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RESEARCH ARTICLE

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Access and benefit-sharing DNA Componentry for plant synthetic biology: Bioparts expressed in plant chassis

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Societal Impact Statement

The "Parts Agenda" is an approach to synthetic biology that fragments genetic resources into functional bioparts to help design and build biological devices and systems. Access and benefit-sharing (ABS), and the issue of how to regulate digital sequence information (DSI) within the current ABS regime, poses a problem for synthetic biology because it assumes fragmented and abstracted bioparts can be traced to their country of origin for the purposes of benefit-sharing, and that contributions to information and knowledge can be quantified and appropriately valued. Any DSI regulatory solutions should account for genetic resource fragmentation and other complexities of modern scientific practice.

Summary

- The inclusion of digital sequence information (DSI, including genetic sequence data) in the existing access and benefit-sharing (ABS) regime will alter the practice of synthetic biology. The potential impediments could be magnified for the "Parts Agenda": the approach to synthetic biology that fragments genetic resources into their smallest functional units to create standardized, interchangeable "bioparts", the building blocks for assembling synthetic biological devices. These biological devices are themselves interchangeable and can be used to engineer higher order synthetic biological systems.
- This article examines how the extension of ABS laws to include DSI could foreseeably apply to the creation and use of plant-derived and other bioparts in engineered biological devices expressed in plant chassis.
- The article demonstrates that ABS issues will be similar for all approaches to synthetic biology, but that the Parts Agenda is uniquely exposed to the potential regulatory burden of bilateral ABS transactions between users and providers of genetic resources.
- The original vision for bioparts was one of openness and sharing, with access and use unencumbered by intellectual property. This article shows that open access to bioparts will not last long if DSI is enclosed within the current ABS regime, destabilizing the values of openness and sharing in synthetic biology that are ostensibly foundational to this still developing field.

KEYWORDS
access and benefit-sharing, BioBricks, bioparts, digital sequence information, Nagoya Protocol, open access, Parts Agenda, synthetic biology

1 | INTRODUCTION

The term synthetic biology means different things to different people, and there is "no one thing called 'synthetic biology'" (Campos, 2012; 116). Broadly speaking, it is the application of engineering principles to biology. The scientific techniques employed under the umbrella of synthetic biology can range from rudimentary site-directed mutagenesis, the use of standardized DNA componentry to make genetic circuits, through to highly complex genome engineering (Gray et al., 2018; 22). Whether or not synthetic biology is evolutionary or revolutionary (Bagley, 2017; Gardner & Hawkins, 2013), there is little doubt that it is heavily dependent on data about genetic resources, particularly genetic sequence data. In many ways, synthetic biology techniques and applications are utilizing genetic resources under various international access and benefit-sharing (ABS) instruments and regimes (Schiele et al., 2015; 100–107).

Multiple United Nations (UN) fora are grappling with how to incorporate digital sequence information (DSI) within ABS regimes that were originally intended to regulate the fair and equitable sharing of benefits derived from use of *physical* genetic resources (Laird et al., 2020). The UN's *Convention of Biological Diversity* (CBD, 1992) defines "genetic resources" as "genetic *material* of actual or potential value" (CBD, Article 2; emphasis added). The *Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity* (Nagoya Protocol, 2010), adopts the same definitions as the CBD, and defines the term "derivative" to mean (in part) "a naturally occurring biochemical compound" (Nagoya Protocol, Article 2), i.e., a physical derivative of a physical genetic resource. The Food and Agriculture Organization of the UN's *International Treaty for Plant Genetic Resources for Food and Agriculture* (Plant Treaty, 2001) defines "[p]lant genetic resources for food and agriculture" as "any genetic *material* of plant origin of actual or potential value for food and agriculture (Plant Treaty, Article 2; emphasis added). The focus on "materials" in the definitions for "genetic resources" means that the scope of these international ABS agreements "may not be sufficiently broad to capture genetic information" (Lawson et al., 2019; 107).

For provider countries, not including DSI within the scope of the CBD, Nagoya Protocol and Plant Treaty presents an intolerable "digital loophole" (ETC Group, 2010; 4): an opportunity for users of genetic resources to avoid benefit-sharing obligations by synthesizing genes (and elements) of interest using publicly accessible genetic sequence data rather than engaging with authorized providers of physical genetic resources to enter into an ABS agreement with the provider's prior informed consent. This loophole stands to undermine the raison d'être of ABS: "the fair and equitable sharing of the benefits arising out of the utilization of genetic resources" (CBD, Article 1), thus creating an incentive for provider countries to start regulating DSI as part of the ABS transaction (Bagley et al., 2020; CBD/DSI/AHTEG/2020/1/5). But for user countries, the enclosure of DSI in the sovereign domain of the nation state represents a threat to the professed open access principles of modern science.

While the CBD, Nagoya Protocol and Plant Treaty regulate physical genetic resources through ABS, they also all contain general obligations "intended to promote the disclosure and exchange of information", which may conflict with the idea of including DSI within the ABS transaction (Lawson et al., 2019; 104). For instance, Article 17 of the CBD on "Exchange of Information" states that "Contracting Parties shall facilitate the exchange of information, from all publicly available sources, relevant to the conservation and sustainable use of biological diversity, taking into account the special needs of developing countries" (CBD, Article 17.1) and that "[s]uch exchange of information shall include exchange of results of technical, scientific and socio-economic research…" (CBD, Article 17.2). The Plant Treaty urges Contracting Parties to "facilitate the exchange of information… on scientific, technical and environmental matters related to plant genetic resources for food and agriculture, with the expectation that such exchange of information will contribute to the sharing of benefits by making information on plant genetic resources for food and agriculture available to all Contracting Parties" (Plant Treaty, Article 17.1). This could be interpreted as requiring the sharing of DSI, including genetic sequence data, as an open access benefit generated through research on genetic resources. However, the ease with which that data can now be rematerialized in the laboratory means that keeping genetic sequence data openly accessible undermines ABS as a tool for ensuring equity and fairness between providers and users of genetic resources.

As a field "[p]oised on the boundary of the informational and the material" (Hilgartner, 2012; 189), synthetic biology is an area of modern scientific practice that is particularly exposed to the DSI policy conundrum. This article will employ the "relatively narrow circuit-based definition" of synthetic biology (Gray et al., 2018; 22); what has been referred to as the "Parts Agenda" (McLennan, 2018; 301). That is, the construction of biological devices and systems using standardized, modular DNA componentry referred to as bioparts. Narrower still, it will look specifically at bioparts for genetic devices that are expressed in plant chassis. This article will examine the various elements that can make up plant synthetic biology devices and systems that could be subject to benefit-sharing obligations under international ABS instruments (including prior informed consent, and mutually agreed terms). The article concludes that even if synthetic biologists are not accessing physical genetic resources from provider countries, there may still be a requirement to share benefits associated with the use of DSI, including genetic sequence data, even if that data has been

significantly altered through human intervention (as is the often case with bioparts) (see Part 2). The legal obligations on users of genetic resources to share benefits with countries of origin can apply to bioparts that were synthesized in the laboratory using downloaded genetic sequence data, and using multiple bioparts originating from multiple jurisdictions could lead to the accumulation of many difficult to trace and enforce legal obligations in a single synthetic product (see Part 3). Using examples drawn from plant synthetic biology, this article aims to help practitioners understand how the regulation of DSI at multiple international ABS fora (and its implementation in domestic laws) will potentially impact their own research. After calls for greater involvement (Laird et al., 2020), scientists are becoming more active in this space (e.g. Scholtz et al., 2020). Their voices are required to ensure their specific needs are accommodated in the legal and regulatory solutions to this problem that will otherwise be adopted in their absence.

2 | DIGITAL SEQUENCE INFORMATION: BIOPARTS FOR PLANT SYNTHETIC BIOLOGY

Synthetic biology can take what is already in nature and modify it in a top-down approach. However, where synthetic biology can really distinguish itself from earlier biology practices is when it takes a bottom-up approach to biology, looking to design and create de novo something that was not in nature to begin with, but was perhaps inspired by nature (Roberts et al., 2013; 1,219). This is where the "Parts Agenda" comes in to play (McLennan, 2018; 30–32). This is a reductionist approach to synthetic biology where biological entities are fragmented into building blocks, and new entities can be designed and engineered using those building blocks.[1] The Parts Agenda starts with standardized, interchangeable "biological parts" (also called "bioparts") with well-characterized functions, made of DNA. These bioparts can be assembled into basic biological "devices", i.e., the smallest assembly that can perform a specified function, such as a basic biological circuit (e.g., an on or off switch) or the translation of a particular protein coding sequence. In turn, these devices, which are themselves interchangeable, can be assembled into "systems" to perform a regulated (programmable) higher-level function within a cell or organism (chassis), such as synthesize a metabolite in response to certain environmental cues (see Baldwin et al., 2016; 73–88).

The Parts Agenda was founded on an ethos of sharing and openness and the creators of BioBricks, the most well-known type of biopart, worked tirelessly to ensure that they would be freely available online (Campos, 2012). Users of BioBricks could take what they needed from the Registry of Standard Biological Parts and would be expected (though not obliged) to contribute back to the Registry any BioBricks they had created themselves (Hilgartner, 2012). The founders wanted to keep BioBricks free of intellectual property so as not to have layers of licensing agreements on new devices that could foreseeably grow to include "50–1000 components" as synthesis technologies continued to improve (Campos, 2012; 127). What they quickly found was that ideals of openness and sharing were not enough – they were always having to walk a tightrope between these ideals and other interests and restrictions, such as market viability (Campos, 2012; 128) and free-riders (Hilgartner, 2012; 193). Open access is rarely as open as it first seems.

Bioparts are both material and immaterial. They exist materially (in physical form in laboratories and in biological devices and systems constructed in laboratories), and while they can be physically exchanged between collaborators, their primary route of transmission between laboratories around the world is over the World Wide Web as digital entities (signs and symbols that represent the physical form). These entities exist in online databases, repositories of DNA parts listing both their DNA sequence and metadata about the characteristics and function of the biopart. They also exist in Computer-Aided Design (CAD) software programs, where synthetic biologists plan biological devices in silico during the "design phase" of the iterative "Design, Build, Test, Learn" engineering cycle (Gray et al., 2018; 17), before being synthesized (rematerialized) and assembled in the laboratory during the "build phase". Publicly accessible online databases, particularly DNA sequence databases like GenBank, bioparts repositories like the Registry of Standard Biological Parts, and protein sequence databases like UniProt are considered a key enabling technology for synthetic biology (Baldwin et al., 2016; 43), and the existence of bioparts in the digital space is just one example of why this is the case – they make the parts easily and readily accessible.

The bioparts found in these repositories are not *completely* novel.[2] They make use of the genetic resources that originate in nature and then recycle them, sometimes modified, sometimes simply isolated from their surroundings, as biopart outputs (Rhodes, 2014; 167). Therefore, the bioparts (or the expression of those bioparts as nucleotide sequences in online repositories or databases) used in

[1]The most famous bioparts are "BioBricks" which were developed by the "leading promotors" of this approach to synthetic biology, including Thomas Knight, Drew Endy, Randy Rettberg and Adam Arkin. Stephen Hilgartner refers to this group as the "BioBricks group" who led the development of "open synthetic biology based on freely available parts" (Hilgartner, 2012; 196). In addition to BioBricks, there are other "syntaxes" that differ depending on the DNA assembly methods and chassis (cells and organisms) of choice. In 2015, Nicola Patron and collaborators proposed a plant-specific assembly standard for plant bioparts, noting that plants are an "ideal chassis for synthetic biology" and having a plant-specific compatibility standard would increase the number of interchangeable genetic tools available to plant synthetic biologists, accelerating innovation in the field (Patron et al., 2015; 13).

[2]The ability of synthetic biology to generate "novel" bioparts depends entirely on what you consider novel. It is worth noting that the use of rational design strategies in synthetic biology are generating products that are getting further and further away from anything found in nature (see, e.g., Peyret et al., 2019 and Cai et al., 2020). If you subscribe to the view that there is nothing genuinely new under the sun, then you may not consider *any* bioparts to be truly novel. But to say that synthetic biologists are simply mimicking nature or tinkering with what nature has already supplied does not come close to adequately describing the current (or future) capabilities of the field. (See the discussion of novelty in synthetic biology, including the use of the term "de novo", in Delgado and Porcar, 2013).

synthetic biology trace their origins back to a genetic resource, or a combination or hybrid of genetic resources found in nature. Those genetic resources may have originated from areas beyond national jurisdiction (such as on the high seas) or from the territory of a nation state. If from the latter, that state regulates access to those genetic resources within their domestic laws either through laws imposing ABS obligations or open access and use (no regulation). Even genetic resources obtained from the high seas in areas beyond jurisdiction may not be exempt from ABS obligations for much longer, with negotiations at the UN *Convention on the Law of the Sea* (UNCLOS) likely to implement benefit-sharing obligations for the use of marine genetic resources (Humphries & Harden-Davies, 2020). All of this is to say that even with extensive modification and human intervention, the DNA componentry (bioparts) used in synthetic biology could be traced back to a physical genetic resource (see Section 4), the use of which potentially falls within the positive obligations of international or national ABS laws. The conception of ABS under the CBD, Nagoya Protocol and Plant Treaty all assume that genetic resources have a clearly identifiable country of origin, that they can be atomized into identifiable parts, tracked and traced through times and interactions with other information and knowledge, and the various contributions of individuals and countries identified, acknowledged, respected and valued. The ABS problem, then, is how the direct and indirect contributions to scientific research and development *can be* properly identified, acknowledged, respected and valued.

The various international ABS instruments (the CBD, Nagoya Protocol and Plant Treaty) are all silent on this matter and it, like most other issues of ABS and interpretation, is left to the nation state to determine when implementing their own legislative, administrative or policy measures for the use of *their* genetic resources. When judging whether bioparts should be subject to benefit-sharing obligations, any thresholds for novelty or non-obviousness (i.e., how different the biopart is to anything found in nature) from patent law are irrelevant here as ABS is not part of patent law. Furthermore, "unlike intellectual property which is a term-limited monopoly, sovereignty may be interpreted as a more enduring form of monopoly rights: a conceptual 'tether' that links genetic resources to their place of origin, perhaps in perpetuity" (Rourke, 2020; 36 employing Hinterberger & Porter's, 2015 "tether" concept). So, countries are free to decide in their domestic ABS measures, and even on a case-by-case basis, whether or not a biopart used in a biological device is sufficiently connected with their original sovereign genetic resource (in terms of sequence homology or temporality) to require some form of benefit-sharing. Indeed, *any* threshold of novelty, non-obviousness or connectedness to nature may simply be irrelevant to some. In 2010, the ETC Group, an international environmental and sustainability action group based in Canada, recommended that "[t]he construction of genetic parts, 'biobricks,' metabolic pathways and synthetic chromosomes for use in synthetic biology should be included under an international ABS regime *whether or not those parts are derived from naturally occurring analogues*" (ETC Group, 2010; 4, emphasis added). If a biopart is simply inspired by a natural genetic resource, then it may be subject to benefit-sharing obligations.

On the issue of temporality, many popular bioparts and chassis used in plant synthetic biology are from plants that have long been model organisms, grown in the laboratory for many generations prior to the entry into force of the CBD, Plant Treaty or the Nagoya Protocol. The temporality issue is whether these agreements apply only prospectively to materials collected from nature *after* the ABS schemes entered into force, or whether the terms "utilization" in the CBD (Articles 1 and 15.7) and Nagoya Protocol (Articles 1 and 3) and "use" in the Plant Treaty (Articles 1.1 and 13.2) apply to each and every utilization/use irrespective of when the materials were collected. This is an issue of interpretation and the use of ex situ genetic resources collected prior to the adoption of the CBD may not present the ABS exemption some may think it does. The CBD and Plant Treaty are silent on the meaning of "utilization" and "use", respectively, but the Nagoya Protocol addresses it directly through its definition of "utilization". "Utilization of genetic resources" "means to conduct research and development on the genetic and/or biochemical composition of genetic resources, including through the application of biotechnology" (Nagoya Protocol, Article 2). Thus, any new instances of utilization of genetic resources collected *at any time* could be subject to benefit-sharing obligations depending on the favored interpretation of the originating state. If genetic sequence data are regulated as genetic resources, the same would likely be true for the utilization of DSI, and this would apply to each and every "utilization" and "use", whether searching sequences on databases in the "design" of a component, deploying a common laboratory technique (e.g. using a commercial plasmid) in the "build" of a component, or experimenting with the component to develop a commercial product in the "test" phase. This also raises the next issue – stacking.

3 | BENEFIT-SHARING "STACKING" FOR MULTIPLE BIOPARTS IN SYNTHETIC DEVICES AND SYSTEMS

A simple device constructed of bioparts might consist of a promotor, a ribosome binding site (RBS), a protein coding sequence (CDS), and a terminator sequence. These bioparts are assembled into an expression vector (a plasmid) and expressed in a host cell, or chassis. In this rather basic example, we are imagining the use of four bioparts, plus the plasmid and the chassis, that is a minimum of six genetic resource inputs, all of which could be derived from different organisms. Additionally, there could be other genetic resources used as tools in the process of creating a device using DNA componentry, such as bacteria required for transformation into the chassis. And multiple devices would come together to make a system.

So far in this very basic hypothetical assembly there are several genetic components that could have benefit-sharing obligations attached to them. Like royalty payments that are made on licensed inputs to research and development (Brett-Major, 2020; 142),

benefit-sharing obligations could start to "stack" from the various bioparts (and processes used to develop these bioparts, e.g., proprietary enzymes, reagents, methods, machines and so on) that are used in synthetic biology products. This is the very same reason the founders of BioBricks fought to keep them free of intellectual property (Campos, 2012; 127); they were concerned patents on individual BioBricks could create legal barriers to using those components thus slowing innovation in the field. If these bioparts are from different organisms originating from nation states with ABS laws that regulate the use of DSI, benefit-sharing obligations could accumulate to the point where the use of bioparts is not commercially viable (see Heller & Eisenberg, 1998). Too many claims will render the negotiations too complex and hence unworkable.

4 | FROM WHERE COULD BIOPARTS, CHASSIS AND RESEARCH TOOLS BE SAID TO HAVE ORIGINATED?

If ABS is to be employed as the tool for sharing the benefits associated with research and development in the biosciences, then the problem becomes one of working out where the genetic resource (and therefore, associated DSI) originates in order to direct those benefits to the authorized providers. This traceability problem can be difficult for physical genetic resources collected from nature, but the problems are magnified in the context of synthetic biology where genetic resources are both material and immaterial (represented as DSI), are fragmented, modified and spliced together with elements from other genetic resources. In this context, it can be difficult to determine what is even meant by "country of origin". Some examples demonstrate the concern.

The most widely used switch in synthetic plant systems (Andres et al., 2019; 865) is "based on [a] mammalian steroid signalling pathway" from rats (Schena et al., 1991; 10,422). The dexamethasone-inducible pOp/LhGR switch is an inducible promotor, meaning there is low-level expression of the gene of interest in the absence of the inducer, in this case a steroid called dexamethasone, and high level of gene expression in the presence of the inducer (Schena et al., 1991; 10,421). In this example, the country of origin of the rats could perceivably enforce their rights over any rats used (as a genetic resource) to develop this switch. But rats are ubiquitous and have been for many thousands of years (see Aplin et al., 2003), and so all states might make claims. Or, as the evolutionary origin of rats is South Asia to Indonesia, are only these states entitled, and which ones?

Chassis species too could be subject to benefit-sharing obligations in some jurisdictions. The most common chassis in plant bioengineering is *Arabidopsis thaliana*, a small flowering plant native to Europe, Asia and Africa and found (as a weed) nearly everywhere else. *A. thaliana* has been researched since the late 1800s and it was proposed as a model organism in 1943 (Meyerowitz, 2001; 15). By the 1980s this species was used widely in laboratories and scientists collected hundreds of accessions from various countries (Meyerowitz, 2001; 15). Many of these are now stored at the Arabidopsis Biological Resource Center (ABRC) at Ohio State University which shares wild-type and modified Arabidopsis seeds and DNA with researchers around the world. Presumably many countries could exercise ABS rights over Arabidopsis species used in synthetic biology applications, but after a century of collecting seeds, cultivating the plant, sharing seeds and genetically modifying them, deciphering precisely which entity might be able to claim such rights to specific accessions could be difficult. The problem for synthetic biologists is that practitioners, as the users of genetic resources, are the party responsible for conducting due diligence. It is not up to the provider (or the entity with possible rights over the genetic resource or associated DSI) to find instances of use in order to attempt to exercise those rights. But it is difficult to know what uses of genetic resources are being regulated by ABS, and how far from the origin that regulation can reach.

Another plant chassis, growing in popularity, is *Nicotiana benthamiana*. This plant is native to northern parts of Australia and was used as chewing tobacco by Australia's First Nations.[3] Goodin et al. (2008) studied the genetic diversity of laboratory accessions of *N. benthamiana* and found that it is probable that they come from a single source (Derevnina et al., 2019; 608). But there are other accessions in use. One study of the origin and evolution of *N. benthamiana* used an isolate that was more than 50 years old, a transgenic line created in the United Kingdom in the mid-1990s (presumably from *N. benthamiana* plants originally from Australia, though this is not explicitly stated, see Ruiz et al., 1998; 944), and a series of wild accessions that appear to have been collected specifically for the purposes of this origin and evolution study (Bally et al., 2015). This study is interesting from an ABS perspective because it uses isolates with three different ABS temporal statuses: the 50-year-old isolate was collected many decades before the CBD, the transgenic line was created after the CBD entered into force but before the Nagoya Protocol, and the newer accessions were collected anew after the entry into force of the Nagoya Protocol. Australia is party to the CBD but not to the Nagoya Protocol, but the use of various isolates of *N. benthamiana* (which can all ultimately be traced back to Australia) from different time points highlights that the use of the same species from the same country could carry different legal obligations depending on the time of collection or use.

Oftentimes, to get a synthetic device that is assembled within a plasmid into the chassis organism, plant synthetic biologists may need to employ a shuttle chassis such as *Agrobacterium tumefaciens* (Boehm et al., 2017; 3). Agrobacterium-mediated transformation is a popular research tool in plant synthetic biology. The bacteria were first isolated in Italy in 1897 from plants with Crown Gall disease (Kado, 2014; 1), but its use as a transformation

[3]This article will not address the various Traditional Knowledge (TK) provisions in the CBD and Nagoya Protocol (see Rourke, 2018) that, in effect, create some of the same ABS obligations for the use of TK associated with genetic resources belonging to Indigenous Peoples and local communities (like prior informed consent and coming to mutually agreed terms). But this is yet another complicating element of accessing and utilizing genetic resources that could well apply to bioparts and other synthetic biology tools.

vector was not recognized until 1977 (Kado, 2014; 7). As bacteria, *Agrobacterium* species are themselves genetic resources within the remit of the CBD and Nagoya Protocol, and therefore, the informal sharing of *Agrobacterium* cultures within the research community would need to be formalized under these international instruments. Again, what this means for researchers using this research tool is unclear.

5 | DISCUSSION: TRACKING AND TRACING NUCLEOTIDES?

While the ABS issues explored in this article and in this special issue of *Plants, People, Planet* are not qualitatively different for the Parts Agenda, they do differ in terms of magnitude and likely impact. The many bioparts used in a single device could be sourced from (or inspired by) multiple genetic resources and could theoretically be subject to separate benefit-sharing obligations with multiple countries of origin, with obligations stacking upon obligations, and possibly conflicting with each other. This article provides an indication of just how complicated the ABS situation could become for those designing and building even the most basic of genetic devices using bioparts for expression in plant chassis.

Access and benefit-sharing laws have been in place since the entry into force of the CBD in 1993. They were designed to help achieve equity and fairness in research and development, and to deal with bioprospecting and the risks of exploiting genetic resources – to generate benefits to ensure the conservation and sustainable use of those genetic resources (CBD, Article 1). The ABS model assumes a clearly identifiable provider and user agreeing about the possible uses of a distinct and simple physical material (e.g., a leaf), and that the provider and user can reach an agreement about benefits in the form of a mutually agreeable contract enforceable through a well-resourced and structured legal system.

But when the layers of abstraction are manifold, as is the case when a biopart barely resembles anything found in nature, when the genetic sequence has been modified (e.g., optimized for the chassis species), when the "thing" being accessed is information and that information originated from a plant that was collected a century ago and propagated in laboratories around the world since, it is harder to determine what best practices should look like. If DSI were included within the current ABS regime, then the regulatory burden for synthetic biologists working with bioparts would be enormous, while the likelihood of any benefits being channelled to originating nation states in a fair and equitable manner are minimal. And this is to say nothing of the conservation and sustainability objectives of these international instruments which appear to have fallen by the wayside in much of the discussion about ABS (Laird et al., 2020).

Given that bioparts exist as both physical DNA componentry and as genetic sequence data on the internet, and that some jurisdictions have already started regulating the use of DSI in their domestic laws (Bagley et al., 2020 CBD/DSI/AHTEG/2020/1/5), some may be left wondering why ABS has not already posed a problem for plant synthetic biologists? In part, plant synthetic biology has been left alone, invisible to ABS rules because it is generally using materials that were collected from in situ conditions prior to the entry into force of the CBD. Many of the model organisms common in the field have been propagated in the lab, shared informally, or sold commercially for decades. But if DSI is incorporated into the existing ABS frameworks at the international level, then the informal exchange of plant-derived bioparts, chassis and research tools like *A. tumefaciens* will likely be impeded (at the very least, it may become hidden). As this article demonstrates, for the current ABS regime to work in synthetic biology applications, each component biopart needs to be considered as the composition of its sub-parts and the origin of each of the sub-parts identified (perhaps down to the level of each base pair). The contributions of any tools in the construction of these bioparts, devices or systems will also need to be identified, and if DSI is included then all information engaged by each component biopart will need to be tracked and traced. Furthermore, academic (non-commercial) researchers should not operate under the assumption that they would be exempted from ABS or ABS-related restrictions if DSI is captured within ABS frameworks. A similar assumption about patented research tools quickly became problematic for academic researchers (Mirowski, 2011; 149–152), who "often care little about the patent status of the parts they use" (Henkel & Maurer, 2009). As Henkel and Maurer (2009) note, "[t]his is shortsighted because it may be expensive to replace patented parts if and when a project is later commercialized". The cost of replacing parts might be the least of a researcher's worries if they are accused of biopiracy under another country's domestic ABS laws, some of which carry harsh penalties including imprisonment (Rochmyaningsih, 2019).

6 | CONCLUSION

The ABS regulations that were designed for simplistic conceptions of bioprospecting activities are now having to meet the challenge of regulating scientific processes that employ a level of abstraction that the negotiators of the CBD and Plant Treaty could never have imagined. Some countries have indicated that they will not implement domestic measures on the regulation of DSI until consensus on the issue is reached at the international level (Bagley et al., 2020, CBD/DSI/AHTEG/2020/1/5; 11). International negotiations for the incorporation of DSI into existing ABS frameworks need to take into account the complexities that arise when using different scientific approaches like the Parts Agenda in synthetic biology. The growing calls for re-thinking ABS (see e.g., Bond & Scott, 2020; Laird et al., 2020; 31) are affirmed by the consequences for synthetic biology. The synthetic biology community made a concerted effort to keep bioparts free from intellectual property claims. Saving bioparts from one regulatory control regime only to have them captured by another will mean that bioparts will not have stayed free for long. The imperative for fair and equitable benefit-sharing arising from the use of genetic

resources is not in question. The future challenge is to find a way to deliver on these important goals without impeding the progress of synthetic biology.

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