‘Five patients at the early stage of the Wuhan seafood market pneumonia virus outbreak’ - bacterial load is much higher than SARS-Cov2 load, Pseudomonas is a definite problem in one patient, and Prevotella is abundant in all patients

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Letter

Here, I analyze the metagenome from the bronchoalveolar lavage fluid of 5 Covid19 [1–3] patients from Wuhan (Accid:PRJNA605983, Table 1). There is no published study on this dataset yet.

Very little viral load

There is very little viral load (in the tens per million reads), similar to the metagenomic study in Brazil [4]. This is a very plausible cause for false negatives, as there is just not enough virus to detect. Thus, it is important to have a large set of RT-PCR primers to cover more of the genome.

Much more bacterial load

While there are a wide range of bacteria, Pseudomonas has definitely colonized patient1, while patient5 seems to have the least bacterial load. Pseudomonas is associated with several diseases, several of which (pneumonia and septicemia) are relevant in Covid19 [5]. The bacterial species and their sequences are submitted in SI5patients on a per patient basis. These bacterial co-infections form the basis of hydroxychloroquine [6] and azithromycin working in clinical trials [7].

Table 1: **Bacterial load is much higher than SARS-Cov2 load in five patients at the early stage of the Wuhan seafood market pneumonia virus outbreak:** PM=per million. Number of reads analyzed: patient1 = 11841722, pat2 = 12882084, pat3 = 12041947, pat4 = 13333138, pat5 = 23201546. Pseudomonas is a definite secondary infection in patient1, while patient5 seems to have the least bacterial load. Patient 4 has the most viral load, otherwise viral load is quite low, just like in the patient from Brazil [4], explaining the high false negatives. As in all previous studies, Prevotella seems to be a common and abundant presence in all patients.

patient1	PM/total	Patient2	PM/total	Patient3	PM/total	Patient4	PM/total	Patient5	PM/total
Pseudomonas	1529/18047	Prevotella	125/1617	Sphingomonas	351/4213	Capnocytophaga	25/333	Neisseria	11/260
Sphingomonas	1166/13766	Pseudomonas	61/790	Prevotella	157/1892	Veillonella	18/250	Capnocytophaga	4/113
Clostridium	400/4720	Streptococcus	30/390	Pseudomonas	141/1696	Streptococcus	5/79	Allo Prevotella	1/43
Sphingobacterium	326/3851	Clostridium	28/370	Clostridium	47/564	Cardiobacterium	5/72	Prevotella	1/38
Lactobacillus	244/2885	Haemophilus	18/236	Escherichia	36/440	Prevotella	3/51	Haemophilus	1/32
Anaerocolumna	217/2564	Lactobacillus	14/181	Sphingobacterium	32/386	Neisseria	3/44	Coxiella	1/26
Delftia	176/2084	Actinobacillus	12/155	Streptococcus	31/376	Schaalia	2/33	Veillonella	0/20
Paenibacillus	170/2006	Anaerocolumna	10/133	Neochlamydia	27/334	Ottowia	1/14	Streptococcus	0/17
Neochlamydia	168/1987	Escherichia	10/129	Lactobacillus	21/262	Coxiella	0/13	Nocardioide	0/16
Methylobacterium	150/1772	Neisseria	9/118	Delftia	19/232	Lautropia	0/11	Campylobacter	0/13
Lysinibacillus	148/1750	Delftia	7/101	Methylobacterium	17/206	Campylobacter	0/10	Fusobacterium	0/12
Pelomonas	123/1461	Paenibacillus	7/99	Haemophilus	17/204	Brachymonas	0/8	Paracoccus	0/12
Prevotella	106/1256	Sphingomonas	7/99	Anaerocolumna	16/199	Pseudomonas	0/8	Pseudomonas	0/11
Chryseobacterium	97/1155	Lysinibacillus	6/78	Paenibacillus	12/151	Eikenella	0/7	Cardiobacterium	0/10
SARS-Cov2	78/923	SARS-Cov2	30/396	SARS-Cov2	18/222	SARS-Cov2	362/4821	SARS-Cov2	19/454

This study reenforces the role of *Prevotella*, which had taken over in a Chinese patient [8]. *Prevotella* also known to lower lymphocyte counts [9], increase IL-6 in plasma [10–12], cause ground glass opacity in lungs [13], and associated with cardiac injury [14] - all symptoms associated with Covid19. Here, a closely related species *Alloprevotella* is also abundant in one patient [15]. In 2003 SARS-Cov1 outbreak, secondary infection and IL-6 was highly correlated with hospitalization and deaths [16].

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