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1	Herpes Simplex Virus Infection, Acyclovir and IVIG Treatment All Independently Cause Gut	
2	Dysbiosis.	
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31 Abstract.

32

33 Herpes simplex virus 1 (HSV) is a ubiquitous human virus resident in a majority of the global 34 population as a latent infection. Acyclovir (ACV), is the standard of care drug used to treat primary 35 and recurrent infections, supplemented in some patients with intravenous immunoglobulin (IVIG) 36 treatment to suppress deleterious inflammatory responses. We found that HSV, ACV and IVIG 37 can all independently disrupt the gut bacterial community in a sex biased manner when given to 38 uninfected mice. Treatment of HSV infected mice with ACV or IVIG alone or together revealed 39 complex interactions between these drugs and infection that caused pronounced sex biased 40 dysbiosis. ACV reduced Bacteroidetes levels in male but not female mice, while levels of the 41 Anti-inflammatory Clostridia (AIC) were reduced in female but not male mice, which is significant 42 as these taxa are associated with protection against the development of GVHD in hematopoietic 43 stem cell transplant (HSCT) patients. Gut barrier dysfunction is associated with GVHD in HSCT 44 patients and ACV also decreased Akkermansia muciniphila, which is important for maintaining 45 gut barrier functionality. Cumulatively, our data suggest that long-term prophylactic ACV treatment 46 of HSCT patients may contribute to GVHD and potentially impact immune reconstitution. These 47 data have important implications for other clinical settings, including HSV eye disease and genital 48 infections, where ACV is given long-term.

49

50 Author Summary.

51

52 Primary and reactivated HSV and VZV infections are treated with Acyclovir (ACV), an 53 antiviral drug that blocks viral DNA synthesis. In some patients IVIG is used as adjunctive therapy 54 to block deleterious inflammation. Long term preventative treatment of patients who receive stem 55 transplants for various blood cancers has been successful in preventing life threatening 56 reactivated HSV and VZV infections, but GVHD remains a major factor limiting transplant

57 success. Studies reported here reveal that HSV infection, ACV and IVIG given alone can all 58 disrupt the gut microbiota and that complex interactions between these drugs and infection results 59 in even more pronounced sex biased changes in the gut bacteria community structure. 60 Importantly, ACV treatment decreased the levels of specific bacterial taxa, including the anti-61 inflammatory *Clostriodia* and *Bacteroidetes* that have been shown to protect against development 62 of GVHD in stem cell transplant patients. These data suggest that long term preventative 63 treatment of patients with ACV may contribute to GVHD in transplant patients and have negative 64 consequences in other HSV induced diseases treated long term with ACV. The health effects of 65 long term ACV and IVIG treatments warrant further clinical studies.

66

67 Introduction.

68

69 Herpes Simplex Virus type 1 (HSV), a ubiquitous human virus is the major cause of HSV 70 encephalitis (HSE), the most prevalent sporadic encephalitis resulting from either primary 71 infection or reactivation of latent virus. However, despite improved diagnostic procedures and 72 effective antiviral therapies, most HSE survivors have persistent neurological impairments, 73 including memory and behavior disturbances, dysphasia and seizures, and only 50-65% of these 74 survivors return to independent living [1, 2]. A delay in initiating Acyclovir (ACV) treatment past 75 the second hospital day is associated with poor neurological outcomes [3, 4]. Recent clinical trials 76 evaluating prolonged oral ACV/valaciclovir (VACV) treatment following standard 14-day 77 intravenous ACV treatment reported improved neurocognitive outcomes in neonates but not 78 adults for reasons that are obscure [5, 6]. Although, it is generally accepted that replication 79 induced pathology underlies HSV related neurological dysfunction, supporting experimental or 80 clinical evidence is lacking. Overwhelming evidence has linked inflammation to the development 81 of various neurological disorders and neuropsychiatric diseases, including Alzheimer's disease

(AD), schizophrenia, autism spectrum disorder (ASD), multiple sclerosis (MS), Parkinson's
disease (PD), depression and anxiety [7-9].

84

85 Having unequivocally established that HSE arises from exaggerated CNS inflammatory 86 responses and that the immunomodulatory activities of intravenous immunoglobulins (IVIG) can 87 prevent HSE in a mouse model [10], we tested the hypothesis that persistent inflammation, which 88 is documented in humans and mice after HSE [11-14], causes neurobehavioral impairments in 89 survivors, that should be impeded by IVIG's anti-inflammatory activity [10]. Compared to treatment 90 of HSV infected mice with ACV or PBS alone, treatment with ACV+IVIG from day 4 pi reduced 91 CNS inflammation and anxiety, consistent with our hypothesis. Strikingly, development of learning 92 and memory (LM) deficits that were evident only in female PBS treated mice, were inhibited by 93 ACV treatment and counterintuitively, aggravated by ACV+IVIG treatment. Treatment of infected 94 male mice with ACV+IVIG also impaired LM compared to ACV or PBS alone, revealing that IVIG 95 antagonized the beneficial effects of ACV [15]. Intriguingly, the differential antagonistic effects of 96 ACV+IVIG on cognitive behavior in HSV infected mice, compared to ACV and PBS treatment 97 alone, were reflected in differential serum proteomic profiles [15]. These reported antagonistic 98 effects of ACV and IVIG on LM present a conundrum, since they are at odds with the known 99 mechanisms of action of these drugs.

100

101 Rapidly accumulating evidence is revealing the critical role of the microbiome in regulating 102 brain homeostasis and function such that perturbation of the gut bacteria community structure 103 and function is increasingly being implicated in a variety of neurodegenerative and 104 neuropsychiatric diseases. In an effort to gain insight into how HSV induces LM impairment and 105 the paradoxical effects of ACV and IVIG, we investigated a role for the gut microbiota. HSV 106 infection, ACV and IVIG were all associated with significant disruption of the gut bacterial 107 community structure that was sex biased. Furthermore, treating HSV infected mice with either ACV or IVIG alone or both drugs together resulted in more pronounced sex-biased shifts in the gut bacterial community structure compared to uninfected mice. These results have significant

110 clinical implications, particularly when patients receive prolonged ACV or IVIG treatment.

111

112 Results.

113

114 Equal numbers (n=8) of female and male C57BL/6 mice were bilaterally inoculated with 115 virulent HSV1 strain 17+ (1x10⁵ PFU/eve) by corneal scarification as previously described [15]. 116 At day 4 post infection (pi), ACV was administered at 1.25 mg / mouse by intraperitoneal injection 117 (ip) daily for 3 days, while IVIG was given as single dose of 25 mg/mouse by ip injection on day 118 4pi [15]. Fresh fecal pellets (n=1-2/ mouse) were collected on day 7 pi and stored at -80°C until 119 processed for Illumina 16S rRNA gene sequencing to determine the effects of infection and drug 120 treatment on the gut microbiome. Normal male and female mice differed in gut bacteria 121 composition and unexpectedly, HSV ocular infection caused further shifts in the gut bacteria 122 community and amplified this sex difference, as shown in a PCoA plot of Hellinger beta diversity 123 distance values for infected compared to uninfected male and female mice (Figure 1A; P<0.05, Adonis Tests). In addition, HSV infection had a greater effect on gut bacterial communities in 124 125 males (P=0.003) compared to females (P=0.011) (Figure 1A). Significant differences were 126 observed at the phyla level, particularly for firmicutes (Figure 1B) with more marked differences 127 evident at the species level for *Clostridium aerotolerans* and other clostridial species, for example 128 *Clostridium XIVa* that ferment carbohydrates in the gut resulting in production of short chain fatty 129 acids (SFCs) that contribute to barrier integrity and also exhibit anti-inflammatory properties 130 (Figure 1C). A notable difference was also observed for Akkermansia muciniphila that has many 131 health promoting activities, including maintaining gut barrier health (Figure 1C).

133 Treating HSV infected mice with ACV from day 4 pi for three days resulted in even more 134 drastic shifts in the gut bacteria composition and exaggerated sex differences (Figure 2A), than 135 for infection alone. Considerable abundance changes were evident at the Phyla level for 136 Bacteroidetes, Firmicutes and Verrucomicrobia (Figure 2B) and at the species level (Figure 2C). 137 Notably, whereas HSV infection reduced the abundance of *Firmicutes* significantly in male but 138 not female mice (Figure 1B), ACV reversed this effect restoring the abundance to the level in 139 uninfected male mice, while also increasing the abundance in female mice (Figure 2B and Figure 140 **1B**). Notable abundance changes at the species level included drastic suppression of *Clostridium* 141 aerotolerans in infected male mice compared to increased abundance in females (Figure 1C), 142 while ACV treatment further increased this abundance only in females (Figure 2C). Akkermansia 143 muciniphila abundance was increased by infection in male mice but reduced in females (Figure 144 **1C**), while ACV treatment resulted in total suppression of this species in female mice compared 145 to a marked reduction in male mice (Figure 2C). There are many other similar changes in species 146 abundance that are differentially impacted by ACV treatment in a sex-biased manner, indicative 147 of complex interactions between infection, ACV effects on infected host cells, and bacteria, as 148 well as metabolites produced by bacterial metabolism of ACV.

149

150 Treatment of uninfected mice with IVIG alone also shifted the gut bacteria community 151 composition with a notable marked sex effect as determined by a beta diversity analysis (Figure 152 3). Males and females showed a major reduction in A. muciniphila, and a lesser reduction of 153 Verrucomicrobia in males, compared to females that showed increased abundance of this phylum 154 in response to IVIG treatment (Figure 4). The abundance of many other bacterial species was 155 differentially altered by IVIG treatment of males and females, for example, Clostridium 156 aerotolerans, Bacteroides acidifaciens and Porphyromonadaceae (Figure 4B). The response to 157 IVIG was distinct in HSV infected mice, and the complex interactions between infection, ACV and 158 IVIG were also evident at the phyla and species levels and were strongly sex biased as well

159 (Figure 4A and 4B). IVIG treatment decreased A. muciniphila abundance markedly in infected 160 males and females as did ACV, whereas in contrast, treatment with ACV+IVIG caused a notable 161 increase in its abundance, indicative of antagonistic effects of these two drugs in the context of 162 infection (Figure 4B) In a similar vein, C. aerotolerans abundance increased markedly in males, 163 but was unchanged in females treated with IVIG, while in contrast, it was strongly decreased in 164 males but slightly increased in females treated with ACV alone. In contrast, treatment with 165 ACV+IVIG suppressed an IVIG-induced increase in males and an ACV-induced increase in 166 females, revealing antagonism between ACV and IVIG in the context of HSV infection (Figure 167 4B).

168

169 Patients with hematologic and other malignancies have benefited immensely from 170 allogeneic hematopoietic stem cell transplantation (allo-HSCT or HSCT), which can be a potent 171 curative immunotherapy. However, life threatening complications such as graft-versus-host 172 disease (GVHD), relapse, and infections that include reactivated HSV and VZV limit its application 173 [16]. HSV and varicella zoster (VZV) reactivation has been successfully suppressed by prophylactic ACV treatment, though ACV-resistant (ACVr) HSV is an emerging problem [17, 18]. 174 175 Long term ACV prophylactic treatment is now routine for HSCT patients, because it was found to 176 correlate with reduced HSV and ACVr HSV disease in those treated for longer than 1 year [19].

177

Given this routine clinical practice, we evaluated the effects of ACV on fecal bacteria, because gut microbes have been implicated in GVHD pathophysiology and because we posit that ACV contributes to the development of GVHD by changing the gut microbiota. First, we identified gut bacterial changes in humans with GVHD [20-30]. Next, we determined whether the ACVinduced changes that we detected in this mouse study matched those GVHD-associated changes. Whenever we identified taxa that were altered in both types of studies, the direction of the change was the same, and it was consistent with our hypothesis that ACV contributes to the development of human GVHD by changing the gut microbiota. In the following, we describe these
results, and we note that these ACV-induced changes were only observed in the HSV-infected
mice and not in the uninfected mice.

188

Reduced levels of several taxa belonging to the phylum *Bacteroidetes* have been shown to be associated with GVHD, indicating that these gut bacteria may play a protective role. In a pediatric study, GVHD patients had lower levels of the family *Bacteroidaceae* and the genus *Parabacteroides* [30]. In a longitudinal study, pediatric patients that had lower levels of *Bacteroidetes* prior to HSCT were more likely to develop GVHD [24]. In our study, all three if these taxa were reduced by ACV treatment in male but not female mice (**Figure 5A**).

195

196 Reduced levels of Anti-Inflammatory Clostridia (AIC) have also been detected in human 197 GVHD patients [20, 23-25, 27-30], indicating that these gut bacteria may play a protective role. 198 This terminology was first introduced by Piper et al. [31] in the context of short bowel syndrome, 199 and then introduced to the GVHD literature by Simms-Waldrip et al. [30]. AIC taxa include 200 members of the families Clostridiaceae, Erysipelotrichaceae, Eubacteriaceae, Lachnospiraceae 201 and Ruminococcaceae. In a pediatric study, decreases in Blautia and Clostridium bolteae were 202 associated with the development of GVHD [30]. In an adult study, lower levels of Blautia, Blautia 203 hansenii, and Blautia stercoris were associated with the development of GVHD [28]. In a 204 longitudinal study, reduced levels of the *Blautia* before HSCT was shown to be a predictive marker 205 for the development of GVHD [27]. In our study, all of these taxa were reduced by ACV treatment 206 in female but not male mice (Figure 5B).

207

In a more detailed analysis of AIC bacteria, we observed that while HSV infection increased the abundance of *Blautia hansenii* only in males, ACV treatment reduced its abundance in females but had no effect on its abundance in males (**Supplemental Figure 1**). Remarkably,

211 a dramatic increase in *B. hansenii* in uninfected females was observed after IVIG treatment, and 212 increase was abrogated by ACV (compare NoHSV F, NoHSV IVIG F and this 213 NoHSV ACVplusIVIG F) (Supplemental Figure 1), a result that supports sex-based differential 214 effects of these drugs. However, during HSV infection, both IVIG and ACV reduced B. hansenii 215 in females, whereas only IVIG reduced abundance in males. Interestingly, HSV infection 216 significantly increased the abundance of the AIC genera Blautia. Allobaculum, and Clostridium 217 XVIII but not *Turicibacter* in both males and females (**Supplemental Figure 2**). ACV treatment of 218 HSV infected female mice resulted in significant decreases in the abundances of 4 AIC genera: 219 Blautia, Allobaculum, Clostridium XVIII and Turicibacter, whereas in infected males, ACV 220 decreased the abundance of Marvinbryantia and Oscillibacter (Supplemental Figure 2). In 221 addition, ACV increased the abundance of *Turicibacter* in uninfected females but not males.

222

223 Finally, the two most abundant operational taxonomic units (OTUs), which exhibited a 224 change in their relative abundances due to ACV treatment, were assigned to the family 225 Porphyromonadaceae and the species A. muciniphila (Figure 5C). While we did not find these taxa associated with GVHD in prior human studies, GVHD has been associated with intestinal 226 barrier dysfunction [32-36]. Supporting our hypothesis that ACV contributes to the development 227 228 of GVHD by changing the gut microbiota, members of the Porphyromonadaceae have been 229 shown to cause gut barrier dysfunction [37, 38], and our Porphyromonadaceae OTU was 230 increased in its abundance by ACV. In addition, A. muciniphila was decreased by ACV treatment 231 in our study, and it has been shown to strengthen gut barrier functioning [39-41].

232

233 Discussion.

234

235 Our intention in this brief report is to alert the scientific community and especially clinicians 236 to the fact that HSV infection, the antiviral drug ACV, and the immunomodulatory biological, IVIG,

can all independently result in significant perturbations of the gut bacterial communities. Our data
 reveal complex interactions between HSV infection and ACV or/and IVIG treatment that result in
 marked alterations to gut bacterial communities. Although the clinical consequences of these
 changes have not yet been elucidated, they could have profound implications in several settings
 including HSCT-associated GVHD.

242

243 Though the mechanisms by which ocular HSV infection causes gut dysbiosis are unclear, 244 neuroinflammatory mechanisms and effects on the enteric nervous system via connected 245 brainstem neuronal circuits can be envisaged [15, 42]. Indeed, recent paradigm-shifting reports 246 reveal that peripheral neurons, including nociceptive and sensory neurons, can directly sense and 247 respond to environmental alarms by releasing neuropeptides that can regulate immune responses 248 in target organs including the gut [43, 44]. Persistence of gut dysbiosis was not evaluated here, 249 but results from a behavioral study alluded to earlier suggest long-term effects of infection and 250 drug treatment on gut bacterial ecology should be investigated [15]. Sex biased effects on HSV 251 induced dysbiosis merit further study, as these may involve microglial responses to HSV infection 252 and the microglial compartment is known to be regulated by the microbiota in a sex biased manner 253 [45-47].

254

255 The mechanism by which ACV, the standard antiviral for HSV infections, changes the gut 256 microbiota likely involves its uptake into bacteria. ACV is preferentially phosphorylated by the viral 257 encoded thymidine kinase (Tk) resulting in cell retention and eventual incorporation into viral DNA 258 resulting in inhibition of viral replication via DNA chain termination. Because Tk is conserved in 259 numerous bacterial species, ACV can be taken up and incorporated into DNA, resulting in 260 bactericidal effects [48-51]. Indeed, early studies on DNA replication mechanisms relied on 261 labeling bacterial DNA with tritiated thymidine and many bacterial taxa can be imaged using 262 nucleoside analogues such as 1-(2 -deoxy-2 -fluoro- -D-arabinofuranosyl)-5-[125] iodouracil

263 ([125I]FIAU) that are substrates for HSV Tk [52-55]. Incorporation of [methyl-³H]thymidine into 264 DNA has been unequivocally demonstrated for members of the Clostridium genus [56] and our 265 data show ACV reduced the abundance of the Blautia genus (order Clostridiales; [57]) Blautia 266 hansenii, Blautia stercoris, and Clostridium bolteae in females but not males. Additionally, 267 interrogating the NCBI reference genome sequence for Blautia hansenii confirmed the presence 268 of a thymidine kinase enzyme. Our data are therefore consistent with ACV causing dysbiosis by, 269 at least in part, inhibiting the growth of various bacteria taxa via the Tk mechanism, though other 270 mechanisms involving bacterial metabolism of ACV cannot be excluded. Clearly, the mechanisms 271 by which ACV affects gut bacterial ecology are complex, which is further supported by the sex-272 biased effects.

273

274 We also explored the effects of IVIG treatment alone and in combination with ACV in HSV-275 infected and uninfected mice, because IVIG has been used to treat HSV encephalitis (HSE) and 276 is also a frontline therapy for autoimmune encephalitis, which is triggered by HSE and other insults 277 [58-60]. Moreover, IVIG is being evaluated in a randomized control trial for children with all-cause 278 encephalitis to determine whether neurological outcomes are improved compared to standard 279 antiviral therapy alone, which is similar to our behavioral study that generated paradoxical results 280 [15, 61]. Reports that IVIG's antigenic repertoire includes reactivities to a variety of gut commensal 281 antigens and metabolites have increased recently [62-64], which is consistent with a report that 282 gut commensals can somehow trigger systemic IgG responses under homeostatic conditions that 283 protect against systemic infection [65, 66]. We speculate that by neutralizing bacterial/host 284 antigens/metabolites, IVIG is able to influence host immunity, the nervous system, and other 285 physiological processes, resulting in perturbation of gut bacteria ecology. We speculate that the 286 disparate and complex effects of ACV and IVIG alone and in combination on the gut bacteria 287 ecology likely account for their antagonistic effects on cognitive behavior in mice latently infected 288 with HSV that we alluded to earlier [15].

289

290 This study has several limitations. Being exploratory in nature, analyses of the gut bacteria 291 were done at a single time point immediately after infection or drug treatment, rather than as a 292 longitudinal study that would have provided information on the persistence of the dysbiotic state 293 as well as mechanistic insights as to how HSV, ACV and IVIG provoke dysbiosis. Ideally, the 294 effects of ACV should be tested in latently infected mice, since virtually all HSCT patients harbor 295 latent HSV. However, because HSV infection alone disrupts the gut bacterial community, 296 assessing the effects of ACV on the gut bacteria community structure in the latently infected mice 297 would likely be difficult. Because ACV was given ip to mice but usually orally to HSCT patients 298 [67], its effects on the gut bacteria community maybe underestimated in our study.

299

300 Notwithstanding these caveats, our finding that ACV treatment of HSV infected mice 301 decreased the relative abundances of several bacterial taxa is important because these bacteria 302 have been negatively correlated with the induction of and mortality from GVHD in HSCT patients 303 [24, 27, 28, 30]. These results are also consistent with our hypothesis that ACV contributes to the 304 development of GVHD by changing the gut microbiota. In the context of allo-HSCT, GVHD occurs 305 when donor immune cells recognize recipient tissues as foreign, leading to immune-mediated 306 damage to several organs and tissues including the gastrointestinal tract. This has led 307 researchers to posit that the reduction of anti-inflammatory bacteria such as AIC contribute to 308 GVHD pathology [30]. The results from our study extend this hypothesis to include ACV treatment 309 as a putative contributor to GVHD, because ACV reduced AIC bacteria in the gut. ACV treatment 310 also decreased the relative abundances of several members of the Bacteroidetes, some of which 311 have been shown to exhibit anti-inflammatory properties [68-71]. More relevantly, the capsular 312 polysaccharide A (PSA) from *Bacteroides fragilis* reduced HSV-associated mortality in mice by 313 dramatically reducing immune-mediated inflammation [72]. In addition, the two most abundant 314 OTUs identified in our study, whose relative abundances were positively (Porphyromonadaceae)

315 and negatively (A. muciniphila) correlated with ACV treatment, have been shown to weaken [37. 316 38] and strengthen [39-41] gut barrier function, respectively. These results provide an additional 317 link between ACV treatment and GVHD, because barrier dysfunction, which can cause systemic 318 inflammation, is a hallmark of GVHD [32-36]. Finally, long-term ACV prophylaxis initiated early 319 after HSCT might also impair immune reconstitution based on results from a study of antibiotic 320 depletion of gut bacteria in a murine model of syngeneic bone marrow transplantation [73]. These 321 tantalizing results warrant independent validation and further detailed studies using a murine 322 autologous BMT model to more rigorously evaluate the impact of long-term ACV prophylaxis on 323 GVHD and engraftment, because results from such studies might eventually lead to improved 324 outcomes for HSCT patients. Ideally, such future studies should be performed with mice harboring 325 wild microbiota, because several recent reports show that immune responses in mice with wild 326 microbiomes model human immune responses more closely than conventional mice with SPF 327 microbiota [74-76].

328

329 Materials and Methods.

330

331 Ethics Statement

All animal procedures were performed with prior approval of the City of Hope Institutional Animal
Care and Use Committee (IACUC) under protocol # 07043 and within the framework of the Guide
for the Care and Use of Laboratory Animals. C57BL6/J (B6) were bred in the vivarium at City of
Hope.

337 Mouse Studies

338

Master stocks of HSV1 strain 17 composed of only of cell-released virus were prepared in
 and their titers determined on mycoplasma-free CV-1 cell monolayers. Single use aliquots of virus

341 in Hanks balanced salt solution supplemented with 2% fetal bovine serum were stored at -80°C. Male and female mice, 6-8 weeks of age, were infected with HSV1 17⁺, a virulent strain. Mice 342 343 were sedated with ketamine (60 mg/kg) and xylazine (5 mg/kg) prior to HSV inoculation by corneal 344 scarification. B6 mice were bilaterally inoculated with 1x 10⁵ PFU per eye and monitored daily as 345 previously described [15, 77]. 346 347 Administration of Acyclovir and Intravenous Immunoglobulins. 348 349 ACV obtained from (APP Pharmaceuticals, Schaumburg, IL) was given at 50 mg/kg of 350 body weight by intraperitoneal (ip) injection daily for 3 days starting on day 4 pi and PBS was 351 given according to the same schedule to control mice. IVIG (Carimune, NF) obtained from CSL 352 Behring (King of Prussia, PA, USA) was given ip as a single 0.5 ml dose (25 mg/mouse) on day 353 4 pi or it was given in combination with a 3 day course of ACV. 354 355 Illumina Bacterial 16S rRNA gene sequencing. 356 357 Illumina bacterial 16S rRNA gene libraries were constructed as follows. PCRs were 358 performed in an MJ Research PTC-200 thermal cycler (Bio-Rad Inc., Hercules, CA, USA) as 25 359 µl reactions containing: 50 mM Tris (pH 8.3), 500 µg/ml bovine serum albumin (BSA), 2.5 mM 360 MgCl₂, 250 µM of each deoxynucleotide triphosphate (dNTP), 400 nM of the forward PCR primer, 361 200 nM of each reverse PCR primer, 1 µl of DNA template, and 0.25 units JumpStart Tag DNA 362 (Sigma-Aldrich, MO, USA). PCR 515F polymerase St. Louis, primers

(GTGCCAGCMGCCGCGGTAA) and 806R (GGACTACHVGGGTWTCTAAT) were used to

targeted the 16S rRNA gene containing portions of the hypervariable regions V4 and V5, with the

reverse primers including a 12-bp barcode [78]. Thermal cycling parameters were 94°C for 5 min;

35 cycles of 94°C for 20 s, 50°C for 20 s, and 72°C for 30 s, and followed by 72°C for 5 min. PCR

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367 products were purified using the MinElute 96 UF PCR Purification Kit (Qiagen, Valencia, CA,368 USA).

369

370 **16S rRNA gene data processing**.

371

372 We used the UPARSE pipeline for de-multiplexing, length trimming, guality filtering and 373 operational taxonomic units (OTU) picking using default parameters or recommended guidelines 374 were initially described in [79] and which have been updated that at 375 https://www.drive5.com/usearch/manual/uparse pipeline.html. Briefly, after demultiplexing, 376 sequences were trimmed to a uniform length of 249 bp, then filtered at the recommended 1.0 377 expected error threshold. Sequences were then dereplicated and clustered into zero-radius OTUs 378 using the UNOISE3 algorithm [80], which also detects and removes chimeric sequences; this 379 method is based on making OTUs at 100% identity. An OTU table was then generated using the 380 otutab command. OTUs having non-bacterial DNA were identified by performing a local BLAST 381 search [81] of their seed sequences against the nt database. OTUs were removed if any of their 382 highest-scoring BLAST hits contained taxonomic IDs within Rodentia, Viridiplantae, Fungi, or 383 PhiX. Taxonomic assignments to the OTUs were performed with SINTAX [82] using RDP 384 Classifier 16S training set number 16 [83] as the reference database.

385

386 **16S rRNA gene data analyses**.

Beta diversity was measured using QIIME 1.9.1 [84] to calculate a Hellinger beta diversity distance matrix, which was depicted using principle coordinates analysis (PCoA), and statistically assessed by performing Adonis tests. Statistical differences among the taxa were determined using edgeR [85, 86]. Taxa relative abundance figures were made using Prism (GraphPad, La Jolla, CA). Comparative analyses of the bacterial taxa between human GVHD studies and our mouse study excluded sequence-selective gPCR, because the selectivity of such assays is

- 393 questionable given the conserved nature of the 16S rRNA gene, and because the results of such
- 394 studies are not typically validated by sequence analyses. The bacterial sequences have been
- 395 deposited in the National Center for Biotechnology Information (NCBI)'s Sequence Read Archive
- 396 (SRA) under the BioProject Accession Number PRJNA549765.
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- 398

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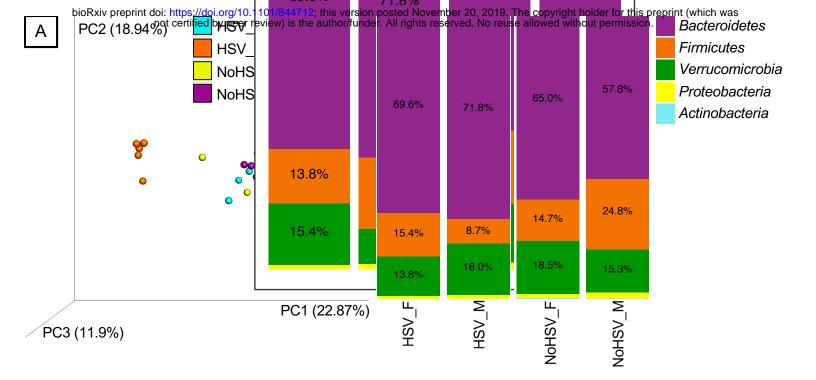
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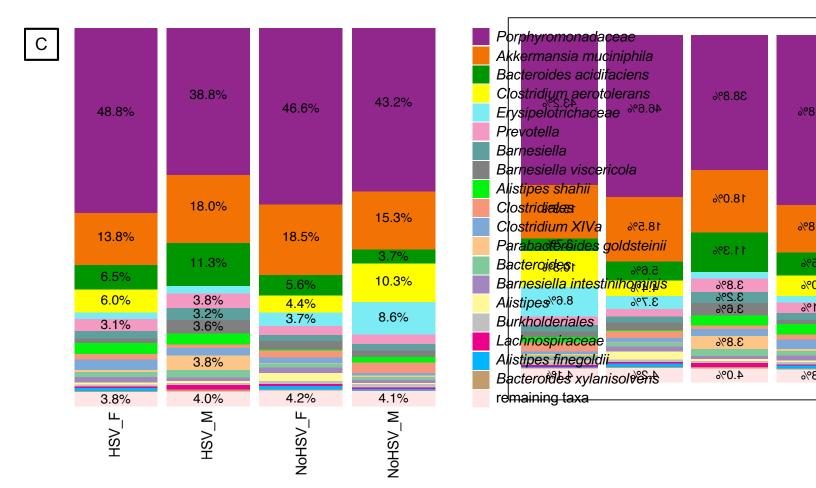
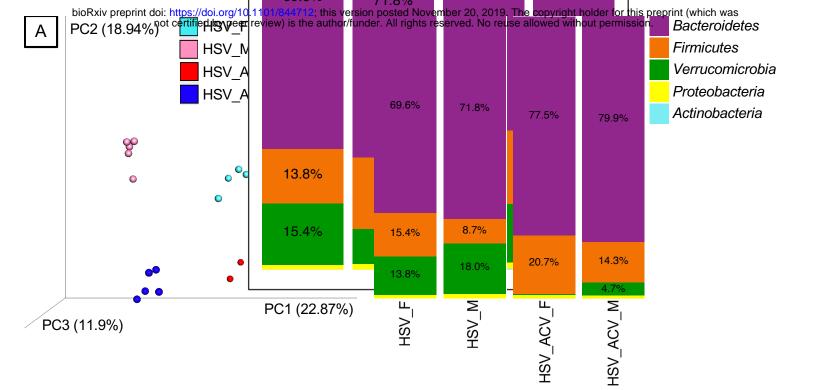


Figure 1. Fecal Bacteria from HSV-Infected and Uninfected Mice. A. Principal-coordinates analysis (PCoA) of Hellinger beta diversity distance values generated from 16S rRNA gene sequences. All four groups were different (P<0.05, Adonis Tests). The number of mice (n) in each genotype-microbiota group are shown in parentheses. B. Bacteria phyla associated with HSV-infected and uninfected mice. C. Bacterial species (or higher taxa) associated with HSV-infected and uninfected mice = _M.



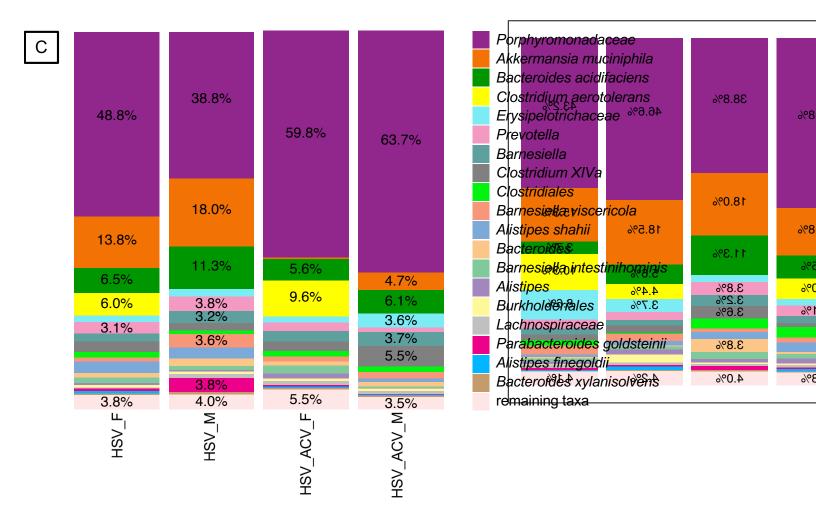


Figure 2. Fecal Bacteria from HSV-Infected Mice Treated and Not Treated with ACV. A. Principal-coordinates analysis (PCoA) of Hellinger beta diversity distance values generated from 16S rRNA gene sequences. All four groups were different (P<0.05, Adonis Tests). The number of mice (n) in each genotype-microbiota group are shown in parentheses. B and C. Bacteria phyla and species (or higher taxa), respectively, associated with HSV-infected mice treated and not treated with ACV. Females = _F and Males = _M.

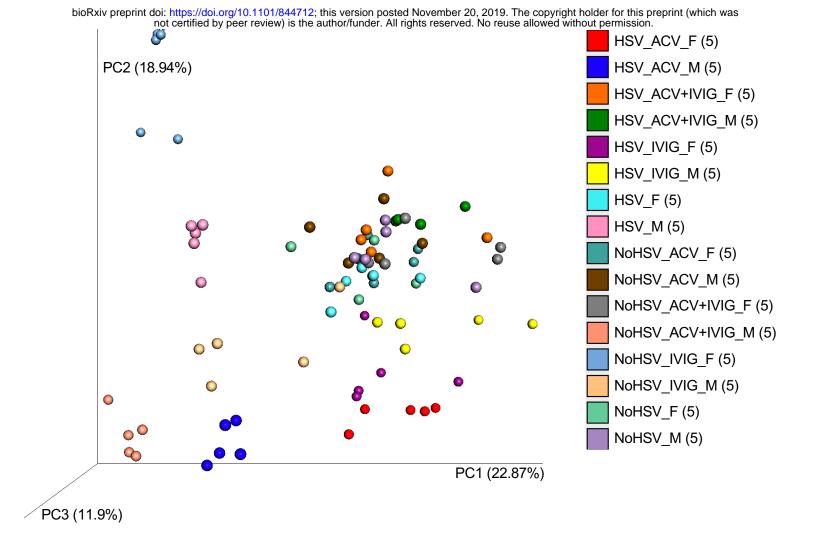


Figure 3. Beta Diversity Analysis of Fecal Bacteria from HSV-Infected and Uninfected Mice Treated and Not Treated with ACV and/or IVIG. Principal-coordinates analysis (PCoA) of Hellinger beta diversity distance values generated from 16S rRNA gene sequences. The number of mice (n) in each genotype-microbiota group are shown in parentheses. Females = _F and Males = _M.

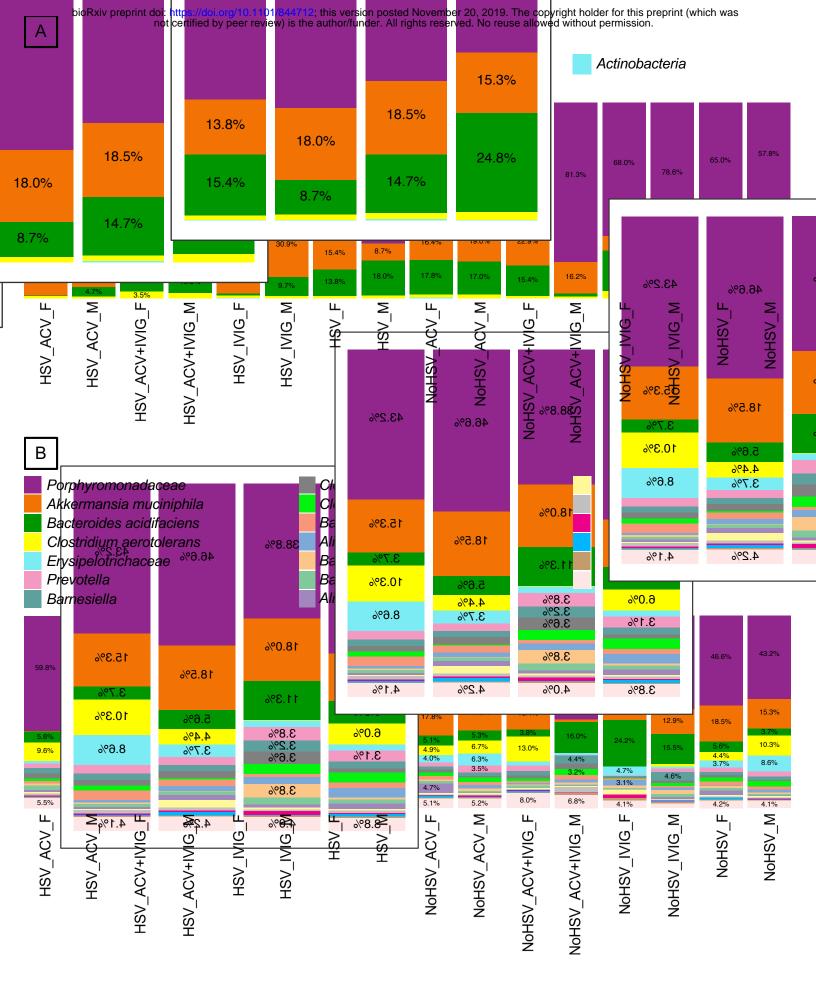


Figure 4. Fecal Bacterial from HSV-Infected and Uninfected Mice Treated and Not Treated with ACV and/or IVIG. A and B. Bacteria phyla and species (or higher taxa), respectively, associated with HSV-infected and uninfected mice treated and not treated with ACV, IVIG, or ACV+IVIG. Females = _F and Males = _M.

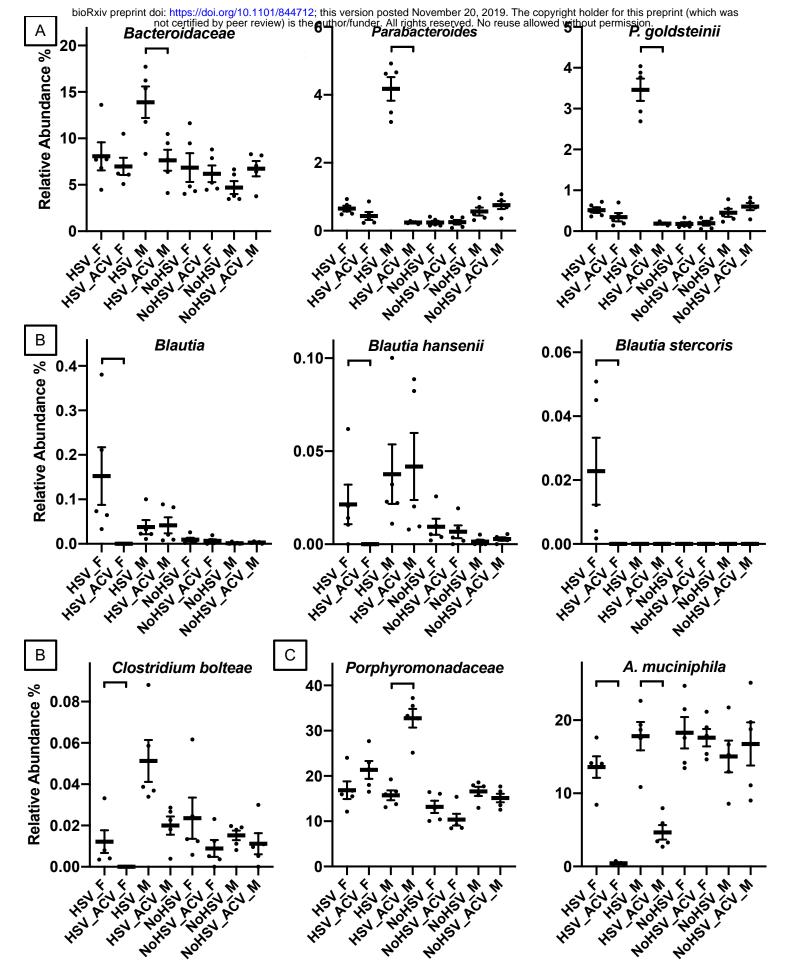


Figure 5. Fecal Bacterial from HSV-Infected and Uninfected Mice Treated and Not Treated with ACV. A and B. Fecal bacterial taxa that were were changed in both human GVHD studies and by ACV in this study. A and B. Members of the *Bacteroidetes* and AIC, respectively. C. The two most abundant bacterial OTUs. The only pairwise differences shown are between ACV treated and untreated mice for each sex (FDR-adjusted P values < 0.05). Bars = standard error. Females = _F and Males = _M.