Illumina/Nanopore reads encoding β -lactamases from plasmids (synthetic vectors) in patient sequencing data from China and Hong-Kong in the suspected coronavirus driven COVID19 outbreak

Sandeep Chakraborty

Letter

I have hypothesized based on sequencing data - two from China [1,2], and one from Hong-Kong [3] - that the SARS-CoV-2 has integrated in the *Prevotella* genome [4,4,5]. The only fly in the ointment in this theory is chimeric reads arising from 16S integrations [6]. These chimeric reads in that region, although some of the are within proteins (SI.plasmid:chimeric.inprotein.fa).

Apart from this, this hypothesis (a chimeric bacteria/virus) explains many of the intriguing observations - the extremely high false negatives (this is now DNA, while we are looking for RNA) [7,8], high incubation periods [9], abdominal problems presenting before respiratory problems [10]. All these, taken one-by-one, probably happen in many viral diseases. But the combination of all observations strongly indicates this is a bacteria+virus.

Plasmid reads encoding β -lactamases

Here, I report plasmid reads encoding β -lactamases in patient sequencing data from China [2] and Hong-Kong [3]. It is not there in the other Chinese study [1].

It is a distant possibility that these reads are from bacteria, given the high homology to plasmids (Fig 1). The origin of these reads, very unlikely to be contamination, in two different geographical locations needs serious investigation. It might also help in choosing the anti-biotics being prescribed.

These sequences can be obtained from SI.plasmid/Study2.HK.blase.fa (N=62) and SI.plasmid/Study3.China.blase.fa (N=35).

References

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Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
☒ Synthetic construct clone 40512BC25_1 beta-lactamase TEM-1 variant gene, complete cds	253	253	100%	1e-63	97.33%	KY725806.1
☒ Synthetic construct clone 101990BC04_1 beta-lactamase TEM-1 variant gene, complete cds	253	253	100%	1e-63	97.33%	KY719820.1
☒ Synthetic construct clone 129619BC27_2 beta-lactamase TEM-1 variant gene, complete cds	253	253	100%	1e-63	97.33%	KY740145.1
☒ Synthetic construct clone 161800_2_2862 beta-lactamase TEM-1 variant gene, complete cds	253	253	100%	1e-63	97.33%	KT417093.1
☒ Synthetic construct clone 125831_1_5967 beta-lactamase TEM-1 variant gene, complete cds	253	253	100%	1e-63	97.33%	KT417137.1
☒ Synthetic construct clone 125831_1_149489 beta-lactamase TEM-1 variant gene, complete cds	253	253	100%	1e-63	97.33%	KT416781.1
☒ Synthetic construct clone 125831_1_123706 beta-lactamase TEM-1 variant gene, complete cds	253	253	100%	1e-63	97.33%	KT416646.1
☒ Synthetic construct clone 161800_2_163137 beta-lactamase TEM-1 variant gene, complete cds	253	253	100%	1e-63	97.33%	KT416483.1
☒ Synthetic construct clone 161800_2_116280 beta-lactamase TEM-1 variant gene, complete cds	253	253	100%	1e-63	97.33%	KT415415.1
☒ Synthetic construct clone 125831_1_20811 beta-lactamase TEM-1 variant gene, complete cds	253	253	100%	1e-63	97.33%	KT412213.1
☒ Synthetic construct clone 125831_1_89266 beta-lactamase TEM-1 variant gene, complete cds	253	253	100%	1e-63	97.33%	KT410839.1
☒ Synthetic construct clone 125831_1_81171 beta-lactamase TEM-1 variant gene, complete cds	253	253	100%	1e-63	97.33%	KT410795.1
☒ Synthetic construct clone 161800_2_123764 beta-lactamase TEM-1 variant gene, complete cds	253	253	100%	1e-63	97.33%	KT408020.1

Synthetic construct clone 40512BC25_1 beta-lactamase TEM-1 variant gene, complete cds
Sequence ID: [KY725806.1](#) Length: 861 Number of Matches: 1

Range 1: 554 to 703 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
253 bits(280)	1e-63	146/150(97%)	0/150(0%)	Plus/Plus
Query 1	CAACAACCTTAAGAAAACCTATTAACTGGCGAATCCTTACTCTAGCTTCCCGCAACAAT	60		
Sbjct 554	CAACAACGTTACGCAAACTATTAACTGGCGAATCCTTACTCTAGCTTCCCGCAACAAT	613		
Query 61	TAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGG	120		
Sbjct 614	TAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGG	673		
Query 121	CTGGCTGGTTTATGCTGATAAATCTGGAG	150		
Sbjct 674	CTGGCTGGTTTATGCTGATAAATCTGGAG	703		

Figure 1: **Reads matching to β -lactamase encoding plasmids:** Plasmid reads encoding β -lactamases in patient sequencing data from China [2] and Hong-Kong [3] in the COVID19 outbreak. It is not there in other Chinese study [1].