

The 2019 Wuhan outbreak could be caused by the bacteria *Prevotella*, which is aided by the coronavirus - *Prevotella* is present (sometimes in huge amounts) in patients from two studies in China and one in Hong Kong

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## Letter

A hitherto unknown cause of the Wuhan coronavirus outbreak [1-3] is reported here - a bacteria from the *Prevotella* genus. The number of Wuhan coronavirus deaths in mainland China has overtaken the SARS epidemic in the country. The high mortality is being caused by targeting only the virus (which is also present). This is a two pronged attack, as previously noted in ‘infection with human coronavirus NL63 enhances streptococcal adherence to epithelial cells’ [4]. *Prevotella* is a well known pathogen, and can induce ‘Severe Bacteremic Pneumococcal Pneumonia in Mice with Upregulated Platelet-Activating Factor Receptor Expression’ [5].

### Study 1 - China, RNA-seq, Illumina

The RNA-seq data from Wuhan, China (PRJNA603194 [6]) has millions of reads of *Prevotella* proteins, and a few thousands from 2019-nCoV (Table 1). SI Tables in this shows the abundance of the bacteria, but there is mention of this in the main paper [6].

### Study 2 - Hong-Kong, RNA-seq, Nanopore

Similarly, the DNA sequences (PRJNA601630) of 6 patients from the same family in Hong Kong [3] shows significant presence of this bacteria. These sequences can be found at SI:China.RNA-seq/SampleSequences.fa(n=480K) and SI:HongKong/ALLsequences.fa(n=50k).

### Study 3 - China, RNA-seq, Illumina

Also, another study from China did bacterial pathogen identification using Metaphlan2 program, ‘which revealed Capnocytophaga sp and Veillonella sp in sample 2 and none in sample 1, and both bacteria identified were not known for their pathogenicity’, and concluded ‘coronavirus is likely to be the main microbial pathogen’ [7]. The sequences of the two patients which are from *Prevotella* are at SI:China.RNA-seq.study3.

### Study 1 - China, expression of proteins

Finally, the expression levels (Table 2) shows that the elongation factor Tu is the most expressed. ‘Elongation factor Tu (Tuf) is a new virulence factor of *Streptococcus pneumoniae* that binds human complement factors, aids in immune evasion and host tissue invasion’ [8].

## Conclusion

These are the three studies I could find. But the clinching evidence is the presence of the same integration point of nCov and *Prevotella* in Study1 and Stud2 [9]/ Moreover, detection of the nCoV can be made very specific by looking for a 500bp in the spike protein [10], which would be a good candidate for vaccine development, protein-inhibition and diagnosis (which was non-specific for SARS in many cases, including the CDC test [11]). And, since this is now DNA, the standard detection tests using RT-PCR, which looks for RNA is having large false negatives [12].

## References

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12. Chakraborty S (2020). Significant false negatives in rt-pcr detection of wuhan coronavirus happens as the usually rna-stranded bacteria is now dna within the *prevotella* genome - and we are looking for rna, which will be made in lesser amount by the bacteria. doi:10.31219/osf.io/85ypb. URL [osf.io/85ypb](https://osf.io/85ypb).

Table 1: *Prevotella* is present in copious amounts in patients from China and Hong Kong

Location	Accid	Reads of nCoV	reads of <i>Prevotella</i>	Tech
China	SRR10971381	44095	4821447	Illumina
Hong Kong	SRR10902284	210	13007	Nanopore
	SRR10948550	313	17040	Nanopore
	SRR10948474	77994	24829	Nanopore

Table 2: **Human lung metagenome from a patient in Wuhan (PRJNA603194) showing most expressed proteins from *Prevotella*.** Ribosomal proteins are not shown. These are raw read counts. Elongation factors proteins seem to be playing a key role in the virulence.

Accid	Description	Counts
WP_009012371.1	elongation factor Tu	6405
SNR97511.1	ATP-dependent Clp protease ATP-binding subunit ClpB	4960
WP_009012398.1	elongation factor G	4716
SNR93756.1	molecular chaperone DnaK	4113
WP_009012372.1	transcription termination/antitermination factor NusG	3038
SNR67224.1	hypothetical protein SAMN06265364.1044	2962
SNS04478.1	phosphoenolpyruvate carboxykinase (ATP)	2815
SNR80995.1	glyceraldehyde 3-phosphate dehydrogenase	2240
SNR91480.1	cysteine synthase A	2145
SNR94701.1	chaperonin GroEL	1984
SNR97358.1	pyruvate-ferredoxin/ferredoxin oxidoreductase	1768
WP_009012245.1	energy transducer TonB	1613
WP_004361631.1	DNA-directed RNA polymerase subunit alpha	1610
SNR93143.1	DNA-directed RNA polymerase subunit beta'	1596
SNR97473.1	Pyruvate phosphate dikinase, PEP/pyruvate binding domain	1533
SNR93835.1	Outer membrane protein OmpA	1488
WP_089365394.1	peroxiredoxin	1483
SNS00213.1	ATP-dependent Clp protease ATP-binding subunit ClpC	1437
SNR60000.1	preprotein translocase subunit SecA	1386
SNR84878.1	hypothetical protein SAMN06265364.11429	1317
WP_089366830.1	translation initiation factor IF-3	1278
SNR68043.1	Biopolymer transport protein ExbD/TolR	1242
SNR68055.1	Biopolymer transport protein ExbD/TolR	1169
WP_009010992.1	elongation factor Ts	1156