

14 May 2021

## LETTERS

## Investigate the origins of COVID-19

Jesse D. Bloom<sup>1,2</sup>, Yujia Alina Chan<sup>3</sup>, Ralph S. Baric<sup>4</sup>, Pamela J. Bjorkman<sup>5</sup>, Sarah Cobey<sup>6</sup>, Benjamin E. Deverman<sup>3</sup>, David N. Fisman<sup>7</sup>, Ravindra Gupta<sup>8</sup>, Akiko Iwasaki<sup>9,2</sup>, Marc Lipsitch<sup>10</sup>, Ruslan Medzhitov<sup>9,2</sup>, Richard A. Neher<sup>11</sup>, Rasmus Nielsen<sup>12</sup>, Nick Patterson<sup>13</sup>, Tim Stearns<sup>14</sup>, Erik van Nimwegen<sup>11</sup>, Michael Worobey<sup>15</sup>, David A. Relman<sup>16,17,\*</sup>

As scientists with relevant expertise, we agree with the WHO director-general (5), the United States and 13 other countries (6), and the European Union (7) that greater clarity about the origins of this pandemic is necessary and feasible to achieve. We must take hypotheses about both natural and laboratory spillovers seriously until we have sufficient data. A proper investigation should be transparent, objective, data-driven, inclusive of broad expertise, subject to independent oversight,

# Biden asks intel community to redouble efforts to trace origins of COVID-19

27 May 2021

By: [PTI](#) | May 27, 2021 8:51 AM

"I have now asked the Intelligence Community to redouble their efforts to collect and analyze information that could bring us closer to a definitive conclusion, and to report back to me in 90 days," Biden said in a statement.



# How many? A. Fauci emails revealed

date? 2021

**From:** Fauci, Anthony (NIH/NIAID) [E]  
**Sent:** Sat, 1 Feb 2020 18:43:31 +0000  
**To:** Kristian G. Andersen  
**Subject:** RE: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Thanks, Kristian. Talk soon on the call.

**From:** Kristian G. Andersen (b) (6) >  
**Sent:** Friday, January 31, 2020 10:32 PM  
**To:** Fauci, Anthony (NIH/NIAID) [E] (b) (6)  
**Cc:** Jeremy Farrar (b) (6) >  
**Subject:** Re: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Hi Tony,

Thanks for sharing. Yes, I saw this earlier today and both Eddie and myself are actually quoted in it. It's a great article, but the problem is that our phylogenetic analyses aren't able to answer whether the sequences are unusual at individual residues, except if they are completely off. On a phylogenetic tree the virus looks totally normal and the close clustering with bats suggest that bats serve as the reservoir. The unusual features of the virus make up a really small part of the genome (<0.1%) so one has to look really closely at all the sequences to see that some of the features (potentially) look engineered.

We have a good team lined up to look very critically at this, so we should know much more at the end of the weekend. I should mention that after discussions earlier today, Eddie, Bob, Mike, and myself all find the genome inconsistent with expectations from evolutionary theory. But we have to look at this much more closely and there are still further analyses to be done, so those opinions could still change.

Best,  
Kristian

On Fri, Jan 31, 2020 at 18:47 Fauci, Anthony (NIH/NIAID) [E] (b) (6) > wrote:

Jeremy/Kristian:

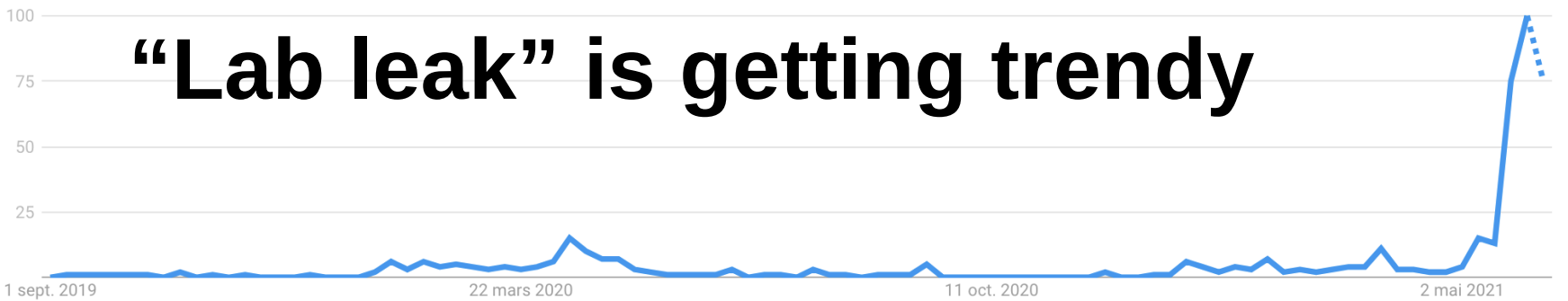
This just came out today. You may have seen it. If not, it is of interest to the current discussion.

Best,  
Tony

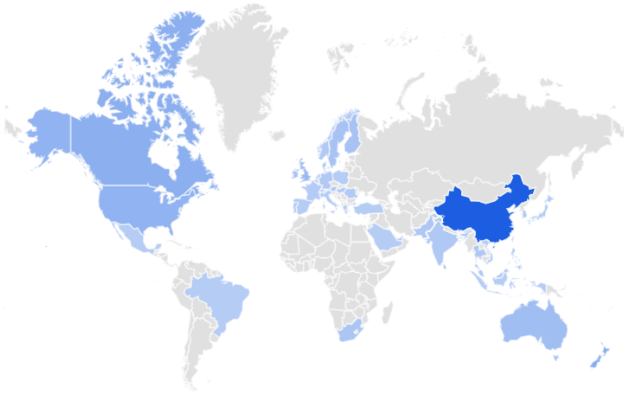
Ref?

Dans tous les pays ▼ 01/09/2019 – 13/06/2021 ▼ Toutes catégories ▼ Recherche sur le Web ▼

Évolution de l'intérêt pour cette recherche ⓘ



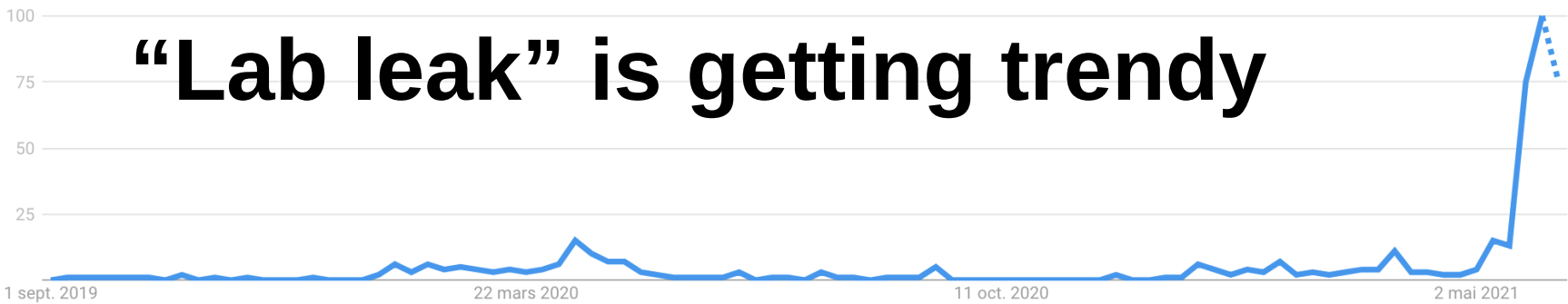
Intérêt par région ⓘ



Région ▼			↓	<>	↻
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2	Nouvelle-Zélande	27	<div></div>		
3	Canada	26	<div></div>		
4	Hong Kong	25	<div></div>		
5	Singapour	23	<div></div>		

Dans tous les pays ▼ 01/09/2019 – 13/06/2021 ▼ Toutes catégories ▼ Recherche sur le Web ▼

Évolution de l'intérêt pour cette recherche ?



Intérêt par région ?

Région ▼

6	États-Unis	22	<div></div>
7	Royaume-Uni	17	<div></div>
8	Australie	13	<div></div>
9	Sri Lanka	13	<div></div>
10	Irlande	10	<div></div>

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