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Greenland's ice is fracturing faster than expected

As glacial ice flows, stress fractures that run tens of metres deep form in the glacier's surface (pictured). These crevasses increase the rate of ice movement, which creates more cracks in a self-reinforcing loop that has the potential to exacerbate ice loss from the land and contribute to rising sea levels. Writing in *Nature Geoscience*, Chudley *et al.* report that in most parts of Greenland, ice crevasses in glaciers are getting deeper and larger — and this is happening more quickly than previously estimated (T. R. Chudley *et al. Nature Geosci.* https://doi.org/n5bg; 2025).

Using satellite images gathered in 2016 and 2021, the authors created 3D maps of crevasses across the Greenland Ice Sheet, the second biggest ice mass on Earth. Chudley *et al.* found that increases in crevasse volume were most extreme where fast-moving glaciers meet the sea, and that the acceleration of crevassing coincided with quickened ice flow caused by a rise in air and ocean temperatures. Predictions of future ice-sheet dynamics will be aided by the vast data set, and the researchers already warn that the effects of crevassing could worsen over the next few years as one of Greenland's fastest-flowing glaciers picks up speed.

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are yet to be discovered. Expanding genomic studies to include under-represented bat families could provide molecular insights into their resilience against diverse viruses.

Furthermore, Morales *et al.* found that the ISG15 protein from bat species that harbour SARS-CoV-2-related coronaviruses is more effective at blocking SARS-CoV-2 than is ISG15 from other bat species. A study published last year showed that certain SARS-CoV-2 proteins, such as the nucleocapsid (N) protein, can be ISGylated[7]. ISGylation of the N protein impairs the synthesis of viral RNA molecules, and thereby inhibits SARS-CoV-2 replication[7]. Investigating whether specific bat species exhibit enhanced ISGylation of coronaviral N proteins could clarify why bats tolerate coronavirus infections that are highly pathogenic in humans. Moreover, the activation of key host proteins in antiviral immunity requires ISG15 conjugation[8,9]. Further studies are needed to establish the precise mechanisms through which adaptations in the bat ISG15 protein confer viral resistance.

The implications of this work extend beyond bats. Integrating genomic data with cutting-edge approaches — such as single-cell transcriptomics to catalogue the RNA transcripts expressed in individual cells, and comparative proteomics analyses to assess the differences in protein expression between bats and humans — could unveil molecular targets for alleviating excessive inflammation in humans. As well as *ISG15*, several other immune genes that underwent positive selection in bats were identified, and these will require functional validation. Decoding bats' viral disease resistance will be crucial for mitigating future pandemics caused by 'spillover' events in which viruses are transmitted from animals to humans. It will also provide valuable insights to aid the design of therapeutic strategies for human disorders that are driven by overactive inflammation.

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