News stories must account for gender bias

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LETTERS

Edited by **Jennifer Sills**

Editorial Expression of Concern

On 21 July 2017, *Science* published the Report "Chiral Majorana fermion modes in a quantum anomalous Hall insulator–superconductor structure" by Q. L. He *et al.* (*1*). Since that time, raw data files were offered by the authors in response to queries from readers who had failed to reproduce the findings. Those data files did not clarify the underlying issues, and now their provenance has come into question. While the authors' institutions investigate further, we are alerting readers to these concerns.

H. Holden Thorp
Editor-in-Chief

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Track Omicron's spread with molecular data

On 26 November, the newly emerged variant Omicron was designated a severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variant of concern (VOC) (*1*). Rapid polymerase chain reaction (PCR) test results could improve estimates of the prevalence of Omicron around the world. The widely used Thermo Fisher TaqPath COVID-19 PCR assay was valuable in tracking the spread of the Alpha (B.1.1.7) VOC (*2*) because a deletion of amino acids 69 and 70 in Alpha's spike gene (Δ69–70) yields a distinct absent S-gene (S^-) despite positive test results. The Delta VOC lacks this deletion and is therefore S-gene positive (S^+) on TaqPath PCR tests (*3*). The Omicron VOC shares the spike Δ69–70 deletion with Alpha, which has dropped to negligible levels worldwide. Therefore, the frequency of S^- results can be used as a rapid proxy for the frequency of Omicron cases, provided initial detection of local circulation had been confirmed by sequencing.

To put these data to use, countries should prioritize the release of daily counts of cases, hospitalizations, and deaths disaggregated by S^+, S^-, and unknown [e.g., (*4*)] as much as possible while taking logistical and privacy concerns into account. S-gene data could serve as a proxy for estimates of Omicron VOC prevalence (*5*) and help us to understand the fraction of infections caused by Omicron (versus Delta) and the severity of Omicron cases, as measured by mortality and hospitalization. In low-resource settings where genomic sampling is absent, infrequent, or characterized by long turnaround times (*6*), S-gene data will help reveal the risk Omicron poses to pandemic control. Finally, through synthesis with serological data (*7*), S-gene data—shared in real time—could help to evaluate the degree of immune protection conferred by natural- and vaccine-elicited immunity in Omicron cases.

Although S-gene data will be informative, preferential sequencing of samples with an S^- result will lead to virus genomic datasets that are unrepresentative of the true underlying spatiotemporal prevalence of Omicron. To provide adequate context for genome sequences, depositors to the Global Initiative on Sharing All Influenza Data (GISAID) database should use the newly introduced nonmandatory "sampling strategy" field to note how cases are selected and sampled for virus genome sequencing, including whether samples were specifically targeted for sequencing based on S^- PCR results. [We have used this field to plot the first 115 Omicron submissions to GISAID, stratified by sampling strategy (*8*).] Virus genomic datasets then can be compiled from cases known to have been sampled randomly from a given population and analyzed to generate more-accurate estimates of Omicron's growth relative to other variants. Standard sampling strategies include random community sampling [the preferred sampling strategy for estimating lineage growth (*6*, *9*)], targeted surveillance of defined subpopulations (e.g., vaccine breakthrough cases or international travelers), and enhanced sampling to investigate specific outbreaks or clusters.

Tracking SARS-CoV-2 lineages and variants, including Omicron, through GISAID (*10*), Pango lineages (*11*), and NextStrain (*12*) has provided valuable information about their spread in close to real time. However, genome sequencing intensities and turnaround times vary substantially across the world; in most countries, it takes more than 21 days after sample collection to deposit data in GISAID (*6*). Moreover, sampling strategies used to select samples for sequencing are heterogeneous across geographic regions (*6*) and often not reported in virus genome metadata. To evaluate risk and guide policy, there is an urgent need to incentivize the quick sharing of well-annotated genomic and S-gene–stratified surveillance data globally. By acting with speed, transparency, and consistency, we can establish

Polymerase chain reaction testing could provide rapid insights into the spread of the COVID-19 Omicron variant.

PHOTO: HANNAH BEIER/BLOOMBERG/GETTY IMAGES

norms to support better global responses to newly emerging variants.

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PHOTO: SUSIE GALLEGOS

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The *Science*Insider piece "Max Planck director loses post after probe of misconduct" (A. Curry, 5 November, p. 671) is the latest in a series of reports of dismissals, demotions, and conflicts involving prominent women in academic research. This story and previous reports have highlighted leadership issues and bullying by women not only at the Max Planck Institute (*1*) but also in top academic positions at ETH Zurich (*2*) and the University of London (*3*). We urge caution

PAST AS PROLOGUE

A uranium miner's daughter

After serving in Vietnam, my dad moved to Grants, New Mexico, to mine uranium. Every day, he drilled out uranium in deep, poorly ventilated, confined, hot, and dangerous underground tunnels. After work, my mom washed his overalls and lunch bucket, soiled with radioactive dirt. One day, when I was in fourth grade, my dad came home early from the graveyard shift and said he was not going back. At the time, I did not understand the circumstances, but I later learned that the industry had collapsed due to declining uranium prices, leaving the local economy in shambles.

Uranium mining has always been controversial. Uranium fuels non–carbon-emitting nuclear energy, but uranium and its radioactive decay progeny may pose health concerns. Even so, my family is proud of my dad's work in the mines because it afforded my parents a livelihood and the means to send their three kids to college, a luxury not given to them. With that opportunity, I pursued degrees in environmental engineering. For my PhD, I moved to Michigan to study iron sulfide–based media for use in cleanup of arsenic-contaminated groundwater. It was a difficult transition moving from sunny New Mexico to the cold, snowy upper Midwest, devoid of blue skies, New Mexico green chile sustenance, and, most importantly, my family. I began to question why I had started down this road, so far away from home without a clear vision of my destination.

The author's father, shown here, mined uranium in Grants, New Mexico.

Fortunately, a series of events allowed me to see the horizon. While on a summer research fellowship in Korea in 2006, I stumbled upon one of the only books in English in the institute's library. It was about the Grants mineral belt. I was amazed to see a book about my hometown halfway around the world. Soon after, I began seeing articles in the Grants newspaper about contamination from former uranium extraction operations, more than three decades after their closure.

I realized that I could apply my expertise to research uranium! The following year, I accepted a Mendenhall postdoc position at the US Geological Survey to study the environmental impacts of uranium mining. Now, with over 14 years of uranium research stimulating my curiosity, I have returned to New Mexico seeking new insights for managing mine waste. It is fitting that my passion for science brought me home again, where it was nurtured from the beginning by a humble, hard-working uranium miner and his wife.

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Call for Submissions Past as Prologue is an occasional feature highlighting the role of family history in the life of scientists. What role did your family background play in your decision to pursue science, your field, or your career? Submit your story to www.submit2science.org.

in reporting such stories given that women face more obstacles to attaining leadership positions and are often held to a different standard than men when it comes to how their behavior is interpreted.

Professional women face many biases that disproportionately delay their advancement along the career track and compromise their effectiveness and even their tenure in positions of power and authority (*4*, *5*). The same biases may result in greater and more detrimental visibility for conflicts involving women. Although gender bias in individual institutions can be difficult to assess because of the small numbers of women in leading scientific positions, the Max Planck Society has a large number of directors. It would be useful to know how many Max Planck Institute directors have left their positions before retirement, whether women are disproportionately represented in this group, and whether the publicity accompanying the departures differed between men and women.

To provide fair coverage, news stories should always pursue the question of possible gender bias, both in the treatment of women in positions of academic leadership and in the reporting on cases of leadership conflicts.

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Editor's Note

We thank J. G. Hering and colleagues for raising important questions about gender bias in cases of alleged bullying at the Max Planck Society and elsewhere. We agree that those issues need to be explored. In our coverage of Nicole Boivin, including a follow-up article published on 6 December (*1*), we note accusations of institutional misogyny at Max Planck and the small proportion of women directors. Our piece on the case at ETH Zurich devoted several paragraphs to the scarcity of women on the physics faculty and possible double standards for judging the behavior of women and men. Because bullying can impact the well-being and careers of young researchers, we believe serious cases should be covered regardless of who is accused—as our stories over the years have shown.

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