

# Codebook

**For the Research Project**

## **Searching for Coronavirus Conspiracy Theories Across Two Search Engines, Six countries, Six languages, and Time**

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### **Acknowledgements**

*This article has received funding from the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation programme (Grant agreement No. 819025). It is part of the ERC consolidator project on 'The Consequences of the Internet for Russia's Informational Influence abroad' ([www.rusinform.uni-passau.de/en](http://www.rusinform.uni-passau.de/en)).*



European Research Council  
Established by the European Commission

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## Part I. Coding Procedure and Intercoder Reliability Tests

### 1. Units of data collection and coding

The **unit of data collection** is the unique query.

The **unit of automated coding** is the **unique query**. For each unique query, we collected its header, its abstract, as well as the full text of the webpage the result linked to (document). For variables coded at this level, see the query-related codes V1-V7.

The **first unit of manual coding** is the **unique top-level domain**. For variables coded at this level, see the unique-source-related codes V8-V10.

The **second unit of manual coding** is the **unique result page**. For variables coded at this level, see the unique-result-related codes V11-V16.

### 2. Coding Procedure

All **query-related codes** were collected and filled in automatically by the Python script that automatically retrieved the data. The codes pertaining to **unique top-level domains (V8-V10)** and **unique result pages (V11-V16)** were filled in in two separate manual coding efforts.

## **Part II. Variables and instructions for coders on how to code them**

### **3. UNIQUE-QUERY-RELATED CODES**

This category of variables is used to locate the search results in space, time and different segments of the internet. These codes were coded automatically.

#### **V1\_ID: Unique ID (Article URL)**

Assigned automatically by the system.

#### **V2\_Country: Location of search**

The geographical location of the "user" in the country of the search (done without personalization and simulated through IP rotation). This variable signifies the location stimulated in the course of data collection, not the physical location of the coder.

- us = USA
- ru = Russia
- ee = Estonia
- de = Germany
- ua = Ukraine
- by = Belarus

#### **V3\_Language: Language of the search term**

- us = English
- ru = Russian
- ee = Estonian
- de = German
- ua = Ukrainian
- by = Belorussian

#### **V4\_Platform: Name of the platform**

The web search engine platform, on which the search was conducted.

- google
- yandex

#### **V5\_Date: Date of search**

The date on which the search was conducted using an **8-date variable (dd.mm.yyyy)**

#### **V6a\_Search\_Term\_Original**

The search term used in the original language

#### **V6b\_Search\_Term\_English**

The search term used translated to English.

### **V7\_Ranking: Ranking of the search result (interval)**

The place of the specific item in the ranking of the search results. A number between 1 and 20 (as we code the first 20 results per search query).

## **4. UNIQUE-SOURCE-RELATED CODES**

The items in this section were coded manually.

### **V8\_Source\_type: Type of source (nominal)**

In this variable, we code the type of actor or organization, which we considered as responsible for the content.

**1 = Professional Academic publishers, Universities, Reputed Academic Institutions**, including professionally organized reference bases, professional academic journals, released in cooperation with the established academic organizations

**Examples:** springer.com, tandfonline.com, mit.edu, medscape.com, Encyclopedia Britannica, theconversation.com, www.poynter.org, scientificamerican.com

#### **Further Instructions:**

Usually, a characteristic of the reputed academic institution is that people with recognized academic degrees work for it, as well as the texts and articles published on the website go through the process of tedious review, usually blind peer reviews.

In case you see an academic institution that might be considered as a government-affiliated organization, for example, John Hopkins Coronavirus Resource Center, check the About Us page, but generally code it as an Academic Institution.

Think tanks and analytical centres should also be coded as Academic Institutions only in case they are well-established, have an academic history and are considered trustworthy in the academic environment, e.g. Reuters Institute for the Study of Journalism or Pew Research Center.

**2 = Wikipedia pages & academic sources with low reput**e (e.g. preprint archives and/or volunteer-based academic websites/ and/or non-profit academic websites)

**Examples:** researchgate.org, sciencedaily.com, jurist.org, wikipedia.com

**Further Instructions:**

In this variable, please code the websites that present themselves as possessing academic authority; however, either the grounds for that are insufficient, and/or the material can be uploaded freely without the peer review or feedback and/or the information presents a commentary or an opinion piece. **Semi-professional and amateur websites specializing in research news and anything journalism-related are coded as 6.**

**3 = Websites operated by government organizations**

**Examples:** osha.gov, coronavirus.gov, arbeitsagentur.de, who.intl, un.org, RKI

**Further Instruction:**

In this variable, we code the websites of both the intergovernmental organizations such as who.int; un.org; as well as the websites of national health authorities that receive the funding from the government or several governments and/or influences the governmental policies. Items with a domain .gov should be coded as government organizations.

Please, do not code under this category the state-owned news websites, such as - [rg.ru](http://rg.ru), [tass.ru](http://tass.ru) and [belta.by](http://belta.by). We code them as 5.

**4 = Non-governmental organizations or parties** (e.g. civil society organizations, NGOs, parties, churches, including local community charity pages, local community initiative pages, etc.)

**Examples:** avma.org, lung.org, Freedom House; Amnesty International, wyandottedaily.com

**Further Instruction:**

In this variable, please code the websites of the non-governmental organizations that are not affiliated with any government explicitly and that receive their funding independently from it.

**5 = Major (mass) news media outlets, including entertainment outlets (including SNS accounts)**

**Examples for Russia:** kp.ru, themoscowtimes.com, ria.ru, rg.ru, tass.ru

**Examples for Germany:** FAZ, SZ, taz, Bild, Welt, Zeit, ARD, ZDF

**Examples for the USA:** Fox, CNN, PBS, The Washington Post, Time.com, vox.com

**Examples for Belarus:** TUT.by

**Examples for Estonia:** postimees.ee, delfi.ee

**Examples for Ukraine:** www.pravda.com.ua

**Examples for the UK:** The Guardian, Financial Times. elle.com/uk, express.co.uk

**Further Instruction:**

In this category, we code mass media and well-established news outlets. In this category, please also code the government-owned mass media news websites, such as rg.ru and tass.ru, in the Russian context and belta.by in Belarus.

**6 = Niche and special interest media (right-wing, left-wing, special interest media, minority media etc.) (including SNS accounts)**

**Examples:** adweek.com (magazine for advertising and marketing); modernghana.com. economictimes.indiatimes.com, theverge.com. innovationorigins.com, newswise.com

**Further Instruction:**

In contrast to the mainstream media, which covers a wide variety of topics and issues, we code the outlets as niche/minority mass media when they are focused either on special area of interest (e.g. health news; marketing news; economic news (but the outlet should be specifically focused on economics, not like Financial Times that covers a wide variety of issues); right-wing news; left-wing news, etc.), local and regional news, and their reach is therefore not as wide as in the mainstream media (following these criteria, for example, forbes.com, despite being focused on finance, should be coded as 5 due to its reach).

One example of a niche website connected to the Russian elites is m24.ru as it is focused on Moscow (i.e. regional) affairs but grounded as a branch of Russian VGTRK, which owns "Rossiya Odin" and the channel was founded as an initiative by Mayor of Moscow, Sergei Sobyenin.

A complex example of the niche media outlet that could theoretically fall into the category **7 = Foreign Communication media** is [Inosmi.com](http://Inosmi.com) - it is a project of RT where the foreign articles are translated into Russian for the Russian audience. The articles

translated are usually biased, as most of its content either praises Russia or criticizes the West. Nevertheless, it shall be coded as niche media, not foreign communications media, as the target population is the Russian domestic audience, not foreign audiences.

The difference between the outlets that fall within this category (6) and category 2 is that this category includes the websites, which might be run voluntarily by scientists, journalists, technology professionals, etc. but they are run by professionals, not amateurs or self-proclaimed specialists, in their field or represent an association of professionals in the field (at different stages),

**7 = Foreign communication media (affiliated with nation-states) (including SNS accounts)**

**Examples:** BBC.com, RT.com, Sputnik.com, cgtn.com, aa.com.tr, www.aljazeera.com, Anadolu Post in Russian, BBC Chinese

**Further Instruction:**

Please consider a media outlet as a Foreign Communication media if at least one of the following conditions 1) it operates in more than three languages (i.e. starting from 4) in order to avoid confusion with the local media outlets e.g. in Estonia, where it can be in Russian, Estonian and English due to the varied character of the society; OR 2) if it operates in the languages other than belonging to its home region AND 3) its primary target audience is located outside the borders of the funding state of such media outlet

**8 = Individual accounts on social networking services/online communities/video sharing platforms, social news aggregation, web content rating, and discussion websites with original user-generated content (not creating content in affiliation with any type of organization)**

**Examples:** Reddit.com, Twitter.com, Pikabu.ru; Facebook.com; YouTube.com

**Further Instruction:**

As for the geographical origin on the social networking site, we code the origin of the content creator, i.e. the origin of the user who made the post, not Reddit.com. In order to determine that, a coder should check the personal profile of the poster, and look into the last 5



posts. If the origin is still unidentifiable (not mentioned by the content creator explicitly, or not easily understandable from the context, i.e. when the content creator participates in the discussion about the location, etc.), please code in V9 the option 99.

**9 = For-profit companies**

**Examples:** apple.com, amazon.de, tesla.com

**10 = Thematic or personal blogs by (teams) of journalists or influences (outside SNS)**

**Examples:** varlamov.ru, nstarikov.ru, wodarg.com

**Further Instruction:**

In this category, please code the items from the thematic websites, which are blogs as a whole (i.e. if it is a blog entry on the university website or a blog entry on the who.it website, it should be coded as such). In this category, only code website blogs (for example, blogs by private persons, journalists, scientists)

**11 = Search Engines**

**Examples:** yandex.ru, bing.com, yahoo.com, yahoo.de

**12 = Fact-Checking website**

**Examples:** snopes.com, fullfact.org

**Further Instruction:**

Code the item as 12 only if it is mentioned specifically that it is a fact-checking website.

**13 = Other, please specify**

**V9\_Source\_Origin: Geographical Origin of Source**

1	Global/Transnational
2	USA
3	Russia
4	Estonia
5	Germany

6	Ukraine
7	Belarus
8	China
9	Great Britain
10	Australia & New Zealand
11	Other, please specify
12	Austria
13	Pakistan
14	Poland
15	India
99	unidentifiable

### Further Instruction:

In order to determine the Geographical Origin of the source of the item, please check the "About us" or "Our History" section of the website. Alternatively, if the geographical location of the source is not explicitly stated, you can use a search engine to find further information about the website. If the Geographical Origin of the source is not explicitly stated or impossible to determine (i.e. in the case of user's posts on Reddit or other social networking platforms), please code 99.

Please, take the domain into consideration as an indicator of the geographical origin i.e. .ua - Ukraine; .ee - Estonia; .by - Belarus; .ru - Russia; .de- Germany (in case of, for example, websites as kp.ua, code it as Ukraine, as in the further variable, V10\_Source\_Influence Russia, you will be able to indicate the connection of the source to the Russian ruling elites)

### V10\_Source\_Influence\_Russia: Connection of Source with Russia's Ruling Elites

#### 0 = Not connected

In this category, please code websites that:

- 1) Have no apparent connection to Russia
- 2) Were never under investigation or suspected to be connected with Russia's ruling elites. A broad range of websites can fall into this category, e.g. the mass media outlets outside Russia; academic websites, special interest websites, government websites, etc.
- 3) Media in Russia that favours an opposition viewpoint and on purpose distances itself from the Russian ruling elites, be that based in Russia (e.g. novayagazeta.ru) or be that opposition media based outside Russia (e.g. meduza.io)

- 4) When the outlet is located in Russia (e.g. local newspaper), but it is owned by a private person/not supported financially by the local administration, and expresses an oppositional viewpoint
- 5) When it is a website of a private company located inside Russia, but nothing is known about its connection to the Russian elites, and it does not seek to exercise influence and political influence in Russia. For example, these can be journals for the people in the pharmacy industry (e.g. rosapteki.ru) or a medical company website which works for profit (e.g. medsi.ru)

### **1 = Connected to Russia's ruling elites**

In this category, we code websites if we could identify credible evidence (i.e. official investigations, contact information with references to the Russian state, etc.) of the influence of Russia's ruling elites on their content. These are:

- 1) Websites that are operated by the Russian government and regional administration
- 2) Major mass media sources located inside Russia and known to be operated by the Russian government (e.g. 1tv.ru, tvzvezda.ru, ria.ru)
- 3) Outlets, that are owned by Kremlin-friendly oligarchs, or people, who work in the Russian government or administration, or the wives of the oligarchs (e.g. lenta.ru)
- 4) State-sponsored Russian outlets aimed at foreign audiences (e.g. rt.com, sputnik.com)
- 5) In case of Yandex.ru – when the content is posted on behalf of Yandex itself or its services, please code it as connected to the Russia's ruling elites

### **2 = Evidence not available or contradictory**

In this category, we code the websites that

- 1) Were suspected or investigated or publicly discussed as a potential Kremlin-supported website, but the allegations were never verified
- 2) If it is a major local Russian newspaper – even in case there is no explicit connection to the local/all-Russian administration, but it is the main newspaper of the region/city
- 4) Private Russian companies that are not owned by the Russian elites directly but express a clear political/societal stance and seek to exercise influence
- 5) When it is unclear who the outlet owner is, and it is purposefully concealed/hidden.

## 5. UNIQUE-RESULT-RELATED CODES

Please code these codes in data set 3 (V11 to V16).

### **V11\_Accessibility: Accessibility of the website**

In this variable, please indicate whether you could still open the website and/or the item, whether it was removed or deleted

- 1 = Link is accessible
- 0 = Link is not accessible

### **V12\_Language of the Actual Item**

- 1 = English
- 2 = Russian
- 3 = Estonian
- 4 = German
- 5 = Ukrainian
- 6 = Belorussian

### **V13\_Publication: Date of Publication**

The date on which the article/website was published using an **8-digit date variable (dd.mm.yyyy)**. If the article was updated over time, please code the date of the last update.

### **V14\_Title: Title of the item (nominal)**

The headline of the website/article (in home language)

### **V15\_Paywall: Presence of a paywall**

Please indicate whether the further content is available behind a paywall or under the registration requirement. If the content is hidden behind a paywall or demands the user to register in order to continue, this is the last variable that you need to code.

- 1 = Yes, content is hidden behind a paywall
- 0 = No, content is not hidden behind a paywall

### **V16\_Presence\_CT: Presence of conspiracy theories (nominal)**

This code indicates whether a conspiracy theory is present in the analyzed item.

- **0 = No conspiracy theories are mentioned** (when no words "conspiracy", "conspiracy theory" or related terms such as 5G, Bill Gates, biological weapon; vaccination, etc. are mentioned in the item)
- **1 = One or several conspiracy theories are mentioned, but all conspiracy theories are exclusively and forcefully debunked or**

when the "conspiracy", "conspiracy theory", or related terms such as 5G, Bill Gates, Biological Weapon; Vaccination, etc. are mentioned in the item, but are not supported and are generally disproved

- **2 = One or several conspiracy theories are mentioned, but at least one conspiracy theory is not forcefully debunked**

#### **Further Instruction:**

When the link forwards you to the Twitter page of the account, please code the first 1 (one) Tweet. When it forwards you to the Facebook group or the Personal page - please, code the first post. When the link forwards you to the YouTube playlist - please, only code the content of the titles of the videos and, if present - a description of the video. If the link forwards you to the website's start page, please code its contents. The tweets and the Facebook posts from the start page of the account or the public page have to be analyzed by the coder using the screenshot of the page.

In order to code whether a conspiracy theory is present in the item, we follow the coding of Uscinski & Parent (2014). Accordingly, narratives qualifying as conspiracy theories must include all four elements found in standard definitions of conspiracy theory: they must suspect "(1) a group (2) acting in secret (2) to alter institutions, usurp power, hide the truth, or gain utility (4) at the expense of the common good" (Uscinski & Parent, 2014, p. 58).

With regard to whether the conspiracy narrative is "forcefully debunked", coders should read/watch the entire item until the end, paying special attention to the final paragraph and closing remarks, as in many cases, they determine the position of the author regarding the conspiracy theory.

By forcefully debunking, we understand when the conspiracy theory is mentioned in the item, but only in the context to disprove it. Often, items that fall within this category include references to reputable scientific studies or other sources with a strong emphasis on the information that debunks a conspiracy theory rather than on discussing the details of the conspiracy theory itself. An example of forceful debunking can be **Article 1** (see in Appendix), which includes scientific data that debunks any speculations about COVID-19 as being man-made, and that among others, includes statements as *"It is improbable that SARS-CoV-2 emerged through laboratory manipulation of a related SARS-CoV-like coronavirus"* and *"However, since we observed all notable SARS-CoV-2 features, including the optimized RBD and polybasic cleavage site, in related coronaviruses in nature, we do not believe that any type of laboratory-based scenario is plausible."*

By not forcefully debunked, we understand several categories of items. Some items that fall within it support conspiracy theories, and others mention conspiracy theories and

bring no evidence to disprove them. Finally, we also include in this category items that might initially claim that they debunk conspiracy theories but that in fact, make little effort to disprove them and rather push the readers/spectators towards further speculations in the direction of conspiracy theories. For the last category of items, looking at the "undertext" that the item promotes, the context referenced and the whole tone of the item under scrutiny is of crucial importance. In the case of the kind, analyzing the last paragraph/ the bottom line can be especially relevant for the correct interpretation of the whole item.

An example of the item that discusses a conspiracy theory and does not forcefully debunk is **Article 2** (see Appendix). This item has statements such as *"Amidst this chaos, there has been misinformation and rumors have been surfacing on social media, the most prominent among them being conspiracy theories regarding the use of COVID-19 as a bioweapon by China"*. While the author labels these speculations as a conspiracy theory and from the first glance could be seen as moving in the direction of debunking, the content of the article is dedicated to the potential lawsuit that the US can form against China for spreading the COVID-19, which places the content of the article in the COVID-19 conspiracy domain. Finally, the last paragraph inserts that *"The only factor which remains in this puzzle is the proper evidence proving such a conspiracy exists. Once a proper investigation is initiated, things will become more clear. However, the behavior of the Chinese government is alarming and appears to be suspicious"*, which seals the conclusion that the article is not aimed at forcefully debunking conspiracy theories, but it is rather aimed at furthering the reader's speculations about COVID-19 being a Chinese biological weapon. Another good example of an article that contains a non-debunked conspiracy theory is Article 3.

The general advice on deciding whether the conspiracy theory (CT) is debunked or not is to closely analyze the last paragraph, as it usually has the key to understanding the author's message. If the last paragraph proclaims that CT can potentially have grounds or does not bring anything in to disprove it as a CT, code 2. If there is a solid reference to the general logic, facts or scientific evidence, and the author is firm in labeling this information as CT and misinformation, code 1.

***If the conspiracy theories are present in the text but are forcefully debunked, this is the last variable you need to code (i.e. you do not need to indicate the number of conspiracy theories even if they are there, but if forcefully debunked).***

**V16a\_Topic\_Related:** Relation of the website content to COVID-19/the pandemic

**Example:** Code 0 (content is unrelated) when the website is about the beer brand "Corona", about the name "Corona", about a software called "Corona" or about the music band "Corona", etc.

**1** = Yes, website content is related to the topic of this study

0 = No, website content is unrelated

## 6. UNIQUE CONSPIRACY THEORY-RELATED CODES

Please code these codes in data set 4 (V17 to V19).

### V17\_Specific plot of the top-5 conspiracies related to COVID-19

In this section, we have listed the 5 most frequently mentioned narratives of CTs plots that have appeared and/or developed in the course of the COVID-19 pandemic.

- V17a: COVID-19 is a biological weapon  
1 = mentioned | 0 = not mentioned
- V17b: COVID\_19 is distributed by 5G towers  
1 = mentioned | 0 = not mentioned
- V17c: COVID-19 is a plot for vaccinating and controlling the population  
1 = mentioned | 0 = not mentioned
- V17d: The origin and (initial) spread of COVID-19 is different from the one proclaimed (not related to the military purposes)  
Examples:
  - a. Laboratory worker carried the virus into the wet market (accidentally)
  - b. The virus was made in a laboratory (not as a weapon, but as a scientific discovery, coincidence, etc. - anything not military-related)
  - c. Virus escaped accidentally
  - d. Chinese people brought the virus into Europe1 = mentioned | 0 = not mentioned
- V17e: The information about the treatment/mortality of COVID-19 is intentionally distorted by someone  
Examples:
  - a. Masks are not an efficient treatment of COVID-19 and they do not stop its spread
  - b. COVID-19 does not exist
  - c. COVID-19 is less dangerous than the cold/ that it is much more dangerous than any other disease

- d. Natural medicine e.g. ginger, lemon/ bleach/ hydroxychloroquine, is an efficient treatment of COVID-19
  - e. The government hides the information/treatment efficient for COVID-19.
  - f. The numbers of infections/deaths are distorted (hyperbolized or intentionally presented as lower)  
1 = mentioned | 0 = not mentioned
- V17f: Other, please specify  
Write a short sentence about a conspiracy theory if it does not fit into any of the above-mentioned categories (e.g. QAnon theory branch with the ring of paedophiles from the secret elites using COVID-19 as a cover-up to traffic the children)

### **V18\_Origin\_Plotter: Geographical origin of the responsible actor (nominal)**

This variable indicates the geographical origin of the actor that is described as standing behind the COVID-19 secret plot. We code this variable for items that don't debunk all the mentioned CTs vehemently. The plotter can be mentioned not explicitly as such, but for example in the context of "who benefits from the events or situations", who advances his or her position through the situation in the context of the plot, who is guilty, who isn't truthful/telling the truth about the events, who is hiding the truth about something or who spreads the distorted information. **Please, code only the main plotter (one tip for determining the main plotter is to code the plotter that was mentioned the most of the times, i.e. repeatedly).**

1	Global/Transnational (including the EU)
	In this option, we code the general reference to the people, mostly unspecified in terms of the nation (without specifying the specific nation, rather stressing mankind or the region or the political entity such as the EU as the victim)
2	USA
3	Russia
4	Estonia
5	Germany
6	Ukraine
7	Belarus
8	China
9	Great Britain
10	Australia & New Zealand



11	Other country/region/entity, please specify
12	No plotter mentioned
13	Austria
99	unidentifiable

### V18a\_Other-Origin-Plotter: Please, Specify

In case the country from which the plotter originates is not mentioned in the list of available plotters, please, specify the country by writing it manually.

### V18b\_Other-Mentioned-Plotters: Please, Specify

We use this variable to write all the specific Plotters that are mentioned either in the capacity or as helping the main Plotter, supporting the main Plotter, etc. This can, for example, be 1) a specific religious group (Zionists, ISIS), 2) specific economic parties or sectors (Biontech; Pfizer), 3) specific persons (e.g. Bill Gates, Donald Trump, etc.), 4) specific media organizations (e.g. CNN, Fox News) or 6) specific organizations (WHO, the Soros Foundation).

### V19\_Origin-Victim: Geographical origin of the victim

We use this variable to indicate where the object of the secret plot against whom COVID-19 is used is located. The victim should be mentioned explicitly to be coded, however in certain cases, such as, for example, with the phrasing as "many will suffer" please consider it coding as 1, or Ordinary people and Global as the Geographical origin, or indicating a specific national connection, if there is such. **Please, code only the main victim (one tip for determining the main victim is to code the victim mentioned most of the times, i.e. repeatedly).**

01	Global/Transnational (including the EU)  In this option, we code the general reference to the people, mostly unspecified in terms of the nation (without specifying the specific nation, rather stressing mankind or the region or the political entity such as the EU as the victim)
02	USA
03	Russia
04	Estonia
05	Germany
06	Ukraine
07	Belarus

08	China
09	Great Britain
10	Australia & New Zealand
11	Other, please specify
12	No victim mentioned
99	unidentifiable

#### **V19a\_Other\_Origin\_Victim: Please, Specify**

In case the country from which the victim originates is not mentioned in the list of the available victims, please, specify the country by writing it manually

#### **V19b\_Other\_Mentioned\_Victim: Please, Specify**

We use this variable to write all the specific victims that are mentioned in the capacity of being the additional victims, not the main ones. This can, for example, be 1) a specific religious/societal group (Muslims, Christians) , 2) specific economic parties or sectors, 3) specific persons, 4) specific organizations, etc.

## 7. APPENDIX

### Article 1

#### The proximal origin of SARS-CoV-2

Source:

<https://www.nature.com/articles/s41591-020-0820-9>

Kristian G. Andersen, Andrew Rambaut, W. Ian Lipkin, Edward C. Holmes & Robert F. Garry

Nature Medicine volume 26, pages450–452(2020)

**To the Editor** — Since the first reports of novel pneumonia (COVID-19) in Wuhan, Hubei province, China<sup>1,2</sup>, there has been considerable discussion on the origin of the causative virus, SARS-CoV-2<sup>3</sup> (also referred to as HCoV-19)<sup>4</sup>. Infections with SARS-CoV-2 are now widespread, and as of 11 March 2020, 121,564 cases have been confirmed in more than 110 countries, with 4,373 deaths<sup>5</sup>.

SARS-CoV-2 is the seventh coronavirus known to infect humans; SARS-CoV, MERS-CoV and SARS-CoV-2 can cause severe disease, whereas HKU1, NL63, OC43 and 229E are associated with mild symptoms<sup>6</sup>. Here we review what can be deduced about the origin of SARS-CoV-2 from comparative analysis of genomic data. We offer a perspective on the notable features of the SARS-CoV-2 genome and discuss scenarios by which they could have arisen. Our analyses clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus.

#### Notable features of the SARS-CoV-2 genome

Our comparison of alpha- and betacoronaviruses identifies two notable genomic features of SARS-CoV-2: (i) on the basis of structural studies<sup>7,8,9</sup> and biochemical experiments<sup>1,9,10</sup>, SARS-CoV-2 appears to be optimized for binding to the human receptor ACE2; and (ii) the spike protein of SARS-CoV-2 has a functional polybasic (furin) cleavage site at the S1–S2 boundary through the insertion of 12 nucleotides<sup>8</sup>, which additionally led to the predicted acquisition of three O-linked glycans around the site.

##### 1. Mutations in the receptor-binding domain of SARS-CoV-2

The receptor-binding domain (RBD) in the spike protein is the most variable part of the coronavirus genome<sup>1,2</sup>. Six RBD amino acids have been shown to be critical for binding to ACE2 receptors and for determining the host range of SARS-CoV-like viruses<sup>7</sup>. With coordinates based on SARS-CoV, they are Y442, L472, N479, D480, T487 and Y4911, which correspond to L455, F486, Q493, S494, N501 and Y505 in SARS-CoV-2<sup>7</sup>. Five of these six residues differ between SARS-CoV-2 and SARS-CoV (Fig. 1a). On the basis of structural studies<sup>7,8,9</sup> and biochemical experiments<sup>1,9,10</sup>, SARS-CoV-2 seems to have an RBD that binds with high affinity to ACE2 from humans, ferrets, cats and other species with high receptor homology<sup>7</sup>.

#### Fig. 1: Features of the spike protein in human SARS-CoV-2 and related coronaviruses.

##### 2. Polybasic furin cleavage site and O-linked glycans

The second notable feature of SARS-CoV-2 is a polybasic cleavage site (RRAR) at the junction of S1 and S2, the two subunits of the spike<sup>8</sup> (Fig. 1b). This allows effective cleavage by furin and other proteases and has a role in determining viral infectivity and host range<sup>12</sup>. In addition, a leading proline is also inserted at this site in SARS-CoV-2; thus, the inserted sequence is PRRA (Fig. 1b). The turn created by the proline is predicted to result in the addition of O-linked glycans to S673, T678 and S686, which flank the cleavage site and are unique to SARS-CoV-2 (Fig. 1b). Polybasic cleavage sites have not been observed in related 'lineage B' betacoronaviruses, although other human betacoronaviruses, including HKU1 (lineage A), have those sites and predicted O-linked glycans<sup>13</sup>. Given the level of genetic variation in the spike, it is likely that SARS-CoV-2-like viruses with partial or full polybasic cleavage sites will be discovered in other species.

The functional consequence of the polybasic cleavage site in SARS-CoV-2 is unknown, and it will be important to determine its impact on transmissibility and pathogenesis in animal models. Experiments with SARS-CoV have shown that insertion of a furin cleavage site at the S1–S2 junction enhances cell–cell fusion without affecting viral entry<sup>14</sup>. In addition, efficient cleavage of the MERS-CoV spike enables MERS-like coronaviruses from bats to infect human cells<sup>15</sup>. In avian influenza viruses, rapid replication and transmission in highly dense chicken populations selects for the acquisition of polybasic cleavage sites in the hemagglutinin (HA) protein<sup>16</sup>, which serves a function similar to that of the coronavirus spike protein. Acquisition of polybasic cleavage sites in HA, by insertion or recombination, converts low-pathogenicity avian influenza viruses into highly pathogenic forms<sup>16</sup>. The acquisition of polybasic cleavage sites by HA has also been observed after repeated passage in cell culture or through animals<sup>17</sup>.

The function of the predicted O-linked glycans is unclear, but they could create a 'mucin-like domain' that shields epitopes or key residues on the SARS-CoV-2 spike protein<sup>18</sup>. Several viruses utilize mucin-like domains as glycan shields involved in immune evasion<sup>18</sup>. Although prediction of O-linked glycosylation is robust, experimental studies are needed to determine if these sites are used in SARS-CoV-2.

### **Theories of SARS-CoV-2 origins**

It is improbable that SARS-CoV-2 emerged through laboratory manipulation of a related SARS-CoV-like coronavirus. As noted above, the RBD of SARS-CoV-2 is optimized for binding to human ACE2 with an efficient solution different from those previously predicted<sup>7,11</sup>. Furthermore, if genetic manipulation had been performed, one of the several reverse-genetic systems available for betacoronaviruses would probably have been used<sup>19</sup>. However, the genetic data irrefutably show that SARS-CoV-2 is not derived from any previously used virus backbone<sup>20</sup>. Instead, we propose two scenarios that can plausibly explain the origin of SARS-CoV-2: (i) natural selection in an animal host before zoonotic transfer; and (ii) natural selection in humans following zoonotic transfer. We also discuss whether selection during passage could have given rise to SARS-CoV-2.

#### **1. Natural selection in an animal host before zoonotic transfer**

As many early cases of COVID-19 were linked to the Huanan market in Wuhan<sup>1,2</sup>, it is possible that an animal source was present at this location. Given the similarity of SARS-CoV-2 to bat SARS-CoV-like coronaviruses<sup>2</sup>, it is likely that bats serve as reservoir hosts

for its progenitor. Although RaTG13, sampled from a *Rhinolophus affinis* bat<sup>1</sup>, is ~96% identical overall to SARS-CoV-2, its spike diverges in the RBD, which suggests that it may not bind efficiently to human ACE2<sup>7</sup> (Fig. 1a).

Malayan pangolins (*Manis javanica*) illegally imported into Guangdong province contain coronaviruses similar to SARS-CoV-2<sup>21</sup>. Although the RaTG13 bat virus remains the closest to SARS-CoV-2 across the genome<sup>1</sup>, some pangolin coronaviruses exhibit strong similarity to SARS-CoV-2 in the RBD, including all six key RBD residues<sup>21</sup> (Fig. 1). This clearly shows that the SARS-CoV-2 spike protein optimized for binding to human-like ACE2 is the result of natural selection.

Neither the bat betacoronaviruses nor the pangolin betacoronaviruses sampled thus far have polybasic cleavage sites. Although no animal coronavirus has been identified that is sufficiently similar to have served as the direct progenitor of SARS-CoV-2, the diversity of coronaviruses in bats and other species is massively undersampled. Mutations, insertions and deletions can occur near the S1–S2 junction of coronaviruses<sup>22</sup>, which shows that the polybasic cleavage site can arise by a natural evolutionary process. For a precursor virus to acquire both the polybasic cleavage site and mutations in the spike protein suitable for binding to human ACE2, an animal host would probably have to have a high population density (to allow natural selection to proceed efficiently) and an ACE2-encoding gene that is similar to the human ortholog.

## 2. Natural selection in humans following zoonotic transfer

It is possible that a progenitor of SARS-CoV-2 jumped into humans, acquiring the genomic features described above through adaptation during undetected human-to-human transmission. Once acquired, these adaptations would enable the pandemic to take off and produce a sufficiently large cluster of cases to trigger the surveillance system that detected it<sup>1,2</sup>.

All SARS-CoV-2 genomes sequenced so far have the genomic features described above and are thus derived from a common ancestor that had them too. The presence in pangolins of an RBD very similar to that of SARS-CoV-2 means that we can infer this was also probably in the virus that jumped to humans. This leaves the insertion of polybasic cleavage site to occur during human-to-human transmission.

Estimates of the timing of the most recent common ancestor of SARS-CoV-2 made with current sequence data point to emergence of the virus in late November 2019 to early December 2019<sup>23</sup>, compatible with the earliest retrospectively confirmed cases<sup>24</sup>. Hence, this scenario presumes a period of unrecognized transmission in humans between the initial zoonotic event and the acquisition of the polybasic cleavage site. Sufficient opportunity could have arisen if there had been many prior zoonotic events that produced short chains of human-to-human transmission over an extended period. This is essentially the situation for MERS-CoV, for which all human cases are the result of repeated jumps of the virus from dromedary camels, producing single infections or short transmission chains that eventually resolve, with no adaptation to sustained transmission<sup>25</sup>.

Studies of banked human samples could provide information on whether such cryptic spread has occurred. Retrospective serological studies could also be informative, and a

few such studies have been conducted showing low-level exposures to SARS-CoV-like coronaviruses in certain areas of China<sup>26</sup>. Critically, however, these studies could not have distinguished whether exposures were due to prior infections with SARS-CoV, SARS-CoV-2 or other SARS-CoV-like coronaviruses. Further serological studies should be conducted to determine the extent of prior human exposure to SARS-CoV-2.

### 3. Selection during passage

Basic research involving passage of bat SARS-CoV-like coronaviruses in cell culture and/or animal models has been ongoing for many years in biosafety level 2 laboratories across the world<sup>27</sup>, and there are documented instances of laboratory escapes of SARS-CoV<sup>28</sup>. We must therefore examine the possibility of an inadvertent laboratory release of SARS-CoV-2.

In theory, it is possible that SARS-CoV-2 acquired RBD mutations (Fig. 1a) during adaptation to passage in cell culture, as has been observed in studies of SARS-CoV<sup>11</sup>. The finding of SARS-CoV-like coronaviruses from pangolins with nearly identical RBDs, however, provides a much stronger and more parsimonious explanation of how SARS-CoV-2 acquired these via recombination or mutation<sup>19</sup>.

The acquisition of both the polybasic cleavage site and predicted O-linked glycans also argues against culture-based scenarios. New polybasic cleavage sites have been observed only after prolonged passage of low-pathogenicity avian influenza virus in vitro or in vivo<sup>17</sup>. Furthermore, a hypothetical generation of SARS-CoV-2 by cell culture or animal passage would have required prior isolation of a progenitor virus with very high genetic similarity, which has not been described. Subsequent generation of a polybasic cleavage site would have then required repeated passage in cell culture or animals with ACE2 receptors similar to those of humans, but such work has also not previously been described. Finally, the generation of the predicted O-linked glycans is also unlikely to have occurred due to cell-culture passage, as such features suggest the involvement of an immune system<sup>18</sup>.

## Conclusions

In the midst of the global COVID-19 public-health emergency, it is reasonable to wonder why the origins of the pandemic matter. Detailed understanding of how an animal virus jumped species boundaries to infect humans so productively will help in the prevention of future zoonotic events. For example, if SARS-CoV-2 pre-adapted in another animal species, then there is the risk of future re-emergence events. In contrast, if the adaptive process occurred in humans, then even if repeated zoonotic transfers occur, they are unlikely to take off without the same series of mutations. In addition, identifying the closest viral relatives of SARS-CoV-2 circulating in animals will greatly assist studies of viral function. Indeed, the availability of the RaTG13 bat sequence helped reveal key RBD mutations and the polybasic cleavage site.

The genomic features described here may explain in part the infectiousness and transmissibility of SARS-CoV-2 in humans. Although the evidence shows that SARS-CoV-2 is not a purposefully manipulated virus, it is currently impossible to prove or disprove the other theories of its origin described here. However, since we observed all notable SARS-CoV-2 features, including the optimized RBD and polybasic cleavage site, in related

coronaviruses in nature, we do not believe that any type of laboratory-based scenario is plausible.

More scientific data could swing the balance of evidence to favor one hypothesis over another. Obtaining related viral sequences from animal sources would be the most definitive way of revealing viral origins. For example, a future observation of an intermediate or fully formed polybasic cleavage site in a SARS-CoV-2-like virus from animals would lend even further support to the natural-selection hypotheses. It would also be helpful to obtain more genetic and functional data about SARS-CoV-2, including animal studies. The identification of a potential intermediate host of SARS-CoV-2, as well as sequencing of the virus from very early cases, would similarly be highly informative. Irrespective of the exact mechanisms by which SARS-CoV-2 originated via natural selection, the ongoing surveillance of pneumonia in humans and other animals is clearly of utmost importance.

## Article 2

### COVID-19: A Well-Planned Conspiracy?

Source:

<https://www.jurist.org/commentary/2020/04/yadav-bajpai-covid-conspiracy/#>

**Shivang Yadav and Rakshitt Bajpai**

APRIL 18, 2020 09:33:15 PM

Edited by: **Gabrielle Wast | U. Pittsburgh School of Law, US**

JURIST Guest Columnists from Dr. Ram Manohar Lohiya National Law University, Lucknow, India, Shivang Yadav, a third-year law student, and Rakshitt Bajpai, a second-year law student, discuss the recent suit filed by US interest group Freedom Watch against the Chinese government amid the COVID-19 pandemic...

Curbing global pandemics like COVID-19 has been one of the most difficult tasks in the history of mankind. The emergence of this virus can be traced back to December of 2019 when China alerted the World Health Organization (WHO) to several cases of unusual pneumonia in Wuhan. However, the virus remained **unknown** at this stage. Only later was it was identified and **named** COVID-19 by WHO. The outbreak was **declared** a public health emergency of international concern.

Amidst this chaos, there has been misinformation and rumors have been **surfacing** on social media, the most prominent among them being conspiracy theories regarding the use of COVID-19 as a bioweapon by China. In one version of the rumor, the virus was engineered in a lab by humans as a bioweapon. In another **version**, the virus was being studied in the lab (after being isolated from animals) and then "escaped" or "leaked" because of poor safety protocol. The fact that Wuhan **has** the only Level 4 microbiology lab that is equipped to handle deadly coronaviruses, the National Biosafety Laboratory (part of the Wuhan Institute of Virology) further reinforces this theory. However, all these rumors lack scientific evidence to support this **conspiracy** theory.



Based on this theory, Freedom Watch **filed** a lawsuit against Chinese authorities in the US over coronavirus outbreak. The plaintiff **seeks** \$20 trillion, a more than China's GDP, claiming coronavirus is the result of a **biological weapon** prepared by the Chinese authorities. The plaintiff also alleged that all the defendants were working together to perpetrate an act of "international terrorism".

### **Issue of Jurisdiction**

Traditionally, US citizens were permitted to sue a foreign state if it was designated as a state sponsor of terrorism by the US, provided that they were harmed by that state's aid for international terrorism. The Justice Against Sponsors of Terrorism Act (**JASTA**) authorized the federal courts to exercise subject matter jurisdiction over a state's support for acts of international terrorism against a US national or property regardless of whether such a state is designated as a sponsor of terrorism. Such types of cases are not new in the legal history of the US. This trend came into the limelight after the case **In re Terrorist Attacks on September 11, 2001**, wherein the JASTA was applied for the first time.

As per Section **1605B(b)** of the JASTA, a foreign state is not immune from the jurisdiction of a US court in cases where money damages are sought against it for physical injury to a person, property or death occurring in the US caused by either an act of international **terrorism** or by a tortious act performed by any agent or official of that state, regardless of the place where it is performed.

Freedom Watch's petition has addressed the question of jurisdiction in a detailed manner and might be admissible in the court.

There have been prior cases wherein a state was held liable for an act of international terrorism and paid hefty damages to the victims. The best example is the case of **Pan Am 103 Bombing** wherein, according to the evidence, the **involvement** of two Libyan intelligence operatives was proven and one of them was found guilty. Initially, the Libyan government did not agree to extradite both of the operatives. Libya finally agreed after being pressured from the Security Council by way of imposing sanctions until the country compensated the victims' families and demonstrated with concrete actions its renunciation of terrorism. Later, the Libyan government also paid a sum of nearly \$3 billion to the victims' families.

However, unlike the **Pan Am 103** case, the issues involved in Freedom Watch's petition still require investigation. Furthermore, the lack of any scientific evidence to support the theory of using COVID-19 as a bioweapon indicates that these are mere theoretical presumptions and are not practically possible as COVID-19 is not fatal enough to be used as a bioweapon. Secondly, the involvement of two nuclear weapons states (**NWS**) in this case which have been involved in a trade war appears to be a mere act of predominance.

### **Further Course of Action and International Overview**

This Freedom Watch petition might be admissible by the court, but what if China, being a superpower, refuses to comply with the decision of the court in order to protect its sovereign immunity? As mentioned above the petition might be rejected on the basis of lack of evidence. Therefore, alternative discourses may be necessary to bring China under



proper jurisdiction and make them accountable for allegedly committing such a heinous and negligent act.

### **Alternative Course of Action Available in International Forums**

Considering the fact that this pandemic has affected more than half of the world's population, it might be best to bring an **Article 7** Crimes Against Humanity case against the Chinese authorities in the International Criminal Court (**ICC**). The ICC is the supreme authority to handle such cases. It is undoubtedly a better alternative to make Chinese authorities responsible for the outbreak.

In the case of **The Prosecutor v. Germain Katanga**, the alleged party was convicted and sentenced to twelve years of prison for committing mass murder and various crimes against humanity. The recent **incident** where China used its veto power to refuse to allow the discussion of the Wuhan epidemic and the spread of COVID-19 in the Security Council has created several questions. The Chinese Ambassador stated that "discussion relating to COVID-19 is not an agenda of the UNSC", which has led to further the suspicion that China is hiding vital details about the origin of the virus.

It may be **inferred** that China is covering up the issue, which itself is a grave and inhumane act during this pandemic. Thus, even if there exists a remote suspicion that China has deliberately used COVID-19 as a biological weapon for committing bio-terrorism, there must be a proper trial held and every suspected authority must be a party.

The People's Republic of China, Major General Chen Wie and Shi Zhengli, Director of the Wuhan Institute of Virology, are the defendants in the Freedom Watch petition. The defendants dealt with the handling of the virus during the pre-pandemic and must be subject to proper investigation. If China is found to guilty of the deliberate release of COVID-19 during the investigation, there would be violations of several treaties China is a party to:

- The **Convention** on the Prohibition of the Development, Production and Stockpiling of Bacteriological (Biological) and Toxin Weapons and on their Destruction: This convention clearly states that the development, production and stockpiling of biological weapons in any manner against mankind would lead to a violation of the treaty. As per the treaty, any party can draw an action against the alleged party in UNSC along with the evidence stated under Article 7.
- **Protocol** for the Prohibition of the Use in War of Asphyxiating, Poisonous or Other Gases, and of Bacteriological Methods of Warfare: This treaty prohibits the use of any bacteriological method for mass destruction of mankind.
- Even if the alleged parties are not found guilty, the International Law Commission's **Liability** for Injurious Consequences exists to try parties for negligence in handling deadly viruses like COVID-19.

### **Conclusion**

The present COVID-19 pandemic has led to serious physical sufferings and mental injury accompanied by damage to the global economy and to man-kind. The proper judicial mechanisms must provide justice to the aggrieved party and convict the culprits behind the conspiracy if it exists. There are also alternatives available in international forums.

The only factor which remains in this puzzle is the proper evidence proving such a conspiracy exists. Once a proper investigation is initiated, things will become more clear. However, the behavior of the Chinese government is alarming and appears to be suspicious.

For more on COVID-19, see our **special coverage**.

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### Article 3

#### Beijing Believes COVID-19 Is a Biological Weapon

Source:

<https://www.globalresearch.ca/beijing-believes-covid-19-biological-weapon/5706558>

By Lucas Leiroz de Almeida

Global Research, March 18, 2020

Region: Asia

Theme: Intelligence, Science and Medicine

*From conspiracy theory to geopolitical realism, the possibility to treat COVID-19 as a biological weapon has been finally accepted in the public sphere. The recent statement by the Chinese spokesman **Zhao Lijian**, formally accusing the US of bringing coronavirus to China, has highlighted a series of new opinions about the pandemic.*

The hypothesis of biological warfare behind the global pandemic had already been raised by Russian experts some weeks ago. Like any opinion that is slightly different from the official version of Western governments and their media agencies, the thesis was ridiculed and accused of being a "conspiracy theory". However, as soon as the official spokesman for the Ministry of Foreign Affairs of the second largest economic power on the planet publishes a note attesting to this possibility, it leaves the sphere of "conspiracy theories" to enter the scene of public opinion and official government versions.

In addition to making the explanation of biological warfare official, Zhao Lijian raised important questions about the pandemic data in the USA: "When did patient zero begin in US? How many people are infected? What are the names of the hospitals? It might be US army who brought the epidemic to Wuhan. Be transparent! Make public your data! US owe us an explanation!"

The supreme leader of the Islamic Republic of Iran, **Ayatollah Khomeini**, ordered on the same day of the declaration of the Chinese Ministry the creation of a unified center of scientific research specialized in the fight against the coronavirus. The motivation, according to the Iranian spiritual and political leader, was motivated by evidence that the pandemic is a biological attack. These are his words:

"The establishment of a headquarters to fight the outbreak [of COVID-19] occurs due to the presence of evidence that indicates the possibility of a biological attack, signaling that it is necessary that all coping services [to the coronavirus] be under the command of a unified headquarters".

In fact, what the mainstream Western media has called a "conspiracy" has been manifested in US defense programs for a long time. We must briefly recall the official document named "[Rebuilding America's Defenses](#)", published by the conservative think tank "Project for a new American Century", where we can clearly read: "(...) advanced forms of biological warfare that can target specific genotypes may transform biological warfare from the realm of terror to a politically useful tool".

Taking into account that the document was published in 2000, we can see that the possibility of biological warfare has been carefully considered and worked on by American strategists for at least two decades. However, the projects are even older. [This article](#) published in Global Research tells a brief history of biological warfare technology, tracing the remote origins of this practice by the American armed forces. In this genealogy of biological warfare, we find reports of the use of bio-weapons in wars in great conflicts of the last century, such as the Second World War, the Korea War and the conflicts with Cuba. Even so, until last Thursday, the mere fact of mentioning this hypothesis for the new coronavirus was rejected as conspiracy.

We must attain to concrete data: [Pentagon has 400 military laboratories](#) around the world, whose activities are still obscure; the USA has not yet made a clear statement about the COVID-19 data in its territory, having not yet informed the identity of its patient zero and maintaining uncertain information about the number of infected; Chinese scientists conducted a complex study in which they concluded that the virus did not originate in China, but that it had multiple and diverse sources from the Huanan marine seafood market from where the virus subsequently spread.

In February, the Japanese media agency [Ashi TV](#) reported that the virus originated in the U.S., not China, and that Washington would be omitting its actual numbers, with some cases of death attributed to influenza being, in fact, camouflaged cases of coronavirus; on February 27, a Taiwanese virologist presented a series of flowcharts on a [TV program](#), corroborating the thesis that the virus has an American origin, providing a scientific explanation to the flow of the virus sources devoid of any geopolitical purpose.

Another curious fact is that China has been unexpectedly affected by epidemic phenomena, particularly during the period of the trade war between Beijing and Washington. Only between 2018 and the beginning of 2020, the country recorded epidemic episodes of H7N4, H7N9 (two variations of bird flu) and African swine flu. Also, the US has not officially responded to any of these notes, remaining silent about the coronavirus situation in its territory.

Not proposing a concrete answer, but only speculations, we can consider that the circumstances of the case present us a very extensive list of possibilities about what in fact the coronavirus is. Obviously, it is possible that it is not a biological weapon – and this is the official version of most of the media agencies and governments – however, once this hypothesis has been raised and no concrete evidence to the contrary is presented, it is also possible that it is a biological weapon.

The most important thing to do is to dispel the myth that biological wars are conspiracy theories. We must begin to take this possibility seriously and analyze the evidences in search of real solutions. Biological weapons are methods that have long been used and

that form a fundamental part of modern warfare, whose costs are less than the methods of direct confrontation of the old wars of mobilization – and whose benefits are greater.

*\*This article was originally published on [InfoBrics](#).*

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The original source of this article is Global Research

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