Metagenomic data of three Covid19 patients submitted by NIAID Bioinformatics and Computational Biosciences Branch is from the gut - and not the lungs (BALF) as stated: Muribaculum is an intestinal microbe

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Letter

The Covid19 anaerobic hypothesis states that SARS-Cov2 is enabling anaerobic bacteria to colonize the lungs, leading to Lemierre's syndrome like symptoms [1]. However, the metagenomic data from 3 Covid19 patients (age M=40, F=20, F=31) submitted by NIAID Bioinformatics and Computational Biosciences Branch (Accid:PRJNA631287) is from the gut - and not lungs (BALF) as stated (Table 1). The Registration date of this sequencing data is : 8-May-2020. Muribaculum is an intestinal microbe [2] - and the microbe composition can be seen to be completely different from that in the lungs.

The data size is very small - 5000 reads per patient. So this should be very easy to verify.

References

1. Chakraborty S (2020). Sars-cov2 enables anaerobic bacteria (Prevotella, et al) to colonize the lungs disrupting homeostasis - symptoms (ARDS, septic shock, blood clots, arterial stroke) finds resonance,

Table 1: **Metagenomic data from 3 Covid19 patients submitted by NIAID Bioinformatics and Computational Biosciences Branch is from the gut - and not lungs (BALF) as stated** Muribaculum is an intestinal microbe [2] - and the microbe composition can be seen to be completely different from the lung microbiome. There are 5000 reads per patient.

M=40 yrs	F=20 yrs	F=31 yrs
Muribaculum-2411	Muribaculum-1460	Muribaculum-1925
Bacteroidales-539	Clostridium-519	Bacteroidales-576
Clostridium-474	Bacteroides-454	Bacteroides-419
Bacteroides-191	Acetatifactor-364	Clostridium-379
Parabacteroides-136	Kineothrix-327	Anaerobacterium-222
Kineothrix-130	Bacteroidales-302	Kineothrix-189
Lactobacillus-122	Oscillibacter-273	Parabacteroides-177
Butyricimonas-108	Parabacteroides-218	Lactobacillus-148
Ruminococcus-89	Butyricimonas-169	Butyricimonas-131
Anaerobacterium-81	Alistipes-111	Ruminococcus-74
Anaerocolumna-75	Eubacterium-102	Peptococcus-70
Acetatifactor-72	Ruminococcus-85	Vallitalea-60
Eubacterium-47	Flintibacter-76	Anaerocolumna-58
Oscillibacter-47	Sporobacter-51	Pseudobacteroides-55
Breznakia-46	Pseudoflavonifractor-50	Eubacterium-44
Alistipes-40	Peptococcus-39	Oscillibacter-39
Flintibacter-37	Phoceia-38	Acetatifactor-37

with key differences, in the ‘forgotten disease’ Lemierre syndrome, caused by anaerobic bacteria enabled by Epstein Barr virus. doi:10.31219/osf.io/usztn. URL osf.io/usztn.

2. Lagkouvardos I, Lesker TR, Hitch TC, Gálvez EJ, Smit N, et al. (2019) Sequence and cultivation study of muribaculaceae reveals novel species, host preference, and functional potential of this yet undescribed family. *Microbiome* 7: 28.

Common Fields	
env_local_scale	hospital ENVO:00002173
env_medium	mucus material ENVO:02000040
geo_loc_name_country	USA
geo_loc_name_country_continent	North America
geo_loc_name	USA:MD,Bethesda
host_disease	COVID-19
Host	Homo sapiens
Instrument	Illumina MiSeq
isolation_source	bronchoalveolar lavage fluid(BALF)

Figure 1: **Annotation of these samples as BALF:** This can be viewed here: <https://www.ncbi.nlm.nih.gov/Traces/study/?acc=SRP260836>