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2 faecal samples from healthy subjects and those treated with antibiotics.

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#### 18 Abstract

A healthy, intact gut microbiota is often resistant to colonisation by gastrointestinal 19 20 pathogens. During periods of dysbiosis, however, organisms such as *Clostridioides difficile* 21 can thrive. We describe an optimised in vitro Colonisation Resistance Assay for C. difficile in 22 Stool (CRACS) and demonstrate the utility of this assay by assessing changes to colonisation 23 resistance following antibiotic exposure. Faecal samples were obtained from healthy volunteers (n=6), and from healthy subjects receiving five days of moxifloxacin (n=11) or no 24 25 antibiotics (n=10). Samples were separated and either not manipulated (raw), or sterilised (autoclaved or filtered) prior to inoculation with C. difficile ribotype 027 spores and 26 anaerobic incubation for 72 hours. Different methods of storing faecal samples were also 27 investigated in order to optimise the CRACS. In healthy, raw faecal samples, incubation with 28 29 spores did not lead to increased *C. difficile* total viable counts (TVC) or cytotoxin detection. By contrast, increased *C. difficile* TVC and cytotoxin detection occurred in sterilised healthy 30 31 faecal samples or those from antibiotic-treated individuals. The CRACS was functional with faecal samples stored at either 4°C or -80°C, but not with those with glycerol (12% or 30% 32 v/v). Our data show that the CRACS successfully models *in vitro* the loss of colonisation 33 34 resistance, and subsequent C. difficile proliferation and toxin production. CRACS could be 35 used as a proxy for *C. difficile* infection in clinical studies, or to determine if an individual is at risk of developing C. difficile infection, or other potential infections occurring due to a loss 36 37 of colonisation resistance.

38

#### 40 Introduction

The burden of *Clostridioides difficile* (previously *Clostridium difficile*) infection (CDI) is 41 42 substantial (1, 2). Asymptomatic carriage of *C. difficile* varies markedly according to risk factors, notably antibiotic exposure and hospitalisation of individuals (3-5). For CDI to occur, 43 44 *C. difficile* spores must reach the colon, germinate and produce toxin. Within a healthy gut 45 microbiota, colonisation resistance to C. difficile is maintained, and so C. difficile proliferation and toxin production in the colon is unlikely to occur. By contrast, in a 46 47 dysbiotic gut microbiota, such as that caused by broad spectrum antibiotic treatment, C. 48 *difficile* can colonise, proliferate and cause disease (6, 7). 49 Investigating C. difficile colonisation resistance can be labour intensive. Current methods include clinical trials (8, 9), animal models (10, 11), and in vitro continuous models (12, 13), 50 51 all of which are extremely time consuming and expensive. Simple models that can quickly 52 determine if colonisation resistance to C. difficile is present or absent are needed, however 53 few studies have used batch culture based models to assess colonisation resistance in 54 humans (14, 15). Borriello and Barclay demonstrated the vegetative growth of C. difficile in the stools of individuals who had received antibiotics but not those of healthy individuals, 55 although this was not demonstrated longitudinally in the same subject. They also showed 56 57 that sterilisation of healthy faecal samples by autoclaving, or by filter sterilisation led to a 58 loss of colonisation resistance to C. difficile, with subsequent C. difficile growth and 59 sporulation.

Building on the study by Borriello and Barclay, we have developed and examined the utility
of an *in vitro* <u>C</u>olonisation <u>R</u>esistance <u>A</u>ssay for <u>C</u>. *difficile* in <u>S</u>tool (CRACS), using *C*. *difficile*spores of a ribotype 027 strain. We have determined the effects of faecal storage

- 63 conditions on the performance of the assay, and successfully used the optimised assay to
- 64 assess the change in colonisation resistance of healthy human subjects following antibiotic
- 65 treatment.
- 66

#### 67 Materials and Methods

68 Study design

69 The CRACS assay provides a measure of colonisation resistance against *C. difficile* for a given stool 70 sample. C. difficile germination and proliferation is expected in sterilised stool samples, whereas the 71 germination and proliferation of C. difficile in raw stool depends on the colonisation resistance of the 72 stool sample. In this study, we have established the premise of this assay, undertaken to optimise 73 conditions for this assay, and then validated the assay using samples from a clinical study. The assay 74 and different conditions evaluated in this study are described in figure 1. 75 During the optimisation phase of this study, healthy volunteers over the age of 18 (n=6) with no 76 history of antibiotic receipt in the last 3 months were recruited to provide anonymous faecal 77 samples. Sample size was determined to ensure at least three individual samples were tested for 78 each condition (sterilisation technique, storage temperature and use of glycerol, effect of freeze-79 thaw). 80 In order to validate the optimised assay, we used faecal samples from a phase 1 clinical study 81 (unpublished). Healthy volunteers provided faecal samples before and after treatment with either 82 moxifloxacin (n=11) or no antibiotic (n=10). All available faecal samples from this study were used. 83

### 84 Faecal samples

Unless otherwise stated faecal samples were provided by healthy volunteers (aged 18-65 years) with no history of antibiotic therapy in the past 3 months. Sample production kits included an AnaeroGen W-Zip Compact Generator system (Oxoid, Hampshire, UK) which maintained the sample in an anaerobic environment prior to processing. Samples were confirmed negative for *C. difficile* by both culture on Brazier's CCEYL agar (cefoxitin [8 mg/L], 90 cycloserine [250 mg/L], lysozyme [5 mg/L], supplemented with 2% lysed, defibrinated horse
91 blood) and by screening for the presence of GDH antigen using the C.DIFF CHEK-60 enzyme
92 immunoassay (DS2, Megellan Biosciences Dynex) before use. Collection of faecal samples
93 was approved by the University of Leeds Research Ethics Committee (Reference numbers:
94 MREC15-070 and MREC17-011).

95 The CRACS assay

The assay and the different conditions evaluated for optimisation are outlined in figure 1. 96 97 Faecal samples were diluted in pre-reduced PBS (1:10 w/v), homogenised in a stomacher 98 and filtered through muslin to remove any large particulate matter. Each sample was 99 processed in raw and sterilised forms (Fig. 1). In an anaerobic environment, samples were inoculated with C. difficile ribotype 027 spores (1:100 v/v of a spore prep containing  $5 \log_{10}$ 100 CFU/mL), and incubated anaerobically at 37°C for 72 hours. At 0, and 72 hours post 101 102 inoculation, C. difficile total viable counts (TVC), spore counts and cytotoxin titres were 103 measured. An observed increase in TVCs and toxin production in raw aliquots at 72 hours 104 compared to 0 hours post inoculation indicates a lack of colonisation resistance. C. difficile clinical strains of ribotypes 027, 078, and 014 were initially tested in raw and 105 106 autoclaved faeces. No strain to strain differences were observed in TVC or spore counts, 107 although the C. difficile ribotype 027 strain yielded slightly higher cytotoxin titres (data not shown). This finding and the high clinical significance/prevalence of ribotype 027 (16) led to 108 109 the selection of this strain for the assay.

110

111 Enumeration of C. difficile total viable counts, spores and cytotoxin

112 Total viable counts were enumerated by serial 10-fold dilution, plating onto Brazier's CCEYL agar and anaerobic incubation for 48 hours. Spore counts were enumerated by the same 113 method following 1 hour incubation in an equal volume of 100% ethanol. Cytotoxin levels 114 115 were measured using the Vero cell cytotoxicity assay as described previously (17, 18). Briefly, sample supernatants were applied 1:10 to a Vero cell monolayer in duplicate, 10-116 117 fold serially diluted and incubated at 37°C in 5% CO<sub>2</sub> (Precision 190, LEEC). Cell rounding was 118 assessed relative to positive and negative controls at 24 and 48 hours using inverted 119 microscopy. C. difficile toxin was confirmed by the presence of ≥80 % cell rounding that was neutralised by Clostridium sordellii antitoxin (1:100 v/v) (Prolab Diagnostics, Bromborough, 120 121 UK).

122

123 CRACS Optimisation

## 124 1. Effect of sterilisation techniques on colonisation resistance

Faecal slurries were separated into equal sized aliquots. Each aliquot was either maintained
anaerobically overnight (raw), autoclaved at 121°C for 15 mins (autoclaved), or centrifuged
at 16000g for 10 minutes prior to filter sterilisation through a 0.22 μm syringe filter (filtered)
prior to anaerobic incubation and use in the CRACS assay (Fig 1). Sterilised samples were
plated onto nutrient agar and fastidious anaerobe agar (FAA, Oxoid, UK)) and incubated
aerobically and anaerobically to evaluate sterility. Sporadic colonies were observed, but not
counted.

132 2. Effect of faecal sample storage on colonisation resistance

133 To determine the effect of different storage conditions on colonisation resistance, faecal samples were stored for 16-24 hours at: room temperature (RT, anaerobic), 4°C (4°C), -80°C 134 (-80°C), -80°C + 12% glycerol (12% glycerol), and -80°C + 30% glycerol (30% glycerol) prior to 135 136 use in the CRACS assay (Fig 1). Samples stored with glycerol were diluted to the same level as those without (1:10), homogenised using a stomacher, filtered through muslin and stored 137 immediately. As required, samples were defrosted thoroughly, at room temperature, prior 138 139 to processing as raw, and sterilised aliquots. Additionally, to determine whether the 140 concentrations of glycerol used had an effect on C. difficile germination and growth, C. 141 difficile spores (1:100 v/v) were inoculated into BHI broth (supplemented with 0.1%142 Taurocholate + 0.4% glycine (Sorg and Sonenshein, 2008)) containing 0%, 12% or 30% glycerol and incubated anaerobically for 72 hours, prior to enumeration of *C. difficile* spores, 143 vegetative cells and toxin as described above. 144

## 145 3. Effect of multiple freeze-thaw cycles on colonisation resistance

Fresh faecal samples were stored anaerobically for 16-24 hours at room temperature, and frozen at -80°C. Faecal samples were thawed, diluted, homogenised using a stomacher, and separated into two, 2 g aliquots (as above). One aliquot was processed through CRACS assay immediately and the other was frozen at -80°C for processing at a later date. These samples were processed using both autoclaving and filtration sterilisation techniques as discussed above.

152

153 Use of the CRACS assay to investigate the effect of antibiotics on colonisation resistance.

Faecal samples from healthy individuals treated with either the fluoroquinolone antibiotic 154 155 moxifloxacin, or a placebo, were provided by Da Volterra (Paris, France). Briefly, healthy volunteers (aged 18-60) with no history of antibiotic therapy in the past 3 months, and 156 devoid of faecal C. difficile colonisation, were either treated with oral moxifloxacin 400 mg 157 158 once a day (Izilox, Bayer HealthCare) for 5 days (treatment group), or did not receive 159 antibiotics (control group). Faecal samples were collected within the last 24h before the first 160 drug administration (D1), and first 24h following the last drug administration (D6), were 161 homogenised using a stomacher, aliquoted and kept frozen at -80°C until processing for the CRACS assay using the filtration sterilisation technique described above. Total viable counts 162 163 and toxin production was measured, but spore counts were not. Treatment of subjects and collection of samples, were approved by ANSM (Agence Nationale de Sécurité des 164 Médicaments) and the Comité de Protection des Personnes Sud-Est IV, and registered as ID-165 166 RCB: 2015-A01899-40, and on Clinicaltrials.gov under number NCT02917200; all subjects 167 had agreed the use of samples for such ancillary biological analysis as informed in their consent form (19). 168

#### 169 *C. difficile spore preparation*

The *C. difficile* PCR ribotype 027 strain 210 (BI/NAP1/toxinotype III) used here was isolated during an outbreak of CDI at the Maine Medical Centre (Portland, ME, USA) and supplied courtesy of Dr Robert Owens (formally at Maine Medical Centre). The *C. difficile* ribotype 078 (R10725) and ribotype 014 (R11446) were sourced from the Anaerobic Reference Unit Cardiff, Wales. *C. difficile* was cultured from -80°C stocks on Brazier's CCEYL agar (cefoxitin [8 mg/L], cycloserine [250 mg/L], lysozyme [5 mg/L], supplemented with 2% lysed, defibrinated horse blood), and checked for purity after 48 hour anaerobic growth at 37°C. Growth was harvested on a sterile swab and transferred to 40 pre-reduced Columbia Blood
Agar (CBA) plates and incubated anaerobically at 37°C for 14 days. Growth from the CBA
plates was re-suspended in 50 % ethanol in saline and vortexed for approximately 5 mins.
The spore preparation was enumerated on Brazier's CCEYL agar and standardised to

181 approximately 5 log10 CFU/mL.

182 Data analysis

- 183 All data presented is the  $\Delta$  change in the geometric mean over 72 hours (geometric mean at
- 184 72h minus geometric mean at 0h). All data were analysed on SPSS version 23, and
- presented on graphs produced in Graphpad prism version 5. Due to the sample size often
- being less than 10 all data were treated as non-parametric and analysed using Kruskal-Wallis
- 187 with Dunns pairwise comparison and Bonferroni correction where applicable. If there was a
- single comparison a Wilcoxon rank sum test was performed.

189 Results

- 190 Stool samples from healthy volunteers (n=6) were used to confirm the utility of this assay,
- and investigate optimal sterilisation technique and storage conditions. The optimised assay
- 192 was then validated using stool samples from healthy volunteers before and after treatment
- 193 with either moxifloxacin (n=11) or no antibiotic (n=10).
- 194 Effect of sterilisation techniques on colonisation resistance

The CRACS assesses colonisation resistance by comparing growth of *C. difficile* in raw vs sterilised faeces. We wanted to compare sterilisation by autoclaving with sterilisation by filtration for use in this assay. Sterilising faeces by either autoclaving or filtration resulted in loss of colonisation resistance to *C. difficile*, with mean TVC increases of 3.4 log<sub>10</sub> cfu/ml and 2.7 log<sub>10</sub> cfu/ml, respectively, after 72 hours of incubation. Colonisation resistance
remained in the raw samples, where there was no observed increase in *C. difficile* TVC (0
log<sub>10</sub> cfu/ml, Figure 2). Similar patterns were observed for spore populations; there was no
increase in spore counts in raw samples, while autoclaved and filtered faeces yielded
increases in spores of 1.9 log<sub>10</sub> cfu/ml and 1.0 log<sub>10</sub> cfu/ml, respectively (supplementary
Figure 1). Cytotoxin was not observed in raw samples, but was universally detected in the
autoclaved and filtered faeces (Table 1).

206

207 Effect of faecal sample storage on colonisation resistance In order for this assay to be 208 clinically useful, the effect of sample storage prior to processing must be investigated, and optimal storage conditions determined. We therefore investigated a range of different 209 210 storage conditions. In the raw faecal samples, there was no effect of sample storage on C. 211 *difficile*  $\Delta$  TVC (Figure 3A) or spores counts (supplementary Figure 2A) at 72 hours, and 212 cytotoxin was not detected (Table 1). In autoclaved samples, storage temperature did not 213 affect the  $\Delta$  change in *C. difficile* TVC, which increased by 2.7 log<sub>10</sub> cfu/ml and 3.1 log<sub>10</sub> cfu/ml for samples stored at 4°C and -80°C, respectively (Figure 3B); similar effects were 214 seen in the spore counts (supplementary figure 2B). However, the presence of glycerol did 215 affect C. difficile growth in autoclaved samples, with the  $\Delta$  change in TVC between 0 and 72 216 217 hours being ~1.5 log<sub>10</sub> cfu/ml and 2.0 log<sub>10</sub> cfu/ml less, in 12% and 30% glycerol containing 218 samples respectively when compared to non-glycerol treated samples stored at -80°C (Fig 219 3B). Cytotoxin detection was also reduced in samples with added glycerol (Table 1). 220 Differences due to storage were even more apparent in the filtered faecal samples. Samples stored at -80°C resulted in a higher  $\Delta$  TVC compared with those held at 4°C. When 221

samples were stored in glycerol, there was no increase in *C. difficile* TVC, which was lower
than samples stored at 4°C (p = 0.026) and -80°C (Figure 3C). In addition, there was no
detection of cytotoxin in samples stored with glycerol. Growth of *C. difficile* in BHI with
taurocholic acid (TCA) was not affected by 12% glycerol, however with 30% glycerol there
was a lower TVC compared with the other conditions, and no cytotoxin was detected (Figure
3D, Table 1).

228

## 229 Effect of freeze-thaw cycles

Two freeze-thaw cycles did not affect *C. difficile* TVC (Figure 4A) nor cytotoxin levels (Table
1). Colonisation resistance was maintained in raw samples (~-0.1 log<sub>10</sub> cfu/ml) but was lost
in the autoclaved and filtered samples (TVC increased 2.4 log<sub>10</sub> cfu/ml and 3.6 log<sub>10</sub> cfu/ml,
respectively). In contrast, freeze-thaw cycles altered the spore counts (Figure 4B).

234

235

*Use of the CRACS assay to investigate the effect of antibiotics on colonisation resistance.* 236 237 CRACS allows a measure of colonisation resistance against C. difficile to be determined for individual faecal samples. We used the assay on stool samples from a clinical study to 238 determine whether antibiotic exposure affected colonisation resistance to C. difficile. 239 240 Healthy individuals were given the fluoroquinolone antibiotic moxifloxacin for 5 days, or no 241 antibiotics (control). Faecal samples were provided before and after treatment, and colonisation resistance to C. difficile was evaluated. Samples were raw or sterilised by 242 filtration. Colonisation resistance in stool samples taken before the beginning of treatment 243

244 (D1) did not differ between the treatment and control groups; no increase in TVCs was observed in raw samples (Figure 5A) but an increase of ~3.2 log<sub>10</sub> cfu/mL was observed in 245 246 sterilised samples (Figure 5B). After 5 days of antibiotic treatment (D6) differences were 247 observed between the treatment and control groups. Colonisation resistance was maintained in the control group, but lost in antibiotic recipient; raw samples taken post 248 antibiotic treatment showed an increase in TVC of 2.4 log  $_{10}$  cfu/ml (p = 0.007, Figure 5A), 249 250 which was associated with an increase in the proportion of samples with detected cytotoxin 251 (Table 1). Filter sterilised samples did not differ irrespective of treatment group or time 252 point; colonisation resistance was lost on all occasions with a TVC increase of ~3.2 log<sub>10</sub> 253 cfu/ml for all samples (Figure 5B) and a high percentage of toxin detection (Table 1).

254

255

### 256 Discussion

We have demonstrated that the CRACS can be used to determine whether colonisation resistance to *C. difficile* expansion is intact in human stool samples. When raw, healthy faecal samples are inoculated with *C. difficile* spores, spore germination, *C. difficile* proliferation, and cytotoxin production do not occur. In contrast, when faecal samples are sterilised either by autoclaving or filtration, spores germinate, *C. difficile* proliferates and cytotoxin is detected.

Our data build on the study by Borriello and Barclay (1986) who used untreated and
sterilised faecal samples from different individuals and found that colonisation resistance is
lost in sterilised samples. We have confirmed this finding, undertaken comparative studies

266 to create a reproducible optimised assay that can be used on faecal samples from human clinical studies, and used the optimised assay to demonstrate longitudinally in healthy 267 268 subjects that colonisation resistance is lost following fluoroquinolone treatment. In 269 previous studies by both Boriello and Barclay and Horvat and Rupnik (2018) investigating colonisation resistance of human stool samples, batch cultures were inoculated with C. 270 *difficile* vegetative cells. Here, we have chosen to inoculate batch cultures with spores. In 271 272 preliminary work (data not shown) we found inoculations of both vegetative cells and spores to work in this assay, however, as spores notably represent the primary 273 274 infective/transmission form of C. difficile (20), and are more straightforward to prepare and 275 manipulate *in vitro*, we found it advantageous to use spores. 276 Importantly, we have also shown that the CRACS can be used to evaluate faecal samples from individuals with potential dysbiosis and provide a measure of colonisation resistance. 277 In individuals treated with the fluoroquinolone antibiotic moxifloxacin for five days, there 278 279 was a significant reduction in colonisation resistance compared with a faecal sample 280 obtained in the 24h prior to the first antibiotic administration (Figure 5). Interestingly, our data appear to show a binary distribution, with approximately half of samples taken following 5 days 281 282 of moxifloxacin therapy supporting large increases in C. difficile growth, while the other half yield 283 results that resemble control samples. The intestinal microbiota varies between individuals, and 284 individualised responses to antibiotic exposure have been reported (21, 22). Therefore, variation in 285 the alterations to the gut microbiota in our participants would be expected. Whist microbiota 286 diversity is thought to be important, and various microbiota changes have been linked to CDI (23), 287 the exact components conferring colonisation resistance are as yet unclear. Our assay is designed to 288 give a qualitative but not a quantitative assessment of colonisation resistance. Thus, according to

our assay and supported by clinical observations, in some patients, microbiota disruption following
 antibiotic exposure leads to loss of colonisation resistance, whilst in others, it does not.

Our results are in line with those of Horvat and Rupnik (2018) who observed a loss of colonisation resistance in dysbiotic faecal samples. Crucially, our data suggest that this assay may also be an effective proxy measurement for risk of *C. difficile* infection prior/ during antibiotic treatment.

295 We have examined potential confounders relating to faecal sample storage, which are 296 important in understanding the utility of this assay, including the desire to batch test and examine specimens retrospectively. Notably, storage temperature had limited effects on 297 298 the assay; raw samples from healthy individuals did not support C. difficile germination, growth or toxin production, irrespective of storage condition. Some variation due to 299 storage temperature was observed in the sterilised portions of assay (which can be used as 300 301 a positive control); greater C. difficile proliferation occurred in sterilised samples stored at -302 80°C compared to those stored at 4°C. Storage temperature of faecal samples has been shown to have little effect on microbial populations, and their amplitude are modest in 303 304 comparison with inter-subject variability (24-26). By contrast, sample storage in glycerol, a common cryoprotectant, was detrimental in terms of CRACS performance. Following 305 glycerol storage, no C. difficile germination, growth or toxin production was observed in the 306 307 sterilised portions of the assay, contrary to expectation and to those samples stored without 308 glycerol. In addition, when inoculated into BHI in the presence of TCA and glycine, known inducers of germination (27), no increases in C. difficile TVC were observed when 30% 309 glycerol was used for storage, although C. difficile growth was unaffected by 12% glycerol. 310 The reasons for this are unknown, but it seems clear that faecal samples should be stored 311

312 without glycerol prior to analysis using CRACS or other colonisation resistance assays reliant on C. difficile growth. One or two freeze-thaw cycles were not detrimental to the 313 314 maintenance or loss of colonisation resistance when assessing C. difficile germination and 315 growth (total viable counts), but spore counts were affected. The reason for this is not clear as C. difficile spores have been demonstrated to be resistant to many different 316 environmental stressors (28). Additionally, the spore counts did not follow the patterns of 317 318 the TVC, or cytotoxin titre (Figure 3, Table 1), something that was already observed after the 319 first freeze-thaw cycle.

320 A key advantage of the CRACS is that it is relatively quick and inexpensive to perform. We recommend that for the assay to function optimally, a sterilisation technique is used as a 321 control, and faecal samples are stored at -80°C without glycerol. One or two freeze-thaw 322 cycles will not affect results of the assay. Continuous culture models have been used 323 repeatedly to demonstrate the capacity of spores to induce CDI and assess the effectiveness 324 325 of therapeutics (12, 13, 29). While these models closely simulate in vivo conditions and indeed are clinically reflective, they are time consuming, technically demanding, low 326 throughput and expensive. 327

328 This study is limited, as the optimised assay has only been validated on stool samples from a 329 relatively small number of healthy volunteers in a clinical study (n=21). We plan to further validate 330 this assay with larger numbers of subjects from a wider range of clinical studies. Additionally, it is 331 difficult to determine the extent to which this assay truly reflects colonisation resistance in patients, 332 as controlled exposure of patients to C. difficile spores is not possible. Prospective studies are 333 problematic. Only a low number of patients receiving antibiotics go on to develop CDI, and so such 334 studies would need to be extremely large (and expensive) to garner meaningful data. However, we 335 believe that some measure of clinical reflectivity could be achieved with retrospective studies, or by examining particular subsets of patients such as those undergoing faecal microbiota transplantation
(FMT), targeted restoration therapy, or microbiota sparing treatments.

338 Interest in microbiota sparing antibiotics and microbiota restoring treatments is high, and 339 multiple clinical studies are underway. Currently, the only way to assess CDI risk in such 340 trials is to determine what proportion of subjects go on to develop C. difficile mediated 341 disease. This will always be a very low number given the clinical dynamics of CDI, and 342 therefore extremely large clinical trials are required to show any difference in CDI rates. 343 Microbiome analyses which use parameters such as microbiota diversity, richness or 344 presence / absence of specific components are therefore used as a proxy measurement. However, as the exact components and factors responsible for C. difficile colonisation 345 346 resistance are unknown, the utility of these are limited. We have demonstrated that CRACS can be used to rapidly assess the presence of colonisation resistance within faecal samples 347 348 from both healthy individuals and those receiving antibiotics. We believe that this assay 349 could be used as a proxy for CDI risk, adding important data to clinical studies, particularly small early phase studies and those investigating the effectiveness of preventative 350 351 approaches.

352

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355 Transparency declarations

A.A. and J.G. are consultants and shareholders of Da Volterra. N.S.L and F.S.G are employees

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<ol> <li>Freeman J, Wilcox MH. 2003. The effects of storage conditions on viability of <em>Clostridium difficile</em> vegetative cells and spores and toxin activity in human faeces. Journal of Clinical Pathology 56:126-128.</li> <li>Ducher A, Mentré F, Donazzolo Y, Latreille M, Burdet C, Nguyen T, Varastet M, Sablier F, Augustin V, Hugon P, Ferreira S, Andremont A, de Gunzburg J. 2018. Dose-effect and safety of DAV132, an activated charcoal based product, when given with oral moxifloxacin on free moxifloxacin fecal concentrations and intestinal microbiota diversity: a randomized controlled trial in 144 healthy volunteers abstr European Congress of Clinical Microbiology and Infectious Diseases (ECCMID), Madrid,</li> <li>Theriot CM, Young VB. 2015. Interactions Between the Gastrointestinal Microbiome and Clostridium difficile. Annual Review of Microbiology 69:445-461.</li> <li>Dethlefsen L, Relman DA. 2011. Incomplete recovery and individualized responses of the human distal gut microbiota to repeated antibiotic perturbation. Proc Natl Acad Sci U S A 108 Suppl 1:4554-61.</li> <li>Fujisaka S, Ussar S, Clish C, Devkota S, Dreyfuss JM, Sakaguchi M, Soto M, Konishi M, Softic S, Altindis E, Li N, Gerber G, Bry L, Kahn CR. 2016. Antibiotic effects on gut microbiota and metabolism are host dependent. J Clin Invest 126:4430-4443.</li> <li>Buffie CG, Bucci V, Stein RR, McKenney PT, Ling L, Gobourne A, No D, Liu H, Kinnebrew M, Viale A, Littmann E, van den Brink MR, Jenq RR, Taur Y, Sander C, Cross JR, Toussaint NC, Xavier JB, Pamer EG. 2015. Precision microbiome reconstitution restores bile acid mediated resistance to Clostridium difficile. Nature 517:205-8.</li> <li>Choo JM, Leong LEX, Rogers GB. 2015. Sample storage conditions significantly influence faced microbiome nerofiles. Scientific Renext E:16250</li> </ol>	422		Chemotherapy 55:974-982.
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<ul> <li>faeces. Journal of Clinical Pathology 56:126-128.</li> <li>Ducher A, Mentré F, Donazzolo Y, Latreille M, Burdet C, Nguyen T, Varastet M, Sablier F, Augustin V, Hugon P, Ferreira S, Andremont A, de Gunzburg J. 2018. Dose-effect and safety of DAV132, an activated charcoal based product, when given with oral moxifloxacin on free moxifloxacin fecal concentrations and intestinal microbiota diversity: a randomized controlled trial in 144 healthy volunteers abstr European Congress of Clinical Microbiology and Infectious Diseases (ECCMID), Madrid,</li> <li>Theriot CM, Young VB. 2015. Interactions Between the Gastrointestinal Microbiome and Clostridium difficile. Annual Review of Microbiology 69:445-461.</li> <li>Dethlefsen L, Relman DA. 2011. Incomplete recovery and individualized responses of the human distal gut microbiota to repeated antibiotic perturbation. Proc Natl Acad Sci U S A 108 Suppl 1:4554-61.</li> <li>Fujisaka S, Ussar S, Clish C, Devkota S, Dreyfuss JM, Sakaguchi M, Soto M, Konishi M, Softic S, Altindis E, Li N, Gerber G, Bry L, Kahn CR. 2016. Antibiotic effects on gut microbiota and metabolism are host dependent. J Clin Invest 126:4430-4443.</li> <li>Buffie CG, Bucci V, Stein RR, McKenney PT, Ling L, Gobourne A, No D, Liu H, Kinnebrew M, Viale A, Littmann E, van den Brink MR, Jenq RR, Taur Y, Sander C, Cross JR, Toussaint NC, Xavier JB, Pamer EG. 2015. Precision microbiome reconstitution restores bile acid mediated resistance to Clostridium difficile. Nature 517:205-8.</li> <li>Choo JM, Leong LEX, Rogers GB. 2015. Sample storage conditions significantly influence faecal microbiome archies. Scientific Reports 5:16250</li> </ul>	424		<pre><em>Clostridium difficile</em> vegetative cells and spores and toxin activity in human</pre>
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<ul> <li>of DAV132, an activated charcoal based product, when given with oral moxifloxacin on free</li> <li>moxifloxacin fecal concentrations and intestinal microbiota diversity: a randomized</li> <li>controlled trial in 144 healthy volunteers abstr European Congress of Clinical Microbiology</li> <li>and Infectious Diseases (ECCMID), Madrid,</li> <li>20. Theriot CM, Young VB. 2015. Interactions Between the Gastrointestinal Microbiome and</li> <li>Clostridium difficile. Annual Review of Microbiology 69:445-461.</li> <li>21. Dethlefsen L, Relman DA. 2011. Incomplete recovery and individualized responses of the</li> <li>human distal gut microbiota to repeated antibiotic perturbation. Proc Natl Acad Sci U S A</li> <li>108 Suppl 1:4554-61.</li> <li>22. Fujisaka S, Ussar S, Clish C, Devkota S, Dreyfuss JM, Sakaguchi M, Soto M, Konishi M, Softic S,</li> <li>Altindis E, Li N, Gerber G, Bry L, Kahn CR. 2016. Antibiotic effects on gut microbiota and</li> <li>metabolism are host dependent. J Clin Invest 126:4430-4443.</li> <li>23. Buffie CG, Bucci V, Stein RR, McKenney PT, Ling L, Gobourne A, No D, Liu H, Kinnebrew M,</li> <li>Viale A, Littmann E, van den Brink MR, Jenq RR, Taur Y, Sander C, Cross JR, Toussaint NC,</li> <li>Xavier JB, Pamer EG. 2015. Precision microbiome reconstitution restores bile acid mediated</li> <li>resistance to Clostridium difficile. Nature 517:205-8.</li> <li>24. Choo JM, Leong LEX, Rogers GB. 2015. Sample storage conditions significantly influence</li> <li>faceal microbiome profiles. Scientific Reports 5:16220</li> </ul>	427		Augustin V, Hugon P, Ferreira S, Andremont A, de Gunzburg J. 2018. Dose-effect and safety
<ul> <li>moxifloxacin fecal concentrations and intestinal microbiota diversity: a randomized</li> <li>controlled trial in 144 healthy volunteers abstr European Congress of Clinical Microbiology</li> <li>and Infectious Diseases (ECCMID), Madrid,</li> <li>20. Theriot CM, Young VB. 2015. Interactions Between the Gastrointestinal Microbiome and</li> <li>Clostridium difficile. Annual Review of Microbiology 69:445-461.</li> <li>21. Dethlefsen L, Relman DA. 2011. Incomplete recovery and individualized responses of the</li> <li>human distal gut microbiota to repeated antibiotic perturbation. Proc Natl Acad Sci U S A</li> <li>108 Suppl 1:4554-61.</li> <li>22. Fujisaka S, Ussar S, Clish C, Devkota S, Dreyfuss JM, Sakaguchi M, Soto M, Konishi M, Softic S,</li> <li>Altindis E, Li N, Gerber G, Bry L, Kahn CR. 2016. Antibiotic effects on gut microbiota and</li> <li>metabolism are host dependent. J Clin Invest 126:4430-4443.</li> <li>23. Buffie CG, Bucci V, Stein RR, McKenney PT, Ling L, Gobourne A, No D, Liu H, Kinnebrew M,</li> <li>Viale A, Littmann E, van den Brink MR, Jenq RR, Taur Y, Sander C, Cross JR, Toussaint NC,</li> <li>Xavier JB, Pamer EG. 2015. Precision microbiome reconstitution restores bile acid mediated</li> <li>resistance to Clostridium difficile. Nature 517:205-8.</li> <li>24. Choo JM, Leong LEX, Rogers GB. 2015. Sample storage conditions significantly influence</li> <li>facal microbiome arefiles. Scientific Reports 5:16250</li> </ul>	428		of DAV132, an activated charcoal based product, when given with oral moxifloxacin on free
<ul> <li>controlled trial in 144 healthy volunteers abstr European Congress of Clinical Microbiology and Infectious Diseases (ECCMID), Madrid,</li> <li>20. Theriot CM, Young VB. 2015. Interactions Between the Gastrointestinal Microbiome and Clostridium difficile. Annual Review of Microbiology 69:445-461.</li> <li>21. Dethlefsen L, Relman DA. 2011. Incomplete recovery and individualized responses of the human distal gut microbiota to repeated antibiotic perturbation. Proc Natl Acad Sci U S A 108 Suppl 1:4554-61.</li> <li>22. Fujisaka S, Ussar S, Clish C, Devkota S, Dreyfuss JM, Sakaguchi M, Soto M, Konishi M, Softic S, Altindis E, Li N, Gerber G, Bry L, Kahn CR. 2016. Antibiotic effects on gut microbiota and metabolism are host dependent. J Clin Invest 126:4430-4443.</li> <li>23. Buffie CG, Bucci V, Stein RR, McKenney PT, Ling L, Gobourne A, No D, Liu H, Kinnebrew M, Viale A, Littmann E, van den Brink MR, Jenq RR, Taur Y, Sander C, Cross JR, Toussaint NC, Xavier JB, Pamer EG. 2015. Precision microbiome reconstitution restores bile acid mediated resistance to Clostridium difficile. Nature 517:205-8.</li> <li>24. Choo JM, Leong LEX, Rogers GB. 2015. Sample storage conditions significantly influence faecal microbione profiler. Scientific Reports 5:163E0</li> </ul>	429		moxifloxacin fecal concentrations and intestinal microbiota diversity: a randomized
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# 463 <u>Tables</u>

# 464 Table 1: Toxin results (Percentage of cytotoxin positive samples at 72 hours) of the experiments shown in figures 2-5. Grey boxes indicate

# 465 **experiment not performed.**

Storage condition or patient group	Raw (n)	Autoclaved (n)	Filtered (n)	BHI and taurocholic acid (n)	Associated figure
Fresh	0 (0/11)	100 (6/6)	100 (5/5)		2
4°C	0 (0/5)	100 (3/3)	100 (3/3)		3
-80°C	40 (3/5)	100 (3/3)	100 (3/3)	100 (3/3)	3
-80°C with 12% glycerol	0 (0/5)	66.6 (2/3)	0 (0/3)	100 (3/3)	3
-80°C with 30% glycerol	0 (0/5)	0 (0/3)	0 (0/3)	0 (0/3)	3
First freeze-thaw	0 (0/3)	66.6 (2/3)	66.6 (2/3)		4
Second freeze-thaw	0 (0/3)	100 (3/3)	100 (3/3)		4
Moxifloxacin D1	9 (1/11)		100 (11/11)		5
Moxifloxacin D6	45 (5/11)		91 (10/11)		5
Control D1	0 (0/10)		100 (10/10)		5
Control D6	0 (0/10)		90 (9/10)		5

466

### 468 <u>Figures</u>



- 470 Figure 1: Manipulation of stool samples undergoing CRACS. The different experimental
- 471 condition investigated during optimisation of the assay are indicated in boxes on the right.









- 478 Untreated vs Autoclaved p = 0.002, Untreated vs Filtered p = 0.006, and Autoclaved vs
- 479 Filtered p = 1.0. Untreated n = 11, Autoclaved n = 6, Filtered n = 5



481

Figure 3: Impact of storage of healthy faecal samples on  $\Delta$  change in the geometric mean *C. difficile* total viable counts over 72 hours. (a). Raw faecal samples(n = 5), (b). Autoclaved faecal samples (n = 3), (c). Filtered faecal samples (n = 3). Faecal samples were stored at 485 4°C, -80°C, -80°C with 12% glycerol or -80°C with 30% glycerol. Panel (d) shows  $\Delta$  change in 486 the geometric mean *C. difficile* total viable counts over 72 hours following growth in BHI 487 broth with taurocholic acid with and without glycerol (n = 3). Individual data points, with 488 the geometric mean are presented. \* indicates p = 0.026



- 491 Figure 4: Effect of multiple freeze-thaw cycles on Δ change in the geometric mean *C*.
- 492 *difficile* total viable counts and spore counts over 72 hours (n = 3). (a); total viable counts,
- 493 (b); spore counts. Individual data points, with the geometric mean are presented.



Figure 5: Effect of five days of antibiotic or control treatment on Δ change in the geometric
mean *C. difficile* TVC over 72 hours. (a). Raw samples, (b). Sterilised samples. \*\* p = 0.006,

498 with Wilcoxon rank sum test, n = 11 for antibiotic treatment group, n = 10 for control

499 group. Individual data points, with the geometric mean are presented.