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Deep-Dwelling Scientists Discover Bubbling CO2 Hotspot

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A Pinoy-led team of scientists discovered bubbling underwater springs that give off high amounts of carbon dioxide (CO2) levels at Secret Bay in Anilao, Batangas.

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The recorded CO2 levels from the springs were twice as high compared to those from the highest reported submarine springs in the world, according to the team's scientific paper.

Noting the soda-like environment where the springs were found, the study's team leader Bayani Cardenas decided

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"The most dramatic levels were found in an area with relatively deep bubble vents. This area, hereafter named Soda Springs, is at a water depth of 55 m and is within Secret Bay," the team wrote.

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Ang lihim ng Secret Bay sa 'Brigada'

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Cardenas, who worked on the study for three years along with several co-authors from various Philippine institutions, confirmed that the CO2 levels measured in the "Soda Springs" were the highest for submarine springs.

"It doesn't mean that higher values do not exist. We used one of the few instruments that can measure CO2 right at the spring itself, and one that can measure very high values. If we probably move that sensor around, we would find even higher values," he told GMA News Online.

Cardenas said this new discovery can help scientists in understanding the effects of increasing atmospheric CO2 levels on coral reefs and how pollution in groundwater can be brought to the reefs.

So, what's the water like in these springs?

Since the springs are located within the area of the active Taal Volcano, the water samples collected from these areas had temperatures as high as 60C.

"The waters are acidic (low pH) compared to seawater but in many ways it also looks like seawater chemically. It is also hot, 50-60C," explained Cardenas.

As seen in a video from the University of Texas Jackson School of Geosciences, lines of small bubbles rose out from hydrothermal vents that were two hundred feet deep from the surface of the bay.

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"As a scientist, we always pursue new knowledge. This also means going to places where knowledge regarding that area is lacking," the University of Texas at Austin professor said. "It is part of the joys of doing science and

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exploration."

The team also discovered another dive site that also has underwater gas vents. This area was named 'Bubbles Point.'

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Other authors of the study included researchers from Utrecht University, University of Texas Bureau of Economic Geology, Agricultural Sustainability Initiatives for Nature, Inc., Planet Dive Resort, Scuba Academy Manila, University of the Philippines Diliman, and Ateneo de Manila University. —MGP, GMA News

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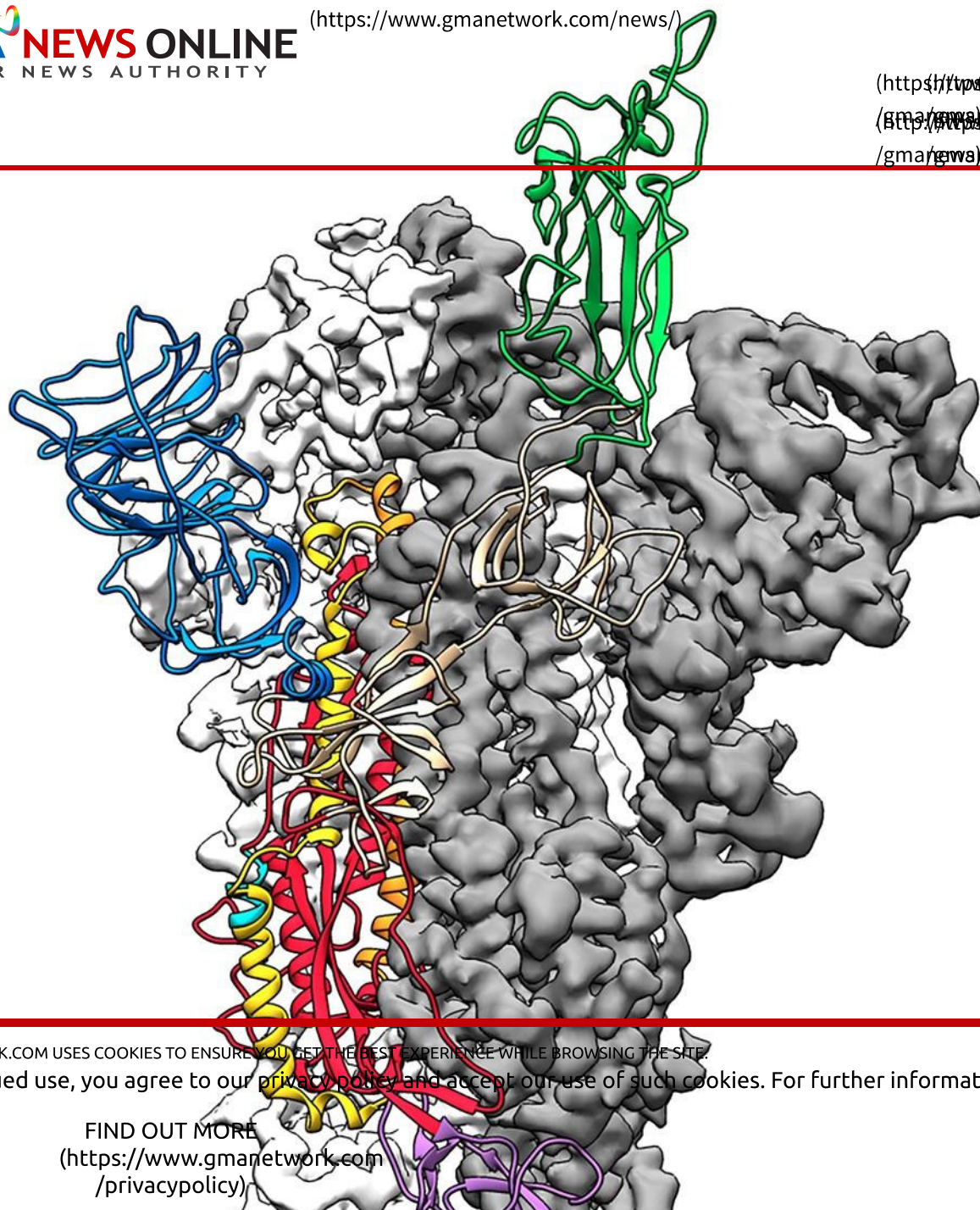
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The first 3D atomic scale map of the part of the 2019 novel coronavirus that attaches to and infects human cells is seen in an illustration provided by the University of Texas at Austin and the National Institutes of Health, US, February 19, 2020. University of Texas at Austin Handout via REUTERS.



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WASHINGTON — US scientists announced Wednesday they had created the first 3D atomic scale map of the part of the novel coronavirus that attaches to and infects human cells, a critical step toward developing vaccines and treatments.

It came as the death toll from the COVID-19 virus jumped past 2,000, almost all of them in mainland China where 74,185 cases of infection have been confirmed since it first emerged in late December.

The team from the University of Texas at Austin and the National Institutes of Health (NIH) first studied the genetic code of the virus made publicly available by Chinese researchers, and used it to develop a stabilized sample of a key part called the spike protein.

They then imaged the spike protein using cutting-edge technology known as cryogenic electron microscopy, publishing their findings in the journal Science.

"The spike is really the antigen that we want to introduce into humans to prime their immune response to make antibodies against this, so that when they then see the actual virus, their immune systems are ready and loaded to attack," UT Austin scientist Jason McLellan, who led the research, told AFP.

He added that he and his colleagues had already spent many years studying other members of the coronavirus family including SARS and MERS, which helped them develop the engineering methods required to keep the spike protein stable.

Their engineered spike protein is itself being tested as a potential vaccine by the NIH.

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The team is sending the map of its molecular structure out to collaborators around the world so they can improve it by making it provoke a greater immune response.

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The model can also help scientists develop new proteins to bind to different parts of the spike and prevent it from functioning, to treat those already infected. These are known as antivirals.

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"This is a beautifully clear structure of one of the most important coronavirus proteins—a real breakthrough in terms of understanding how this coronavirus finds and enters cells," said virologist Benjamin Neuman at the Texas A&M University-Texarkana, who was not involved in the work.

"The structure shows that although the spike is made of the three identical proteins, one flexes out above the rest, effectively giving the virus a longer reach," he added.

A useful aspect of the structure for vaccine development is that it maps out the size and location of chains of sugar molecules the virus uses in part to avoid being detected by the human immune system, added Neuman.

Cryogenic electron microscopy uses beams of electrons to examine the atomic structures of biomolecules that are frozen to help preserve them.

Three scientists credited with developing the technology were awarded the 2017 Nobel prize in chemistry. —
Agence France-Presse

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