Possible hospital acquired Acinetobacter, Klebsiella, Mycoplasma and Legionella secondary infections in Covid19 patients from Russia

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Letter

The hypothesis that SARS-Cov2 enables anaerobic bacteria to colonize the lungs disrupting homeostasis, causing long-drawn chronic symptoms, and acute severe symptoms (ARDS, septic shock, clots, arterial stroke) which finds resonance, with key differences, in the ‘forgotten disease’ Lemierre Syndrome [1], enabled by Epstein Barr Virus [2] has found corroboration in other studies. An assessment of immunity in mild versus severe COVID-19 infection in humans found that severity correlated with increased bacterial products in plasma [3], while another study reported endotoxemia and circulating bacteriome in severe COVID-19 patients [4]. *Fusobacterium nucleatum* bacteremia was reported in Covid19 patients in Belgium [5]. The overlapping symptoms can often confuse diagnosis [6, 7]. ‘Jugular vein distention’ should have led to a Lemierre like diagnosis [8].

While, these are commensal lung microbiome, hospital acquired infections (HAI) also play a major role in fatal outcomes for Covid19 patients.

Secondary infections in samples from Russia

Acinetobacter/Legionella/Mycoplasma/Klebsiella possible co-infections in Covid19 patients from Russia (Accid:PRJNA682735). Some of these samples have no SARS-Cov2 reads - these could be control samples. The viral load is quite low in many patients, indicating that these might lead to false negative results [9]. It is interesting to note that samples with higher viral load also have higher % of anaerobic bacteria.

Table 1: **Acinetobacter/Legionella/Mycoplasma/Klebsiella co-infections in Covid19 patients from Russia (Accid:PRJNA682735):** The viral load is quite low in all but four samples. Reads are per 100k.

Accid	Bacterial	Cov2
SRR13300913	Acinetobacter=26320 HOMO=621 Legionella =253	0
SRR13300932	Stenotrophomonas=10329 Pseudomonas=5139 Acinetobacter=4162	0
SRR13300811	Acinetobacter=21025 Klebsiella=1549 Citrobacter=310	0
SRR13300860	Neisseria=4635 HOMO=3607 Streptococcus=3172	0
SRR13300797	Acinetobacter=27550 HOMO=1546 Moraxella=290	1
SRR13300858	Acinetobacter=17845 HOMO=2530 Moraxella=78	1
SRR13300898	Acinetobacter=15613 Klebsiella=645 Citrobacter=148	1
SRR13300909	Acinetobacter=7677 Klebsiella=2300 Mycoplasma=1625	1
SRR13300918	Acinetobacter=13441 Klebsiella=1374 Raoultella=274	1
SRR13300947	Acinetobacter=27400 Klebsiella=1243 Legionella =300	1
SRR13300878	Klebsiella=8925 Raoultella=1691 Enterobacter=1599	4
SRR13300802	Mycoplasma=1538 Prevotella=936 Treponema=721	32
SRR13300884	Streptococcus=4542 Prevotella=1376 Mycoplasma=1229	76
SRR13300914	Streptococcus=8093 Prevotella=2339 Haemophilus=1001	466

Previous *Acinetobacter*/*Legionella*/*Klebsiella*/*Mycoplasma* co-infections in Covid19 patients

Ventilator-associated pneumonia (VAP) caused by carbapenem-resistant *Acinetobacter baumannii* (CRAB) was a source of concern [10].

An acute care hospital in New Jersey saw an Increase in hospital-acquired CRAB infection and colonization [11]. In another example, all 19 patients were found positive for bacterial infections (17 *Acinetobacter baumannii* and 2 *Staphylococcus aureus*) [12]. There have been isolated incidents of *Legionella* and SARS-CoV-2 co-infection, one of which led to a fatal result in an 80 year old patient returning from a Nile cruise [13]. In another case, which made a full recovery with antibiotics, CSF was PCR positive for *Neisseria meningitidis* [14]. *Klebsiella pneumoniae* infections were reported in an Italian hospital [15], while fatal sepsis hypervirulent *Klebsiella pneumoniae* was reported in a Japanese Covid19 patient [16] A concurrent infection with *Klebsiella pneumoniae* in Taiwan also led to a fatal outcome [17].

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