 bacteria, as demonstrated in gnotobiotic mice.<sup>65,66</sup> Therefore, which gut  
311 bacteria are going to be affected by phage predation during FMT, to what  
312 extent and in what direction, present an unpredictable and daunting  
313 challenge. Equally complex and unpredictable is the subsequent effects of  
314 microbiome manipulations on the overall health of the human host. In  
315 addition, horizontal gene transfer (HGT) from one bacterial strain to another,  
316 mediated by bacteriophages (phage transduction) can be a significant  
317 contributor to dissemination of antibiotic resistance genes, virulence genes  
318 and other unwanted genetic material.<sup>67</sup> A number of bacteriophages encode  
319 toxins (such as diphtheria toxin, Shiga toxin and erythrogenic toxin) that  
320 increase survival and virulence of their bacterial host during lysogenic  
321 conversion.<sup>68,69</sup> FMT may transfer the bacteriophages carrying these toxin  
322 genes to confer a virulent phenotype to the co-resident bacteriome in the gut  
323 of the recipient, posing another health concern.

324

325 Administering rats with a bacteriophage cocktail led to an increased intestinal  
326 permeability, weight loss, and decreased activity.<sup>70</sup> This study demonstrates  
327 that increased intestinal permeability may be induced by bacteriophages that  
328 affect the microbiota. Recently, a temperate filamentous bacteriophage was  
329 found to integrate into the genome of a multidrug-resistant *Pseudomonas*  
330 *aeruginosa*, resulting in inappropriate antiviral immune responses and

331 impaired clearance of bacterial infection in the host.<sup>71</sup> These evidence  
 332 suggest that akin to the transfer of certain eukaryotic viruses, the transfer of  
 333 unwanted bacteriophages may also confer undesired health concerns to the  
 334 human host.

335

### 336 **Mechanisms of virome function underlying FMT**

337 The mechanisms of viral action contributing to FMT therapies include  
 338 tripartite mutualistic interactions between bacteriophages/eukaryotic viruses,  
 339 bacteria, and the mammalian host (figure 1b).<sup>6</sup>

340

### 341 ***Functions of bacteriophages colonisation***

342 Bacteriophage transfer engraftment can modulate not only the taxonomic  
 343 composition but also the functional capacity of the gut bacteriome.<sup>65,66,72</sup>  
 344 Faecal multi-omics profiling of mice receiving a transplant of a defined  
 345 consortium of bacteriophages revealed shifts in both the microbiome and gut  
 346 metabolome after bacteriophage colonisation.<sup>66</sup> The result showed that a  
 347 large diversity of metabolites was altered after bacteriophage transplantation,  
 348 including nearly all KEGG pathways (amino acids, peptides, carbohydrates,  
 349 lipids, nucleotides, cofactors, vitamins, and xenobiotics).<sup>66</sup> A recent study  
 350 also showed that *Bacteroides* phage BV01 altered the genome-wide  
 351 transcriptome profiles and bile salt hydrolase activity in its bacterial host,  
 352 leading to an altered profile of bile acids.<sup>72</sup> In return, bile acids are well known  
 353 to regulate both host microbiome (including *C. difficile*) and host  
 354 physiology.<sup>73,74</sup> Such changes in gut bacteriome composition and functionality  
 355 induced by bacteriophage colonisation are important for host health.

356

357 Accumulating data suggest that bacteriophages can modulate the immune  
 358 system both directly and indirectly. Indeed, bacteriophages can colonise the  
 359 intestinal mucus layer, directly binding to mucin glycoproteins via their  
 360 capsids, and provide the mammalian host with a defence mechanism against  
 361 the bacteria trying to breach through the intestinal barrier.<sup>75</sup> Certain

362 bacteriophages, such as phage 536\_P1, directly promote the production of  
 363 antiviral cytokines, such as IFN- $\gamma$  and IL-12, as well as chemokines, even in  
 364 the absence of their host bacteria.<sup>76</sup> Bacteriophages can interact with the  
 365 host immune system in various ways, by inducing the innate defenses  
 366 against bacterial colonisation, stimulating production of inflammatory  
 367 cytokines, and activating dendritic cells (DCs) and innate lymphoid cells  
 368 (ILCs) to produce IFNs (figure 1b).<sup>77</sup>

369

### 370 ***Functions of eukaryotic viruses colonisation***

371 In addition, colonisation with eukaryotic viruses in the gut is critical for the  
 372 maintenance of gut microbial homeostasis and host immunity. Recognition of  
 373 the bulk of enteric viruses via surface receptors TLR3 or TLR7 induces  
 374 production of IFN- $\beta$ , which protects the host from developing inflammation.<sup>27</sup>  
 375 The RIG-I receptor for viral RNA recognition in the cytosol signals IL-15  
 376 production to maintain homeostasis of intraepithelial lymphocytes.<sup>78</sup> Another  
 377 prime example of protective effects of intestinal eukaryotic virome was  
 378 demonstrated in murine norovirus (MNV)-colonised mice.<sup>79</sup> The viral protein  
 379 NS1/2 from MNV evoked a host protective response with increased  
 380 production of IFN-I and IL-22, which conferred a critical protection against  
 381 *Citrobacter rodentium* infection and promoted proliferation of the intestinal  
 382 epithelial cells.<sup>79</sup> A recent comprehensive murine study profiled the immune  
 383 responses to a panel of eukaryotic viruses and found a widespread capacity  
 384 for asymptomatic intestinal colonisation and durable alterations that the both  
 385 strain-specific and common to multiple viruses.<sup>28</sup> Most enteric viruses  
 386 promoted T cell differentiation, Th1 polarization, and production of IL-22, a  
 387 cytokine central to the dialog between host and microbiome at epithelial  
 388 barriers.<sup>28,80</sup> Such enteric viruses could transcriptionally upregulate anti-  
 389 bacterial peptides, though to a lesser extent than a consortium of 15 bacterial  
 390 strains in germ-free (GF) mice.<sup>28</sup> In addition, astrovirus supplementation in  
 391 immunocompromised mice can protect the mice from enteric pathogens via  
 392 IFN- $\lambda$ , transferable by cohousing and faecal transplantation.<sup>81</sup> These data  
 393 together suggest that gut eukaryotic viruses also tune host homeostasis by  
 394 orchestrating both the host immunity and the co-resident microbiome.

395

396 Taken together, these studies indicate that colonisation by gut viruses, both  
397 prokaryotic and eukaryotic, is essential to calibrate host immunity and  
398 physiology. Transfer and engraftment of gut viruses via FMT can have broad  
399 cascading effects on the mammalian host, including modulation of host  
400 microbiome, metabolome, and immunity.

401

## 402 Roles of gut mycobiome in FMT

### 403 The human gut mycobiome

404 The human GI tract is also home to a large diversity of fungi, collectively  
405 known as the gut mycobiome. Fungi constitute a minor component of the gut  
406 microbiota, making up approximately 0.1% of the microorganisms shown by  
407 metagenomics sequencing.<sup>4,82,83</sup> Studies have shown that the gut harbours  
408 >50 genera of fungi with *Candida*, *Saccharomyces*, *Cladosporium* and  
409 *Malassezia* being the most abundant genera (figure 2a).<sup>4,82,83</sup> However, the  
410 gut fungi are highly under-explored relative to the gut bacteria, and hence are  
411 underrepresented in current mycobiome databases, hindering gut  
412 mycobiome profiling and functional characterisation.<sup>84</sup> Gut resident fungi  
413 have both mutualistic and antagonistic relationships with the gut bacteria,  
414 together shaping the host immunity.<sup>85</sup> Intestinal fungi have been shown to be  
415 causally implicated in microbiome assembly and immune development.<sup>86</sup>  
416 Accumulating evidence points to that the gut mycobiota can strongly  
417 influence the host immune system and this interaction is linked to bacteria  
418 activities.<sup>87,88</sup> Recent observations of dysbiosis in gut mycobiome across  
419 various diseases highlight a critical role of gut fungi in disease  
420 pathogenesis<sup>89–91</sup>, suggesting that targeting gut mycobiome may represent a  
421 promising therapeutic modality.

422

### 423 Translational studies investigating FMT and mycobiome

424 Emerging studies report that FMT involves transfer of fungi, which may affect  
425 treatment outcomes.<sup>8,9</sup> Our FMT-fungi study in CDI (n=16) showed that donor

426 fungi were substantially transferred to recipient after FMT, and cure after  
427 FMT was associated with increased colonisation of donor-derived fungal taxa  
428 in recipients.<sup>8</sup> After FMT, responders displayed a high relative abundance of  
429 *Saccharomyces* and *Aspergillus*, whereas non-responders and patients  
430 treated with antibiotics displayed a dominant presence of *Candida* in faeces.<sup>8</sup>  
431 CDI patients who responded to the treatment showed a reduction in the  
432 abundance of *C. albicans* after FMT, while those who did not respond to FMT  
433 showed a still high abundance of *C. albicans* in faeces.<sup>8</sup> In favor of this  
434 finding in humans, we observed that *C. albicans* also negated FMT efficacy  
435 in a mouse model of CDI.<sup>8</sup> In a separate experiment, we showed that  
436 antifungal treatment to eliminate *C. albicans* in recipient mice before FMT re-  
437 established FMT efficacy using the same donor stool without presence of *C.*  
438 *albicans*.<sup>8</sup> These evidence together highlight a causal relationship between  
439 gut fungal dysbiosis and FMT outcome in CDI.

440

441 Interestingly, a recent FMT study conducted in patients with UC (n=24)  
442 observed a different association between faecal *C. albicans* levels and  
443 treatment outcome: UC patients with higher *C. albicans* abundance pre-FMT  
444 were much likely responsive to FMT.<sup>9</sup> On the other hand, in agreement with  
445 the finding in CDI, FMT resulted in a reduction of *C. albicans* in UC patients.<sup>9</sup>  
446 Decreased *Candida* abundance post-FMT was indicative of ameliorated UC  
447 severity.<sup>9</sup> These findings suggest that FMT reduces *C. albicans* abundance,  
448 and a decreased *C. albicans* abundance after FMT is associated with  
449 disease amelioration in both CDI and UC. The discordant findings between  
450 CDI and UC that a high faecal abundance of *C. albicans* in recipients pre-  
451 FMT may lead to discrepant treatment outcomes after FMT underscores that  
452 gut fungi in recipient baseline may affect FMT efficacy in a disease-  
453 dependent manner. Similarly, patients with CD had higher fungal burden and  
454 *Candida* colonisation in the gut, however CD patients were less responsive to  
455 FMT compared to UC.<sup>10,92–94</sup> Different immunophysiology and  
456 immunopathophysiology mechanisms, though calibrated by the same fungi,  
457 in different disease settings may underlie this discordance in FMT efficacy  
458 between diseases.



459

460 Overall, FMT treatment is able to reduce *C. albicans* levels in recipient and  
461 produce a positive treatment outcome in CDI and IBD. This effect is also  
462 evidenced in different mouse models, demonstrating that FMT prevented *C.*  
463 *albicans* colonisation.<sup>8,95,96</sup> In a pilot study, a patient with UC was cleared of  
464 recurrent *C. glabrata* infection after FMT<sup>97</sup>, suggesting FMT may be able to  
465 deliver a possible beneficial effect on patients who are complicated with  
466 fungal infection. Another clinical study showed that FMT was effective to  
467 reduce the likelihood of developing blood stream fungal infection in rCDI  
468 patients compared to antibiotics treatment.<sup>98</sup> These studies further support  
469 that FMT is capable of modulating recipient fungi, including *Candida* species.

470

471 Another intestinal disorder IBS is also characterised by a significant alteration  
472 in the gut mycobiome, featured by predominance of two fungal species *C.*  
473 *albicans* and *Saccharomyces cerevisiae* compared to healthy individuals.<sup>99</sup>  
474 Interestingly, IBS-related visceral hypersensitivity was transferable between  
475 rats by FMT, suggesting a causal role of gut microbiome in IBS.<sup>99</sup> To date,  
476 whether FMT is effective in IBS is still controversial in clinical practices. One  
477 randomized clinical trial (n=90) conducted in a cohort of IBS patients in  
478 northern Norway showed that FMT relieved IBS symptoms compared to the  
479 placebo arm, whereas another randomized clinical trial (n=48) conducted in  
480 three US centres showed that FMT was ineffective in reducing IBS symptoms  
481 compared with placebo.<sup>100</sup> Whether gut fungi play a role in such  
482 heterogenous clinical efficacy of FMT in IBS warrants further investigation.

483

484 FMT is a promising agent for treating infectious diseases and gastrointestinal  
485 disorders, it has been utilised for treating severe colitis in GvHD patients  
486 following allogeneic HSCT.<sup>12</sup> The antifungal drug fluconazole has been shown  
487 to prevent *C. albicans* colonisation and to reduce the likelihood of developing  
488 GvHD after HSCT, suggesting that modulation of gut mycobiota may be  
489 associated with the pathogenesis of GvHD post HSCT.<sup>101</sup> More recently, our  
490 observational FMT study on a single GvHD case reported some changes in

the gut mycobiome following a successful treatment of 4-dose FMT.<sup>12</sup> The serial FMT treatments altered the fungal composition and diversity in the faeces of this GvHD patient, which was more similar to the donor's faecal fungal profile after FMT compared to his pre-FMT profile.<sup>12</sup> However, as this pilot study was exploratory, an expanded sample size is needed in future to address any biologically meaningful changes in recipient's gut mycobiome by FMT underlying cure of GvHD.

498

The role of gut mycobiome in FMT is elusive and there is a significant lack of human and animal studies centered on fungal transfer in FMT treating different diseases. The keystone fungal species as well as their functions in the gut and FMT remain to be discovered in different disease settings.

503

#### 504 **Donor and recipient effect**

As aforementioned, our FMT-CDI study in both humans and mice found that existence of *C. albicans* in donor and high abundance existence of *C. albicans* in CDI recipient pre-FMT were both detrimental to FMT outcome.<sup>8</sup> Similarly, two filamentous fungi *Penicillium brocae* and *Aspergillus penicillioides*, present in either donor or recipient pre-FMT, also nullified the treatment efficacy of FMT in CDI mice, highlighting a generic deleterious role of overrepresentation of certain fungi in donor or recipient in FMT.<sup>8</sup> Antibiotics are always the primary treatment for patients with CDI, which may lead to a fungal bloom and a high likelihood of developing fungal infections in patients, particularly expansion of *Candida* species.<sup>102</sup> These data underscores the importance of donor selection (exclusion of invasive *Candida* carriers) and appropriate recipient preparation based on their faecal fungal profiles, to enhance FMT efficacy in CDI. In contrast, a high faecal abundance of *C. albicans* in UC patients pre-FMT was associated with a favourable FMT outcome.<sup>9</sup> Taken together, it suggests that the gut mycobiome composition of donor and recipient should be considered separately in different disease settings when employing FMT.

522

### 523 **Safety concerns of mycobiome transfer in FMT**

524 Analogous to gut bacteria, a lot of gut fungi are opportunistic species which  
525 can mount detrimental immune responses in the host under non-homeostatic  
526 conditions, including *C. albicans*. Therefore, to avoid transfer of fungal  
527 pathogens and opportunistic fungal pathogens, thorough donor screening  
528 based on the faecal fungal profile is necessary during FMT practice. To date,  
529 there has no report of death or infection caused by transmission of life-  
530 threatening fungi from FMT, but screening for fungal candidates in the donor  
531 and susceptible recipients should also be cautious. Fungal infection is often  
532 seen in immunocompromised patients with CDI, IBD and GvHD, and the  
533 responsible candidates are *Candida* species that contribute to the majority of  
534 infections.<sup>97,98,101</sup> Most common fungal infections in CDI are caused by *C.*  
535 *albicans*, *C. parapsilosis*, and *C. tropicalis* in the blood stream due to  
536 prolonged use of antibiotics.<sup>98</sup> These fungi constitute a health concern to the  
537 host, and may nullify FMT efficacy and invoke undesired immune responses  
538 after FMT.

539

540 Other fungi, such as *Malassezia restricta* and *Histoplasma capsulatum*  
541 should also be checked in donor screening.<sup>103,104</sup> *M. restricta* is a skin  
542 commensal that preferentially colonises in CD patients with CARD9  
543 polymorphism, whereas *H. capsulatum* preferentially infects IBD patients with  
544 immunocompromised condition.<sup>103,104</sup> CARD9 and dectin-1 are well known  
545 fungal recognition receptors, and polymorphisms in these genetic loci are  
546 associated with increasing susceptibility to fungal infections.<sup>105–107</sup> It is known  
547 that antibiotics can alter the gut bacterial-fungal community structure and that  
548 antibiotics treatment was found to offer longer-lasting impact on gut fungi  
549 other than bacteria.<sup>108</sup> Hence, fungal profiling in the donor, the genetically  
550 susceptible or immunosuppressive recipient, as well as those with a drug or  
551 antibiotics history, are needed to avoid potential fungal bloom or infection  
552 following FMT.<sup>105–107,109</sup>

553

## 554 **Mechanisms of protective immunity elicited by the gut fungi**

555 The commensal fungi in the gut can evoke protective immunity in the host  
 556 and impact gut microbiome assembly.<sup>6,88,105,110,111</sup> The mechanisms of  
 557 mycobiome action underlying FMT treatment of diseases hence also involve  
 558 a tripartite interaction between fungi, bacteria, and the mammalian host  
 559 (figure 2b).

560

561 It is shown in gnotobiotic mice that commensal fungi can functionally  
 562 recapitulate the protective benefits of intestinal commensal bacteria, by  
 563 mitigating tissue injury and extra-intestinal infection as well as calibrating the  
 564 activation of protective CD8<sup>+</sup> T cells.<sup>112</sup> Elimination of the gut fungi by oral  
 565 antifungals in mice worsened the outcome of colitis and allergic airway  
 566 disease<sup>91</sup>, where both the host immune profile and the gut bacteriome  
 567 composition were disrupted, suggesting that colonisation of gut commensal  
 568 fungi plays an import role in host immune and microbiome homeostasis.  
 569 Fungi can stimulate host cells through a variety of microbial pattern  
 570 recognition receptors (PRRs).<sup>6,105,110,113–117</sup> Surface receptors, such as dectin-  
 571 1, dectin-2, mincle and CX3CR1 receptors on mononuclear phagocytes  
 572 (MNP) can recognize  $\beta$ -glucans in the fungal cell wall.<sup>6,105,110,113–117</sup> Fungal  
 573 sensing by CARD9 signalling induces release of IL-18 for reconstitution of  
 574 intestinal epithelial cells (IECs).<sup>6,105,110,113,118</sup> IL-22 elicited by fungal sensing  
 575 restricts inflammasome from triggering immune pathology.<sup>119</sup> Fungal-derived  
 576 molecules and metabolites, such as mannans and glucans, are also critical  
 577 components to calibrate host immunity by changing the cytokine profile.<sup>120,121</sup>  
 578 These mechanistic studies underscore the sophisticated molecular pathways  
 579 underlying gut fungi regulating host immunity.

580

581 Another aspect of mycobiome function on the host is its interactions with gut  
 582 bacteria and other co-resident fungi. In steady state, bacteria and fungi keep  
 583 each other in check in the gut. One study demonstrated that *C. albicans*  
 584 affects the recolonisation of the cecum by the microbiota in mice treated with  
 585 antibiotics.<sup>122</sup> The presence of *C. albicans* in the gut increased colonisation

by the bacterium *Enterococcus faecalis* and reduced colonisation of probiotic *Lactobacillus* strains.<sup>122</sup> A follow-up study revealed that antibiotic-treated *C. albicans*-colonised mice had reduced expression of specific immune genes, hinting at dual role of *C. albicans* on host immunity and bacteriome assembly.<sup>123</sup> Several studies have shown that *Saccharomyces boulardii* can suppress *C. difficile* by the production of a protease to degrade toxins A and B of *C. difficile*.<sup>124,125</sup> These studies imply that colonisation of *Saccharomyces* species by FMT may favour a positive outcome in CDI. Moreover, *S. boulardii* has a protective effect against various other bacterial gastrointestinal pathogens, including *Helicobacter pylori*, *Vibrio cholerae*, *Salmonella enterica* serovar *Typhimurium*, *Shigella flexneri*, and *Escherichia coli*.<sup>85</sup> Both *E. coli* and *S. Typhimurium* bind to the surface of *S. boulardii*, potentially preventing adhesion to intestinal epithelial cells and thus allowing quicker excretion through faecal matter.<sup>126,127</sup> *S. boulardii* was found to suppress colonisations of both *C. albicans* and Adherent-invasive *Escherichia coli* (AIEC) and to alleviate colitis in mice.<sup>128–130</sup> Overall, FMT is able to cause a collection of fungi colonised in recipient, where they individually or together with gut bacteria regulate host immunophysiology influencing FMT outcome.

605

## 606 Conclusions

A large body of studies demonstrated efficacy of FMT in re-shaping the microbial composition and function in the recipients in a number of human diseases, though resolution of symptoms and cure can only be consistently achieved in CDI and inconsistently achieved in other diseases, such as IBS, IBD and obesity. Successful FMT is not only ascribed to the restoration of healthy gut bacteriome, but also involves modulation of the virome and mycobiome. The intricate relationships between the bacteriome, the virome and the mycobiome on one hand, and the human host on the other, underpin clinical and microbiological effects, and overall efficacy of FMT. Enhanced understanding of gut virome and mycobiome will guide and facilitate future precision FMT-based therapies of various human diseases. Well-designed

618 clinical trials based on targeted bacterial-, viral/phage- and fungal-transfer will  
619 be required, so are preclinical mechanistic studies investigating functions of  
620 the individual components of the microbiome. Of particular interest are  
621 different lineages and combinations of *Caudovirales* phages, as well as fungi  
622 from the genera *Candida* and *Saccharomyces*, due to their possible  
623 contributions to FMT efficacy. Precision FMT should be adopted in future,  
624 including FVT and/or defined consortia of phages-fungi-bacteria  
625 combinations, in a personalised, disease-specific manner. We look forward  
626 with optimism to the future of precision FMT, as it transfers a holistic, tailor-  
627 made, and well donor-recipient paired microbiome for disease treatment.

628

## 629 **Search strategy and selection criteria**

630 A literature search was performed on Pubmed, Google Scholar and Web of  
631 Science using the keywords “Faecal microbiota transplantation”, “FMT”,  
632 “Faecal viral transfer”, “FVT”, “Fungal microbiota”, “Gut virus”, “Virome”, “Gut  
633 fungi” and “Mycobiome” to select relevant clinical and animal studies.

634

### 635 **Contributors:**

636 TZ conceived the manuscript. TZ and SL wrote the manuscript. ANS, PL and XJW  
637 provided significant intellectual contribution and edited the manuscript. TZ, PL and  
638 XJW supervised this study. HP and XWB provided critical comments.

639

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641 The authors declare no conflict of interest.

642

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650

651

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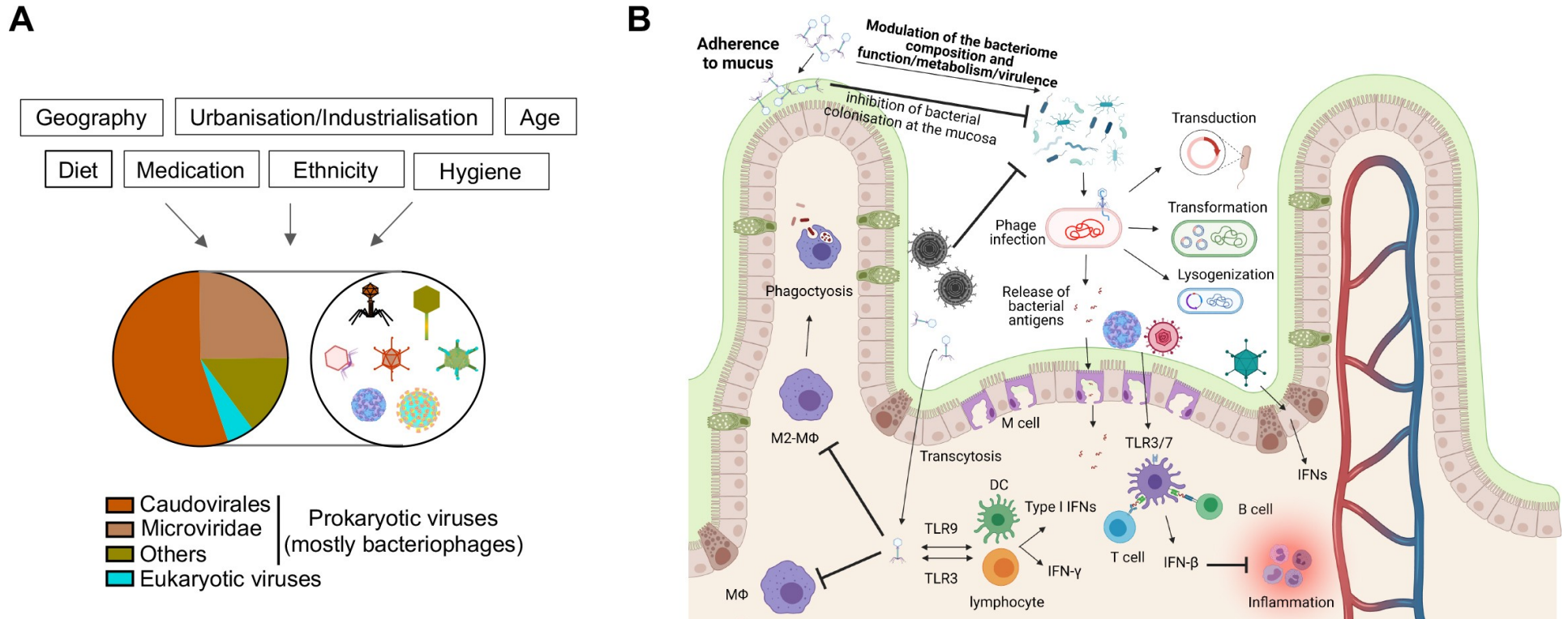
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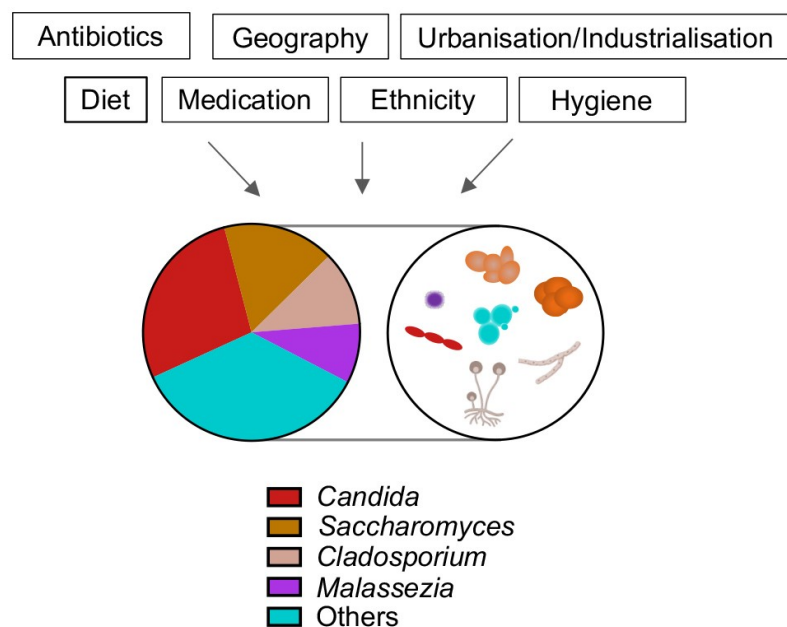
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1050 Figure 1. Composition and function of the gut virome. A. The composition of human gut virome and factors influencing its composition. B.

1051 Functions of the gut virome on the host.

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A



B

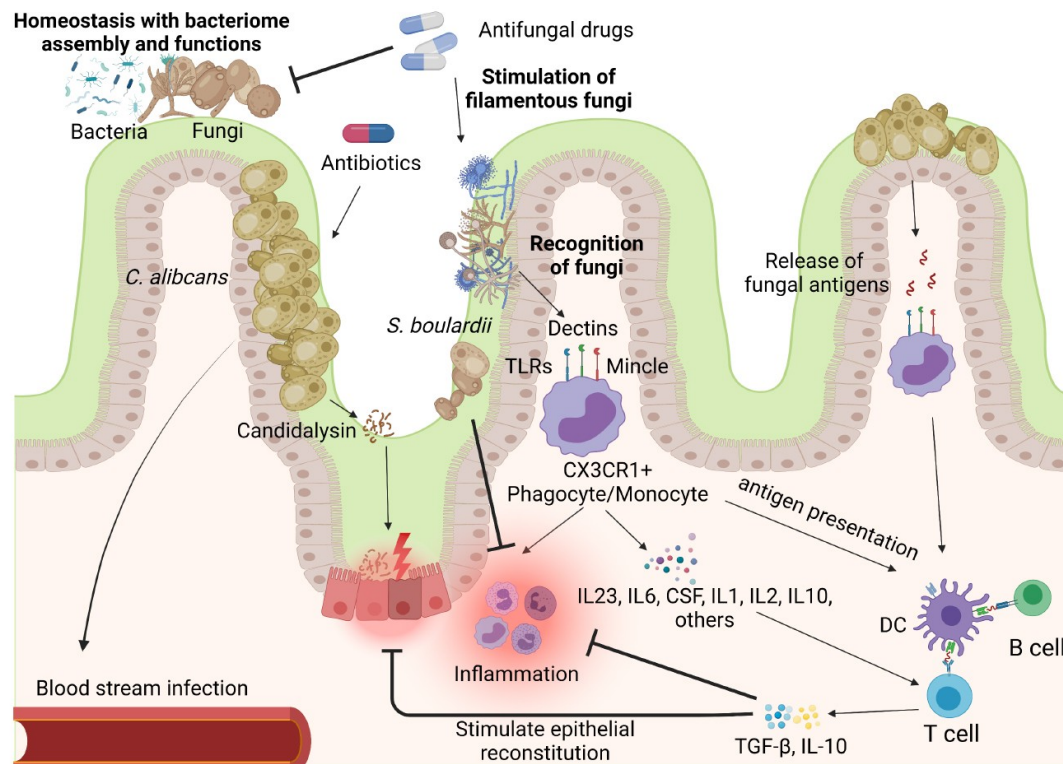


Figure 2. Composition and function of the gut mycobiome. A. The composition of human gut mycobiome and factors influencing its composition. B. Functions of the gut mycobiome on the host.

Table 1. Summary of human studies investigating FMT and gut virome/mycobiome

Indication	Number of study subjects	Type	Methodology	Treatment outcome in association with gut virome/mycobiome alterations	Reference
CDI	N=44	Randomized Controlled Trial	Faecal virome and bacteriome were profiled in association with treatment outcome	<i>Caudovirales</i> derived from the donors with increased richness displayed responsiveness	7
	N=55	Randomized Controlled Trial	Faecal mycobiome and bacteriome were profiled in association with treatment outcome	High abundances of <i>Candida albicans</i> in donor or recipients led to failure of FMT; FMT decreased <i>Candida albicans</i> abundance	8
	N=9	Pilot-study	Analysis in the metagenome, prophage- and CRISPR-based bacteria-phage association and gene functions of the bacteriome and virome after FMT treatment	Successful FMT resulted in functional restoration in the bacteriome and virome resembling donors' profiles. A negative correlation between <i>Microviridae</i> and <i>Proteobacteria</i> was found before and after FMT	35
	N=1	Case-study	Longitudinal investigations up to 42 months on patient's bacteriome and virome after a successful FMT	Bacteriome and virome in the patient resembled the donor's profile long-term; low phage abundance is associated with a 'healthy' virome profile	47
	N=14	Pilot-study	Investigations up to 12 months on the viral transfer from 3 donors to 14 patients	A successful FMT was associated with durable virome alterations up to 12 months in recipients	46
IBD	N=39	Randomized Controlled Trial	Faecal mycobiome was profiled in association with treatment outcome	FMT responders showed lower faecal <i>Candida albicans</i> abundances and anti- <i>Candida</i> antibody levels after FMT	9
	N=9	Pilot-study	Analysis in the UC faecal virome and its association with induction of clinical and endoscopic remission	FMT responders showed lower baseline eukaryotic virome richness	44
GvHD	N=1	Case-study	Faecal virome, mycobiome and bacteriome were profiled longitudinally in one patient treated with 4-dose FMT	Decreased faecal fungal diversity after serial FMTs, while virome maintained stable after FMT; relative abundance of Torque teno viruses was decreased, whereas <i>Caudovirales</i> bacteriophages was increased in faeces after FMT	12