The international political process around Digital Sequence Information under the Convention on Biological Diversity and the 2018–2020 intersessional period

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Societal Impact Statement
The international conservation of biological diversity is addressed under the Convention on Biological Diversity (CBD) and goals for the next decade will be discussed at the next Conference of the Parties. One issue under negotiation in the CBD is Digital Sequence Information (DSI), which has created tension between parties calling for preserving open access to DSI who also note its importance in addressing biodiversity and the UN Sustainable Development Goals and those parties calling for fair and equitable benefit sharing from DSI. This article introduces scientists to the current debate and political process on DSI within the CBD.

Summary
Most biologists take open access to sequence data for granted. This open system, while a hallmark of innovation and collaboration for the scientific community, is being called into question as some parties to the Convention on Biological Diversity (CBD) assert that this access undermines their sovereign rights over their genetic resources and corresponding benefit sharing. The governance of sequence data and potentially other types of biological data, known in international policy circles as “Digital Sequence Information” (DSI), a placeholder term invented by negotiators, could be dramatically altered and ultimately change the way scientific research and publishing on sequence data is conducted. Many sequence-using scientists are unfamiliar with the international political processes around DSI even though it could lead to irreversible decisions that might have significant impacts on research. This paper bridges that gap by providing an overview of the ongoing political process with a focus on the most recent studies on DSI commissioned by the Secretariat of the Convention on Biological Diversity (SCBD) and what these studies forecast about the political debate. With this information in hand, the scientific community can hopefully better engage with the political process and proactively promote evidence-based decisions or even solutions that can bridge the demand for benefit sharing with the scientific need for open access to DSI.

Keywords
access and benefit sharing, Convention on Biological Diversity, CBD, digital sequence information, DSI, genetic resource, genetic sequence data, International Treaty on Plant Genetic Resources for Food and Agriculture, Nagoya Protocol, nucleotide sequence data
INTRODUCTION

Over the past 8 years, parties to the Convention on Biological Diversity (CBD) have been debating whether or not the use of sequence data should require the sharing of benefits under this international treaty. Many scientists that use sequence data as a routine part of their work, when first learning about these policy discussions that have the potential to limit or disrupt access to this critical research component, may feel a sense of concern, disbelief, or even resentment. After all, these data cost significant financial and personnel resources to generate and understand, are available to the entire world, and are often used towards research for the public good—biodiversity, health, and agriculture. These concerns are understandable and valid, but, as scientists, we also have a responsibility to look objectively at the situation and understand the political nuance and complexity.

This article brings readers up-to-date on the current state of the policy discussion around digital sequence information (DSI), sovereign rights, and benefit sharing. We explore what the ongoing policy process shows us about where the decision around DSI could go and what the studies commissioned by the Secretariat of the CBD (SCBD) tell us about the scientific and legal landscape. The goal of this paper is to encourage more scientists to engage in the search for practical, evidence-based compromise in order to avoid worst-case outcomes. Because of the political deadlock, the complex CBD policy process, and lack of a common language between scientists (highly comfortable with DSI, databases, and technical details) and policymakers trying to resolve historical injustices, it can be extraordinarily challenging for scientists to understand how and where they can make a difference. Because the ongoing SARS-CoV-2 pandemic has delayed the DSI decision by at least a year, this article can hopefully inspire scientists, the primary users of DSI, and, thus, those with the most at stake, to engage and search together for compromise.

1.1 The concept of access and benefit sharing

The CBD, opened for signatures in 1992, states as its third objective, after conservation and the sustainable use of biodiversity, "... the fair and equitable sharing of the benefits arising out of the utilization of genetic resources..." (Secretariat of the CBD, 1992), which is commonly referred to as Access and Benefit Sharing (ABS). The term "genetic resource" refers to "genetic material of actual or potential value" (Secretariat of the CBD, 1992), which can range from the whole organism down to DNA, proteins, or even metabolites. The idea behind the third objective is that the country from which a genetic resource originated should also benefit from any (monetary or nonmonetary) value generated from that genetic resource. Ultimately, this should motivate countries and indigenous people to preserve and sustainably use their biodiversity.

In order to strengthen ABS, the Nagoya Protocol (NP) on ABS came into force in October 2014. It requires anyone wanting to access or use a genetic resource from a country that is party to the NP to notify a designated representative or agency, called the national focal point, and sign a transfer/use agreement based on prior informed consent and mutually agreed terms (MATs; Secretariat of the CBD, 2011). The legal "hook" to the NP is that all parties (signatory countries) must check the compliance of their domestic users with these foreign agreements, the principles of which are further explained in Greiber et al. (2012).

1.2 Why is DSI a political issue?

Although countries can exert sovereign rights over their biological diversity, many parties now argue that the digitalization of biological information and genomic technologies, combined with advances in synthetic biology and genome editing, enables users to bypass the system established by the CBD and its NP. The data explosion in "Omics" technologies raises overarching concerns about the dematerialization of genetic resources, especially the rapid advancement in sequencing technologies and their connection to synthetic biology (Gilliot & Gorochowski, 2020). For example, a complete genome of a plant variety can be openly accessed via GenBank, and tools like CRISPR-Cas enable rapid modification of the genome of a local plant, possibly making physical access unnecessary. In general, the fear is that as more biological information is published online, the easier it is to synthesize and edit genetic sequences, and the more fundamental principle of ABS is threatened.

These rapid improvements in DNA sequencing and biotechnology were simply not foreseen by policymakers in 2010, and some parties argue that a loophole has thus been created. At the same time, the open access to sequence data provided by public sequence databases is a basic requirement for research in the life sciences, including biodiversity protection and research on pathogens. While the scientific community thrives on openness and public availability of sequences, many countries fear that open access undermines their sovereign rights. This conflict will likely require compromise from both sides, and scientists working with sequence data should be informed and, ideally, involved in this debate.

2 OTHER INTERNATIONAL FORA AND TREATIES AROUND DSI

Although the focus of this article is on the DSI–CBD intersection, several other international organizations and instruments are currently discussing the governance of DSI and whether DSI should be regulated (Lawson et al., 2019; Smyth et al., 2020).

The sovereign rights provided by the CBD and NP exist in parallel to the intellectual property rights provided by the World Intellectual Property Organization (WIPO). Sequence data, if relevant (to enable the intellectual property rights provided by the World Intellectual Property Organization (WIPO). Sequence data, if relevant (to enable a practitioner skilled in the art to reproduce the invention), are already disclosed within a patent application and usually simultaneously submitted to the International Nucleotide Sequence Database..."
All pathogens (except pandemic influenza, which is handled within a specialized instrument under Art. 4 of the NP) are within the scope of the CBD and NP. As the current pandemic caused by SARS-CoV-2 has highlighted, the rapid sharing of pathogen genetic resources and DSI (called genetic sequence data under the auspices of the World Health Organization, WHO) is essential, as every delay or missing information can have wide-reaching effects on public health. In 2007, Indonesia refused to share influenza samples, as the country feared that developed medications would be unobtainable to its population. This ultimately led to the creation of the multilateral Prepared Influenza Preparedness (PIP) Framework in 2011 (Fidler & Gostin, 2011). The issue of DSI/GSD is subject to robust discussion within the PIP framework, but so far, the multilateral framework has been a successful instrument to reconcile the different perspectives and needs of stakeholders, while enabling the benefits for global health (Nicholson et al., 2019). The example of SARS-CoV-2 emphasizes both the need for an expanded multilateral benefit-sharing mechanism for public health emergency-causing pathogens or even all pathogens as well as a timely resolution to pathogen DSI/GSD discussions, and indeed there is an active, but pandemic-delayed, policy dialog underway between the WHO and CBD.

The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) under the auspices of the Food and Agriculture Organization (FAO) of the United Nations aims to support food security by acknowledging farmers’ rights and establishing a multilateral system of ABS. Like the PIP framework, the topic of DSI is currently a major topic within the ITPGRFA (Aubry, 2019; Heinemann & Thaler, 2018; Welch et al., 2017), and recent negotiations in November 2019 fell apart at least in part because of the DSI issue. Both ITPGRFA and WHO frameworks have the potential to set up rules for specific subsets of DSI that are crucial for humanity beyond the scope of environmental protection and economic endeavors.

Finally, the United Nations Convention on the Law of the Sea (UNCLOS) governs international waters and the deep sea. As these areas belong to no nation, there is an opportunity for a “holistic” ABS system that does not divide up DSI and GR. Therefore, the ABS focus is perhaps more straightforward within UNCLOS where the balance is how to foster biodiversity protection, access to GR and sequencing, while sharing the benefits (Rabone et al., 2019).

### 3 | THE CBD PROCESS FOR DSI

The topic of DSI was first introduced in the 13th Conference of the Parties (COP) in December 2016 (Figure 1). COPs are the decision-making tool of the CBD; the 2 years between each COP are “intersessional periods” used for submeetings and information gathering. On controversial issues, the parties can convene a technical expert meeting, called an Ad Hoc Technical Expert Group (AHTEG), which is composed of individuals nominated by parties and relevant stakeholders, for example, science associations or indigenous communities. Parties can also call for studies on the topic, which are commissioned and supervised by the SCBD. Before COP, the Subsidiary Board on Scientific, Technical and Technological Advice (SBSTTA) meets to discuss technical and scientific issues and prepare initial documents that will be discussed during the COP.

![Figure 1](image-url)
Figure 1 shows the sequence of meetings in which DSI was and will be discussed. The procedure is common for controversial issues within the CBD, except for two aspects that stand out for DSI. The first aspect is that a total of four different studies on DSI were commissioned at COP 14 rather than just one. This can be seen as further demonstration of the disagreement among parties, but the unprecedented number of studies also shows the complexity of the DSI topic. The second aspect is that the findings of the 2020 AHTEG will not be discussed in the SBSTTA, as in the 2016–2018 intersessional period, but rather within the Open-ended Working Group (OEWG), specifically under the third meeting of the OEWG (OEWG 3) for the Post-2020 Global Biodiversity Framework (GBF; Secretariat of the CBD, 2020a, 2020b). The GBF will lay out the goals of the CBD for the next decade (2030) and beyond (to 2050) and allocates its funds. The decision to put the topic of DSI not under the SBSTTA but under the OEWG and thus tie it to future biodiversity goals, targets, and financing means that DSI becomes an “all or nothing” issue. Should no agreement on DSI be achieved, the GBF and, thus, progress on biodiversity loss and conservation over the next decade or more would be in danger, which thereby increases pressure on parties that so far have disputed an integration of benefit-sharing for DSI into the CBD.

4 | THE STUDIES ON DSI

The scientific studies commissioned by the SCBD have a particular importance for the discussions within the CBD, as parties have to take the studies and their findings into consideration and are therefore allowed an extensive feedback process (called peer-review but not to be confused with the scientific peer-review process). This also means that these studies are highly visible for representatives of parties and stakeholders, which is often not the case with publications in peer-reviewed journals. The first study on DSI was drafted in 2017 (finalized in 2018), after the topic of DSI was put onto the agenda of the CBD. It is called the “Fact finding and scoping study” (Laird & Wynberg, 2018) and provides an introduction on DSI and its utilization. (Note: The following three studies were commissioned in the 2018–2020 intersessional period, and the “numbering” starts again at 1 in spite of the first 2017 fact-finding study.)

4.1 | Study 1: Concept and scope

Study 1 on DSI Concept and Scope (Houssen et al., 2020) gives an overview of all information that can be obtained/linked to a biological sample and deals with the question of how DSI could be defined. The advances and the decreasing costs in sequencing are explained, as well as the rise of “Omics” technologies, which generate vast quantities of biological information.

It may seem self-evident that in order to discuss possible regulation of DSI, that term would need a clear definition. However, until Study 1, there was only a placeholder list of things that could potentially fall under the term DSI, established by the AHTEG in 2018 (Secretariat of the CBD, 2018), which was never taken up by SBSTTA and was viewed by many as being unrealistic. Study 1 gave four consecutive options for defining DSI, with each option containing and expanding the previous one. The structure of the options provided by Study 1 was generally adopted by the AHTEG report in 2020 (Secretariat of the CBD, 2020a, 2020b), as shown in Table 1 and which will be discussed at OEWG 3 and taken up at COP15.

The three groups of Table 1 are cumulative (i.e., Group 2 includes Group 1) and cover the whole range from a narrow to a broad definition for DSI. This allows stakeholders and experts to assess impacts and feasibilities of different policy options for every of the three different groups in detail, in turn, allowing policymakers to make informed decisions. Without definitions and data, policy discussions are blurry because parties and stakeholders choose definitions and data suitable to their position and political strategy. Importantly, the information listed under “associated information” is not likely to be in the definition of DSI.

In summary:

- Three biological groups exist as potential definitions for DSI.
- The larger the group, the more aspects of biological information are covered, and the thinner the connection to the physical genetic resource becomes, and the less likely that tracking and tracing mechanisms will be feasible.

4.2 | Study 2 + 3: Traceability and databases

Due to their thematic connectedness, the studies on traceability of DSI and on public and private databases on DSI were merged together into one combined large study (Rohden et al., 2020).

4.3 | Overview of public DSI

As no agreed definition of DSI existed, the study used nucleotide sequence data (NSD) as a starting point to facilitate quantifiable analysis, databases, and the associated traceability system within scientific publishing of NSD. The usage of the term NSD in Study 2 + 3 is equivalent to Group 1 (Table 1). The largest and core public collection of NSD is held within the INSDC, consisting of GenBank, EMBL-EBI, and the DNA Data Bank of Japan (DDBJ), three different databases that synchronize and mirror their datasets. Because their dataset is identical, the GenBank platform was used as representative of the whole INSDC throughout the study.

This analysis shows that NSD in the database are biologically diverse and that not all DSI in them is “under the CBD” (e.g., human genetic resources, influenza flu virus, and some food and agriculture plants). There are two data subsets that represent “grey areas” under the CBD: model organisms and “other/synthetic” sequences (Figure 2). Model organisms contain many organisms of different
### TABLE 1 Clarifying the scope of digital sequence information on genetic resources

| Information related to a genetic resource | Genetic and biochemical information | Asssociated information |
|------------------------------------------|-------------------------------------|-------------------------|
| **Group reference**                      | **Group 1**                         | **Group 2**             | **Group 3** |
| High-level description of each group     | DNA and RNA                         | Group 1 + proteins + epigenetic modifications | Group 2 + metabolites and other macromolecules |
| Examples of granular subject matter      | Nucleic acid sequence reads;        | Amino acid sequences;   | Information on the biochemical composition of a genetic resource; |
|                                          | Associated data to nucleic acid reads; | information on gene expression; | Macromolecules (other than DNA, RNA and proteins); |
|                                          | Noncoding nucleic acid sequences;   | Epigenetic modifications (for example, methylation patterns and acetylation); | Cellular metabolites (molecular structures); |
|                                          | Genetic mapping (for example, genotyping, microsatellite analysis, and SNPs); | Molecular structures of proteins; | Other types of information associated with a genetic resource or its utilization. |
|                                          | Structural annotation.              | Molecular interaction networks. | |

**Note:** The table from the 2020 AHTEG report shows the three different groups that could be used as definition for DSI, as well as associated information and examples for each.

**Abbreviation:** SNPs, single-nucleotide polymorphisms.

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A key political and scientific aspect surrounding DSI is where NSDC entries were sourced from, that is, what their country of origin originally was (not where they were sequenced). When sequences are uploaded, a field for the country of origin (https://www.ncbi.nlm.nih.gov/GenBank/collab/country/) can be filled out by the submitter. Sixteen percent of NSDC entries have a valid country field, and their distribution is depicted in Figure 3. China and the United States are the primary countries of origin and, together with Canada and Japan, make up over half of all sequence entries with a country tag. This may not be surprising for biologists, but within the CBD and the NP, many policymakers initially supposed that DSI origin mirrors macroorganism biodiversity distribution patterns, which would mean DSI is predominantly sourced from mega-biodiverse countries (LMICs) that are often low- and middle-income countries (LMICs). Based on the current NSDC dataset, this is not the case. Whether this pattern will change and more DSI will originate from LMICs, which are often low- and middle-income countries (LMICs) that do not claim sovereign rights over their sequences, will likely increase over time.

The DSI geographic distribution patterns also have additional legal implications, as the United States, Canada, Japan, and much of Northern Europe that contribute DSI to the database also do not claim sovereign rights over their sequences but instead have given true access. Indeed, one unaddressed “elephant in the CBD room” is how the United States, as a nonparty to the CBD that has no seat at the negotiating table and thus no direct impact on negotiations, fits into the puzzle.
American-sourced DSI is at the top of the DSI provider list, and American scientists are at the top of the user lists. Furthermore, the U.S. Government funds one of the three INSDC databases (GenBank). In short, there are many unresolved complexities. The NSD dataset is not only biologically “mixed” (see above) but also “legally mixed” or geographically complex in terms of ABS (or the absence of) requirements.

An important conclusion from the data can be drawn here: The amount of sequences that would not fall under any ABS obligations (if a DSI framework is based on individual sequences), either due to it being not applicable (model organisms, human, synthetic, etc.) or coming from countries that do not have ABS obligations, is quite significant.

Because the country data are critical for political discussions, it was important to test whether country information is filled out correctly. A set of 150 random sequences with country information were analyzed manually by reading associated publications. For all sequences (86) for which a publication was available, the country field was correctly filled out (no errors found).

Although the country field is highly accurate, only 16% of sequence entries in GenBank have country information available. Although sequences will sometimes not have a country of origin, this percentage still seemed very low. The study authors showed that in 43% of cases, NSD with no country information should have listed country information based on descriptions given in the publication. (For the other 57%, the absence of country information seemed scientifically reasonable, i.e., of human origin, model organism or inbred lines, all of which do not normally require a country of origin). The scientific community could and should work towards increasing awareness and filling out the country field more diligently. However, a small analysis of the geographical distribution of “missing” country information (where the authors manually read the publications) showed a similar geographical distribution patterns as seen in Figure 3. This suggests that this missing country information is likely caused by oversight or carelessness on behalf of the submitting scientist rather than deception or a wish to “hide” country of origin.
4.5 | Scientific flow of DSI

The concept of “tracking and tracing” refers to the monitoring of genetic resource utilization, which is necessary for identifying user compliance and potential ABS obligations. However, tracking and tracing DSI is challenging. Once data are uploaded and publicly available, it can be downloaded and multiplied ad infinitum. A major problem for tracking and tracing is that the flow of information is not centralized. The 2020 *Nucleic Acid Research* database issue and molecular biology database collection (Rigden & Fernández, 2020) lists over 1,600 public databases that store DSI (the 2019 version used in Study 2 + 3 listed over 1,700). Even these databases do not include every repository of biological information or the DSI within scientific publications, and furthermore, most DSI-using companies have private databases and collections beyond the public databases.

The INSDC, though, is a centerpiece of NSD flow, as its databases serve as the core repository for sequences and because they create the unique identifier for sequence data, the accession numbers (ANs), which serve as an identifier used by other databases and within scientific publications. A general requirement from journals for publishing a scientific paper is that the sequences mentioned in the paper must be made publicly available, which is verified by the listing of ANs in the publication. At the same time, the open publication of a sequence also means that commercial stakeholders can access it freely and profit from it, without being monitored.

Resolving these opposing interests between the scientific community and some CBD parties will be the major challenge of any future DSI regulation. Setting up restricted and controlled access for all databases would not be possible for most of the smaller databases and put a huge and unsustainable burden on the few well-funded ones. Additionally, the download of data would need to be restricted and controlled as well, which again could severely impede scientific research. The complexity of data flow will increase even further as cloud computing is beginning to enable laboratories to put all their research data into the cloud and work jointly on the data with collaborators around the world.

Importantly, the distribution of unique users that accessed GenBank in the year 2018 (Figure 4) shows that although being distributed unevenly between countries, every country in the world and its scientists use and profit from open access to NSD. Any financial or administrative burden for accessing NSD will affect all scientists, anywhere in the world, and their ability to collaborate, share, and exchange NSD.

**In summary:**

- Sequence databases are biologically, legally, and geographically diverse.
- The country of origin of NSD in public databases does not mirror macroorganism biodiversity distribution patterns. From the available information, four countries currently contribute the majority of NSD to the databases.
- Tracking and tracing of NSD movement is challenging, especially for downloads, but sequence ANs are already in widespread use in the scientific community.
- Users of public databases are in every country of the world.

![Figure 4](image_url) Location of Digital Sequence Information (DSI) users. The world map shows, on a logarithmic scale, the unique users per country that accessed GenBank in 2018. The table on the left shows the Top 10 countries with the highest numbers of unique users and their percentage of total users (Figure 5a from Study 2 + 3, page 32)
available. As countries lose control upon open access publication of DSI, they are faced with a dilemma between prohibiting sequencing, and thus decreasing the utility of their genetic resource, or relinquishing control and taking a risk that a future commercial endeavor will not return benefits to them.

DSI is not directly regulated by the NP, and many countries do not have ABS requirements for DSI in place although it can be covered under bilateral MATs. However, so far, 15 countries have created national legislation on DSI that originated (i.e., country of origin) from the country. Another 18 countries indicated that they are in the process of or planning to generate national legislation on DSI. As this legal information is not connected to the sequence entries, researchers may often break national legislation without knowing it, creating a high amount of legal uncertainty for users. However, in many cases, the national DSI legislation distinguishes between commercial and noncommercial use. These rules are often triggered upon commercialization or patent application, leaving DSI open for noncommercial scientific access. Yet even for noncommercial use, certain procedures and necessary notifications may apply.

Brazil has a sophisticated and, so far, unique ABS system in place. Users (only Brazilians) are required to sign up to an online system, the National System of Genetic Resource Management and Associated Traditional Knowledge (SisGen), and report on use of Brazilian GR, for example, by providing information on patent applications filed, commercialization, research publications, and any distribution of Brazilian GR outside of Brazil. Although monetary benefit sharing is only required when commercial outcomes are generated, researchers are required to sign up and register, whenever they publish results based on DSI coming from Brazil (including sequences available in public database even if physical material was never accessed). However, at present, only Brazilian scientists can register themselves and their research, so scientists outside of Brazil must find a Brazilian partner to conduct research on Brazilian DSI. It should be noted that Brazil’s approach is not without critique among scientists, including Brazilians (Alves et al., 2018).

In summary, national legislation around DSI has already begun and has created legal uncertainties. Scientists accessing publicly available DSI can unintentionally overlook compliance with national legislation. And this challenge will remain unless there is harmonization at the international level. Some countries have passed legislation to prohibit having “their” genetic resources used without their consent because no international decision has been yet been reached, whereas others are waiting with that decision to see what comes out of the CBD process. If a future CBD DSI framework is adopted, more countries will likely put forward new or expand their existing legislation. When compared with the status quo, any regulation of DSI under the CBD will likely cause some challenges for international research collaborations and access to DSI. However, having internationally standardized and recognized rules around DSI and benefit sharing might be better than having a patchwork of completely different rules for every country. Furthermore, ideally, the other international fora (ITPGRFA, WHO, UNCLOS, and WIPO) should also harmonize with any new framework to minimize bureaucratic and practical hurdles for scientists working across all these fora.

In summary:

- Fifteen countries have adopted legislation on DSI; 18 more are planning to do so. These different frameworks create legal uncertainty for users.
- Different rules around DSI for every country will be more burdensome for scientists and collaborations than a single, international multilateral regulation.

5 | The Way Ahead

As our societies and economies become more and more driven by data and information, the governance of information is increasingly important. In parallel, as biodiversity continues to decline, shown once more by the latest report of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (Brondizio et al., 2019), the status quo is not acceptable and new solutions need to be found.

In the case of DSI, the debate focuses on biodiversity, benefit sharing, intellectual property, economic growth, food security, and public health. While all these aspects have various legal instruments, stakeholders, and organizations engaged, the scientific community as the primary user of DSI needs to have a strong representation at the negotiation table as well. We therefore echo the call to researchers and scientific associations to participate in the CBD process (Laird et al., 2020).

A recently published white paper by the German WiLDSI project lists five different policy options under which DSI could be governed, generate revenues for benefit sharing or environmental protection, and at the same time preserve the scientific system of open access and publication (Scholz et al., 2020). It demonstrates that the scientific community can be proactive and offer solutions to inform the policy process. Indeed these options were taken up, along with others, in a February 2021 DSI options webinar hosted by the SCBD (https://www.cbd.int/article/dsi-webinar-series-2020).

Although a range of possible solutions exist, one thing is clear: For the scientific community, a multilateral, universal framework for DSI is overwhelmingly preferable to a bilateral system, such as that in place for physical genetic resources. And a multilateral framework will be absolutely necessary for those DSI for which a bilateral approach is impossible (Bagley & Perron-Welch, 2020). The burden of having to deal with a hundred different rules and forms will place unreasonable and unfeasible burden on individual scientists, as well as discourage international collaboration. The scientific community should emphasize their legitimate concerns and help lead the way towards a multilateral, ideally universal, solution.
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