Prevotella/Streptococcus and other anaerobes colonize the metagenome (nasopharyngeal swab) submitted by Emory University School of Medicine, Georgia in Covid19 patient, corroborating the hypothesis that SARS-Cov2 is enabling anaerobes

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Letter

The hypothesis [1] that SARS-Cov2 [2,3] enables anaerobic bacteria (Prevotella, et al) to colonize the lungs disrupting homeostasis finds resonance in the ‘forgotten disease’ Lemierre’s Syndrome [4–9,9,10]. Lemierre’s Syndrome is also caused by anaerobic bacteria enabled by Epstein Barr Virus [11,12]. Symptoms common to both diseases include ARDS, septic shock, blood clots and arterial stroke [?,13–17]. Covid19 starts from the lungs (possibly making it easier to treat), in contrast to Lemierre’s Syndrome that originates in the jugular vein.

Nasopharyngeal swab(Accid:SRR11829376)

Here, metagenome from a Covid19 patient in Emory University School of Medicine, Georgia is analyzed (Table 1, Fig 1). Prevotella/Streptococcus and other anaerobes colonize the metagenome, corroborating the hypothesis that SARS-Cov2 is enabling anaerobes [1]. The bacterial load is quite high, the first five species comprise 70% of the load.

Atopobium - a biofilm producing bacteria implicated in bacterial vaginosis (BV)

The Bangladesh metagenome had a new hard-to-culture anaerobe implicated in disease - Lawsonella [1]. Here, Atopobium [18, 19] is another anaerobe with significant abundance ((Table 1, Fig 1). Atopobium is implicated in bacterial vaginosis and ‘around 80% of the cases and might be involved in therapeutic failure’ [20]. BV biofilm formation, and antibiotic resistant *A. vaginae* could explain therapeutic failures and recurrences of BV [19]. Long drawn symptoms in Covid19 have caused great consternation, and could be similarly explained by persistence of biofilms [21]. Also, the synergy between Atopobium and Gardnerella Vaginalis is a key virulence factor implicated in disease, since *G. vaginalis* displaces protective lactobacilli, and the initial colonization [22] establishes the biofilm structures to which secondary colonisers, such as *A. vaginae* attach.

Gut metagenome (Accid:SRR11827437)

Another sample shows Enterococcus colonization, and although the source of the sample is mentioned as nasopharyngeal swab, most of the bacteria are gut related (Table 2).

Figure 1: **Krona figure generated from the NCBI analysis:** The Prevotella abundance is visible (light green). Atopobium (5%) of the reads is around 11 o'clock.

Table 1: **Bacterial reads in sequencing data (nasopharyngeal swab) of submitted by Emory University School of Medicine, Georgia** Prevotella/Streptococcus and other anaerobes colonize the metagenome, corroborating the hypothesis that SARS-Cov2 is enabling anaerobes. The bacterial load is quite high, the first five species comprise 70% of the load. FAC-ANE=facultatively anaerobic (aerobic, but capable of switching to fermentation if oxygen is absent).

PerMillion	Bacteria	Type	Diseases
218827	Veillonella	obligateanaerobic	rare cases of meningitis, osteomyelitis, and periodontal disease [23]
202862	Prevotella	obligateanaerobic	aspiration pneumonia, lung abscess, pulmonary empyema, etc [24, 25]
191362	Streptococcus	FAC-ANE	pneumonia, bacteremia [26]
66431	Schaalia	FAC-ANE	similar to Actinomyces, alimentary tract diseases [27]
33327	Atopobium	anaerobic	Bacterial vaginosis [20]
23896	Leptotrichia	FAC-ANE	Endocarditis [28]
23534	Moraxella	aerobic	otitis media in infants and children [29]
15448	Bacteroides	obligateanaerobic	‘genus Bacteroides have the most antibiotic resistance mechanisms’ [30]
12172	Actinomyces	FAC-ANE	alimentary tract diseases [27]
9603	Megasphaera	obligateanaerobic	Bacterial Vaginosis [31, 32]
8482	Porphyromonas	obligateanaerobic	periodontal disease [33]
7103	Campylobacter	aerobic	diarrhoea [34]
6706	Fusobacterium	obligateanaerobic	periodontal, tonsillitis, peritonsillar abscess, etc [35]
6689	Selenomonas	obligateanaerobic	periodontal disease [36]
4793	Lachnoanaerobaculum	anaerobic	new genus [37]

Table 2: **Bacterial reads in sequencing data, most likely from the gut, submitted by Emory University School of Medicine, Georgia:** Although the source of the sample is mentioned as nasopharyngeal swab, most of the bacteria are gut related. Here, Enterococcus, which can be pathogenic, is seen to be colonizing. FAC-ANE=facultatively anaerobic (aerobic, but capable of switching to fermentation if oxygen is absent).

PerMillion	Bacteria	Type	Diseases
104097	Enterococcus	FAC-ANE	urinary tract infections; intraabdominal [38]
8612	Escherichia	FAC-ANE	cholecystitis, bacteremia, cholangitis, urinary tract infection [39]
6383	Corynebacterium	aerobic	diphtheria toxin [40]
3888	Klebsiella	FACANE	pneumoni [41] and intestinal colonization [42]
3307	Salmonella	FAC-ANE	typhoid [43]
2968	Shigella	FAC-ANE	leading cause of diarrhoeal death among children [44]
1365	Dolosigranulum	FAC-ANE	multiple sclerosis [45]
787	Staphylococcus	FAC-ANE	Boils, impetigo, food poisoning, cellulitis, and toxic shock syndrome
593	Carnobacterium	anaerobic	frequently isolated from natural environments and foods [46]
545	Bacillus	FAC-ANE	Inhalation or respiratory anthrax
414	Lactobacillus	FACANE	mutualistic beneficial relationship with the human body, [47]
317	Streptococcus	FAC-ANE	pneumonia, bacteremia [26]
313	Aerococcus	aerobic	Urinary tract infection [48]
310	Erwinia	FAC-ANE	dermohypodermatitis and bacteraemia [49]
286	Sphingomonas	aerobic	causative agent of infection in immunocompromised patients [50]

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