The international journal of science / 28 May 2020

nature

Coronavirus misinformation needs engagement

Researchers must be open and transparent – acknowledge what is known and what isn't.

The past few weeks have seen an explosion in misleading claims about COVID-19. These are mostly online, and many are intended to sow doubts about vaccination as a way to protect against infection. For the individuals and organizations involved in such disinformation, the pandemic is a gilded opportunity. They are capitalizing on both the many unknowns about the SARS-CoV-2 virus and the disease it causes, as well as the many legitimate questions about safety and efficacy as vaccines are being developed at unprecedented speed.

Vaccines must be safe and effective. Once (and only once) this is proven, immunization campaigns need to be comprehensive to succeed. But this presents many challenges. For low-income countries, and in those without universal health care, a key obstacle is ensuring that vaccines are available and affordable. For certain higher-income countries – for example some in Europe – the challenge for coronavirus will be to overcome scepticism about vaccines, which is being fuelled by false information.

Researchers can play a part. Knowing what to do in the middle of a pandemic isn't straightforward. But for those considering how to respond to the kinds of questions that everyone is asking, and what to do about disinformation, there are ways to help.

Tackling disinformation

As *Nature* reports on page 371, misinformation (false information) and disinformation (information that is deliberately misleading) are complex. Some politicians are spreading virus disinformation to burnish their image and influence among their supporters. There are organizations that have set up disinformation websites – including money-making scams. Very little, if any, of this information will have been put through an open process of verification and review. For consumers, it can be a double whammy – they are paying, and also being misinformed or misled.

Public-health agencies and technology firms are aware of the harm being done and are working to respond. To their credit, platforms such as Facebook and YouTube are more active in taking down posts where there is a clear risk to public health. When questions such as "are vaccines safe" are typed into Google, the search algorithms are listing sources that provide evidence-based information. But for every item of misinformation and disinformation that are dealt with, more pop up. Moreover, sites have discovered ways to circumvent artificial-intelligence tools and harried moderators, and that makes the role of human fact-checkers more important.

> "Involving communities helps to create and maintain trust."

One thing that researchers can do is to work with organizations that are responding to disinformation. They can support or join in the work of professional fact-checkers, journalists and academics, doggedly following bots and disinformation-news sites, flagging their content to the media organizations and social-media firms that host these sites. Groups all over the world are involved in this response – including professional bodies, learned societies and media-facing organizations. The work they do is labour-intensive and can seem never-ending, but it is needed now more than ever.

Public engagement and transparency

Many people are asking important questions on subjects such as the safety of proposed vaccines, the security of contact-tracing apps and how intellectual property rights and profits from new drugs and vaccines will be shared. These are questions that researchers from fields such as public health, data security and health-care finance are also asking. If they are not already doing so, now is the time for these and other researchers to expand their public engagement.

It might be that a definite answer isn't known, or that there are a range of possible answers. That is often the case in science. The study and practice of public engagement in science has shown that involving communities in the kinds of conversations that researchers have – conversations about how scientists search for evidence, and being transparent about what is known and not known – all helps to create and maintain trust.

A year ago, the UK biomedical funding charity Wellcome published the results of a large global survey into vaccines, involving 140,000 participants in 140 countries. It found that around 80% of respondents considered vaccines safe and effective. Confidence was highest in low-income countries – notably Bangladesh and Rwanda – where public-awareness campaigns against infectious diseases such as malaria, typhoid and hepatitis are common.

By contrast, confidence in the importance of vaccines was lower in Europe, where populations are comparatively free of infectious diseases, but now have some of the highest deaths and infections from COVID-19. Some 22% of respondents from Europe are not confident that vaccines are safe, and this figure increases to 33% for France. Wellcome's findings reflect those from the European Commission's own *State of Vaccine Confidence* report from 2018. Across the European Union, health ministries are unable to meet their own target – set after the 2009 H1N1 swine flu outbreak – of vaccinating 75% of over-65s against flu.

Last November, Heidi Larson, an anthropologist at the London School of Hygiene and Tropical Medicine – and a co-author of the European Commission report – warned in an interview with *Nature* that if there is "another very serious influenza pandemic sooner or later, and if the public opt to forgo vaccination the way they did during the 2009

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swine-flu pandemic, we're in deep trouble" (S. el-Showk *Nature* **575**, S57; 2019).

That is why there is work to be done. When it comes to communicating emerging information on research, the lessons from studies and from past practice are clear: not to over-promise, nor oversell and to emphasize what is known and what isn't. In the case of vaccines, it means being as transparent as possible about how vaccines are made, how they work, what they contain and how they will be tested, and always being upfront about the evidence for their effectiveness, possible risks and side effects.

Researchers should play a part — no matter how small — in the response to misinformation and disinformation. We need to build a society that is resilient to falsehoods about COVID-19, a task that will only become more vital as vaccines near.

Milestone in human genetics highlights diversity gap

Landmark study identifies genes that it seems people can and cannot live without. But such data still need to be more representative.

From the time that the nineteenth-century monk Gregor Mendel squinted at the pea plants in his garden and wondered why some had white flowers or wrinkled seeds, it has been a tradition in biology to observe what goes awry when a DNA sequence is altered — whether that variation occurs naturally or through human intervention.

Although geneticists have long been able to introduce genetic mutations into model organisms such as the fruit fly — first with X-rays or chemicals, and now with more sophisticated gene-editing tools — where humans are concerned, the toolbox is more limited. Researchers clearly cannot intentionally introduce mutations into humans; instead, they must use what nature provides. As a result, they comb through genomes in search of variations in DNA sequences, and use statistical tools to determine whether those variations contribute to traits and diseases. As genome sequencing has become quicker and cheaper, those studies have become bigger and more complex.

This week, three journals in the *Nature* family are publishing the results of the latest effort: a study of a staggering 125,748 exomes (the part of the genome that codes for proteins) and 15,708 whole genomes (see go.nature.com/2zgfxr2). The study — the most extensive publicly accessible analysis carried out so far — sheds light on which genes are essential and which a person might be able to live without. The results are compiled in the Genome Aggregation Database (gnomAD) and will help researchers to better understand the roots of genetic disorders, and, eventually, how best to treat them. That mutations can inactivate genes is hardly new, but this study adds to the surprisingly long list of mutations that can obliterate a gene's function without causing obvious harm. The study also identified a flurry of genes that are probably vital for life, because people rarely harbour drastic mutations predicted to cause 'loss of function' in these genes.

> **"Around half of the samples were donated by people of European descent."**

The study's large scale made it possible for the authors to devise a measure of how tolerant to loss-of-function mutations a given gene might be. This is a useful tool with which to study the function of known and newly identified genes, to pinpoint candidate disease-causing mutations, and to find new drug targets in the human genome.

One example is the team's evaluation of the gene *LRRK2*, which has been implicated in Parkinson's disease (N. Whiffin *et al. Nature Med.* https://doi.org/10.1038/s41591-020-0893-5; 2020). DNA variants that increase the activity of the LRRK2 protein have been associated with a higher risk of the disease, leading scientists to think that a drug that switches the gene off could be beneficial. But would turning off *LRRK2*, which is active in the brain, as well as in other tissues, be dangerous? Looking through gnomAD's 140,000 genomes and exomes, the authors found many naturally occurring DNA sequence variants that switch off *LRRK2*. That suggests — at least in principle — that a drug that can mimic this effect might not be harmful.

To answer such questions, a very large number of samples is needed, in part because DNA sequence variations that wipe out the function of an important gene are likely to be rare. This means that the more genomes scientists can analyse, the more variants they can find and the better they can pick apart the effects of each one. But such projects also need a greater diversity of participants than they have had thus far.

In the current studies, around half of the samples were donated by people of European descent. Although this is an improvement on previous studies, people from regions such as Central Asia, Oceania, the Middle East and much of Africa are almost absent. This means researchers are probably missing variants that are important for understanding gene function — and disease risk — in these regions. This is something that consortium members recognize, but progress is slow. Researchers and funders must incentivize such work to ensure that it continues to expand.

The gnomAD database is an outstanding resource. The willingness of participants to contribute — along with the willingness of researchers to share — has been key to its success. Further insights will come from combining sequence data with clinical information. Projects such as the Estonian Biobank, which includes more than 200,000 participants, and the UK Biobank, which has DNA and health information from 500,000 people, are paving the way. But such efforts need the involvement of more-diverse populations.

With these improvements, researchers will be able to maximize the contribution of everyone who provided their DNA samples to improve our knowledge of human biology and to fully harness genetic differences to benefit us all.