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Coronavirus: keep sharing research

Researchers must ensure that their work on this outbreak is shared rapidly and openly.

Twenty thousand cases; more than 400 lives lost. The coronavirus first reported last December is now a public-health emergency of international concern. In China, cities have been sealed off, and the authorities have built an entire new hospital in Wuhan, where the outbreak started.

Along with medical workers, the country's researchers are playing a vital part. Epidemiologists are working to update estimates of case numbers; genome samples of the pathogen are being sequenced and results are being shared.

In two papers in *Nature*, teams led by researchers at the Wuhan Institute of Virology and at Fudan University, Shanghai, confirm that the virus is similar to the one that caused severe acute respiratory syndrome (SARS), and that there's evidence it originated in bats. The Wuhan team analysed viral-genome samples from a small number of patients, all of whom worked at the animal market from which the first cases were reported (P. Zhou *et al. Nature* http://doi.org/ggj5cg; 2020). The Fudan team sequenced a sample from one infected market worker (F. Wu *et al. Nature* http://doi.org/dk2w; 2020).

In the first days after the outbreak became known, we confirmed that reporting research and data will in no way affect consideration of submissions to *Nature*. *Nature* and its publisher Springer Nature have now signed a joint statement with other publishers, funders and scientific societies to ensure the rapid sharing of research data and findings relevant to the coronavirus. In the statement, we commit to working together to help ensure that:

• All peer-reviewed research publications relevant to the outbreak are made immediately open access, or freely available at least for the duration of the outbreak.

• Research findings relevant to the outbreak are shared immediately with the World Health Organization (WHO) upon journal submission, by the journal and with author knowledge.

• Research findings are made available via preprint servers before journal publication, or via platforms that make papers openly accessible before peer review, with clear statements regarding the availability of underlying data.

• Researchers share interim and final research data relating to the outbreak, together with protocols and standards used to collect the data, as rapidly and widely as possible — including with public health and research communities and the WHO.

The priority now is to stop the virus's spread and help those affected. That includes understanding how the virus is transmitted between people, ramping up supplies of diagnostic equipment and accelerating vaccine development. Beyond this, questions are being asked about whether there were delays in sounding the alarm. Answering this honestly is necessary if we are to learn lessons for next time. It's also essential to improve regulation of animal markets, because lax oversight increases the risk of new viruses transferring from animals to humans. And funds must be released for better disease surveillance in the poorest countries — the main reason the WHO declared the virus a public-health emergency of international concern.

For researchers, the message is simple: work hard to understand and combat this infectious disease; make that work of the highest standard; and make results quickly available to the world.

> **"The priority now is to stop the virus's spread and help those affected."**

Cancer genomics gets new focus

To realize the full potential of cancer genomics studies, tumour sequence data needs to be paired with clinical background information.

This week, *Nature* is publishing a suite of papers that sheds new light on the genetic causes of cancer. The results show how far our understanding of cancer has come — and how far we still have to go.

The Pan-Cancer Analysis of Whole Genomes Consortium brought together researchers with nearly 750 affiliations across 4 continents. Between them, they sequenced full genomes from more than 2,600 samples representing 38 different types of cancer. The work is summarized in a News & Views article on page 39.

The project is remarkable in both scope and complexity, and, partly because of this, faced challenges at every step; from acquiring samples to protecting patient privacy while putting terabytes of data into the hands of researchers.

Thanks to these efforts — and previous full-genome sequences — scientists now have an unprecedented view of the genetic changes that can contribute to cancer, and a clearer idea of where gaps in knowledge remain. Altogether, the team pinpointed 705 mutations that occurred repeatedly in the cancer genomes, suggesting that they are important for tumour growth. Of these, about 100 fell outside the protein-coding regions of the genome, but more such mutations might be uncovered with improvements in computational techniques for analysing non-coding regions. Overall, the authors found that cancer genomes contain an average of four to five mutations that drive tumour growth. In 5% of cases, however, they found no such mutations.

Cancer genomes have been sequenced for more than a decade, but now researchers and the funders who support them must tackle the next challenge. The goal has always

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been to improve the lives of those affected by cancer, and the reams of data amassed by sequencing projects have helped. They are used by researchers to find new drug targets, and to generate new markers that can be used to match patients with the treatment most likely to help.

But most of the data so far have been limited in one crucial respect: clinical details of the sample donors are often missing. The first samples collected for the Cancer Genome Atlas, a sequencing project that ran from 2006 to 2018, co-funded by the US National Cancer Institute and the National Human Genome Research Institute, typically came with little more than the donor's gender, diagnosis and age at diagnosis. Rarely would there be a record of that person's family or medical history, what therapy they had received and how they had responded – all crucial information if genome sequences are to be put to work to help patients.

The next generation of cancer-genome sequencing projects is trying to change that. But gathering detailed clinical information is more difficult – and more expensive – than sequencing genomes, particularly in the many countries that lack a unified health-care system. There, accessing hospital records is complicated: different hospitals keep records differently; patients often move from one treatment centre to another; and the quality of records varies enormously. More-detailed records also mean greater risk of personal exposure if there is a privacy violation, raising the bar yet again for participant protection.

These are all pressing issues, not only in cancer research, but in health care generally. Efforts are already under way to transform health records into a format that can be more readily, but securely, accessed and studied. The American Association for Cancer Research's project GENIE, for example, has compiled 70,000 records of tumour DNA sequences, and real-world clinical data. The United Kingdom's 100,000 Genomes Project also aims to match DNA sequences with clinical information for a variety of conditions. And the International Cancer Genome Consortium, which has coordinated much of the tumour sequencing work so far, has launched a new phase, this time with a focus on clinical information.

Pooling large numbers of samples is a powerful way to find genetic changes that can drive cancer, and provides a starting point for learning how they do so. But the real return on investment will come when that information can be used to tailor therapy to individual patients. And for that to be achieved, clinical background information on study participants is essential.

When cancer-genome sequencing projects were first launched, it was hoped that they would provide a catalogue of mutations that could give rise to cancer – and reveal broad patterns on which researchers could base drug development. The core of that mission has been achieved, but many cancers have proved more complex than expected. Seemingly similar cancers can contain very different sets of mutations – no two cancers are quite the same.

As is often the case in biomedical research, the answers to a question are more complex than originally imagined. But recognizing the complexity is empowering, and harnessing it will be necessary in the search for better treatments.

> **"The answers are more complex than originally imagined."**

Read all about it

***Nature* will trial the publication of peer-review reports.**

Research communities are unanimous in acknowledging the value of peer review, but there's a growing desire for more transparency in the process. As part of that, researchers want to see how publishing decisions are made, and they want greater assurance that referees and editors act with integrity and without bias.

For many journals, including *Nature*, peer review has typically been single-blind – that is, authors do not know who is reviewing their paper. At the same time, the contents of peer-review reports, and correspondence between authors, reviewers and editors, are kept confidential.

This prevents readers from seeing the often fascinating and important discussions between authors and reviewers, which are crucial in shaping and improving research and checking its integrity. Keeping these debates confidential also helps to reinforce perceptions that the research paper is the last word on a subject – when the latest finding is often simply a milestone along the scholarly journey.

Our authors have told us they want change. In a 2017 survey of *Nature* referees, 63% of respondents said publishers should experiment with alternative models, and more than half said peer review could be more transparent.

Four years ago, *Nature* invited referees to be acknowledged in papers – with the consent of both author and reviewer. Around 3,700 *Nature* referees have chosen to be publicly recognized, and around 80% of the journal's papers have at least one referee named.

Beginning this week, authors of new submissions to *Nature* will be offered the option to have anonymous referee reports published, along with their own responses and rebuttals, once a manuscript is ready for publication.

Those who agree to act as reviewers should know that their anonymous reports – and their anonymized correspondence with authors – might be published. Referees can also choose to be named, should they desire.

In making this change, *Nature* is following seven other Nature Research journals. And we're joining the pioneering efforts of *The EMBO Journal* and BMC journals – and, more recently, *Nature Communications*, which has been publishing reviewer reports since 2016.

We will report back as the trial progresses, but the experience of *Nature Communications* has been positive. In 2018, the overwhelming majority (98%) of the journal's authors who had published their reviewer reports told us they would do so again.

Published peer reviews are intended to advance scholarly discussion about a piece of research and it is important that our readers and the research community at large can benefit from such discourse. We are pleased to be playing a small part in making that happen.