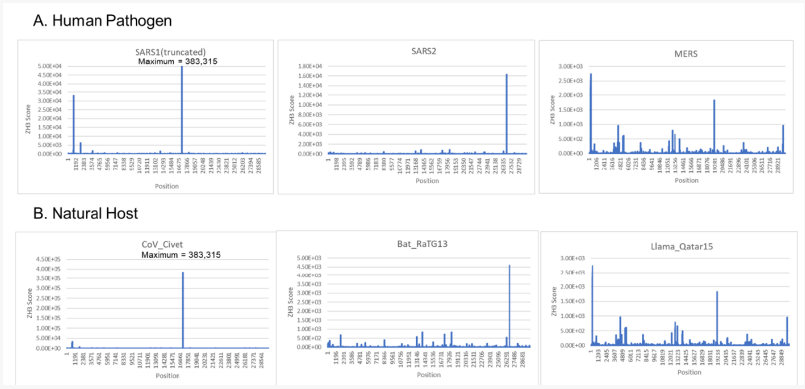
A flipon signature allows tracing of the SARS virus origin

A fingerprint for SARS viruses that allows identification of the hosts from which they originated.



The fingerprint for the human viruses on the top row align with the animal virus from where they came on the bottom row

CHARLESTOWN, MA, UNITED STATES, March 1, 2022 /EINPresswire.com/ -- One of the many mysteries is where the coronaviruses that cause human disease came form. Today, in a pre-print, Alan Herbert form InsideOutBio along with Ale Shein and Maria Poptsova from the Higher School of Economics and Computer Science (HSE) provide an answer to this question. They analyzed different coronavirus strains to generate a signature based on their RNA sequence, one unique for each virus. Using this molecular fingerprint the authors show unambiguously that the Middle East respiratory syndrome (MERS) signature is identical to the Llama coronavirus (CoV), Severe Acute Respiratory Syndrome-CoV1 (SARS1) is the same as for civet CoV and a SARS-CoV2 (SARS2) matches that from bat CoV RaTG13. The approach confirms previous findings but provides an extremely easy way to analyze the relationship between different CoV strains. The work is consistent with a natural origin for the disease viruses.

> Teh discovery of Z-DNA has lead to many unexpected findings both in biology and therapeutics. The work has now rather surprisingly identified unique signatures for coronavirus strains"
>
> *Alan Herbert*

The signature is based on the propensity of double-stranded nucleic acids to flip from the right-handed Watson Crick conformation to the left-handed Z-DNA and Z-RNA conformation. It builds on many decades of work following the unexpected discovery of Z-DNA. Once controversial, a biological role for Z-RNA in regulating immune responses against viruses has been confirmed by recent breakthroughs. The finding build on previous work showing that those sequences adopting the Z-conformations under physiological conditions, called flipons, have additional important functions in cellular dynamics.

The preprint examines Z-RNA dependent host responses to coronaviruses, proposing a number of features that will require additional experimental validation. The manuscript has been submitted for peer-review.

InsideOutBio is a privately held biotech working in cancer therapeutics. HSE is a top ranked computer science institution located in Moscow.

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