

Opinion

# Hypothesis about pathogenic action of Sars-COV-2

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## Abstract

The Hypothesis born on a simple clinical data noted by some Chinese Reserchers during the starting point of epidemic began in the dicember of the 2019, for the novel member of human coronavirus, officially named as SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) by International Committee on Taxonomy of Viruses (ICTV) is a new strain of RNA viruses that has not been previously identified in humans [1]. Sars-COV and SARS CoV-2 have some clinical differences. First: The Sars, severe acute respiratory sindrome induce a respiratory disease in immunocompetent hosts, although can cause severe infections in infant, young children and elderly individuals; Sars-CoV-2 induce a middle infection into the young children but the mortality is more high in to the adult population. We made a machting with balst p of these sequences, Sars COV-2, taken on GENE BANK with H1N1 neuraminidase and the not structural protein NS1 and NS2 an interferon antagonist that may also stimulate proinflammatory cytokines in infected cells We can speculate that the mutation is occurred on accessories protein making a different virulence action between the two species Sars Cov and Sars Cov-2, same action we have founded in the H<sub>1</sub>N<sub>1</sub> viral pandemic of the 2019.

## Introduction

The Hypothesis born on a simple clinical data noted by some Chinese Reserchers during the starting point of epidemic began in the dicember of the 2019, for the novel member of human coronavirus, officially named as SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2) by International Committee on Taxonomy of Viruses (ICTV) is a new strain of RNA viruses that has not been previously identified in humans [1]. Sars-COV and SARS CoV-2 have some clinical differences. First: The Sars ,severe acute respiratory sindrome induce a respiratory disease in immunocompetent hosts, although can cause severe infections in infant, young children and elderly individuals; Sars-CoV-2 induce a middle infection into the young children but the mortality is more high in to the adult population: this way of infection it isn't a classic way because the child doesn't have a strong immunitary response, therefore this atypical response remember us the infection of Spanish influenza just known as pandemic spanish influenza; it had an high score of mortality between the 1918 and the 1920, killing millions of persons all around the world. In the 2009 we had another pandemic influenza from H<sub>1</sub>N<sub>1</sub> virus and it was characterized by at similar mortality score. At this regarding the risk factors for severe disease, obesity was an important predisposing factor, in addition to extremes of age,

pregnancy, and underlying medical illness [2]. In patients with severe disease, viral clearance was delayed, with a persistent elevation of pro-inflammatory cytokines and associated multiorgan damage despite antiviral therapy [2]. Additionally, a lower serum IgG2 level appeared to be associated with disease severity, especially in pregnant patients. Severe disease and lung pathology were associated with immune complex deposition. The second element of this pathogenic coronaviruses SARS-CoV-2 is a cytochine storm\*6 [3]. It was demonstrated that SARS-COV and SARS-CoV-2 are similiar, so we have supposed that both these viruses can doing matching in them hotspot mutation. In the lecterature these hot spots are orf8 and orf3 [4]. We, in our hypothesis, considered also another hot spot; Orf 1 ab as an interest point [5]. We made a machting with balst p of these sequences, Sars COV-2, taken on GENBANK with H<sub>1</sub>N<sub>1</sub> neuraminidase and the not structural protein NS1 and NS2 an interferon antagonist that may also stimulate proinflammatory cytokines in infected cells [6,7], (Death is aborted by blockade of interferon-1 (IFN-1) signaling or deletion of CD8 T cells).

## Materials and methods

We used to identify, a possible genomic correspondence between H<sub>1</sub>N<sub>1</sub> and Sars COV-2, Gene Bank for identification of amminoacids sequence of Orf 1ab, Orf 3a (hot spot mutation

## More Information

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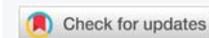
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for Sars COV-2), Neuraminidase segment and NS1/NS2 (factor of H<sub>1</sub>N<sub>1</sub> virulence) and BLASTp ncbi program for matching these sequences. We match before Orf 3a with neuraminidase aminoacids sequence then Orf 1ab with NS1/NS2 aminoacids sequence.

Results are for Orf 3a and neuraminidase of H<sub>1</sub>N<sub>1</sub>: e-value 0.23; Query cover of 22% and percent identity of 22,22%, but the most important data is in the range2 where we find an identities of 100% with positivity of 100% for sequence 311-315 of neuraminidase H<sub>1</sub>N<sub>1</sub> the sequence expressed in both is: DYQIG. The results of matching between Orf 1ab of Sars-COV-2 and NS1/NS2 of H<sub>1</sub>N<sub>1</sub> present an e-value of 1.2 (little bit significance) but with an Query cover of 51% and a percent identity of 40%. Even if the e-value is little bit high we have a significance match score and query cover; that purpose an hypothesis of mutation of the Sars-COV-2 in sense of H<sub>1</sub>N<sub>1</sub>. At last we made another analysis matching between ORF8a of Sars-COV-2 and neuraminidase of H<sub>1</sub>N<sub>1</sub>; these sequence matching have expressed an evalue of 2.2 with a query cover of 15% and percent identity of 23,3%, in this case we can say that we not have a significative correspondence between these sequences not only for the e-value to much high but also for the query cover that is not too significance. To support our theory we have made some control test matching between Sars-COV Orf 1ab and Orf 1ab Sars-COV-2 that present a query cover of 100% e-value 0.0 and identity percent of 86,16%, so we speculate that in Orf 1ab Sars COV have lose some aminoacids passing to COV-2 (our control). Then we matching, for control analisis too Orf 3 of Sars COV and Orf 3a of Sars COV-2 with a query cover of 64% e-value 3e-154 and an identity percent of 72%; we match also neuraminidase with Orf3 Sars COV with a query 4%, e-value 0,74 and an identity percent of 62,5%.

We can speculate that the mutation is occurred on accessories protein making a different virulence action between the two species Sars Cov and Sars Cov-2 infact in the licterature we know that the Sras Cov has like target children and seniors; this aspect in Sars COV-2 is less present; Furthermore Sars COV-2 presents a citokine storm like immune reaction at this virus. This fact can suggest a direct attack on the immune system or a specific defense mechanism of the virus. The same action we have founded in the H<sub>1</sub>N<sub>1</sub> viral pandemic of the 2019; the citokine storm is the principal cause of the high mortality and morbidity of this virus that attack respiratory ways.

## Results

Table 1
ORF 3a Sars COV-2 match H <sub>1</sub> N <sub>1</sub> neurominidase
Range 2: 183 to 187
Score:15.4 bits(28), Expect: 2.4,
Method: Compositional matrix adjust.,
Identities: 5/5 (100%), Positives: 5/5 (100%), Gaps:0/5(0%)
Query 311 DYQIG 315 Sbjct
183 DYQIG 187
We can see a strong matching between Query sequence H <sub>1</sub> N <sub>1</sub> neurominidase and Sars COV2 Orf 3a.

## Discussion and conclusion

Our Hypothesis is that Sars COV-2 could near at H1N1 for two reasons; first one the action of the virus on guest immune system and the second one the strong similarity in the matching supposed. If this correspondence could be true, we can considerate the Orf3a and Orf 1ab as target of some drugs already useful against neurominidase and Ns1/NS2 of H<sub>1</sub>N<sub>1</sub>. Our Hypothesis is sustained by the new Italian datas of infection; the patient are treated with cortisone and tocilizumab that intervenc on cytochine storm.

## Declaration

### Ethical approval

All procedures performed in studies involving human participants were in accordance with the ethical standards of the institutional national research committee and with the 1964 Helsinki declaration and its later amendments or comparable ethical standards.

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