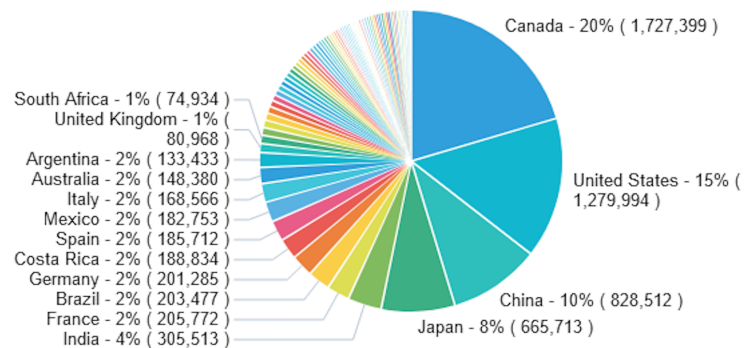


Use of Digital Sequence Information: Traffic-Circle instead of One-Way Street

Joint press release IPK Leibniz Institute and Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures

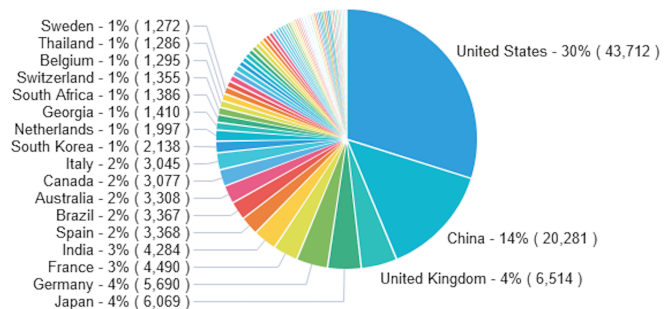
BRAUNSCHWEIG, LOWER SAXONY, GERMANY, January 19, 2022 /EINPresswire.com/ -- In the life sciences, globally available digital sequence information (DSI) or nucleotide sequence data (NSD) is a crucial building block for research. Knowledge often only emerges through the analysis and comparison of a large number of such data. For this reason, many researchers and science organisations are critical of political considerations according to which free access to these data should be restricted. Researchers at the IPK Leibniz Institute and the Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures GmbH have investigated how such data has been processed and used to date. Their results have been published in two studies in the journal "Giga Science".

Providing countries of DSI used in all publications



Source: IPK

Using countries based on publications



Source: IPK

The United Nations Convention on Biological Diversity officially recognised the rights of nations over the diversity of their ecosystems - that is, over all non-human living things. The treaty implies the idea that states with a large biodiversity provide the corresponding genetic resources. Scientists can use these resources and later share the resulting research results with the country of origin. However, the country of origin can also benefit in other aspects such as training and technology transfer. Ultimately, it is a matter of "access and benefit sharing".

The contracting parties are currently debating whether to restrict free access to DSI and establish monetary benefit sharing for the use of sequence data. Science organisations such as the Leopoldina reject this. Instead, they call for continued free access to data, but also support the principles of benefit sharing.

At this critical time in the international negotiations, which are to be continued in China in the summer of 2022, an international research team led by the IPK and the DSMZ has now examined how and according to which patterns access to and use of this data has taken place so far. It comes to the conclusion that the simple model of an exclusive provider-user relationship falls far short.

The simplistic notion that biodiverse countries only provide access to genetic resources and that science only uses and adds value to this data in rich countries is no longer tenable. "Our data point to a much more complex flow of information for digital sequence information," affirms Dr. Amber Hartman Scholz from the Leibniz Institute DSMZ and lead author of one of the two studies (1). "Many people think it's like a one-way street. But that's wrong. It's a kind of traffic-circle with entrances and exits," says Dr. Amber Hartman Scholz. "The use of DSI by scientists in the countries of origin is much stronger than we expected. We estimate it is precisely this open DSI ecosystem that leads to DSI being used more than thought in countries with a rather low GDP," says the DSMZ researcher. "Therefore, all policy decisions should aim to preserve open access to this important commons."

Nucleotide sequence data are collected and archived in the European Nucleotide Archive, among other places. Researchers at the IPK Leibniz Institute have analysed 263 million data sets from this collection and have investigated two questions: Which nation provided the biological material for the sequencing? And which researchers from which nations have subsequently used this sequence data for their own work? The result is an interactive Web-Portal to screen the use of DSI.

New discoveries in the life sciences rely on open data," say Dr. Matthias Lange from the "Bioinformatic and Information Technology" research group at IPK and lead author of the second study (2) and Dr. Guy Cochrane, Head of the European Nucleotide Archive at EMBL-EBI. "Researchers all over the world depend on the seamless flow of sequence data to find solutions for global challenges, from biodiversity to agriculture and human health. These studies show that reducing the flow of data will be damaging for everyone."

Together, Dr. Amber Hartman Scholz, Dr. Guy Cochrane and Dr. Matthias Lange appeal to policymakers to maintain free access to digital sequence information in the future. "If free access were to be restricted, it would make global scientific progress much more difficult," they both warn, referring to research on vaccines against Covid-19. "Certainly, science would not be as far along today as it is if researchers had had to pay for access to SARS CoV-2 sequence data and it were restricted."

Original publications:

(1) Scholz et al. (2021) Myth-busting the provider-user relationship for digital sequence information. Giga Science. [DOI: 10.1093/gigascience/giab085](https://doi.org/10.1093/gigascience/giab085)

(2) Lange et al. (2021) Quantitative monitoring of nucleotide sequence data from genetic resources in context of their citation in the scientific literature.

Giga Science. [DOI: 10.1093/gigascience/giab08](https://doi.org/10.1093/gigascience/giab08)

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Sven David Mueller
Leibniz-Institut DSMZ

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