Dr. Tom Cowan & Biotech Scientist Mike Donio: A Close Examination of the Evidence of Snake Venom in “the Virus” & in the Water Supply

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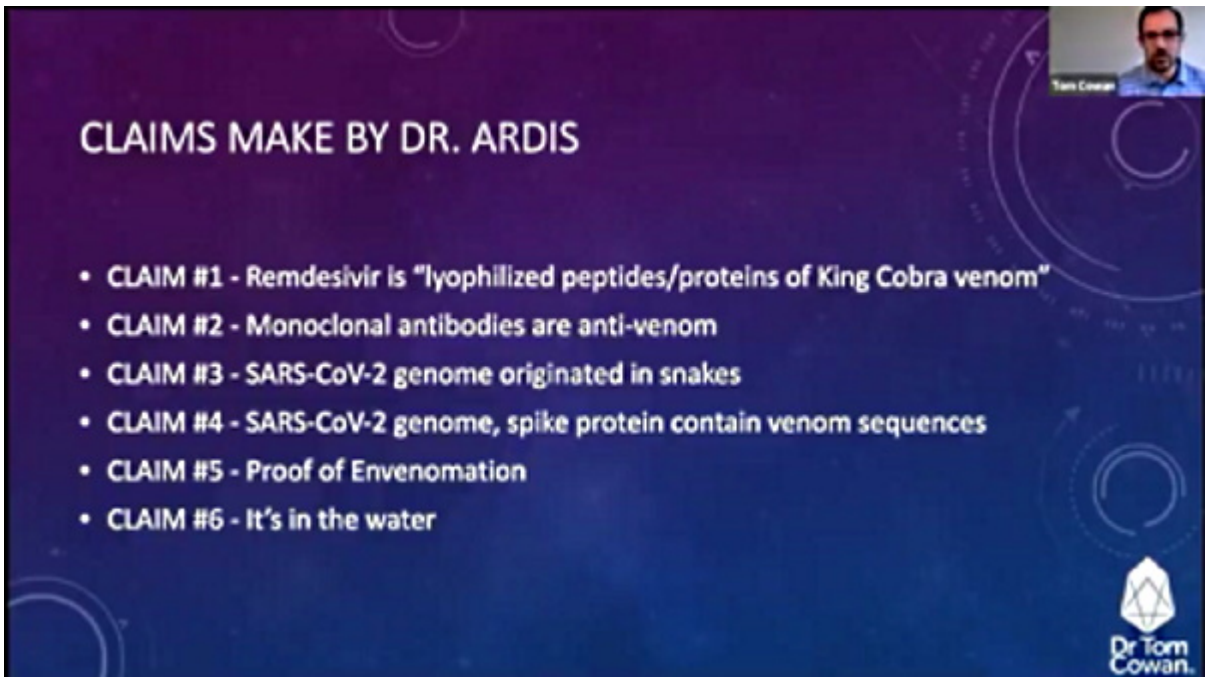
Getting to the Head of the Snake – Is Covid 19 Toxic Envenomation?

by **Dr. Tom Cowan** with **Mike Donio**
April 22, 2022

In this webinar, my friend and colleague Mike Donio analyzed the main points of Dr. Ardis’ recent snake venom warning. Tune in to find out what we think of these claims.

Slides Outlining the Presentation:


Dr Tom Cowan™
GETTING TO THE HEAD OF THE SNAKE
IS COVID-19 TOXIC ENVENOMATION?


CLAIMS MAKE BY DR. ARDIS
• CLAIM #1 - Remdesivir is "lyophilized peptides/proteins of King Cobra venom"
• CLAIM #2 - Monoclonal antibodies are anti-venom
• CLAIM #3 - SARS-CoV-2 genome originated in snakes
• CLAIM #4 - SARS-CoV-2 genome, spike protein contain venom sequences
• CLAIM #5 - Proof of Envenomation
• CLAIM #6 - It's in the water
Dr Tom Cowan.

QUALIFYING STATEMENTS

- As we have extensively shown, there is no evidence that the SARS-CoV-2 virus exists.
- All claimed isolation of a virus evidenced by the creation of a new genome is fallacious.
- Any SARS-CoV-2 test, PCR or otherwise, derived from said genomes are also invalid.
- Therefore, data and conclusions based on stratification of patients solely by test results are unreliable.
- We hope to clearly demonstrate that SARS-CoV-2 is neither a virus or snake venom.

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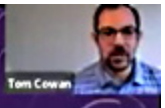
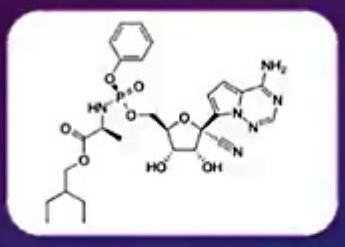


CLAIM #1: REMDESIVIR IS LYOPHILIZED KING COBRA VENOM PEPTIDES/ PROTEINS



- **Claim:** "Remdesivir is lyophilized peptides/proteins of King Cobra venom."
- According to Tchesnokov et al. Remdesivir is a "1'-cyano-substituted adenosine nucleotide analog prodrug".
- Remdesivir, structure shown above, is metabolized to form the active drug or the triphosphate form.
- The proposed mechanism of action is inhibition of the viral RNA dependent, RNA polymerase (RdPp).
- **Conclusion:** False, Remdesivir is not King Cobra venom peptides or proteins.
- Note: We in no way are saying that Remdesivir isn't toxic because it is.

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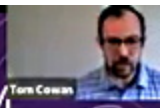

CLAIM #2: MONOCLONAL ANTIBODIES ARE ANTI-VENOM

- **Claim:** All monoclonal antibodies are anti-venom.
- Dr. Ardis describes a process whereby venom toxins are injected into horses and the serum is collected.
  - The antibody cocktail generated in the horse sera is referred to anti-venom.
- Therefore, he concludes, all monoclonal and polyclonal antibodies are anti-venom.
- Reality: This is how all antibodies are generated for research and therapeutic purposes.
- **Conclusion:** Partly False
  - Not all antibodies are anti-venom, only those specifically raised against venom toxins.

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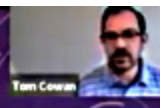


CLAIM #3 - SARS-COV-2 ORIGINATED IN SNAKES

RESEARCH ARTICLE

JOURNAL OF MEDICAL VIROLOGY WILEY

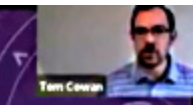
Cross-species transmission of the newly identified coronavirus 2019-nCoV

Wei Ji[1] | Wei Wang[2] | Xiaofang Zhao[3] | Junjie Zai[4] | Xingguang Li[5]

- **Claim:** SARS-CoV-2 originated in snakes
  - Study by Ji et al. showed 2019-nCoV genome has lowest RSCU distance with snakes
  - RSCU is Relative Synonymous Codon Usage
- Let's take a closer look at the paper

Dr Tom Cowan.

CLAIM #3 - SARS-COV-2 ORIGINATED IN SNAKES



2 | MATERIALS AND METHODS

2.1 | Sequence data collection

The newly sequenced Beta-coronavirus (MN908947) genome was downloaded from the GenBank database. Five hundred closely related sequences were also downloaded from GenBank. Out of them, 271 genome sequences (>19 000 bp in length) were used in this study together with the above-described Beta-coronavirus (2019-nCoV, MN908947) genome sequence (Table S1). The geographic origins of the sequences were from Bulgaria (n = 1), Canada (n = 2), China (n = 67), Germany (n = 1), Hong Kong (n = 5), Italy (n = 1), Kenya (n = 1), Russia (n = 1), Singapore (n = 24), South Korea (n = 1), Taiwan (n = 11), United Kingdom (n = 2), United States of America (n = 67), and unknown (n = 88). Sequences were aligned using MAFFT v7.222,[17] followed by manual adjustment using BioEdit v7.2.5.[18]

- The reference genome sequence used is 2019-nCoV, MN908947 also known as WH-Human 1.
- The genome was generated by Wu et al. in January 2020 from a single patient.
- RNA was isolated from lung fluid and sequenced.
- Then the genome was created in silico.
- They did not isolate any viral particles to confirm that the genome actually came from a virus.

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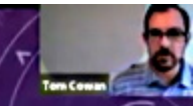
CLAIM #3 - SARS-COV-2 ORIGINATED IN SNAKES



virus,[15] hepatitis B virus,[16] hepatitis C virus,[17] and classical swine fever virus.[18] Similarity plot analysis of the 2019-nCoV revealed that homologous recombination may occurred between Clade A strains (bat-coronaviruses) and the origin-unknown isolates, located within the spike glycoprotein that recognizes cell surface-receptor (Figure 2). These characteristics indicate that cross-species transmission may be caused by homologous recombination.

3.3 | Relative synonymous codon usage analysis

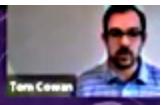
As parasitic microorganism, virus codon usage pattern resembles its host to some extent. The RSCU bias shows that the 2019-nCoV, bat-SL-CoVZC45, and snakes from China have similar synonymous codon usage bias (Figure 3A, Table 1). The squared euclidean distance indicates that the 2019-nCoV and snakes from China have the highest similarity in synonymous codon usage bias compared to those of bat, bird, Manmota, human, Manis, and hedgehog and (Figure 3B). Two types of snakes, containing B. multicinctus (many-banded krait) and N. atra (Chinese cobra) were used for RSCU analysis. Squared Euclidean distance between the 2019-nCoV and B. multicinctus is 1334. The distance between the 2019-nCoV and another snake N. atra is 1649. The distance between the 2019-nCoV and Rhinolophus sinicus is 2246. However, the distance between the 2019-nCoV and other animals is greater than 26, specifically 2693 for bird, 34.79 for Manmota, 35.36 for human, 34.71 for Manis, and 37.96 for hedgehog. These data suggest that the 2019-nCoV might more effectively use snake's translation machinery than that of other animals.

Two types of snakes are common in Southeastern China including the city of Wuhan (Figure 4). Geographical distributions of B. multicinctus include Taiwan, the Central and Southern China, Hong Kong, Myanmar (Burma), Laos, and Northern Vietnam.[19] N. atra is found in Southeastern China, Hong Kong, Northern Laos, Northern Vietnam, and Taiwan.[19] Snakes were also sold at the

- They use RSCU to predict the closest native host.
- The idea is virus codon usage pattern is supposed to resemble its host to some extent.
- A lower number or distance means a closer resemblance.
- According to their calculations, comparisons with 2019-nCoV and two snake species were closest.

Dr Tom Cowan.

CLAIM #3 - SARS-COV-2 ORIGINATED IN SNAKES



- Letters to the Editor from other scientists challenged the claims by Ji et al.

LETTER TO THE EDITOR

JOURNAL OF MEDICAL VIROLOGY WILEY

Comments on "Cross-species transmission of the newly identified coronavirus 2019-nCoV"

Dear Editor,

After reading the article speculating that novel coronavirus from Wuhan may be transmitted to humans through snakes, I think the most critical analysis method is the synonymous codon usage analysis, which estimated the relative synonymous codon usage (RSCU) of the 2019-nCoV (novel coronavirus) and its potential hosts. Here, I would like to make a few comments:

First, there exists a large difference in the number of codons used in potential hosts, which would obviously cause biases and lead to an unreliable conclusion. Only 5381 codons, 9567 codons, and 8085 codons were used in *Bungarus multicinctus*, *Naja atra*, and *Rhinolophus sinicus*. While 16 717 458 codons, 21 090 600 codons, 22 980 491 codons, 36 086 657 codons, and 40 662 582 codons were used in *Enhydra lutris*, *Mustela putorius furo*, *Manis javanica*, *Gallus gallus*, and human. The genome of *Ophiophagus hannah* (GCA_000516915.1) and *Rhinolophus ferrumequinum* (GCA_004115265.2) might be alternatives to estimate the RSCU in snake and bat.

Second, the measure of judgment on putative wildlife reservoir hosts is lacking. I do not think it is appropriate to conclude that *Manis* was the reservoir host when *B. multicinctus* and *N. atra* were removed from the comparison.

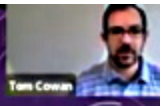
Finally and most importantly, the result of comparison of RSCU between 2019-nCoV and its putative wildlife reservoir hosts was lacking adequate support (Figure 1). Theoretically the patterns and factors that affect codon usage of viruses should reflect evolutionary changes that allow them to optimize their codon usage in their hosts. But there is no evidence showing that this rule worked for coronavirus also. To make it more convincing, Middle East respiratory syndrome-coronavirus (MERS-CoV) and its host *Camelus dromedarius* (GCA_000803125.3) should be included as control. While even taking camel into consideration, we can see that it is still far away from these CoVs.

In summary, we think the conclusion that the newly identified coronavirus may boast cross-species transmission from snake to human is inadequate, and it can lead to public misperception.

As for the reason why snakes share the most similar codon usage pattern with SARS-CoV-2, we believed that is because of the inherent A/T(U)-rich base compositions in both the genomes of the coronaviruses[7] and snakes.[8] Base composition, like GC_3 (guanine-cytosine [GC] content on the third codon position) value has been illustrated as a strong determinant in shaping codon usage both in viruses[9,10] and higher multicellular eukaryotes.[7] In a bid to test our speculation, we added viruses with known hosts and different AU_3 values, as well as several host animals into Ji et al's[1] sampling pool. Coding sequences of their genomes were obtained from GenBank and the RSCU similarity was calculated using the same method by Ji et al[1] (see detailed information in Supplementary Information Appendix 1). It turned out that viruses with high AU_3 values are closer to animals have comparatively high AT_3 values (herein *N. atra*, *B. multicinctus*, and *M. oondyiurus*) rather than AT_3 low-value species in RSCU distance (Figure 1). The result designated most investigated viruses (10/12) to infect snakes, regardless of their actual hosts.

In conclusion, the RSCU similarity analyses only links virus to animal(s) that possesses comparable GC content. We did not rule out the speculation that snakes would be the intermediate host of SARS-CoV-2, but we suspect if the possibility of these species was higher than any other creature in transmitting the virus. Scientific research that gives a quick response to public emergencies is imperative and appreciative, yet the methodology applied within has to be carefully examined.

CLAIM #3 - SARS-COV-2 ORIGINATED IN SNAKES



Response to comments on "Cross-species Transmission of the Newly Identified Coronavirus 2019-nCoV" and "Codon bias analysis may be insufficient for identifying host(s) of a novel virus"

To the Editor,

We have recently reported for the first time that severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) maybe a bat-originated coronavirus with a recombination occurred within the spike (S) protein gene based on phylogenetic and simplot analyses.[1] These two conclusions are supported by findings recently reported by others and are well accepted in the field of SARS-CoV-2 research.[2,3] In addition, we speculated that snake may serve as a potential reservoir for cross-species transmission of SARS-CoV-2 to humans based on limited information obtained from relative synonymous codon usage (RSCU) bias among different animal species. The later speculation was questioned by Yuzhou Gong et al and Jiating Qian et al in the preceding letters to editors. We concur with the argument that SARS-CoV-2 genomes used in the study were inconsistent. In fact, we used several SARS-CoV-2 sequences released at the time for phylogenetic analysis. However, we only included 2019 novel coronavirus (2019-nCoV/MHV0847 pressure but also natural selection,[1] which indicate that forecasting host reservoir only by RSCU are questionable. The true animal reservoir for SARS-CoV-2 remains controversial at present time and is warranted for further investigation.

Wei Ji[1]
Xingguang Li[2]

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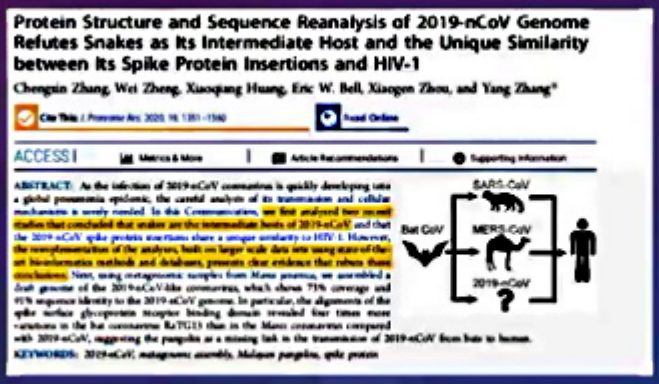
[2]Hubei Engineering Research Center of Viral Vector, Wuhan University of Bioengineering

Correspondence
Wei Ji, Medical school, Liaocheng university, Liaocheng, China
Email: ji102306@126.com

- Response from author Wei Ji.
- True animal reservoir remains controversial and further investigation is warranted.

CLAIM #3 - SARS-COV-2 ORIGINATED IN SNAKES



Protein Structure and Sequence Reanalysis of 2019-nCoV Genome Refutes Snakes as Its Intermediate Host and the Unique Similarity between Its Spike Protein Insertions and HIV-1

Chengxin Zhang, Wei Zheng, Xiaoqiang Huang, Eric W. Bell, Xiaogen Zhou, and Yang Zhang*

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ABSTRACT: As the infection of 2019-nCoV coronavirus is quickly developing into a global pneumonia epidemic, the careful analysis of its transmission and cellular mechanisms is newly needed. In this Communication, we first analyzed two recent studies that concluded that snakes are the intermediate hosts of 2019-nCoV and that the 2019-nCoV spike protein insertions share a unique similarity to HIV-1. However, the reexamination of the analyses, built on larger scale data sets using state-of-the-art bioinformatics methods and databases, presents clear evidence that rebuts those conclusions. Next, using metagenomic samples from Manis genetics, we assembled a draft genome of the 2019-nCoV-like coronavirus, which shows 73% coverage and 91% sequence identity to the 2019-nCoV genome. In particular, the alignments of the spike surface glycoprotein receptor binding domain revealed four times more variations in the bat coronavirus RaTG13 than in the Manis coronavirus compared with 2019-nCoV, suggesting the pangolin as a missing link in the transmission of 2019-nCoV from bats to human.

KEYWORDS: 2019-nCoV, metagenomic assembly, Malayan pangolins, spike protein

- A follow up commentary by Zhang et al directly refutes the study by Ji et al.
- Claims clear evidence to rebut the conclusion that snakes are the intermediate hosts of 2019-nCoV.
- **Conclusion:** False, the 2019-nCoV genome did not originate in snakes.

Dr Tom Cowan.

CLAIM #4: SPIKE PROTEIN CONTAINS SNAKE VENOM SEQUENCES

- **Claim:** SARS-CoV-2 Spike protein contains snake venom sequences.
- Performed nBLAST searches comparing the following:
  - SARS-CoV-2 and human PLA2
  - SARS-CoV-2 and King Cobra PLA2
  - SARS-CoV-2 and ophiophagus hannah (King Cobra)
- Performed pBLAST searches comparing the following:
  - SARS-CoV-2 spike protein and sPLA2 protein
  - SARS-CoV-2 spike protein and alpha-conotoxin
  - SARS-CoV-2 spike protein and alpha-bungarotoxin
- No significant similarities or homologies were found for any of the comparisons.
- **Conclusion:** False

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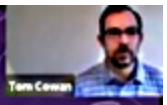
CLAIM #5: PROOF OF ENVENOMATION



- Dr. Ardis used two key studies as proof of envenomation.
  - Increased sPLA2-IIA levels in COVID-19 patients (Snider et al. 2021).
  - Peptides closely related to venom toxins found in plasma, urine and fecal samples of COVID-19 patients (Brogna et al. 2021).
- We will examine each one individually.

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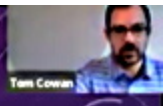
CLAIM #5: PROOF OF ENVENOMATION



- Increased sPLA2-IIA levels in COVID-19 patients (Snider et al. 2021).
- Analyzed 127 plasma samples from COVID-19 positive patients via SARS-CoV-2 test.
  - Stratified into 4 groups with approximately 30 patients each:
    - Group A: Mild symptoms
    - Group B: Severe symptoms
    - Group C: Deceased
    - Non-COVID-19 group
  - Found elevated metabolites associated with secreted phospholipase A2 (sPLA2) activity and mitochondrial dysfunction.
- Soluble phospholipase A2 (sPLA2) was supposedly first discovered as a component of cobra venom.
- Dr. Ardis claims that it shows how all the symptoms and drug/vax side effects are all related to snake venom poisoning.
- Let's look at the paper to verify the claims.

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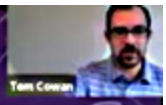
CLAIM #5: PROOF OF ENVENOMATION



- What is phospholipase A2 (PLA2)?
- PLA2s are enzymes that largely function to hydrolyze fatty acids - breaks them down into something else.
- Generates two new molecules: free arachidonic acid (AA) and lysophospholipids.
- One type of molecule that can be generated from AA are prostaglandins (PGs).
- PGs are pro-inflammatory lipid mediators which stimulates inflammatory cytokines.
- Bottom line: these are markers for inflammation.
- "Levels in sera/exudating fluids are well correlated with the severity of inflammatory diseases" - Murakami et al. 2001.
- Humans make roughly 20 different PLA2 isoforms alone - different versions with similar activities.

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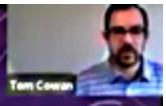

propriate patient selection probably contributed to patient heterogeneity, resulting in negative findings. A recent study reported that, using a cutoff value of 25 ng/mL, $sPLA_2$-IIA is highly sensitive and specific in detecting sepsis (20). Given that deceased COVID-19 patients in this study had elevated $sPLA_2$-IIA levels (≥10 ng/mL), we propose incorporating $sPLA_2$-IIA levels and the PLA-BUN index as prognostic clinical parameters. Our study further highlights the merit of exploring $sPLA_2$-IIA inhibitors to reduce COVID-19–related morality.

Methods

Study design. The study was designed according to Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) guidelines (41). COVID-19 was diagnosed by real-time reverse transcriptase PCR (RT-PCR), and COVID-19–positive patients were classified into 3 groups: (a) mild, in which patients had mild symptoms without pneumonia on imaging and were discharged from inpatient care; (b) severe, in which patients had respiratory tract or nonspecific symptoms, pneumonia confirmed on imaging, an oxygenation index below 94% on room air, and were discharged from inpatient care; and (c) deceased, in which the patients died during inpatient care. All plasma samples were collected during each patient's hospital stay, except for the late (2nd) time points for patients with mild COVID-19 (Supplemental Figure 6). Only non-COVID-19 patients and those with mild COVID-19 with NEWS2 scores of 3 or lower were included in this study in order to exclude patients hospitalized for unrelated, possibly confounding major clinical presentations.

Sample processing and lipidomics analysis. Frozen EDTA plasma samples were processed using Biosafety Level 2 conditions following the CDC Guidelines for the handling and processing of specimens associated with COVID-19. Metabolites were isolated from plasma via methanol-based extraction containing 10 μL Splash Lipidomix (Avanti Polar Lipids) and separated using reversed-phase chromatography as previously described by Najdekr et al. (43). Samples were analyzed using an ultra-high-performance liquid chromatography–electrospray ionization–tandem mass spectrometry (UHPLC-ESI-MS_2/MS) system (UHPLC: Thermo Horizon Vanquish Duo System from Thermo Horizon; MS: Thermo Exploris 480, both from Thermo Fisher Scientific, and separation was achieved using a Hypersil GOLD aQ UHPLC column (100 × 2.1 mm, 1.9 μm, Thermo Fisher Scientific, part no. 25302-102130) with mobile phases composed of water containing 0.1% formic acid and methanol containing 0.1% formic acid. Metabolites were eluted over a 15-minute gradient with the Exploris 480 operating in positive ion mode, at an ion transfer tube temperature of 350°C, a sheath gas of 45, an aux gas of 5, and a spray voltage of 4000. Mass spectrometric data for all samples were collected using dynamic exclusion and then aligned with pooled samples collected using the Thermo AquireX to achieve optimal metabolite identification in LipidSearch 4.0 and Thermo Compound Discoverer 2.3 software (both from Thermo Fisher Scientific).

Targeted lipidomics analysis was performed using an Agilent 1200 HPLC Tandem Thermo Quantum Ultra triple quadrupole mass spectrometer (Agilent Technologies) to quantify levels of major molecular species of lyso-PLs. C16, C18:1, C18:2, and C20:4 molecular species for lyso-PC, lyso-PE, and lyso-PS (Cayman Chemical) were used as standards and deuterated Splash Lipidomix (Avanti Polar Lipids) as internal standards. Lyso-PLs were separated using an Agilent Poroshell 120

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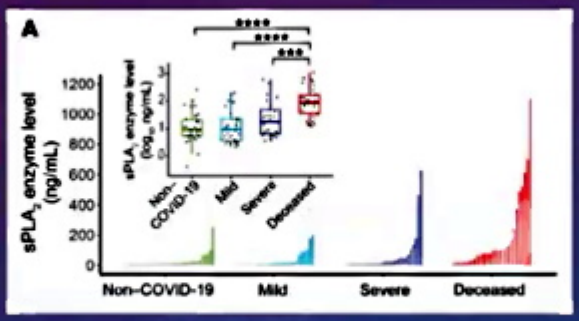

- Appears to be mostly a trend with patients having varying levels of sPLA2 in each group, as seen in panel A above.
- It isn't surprising to find that very sick patients had high levels of an inflammatory marker.
- The authors simply suggest incorporating sPLA2-IIA levels a prognostic clinical parameters.
- There is no suggestion or implication that these findings are in any way related to snake venom.
- **Conclusion: False**

Dr Tom Cowan.

CLAIM #5: PROOF OF ENVENOMATION

Abstract

Background: SARS-CoV-2 that causes COVID-19 disease and led to the pandemic currently affecting the world has been broadly investigated. Different studies have been performed to understand the infection mechanism, and the involved human genes, transcripts and proteins. In parallel, numerous clinical extra-pulmonary manifestations co-occurring with COVID-19 disease have been reported and evidence of their severity and persistence is increasing. Whether these manifestations are linked to other disorders co-occurring with SARS-CoV-2 infection, is under discussion. In this work, we report the identification of toxin-like peptides in COVID-19 patients by application of the Liquid Chromatography Surface-Activated Chemical Ionization – Cloud Ion Mobility Mass Spectrometry.
Methods: Plasma, urine and faecal samples from COVID-19 patients and control individuals were analysed to study peptidomic toxins' profiles. P precipitation preparation procedure was used for plasma, to remove high molecular weight proteins and efficiently solubilize the peptide fraction; in the case of faeces and urine, direct peptide solubilization was employed.
Results: Toxin-like peptides, almost identical to toxic components of venoms from animals, like conotoxins, phospholipases, phosphodiesterases, zinc metal proteinases, and bradykinins, were identified in samples from COVID-19 patients, but not in control samples.
Conclusions: The presence of toxin-like peptides could potentially be connected to SARS-CoV-2 infection. Their presence suggests a possible association between

- Peptides closely related to venom toxins found in plasma, urine and fecal samples of COVID-19 patients (Brogna et al. 2021).
- Authors claim that toxic-like peptides were identified in samples from COVID-19 patients but, not in controls.
- "Almost identical to toxic components of venoms in animals..."
- Concluded that the presence of toxin-like peptides could potentially be connected to SARS-CoV-2.

Dr Tom Cowan.

CLAIM #5: PROOF OF ENVENOMATION

- Harsh chemicals were used in the preparation of samples.
  - Can possibly lead to generation of artifacts.
- Patients stratified simply either as COVID-19 positive or negative by SARS-CoV-2 test.
- Specifically excluded those affected by other conditions like cancer or autoimmune diseases.
- Sample sizes are very low, especially in the urine and stool groups.
- Should have included additional control groups to rule out other disease conditions or pharmacologic effects that could result in a similar peptide profile.

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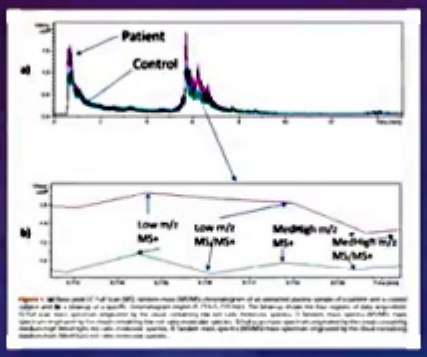
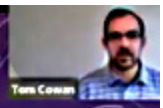


- Only show data for one patient sample compared to control.
- There is usually high variability in these sorts of proteomic analyses.
- Proteins are determined by aligning peptides and searching databases - can be very biased.
- Significance is represented by arbitrary statistics and cut-off values.

Dr Tom Cowan.

CLAIM #5: PROOF OF ENVENOMATION



Reader Comment 19 Jul 2021

Ernesto de Bernardis, ASP SR, Italy

I don't understand why the Authors' hypotheses about the origin of these peptides don't include the host response during severe inflammation or ARDS, or during a pharmacological therapy similar to those given to COVID patients.

The paper compares peptides from COVID patients with those from healthy controls, but doesn't include controls with other diseases, e.g. inflammatory diseases, other viral diseases, or people treated with the same medications that were administered to their sample of COVID patients.

So, I guess it can't be excluded that the findings aren't specific to COVID and that might be common to other conditions.

Competing Interests: No competing interests were disclosed.

- There was a comment from another scientist in Italy at the end of the study.
- This scientist questions the conclusions being made as to whether they are specific to COVID.

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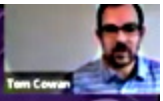

Mauro Petrillo, European Commission, Joint Research Centre (JRC), Ispra, Italy

Dear Dr. de Bernardis,

Thanks a lot for your valuable comment.

You are perfectly right: *it can't be excluded that the findings aren't specific to COVID and that might be common to other conditions.*

And in fact, one of the questions of the Conclusions section of the manuscript is "*Are toxin-like peptides associated with SARS-CoV-2 infection or to other viral infections or, more in general, a their presence related to sickness condition?*"

The aim of our manuscript is to immediately share these observations with the scientific community as they are (together with a series of other observations which we have recently reported in https://doi.org/10.12688/f1000research.52540.3) quite unexpected, at least to us.

Thanks again for your time and interest. I am happy to further discuss, also privately.

Best regards,
Mauro Petrillo

Competing Interests: None

- The author, Mauro Petrillo, responds and agrees with the comment.
- "It can't be excluded that the findings aren't specific to COVID and that might be common to other conditions."
- **Conclusion:** False
  - The claims aren't certain to be specific to COVID and certainly don't offer proof of venom poisoning.

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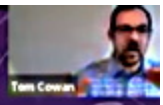

- Each of the two studies used by Dr. Ardis to make this claim are unsubstantiated.
- The claims in one study was questioned by another scientist and the author agreed.
- Neither study directly links or implicates snake envenomation as the cause of COVID-19 disease.
- **Conclusion:** False, there is no proof based on these studies or others that COVID-19 is envenomation.

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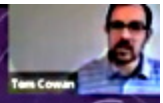
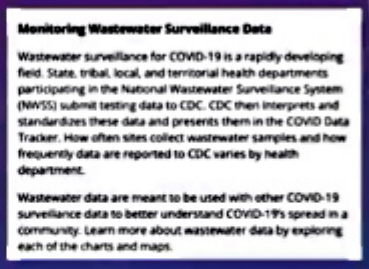
CLAIM #6: IT'S IN THE WATER





- **Claim:** "They" are putting toxic peptides (aka venom or from venom) into the water.
- Dr. Ardis says that on the CDC website it says they are testing the wastewater to track SARS-CoV-2 spread.
- They are using the SARS-CoV-2 PCR test.
- Says the test is actually for snake venom.

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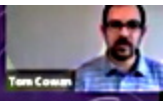

- **Conclusion: False**
  - The SARS-CoV-2 PCR test is invalid and carries an approximately 100% false positive rate.
  - There is no evidence of a PCR test being used to detect snake venom in water.
  - Snake venom added to water wouldn't be toxic via ingestion as stomach acids would break it down.
  - Only direct injection with a concentrated stock of venom would result in symptoms and illness.

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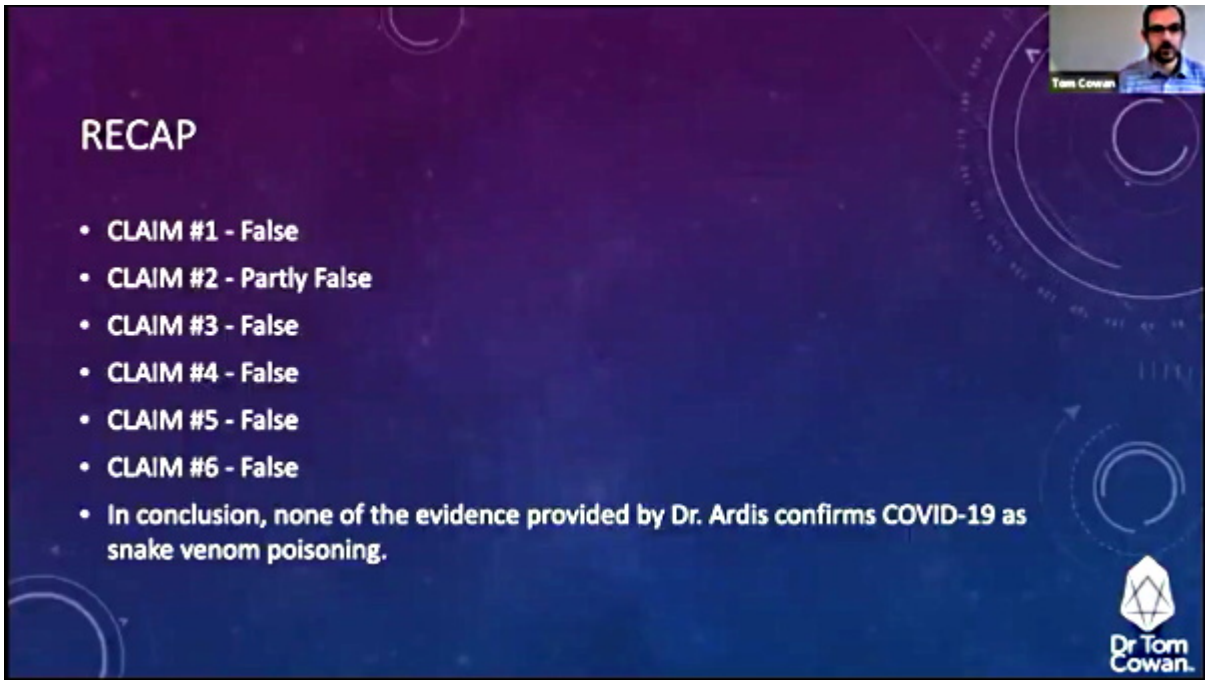
IMPORTANT ADDITIONAL POINTS

- Snake venom and other animal derived toxins have been used in drug development for decades.
- It is very hard to source these products and typically you can only get them in small amounts.
- Sustaining adequate levels of snake venom peptides/proteins in the water would be impossible.
- Animal derived products such as enzymes are commonly used tools in labs.
- Understand how materials and reagents in methods sections are used prior to drawing conclusions.

Dr Tom Cowan.



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