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Proteolytic reversibility of COVID19-associated phenotype

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Abstract

I. The remote, in vivo, and chemogenetic activation of COVID19 phenotype is fully reversible.

Persistent ultrasonic-mediated stimulation of the caudate-putamen (CPu) brain region with low-intensity (PSRF-encoded) ultrasounds may trigger GPCR-mediated inhibitory dopamine (D2R) release in the striatum and is associated to increased glucocorticoid (GC) signaling and NLRP3-dependent inflammasome activation in the pathology of COVID19. [1]

II. Adenosine-dependent reversal of COVID19 rna-binding-protein (RBP) is mediated by furin convertase proteolysis.

In addition the unusual specificity of the chimeric RBP driving viral entry in the pathology of "COVID19" may indicates the existence of a 19th O-linked glycolysation site highly specific to Ebola virus (Makina C07) (https://https://www.ncbi.nlm.nih.gov/nuccore/KJ660347.2) phenotype and may require functional (and reversible) furin-mediated proteolytic cleavage to trigger a CCR5-mediated pro-inflammatory response in epithelial cells. [2][3]

III. COVID19 RBP is a chimeric/mutant glycoprotein derived from R26-LSL-Gq-DREADD.

Our current report suggest COVID19 cellular reversibility is evidence of engineered GPCR (CCR5) trafficking mecanism and may exploit a clathrin-dependent endocytosis feature to activate a CD4-dependent proinflammatory pathway (THP-1) in the pathology of COVID19.[4][5]

Introduction

Chloroquine is a clathrin-mediated endocytosis (CME) inhibitor of CCR5 in the pathology of COVID19.

New evidences suggests chloroquine may inhibits clathrin-mediated (CCR5) endocytosis and knockdown NLRP3-dependent inflammasome activation in the pathology of COVID19: Yen. et al (2006) reported a functional role of the chemokine receptor CCL5 (CCR5) in the pathology of SARS-CoV-1 and this ligand is a well-known HIV/AIDS co-receptor activated via DC-SIGN expressing mononuclear cells (THP-1) in vitro.

Method

Identification of synthetic constructs in recombinant COVID19 spike protein (QHD43416.1)

The goal is of this strategy is to compile and identify chimeric genes (ie: designer-like receptors) in the COVID19 structural glycoprotein using COBALT generated multiple sequence alignments (MSA).

Protocol: Magic-BLAST (blastn)

Primary paper: https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-019-2996-x

Reference GenBank accessions (FASTA):

- 1. QHD43416.1 (Subject) sars-cov-2 RBP (21563-25384)
- 2. MN908947.3 sars-cov-2 full genome

Experimental data and results

Multiple Sequence Alignments

- pAAV-hSyn-DIO-hM3D(Gq)-mCherry : MSA dataset (Last modified: 20/07/02)
- NM 000579.3 (Human CCR5 locus) : MSA dataset (Last modified: 20/07/04)

Discussion

Early genetic evidences of the structural design and assembly of the recombinant SARS-CoV-2 S protein

The discovery or a functional and recombinant CCR5 domain (SHS) in the CODIV19 spike GP has several highly important implications to the scope and relevancy of this report. In specific, our experimental data may suggest reliable genetic evidences on the existence of a cryptographic 20bp "DNA barcode" located into the COVID19 "spike" GP, region 23405-23394.

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AgRP neurons regulate development of dopamine neuronal plasticity and nonfood-associated behaviors

See also

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- Clustal Omega: https://www.ebi.ac.uk/Tools/msa/clustalo/
- GenBank to FASTA: https://www.bioinformatics.org/sms2/genbank fasta.html
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