Highly expressed host genes in the cells of monkeys infected with SARS-Cov2 - eukaryotic translation elongation factors, cathepsin L, galectin, vimentin

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Letter

A recent pre-print has used Nanopore sequencing to ‘describe aspects of coronavirus evolutionary genetics revealed from these data, and provide the first direct RNA sequence of SARS-CoV-2, detailing coronavi-ral subgenome-length mRNA architecture’ [1]. They have analyzed reads matching to the SARS-Cov2. Here (Table 1) I analyze reads matching to the host cell (ignoring ribosomal genes) - the full list is in SI:hostgeneexpression.txt.

Eukaryotic translation elongation factors

This review details how ‘viral pathogens usurp these abundant cellular proteins for their replication’ [2].

S100 calcium binding proteins

These proteins seem to be host defence mechanisms as in this study ‘S100A1, S100A2 and S100A6 in sO cells resulted in the efficient inhibition of HCV replication’ [3].

Cathepsin L

This - and not TMPRSS2 [4] - seems to be the protease involved in SARS-Cov2 [5]. Note, Cathepsin L ‘functionally cleaves the severe acute respiratory syndrome coronavirus class I fusion protein upstream of rather than adjacent to the fusion peptide’ [6] and its inhibition prevented virus entry’ [7]. There is also a contrarian view since human coronavirus NL63 does not use Cathepsin L to infect ACE2-expressing cells [8].

Galectin

Galectins have a role in virus infection [9]. In fact this is a ‘viral evolution strategy in which coronaviruses stole a galectin from hosts, incorporated it into their spike protein, and evolved it into viral receptor-binding domains with altered sugar specificity in contemporary BCoV or novel protein specificity in contemporary MHV’ [10].

Vimentin

‘Surface vimentin is critical for the cell entry of SARS-CoV’ [11].

References

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Table 1: **Highly expressed host genes in the cells of monkeys infected with SARS-Cov2:** Sequencing data obtained from Accid:PRJNA608224 [1]. Excluded ribosomal and mitochondrial genes.

Read counts	Description (Human accession id)
2442	NM.001402.6 eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA
1519	XM.017002033.1 S100 calcium binding protein A6 (S100A6),
1309	NM.006098.4 receptor for activated C kinase 1 (RACK1), mRNA
1189	XM.011516549.3 VGF nerve growth factor inducible (VGF),
1134	NM.021103.4 thymosin beta 10 (TMSB10), mRNA
1070	XM.024446695.1 aldo-keto reductase family 1 member B (AKR1B1),
1063	XM.017014293.2 cathepsin L (CTSL),
1025	NM.002305.4 galectin 1 (LGALS1), mRNA
1024	NM.006082.3 tubulin alpha 1b (TUBA1B), mRNA
970	NM.021109.4 thymosin beta 4 X-linked (TMSB4X), mRNA
898	NM.021009.7 ubiquitin C (UBC), mRNA
782	NM.003295.3 tumor protein, translationally-controlled 1 (TPT1),
735	XM.017012224.2 aldo-keto reductase family 1 member B15 (AKR1B15),
710	NM.002520.6 nucleophosmin 1 (NPM1),
676	XM.011511522.2 prothymosin alpha (PTMA),
670	XM.006717500.2 vimentin (VIM),
643	NM.001909.5 cathepsin D (CTSD), mRNA
642	XM.017022313.2 pyruvate kinase M1/2 (PKM),
632	NM.002415.2 macrophage migration inhibitory factor (MIF), mRNA
628	NM.003329.4 thioredoxin (TXN),
626	NM.001353346.2 enolase 1 (ENO1),
608	XM.011542798.1 heat shock protein family A (Hsp70) member 8 (HSPA8),
595	NM.001404.5 eukaryotic translation elongation factor 1 gamma (EEF1G), mRNA
564	NM.001145199.1 chromosome 12 open reading frame 75 (C12orf75), mRNA
553	XM.017024761.1 profilin 1 (PFN1),
551	NM.001961.4 eukaryotic translation elongation factor 2 (EEF2), mRNA
543	NM.178014.4 tubulin beta class I (TUBB),
509	XM.024450193.1 aldolase, fructose-bisphosphate A (ALDOA),
494	XM.017021370.1 serpin family A member 1 (SERPINA1),
485	XM.024449908.1 annexin A2 (ANXA2),
479	NM.016139.4 coiled-coil-helix-coiled-coil-helix domain containing 2 (CHCHD2),
457	NM.002032.3 ferritin heavy chain 1 (FTH1), mRNA

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