The usual anaerobic bacterial suspects extracted from a global metagenomic database of Covid19 patients from Peru, Cambodia, China, Brazil and the US - *Prevotella*, *Veillonella*, *Capnocytophaga*, *Fusobacterium*, *Oribacterium* and *Bacteroides* should be monitored for colonization

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Letter

The Covid19 pandemic [1], triggered by novel strain of a coronavirus SARS-Cov2 [2] has spread globally like a wildfire [3] after being first detected in Wuhan.

Previous studies from China, Brazil and the US:

Previously, several sequencing datasets - some of them published [4–9], others having sequencing data submitted in NCBI (with no associated publications) [10–13] - have revealed the metagenome in these patients from different parts of the world. The overwhelming presence of anaerobic bacteria (very low concentration of oxygen kills them) in these patients has led to the theory that antibiotics (like doxycycline/Metronidazole) targeting these specific organisms may provide better clinical results [14].

Two more studies added - patients from Peru and Cambodia:

Here, two more studies from Peru (Table 1) and Cambodia (Table 2) provide further corroboration to the anaerobic bacteria theory. These anaerobic bacteria have virtually colonized the metagenome - pushing other aerobic species out of the niche, disrupting the homeostasis. Around 30% and 23% of the reads from Peru and Cambodia are bacterial, respectively. This is not observed in other patients, even when having chronic issues [15].

Common opportunistic anaerobic bacteria in this global metagenomic Covid19 dataset

Here, I enumerate common opportunistic anaerobic bacteria present in this global metagenomic Covid19 dataset (Table 3). Any or multiple of these might become the main colonizer after SARS-Cov2 infection in Covid19. The trigger of such an event is still elusive. However, once this happens, some of these bacteria express hemoglobin degrading proteins [16], heme-binding proteins sequestering heme after hemoglobin degradation [17], ‘plundering’ iron, and thereby sequestering oxygen [18]. Hypoxia could also result from formate, the by-product of anaerobic respiration, which inhibits mitochondrial cytochrome oxidase, causing hypoxia at the cellular level [19].

Table 1: **Bacterial reads in a patient from Peru (Accid:PRJNA623683)**: Total number of reads - 2.3Million, of which around 700K, approximately 30% are bacterial reads. There are about 14K viral reads. And among the first 20 such species, all, barring one (highlighted), are either obligate-anaerobic (ie that cant survive even in low concentrations of oxygen) or facultatively anaerobic (FAC-ANE, aerobic, but capable of switching to fermentation if oxygen is absent). In fact, its the percentage of obligate-anaerobic thats more important, they seem to have colonized the lungs. Also the upper and lower airway microbiota in children with chronic lung diseases shows homeostatis with aerobic bacteria [15], something that seems to be broken in Covid19.

Reads	Bacteria	Description	Disease
291478	Veillonella	obligateanaerobic	rare cases of meningitis, osteomyelitis, and periodontal disease [20]
88835	Prevotella	obligateanaerobic	aspiration pneumonia, lung abscess, pulmonary empyema, etc [21]
62091	Fusobacterium	obligateanaerobic	periodontal, tonsillitis, peritonsillar abscess, etc [22]
35808	Streptococcus	FAC-ANE	pneumonia, bacteremia [23]
25789	Oribacterium	obligateanaerobic	periodontal disease [24]
25636	Porphyromonas	FAC-ANE	periodontal disease [25]
25436	Selenomonas	obligateanaerobic	periodontal disease [26]
20951	Leptotrichia	FAC-ANE	Endocarditis [27]
15906	Megasphaera	obligateanaerobic	Bacterial Vaginosis [28]
13417	Bacillus	FAC-ANE	Inhalation or respiratory anthrax
13246	Campylobacter	aerobic	diarrhoea [29]
10786	Haemophilus	FAC-ANE	pneumonia, meningitis and bloodstream infection
9894	Gemella	FAC-ANE	Infective Endocarditis [30]
6275	Streptobacillus	FAC-ANE	Rat bite fever [31]
5697	Granulicatella	FAC-ANE	Bacterascites [32]
4573	Bacteroides	obligateanaerobic	‘genus Bacteroides have the most antibiotic resistance mechanisms’ [33]
4505	Stomatobaculum	obligateanaerobic	[34]
4351	Centipeda	obligateanaerobic	Periodontitis Lesions [35]
4297	Dolosigranulum	FAC-ANE	multiple sclerosis [36]
3820	Solobacterium	obligateanaerobic	Bacteremia [37, 38]

Table 2: **Bacterial reads in a patient from Cambodia (Accid:PRJNA623895)**: Total number of reads - 3.8Million, of which around 864K, approximately 23% are bacterial reads. There are about 3.5K viral reads. And among the first 20 such species, all, barring one (highlighted), are either obligate-anaerobic (ie that cant survive even in low concentrations of oxygen) or facultatively anaerobic (FAC-ANE, aerobic, but capable of switching to fermentation if oxygen is absent). In fact, its the percentage of obligate-anaerobic thats more important, they seem to have colonized the lungs, disrupting the homeostatis with aerobic bacteria [15].

Reads	Bacteria	Description	Disease
135955	Prevotella	obligateanaerobic	aspiration pneumonia, lung abscess, pulmonary empyema, etc [21,39]
134787	Veillonella	obligateanaerobic	rare cases of meningitis, osteomyelitis, and periodontal disease
103875	Haemophilus	FAC-ANE	pneumonia, meningitis and bloodstream infection [40]
95675	Neisseria	FAC-ANE	infection and persistence in the upper respiratory tract [41]
51421	Capnocytophaga	FAC-ANE	usually occur with dog or cat bites
45859	Streptococcus	FAC-ANE	pneumonia, bacteremia [23]
34820	Fusobacterium	obligateanaerobic	periodontal, tonsillitis, peritonsillar abscess, etc
23228	Leptotrichia	FAC-ANE	Endocarditis [27]
21831	Actinobacillus	FACANE	wooden tongue disease [42]
19160	Morococcus	aerobic	periodontal [43]
15051	Campylobacter	aerobic	diarrhoea [29]
11195	Parabacteroides	obligateanaerobic	[44]
10252	Rodentibacter	FACANE	[45]
9626	Aggregatibacter	FACANE	endocarditis, periodontal infection [46]
9287	Bacteroides	obligateanaerobic	‘genus Bacteroides have the most antibiotic resistance mechanisms’ [33]
8446	Porphyromonas	FAC-ANE	periodontal disease [25]
6415	Pasteurella	FACANE	respiratory disease [47]
3717	Gemella	FAC-ANE	Infective Endocarditis [30]
3700	Kingella	weak FACANE	pneumonia, meningitis, ocular infections, pericarditis and peritonitis [48]
3564	Bergeriella	FACANE	[49]

Table 3: **Common opportunistic anaerobic bacteria in this global metagenomic Covid19 dataset:** The metagenomic database comprises of Covid19 patients from Peru, Cambodia, China, Brazil and the US. Any or multiple of these might become the main colonizer after SARS-Cov2 infection in Covid19. The trigger of such an event is still elusive. However, once this happens, some of these bacteria express hemoglobin degrading proteins [16], heme-binding proteins sequestering heme after hemoglobin degradation [17], ‘plundering‘ iron, and thereby sequestering oxygen [18]. Hypoxia could also result from formate, the by-product of anaerobic respiration, which inhibits mitochondrial cytochrome oxidase, causing hypoxia at the cellular level [19]. For example, in this study [6] found Capnocytophaga sp and Veillonella sp in sample 2 and none in sample 1, but ignored both bacteria identified as they ‘were not known for their pathogenicity’. Covid19 is different - here anaerobes are always suspect.

Species	Occurences	Implicated in diseases
Prevotella	high-common	aspiration pneumonia, lung abscess, pulmonary empyema, etc [21, 39]
Veillonella	high-common	rare cases of meningitis, osteomyelitis, and periodontal disease [50]
Capnocytophaga	high-common	‘but do not grow under aerobic conditions, but in a CO2-added anaerobic environment’ [52]
Fusobacterium	high-common	periodontal, tonsillitis, peritonsillar abscess, etc [53]
Oribacterium	high-common	periodontal disease [24]
Bacteroides	high-common	‘genus Bacteroides have the most antibiotic resistance mechanisms’ [33]
Cutibacterium	common	chronic blepharitis and endophthalmitis [51]
Clostridium	common	[54]
Centipeda	rare	Periodontitis Lesions [35]
Megasphaera	rare	Bacterial Vaginosis [28, 55]
Porphyromonas	rare	periodontal disease [56]
Selenomonas	rare	periodontal disease [26]
Solobacterium	rare	Bacteremia [37, 38]
Stomatobaculum	rare	[34]
Parabacteroides	rare	[44]
Peptostreptococcus	rare	[57]

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