



UNIVERSITY OF LEEDS

This is a repository copy of *Can SARS-CoV-2 be transmitted via faeces?*.

White Rose Research Online URL for this paper:

<https://eprints.whiterose.ac.uk/180503/>

Version: Accepted Version

Article:

Moura, IB orcid.org/0000-0002-3019-7196, Buckley, AM orcid.org/0000-0002-2790-0717 and Wilcox, MH (2021) Can SARS-CoV-2 be transmitted via faeces? *Current Opinion in Gastroenterology*. ISSN 0267-1379

<https://doi.org/10.1097/mog.0000000000000794>

© 2021 Wolters Kluwer Health, Inc. This is an author produced version of an article published in *Current Opinion in Gastroenterology*. Uploaded in accordance with the publisher's self-archiving policy.

Reuse

Items deposited in White Rose Research Online are protected by copyright, with all rights reserved unless indicated otherwise. They may be downloaded and/or printed for private study, or other acts as permitted by national copyright laws. The publisher or other rights holders may allow further reproduction and re-use of the full text version. This is indicated by the licence information on the White Rose Research Online record for the item.

Takedown

If you consider content in White Rose Research Online to be in breach of UK law, please notify us by emailing eprints@whiterose.ac.uk including the URL of the record and the reason for the withdrawal request.



eprints@whiterose.ac.uk
<https://eprints.whiterose.ac.uk/>

Can SARS-CoV-2 be transmitted via faeces?

Ines B. Moura¹, Anthony M Buckley¹, and Mark H. Wilcox^{1,2}

¹Healthcare-Associated Infections Group, Leeds Institute of Medical Research, Faculty of Medicine and Health, University of Leeds, Leeds LS1 9JT U.K.

²Microbiology, Leeds Teaching Hospital NHS Trust, Old Medical School, Leeds General Infirmary, Leeds LS1 3EX U.K.

*Corresponding author:

Dr Ines Moura

Healthcare Associated Infections research group

Old Medical School

Leeds General Infirmary

Leeds LS1 3EX U.K.

Email: i.b.moura@leeds.ac.uk

Tel: +44 113 392 8663

Keywords

SARS-CoV-2, COVID-19, faecal transmission, gastrointestinal symptoms, gut microbiota

Abstract

Purpose of review: COVID-19 patients can present gastrointestinal symptoms, being diarrhoea one of the most frequent, suggesting intestinal health can be impacted by COVID-19. Here we will discuss whether there is a correlation between the presence of SARS-CoV-2 RNA in faeces and diarrhoea, the relevance of gastrointestinal symptoms is disease diagnosis and transmission, and how COVID-19 can impact the gut microbial balance.

Recent findings: SARS-CoV-2 RNA has been reported in faeces or rectal swabs of COVID-19 patients with and without diarrhoea, suggesting faecal shedding can occur independently to gastrointestinal symptoms. However, the presence of the virus in the intestine can persist beyond its presence in the respiratory tract, with some reports suggesting that SARS-CoV-2 in the faeces can be infectious. COVID-19 can impact in the gut microbiota causing an enhancement of biosynthesis pathways that favour the expansion of bacterial pathogens in the inflamed gut, and causing a decline in commensals involved in the human immune response.

Summary: Gastrointestinal symptoms may be the first indication of COVID-19. SARS-CoV-2 in faeces can potentiate routes of disease transmission, particularly as the high viral loads reported in patients with severe illness suggest virus replication in the intestine may be possible.

Introduction

The main pathway of transmission of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the etiological agent of coronavirus disease 2019 (COVID-19), is through exposure to respiratory droplets which can transfer more easily in closed environments and through human contact [1].

In addition to respiratory symptoms, COVID-19 patients can also present gastrointestinal manifestations, such as nausea, abdominal pain, vomiting, and diarrhoea, with the latter being the most frequent [2-4]. Incidence of diarrhoea as a symptom in COVID-19 patients can vary between 5% and 55% [2-10]. However, comparison between studies can be difficult as samples sizes and patient recruitment criteria vary between studies. Nonetheless, diarrhoea has been more commonly reported in patients of America and Europe, with one study observing a 31% higher risk of hospitalisation in patients with diarrhoea [7], whereas others suggested this symptom is not associated with higher disease severity or poorer outcome [2, 3, 8, 9].

COVID-19 occurs when the SARS-CoV-2 spike glycoproteins bind to the extracellular-facing N-terminal domain of the angiotensin-converting enzyme 2 (ACE2) receptors present in the lungs epithelial cells [11, 12], allowing the virus to enter the host cells [13]. These receptors are also expressed in epithelial cells of the large and small intestine, where ACE2 can act as a potential entry point for the virus [11, 14]. This has been confirmed by visualization of the viral nucleocapsid protein in the cytoplasm of gastric, duodenal, and rectum epithelial cells [14].

It is therefore important to understand the potential implications of SARS-CoV-2 faecal excretion in disease transmission and whether there is a correlation between the presence of virus in faeces and diarrhoea as a symptom of COVID-19. Here we will discuss the relevance of these manifestations in disease diagnosis and transmission, and how COVID-19 can impact the gut microbial balance.

SARS-CoV-2 can persist in the intestine of COVID-19 patients

Most studies focusing on SARS-CoV-2 detection in different tissues/samples use RT-PCR assays to target the presence of viral RNA [15, 16]. This is due to the speed, reliability and low limits of detection of molecular testing, but also due to the difficulties to isolate and culture the live virus [17]. In addition to the nose and throat swabs used for COVID-19 diagnosis, SARS-CoV-2 RNA has also been detected in faeces or rectal swabs of patients with COVID-19 [5-7, 10, 14, 15, 18-20]. In early 2020, faecal samples of 41 (out of 74) patients tested positive for the virus for an average of 28 days. The respiratory samples of the patients showing faecal excretion of SARS-CoV-2 remained positive for approximately 17 days, 11 days less than the faecal samples, but over a day longer than the observed for the COVID-19 patients with negative faecal samples [10]. Other studies have also suggested that SARS-CoV-2 shedding through the faeces continues to occur after the respiratory samples have converted to negative [14, 19, 21]. In two reports, over 40% of the patients investigated were positive for viral RNA in faeces for up to 14 days after pharyngeal swabs tested negative [10, 21]. In one other study, a patient with a clinical presentation consistent with COVID-19, including respiratory symptoms and lung damage, tested negative for SARS-CoV-2 on the pharyngeal swab but positive on the faecal sample [18].

The detection of SARS-CoV-2 RNA in faeces for such lengthy periods of time raises the question whether patients should be considered free of the virus based just on negative nasopharyngeal swabs [14, 19]. Furthermore, as intestinal cells express the ACE2 receptors required for SARS-CoV-2 infection [11], the possibility of a faecal-oral route of transmission cannot be excluded [14, 18].

These concerns gathered additional relevance as Wang et al. reported SARS-CoV-2 RNA in 44% of 153 faecal samples tested, 2 of which also shown presence of live virus [15]. Similarly, Xiao et al. cultured SARS-CoV-2 from stool samples of 2 patients, one of which showing higher viral loads in the faeces compared to nasopharyngeal samples [17]. In both these studies, cycle threshold values in stool were consistent with a high viral load, suggesting the virus can persist and potentially replicate in the digestive tract [15, 17]. These observations were further supported by the sequencing of

SARS-CoV-2 in stool samples of COVID-19 patients, showing a higher density and coverage of the virus genome at the of the 3' end region which is associated with viral activity, replication and infection of the host cells [22].

Relevance of gastrointestinal symptoms in disease transmission

As the presence of SARS-CoV-2 genetic material and live virus in patients faeces became apparent, apprehension increased as COVID-19 patients can also present gastrointestinal symptoms such as diarrhoea [3-9, 17]. The occurrence of loose stools in COVID-19 patients extends the risk of environmental contamination of toilets and contact surfaces through aerosols or faecal matter deposition [23]. Facilities in areas shared by individuals more susceptible to severe illness such as wards or care homes are of particular concern, since patients are deemed virus-free upon negative nasopharyngeal tests, even though the presence of virus in the intestine can outlast its presence in the respiratory tract [10, 14, 19, 21].

Despite the evidence of gastrointestinal symptoms in COVID-19, a direct association between SARS-CoV-2 in faeces and diarrhoea has not been clearly established. In a study involving 22 patients with mild COVID-19 in China, the virus was most frequently detected in faeces of patients with digestive symptoms, being diarrhoea the most prevalent [6]. These observations are consistent with other reports from China [4], South American [7] and Hong Kong [16], but while one study found similar viral loads in stools of patients with gastrointestinal symptoms and in those asymptomatic [7]; in another study patients with diarrhoea showed higher concentration of virus ($5.1 \log_{10}$ copies/ml) compared to those without loose stools ($3.9 \log_{10}$ copies/ml) [16]. However, a study involving 9 COVID-19 patients with diarrhoeal symptoms at time of stool collection, 13 patients in which diarrhoea had ceased prior to sample collection, and 22 patients without any diarrhoeal symptoms, SARS-CoV-2 RNA was only detected in stools of asymptomatic patients or in those in which symptoms had already ceased [5], suggesting patients without diarrhoea can also show SARS-CoV-2 shedding through the faeces.

Faecal excretion of SARS-CoV-2 can be a factor in disease transmission, particularly as gastrointestinal symptoms may be the only manifestation of COVID-19 at illness onset, increasing the risk of exposure to the virus. Song et al. reported the case of a patient experiencing 3 to 4 episodes of diarrhoea daily for 4 days, accompanied by low fever prior to receiving medical assistance. This clinical presentation suggested gastrointestinal illness. Further testing revealed the patient was negative for all common pathogens associated to digestive illness and was indeed positive for SARS-CoV-2 [24]. Similarly, a study by Pan et al. reported 103 patients with COVID-19 and showing digestive symptoms. Six of those patients did not present respiratory symptoms and one also did not present fever [3]. Although diarrhoea was present in 34% of the patients with gastrointestinal symptoms, the study did not specify if that was the case for the 6 patients without respiratory symptoms [3]. One other study identified 183 COVID-19 patients reporting only digestive symptoms, including 69 patients with diarrhoea [25]; whereas a study following mild disease in 67 patients, observed 13 patients that experienced diarrhoea as the first symptom prior to developing respiratory symptoms [6].

SARS-CoV-2 shedding can occur through the faeces and evidence suggests COVID-19 may present initially via digestive symptoms only, leading to longer times from disease onset to hospital admission [3], therefore the potential for virus transmission in the community through the faecal-oral route should not be disregarded.

Role of gut microbiota in COVID-19

The intestinal flora plays an important role in human immunity and physiological balance required for disease prevention. Infection by SARS-CoV-2 disrupts this equilibrium leading to gastrointestinal manifestations such as diarrhoea, which are potentially aggravated by antibiotic therapy during COVID-19 treatment [4]. Additionally, a biomarker of intestinal inflammatory response, faecal calprotectin, has been found elevated in patients with COVID-19 with diarrhoea [5]. As the virus binds to ACE2 receptors which are also present in human upper and lower intestinal cells [11, 14], and

have a role in regulation of intestinal inflammation and the ecology of the gut microbiome [20]; it has been hypothesised SARS-CoV-2 presence may also affect composition and diversity of the gut microbiota [3], which is naturally decreased in the elderly [26], those more affected by severe COVID-19.

Metagenomics analysis of faecal samples from 6 COVID-19 patients showed a depletion of bacterial commensals that are suspected to be involved in the human immune response, namely *Faecalibacterium prausnitzii*, *Eubacterium rectale*, *Ruminococcus obeum*, and *Dorea formicigenerans*. Independent of antibiotic use or gastrointestinal symptoms, samples of COVID-19 patients also showed a higher prevalence of opportunistic pathogens (*Clostridium hathewayi*, *Actinomyces viscosus*, and *Bacteroides nordii*) compared to a pre-pandemic cohort of controls [20]. This agrees with a previous study from the same authors reporting an enhancement of amino acid biosynthesis pathways such as L-serine in patients with higher SARS-CoV-2 infectivity, which can favour the expansion of bacterial pathogens in the inflamed gut of COVID-19 patients [22]. While *F. prausnitzii*, *E. rectale* and some *Bacteroides* species that have been associated with the downregulation of ACE2 were underrepresented in COVID-19 patients; the opposite was observed for bacteria of the genus *Coprobacillus* like *C. hathewayi*, known to upregulate the expression of this receptor [20]. These results were largely confirmed in a subsequent study involving 87 COVID-19 patients where, in addition to the previously observed changes, bifidobacteria was also depleted in ill patients [27]. While no significant differences in diversity were observed between COVID-19 patients and controls [27], in both studies the gut dysbiosis persisted after the patients nasopharyngeal swabs tested negative for the virus [20, 27].

An increase in opportunistic pathogens seems to be generically observed in COVID-19 patients, even with less discriminatory analysis such as 16S sequencing. Gu and colleagues observed a predominance of genus *Streptococcus*, *Rothia*, *Veillonella*, and *Actinomyces* in 30 COVID-19 patients, and a reduction in the abundance of several genera from the Lachnospiraceae family. This analysis

also showed a decline in bacterial diversity compared to healthy individuals, which reflected the low relative abundance of beneficial commensals [28].

Microbial analysis of faecal samples suggests a long-term increase in opportunistic gut pathogens, an imbalance that may affect the human inflammatory responses in COVID-19 [20, 27]. Further studies will potentiate the clear identification of biomarkers of disease severity and create opportunities for modulation of the gut microbiota through replacement therapies.

Conclusion

The human gut plays a key role in immunity and disease prevention. Detection of SARS-CoV-2 RNA in the faeces of COVID-19 patients at high levels suggests virus replication in the intestine may be possible. The reports of patients showing only gastrointestinal symptoms as the first indication of COVID-19 further strengthens this possibility. Infection by SARS-CoV-2 appears to impact the microbial balance of the gut population, causing a reduction of beneficial commensals and an increase of opportunistic pathogens associated with the upregulation of ACE2 receptors in the intestine. Although reports of viable virus in faeces are rare, this may be a reflection of the difficulties associated with culture of a highly infectious virus compared to use of molecular techniques, particularly during periods of heavy burden to healthcare systems. Therefore, the risk of disease transmission through the faecal-oral route cannot be excluded.

Conflict of interest: None

Acknowledgments: None

Funding support and sponsorship: None

References

1. Chan JF, Yuan S, Kok KH, *et al.* A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster. *Lancet.* 2020; 395:514-23.
2. Ferm S, Fisher C, Pakala T, *et al.* Analysis of Gastrointestinal and Hepatic Manifestations of SARS-CoV-2 Infection in 892 Patients in Queens, NY. *Clin Gastroenterol Hepatol.* 2020; 18:2378-9.e1.
3. Pan L, Mu M, Yang P, *et al.* Clinical Characteristics of COVID-19 Patients With Digestive Symptoms in Hubei, China: A Descriptive, Cross-Sectional, Multicenter Study. *Am J Gastroenterol.* 2020; 115:766-73.
4. Lin L, Jiang X, Zhang Z, *et al.* Gastrointestinal symptoms of 95 cases with SARS-CoV-2 infection. *Gut.* 2020; 69:997-1001.
5. Effenberger M, Grabherr F, Mayr L, *et al.* Faecal calprotectin indicates intestinal inflammation in COVID-19. *Gut.* 2020; 69:1543-4.
6. Han C, Duan C, Zhang S, *et al.* Digestive Symptoms in COVID-19 Patients With Mild Disease Severity: Clinical Presentation, Stool Viral RNA Testing, and Outcomes. *Am J Gastroenterol.* 2020; 115:916-23.
7. Díaz LA, García-Salum T, Fuentes-López E, *et al.* Symptom Profiles and Risk Factors for Hospitalization in Patients With SARS-CoV-2 and COVID-19: A Large Cohort From South America. *Gastroenterology.* 2020; 159:1148-50.
8. Aghemo A, Piovani D, Parigi TL, *et al.* COVID-19 Digestive System Involvement and Clinical Outcomes in a Large Academic Hospital in Milan, Italy. *Clin Gastroenterol Hepatol.* 2020; 18:2366-8.e3.
9. Livanos AE, Jha D, Cossarini F, *et al.* Intestinal Host Response to SARS-CoV-2 Infection and COVID-19 Outcomes in Patients With Gastrointestinal Symptoms. *Gastroenterology.* 2021; 160:2435-50.e34.

10*. Wu Y, Guo C, Tang L, *et al.* Prolonged presence of SARS-CoV-2 viral RNA in faecal samples. *Lancet Gastroenterol Hepatol.* 2020; 5:434-5.

Study reported that SARS-CoV-2 RNA can be detected in faecal samples several days after the virus is no longer detected in nasopharyngeal swabs tested negative.

11*. Hoffmann M, Kleine-Weber H, Schroeder S, *et al.* SARS-CoV-2 Cell Entry Depends on ACE2 and TMPRSS2 and Is Blocked by a Clinically Proven Protease Inhibitor. *Cell.* 2020; 181:271-80.e8.

Study demonstrated that ACE2 receptor is essential to host cell infection by SARS-CoV-2.

12. Zhou P, Yang XL, Wang XG, *et al.* A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature.* 2020; 579:270-3.

13. Qi F, Qian S, Zhang S, Zhang Z. Single cell RNA sequencing of 13 human tissues identify cell types and receptors of human coronaviruses. *Biochem Biophys Res Commun.* 2020; 526:135-40.

14*. Xiao F, Tang M, Zheng X, *et al.* Evidence for Gastrointestinal Infection of SARS-CoV-2. *Gastroenterology.* 2020; 158:1831-3.e3.

Study demonstrating that ACE2 receptor in intestinal cells is active in COVID-19 patients.

15. Wang W, Xu Y, Gao R, *et al.* Detection of SARS-CoV-2 in Different Types of Clinical Specimens. *JAMA.* 2020; 323:1843-4.

16. Cheung KS, Hung IFN, Chan PPY, *et al.* Gastrointestinal Manifestations of SARS-CoV-2 Infection and Virus Load in Fecal Samples From a Hong Kong Cohort: Systematic Review and Meta-analysis. *Gastroenterology.* 2020; 159:81-95.

17**. Xiao F, Sun J, Xu Y, *et al.* Infectious SARS-CoV-2 in Feces of Patient with Severe COVID-19. *Emerg Infect Dis.* 2020; 26:1920-2.

Study reporting infectious SARS-CoV-2 was isolated from the faeces of a patient with severe disease.

18. Chen L, Lou J, Bai Y, Wang M. COVID-19 Disease With Positive Fecal and Negative Pharyngeal and Sputum Viral Tests. *The American journal of gastroenterology*. 2020; 115:790-.
19. Chen C, Gao G, Xu Y, *et al*. SARS-CoV-2-Positive Sputum and Feces After Conversion of Pharyngeal Samples in Patients With COVID-19. *Ann Intern Med*. 2020; 172:832-4.
- 20**. Zuo T, Zhang F, Lui GCY, *et al*. Alterations in Gut Microbiota of Patients With COVID-19 During Time of Hospitalization. *Gastroenterology*. 2020; 159:944-55.e8.
Metagenomics analysis of faecal samples from COVID-19 patients showed changes in the composition of the gut microbiota of ill patients.
21. Chen Y, Chen L, Deng Q, *et al*. The presence of SARS-CoV-2 RNA in the feces of COVID-19 patients. *J Med Virol*. 2020; 92:833-40.
22. Zuo T, Liu Q, Zhang F, *et al*. Depicting SARS-CoV-2 faecal viral activity in association with gut microbiota composition in patients with COVID-19. *Gut*. 2021; 70:276-84.
23. Amoah ID, Pillay L, Deepnarian N, *et al*. Detection of SARS-CoV-2 RNA on contact surfaces within shared sanitation facilities. *Int J Hyg Environ Health*. 2021; 236:113807.
24. Song Y, Liu P, Shi XL, *et al*. SARS-CoV-2 induced diarrhoea as onset symptom in patient with COVID-19. *Gut*. 2020; 69:1143-4.
25. Luo S, Zhang X, Xu H. Don't Overlook Digestive Symptoms in Patients With 2019 Novel Coronavirus Disease (COVID-19). *Clin Gastroenterol Hepatol*. 2020; 18:1636-7.
26. Zhang X, Zhong H, Li Y, *et al*. Sex- and age-related trajectories of the adult human gut microbiota shared across populations of different ethnicities. *Nature Aging*. 2021; 1:87-100.
27. Yeoh YK, Zuo T, Lui GC-Y, *et al*. Gut microbiota composition reflects disease severity and dysfunctional immune responses in patients with COVID-19. *Gut*. 2021; 70:698-706.
28. Gu S, Chen Y, Wu Z, *et al*. Alterations of the Gut Microbiota in Patients With Coronavirus Disease 2019 or H1N1 Influenza. *Clin Infect Dis*. 2020; 71:2669-78.