Food and Agriculture Organization of the United Nations

COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE

THE ROLE OF DIGITAL SEQUENCE INFORMATION IN THE CONSERVATION AND SUSTAINABLE USE OF GENETIC RESOURCES FOR FOOD AND AGRICULTURE: OPPORTUNITIES AND CHALLENGES

BACKGROUND STUDY PAPER NO. 73

THE ROLE OF DIGITAL SEQUENCE INFORMATION IN THE CONSERVATION AND SUSTAINABLE USE OF GENETIC RESOURCES FOR FOOD AND AGRICULTURE: OPPORTUNITIES AND CHALLENGES

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Abbreviations

AHTEG	Ad Hoc Technical Expert Group
ABS	access and benefit-sharing
BCA	biological control agent
BOLD	Barcode of Life Data System
BRICS	Brazil, Russian Federation, India, China and South Africa
CBD	Convention on Biological Diversity
CABI	CAB International
CGIAR	Consultative Group on International Agricultural Research
CNVs	copy number variants
COP	Conference of the Parties
CRISPR	clustered regularly interspaced short palindromic repeats
CRISPR-Cas	CRISPR assisted protein
DDBJ	DNA Data Bank Japan
DNA	deoxyribonucleic acid
DSD	Digital sequence data
DSI	digital sequence information
EBI	European Bioinformatics Institute
EMBL	European Molecular Biology Laboratory
ENA	European Nucleotide Archive
FAIR	findability, accessibility, interoperability and reusability
FAO	Food and Agriculture Organization of the United Nations
G77	Group of 77 (lower-income countries) at the United Nations
GBC	Global Biodata Coalition

GBS	genotyping by sequencing
GI	genetic information
GRFA	genetic resources for food and agriculture
GRSD	Genetic resource sequence data
GSD	genetic sequence data
GWAS	genome-wide association studies
HRMS	high resolution mass spectrometry
INSDC	International Nucleotide Sequence Database Collaboration
iBOL	International Barcode of Life
LMICs	low- and middle-income countries
MAT	mutually agreed terms
mRNA	messenger RNA
NASD	Nucleotide and amino acid sequence data
NASSI	Nucleotide and amino acid sequence and structural information
NASSFI	Nucleotide and amino acid sequence, structural and functional information
NBA	National Biodiversity Authority
NCBI	National Center for Biotechnology Information
NFP	national focal point
NGDC	National Genomics Data Centre
NGS	next-generation sequencing
NIH	National Institutes of Health
NSD	nucleotide sequence data
NSI	nucleotide sequence information
OECD	Organisation for Economic Co-operation and Development
OEWG	Open-ended Working Group
PCR	polymerase chain reaction

PIC	prior informed consent
PubMed	Public/Publisher MEDLINE
R&D	research and development
RNA	ribonucleic acid
SDG	Sustainable Development Goal
SNP	single nucleotide polymorphism
WDCM	World Data Centre for Microorganisms
WiLDSI	“Wissenschaftsbasierte Lösungsansätze für Digitale Sequenzinformation” – Scientific approaches for digital sequence information

Abstract

This study discusses applications of digital sequence information (DSI) that are relevant to genetic resources for food and agriculture (GRFA), including DSI that is not derived from GRFA but nevertheless contributes to their identification, characterization, use, improvement and conservation. DSI is also fundamental to the characterization of other components of biodiversity for food and agriculture and is an important tool in efforts to make agriculture more sustainable.

Searches of CABI's literature database, CAB Abstracts, which contains 10.9 million records, revealed many examples of publications that demonstrate the important contribution of DSI to the sustainable use and conservation of GRFA. These publications cover animal genetic resources, aquatic genetic resources, forest genetic resources, plant genetic resources and microorganisms. The database searches revealed a rise in the number of publications on DSI from 20 000 in 2002 to 1 180 915 in 2022 (almost 11 percent of the records) and demonstrated a continued annual rise in the contribution of DSI to research (15 percent of the records added between 1 April 2022 and 2 June 2023). Most of the literature published up to 2022 concerned plant genetic resources. However, most of the literature citing DSI during the period April 2022 to June 2023 concerned animal genetic resources and the percentage of publications on aquatic genetic resources doubled.

Scientific literature focusing on climate change adaptation and on improving yields was found to include publications that address the discovery of candidate genes for improved abiotic stress tolerance in wheat, the contribution of DSI to progress on drought and heat tolerance in rice, use of DSI-based technologies to increase grain yield and starch content in maize, and DSI-assisted development of disease resistance and drought and salt tolerance in chickpea. These are clear examples of DSI playing an increasingly important role in research on climate change adaptation, crop production and plant health.

The increasing significance of DSI is further confirmed by the fact that the quantity of DSI available in public databases is growing exponentially: the content of the International Nucleotide Sequence Database Consortium (INSDC) exceeded 9 petabytes in 2020. Analysis of the Science-based Approaches for Digital Sequence Information (WiLDSI) Data Portal[1] demonstrates that data on biodiversity are generated globally and are being used extensively to help characterize biodiversity and to create innovative solutions to growing problems and threats.

Making DSI available through public databases does not, however, mean that it is accessible to everyone in the same way. Many countries face serious obstacles to accessing and using DSI. CABI received feedback from several of its Member Countries via its regional centres. This confirmed that the Bahamas, Brazil, China, Ghana, India, Kenya, Malaysia, Pakistan, Trinidad and Tobago, the United Kingdom and Zambia were using DSI but that in most cases the infrastructure needed to generate it and make optimum use of it were not in place. Feedback from China confirmed, however, that the country was in a good position with respect to the generation, storage, management and use of DSI.

There are currently several options on the table for how access to, and use of, DSI can be guaranteed while at the same time equitably sharing benefits associated with this use, especially within countries in need of capacity building and support in the field of GRFA conservation. There is some convergence towards a global multilateral solution, while some countries are anticipating hybrid approaches that will incorporate both bilateral and multilateral systems of benefit-sharing. However, there is currently insufficient information available to carry out a cost–benefit analysis on these options.

The key messages of this study are as follows:

1. There are many different existing and potential applications of DSI that are highly relevant to GRFA, including applications of DSI that is not directly derived from GRFA.

2. The current and potential applications of DSI show that its generation, storage, accessibility and use are fundamental to the characterization

[1] https://apex.ipk-gatersleben.de/apex/wildsi/r/wildsi/home

of GRFA and are important in efforts to make agriculture more sustainable.

3. Access to and use of DSI face serious obstacles in many countries. There is an urgent need to address the root causes of these problems, which include lack of technical infrastructure, financial and human resources, educational and training opportunities, scientific collaboration, computing infrastructure, reliable electricity and high-speed internet, and may in the future possibly include prohibitive charges for database use.

4. There is a need for a regulatory environment that facilitates access to DSI and the fair and equitable sharing of benefits arising from its use.

Introduction

This study contributes to the work stream on digital sequence information (DSI) of FAO's Commission on Genetic Resources for Food and Agriculture (Commission). It presents key practices and experiences related to the ways in which DSI is generated, stored, accessed, and used for research and development (R&D) related to genetic resources for food and agriculture (GRFA). It also explores the availability and accessibility of DSI to the research community and the private sector in all parts of the world and presents solutions currently being discussed for access to and use of DSI and the sharing of benefits arising from its use. The term "DSI" was first used by the Convention on Biological Diversity (CBD) in discussions about the issue of data on genetic resources being accessible without precipitating the benefit-sharing measures anticipated by the CBD and the Nagoya Protocol for the genetic resources themselves (CBD, 2011; 2016; 2018).

The debate began at the Conference of the Parties (COP) to the CBD and spread to other major fora such as the United Nations Convention on the Law of the Sea, the World Intellectual Property Organization, the World Health Organization and the Commission, each of which has explored how DSI affects its fields of responsibility. It has become clear from these discussions that the use of digital information relating to genetic resources delivers benefits: the current focus is on how these benefits should be shared. There has been some convergence on what DSI could cover, but the route to a solution for equitable benefit-sharing remains unclear. Given this lack of agreement and the importance of DSI to research and development, the ongoing debate is of considerable significance to the food and agriculture sector.

One argument is that the conservation of biological resources under the CBD could be supported without controlling access to DSI and sharing monetary benefits from its use. The alternative view is that, because of the direct link between DSI and genetic resources more broadly, there is an obligation to share the benefits arising from the use of DSI.

Genomics is revealing previously undiscovered biodiversity that has an important role in ecosystems and is responsible for functions that are essential to biological cycles. It also provides a deeper understanding of how organisms function and thereby enables constructive manipulation and utilization of genetic resources. These developments provide opportunities for important advances in food and agriculture. The present study provides examples of the impact of DSI and demonstrates that developments and innovations in genomics are not bound to particular species or sectors. Work on species considered to be outside the remit of GRFA may also have relevance to the field (and vice versa). The study presents examples of how the generation and use of DSI-nucleotide sequence data (NSD) enables advances in agriculture, food production and food security.

Resources used in this study (materials and methods)

To track the use of DSI, the outputs of the Wissenschaftsbasierte Lösungsansätze für Digitale Sequenzinformation (Science-based Approaches for Digital Sequence Information) (WiLDSI) Data Portal[1] were consulted. This portal provides access to data from 198 countries that can be used for biogeographical studies, exploration of collaborative networks, and profiling of access to and use of sequence data (DNA and RNA grouped as NSD). An analysis by Lange *et al.* (2021) connected publications with NSD records, geographical information and author contributions based on their country of origin to infer trends in scientific knowledge-gain at the global level. These data were further analysed to determine whether there was an imbalance in the generation and use of the data from a sample of the 198 countries.

The present study used the CAB Abstracts database to analyse growth in the generation and the application of DSI. CABI has been gathering data on agriculture for over 100 years, and much of this is presented via CAB Direct.[2] The CAB Abstracts bibliographic database is part of this resource and covers applied life sciences, including agriculture, plant sciences, animal sciences and related subjects. It contains over 10.9 million records dating from 1973 to the present (and an archive covering the period from 1912 to 1973). It is searchable on several

[1] https://apex.ipk-gatersleben.de/apex/wildsi/r/wildsi/home
[2] https://www.cabdirect.org

Table 1. Search terms used to find DSI-related studies

Search terms	Database
"digital sequenc*" or "genetic engineer*" or "genetic sequenc*" or "dna sequenc*" or "nucleotide sequenc*" or "RNA sequenc*" or "genomic*" or "gene expression" or "recombinant dna" or "ngs" or "mRNA" or "transcription" or "genetically engineer*" or "metagenomic" or "next generation sequenc*" or "genome*" or "genetic manipulation" or "molecular genetic*" or "polymerase chain*"	CAB Abstracts

Source: Authors elaboration for this background paper.

platforms including CAB Direct, which was used in this study. The search strategy employed was to filter out the DSI-related studies from CAB Abstracts and group the "hits" obtained into various categories such as "dominant crops in FAO regions", various terminologies for describing DSI, and examples of actual and potential applications of DSI in food and agriculture. The terms used to identify the DSI-related records in CAB Abstracts (Table 1) were in accordance with the three DSI groups identified by the Ad Hoc Technical Expert Group (AHTEG) on DSI on Genetic Resources (AHTEG, 2020). The analysis is described in more detail in Appendix 1.

Searches were carried out in PubMed for comparison. A direct comparison with Google Scholar was not possible because its 256-character limit for searches precluded the inclusion of all the search terms. A search for DSI on Google Scholar resulted in only 876 hits.

The following parameters were used to filter publications citing microorganism and invertebrate DSI in CAB Abstracts:

- Microorganisms gave 375 509 records [using ("digital sequenc*" or "genetic engineer*" or "genetic sequenc*" or "dna sequenc*" or "nucleotide sequenc*" or "RNA sequenc*" or "genomic*" or "gene expression" or "recombinant dna" or "ngs" or "mRNA" or "transcription" or "genetically engineer*" or "metagenomic" or "next generation sequenc*" or "genome*" or "genetic manipulation" or "molecular genetic*" or "polymerase chain*" AND ("bacteri*" OR "fung*" OR "microbe*" OR "microorganism*" OR "micro-organism*" OR "protist*")]
- Invertebrates gave 165 440 records [using ("digital sequenc*" or "genetic engineer*" or "genetic sequenc*" or "dna sequenc*" or "nucleotide sequenc*" or "RNA sequenc*" or "genomic*" or "gene expression" or "recombinant dna" or "ngs" or "mRNA" or "transcription" or "genetically engineer*" or "metagenomic" or "next generation sequenc*" or "genome*" or "genetic manipulation" or "molecular genetic*" or "polymerase chain*" AND ("invertebrate*" OR "arthropod*" OR "insect*" OR "mollusc*" OR "annelid*" OR "tardigrad*" OR "echinoderm*" OR "bryozo*")

The search terms were selected in consultation with the CABI Abstracts database managers, matching key words known to be present in the records. It was considered impractical to try and include all organism taxonomic groups.

To assess the availability/accessibility of DSI to the research community and the private sector in all parts of the world, key managers and researchers in CABI's regional and national centres carried out local enquiries with contacts, national authorities and project partners to determine the extent to which they generated, accessed and utilized DSI/NSD (see Appendix 2).

The term digital sequence information (DSI)

The term DSI was originally developed in the context of the CBD and the Nagoya Protocol, although with the caveat that it "may not be the most appropriate term and … is used as a placeholder until an alternative term is agreed" (CBD, 2018). Although it is still not clearly defined, DSI in its narrowest sense refers to digitally recorded DNA and RNA sequences. However, in many cases the term is also used to refer to data generated from proteomic studies (protein sequences) and sometimes also to data from metabolomics (relating to primary and secondary metabolites, and other chemical entities). So-called "omics"-based techniques provide genomic blueprints of microorganisms, allowing their functions and their roles in water, carbon, nitrogen, phosphorus and sulphur cycles to be elucidated (Zhou *et al.*, 2022).

There is a pressing need for an agreed definition of DSI that can encompass potential future discoveries and new technologies, but this is proving difficult to achieve. It has been suggested that the term could be taken to encompass "the kind of information in, or that might be added to, databases of the kind currently in use and collated by the scientific journal *Nucleic Acids Research*" (Heinemann, Coray and Thaler, 2018). The authors that made this suggestion cited the 2017 Database Issue of *Nucleic Acids Research* (2017), which documented 54 new databases added

since the previous review. Subsequent reassessments have been made annually, with the latest in 2022 (Rigden and Fernández, 2022). This definition is associated with, but goes beyond, DNA sequences in that it encompasses proteomics and metabolomics, which are also included in the *Nucleic Acids Research* database lists.

The AHTEG and the Open-ended Working Group on the Post-2020 Global Biodiversity Framework (OEWG) did not attempt to define DSI. Their approach was to compartmentalize the scope of DSI into three subgroups of information (Table 2) (AHTEG, 2020; OEWG, 2021a). Group-1 includes DNA and RNA. Group-2 includes Group-1 and adds proteins and epigenetic modifications. Group-3 includes Groups 1 and 2 and adds metabolites and macromolecules. However, it was not agreed whether Groups 2 and/or 3 should be considered DSI.

Data/information flows linking genetic resources and related NSD generated by research are summarized in Figure 1. According to Lyal (2022), "the main basis for accepting DSI as coming under the CBD and Nagoya Protocol is the (disputed) proposition that DSI is the 'intangible equivalent' of a physical genetic resource and as such falls under the sovereign rights of the country from which the original genetic resource was accessed." Lyal describes DNA or RNA sequences (NSD) as "the closest functional analogy between a genetic resource and an intangible equivalent" and notes that "a number of countries have apparently adopted this concept. 'GSD' (genetic sequence data) is used in the World Health Organisation pandemic influenza preparedness framework and has the same meaning. This is the Group-1 of the latest AHTEG" (Lyal, 2022).

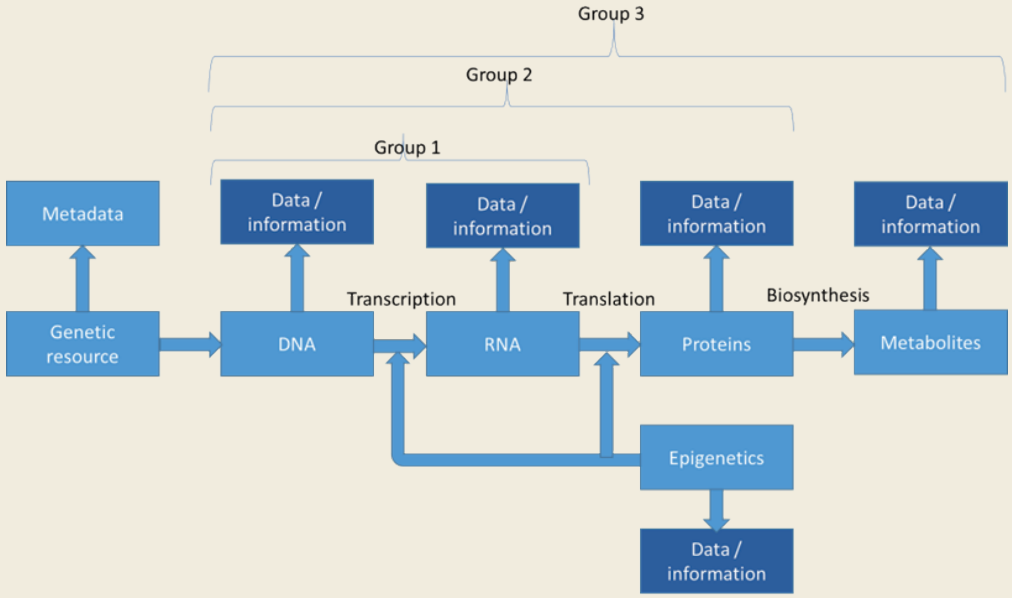
Ruiz Muller (2018) introduced the term "natural information" to the debate and defined it as "any non-uniformity, difference, or distinction not intentionally produced by *H. sapiens* which derives from thermodynamically open systems to dissipate energy gradients and create copies of itself", also putting forward the concept of "bounded openness for natural information", which includes sequence data and all "natural information" . This would include the "associated information" mentioned in Table 2. Vogel *et al.* (2022) note that a "more colloquial and

Table 2. Grouping and scope of DSI

Information related to a genetic resource				
	Genetic and biochemical information			
Group reference	Group-1	Group-2	Group-3	Associated information
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 • Associated data to nucleic acid reads • Non-coding nucleic acid sequences • Genetic mapping (e.g. genotyping, microsatellite analysis, single nucleotide polymorphisms [SNPs], etc.) • Structural annotation	• Amino acid sequences • Information on gene expression • Functional annotation • Epigenetic modifications (e.g. methylation patterns and acetylation) • Molecular structures of proteins • Molecular interaction networks	• Information on the biochemical composition of a genetic resource • Macromolecules (other than DNA, RNA and proteins) • Cellular metabolites (molecular structures)	• Traditional knowledge associated with genetic resources • Information associated with DSI Groups 1, 2 and 3 (e.g. biotic and abiotic factors in the environment or associated with the organism) • Other types of information associated with a genetic resource or its utilization

Source: AHTEG (Ad Hoc Technical Expert Group). 2020. *Report of the Ad Hoc Technical Expert Group on Digital Sequence Information on Genetic Resources*, Montreal, Canada, 17–20 March 2020. CBD/DSI/AHTEG/2020/1/7. Montreal, Canada. https://www.cbd.int/doc/c/ba60/7272/3260b5e396821d42bc21035a/dsi-ahteg-2020-01-07-en.pdf

Figure 1. The concept and scope of DSI and its generation



Source: Lyal, C.H.C. 2022. Digital sequence information on genetic resources and the convention on biological diversity. In: E. Chege Kamau, ed. *Global transformations in the use of biodiversity for research and development.* Ius Gentium: Comparative Perspectives on Law and Justice, 95, pp. 589–619. Cham, Switzerland, Springer, after AHTEG (Ad Hoc Technical Expert Group). 2020. *Report of the Ad Hoc Technical Expert Group on Digital Sequence Information on Genetic Resources*, Montreal, Canada, 17–20 March 2020. CBD/DSI/AHTEG/2020/1/7. Montreal, Canada. https://www.cbd.int/doc/c/ba60/7272/3260b5e396821d42bc21035a/dsi-ahteg-2020-01-07-en.pdf (reproduced with permission).

maybe legal definition could also be 'any non-uniform expression, difference or distinction produced by nature.'" They conclude that "natural information (biotic) captures what should fall within the scope of the CBD while excluding information that is artificial or natural but abiotic." Vogel *et al.* (2022) include "*in silico* utilization" (ISU) of genetic resources, genetic information, GSD and NSD of the biotic natural information within the natural information category. They believe that "once artificial or natural information is interpreted as the object of access in R&D, a multilateral system can be constructed in a way that all the international agreements that concern ABS become harmonious. The optimal modality is bounded openness ..." (Vogel *et al.*, 2022). The authors define "bounded openness", in turn, as "legal enclosures which default to, yet depart, from *res nullius* [property of no one] to the extent the departures enhance efficiency and equity, which must be balanced when in conflict." They go on to say that it "satisfies ... three criteria: genetic resources flow freely for R&D ...; royalties are due only on the value added through intellectual property and distributed proportional to custodianship ...; and transaction costs are minimized ..." (Vogel *et al.*, 2022).

The various concepts described here would result in different outcomes if used to define the scope of access and benefit-sharing (ABS) regimes and would result in different levels of complexity in traceability and monitoring. The ultimate outcome depends on how far into the metabolism of the genetic resource (the flow of information) the scope extends and is justifiable; human (research) intervention is required at several stages (see Figure 1). Lyal (2022) discusses the elements along the information flow illustrated in Figure 1 that "reflect the degree of biological processing and the proximity to the underlying genetic resource." Human interventions include those related to the further analysis of the raw nucleotide sequence, the technical aspects of sequencing, the "associated data" to which the AHTEG referred and metadata from the collection of the genetic resource. They also include additional information processing related to aligned nucleotide sequences, information on sequence assembly, structural annotation of genomic elements, biochemical and biological function, behavioural observations, the structure of organisms, the molecular structures of gene products and derivatives (cell metabolites, etc.), and patentable discoveries and inventions.

Table 3. Numbers of records in the CAB Abstracts citing DSI (the data pool) for the three AHTEG-defined groups

	Information related to a genetic resource			
	Genetic and biochemical information			
Group reference	Group-1	Group-2	Group-3	Associated information
High-level description of each group	DNA and RNA	Group-1 + proteins + epigenetic modifications	Group-2 + metabolites and other macromolecules	
CABI DSI data pool hits	4 965	23 246 (additional) i.e. 28 211 (Groups 1 and 2) in total	320 (additional) i.e. 28 531 (all groups) in total	All 1.8 million records in the DSI data pool

Source: Authors elaboration for this background paper.

Table 3 shows the number of hits from the CAB Abstract database for DSI Groups 1 to 3 as defined by the AHTEG. If the terms chosen by the AHTEG to characterize these groups are used to search the database for DSI, the numbers of publications found is relatively low for Group-1 (4 965 hits). When the search is expanded to include Group-2, an additional 23 246 hits are obtained, and for Group-3 an additional 320 hits are obtained. This is considerably short of the 1 180 915 hits obtained in the CAB Abstracts database using the comprehensive set of search terms listed in Table 4, where the numbers were 10- to 100-fold larger (see Section 1.2), demonstrating the complexity of the scope of DSI.

These figures reflect the research covered in the CAB Abstracts database, which in turn reflects current research in agriculture. The database contains fewer publications specifically on RNA and DNA sequences, but when searches include their direct products, proteins and epigenetic modifications (i.e. Group-2), there is an almost five-fold increase in the number of hits. The creation of the DSI data pool required the use of all relevant terms for Groups 1 to 3. The high-level description of each group, as given in Table 2, fails to find all publications citing DSI. This reflects the complexity of the subject and potentially raises issues around our ability to monitor and trace DSI usage.

Table 4 presents the list of terms put forward in the AHTEG report related to activities and processes in the generation of DSI. They represent elements of the genetic information on an organism that may potentially be utilized to generate products. When the terms presented in Table 4 were used to create the CABI DSI data pool, significantly higher hit rates were obtained, with a total of 1.18 million records found.

Aside from genetic/biochemical factors, there is a need to address the data side: published research results (see Figure 1). The process of data generation, storage and management is complex; data may be generated – or even computationally derived – from other data. For example, sequence databases contain the sequence of "bases" (components of DNA), with associated metadata describing the source of the organism from which the sequence was obtained along with related information. It is not just "data": in each case there has been some processing, and thus more "information" is included, i.e. the process includes a human judgemental element that adds to its ultimate value. This is particularly relevant to the development of any potentially valuable end product, and ultimately the generation of benefits, in that the process is one-way: it is possible to deduce a protein's composition from the gene but not the gene from the protein (or from a given metabolite). This is because more than one gene can code for the same protein (and more than one codon may code for the same amino acid).

Table 5 provides further details of the methodologies used to create DSI related to GRFA, briefly describing the uses of the technologies, the type of data produced and the number of hits obtained in the CAB Abstract database. The latter are presented under the AHTEG groups, and the number of papers in the CAB Abstracts database citing these technologies gives an indication of the extent of their use. There were 86 655 hits for genome sequencing (Group-1), 81 528 hits for proteins and epigenetic modifications (Group-2 additions) and 6 208 hits for Group-3 additions. Thus, Groups 1 and 2 had the most hits.

The technologies used to generate DSI include epigenome-guided crop improvement. The

Table 4. The AHTEG options for terminology to describe DSI on genetic resources

Group reference	Group-1	Group-2	Group-3	Associated information
Category/term	Nucleotide sequence data (NSD); Genomic sequence information; Genomics information; Nucleotide sequence information (NSI); Genetic resource sequence data (GRSD); Digital sequence data (DSD); Data on the genomic DNA (or RNA) of a sample genetic resource	Genomic and proteomic sequence information Nucleotide sequence information (NSI) and genetic information (GI); Sequence data; Nucleotide and amino acid sequence data (NASD); Nucleotide and amino acid sequence and structural information (NASSI); Nucleotide and amino acid sequence, structural and functional information (NASSFI); Functional digital information of NSD Proteomic data Genomic and proteomic sequence information Data on the macromolecular composition of a sample genetic resource	Genomic, proteomic and metabolomic information; Genetic and "omics" information; Metabolomic data; "Omics" information; Genomic, proteomic and metabolomic information; Data on the biochemical and genetic composition of a sample genetic resource	Associated information Contextual information Subsidiary information

Source: AHTEG (Ad Hoc Technical Expert Group). 2020. *Report of the Ad Hoc Technical Expert Group on Digital Sequence Information on Genetic Resources*, Montreal, Canada, 17–20 March 2020. CBD/DSI/AHTEG/2020/1/7. Montreal, Canada. https://www.cbd.int/doc/c/ba60/7272/3260b5e396821d42bc21035a/dsi-ahteg-2020-01-07-en.pdf

Table 5. Methods for analysing DSI in food and agriculture

Method	Description	Uses	Data type	CABI Search hits
Genome Sequencing (AHTEG Group-1 DSI)				
De novo sequencing	A step towards understanding the genetic component of a plant or animal's traits and interactions with the environment	Assigning map positions and breed information for subsequent resequencing to discover single nucleotide polymorphisms (SNPs) and other genetic variations	DNA sequence data free of any constraints or assumptions	9 877
Whole-genome resequencing	A comprehensive method for analysing the entire genome when a species' reference genome is available	Identifying genes, SNPs and structural variants while simultaneously determining genotypes	Sequence differences from the reference genome	8 469

Method	Description	Uses	Data type	CABI Search hits
Transcriptome sequencing	A method that provides novel insights into changing gene expression levels that occur in development and during disease and under conditions of stress	Elucidating gene and protein function and interactions, identifying tissue-specific lists of RNA transcripts and discovering new SNPs	Messenger RNA expressed in the tissue sample at the time of extraction	32 945
Epigenetics	Adaptive responses to changes in the environment (e.g. in food availability or drought conditions) can trigger phenotypic changes in plants and animals that affect their viability and reproductive fitness. Note: Epigenetic changes are not always adaptive; many are heritable (e.g. "imprinting"-based diseases). Phenotypic changes can be independent of genetic and/or epigenetic changes (e.g. abiotic stress).	Using sequencing to identify changes in DNA methylation, chromatin structure and small RNA expression to better understand how epigenetic factors contribute to controlling these and other traits in a species of interest	Generally, changes in cytosine methylation at position 5 when sequencing methods are used	10 992
Genome Sequencing (AHTEG Group-1 DSI)				
Targeted resequencing	A method for sequencing predetermined areas of genetic variation over many samples	Identifying common and rare variants – such as SNPs and copy number variants (CNVs) – to help inform breeding decisions or characterize disease susceptibility	Sequence variants compared to a reference sequence at each locus	2 558
Genotyping by sequencing (GBS)	A low-cost genetic screening method for discovering novel plant and animal SNPs and performing genotyping studies, often simultaneously in many specimens	Include genetic mapping, screening backcross lines, purity testing, constructing haplotype maps, and performing association and genomic evaluation for plant genome studies	SNPs in genotyping studies, such as genome-wide association studies (GWAS); GBS uses restriction enzymes to reduce genome complexity and genotype multiple DNA samples	16 213

Method	Description	Uses	Data type	CABI Search hits
Environmental DNA sequencing	An effective biomonitoring tool that allows characterization of both bacterial and eukaryotic species in aquatic, soil and other samples	Include port monitoring, biodiversity surveys, ballast-water testing and soil testing	eDNA from environmental samples, rather than directly sampled from an individual organism	483
Genome editing	CRISPR (clustered regularly interspaced short palindromic repeats) genome editing holds great potential for agriculture, food science, environmental science and a broad range of other applications	Confirming gene knockouts, analysing on- and off-target effects and assessing the functional impact of gene edits	Edited DNA from a cell expressing specific properties	5 118
Proteins and epigenetic modifications (AHTEG Group-2 additions)				
Mass spectrometry	Determines mass-to-charge ratio of ions (e.g. from gas or liquid chromatography)	Identifying and characterizing small molecules and proteins (proteomics)	Data that allow protein identification and annotation of secondary modifications, and determination of the abundance of individual proteins	13 887
Proteins and epigenetic modifications (AHTEG Group-2 additions)				
ELISA	Enzyme-linked immunosorbent assay an immunological assay commonly used to measure antibodies, antigens, proteins and glycoproteins in biological samples	Detection of antigen	Antigen presence, and possibly quantitation	24 332
Gel electrophoresis	A method in which an electric current is applied to samples, separating fragments that can be used for comparison between samples	Separation of DNA, RNA and protein samples	Separate bands of DNA, RNA or protein molecules based on their size and electrical charge	23 546

Method	Description	Uses	Data type	CABI Search hits
Chromatography	A method in which a mixture is dissolved in a fluid solvent (gas or liquid) that is carried through a system; components move at different rates and are thus separated	Separation of a mixture into its components	Fractionation position and abundance	19 665
Protein microarrays	Application of small amounts of sample to a "chip" for analysis	Detection of protein–protein interactions	Data on the presence of antigens	98
Metabolomic information (AHTEG Group-3 additions)				
MALDI-ToF-MS	Matrix-assisted laser desorption/ ionization coupled to time-of-flight mass spectrometry	Bacterial identification	Molecular weight for acid-soluble proteins, with identification from comparison of unknowns with a database of knowns	2 813
Nuclear magnetic resonance (NMR) spectroscopy	A method for determining the structures of complex molecules by measuring the interaction of nuclear spins when placed in a powerful magnetic field and exposed to radiofrequency (RF) radiation	Determining the molecular structure of proteins; also used to generate metabolic profiles from biological fluids by simple proton-resonance and peak-identification from databases	Data on the structure, dynamics, reaction state, and chemical environment of molecules	3 130
Metabolomic information (AHTEG Group-3 additions)				
High-resolution mass spectrometry (HRMS)	Modern separation techniques such as liquid chromatography, gas chromatography or capillary electrophoresis, are often coupled with HRMS	Fractionation of molecules and protein sequencing (e.g. ion-cyclotron-resonance peptide separation linked to collisional-fragment peptide sequencing)	Fractionation position, abundance and protein sequence	265

Source: The list of techniques and the descriptions is a compilation of technologies used in sequencing from a Google search and the CAB Abstracts records, enhanced by personal experience and knowledge of the CABI molecular biology team. The uses and data types are summarized by the authors based on personal knowledge and a summary compilation of descriptions found in the literature search.

epigenome is described as a "multi-modal layer of information superimposed on DNA sequences" that influences gene expression and can improve crop performance (Zhang *et al.*, 2022b). Epigenetics concerns the heritability of traits that is not associated purely with base-related DNA sequence. Some consider that epigenetic data do not qualify as DSI and should be outside the scope of any benefit-sharing regime. However, epigenetics is considered part of the digital flow of information from biodiversity and is included under the AHTEG groupings of the scope of DSI (AHTEG, 2020) (see Group-2 in Table 2). Epigenome-guided crop improvement can "identify and select for heritable epialleles that control crop traits independent of underlying genotype" (Zhang *et al.*, 2022b). In doing so, specific opportunities and challenges related to grain and horticultural crops have been identified, for example the genomic profile of a leaf in fruit and grain crops could potentially be extrapolated to predict genes and guide genome modification in other tissues or organs (Zhang *et al.*, 2022b).

Chapter 1. Relevance of DSI in general

DSI underpins much of current research in the life sciences, contributing to advances in medicine, conservation, agriculture and other fields. Since the first complete bacterial genome was sequenced in 1995 (Fleischmann *et al.*, 1995), over 200 000 bacterial and archaeal complete or draft genomes have been uploaded to public databases, and this has been happening at an increasing rate thanks to advances in sequencing technology and associated decreases in "per base" costs (Land *et al.*, 2015). The rapid increase in the rate of sequence-data acquisition since the end of the 1990s has been driven by matched advances in the fields of high-throughput (massively parallel) nucleic-acid sequencing and computing power for data analysis. This has enabled increases in per-machine output from about 5 kilobase pairs per day in the mid-1980s (early automated "Sanger sequencing" machines) to up to 180 gigabase pairs per day from a current Illumina NextSeq. The total amount of sequence data maintained by the International Nucleotide Sequence Database Consortium (INSDC), comprising the DNA Data Bank of Japan (DDBJ),[1] the European Nucleotide Archive (ENA)[2] and GenBank,[3] exceeded 9 petabytes in 2020 (Arita Karsch-Mizrachi and Cochrane, 2021). The DSI that is now available is thus a product of recent and unprecedented improvements in genetic sequencing technology. This vast amount of data can be utilized by scientists to obtain an understanding of an organism's DNA, its genes and ultimately the function of these genes. The data can help identify changes in particular genes and – through comparison with other examples from the species – provide information on the role of genetic change in susceptibility to disease and response to environmental influences. This can provide vast potential for diagnostics and therapies (see the National Human Genome Institute Fact Sheet [NHGRI, 2020] for further information on the latter).

In non-medical applications, DSI is mainly generated for the purpose of identifying and characterizing biodiversity. When a DNA sequence (partial [barcode] or whole genome) is generated from a genetic resource, it is compared to existing data to determine its similarity to previously generated sequences. If a close match is found, the genetic resource can be identified. The information obtained can be utilized in multiple sectors for research and product development.

GRFA can be relevant for uses in other sectors, for example where sequence data from GRFA are utilized for comparison with sequence data from other organisms; such data can also lead to the discovery of enzymes and metabolites for use in industry and healthcare. Once a resource has been sequenced, it can be compared with existing sequences derived from other sectors. Such cross-over between sectors presents a potential challenge for ABS instruments and schemes that address the use of DSI for specific uses such as food and agriculture.

Scientists use DSI in various ways to inform their research and provide the baseline for solutions to challenges such as those involved in the identification of organisms or the selection of the most appropriate production and application strains for microorganisms. Analysis of specific regions of DNA can provide insight into genes that are essential to regulatory mechanisms and the switching "on" or "off" of their activity. Increasingly, such comparisons can tell us which genes cause or increase susceptibility to disease, taking the influence of both inheritance and the environment into account.

Zhou *et al.* (2022) considered the effect of current technologies such as metagenomics and single-cell genomics on the reconstruction of genomes from mixed microbial communities. They concluded that such approaches allow scientists to "read genomic blueprints of microorganisms, decipher their functional capacities and activities, and reconstruct their roles in biogeochemical processes."

DSI can help explain the molecular basis and evolutionary theory of life and provide new methods for the conservation and sustainable use of biodiversity (Li and Xue, 2019). It is now possible to design and build products from DSI, removing the need to access the genetic resource itself: a key argument in the case for conservation and benefit-sharing. The generation and characterization of DSI has allowed the establishment of biofoundries, highly automated facilities that enable products and discoveries to be obtained from DSI (Hillson *et al.*, 2019; Si *et al.*, 2017; Richardson *et al.*, 2017). The Global Biofoundry Alliance (GBA, 2022) develops, promotes

[1] https://www.ddbj.nig.ac.jp
[2] https://www.ebi.ac.uk/ena/browser/home
[3] https://www.ncbi.nlm.nih.gov/genbank

Table 6. A snapshot of the growth in the number of nucleotide base pairs in selected GenBank Divisions, 2020–2021

	GenBank division	Number of base pairs of sequence in GenBank in August 2021	Growth in sequence databases in the year to August 2021 (%)
	Plants	350 590 744 188	30.12
	Phages	935 884 237	19.59
	Viruses	39 351 597 469	575.68
	Bacteria	130 518 385 589	32.07
	Primates	15 165 437 356	72.97
	Rodents	23 336 550 435	93.02
	Other mammals	28 568 850 588	37.06
	Other vertebrates	85 320 979 451	34.22
	Invertebrates	108 680 334 593	450
Total increase (August 2020 to August 2021)	Above sets plus 12 other GenBank divisions	15 309 209 714 374	54.79

Source: Sayers, E.W., Cavanaugh, M., Clark, K., Pruitt, K.D., Schoch, C.L., Sherry, S.T. & Karsch-Mizrachi, I. 2022a. GenBank,.*Nucleic Acids Research*, 50: D161–D164. https://doi.org/10.1093/nar/gkab1135

and collaborates on biological engineering to allow researchers to test large-scale genetic designs and apply artificial-intelligence machine learning to enhance the design process.

Sayers *et al.* (2022a) reported that, as of 2021, GenBank®, a comprehensive public database, contained over 15.3 trillion base pairs from over 2.5 billion nucleotide sequences from 504 000 formally described species. Daily data exchange with ENA and DDBJ ensures worldwide coverage (Benson *et al.*, 2011). The database has 21 main divisions (Sayers *et al.*, 2022a). A snapshot of the figures on the growth of the database (Table 6) shows huge increases in the number of base pairs of sequence added in the year from August 2020, with the largest increases being in invertebrate and virus sequences (the latter unsurprisingly in view of the worldwide coronavirus pandemic during this period).

Over the past 20 years, the sequences of over 1 000 plant genomes have been published, representing 788 highly diverse species (Sun *et al.*, 2022a). However, this remains a small proportion of the more than 390 000 plant species known to science. Although the cell and taxon proportions of genome-sequenced bacteria or archaea on Earth remain unknown, 155 810 prokaryotic genomes can be found in public databases (Zhang *et al.*, 2020). These studies reveal the current status of prokaryotic genome sequencing for the Earth's biomes: only 2.1 percent of known prokaryotes are represented by sequenced genomes. Among insects, only 28 species of agricultural pest have had their complete genomes sequenced (Li *et al.*, 2019), as compared to a total of 601 insect species that have been sequenced and made publicly available in GenBank (Hotaling *et al.*, 2021a). Despite the increasing amount of data generated, understanding of genomic information remains limited. Further analysis will accelerate advances towards a comprehensive understanding of microbial ecological functions in different environments (Zhang *et al.*, 2020). Forin *et al.* (2018) note that "recent studies have reported only about ... 35 000 correctly identified fungal species represented by DNA sequences in public databases." There is much work still to be done, as the

numbers of species sequenced are far short of current global estimates of total numbers of species on the planet; there are 3.8–5.1 million extant fungal species (Blackwell, 2011; Hawksworth and Lücking, 2017), up to 1 million species of prokaryotes (Louca *et al.*, 2019), and up to 10 million species of insects, of which only just over 1 million have been described (Royal Entomology Society, 2023).

Chapter 2. Generation and storage of DSI

Generating DSI is expensive, although the cost is falling as methods improve and become more efficient. The Earth BioGenome Project, which aims to sequence the DNA of all 1.5 million known eukaryotic species, is projected to cost USD 4.7 billion. The AfricaBP effort to sequence the genomes of 105 000 eukaryotic species in Africa will cost a total of USD 1 billion over ten years. These estimates of sequencing costs are based on the plateauing cost per megabase of sequence. The National Human Genome Research Institute estimates that the cost of DNA sequencing at its sequencing centres (NHGRI, 2022) has come down to around USD 0.10 per megabase of raw sequence (though their subsequent cleaning up or annotation takes considerable additional investment in computing resources and trained bioinformaticists). Given that costs have plateaued and the (likely continuing) increase in energy costs and reagent costs – especially single-use plastics – it appears that the cost per megabase is unlikely to drop below USD 0.075 in the near future.

If such a data resource were to be built elsewhere, or if it needed to be recreated, for example under a single standard, on the basis of a cost of USD 0.075/megabase, the 6.25 trillion bp of sequence data held by the European Bioinformatics Institute (EBI) would cost USD 468 750. However, if we take the more pragmatic view that it would be necessary to (re)sequence the 1.6 billion individually deposited sequences in EBI at USD 0.075 per sequence, the cost would be USD 120 million.

The costs are not negligible. One way in which this issue could be addressed is to look to distributing the effort (e.g. with data-brokering arrangements) so that globally distributed expertise could contribute to the building of ENA/INSDC and the costs could be shared. The rewards to countries would relate initially to growth of the science sector but could later translate into societal benefits from new-found national influence within the global scientific effort. Building these kinds of distribution arrangements is an ongoing priority for ENA (and INSDC as a whole) and would address INSDC operational issues as well as the global imbalance of DSI generation, storage and analysis.

Data are held in many places, in databases managed by different organizations. The resources are often termed "archival data repositories"; their data are not just stored but actively curated and managed. Examples include INSDC, Worldwide Protein Data Bank[1] (3D structure of proteins) and the ProteomeXchange[2] collaboration. Knowledge bases integrate information from multiple sources, often using computational approaches, for example the Universal Protein Resource[3] (protein sequences and function). Many, but not all, such repositories are public. INSDC content is transmitted to more than 1 700 other public databases with specialized content, processes and uses; many databases use and repurpose content from other databases. Figure 2 illustrates the data movements between EMBL-EBI's data resources and external data resources. It shows 468 separate external data resources that are linked to 39 EMBL-EBI resources by 1001 separate data connections (Cook *et al.*, 2020).

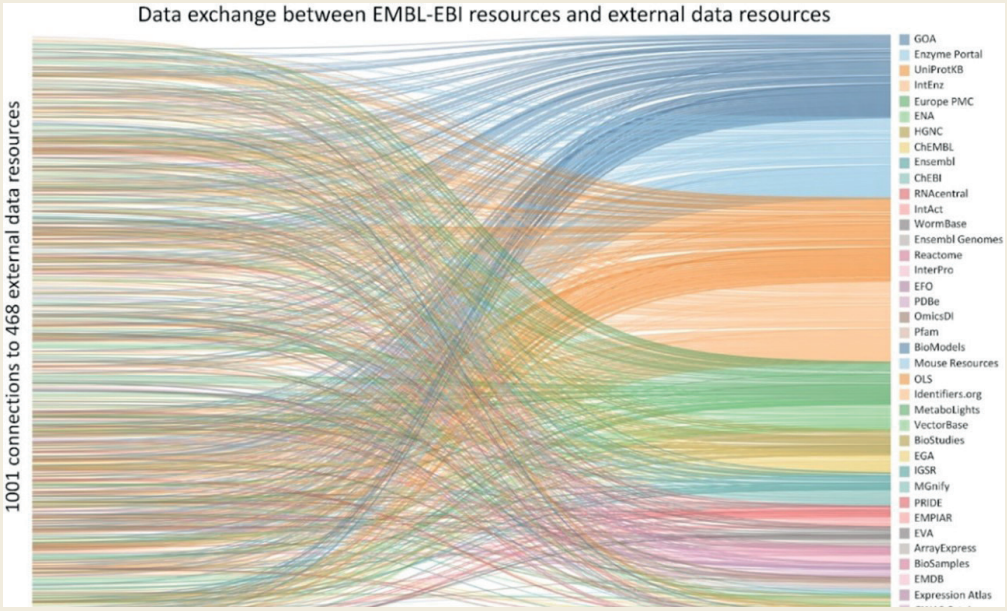
DSI generated by publicly funded research or published in scientific literature usually has to be made freely available; this is normally achieved through open-access public databases. A mechanism for making public databases more inclusive and ensuring balanced global coverage is needed. There is a broad range of opinions on this topic, and a full discussion of them goes beyond the scope of this study. One example is the suggestion that it may help to bring in key persons from regional bioinformatics networks, such as the Pan African Bioinformatics Network for the Human Heredity and Health in Africa consortium (H3BioNet)[4] (Ebenezer *et al.*, 2022).

2.1 Where is DSI generated and used?

Scholtz *et al.* (2021) concluded that the vast majority of countries use and provide access to genetic resources from which DSI has been generated, albeit to varying extents. These authors reported that the total output of publications in 2021 from scientists in low- and middle-income countries (LMICs) is 40

[1] http://www.wwpdb.org
[2] http://www.proteomexchange.org
[3] https://www.uniprot.org
[4] https://h3africa.org

Figure 2. Data exchange between EMBL-EBI resources and external data resources



Source: Cook, C.E., Stroe, O., Cochrane, G., Birney, E. & Apweiler, R. 2020. The European Bioinformatics Institute in 2020: building a global infrastructure of interconnected data resources for the life sciences, *Nucleic Acids Research*, 48(D1): D17–D23. https://doi.org/10.1093/nar/gkz1033

percent less than that from their counterparts in high-income countries. However, scientists are using DSI in almost every country in the world – and thus DSI is truly being generated and used on a global scale (Scholtz *et al.*, 2021).

The WiLDSI Data Portal enables discovery of data for biogeographical studies, exploration of collaborative networks, and profiling of the flow of access and benefits relating to sequence data (DNA and RNA, grouped as NSD). To explore NSD provenance and scientific use and reuse in the community, Lange *et al.* (2021) extracted NSD records from ENA and linked them to citations in open-access publications aggregated at Europe PubMed Central. By connecting publications with NSD records, NSD geographical-provenance information and author geographical information, Lange *et al.* were able to assess the contribution of NSD to scientific knowledge, and to infer global trends. A total of 8 464 292 ENA accessions with geographical-provenance information were found to be associated with publications, and the authors concluded that global provision and use of NSD enable scientists worldwide to join literature and sequence databases in a multidimensional fashion. The WiLDSI data portal shows that most countries (to varying extents) use and provide DSI for basic and applied research in both the public and private sectors. For example, DSI from Kenya is being used by 79 countries worldwide, while scientists in Kenya use DSI from 83 countries; DSI from Brazil is used by 111 countries, while scientists in Brazil use DSI from 153 countries.

The WiLDSI Data Portal currently presents data on 198 countries. The United States of America (7 726 083 sequences) and China (5 399 676 sequences) are the biggest providers of the genetic resources used to generate DSI. The next biggest providers are the United Kingdom of Great Britain and Northern Ireland (2 518 762) and Canada (2 158 026). These four countries are also among the greatest users of DSI. Only six countries have produced more than 1 million sequences, the other two being Japan and Germany. One hundred and fifty-seven countries have produced fewer than 100 000 sequences each, and 27 countries have produced fewer than 2 000 sequences each. The latter are Andorra, Antigua and Barbuda, Barbados, the Democratic People's Republic of Korea, Dominica, Eritrea, Eswatini, Grenada, Kiribati, Lesotho, Libya, Liechtenstein, Maldives, the Marshall Islands, Mauritania, Monaco, Nauru, Palestine, Saint Kitts and Nevis, Saint Vincent and the Grenadines, Saint Lucia, Somalia, San Marino, South Sudan, Timor-Leste, Turkmenistan and Tuvalu.

These data are based on the metadata/country tag used by the three INSDC databases. They refer to the **country of origin** of the genetic material that was sequenced and **not** to the location where sequencing took place. The 27 lowest-producing countries have provided access to genetic resources that have produced less than 0.1 percent of the total sequence information. Genetic and genomic analysis is often conducted in collaboration, and usually uses DSI that is from the local region. Nevertheless, China provides 26 percent of the DSI used globally and is responsible for the use of 23 percent of the sequence data analysed on the WiLDSI Data Portal. Thirty-six countries qualify for the table of top user and provider countries. These include countries in five of the six FAO regions, as listed below.

Africa: South Africa, United Republic of Tanzania.

Asia and the Pacific: Australia, China, India, Iran (Islamic Republic of), Japan, New Zealand, Republic of Korea, Thailand.

Europe and Central Asia: Austria, Belgium, Czechia, Denmark, Finland, France, Germany, Italy, Netherlands (Kingdom of the), Poland, Portugal, Russian Federation, Spain, Sweden, Switzerland, United Kingdom.

Latin America and the Caribbean: Argentina, Brazil, Costa Rica, Mexico, Panama, Peru.

North America: Canada, United States.

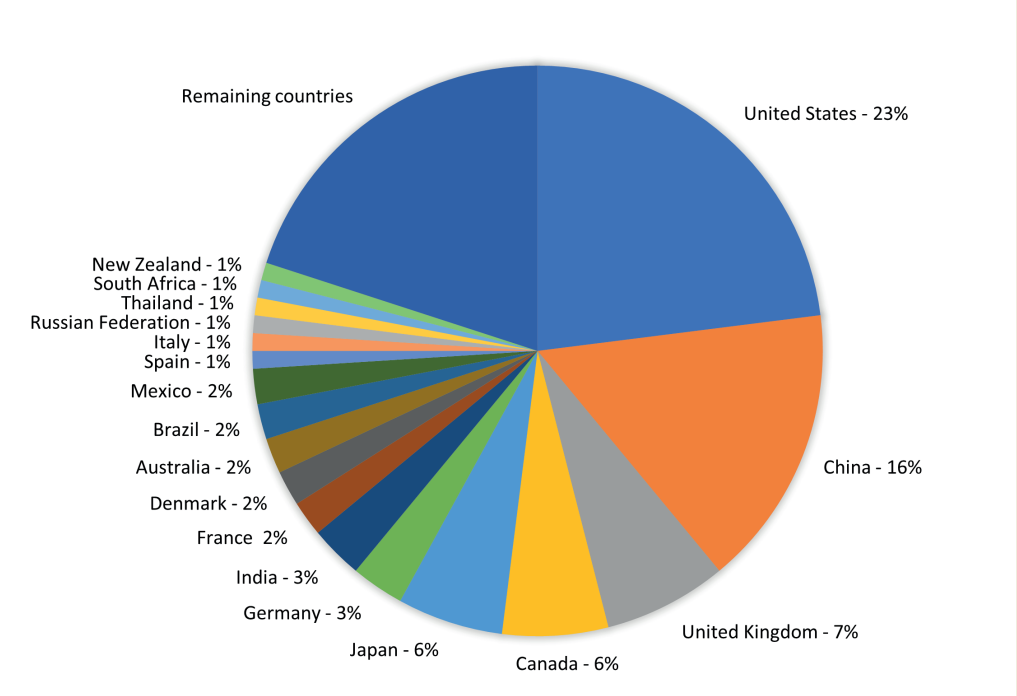
Scholz *et al.* (2021) explored the range of countries from which DSI has originated and the range of countries accessing and utilizing it. Although DSI is utilized quite broadly, the level of use does not reflect the traditional rhetoric around the provider–user relationship, which assumes that provision (access) to genetic resources happens in the Global South and that the subsequent use occurs in the Global North. Instead, the situation is much more complex, with use **and** provision happening in both directions (see below). The study considered the 17 816 729 sequences in the INSDC database that carry a tag showing the country of origin (of the genetic resources from which the DSI was generated), representing around 16 percent of the global database holdings. For each of these sequences, a publication listed within the INSDC database was counted as a "primary" publication, and any publication in the Europe PubMed Central database that listed the sequence was counted as a "secondary" publication. A total of 117 483 publications were included in the analysis.

Scholz *et al.* (2021) found that DSI is both provided and used by more than 99 percent of countries and that DSI use and provision often occur in roughly similar proportions. The figures from the WiLDSI Data Portal also show North–South collaboration (Europe and North America collaborating with South America, Africa and Asia) and South–South collaboration. The same study compared the "users" (based on counting publications not individuals) of nationally generated sequence information for lower-income (Group of 77 [G77]), middle-income (BRICS: Brazil, Russian Federation, India, China, South Africa) and high-income countries (Organisation for Economic Co-operation and Development – OECD). They found that in each case, the biggest users of a given economic group's DSI were users located in the same economic group (i.e. users appear to be mostly using their own DSI). However, there were significant differences in the numbers of publications for the different groups, with a total of 64 178 publications in low-income countries, 52 039 in BRICS countries and 82 971 in OECD countries.

Some countries that are heavy providers (see Figure 3) are also heavy users of DSI, which in turn could drive innovation. To an extent, the use of DSI data correlates to their provision. The United States, for example, provides a great deal of access to DSI while also being a major user of DSI data. Other countries, especially in Africa, provide less DSI and are also relatively light users. Given that much of the DSI data in public databases does not have "country-of-origin" tags, the scope for tracing DSI provision and use by country is limited.

As the data in the global resources cannot be split by sector, it is not possible to determine easily whether the above-described situation reflects the use of DSI on GRFA. However, searches of the agriculture-specific CABI database revealed a similar pattern (see Appendix 1), although country data were limited to author institution and thus did not necessarily indicate where the sequencing was conducted or where the source genetic resource that was sequenced originated. The analysis does demonstrate that researchers globally are using DSI in their research. A significant amount of DSI data generated from African species is housed in European and North America museums (e.g. the Natural History Museum in the United Kingdom, the National Museum of Denmark and the Smithsonian Museum in the United States), as are many specimens of such species. In many cases, there are more museum-held African samples outside Africa than in Africa, although many of the non-African institutions have active outreach, project and visiting-scientist programmes. Again, analysis of such data must be based on the source of the genetic resources and not the generator and depositor.

Figure 3. Number and percentage of sequences provided, by country



Source: WiLDSI. 2022. Overview of DSI use. In: *WiLDSI Data Portal*. Cited 12 December 2022. https://wildsi.ipk-gatersleben.de/apex/wildsi/r/wildsi/1233 (reproduced with permission).

The WiLDSI Data Portal also presents "country use of DSI", which makes it possible to explore how each country's scientists use their own DSI. LMICs both provide and use less DSI than, for instance, the United States, where almost 49 000 of the country's authors are using the country's data. Although the usage level varies greatly, the pattern of authors using their own country's DSI remains similar elsewhere: for example, the majority of authors (2 348) from South Africa use South African data. When it comes to authors using DSI from countries other than their own, the WiLDSI Data Portal reports that by far the greatest number, 118 980, are authors affiliated to the United States. As mentioned above, much work is carried out in, and for, LMICs through collaborations with higher-income countries, as demonstrated by the presence of more than twice as many North–South collaborations as South–South collaborations in the WiLDSI Data Portal.

2.2 Public databases

Currently, a vast amount of DSI is openly accessible, meaning that it is freely and easily available for anyone to access and analyse using public data resources, such as those managed by EMBL/EBI (Cochrane, 2022). Taking AHTEG's DSI Groups 1 to 3 together, the main resources for storing and distributing sequence data are: the National Institutes of Health (NIH) Sequence Read Archive, maintained by National Center for Biotechnology Information,[5] ENA and DDBJ.

As of August 2021, 15 309 209 714 374 sequences were stored in INSDC databases; at the same point, the NIH Sequence Read Archive comprised 11.5 petabytes of publicly accessible data (Sayers *et al.*, 2022b). The above "mirror" databases make DNA, RNA and protein sequence data available for free. They exchange data on a regular basis and therefore contain essentially the same content – all available within a single unified accession-number scheme. Importantly, these data are available to all, with evidence for use, for example, by approximately 1 700 other databases that curate, organize, integrate, annotate or add some further value to the holdings.

The 2022 database issue of the journal *Nucleic Acids Research* (NAR) (Rigden and Fernández,

[5] https://www.ncbi.nlm.nih.gov

2022) contains 185 papers spanning a wide range of biological fields and types of investigation. It includes 87 papers reporting on new databases and 85 covering recent changes to resources previously published, starting with reports from the major database providers NCBI, ENA-EBI and the National Genomics Data Centre (NGDC) in China (Sayers *et al.*, 2022a; Cantelli *et al.*, 2022; CNCB-NGDC, 2022). The NAR database issue also reports on data created and stored on (i) nucleic acid sequence and structure, transcriptional regulation, (ii) protein sequence and structure, (iii) metabolic and signalling pathways, enzymes and networks, (iv) genomics of viruses, bacteria, protozoa and fungi, (v) genomics of human and model organisms, plus comparative genomics, (vi) human-genomic variation, diseases and drugs, (vii) plants and (viii) other topics, such as proteomics databases.

Vast quantities of sequence data are generated annually, and these are stored with their associated metadata. INSDC has announced that, from 2022, it will make spatio-temporal metadata mandatory for new submissions (EMBL-EBI, 2022a).

The Global Biodata Coalition (GBC)[6] brings together research funders to coordinate and organize the rapid growth of biodata (GBC, 2022). There is a growing need to share approaches that allow the efficient management of this process, to address associated challenges such as fragmentation and duplication of effort, and to develop a strategy for long-term sustainability. The direct interest of GBC, as a coalition of research funders, is the sustainability of biodata resources that comprise an essential infrastructure for research. To achieve this, however, GBC also needs to address global inclusion, as the life sciences require samples/data from all parts of the world, and biologists in all countries have expertise to add to global science. GBC will be trying to engage with parties and bring them together to push for global distribution of effort and benefit in the operation and use of biodata resources such as DSI databases (GBC, 2022).

The data in the databases covered here originate from genetic resources from all parts of the world, as demonstrated by the WiLDSI Data Portal. Not all DSI has full associated metadata that identifies the country of origin of the genetic resources from which it was derived. Public databases are addressing this issue. Without information on the country of origin, it is difficult to ensure that benefits arising from the use of the DSI are shared with the country that provided the genetic resources. Public databases, including INSDC, store information on patented sequences, which are often deposited in publicly accessible databases in order to properly disclose inventions in line with the disclosure requirement of patent law.

2.3 Private databases

By their very nature, little information is available about privately held databases. It is clear that companies and organizations are generating sequence data and harvesting what they need from publicly available databases in order to undertake their research, which they then wish, and need, to keep confidential. In 2020, a study on DSI in public and private databases (Rohden *et al.*, 2020) showed that the DSI stored is very diverse and that such databases are often distributed internally according to the end uses and types of data stored, which include data on proteins (see Table 7). The study goes on to say that, in general, it seems that at least half the biological data stored in private databases originated from public databases, although this is only an estimate. The authors of the study noted that privately generated DSI can also be fed back into the public domain, primarily in the form of publications or the registration of patents. The study also found that there are large quantities of unpublished private DSI that do not become part of patents and would not necessarily need to be kept private. However, there are few incentives for companies to publish these NSD. The fact that huge quantities of DSI are freely available to the private sector has not so far convinced the private sector to make its DSI similarly available (Rohden *et al.*, 2020). Unfortunately, for the purpose of the present and other studies, DSI in private databases cannot be analysed to quantify the volume of data or their uses, users or biological scope.

Rohden *et al.* (2020) concluded that there are likely to be thousands of companies that use the public DSI available from the INSDC and integrate it into their in-house databases, noting that some of these companies do add data to public databases, especially in the context of collaborations with public institutions. They further concluded that backtracking to the original genetic resources by the company itself works in general for DSI generated in-house but not for all data obtained from the public databases. The study also found that companies use patent NSD databases (commercial databases) to check for already-existing patents but that other commercial NSD databases are uncommon. The authors note that this finding may suggest that such databases represent a challenging business model, as NSD is freely available at the INSDC and many downstream NSD and sequence information databases.

[6] https://globalbiodata.org

Table 7. Overview of private database case studies

Case Study	Employees	Focus for NSD+SI	% of public data	Submit data to public databases	P&P partnerships	Use patent databases
1. Novozymes	>6 000	Enzymes	-50%	yes	yes	yes
2. Company X	>20 000	Health, materials and nutrition	-95%	yes	yes	yes
3. Company Y	>2 000	Plant breeding and seed production	-50-80%	yes	yes	yes
4. TraitGenetics	>20	Molecular markers and genotypes in plants	?	yes	yes	no
5. BASF SE	>122 000	Various areas	-50-90%	yes	yes	yes
6. Company Z	>350	Enzymes for DNA handling	?	yes	yes	yes

Source: Rohden, F., Huang, S., Dröge, G. & Scholz, A.H. 2020. *Combined study on digital sequence information in public and private databases and traceability*. Annex 1. Ad Hoc Technical Expert Group on Digital Sequence Information on Genetic Resources, Montreal, Canada, 17–20 March 2020. CBD/DSI/AHTEG/2020/1/4. Montreal, Canada, Secretariat of the Convention on Biological Diversity. https://www.cbd.int/doc/c/1f8f/d793/57cb114ca40cb6468f479584/dsi-ahteg-2020-01-04-en.pdf

Chapter 3. The role of DSI in the conservation and use of genetic resources for food and agriculture

This section discusses the genetic sequencing technologies that generate DSI. It then describes how DSI on GRFA is used for research and development. This is followed by a discussion of where and how DSI is stored, and finally an analysis, based on DSI data flows and a literature review, of where and by whom DSI is used.

3.1 Use of DSI for food and agricultural research and development

The opportunities, challenges and implications associated with the use of DSI for GRFA are described in an earlier FAO document (FAO, 2021). The present study adds to this information through the survey of literature in the CAB Abstracts database (Appendix 1) and several case studies of CABI Member Countries, which confirmed that many countries are not yet in a position to make full use of DSI (Appendix 2).

3.1.1 Characterization

Elements of DSI are now used in taxonomy to characterize unknown organisms and partial sequences of genomes by comparing taxonomically informative genetic sequences with those available in databases. It is possible to extract such sequences from dead and dried specimens in museums and botanical gardens (Kates *et al.*, 2021). Comparison of new sequences against this massive, authenticated database resource enables the unknown organism to be identified.

Identifying pests (*sensu lato*) and their natural enemies (for biological control potential) is of high and direct relevance to GRFA. Using "DNA barcodes" (and more sophisticated DSI) that are compared against the Barcode of Life Data System (BOLD),[1] GenBank and other major repositories, Morand (2018) reported on advances and challenges in barcoding microbes, parasites and their vectors and reservoirs. He stated that BOLD held more than 6 million barcodes from over 270 000 species (including animals, plants and fungi). Where reference barcodes are not available for the species sampled, the most similar barcodes (which may not be generated from GRFA) often give clues to the identity of the test sample. This approach can be applied to all animals, plants and microorganisms. Just a short genetic sequence (e.g. 400–800 base pairs) is enough to identify most species (Whitfield, 2003). The Barcoding Table of Animal Species, for example, provides a new tool for selecting appropriate methods for identifying animal species using DNA barcoding (Matthes *et al.*, 2020). Hotaling, Kelleya & Frandsen (2021) reported 3 278 unique animal species in GenBank. There is still a lot of work to do to barcode all organisms and more still to whole-genome sequence them, but huge projects have been initiated to produce the overall "Tree of Life", including the Earth BioGenome project, a global enterprise with ambitions to sequence genomes for all of Earth's eukaryotic diversity (Lewin *et al.*, 2018, 2022).

3.1.2 Use and development

Substantial advances in DNA sequencing bring the potential to enhance food security and the sustainable use of global biodiversity, and hence to benefit the world's poorest people (Cowell *et al.*, 2022). The sharing of sequence information has underpinned these advances and has been critical in allowing evolutionary relationships, population dynamics and gene function to be inferred from the comparison of multiple sequences. The DSI generated, in combination with other data, such as predictive climate models, provides the foundation for finding nature-based solutions to current global challenges (Antonelli *et al.*, 2020).

Sequencing genes to discover their products is providing a rich foundation for further discovery, which in turn could generate products for the market and lead to the generation of monetary benefits. Numerous publications demonstrate the impact of DSI studies on R&D in the field of GRFA. "Omics" technologies can drive plant engineering, ecosystem surveillance, and human and animal health. Hurgobin and Lewsey (2022a) provide a collection of reviews that introduce readers to current and future uses of "omics" technologies to solve real-world problems. The authors describe "omics" as a "collection of research tools and techniques that enable researchers to collect data about biological systems at a very large, or near-complete, scale. These include

[1] https://www.boldsystems.org

Table 8. Benefits of DSI studies

Activity	DSI component of research	Benefits
Identification of biodiversity and its characterization	DNA barcoding and whole genome sequencing (WGS) to name the organism; annotated sequences can reveal potential traits and properties	Contributing to biodiversity inventories and data comparison, allowing biodiversity to be monitored and conservation to be improved
Diagnosis and identification of pests and diseases	Identification of causative organisms using barcoding or WGS	Enabling appropriate management recommendations and improving yields; combatting threats to livelihoods, agriculture and the environment from pests and diseases
Rapid identification of newly introduced (invasive) alien species	Sequencing and some automated identification systems based on proteomics and metabolomics with extensive databases can accelerate the identification process	Early warning that facilitates containment and management and reduces losses
Assessment of the impact of land-use and climate change on biodiversity and ecosystem services, which often involves finding species new to science	Population genomic studies are often carried out and can create baseline data that can be compared following environmental and climatic changes	Providing vital information for biodiversity inventory and for monitoring climate change and soil health; identifying interventions that can result in improved agricultural production
Development of microbial solutions to improve health and nutrition security	DSI observations can lead to identification of traits and properties that can be utilized	Improving yields and reducing losses of biodiversity for food and agriculture; monetary benefits arise when products are placed on the market
Development of biological control agents (BCAs)	Identification and characterization of suitable BCAs	Management of invasive species; reduction of crop losses and minimization of unnecessary pesticide use
Increasing and improving access to agricultural and environmental scientific knowledge	Sequencing of DNA and RNA and characterizing proteins and the metabolome can provide chemical profiles of species	Improvement of the knowledge base that all can use for innovation and discovery

Source: Authors elaboration for this background study paper.

sequencing individual and community genomes (genomics, metagenomics), characterisation and quantification of gene expression (transcriptomics, meta-transcriptomics), metabolite abundance (metabolomics), protein content (proteomics) and phosphorylation (phospho-proteomics). Though initially exploited as tools for fundamental discovery, 'omics techniques are now used extensively in applied and translational research, e.g. in plant and animal breeding, biomarker development and drug discovery."

Numerous benefits can arise from DSI activities. Table 8 gives some examples.

The results of the literature survey of the CAB Abstracts database show that an increasing

Table 9. DSI publication records in CAB Abstracts for different elements of GRFA

Type of genetic resource	Literature records citing DSI (10.9 million in database) 1973 to March 2022		Literature records citing DSI added between 1 April 2022 and 2 June 2023 (658 945 records added to database in total)	
	Number	Percentage	Number	Percentage
Animal	628 518	30.7%	56 672	45.9%
Aquatic	56 241	2.7%	6 668	5.4%
Forest	128 661	6.3%	5 533	4.5%
Plant	857 580	42%	48 126	39%
Microorganism	375 509	18.3%	6 419	5.2%
Total records citing DSI	1 180 915*	11% (of database records)	99 149*	15% (of literature records added)

**Some publications mentioned more than one type of genetic resources.*
Source: Authors elaboration for this background study paper.

proportion of publications are citing DSI in research on GRFA: 11 percent of the records from the period 1973 to March 2022 and 15 percent of the records added between 1 April 22 and 2 June 2023. They also show that there was a relatively larger increase in the proportion of papers on animal and aquatic genetic resources (Table 9).

Animal genetic resources (including invertebrates)

DSI leads to a better understanding of the genetic basis of an animal's traits for use in breeding programmes, for example how adaptive responses to environmental changes (e.g. in feed availability or rainfall) can trigger phenotypic changes that affect viability and reproductive fitness (Chen *et al.*, 2022).

DSI allows the genetic variability within populations to be maintained and hence contributes to the sustainable use of animal genetic resources. It can advance the discovery and development of new livestock breeds, with enhanced outcomes for sustainable and resilient livestock systems and food security.

Whole-genome sequencing data from the 1000 Bull Genomes Project are aiding the discovery of positive and negative traits and thus benefiting the cattle industry globally (Hayes and Daetwyler, 2019). More recent analyses in cattle include a genome-wide association study aimed at detecting genetic variants associated with bone weight (Niu *et al.*, 2021). Only 14 of the 364 variants detected in this study were present in the widely used Illumina "BovineHD SNP array". Several candidate genes with putative links to body measurement and growth traits that could be of direct relevance to future breeding programmes were noted. In the case of dairy cattle, DSI tools have enabled the detection of candidate genes with potential as markers for increased milk production. Recent research in Ethiopia explored the relationship of one such candidate gene, *DGAT1*, to milk production levels (Samuel *et al.*, 2022). The gene was found to be polymorphic across cattle populations in Ethiopia and is considered to be very important in terms of determining a baseline that can serve to increase understanding of a range of traits related to milk production levels (Samuel *et al*, 2022). Another recent study, which focused on dairy cattle belonging to a population considered to be ancestral to the renowned Holstein breed, identified several further trait-related genetic variants (in addition to *DGAT1*) with relevance to fat, protein or overall milk yields (or more than one of these) (Korkuć *et al.*, 2023). A different aspect of milk production was investigated in water buffalo, with DSI-related methods used to study DNA methylation specifically related to subclinical mastitis susceptibility in the Murrah breed; the work provided researchers with access to a genome-wide resource that could lead to better control of this problematic condition in the Murrah and beyond (Nayan *et al.*, 2022).

Whole-genome sequencing has also been used to try to discover gene traits in goats, for example a recent study on Hainan black goats in China (Chen *et al.*, 2022). This breed is renowned in China for its meat, but it also known to be well-adapted to hot, humid conditions. The results of the comparisons between the genetic make-up this breed and that of six other breeds could be of great importance in breeding programmes in the context of climate change (Chen *et al.*, 2022). A broader study of mitochondrial DNA from 250 goat breeds in China and 71 other countries showed the likely route of migration of this important livestock species, thereby providing insights into the development and evolution of preferred traits (Peng *et al.*, 2022).

Whole-genome sequencing was recently used to determine preferred traits across different pig breeds in China (Yang *et al.*, 2022). The researchers compared a total of 90 individuals across nine breeds, including the Beijing Black, annotating potential functions and proposing candidate genes for key developmental traits and disease resistance (Yang *et al.*, 2022). Biotechnological approaches combining whole-genome sequencing and CRISP-Cas technology have also enabled the recent development of commercializable disease-resistant pigs (Mark Cigan and Knap, 2022).

Javal *et al.* (2021) report that DNA barcoding has been used successfully for biosurveillance of forest and agricultural pests but point out the urgent need to develop advanced tools for the early detection and accurate identification of new or emerging insect pests. They note that the online database BOLD allowed them to automatically identify species based on their DNA barcodes.

Although barcode databases are far from comprehensive for insects, DNA barcoding can complement existing morphological identification tools and will facilitate the identification of the most common species, irrespective of the taxonomic skills of the observer or the developmental stage of the insect (Javal *et al.*, 2021).

Aquatic genetic resources

DSI can enable the characterization of genes and identification of genetic sequences for use in population genetics and stock assessment. It can also enable the identification of molecular markers for use in disease diagnosis and prevention, and in pedigree assignment in breeding programmes. Having DSI data can contribute to improved market access and consumer confidence in supply chains by improving traceability and identifying product substitution, and can support product labelling and certification schemes (OEWG, 2021b).

DSI is used in the breeding of pikeperch (*Sander lucioperca)*, a fish species of growing economic significance (de los Rios-Pérez *et al.*, 2020). The quality of the meat of the pikeperch, which has low fat and high protein content, gives it high commercial value, and the species has become a candidate for intensive inland aquaculture. Knowledge of the pikeperch's genome enables selection of the best candidates for breeding.

Marine biotechnology is a growing and globally significant economic sector that can help address global economic challenges (Rotter *et al.*, 2021).

DSI can be applied in various ways to aquaculture and the use of aquatic organisms for human nutrition. There is growing scope for using it to improve understanding of global challenges to aquatic production, such as climate change. For example, a recent study of the impact of marine heatwaves on farmed mussels in Greece showed that they led to increased levels of stress and vulnerability to parasitism in both traditional and modern aquaculture environments (Lattos *et al.*, 2022). The Thermaikos Gulf region produces 90 percent of Greece's farmed mussels, more than three-quarters of which are destined for other European countries (Kalaitzidou *et al.*, 2022). Mass deaths of farmed mussels in the region in 2021 and 2022 (up to 100 percent losses) led to investigation of the threat. Several biochemical and molecular markers from *Mytilus galloprovincialis* were screened to determine the extent of the mussels' pathophysiological response to a combination of biotic and abiotic stresses (Lattos *et al.*, 2022). The authors note that DSI-based methods will be a key part of the toolbox available for use in ongoing surveillance and research. The likely effects of increased temperatures associated with climate change have also been investigated in the economically important razor clam *Sinonovacula constricta*. This bivalve mollusc is able to tolerate a broad range of temperatures, but specimens were subjected to a period of controlled thermal stress in an attempt to determine the specific genes affected and the nature of the effect on the expression of those genes, with the ultimate aim of improving understanding of which genes/traits should be considered in future efforts to improve thermal tolerance (Kong *et al.*, 2022).

The issue of how to cope with fluctuations in abiotic factors has led to the publication of several papers on the tolerance of increased or decreased salinity in

aquatic food-producing stocks. A recent investigation of the impact of low salinity on the Pacific abalone compared the transcriptome of gill tissue from *Haliotis discus hannai* to that of an interspecies hybrid (*H. discus hannai x H. fulgens*) (Boamah *et al.*, 2022). The authors found that in both cases the abalone increased expression of genes related to antioxidation and anti-inflammation and decreased the expression of those involved in the promotion of inflammatory responses; they also noted that the hybrid appeared to respond better to the low-salinity stress, which has potential implications for future breeding programmes. It is known that intertidal organisms are subject to considerable changes in several abiotic factors. A recent study of the Manila clam, *Ruditapes philippinarum*, that aimed to elucidate the genes that enable it to tolerate a broad range of salinity levels used transcriptomic and metabolomic analyses to pinpoint potential indicators of exposure to salinity stresses (Sun *et al.*, 2022b).

The tilapia *Oreochromis niloticus* is one of the most important fish in terms of human nutrition in LMICs and has been a focus of studies using DSI-based tools in the fields of responses to dietary supplements (Li *et al.*, 2022), antiviral vaccine development (Yu *et al.*, 2022a) and the investigation of potential quantitative trait loci for swimming performance and its relation to growth (Yu *et al.*, 2022b).

Forest genetic resources

DSI is contributing to the assembly of breeding populations in newly developed and advanced breeding programmes, and to the selection of genetic material for storage or micropropagation. It can potentially be used as a powerful tool for breeding forest trees as well as for enhancing the productivity of plantation forests and enabling judicious control of pest infestation. Using predictive genomics may help in the conservation of trees by identifying the environment most suited to the particular genotype and by providing information to support assisted migration. Accumulated DSI enables comparison of large numbers of individuals and populations of the same and related species to identify their current distribution areas and project changes related to climate change. Even "simple" DNA barcoding has been used in Nigeria to obtain markers for forest species listed under the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) and other endangered forest species (Onyia *et al.*, 2022). This development has important implications for the conservation of endangered species and the detection of illegal processing of timber products. DNA barcodes (generated from whole chloroplast genomes) have also been used in the creation of a resource for use in the detection of illegal logging of rosewood (*Dalbergia* spp.) in China (Hong *et al.*, 2022).

Metagenomic and metabarcoding approaches are providing a wealth of information on the composition of forest soil. Metagenomic profiling was used in combination with chemical analyses to study the relative contributions of biotic and abiotic factors to soil fertility in a comparison of forest soil management mechanisms – tilled versus undisturbed – in Indonesia (Wiryawan *et al.*, 2022). The main finding of the investigation was that there was greater species richness in the undisturbed soil, which indicated the greater potential of natural forest soil to encourage microbial diversity (Wiryawan *et al.*, 2022). A more basic study using microbial isolation from forest soils followed by DNA-sequence analysis resulted in the identification of several potential plant growth-promoting bacteria from forest soil in Egypt, the ultimate aim being to use such organisms as biofertilizers (Chowhan *et al.*, 2023).

Increasingly, forest soils (and forest trees and other plants) are seen as untapped sources of potentially useful organisms and natural products. A recent study of mangrove forest sediment screened for, and isolated, bacteria that are able to remove sodium from high-sodium laboratory media (Duy *et al.*, 2022). DNA barcoding showed that the isolated strains belonged to the genus *Rhodobacter*, and they are viewed as having potential for use in the decontamination of heavily salinated soils (Duy *et al.*, 2022). A study in mangrove forests (Octaviana *et al.*, 2023) sought to identify Myxobacteria with putative antimicrobial properties, and obtained promising results by isolating strains in the laboratory, identifying them using 16S sequence analysis and then screening them for antimicrobial activity by testing crude extracts on target organisms and then screening by high performance liquid chromatography.

Microbial genetic resources

DSI is commonly used in microbiology, as microorganisms, by definition, cannot be seen with the naked eye and most often require sequence-based technologies to detect their presence and describe them. It is now routine to use barcoding to identify microorganisms. Automated identification tools that depend on comparisons with reliable and complete databases are proving extremely useful, especially for detecting organisms of regulatory importance. For example, matrix-assisted laser desorption/ionization-time of flight (MALDI-ToF) mass

spectrometry is used for almost all bacterial disease diagnostics in the United Kingdom's National Health Service. It is also possible to express novel properties through genome engineering and even produce chemically synthesized genomes (see Box 1).

The development of high-throughput molecular methods utilizing specific gene regions (barcodes) provides massive amounts of DSI on microorganisms. Although a large fraction (more than 50 percent) of the detected genes have no assigned function to date, the use of functional metagenomics applications has led to the discovery of novel enzymes. Importantly, shotgun metagenome analysis allows the genomes of all microbial species in a sample to be sequenced if there is enough sequence coverage, for example a sample from the marine environment, where the majority of microorganisms remain to be discovered. This enables enzymes of interest to be linked directly to organisms and thus allows the properties of unculturable microbes to be accessed (Rotter *et al.*, 2021). Improved technologies have led to the discovery of many novel bioactive compounds through the sequencing of complete microbial genomes from selected niches, enabling bioprospecting for marine microorganisms. Open-access knowledge bases containing tandem mass spectrometry (MS/MS) data or structures of microbial natural products have been greatly improving dereplication processes (processes for excluding items that have already been discovered), leading to the identification of new molecules and natural products (Rotter *et al.*, 2021).

Fungi are often employed as biological control agents (BCAs), and their conidiation capacity (capacity to produce spores – propagules) and conidial quality are critical to their production and application, for example in the mass production of the fungal insect pathogen *Metarhizium acridum* (Zhang, Peng and Xia, 2010).

Metabolomics is an emerging tool for studying plant–microbe interactions (Gupta, Schillaci and Roessner, 2022). It enables access to cellular metabolites, which belong to the AHTEG's Group-3 (see Section 1.2). Gupta, Schillaci and Roessner (2022) report that "metabolomics research based on mass spectrometric techniques is one of the crucial approaches that underpins system biology and relies on precision instrument analysis. In the last decade, this emerging field has received extensive attention. It provides a qualitative and quantitative approach for determining the mechanisms of symbiosis of bacteria and fungi with plants" before reaching the conclusion that "application of metabolomics to study plant microbe interactions comes with several challenges, such as the differentiation of the origin of metabolites analysed, uncovering the metabolic complexity of two or more organisms interacting and linking metabolome information with other omics data such as transcriptomics, proteomics or phenomics."

The use of locally acclimatized rhizobial strains can replace the use of nitrogen-based fertilizers for the cultivation of soybean. Chibeba *et al.* (2017) used DSI-generating technologies (BOX-PCR fingerprinting) to select ten isolates from Mozambique that out-

Box 1. *Saccharomyces* cerevisiae as an example organism

Genome-scale engineering is being employed as an automated platform for the yeast *Saccharomyces cerevisiae* (Si *et al.*, 2017). This yeast is an important eukaryotic model and a widely used microbial cell factory. Standardized portions of the genome are created in a single step from a full-length complementary DNA library with the aid of CRISPR-Cas technology (removing, adding or altering sections of a sequence) (Pickar-Oliver and Gersbach, 2019). These genetic parts are iteratively integrated into the repetitive genomic sequences in a modular manner using robotic automation. This allows expression of diverse phenotypes, including cellulase expression, isobutanol production, glycerol utilization and acetic-acid tolerance, and may accelerate genome-scale engineering endeavours in yeast (Si *et al.*, 2017). A complete synthetic version of a highly modified *Saccharomyces cerevisiae* genome, reduced in size by nearly 8 percent, has been designed. Chemically synthesised genomes of this kind are customizable and allow scientists to attempt to answer questions about chromosome structure, function and evolution by using a bottom-up design strategy (Richardson *et al.*, 2017).

Source: Pickar-Oliver, A. & Gersbach, C.A. 2019. The next generation of CRISPR–Cas technologies and applications. *Nature Reviews Molecular Cell Biology*, 20: 490–507. https://doi.org/10.1038/s41580-019-0131-5; Richardson, S.M., Mitchell, L.A., Stracquadanio, G., Yang, K., Dymond, J.S., Dicarlo, J.E., Lee, D. *et al.* 2017. Design of a synthetic yeast genome. *Science*, 355(53223): 1040–1044. https://www.science.org/doi/10.1126/science.aaf4557; Si, T., Chao, R., Min, Y., Wu, Y., Ren, W. & Zhao. H. 2017. Automated multiplex genome-scale engineering in yeast. *Nature Communications*, 8: 15187. https://doi.org/10.1038/ncomms15187.

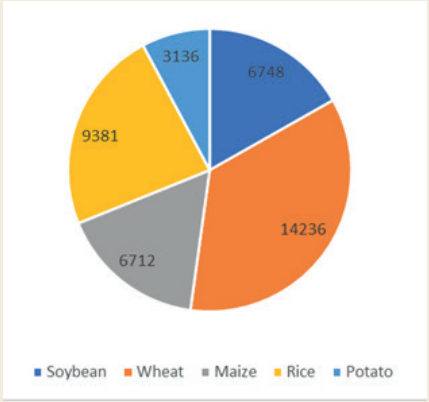
performed a commercially available strain, providing a possible strategy for increasing soybean yields.

Crop rotation can improve soil properties and is an important way of preventing soil-borne diseases. A study (Zhang *et al.*, 2022a) that used different preceding crops and combinations of soil microorganisms to control clubroot disease in Chinese cabbage showed that growth and disease resistance could be improved. Different combinations of preceding crops, including soybeans, potato, onions and wheat, were used, and metagenomic sequencing demonstrated the differences they induced in the abundance and diversity of the bacteria and fungi. The study showed that the preceding crops changed the structure of soil microbial communities, reduced clubroot disease in Chinese cabbage and promoted growth.

Another study (Bonanomi *et al.*, 2020) showed how intensive agricultural practices negatively affect soil fertility and soil microbial communities, and compromise the crop quality and yield of rocket (Eruca sativa). High-throughput sequencing was used to monitor changes in populations of bacteria and fungi after chemical applications. This demonstrated that synthetic fertilizer and fumigation induced soil acidification and increased soil salinity, with a detrimental impact on microbial diversity, activity and function, and consequent negative effects on crop yield. The application of organic amendments significantly improved crop yield, especially when alfalfa and glucose were applied as a single dose.

It is now possible to explore microbial communities that are present in the environment surrounding plants, animals and humans. These communities comprise bacteria, archaea and fungi, among other microorganisms. They include organisms that have properties that improve plant growth and crop yield as well as human and animal health. Harnessing these organisms to improve poor agricultural soil and production systems may well become common, for example replacing the use of manure with a targeted mix of key organisms. The composition and differentiation of microbial communities are now being explored, but understanding the microbiome remains challenging. For example, there is a need to understand the microbial community's interactions with other organisms and its environment and to identify ways of optimizing the taxonomic composition of microbiomes to improve the overall health and fitness of plants and the soil, and hence to help make agriculture more sustainable (Singh and Goodwin, 2022). With regard to the maize microbiome, Singh and Goodwin point out the huge opportunities that genomics may offer in terms of improving yields and facilitating adaptation to climate change. It is clear that generation of DSI will only increase and that its importance in the food and agriculture sector is still becoming apparent.

Figure 4 The number of literature records for soybean, wheat, maize, rice and potato referencing DSI in the CAB Abstracts database



Source: CAB Abstracts output.

Plant genetic resources

The literature survey carried out on CAB Abstracts (Appendix 1) provided many examples of the use of DSI to improve crops. Figure 4 summarizes the number of literature records for soybean, wheat, maize, rice and potato.

DSI is used in several ways to improve crop yields and resistance to disease, and to address threats to biodiversity such as invasive species and climate change. Examples from the publications on wheat, rice, maize and soybean of how DSI is being used in crop improvement and sustainability are presented in Box 2. In addition to the use of DSI from specific crops to improve production of the respective species, there are also examples in which it is being used to enhance other crops: this is discussed in Section 3.1.3.

3.1.3 Cross-species knowledge transfer and research on metabolism

Plants produce many specialized metabolites with distinct biological activities and potential applications outside agriculture (Muhich, Agosto-Ramos and Kliebenstein, 2022). Despite this potential, most biosynthetic pathways, including for metabolite production, remain poorly understood. However, advances in genomic technologies have enabled the identification of some specialized

Box 2. DSI from food crops

Wheat is the most widely grown crop globally, providing 20 percent of all human calories and protein (Calderini *et al.*, 2021). Candidate genes for improved abiotic stress tolerance have been discovered (Schmidt *et al.*, 2020). Wheat characteristics such as leaf chlorophyll content, leaf greenness, cell-membrane thermostability and canopy temperature have been proposed as candidate traits for improving adaptation and yield potential under high temperatures (Pradhan *et al.*, 2020). Marker-trait associations have been discovered that affect grain yield (e.g. in genes encoding different types of proteins associated with heat stress) and can be used in breeding to develop varieties with high stability for grain yield under high temperatures (Pradhan *et al.*, 2020). Similar markers linked to fruiting efficiency, grain number and spikelet weight have been found and can potentially be used in breeding programmes as selection criteria for increasing yield potential (Hutter, 2022; Gerard *et al.*, 2019). In the case of multigene complex traits, such as yield, there is a need for improved strategies for research into which genes are responsible and how new varieties can be generated (Skraly *et al.*, 2018). Predictive models facilitate the identification of gene targets, and trait engineering can affect commercialization cost and timeline (Skraly *et al.*, 2018).

Rice is a staple food crop for more than half the world's population; it is grown in more than 100 countries, with 90 percent of total global production occurring in Asia (Fukagawa and Ziska, 2019). Studies using DSI have been carried out on rice to improve drought tolerance and increase grain yield by modulating expression of osmolytes, antioxidants and abiotic stress-responsive genes (El-Esawi and Alayafi, 2019). A combination of stress tolerance (e.g. to salinity and drought) and enhanced grain yield is a major focus of rice-breeding strategies; modifying the function of the drought and salt-tolerance gene produced transgenic plants that had higher stress tolerance and better yields (Faisal *et al.*, 2017).

Maize is one of the most important food crops in the world after wheat and rice (Shiferaw *et al.*, 2011). Erenstein *et al.* (2022) note that "together, the three big global staple cereals – wheat, rice, maize" account "for an estimated 42 percent of the world's food calories." DSI studies on maize are helping provide information that improves our ability to provide the ever-increasing volumes now needed. Cell wall invertase genes increase maize grain yield and starch content by up to 145.3 percent, as confirmed in two-year field trials at different locations (Li *et al.*, 2013). Simmons *et al.* (2020) describe how DSI studies could identify genes that could be harnessed to enhance yield in commercial strains of maize. Hannah *et al.* (2012) found that the maize shrunken-2 (*Sh2*) gene encodes the large subunit of the rate-limiting starch biosynthetic enzyme ADP-glucose pyrophosphorylase. Expression of a transgenic form of the enzyme with enhanced heat stability and reduced phosphate inhibition increased maize yield by up to 64 percent. These DSI studies have enabled a greater understanding of maize production and helped identify interventions that can improve production and contribute to climate change adaptation.

Chickpea is a highly nutritious grain legume crop that is widely consumed, especially in the Indian subcontinent. The major constraints to chickpea production are biotic stresses (*Helicoverpa*, bruchid beetles, aphids, *Ascochyta*) and abiotic stresses (drought, heat, salt, cold), which reduce yield by up to 90 percent (Kumar *et al.*, 2018). Recent advances in gene technologies have enabled the development of genetically modified chickpeas, including ones that are resistant to Helicoverpa armigera, *Callosobruchus maculatus* and *Aphis craccivora* and to drought and salt stress (Kumar *et al.*, 2018).

metabolic pathways, including those involved in improving abiotic and biotic stress resistance and in boosting nutritional content. Muhich, Agosto-Ramos and Kliebenstein (2022) reviewed the potential and limitations of (1) identifying these metabolic pathways and (2) using the discovered enzymes in synthetic biology or crop engineering. This technology demonstrates that the use of DSI in plants is not restricted to one sector, with DSI enabling discoveries that can be utilized in other sectors, for example industrial enzymes.

Cell- and tissue-specific "omics" techniques can be used to improve plant productivity. Hurgobin and Lewsey (2022b) report that plants have unique patterns of gene expression and protein and metabolite content, enabling specific patterns of growth, development and physiology. They explain that plants normally considered as resources for agriculture can provide properties for use in other sectors such as pharmaceuticals and bioindustry. Many instances of cross-species knowledge transfer are reported.

Soybean is a major animal feed crop that is being negatively affected by climate change and for which future yield losses are predicted (Fodor *et al.*, 2017). DSI studies in soybean have explored the roles of a transcription factor in regulating fatty-acid biosynthesis and have demonstrated that it could influence many aspects of plant structure and growth. Overexpression of the gene *GmWRI1b* improves yields and increases total seed oil production under field conditions (Guo *et al.*, 2020).

Sources: Calderini, D.F., Castillo, F.M., Arenas-M, A., Molero, G., Reynolds, M.P., Craze, M., Bowden, S. *et al.* 2021. Overcoming the trade-off between grain weight and number in wheat by the ectopic expression of expansin in developing seeds leads to increased yield potential. *New Phytologist*, 230(2): 629–640. https://doi.org/10.1111/nph.17048; El-Esawi, M.A. & Alayafi, A.A. 2019. Overexpression of rice Rab7 gene improves drought and heat tolerance and increases grain yield in rice (*Oryza sativa* L.). *Genes*, 10(1): 56. https://doi.org/10.3390/genes10010056; Erenstein, O., Jaleta, M., Sonder, K., Mottaleb, K. & Prasanna, B.M. 2022. Global maize production, consumption and trade: trends and R&D implications. *Food Security*, 14: 1295–1319. https://doi.org/10.1007/s12571-022-01288-7; Faisal, A., Biswas, S., Zerin, T., Rahman, T. & Seraj, Z. 2017. Downregulation of the DST transcription factor using artificial microRNA to increase yield, salt and drought tolerance in rice. *American Journal of Plant Sciences*, 8(9): 2219–2237. https://doi.org/10.4236/ajps.2017.89149; Fodor, N., Challinor, A., Droutsas, I., Ramirez-Villegas, J., Zabel, F., Koehler, A-K. & Foyer, C.H. 2017. Integrating plant science and crop modeling: Assessment of the impact of climate change on soybean and maize production. *Plant and Cell Physiology*, 58(11): 1833–1847. https://doi.org/10.1093/pcp/pcx141; Fukagawa, N.K. & Ziska, L.H. 2019. Rice: importance for global nutrition. *Journal of Nutritional Science and Vitaminology*, 65(Supplement): S2–S3. https://doi.org/10.3177/jnsv.65.S2; Gerard, G.S., Alqudah, A., Lohwasser, U., Börner, A. & Simón, M.R. 2019. Uncovering the genetic architecture of fruiting efficiency in bread wheat: a viable alternative to increase yield potential. *Crop Breeding & Genetics*, 59(5): 1853–1869. https://doi.org/10.2135/cropsci2018.10.0639; Guo, W., Chen, L., Chen, H., Yang, H., You, Q., Bao, A., Chen, S. *et al.* 2020. Overexpression of *GmWRI1b* in soybean stably improves plant architecture and associated yield parameters, and increases total seed oil production under field conditions. *Plant Biotechnology Journal*, 18(8): 1639–1641. https://doi.org/10.1111/pbi.13324; Hannah, L.C., Futch, B., Bing, J., Shaw, J.R., Boehlein, S., Stewart, J.D., Beiriger, R. *et al.* 2012. A shrunken-2 transgene increases maize yield by acting in maternal tissues to increase the frequency of seed development. *The Plant Cell*, 24(6): 2352–2363. https://doi.org/10.1105/tpc.112.100602; Hutter, C. 2022. Genome-wide association studies. In: *National Human Genome Research Institute*. Bethesda USA. Cited 13 December 2022. https://www.genome.gov/genetics-glossary/Genome-Wide-Association-Studies#:~:text=A%20genome%2Dwide%20association%20study,disease%20or%20a%20particular%20trait; Kumar, M., Yusuf, M.A., Nigam, M. & Kumar, M. 2018. An update on genetic modification of chickpea for increased yield and stress tolerance. *Molecular Biotechnology*, 60: 651–663. https://doi.org/10.1007/s12033-018-0096-1; Li, B., Liu, H., Zhang, Y., Kang, T., Zhang, L., Tong, J., Xiao, L. & Zhang, H. 2013. Constitutive expression of cell wall invertase genes increases grain yield and starch content in maize. *Plant Biotechnology Journal*, 11(9): 1080–1091. https://doi.org/10.1111/pbi.12102; Pradhan, S., Babar, M.A., Bai, G., Khan, J., Shahi, D., Avci, M., Guo, J. *et al.* 2020. Genetic dissection of heat-responsive physiological traits to improve adaptation and increase yield potential in soft winter wheat. *BMC Genomics*, 21: 315. https://doi.org/10.1186/s12864-020-6717-7; Schmidt, J., Garcia, M., Brien, C., Kalambettu, P., Garnett, T., Fleury, D. & Tricker, P.J. 2020. Transcripts of wheat at a target locus on chromosome 6B associated with increased yield, leaf mass and chlorophyll index under combined drought and heat stress. *PLoS ONE*, 15(11): e0241966. https://doi.org/10.1371/journal.pone.0241966; Shiferaw, B., Prasanna, B.M., Hellin, J. & Bänziger, M. 2011. Crops that feed the world 6. Past successes and future challenges to the role played by maize in global food security. *Food Security*, 3: 307. https://doi.org/10.1007/s12571-011-0140-5; Simmons, C.R., Weers, B.P., Reimann, K.S., Abbitt, S.E., Frank, M.J., Wang, W., Wu, J., Shen, B. & Habben, J.E. 2020. Maize BIG GRAIN1 homolog overexpression increases maize grain yield. *Plant Biotechnology Journal*, 18(11): 2304–2315. https://doi.org/10.1111/pbi.13392; Skraly, F.A., Ambavaram, M.M.R., Peoples, O. & Snell, K.D. 2018. Metabolic engineering to increase crop yield: from concept to execution. *Plant Science*, 273: 23–32. https://doi.org/10.1016/j.plantsci.2018.03.011.

Capacity to assimilate carbon and nitrogen and to transport and convert incoming sugars and amino acids into storage compounds is a key determinant of crop yield (Vallarino *et al.*, 2020). Vallarino *et al.* (2020) demonstrated that genes artificially introduced into tomato from various sources, including potato and Arabidopsis, increase carbon and nitrogen flows and boost fruit yield by up to 23 percent. Lack of potassium in soil limits crop yield, and under such circumstances crops require improved potassium-use efficiency. Many genes influence this in plants. A pyrophosphatase-encoding gene that was induced by low potassium stress was identified by Zhou *et al.* (2020), who report that overexpression of this gene in two wheat varieties resulted in increases in yield, grain number per spike, plant height and potassium uptake in four transgenic lines over several years.

Understanding of the mechanisms that can be used to increase crop yield can be explored and improved by studying relevant DSI. For instance, a study found that overexpression of transcription factors regulating photosynthesis and related metabolism in switchgrass gave rise to an increase of 160 percent in above-ground biomass (Ambavaram *et al.*, 2018).

DSI has been used to improve plant-breeding programmes for cereal varieties with better salinity

tolerance and more profitable grain yields in saline soils. The Arabidopsis gene encoding a vacuolar proton-pumping pyrophosphatase has been shown to improve the salinity tolerance of transgenic barley plants in greenhouse conditions (Schilling *et al.*, 2013). The transgenic barley was found to have higher grain yield per plant in field studies under saline conditions.

Studies on DSI relating to cell proteins can also be carried out with the aim of improving crop resilience and making discoveries that can be used in breeding programmes. Targeted overexpression of an α-expansion in early developing wheat seeds led to an increase in grain yield of 11.3 percent in field experiments (Calderini *et al.*, 2021). In photosynthetic organisms, the photosystem II complex is the system most vulnerable to thermal damage, and it is therefore an obvious target for efforts to improve a crop's resilience to climate change. Expression of the chloroplast-based gene driven by a heat-responsive promoter protects transgenic rice plants from severe loss of protein, and dramatically enhances their biomass and grain yield under heat. These findings represented a breakthrough in bioengineering plants to achieve efficient photosynthesis and increase crop productivity under both normal and heat-stress conditions (Chen *et al.*, 2020).

A study of regulated expression of isopentenyltransferase, a critical enzyme in the cytokinin biosynthetic pathway, demonstrated how to significantly improve the drought tolerance of groundnuts in both laboratory and field conditions (Qin *et al.*, 2011). To understand the role of jasmonate plant hormones in tuberization in potato, the *Arabidopsis* jasmonic acid carboxyl methyltransferase gene was constitutively overexpressed in transgenic potato plants (Sohn *et al.*, 2011). Increases in tuber yield and size, as well as in in vitro tuberization frequency, were observed in the transgenic plants.

In summary, plant genome sequencing for crop improvement enables the discovery of genes and molecular markers associated with diverse agronomic traits. This, in turn, creates new opportunities for crop improvement (Edwards and Batley, 2009). However, converting these data into knowledge that can be applied in crop breeding programmes remains a challenge.

Genomic sequence information, coupled with phenotypic and other data, may also identify genotypes that are adapted to diverse, and changing, agroecological conditions. When integrated into crop breeding programmes, genomic sequence information is increasingly useful in efforts to achieve targeted, efficient uses of genetic diversity in sustainable agriculture.

3.2 The role of DSI in the conservation of genetic resources for food and agriculture

DSI is an important tool in conservation in that it enables both the identification and the characterization of genetic diversity. It is helping us understand life and evolutionary processes and enabling the discovery of new approaches to the conservation of endangered species. The DNA unique digital barcode is increasingly used to identify species, describe the composition of communities, and combat poaching and illegal wildlife trade (Pedris, 2017) by identifying closely related animal species when trade in some but not all of them are illegal, for example among sharks and rays (Palminteri, 2017). Efforts are also ongoing to apply the technology to plant products, such as timber (John, 2016). Inclusion of molecular data in biodiversity inventories allows changes over time to be tracked, as required for countries' biodiversity monitoring activities under the CBD (Cowell *et al.*, 2022). Genomic analysis provides an alternative method for evaluating long-term *in situ* conservation programmes.

Digital genomic sequence data are used to assess the genetic diversity of *ex situ* collections and to identify unique germplasm in farmers' fields that is not included in collections. This baseline information is essential for developing more effective *ex situ* and *in situ* conservation strategies (Halewood *et al.*, 2017).

Supple and Shapiro (2018) discuss how genome-scale data can inform species delineation in the face of admixture (the mix of diverged or isolated genetic lineages) and identify adaptive alleles, and thus enhance evolutionary rescue based on genomic patterns of inbreeding. "Conservation genomics" (Supple and Shapiro, 2018) encompasses the idea that genome-scale data will improve the capacity of resource managers to protect species. It has only recently become possible to generate genome-wide data at a scale that is useful for conservation, and in future this will have a positive impact on policy and management.

Chapter 4. Obstacles to access and use of DSI, and the need for capacity building

Almost all research that leads to DSI will be built on reference to existing DSI in some way, requiring information on the prior use of the methods, i.e. resequencing a crop variety needs a reference genome, while *de novo* sequencing needs gene models for annotation, expression and related studies. It is therefore important for data to be openly accessible and held in a single, uncomplicated system. In almost all common scenarios, a given sequence is only useful for research or development if it can be compared with existing characterized sequences (data from other studies, countries, species, etc.). In order to encourage the widest possible access to the existing and future benefits of DSI-based science, all data need to be findable, accessible, interoperable and reusable, i.e. comply with the so-called FAIR (*findability, accessibility, interoperability* and *reusability*) principles (Wilkinson *et al.*, 2016). Any ABS system must consider such principles for data accessibility and use. The INSDC collaboration of publicly accessible, open-access databases enables this to occur, but the process would benefit from the use of standard methodologies for data collection, recording and sharing to maintain the consistency and reproducibility of results. Currently, data are often deposited by researchers to meet the policy requirements of funders and/or scientific journals when publishing their findings. It is important that sample (and DSI) metadata not only cite the country where the genetic resource originated but also provide details of the methodology used to produce it. Views from a recent report on open access are presented in Box 3.

DSI databases offer a crucial research infrastructure for the global research community. Beagrie and Houghton (2021) estimated that the annual return on investment in R&D depending on EMBL-EBI-managed data is GBP 1.3 billion. More than 4 900 researchers participated in the study. The most direct measure of the value is the time researchers spend using EMBL-EBI data resources. This added up to more than 140 million hours during 2020, equivalent to an estimated GBP 5.5 billion.

In some areas of research, tracing a sample to its country of origin could be crucial. Adding this information will enrich the scientific value of the data, especially for scientists working on infectious disease, biodiversity and ecology. Cochrane (2022) discussed how to ensure that countries rich in biodiversity can benefit from research on this biodiversity and discoveries resulting from such research. He reported that megaprojects such as the Darwin Tree of Life,[1] the African BioGenome Project[2] and the Earth BioGenome Project[3] are daily sequencing hundreds of new species, and discussed how the data generated are made available to the scientific community. The INSDC currently names only those who have submitted samples or sequence data and not the primary owners or custodians of the sample (Ebenezer *et al.*, 2022). The new proposals to include improved metadata with submitted samples (EMBL-EBI, 2022a) may need to be extended to enable links to the locality of the genetic resources sequenced and to those who manage it, for example to the Indigenous Peoples or local communities that provided the material, rather than only to the person/entity that submitted the samples (Ebenezer *et al.*, 2022).

Databases are constantly exchanging data to ensure that they are all up to date (see Figure 2). Currently, sequence data are available to all from public databases such as INSDC, and free online training is available (HBC, 2022). GenBank also provides instructions and tools for accessing and utilizing the data. Theoretically, therefore, DSI data are available to all given a little knowledge and computer capacity. However, full analysis requires more specialist knowledge and bioinformatic skills. The ENA and INSDC have a uniform policy (EMBL-EBI, 2022b) of granting free and unrestricted access to all their data records, giving scientists worldwide access to these data and the freedom to publish any resulting analysis as long as the original submission is cited. This practice enables traceability to source and follows the accepted practices of scientists utilizing published scientific literature. The journal *Nature* provides data-repository guidance (Nature, 2022) to facilitate access to data. In the health sciences, some repositories have datasets requiring restricted data access, for example where there is a need for participant anonymity in clinical datasets. There is overwhelming support for keeping access to DSI data open provided that the source metadata are

[1] https://www.darwintreeoflife.org
[2] https://africanbiogenome.org
[3] https://www.earthbiogenome.org

Box 3. A perspective on the debate on benefit-sharing and DSI

Frictionless data sharing and use of DSI in public databases minimize transaction costs in accessing and using data, but this has implications for the design of benefit-sharing from DSI. First, to maintain the high degree of interoperability that characterizes the *status quo*, a multilateral access model applied as universally as possible (i.e. across all DSI and all international benefit-sharing fora) is needed. This could take the form of uniform terms of access for DSI across public databases. Benefit-sharing obligations that apply to the entire DSI dataset globally will best protect the open system because the technological infrastructure that facilitates DSI use to generate knowledge would not require massive changes. These types of benefit-sharing obligations are decoupled from access, which remains open. In comparison, options that require accounting of DSI access, movement and use (bilateral mechanisms) appear more likely to impair interoperability and to generate high transactions costs and frictions to data flow that will significantly hinder research.

A historical perspective on open access and open scientific research data can serve as a starting point for characterizing and defining open access in the context of DSI. This may assist in the development of a working definition tailored to DSI. However, a consensus definition may not necessarily need to be the primary focus. Instead, it might be advisable for policy discussions to pay closer attention to whether, and to what extent, scientific research and innovation would be significantly hindered by changes to the current "open and unrestricted" access to and use of DSI in public databases. This lens appears better suited to guiding discussions on the design of the access pillar of any potential benefit-sharing solution.

Taking inspiration from the Scholarly Publishing and Academic Resources Coalition approach, it is useful to look beyond the question "what is open access?" towards a more nuanced approach to the design and evaluation of ABS policy solutions based on the question "is it as open as possible?" Efforts should be made to ensure that any necessary changes made to the *status quo* are proportionate and justified. Applying this nuanced approach to benefit-sharing objectives suggests that a multilateral and universal mechanism for DSI should be "as open as possible" provided it can be designed to deliver benefits that are deemed acceptable by the Parties to the Nagoya Protocol. Certainly, the scientific community's quest to ensure that open access to DSI will continue to be guaranteed, and that biological data will be publishable, available, linkable, downloadable and continue to flow into the downstream databases and software that they use, is strongly aligned with international, regional and national policies concerning science and innovation. Globally, there is a move towards a greater openness aimed at promoting research, innovation, technological development and ultimately sustainable economic development. The outstanding questions are whether the CBD and the broader benefit-sharing community will follow or go against this trend, and what the consequences of that choice will be.

Source: adapted from Rodrigo, S., Hufton, A.L., Sett, S. & Scholz, A.H. 2022. A technical assessment for the debate on benefit-sharing and digital sequence information. *Zenodo*. DOI: 10.5281/zenodo.5849643. https://zenodo.org/record/5849643.

published with the DSI, thus enabling traceability back to the provider country.

The outcomes of the analysis of the WiLDSI Data Portal data suggest that the global goal should be to increase the scientific output and generation of DSI from LMIC (G77) and BRICS countries to levels similar to those observed in the OECD (Scholz *et al.*, 2021). Increased research capacity in LMICs would have global benefits and would allow global biodiversity knowledge gaps to be filled more effectively. To achieve this, any DSI policy mechanism should recognize the existing divide between richer and poorer countries, and encourage DSI use, publication and collaboration, perhaps explicitly dedicating significant capacity-building to levelling the DSI playing field in scientific terms.

Access to and use of DSI in many countries are still constrained by serious obstacles. There is an urgent need to address issues such as lack of technical infrastructure, financial and human resources, educational and training opportunities, scientific collaboration, computing infrastructure, reliable electricity and high-speed internet, and potentially in the future prohibitive charges for database use. The feedback received by CABI centres from their own researchers and their partner institutions supports this finding (Table 10). CABI has centres (CABI, 2022a) in Brazil, China, Ghana, India, Kenya, Malaysia,

Pakistan, Switzerland, Trinidad and Tobago, the United Kingdom and Zambia that use GRFA in their research and development activities. All run projects with numerous partners (CABI, 2022b) under the following seven main themes (CABI, 2022c) (numbers of projects given in brackets): climate change (2), crop health (57), development communication and extension (40), digital development (23), invasive species (81), publishing (4), and value chains and trade (40). These are carried out in 85 countries (CABI, 2022c) in the following regions: Africa (51), Asia (49), Central America and the Caribbean (8), Europe (25), North America (29), Oceania (6) and South America (3). Feedback was obtained from CABI Centres and partners in Brazil, the Caribbean (including the Bahamas and Trinidad and Tobago), China, Ghana, Kenya, Pakistan and Zambia.

All those consulted reported (Table 10) that they use DSI in the course of their work, mainly for the identification and characterization of organisms. However, they noted that this DSI is often generated through collaboration, for instance with Australia, the United States, European countries or South Africa. Pakistan, for example, identified microorganisms through the use of DSI in collaboration with China and Saudi Arabia. The CABI Centre in India has been working in the region since 1948 and has witnessed rapid growth in the generation and use of DSI. It reported that "what started as a trickle in early 2000 is now a flood." The resulting data are mostly published in public databases. Researchers in all the countries consulted have accessed DSI from other countries for genetic improvement programmes. In India, some institutions have online databases, while others do not but are working to create them. However, much of the DSI generated is for local use and it is often not published or shared.

Globally, the generation and use of DSI are expanding rapidly, but for the majority this is often still hindered by a lack of resources, including funding and expertise. Even in China, recognized by the DSI network analysis of the WiLDSI Data Portal as one of the world's largest generators and users of DSI, the ability to use DSI fully is not shared evenly by all researchers across the country.

The CABI centres' responses to questions on accessibility and the ability to use DSI are summarized in Table 10, where a number of constraints to the generation of DSI, access to DSI, analysis of DSI and utilization of DSI to its full potential are reported. Many respondents mentioned a lack of investment in sequencing infrastructure, problems with internet access, shortages of trained staff, financial constraints to paying fees for access, and a major shortage of people to carry out data analysis. Redressing the imbalance in the ability to access and fully use DSI will require capacity building.

Capacity building

Coordinated and targeted capacity-building activities are crucial and could include:

(a) on-site and/or virtual courses;

(b) case studies, exchange of information and experiences, and sharing of lessons learned;

(c) joint scientific research, technology transfer, scientific visits, partnerships and collaborations, including through regional networks;

(d) support for the development of scientific infrastructure, including through regional approaches (e.g. CGIAR centres);

(e) intercultural dialogue through face-to-face meetings for Indigenous Peoples and local communities using culturally appropriate tools and methodologies in Indigenous languages, which could include dialogue between scientists and holders of traditional knowledge;

(f) integration in academic curricula; and

(g) integration in regional and international development agendas.

Table 10. Commonalities from CABI centre feedback on capacity and ability to access and use DSI

	Bahamas	Brazil	China	Ghana	India	Kenya	Malaysia	Pakistan	Trinidad and Tobago	United Kingdom	Zambia
1. Does the centre operate across a region?	-	Y	-	Y	-	Y	Y	-	Y	Y	Y
2. Does the country use DSI?	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
2.1 Private sector use of DSI	-	Y	-	-	Y	-	-	-	-	Y	-
2.2 Public sector use of DSI	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
3. Does the country generate DSI?	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
3.1. In-country	-	Y	Y	N	Y	-	Y	Y	N	Y	Y/N
3.2 By out-sourcing	Y	Y	-	Y	N	Y	N	Y	Y	Y	Y
4. Is there country legislation covering use of genetic resources/ DSI?	-	Y	-	-	Y	-	Y	-	-	N	-
4.1. Require benefit-sharing at access	-	-	-	-		-	-	-	-	N	-
4.2 Benefits triggered by product on the market	-	Y	-	-		-	-	-	-	N	-
5. Are there constraints to generation of or access to DSI?	Y	Y	Y	Y	Y	Y	Y	N	Y	Y	Y
5.1. Sequencing Infrastructure	Y	Y	N	Y	N	Y	N	N	Y	Y	Y
5.2 Internet access	Y	N	Y	Y	-	Y	Y	N	-	N	Y

	Bahamas	Brazil	China	Ghana	India	Kenya	Malaysia	Pakistan	Trinidad and Tobago	United Kingdom	Zambia
5.3 Trained staff	-	Y	-	Y	Y	Y	Y	N	Y	Y	Y
5.4 Financial	-	Y	-	Y	Y	Y	Y	N	Y	Y	Y
5.5 Other IT infrastructure	Y	Y	Y	Y	-	Y	Y	N	Y	Y	Y
5.6 Data analysis	Y	Y	Y	Y	-	Y	-	N	Y	Y	Y
6. Are data easily accessible?	Y	Y	N	Y	Y	Y	Y	Y	Y	Y	Y

Notes: Bahamas and Trinidad and Tobago are covered by the same CABI centre. Y = Yes; N = No; - = no stated view.
Source: Authors elaboration for this background study paper.

Chapter 5. Access and benefit-sharing for DSI

Bagley *et al.* (2020) explored how domestic measures address benefit-sharing arising from commercial and non-commercial use of DSI. The study identified 16 countries and one subnational jurisdiction as having domestic ABS measures addressing DSI. The study reported that 18 countries indicated that ABS measures on DSI were under preparation. Most domestic ABS measures allow for the inclusion of specific obligations, including benefit-sharing obligations relating to DSI, as part of mutually agreed terms (MAT) for genetic resources.

The study found that countries' domestic measures take different approaches to addressing DSI. While some consider DSI only in the context of the utilization of the tangible resource, others require prior informed consent (PIC) and MAT for DSI. Others do not require PIC for access to DSI for research and development but require the sharing of benefits derived from DSI that has been generated from their genetic resources. A fourth group of countries has taken a conscious decision not to address DSI in their ABS measures, and a fifth group addresses DSI in some other way (Bagley *et al.*, 2020).

Reports of monetary benefit-sharing are difficult to find, and given that the measures that are in place are fairly early in their implementation, there is not a great deal to report on benefit-sharing related to DSI. Most countries are participating in negotiations towards a common approach, for example the outputs reported from COP 15 (CBD, 2022).

5.1 Benefit-sharing practices

Even where there are no legal obligations to share the benefits resulting from DSI, there may be voluntary benefit-sharing arrangements involving DSI. There are cases where the parties involved did not explicitly address DSI and benefit-sharing but in fact collaborated on DSI and shared benefits, even if these benefits may not have been monetary. This has been the case for CABI United Kingdom Centre projects, where the benefit-sharing arising from 116 projects active in 2019 that involved access to genetic resources was analysed by Smith *et al.* (2021). The majority of these CABI projects were carried out jointly with partners in the provider countries and often with joint funding. However, fewer than 20 were in countries with Nagoya legislation that required compliance with ABS, and most of the projects were outside the scope of Nagoya legislation. CABI shares benefits with all its partner countries, including in the following ways: sharing results; collaboration in education, training and research; joint authorship of publications; joint ownership of intellectual property rights; and provision of access to CABI facilities and databases. The projects also invariably result in knowledge and technology transfer that helps the partners to develop their own products and in institutional capacity development to help build or maintain local collections of biodiversity. For instance, projects in Brazil include discovery, formulation and application of BCAs such as *Metarhizium* and *Beauveria* spp. to tackle resistance to pesticides used against insect crop pests. The biopesticide product will be owned by the Brazilian partners, who also benefit from CABI's know-how and technology. Another biological control project involves a partnership with India to address the invasive weed problem caused by Himalayan balsam in the United Kingdom. An Indian strain of the rust fungus *Puccinia komarovii var. glanduliferae* was approved for release in England and Wales in 2014 (Ellison, Pollard and Varia, 2020). A second strain, from Pakistan, was released in 2017 to control a different cohort of Himalayan balsam. However, there are several weed genotypes in the British Isles that are not susceptible to either rust strain, and further collaborative surveys with scientists from India are now taking place. Benefits shared to date include joint papers and training activities with Indian and Pakistani collaborators, plus collaborative payments. Training was provided for an MSc student from Kenya and a PhD student from Malaysia. The project has also been extended to include control of Himalayan balsam in Canada.

CABI shares benefits with provider countries regardless of their status under the Nagoya Protocol (CABI, 2022d). The 27 projects covered in the Smith *et al.* (2021) report involved the use of genetic resources, all characterized with DSI, from 22 countries. Of these, nine countries are parties to Nagoya Protocol with implementing law, eight are parties to the Nagoya Protocol with no implementing law (as indicated as of 8 July 2021 on the Access and Benefit-Sharing Clearing House) and five are not parties to the Nagoya Protocol. Nevertheless non-monetary benefits were shared with all the countries.

5.2 Examples of triggered benefit-sharing

While most countries addressing DSI expect monetary benefit-sharing arising from its use, to date no country has reported receiving such benefits (Bagley *et al.*, 2020). Those countries that omit DSI from domestic benefit-sharing measures because they consider it out of the scope of the CBD and the Nagoya Protocol nonetheless facilitate scientific advancement through open access to DSI and regard it as a form of non-monetary benefit-sharing. The WiLDSI (2020) white paper offers five monetary benefit-sharing open-access policy options for DSI. The details are given in the white paper and include a "micro-levy", membership fee, cloud-based fees, commons licenses and blockchain metadata for open access to DSI. The idea is that open access does not equal "free of any obligations" and models can be implemented that make DSI "visible to all" but subject to conditions. The authors of the white paper conclude that "benefit-sharing is most likely to materialise when free exchange can happen" and that any system should avoid "attempts at monitoring/tracing/controlling this highly complex, dynamic ecosystem", as this would require huge investment and be unlikely to result in cost-effective benefit-sharing.

The above-mentioned CABI report on its ABS policy and practices (Smith *et al.*, 2021) puts forward the argument that amendments to the Nagoya Protocol are not necessary with respect to DSI and that the issue should be treated at country level. It notes that DSI is akin to derivatives, naturally occurring biochemical compounds resulting from a cell's metabolism, and that it is clear that if DSI is accessed with the genetic resource on which it is based or generated the DSI may be covered by MAT. The report argues, however, that this would mean that each country would take its own position, potentially making international collaboration and usage difficult. To avoid this problem, it would be beneficial to have a common agreement on the generation of DSI and how it can be used in a way that facilitates innovation in the life sciences.

Both monetary and non-monetary benefits are possible for DSI, as is the case for the genetic resources themselves, and the decision on which type of benefit is most appropriate might potentially be determined by the type of use (Smith *et al.*, 2021). For example, where generating and publishing sequence data produces descriptive information on the organism and does not amount to utilization, benefits to be shared could be non-monetary. These might include access to the data and elements of capacity building, for example assistance with generating, publishing and analysis of the sequence data. DSI can be used at many non-exploitative levels: for example, its use to confirm organism identification is an observation rather than research; in most cases the resulting sequence data are published in public databases. There could be similar non-monetary arrangements related to uses delivering public good, such as addressing the Sustainable Development Goals (SDGs). However, if DSI is used for financial benefit then this should be considered utilization and could trigger monetary benefit-sharing. The full benefit-sharing arrangement could be negotiated with the provider country, as would be the case for access to the organism itself, or managed in a similar way in a multilateral system. The latter could reduce transaction costs and provide a global system that might not require tracking and tracing the source of the DSI. Such use and its implications should be made clear in the terms and conditions for the use of public databases containing DSI. Currently, for some countries, the generation and use of DSI must be considered when negotiating access – i.e. be expressed in the MAT and presented in any material transfer agreement to make it clear what can and cannot be done regarding DSI (at least until clarification is given by the COP in guidance or regulation).

5.3 Resolving the common approach to DSI use and benefit-sharing

Prior to COP 15 there were several different proposed options for a common approach to DSI and the sharing of benefits from its use (OEWG 2021a, 2021c; CBD, 2021). Parties to the CBD had not been able to agree on a single way forward, and there was still some way to go to reach consensus. COP 15 took the discussions further, taking decisions on some aspects, but several issues remained unresolved. Decision 15/9 on DSI on genetic resources (CBD, 2022) reports on key issues where actions are to be taken but highlights the divergent views expressed. It notes the work of the "Informal Co-Chairs' Advisory Group on DSI on genetic resources established by the Co-Chairs of the Open-ended Working Group on the Post-2020 Global Biodiversity Framework and the Executive Secretary, and the work on digital sequence information on genetic resources undertaken by the Advisory Group, including consideration of policy options." Decision 15/9 (CBD, 2022) also recognizes that there are "divergent views on DSI with regard to its scope under the Convention on Biological Diversity." The key outputs with respect to further action were:

- the decision to establish, as part of the Kunming-Montreal Global Biodiversity

Framework, a multilateral mechanism for benefit-sharing from the use of DSI on genetic resources, including a global fund;

- the decision to establish a fair, transparent, inclusive, participatory and time-bound process to further develop and operationalize the mechanism, to be finalized at the sixteenth meeting of the COP;
- the establishment of an ad hoc open-ended working group on benefit-sharing from the use of DSI on genetic resources to undertake further development of the multilateral mechanism, including the elements identified in an annex to the decision, and to make recommendations to the COP at its sixteenth meeting; and
- issues listed in the above-mentioned annex, indicate the breadth of issues that will have to be further considered in the development of the multilateral mechanism, including policy options other than a multilateral mechanism.

Resolving the policy issues around DSI would be desirable, as uncertainty could slow the publication and exchange of DSI. A legal vacuum around DSI could even hinder the sharing of genetic resources. FAO has the opportunity to contribute to the continued process of discussion and experimentation towards the establishment of a system that better facilitates the generation and use of DSI to improve the production and sustainability of agricultural and food products.

5.4 Addressing utilization for the public good

A number of interested parties have argued that activities that result in delivery of public goods, such as contributing to the SDGs, should be exempt from benefit-sharing obligations. However, as mentioned earlier, rather than exemption, an alternative might be for such activities only to generate non-monetary benefits, particularly with regard to reducing losses and improving yields from food and agricultural biodiversity. Identification of emerging plant and animal diseases and research on how to minimize their impact would be of high relevance here, and such an approach would be similar to the WHO position on emerging human diseases (WHO, 2017). Research and development of agents for classical biocontrol (the release of a natural enemy to control a pest or disease) is a case in point: here benefits could include sharing the knowledge base and giving facilitated access to BCAs (Smith *et al.*, 2018). This might be achieved through an intergovernmental agreement (binding or non-binding) through which governments commit themselves, on the basis of reciprocity, to share access to, information on and use of BCAs with participating countries. A country giving access to its genetic resources for such activities would benefit from solutions developed by other countries. This meets the intentions of the CBD and the Nagoya Protocol and provides the appropriate level of benefit-sharing that countries are seeking (Smith *et al.*, 2018). Silvestri *et al.* (2019) concluded that it is important to raise awareness among policymakers of the key role that classical weed biocontrol could play in different sectors and to persuade them to develop ABS legal frameworks tailored to this. Classical biological control studies almost exclusively result in the release of the BCA and may not result in a product being released onto the market, although the results, including formulation and the genetic resource itself, may be published. Clearly, where a biopesticide product is developed this could trigger monetary benefit-sharing via the relevant agreements.

Chapter 6. Discussion and conclusions

The definition of DSI remains controversial. The scope of DSI can range from only covering DNA and RNA sequences (NSD) to also including protein sequences, metabolites and macromolecules; it may also include associated information and traditional knowledge. This study does not take a position on this issue.

DSI is highly and increasingly relevant to R&D in all sectors of GRFA. Multiple reports and studies as well as literature surveys carried out for this study indicate that DSI is used extensively to identify, characterize and monitor GRFA. Furthermore, DSI on GRFA is enabling crops and livestock to be improved, increasing yields and – by providing resistance to pests and diseases and tolerance to drought and heat – enhancing resilience to climate change. Additionally, DSI from biodiversity outside the food and agriculture sector contributes to and is used for research on GRFA. Identifying sequences and their properties utilizes biodiversity data from all sectors, within and beyond food and agriculture, and often genes from organisms considered to be outside food and agriculture are used to improve agricultural productivity and disease resistance. The most common point of entry to DSI databases is for a given user to identify their sequence by comparison against the database content, looking for similarities or close matches. In such cases, all DSI may be relevant, no matter the sector from which it derives. Similarly, researchers that are looking for a particular sequence-encoded function will compare their sequence against the database content. Alternatively, users may choose to focus on the subset of the database that covers their organism of interest, while still others may focus on the protein/metabolite of interest and look across the broader database for the common ways that very different organisms have found to solve similar problems.

It is clear from this study that the scope of DSI is complex, and as more information is gathered, the complexity increases further and discussions on potential solutions expand. Scientifically, DSI represents a continuum: scientists may use both genomic sequence and systems biology data from metabolomics and proteomics to explore their research questions. The CABI Abstracts database survey found most hits for technologies that generate NSD (86 655), although work on proteins and epigenetic modifications gave only slightly fewer hits (81 528). However, hits for the metabolome were significantly fewer (6 208).

In science, the primary benefit that is generated and shared is information, which in turn enables discoveries and allows public goods to be generated, as discussed above. To this end, DSI is deposited freely, openly and transparently into public databases by its generators, thereby also meeting the requirement of scientific journals that DSI (e.g. DNA and RNA sequences) be deposited with a unique identifier that is quoted in the publication to enable tracking. A given sequence is only useful for research or development if it can be compared with existing characterized sequences (data from other studies, countries, species, etc.). This allows the source genetic resource to be identified and gives some indication of its characters and properties.

The generation of DSI should be encouraged for the benefit of science and discovery. A system that only recognized the source country of the genetic resources for benefit-sharing might disincentivize DSI producers, who may not reside in the country from which the genetic resources originate. It has been proposed that access to DSI should be "decoupled" from benefit-sharing (DSI Network, 2022): this could be achieved by establishing mechanisms that do not limit access to DSI but enable countries to receive appropriate benefits from a possible global fund. However, it is very clear that ability to generate, manage and utilize DSI is not distributed equally across the world. LMICs such as the CABI Member Countries the Bahamas, Ghana, Kenya, Malaysia, Trinidad and Tobago, and Zambia, often do not have the requisite facilities and capacity. DSI from these countries are often generated in one of the following ways: by foreign scientists who access the genetic resources; through collaboration between local scientists and partners in other countries that have access to facilities; or by buying in the necessary services. Feedback via the CABI centre in China also indicated that not all scientists in China have equal access to DSI and ability to utilize it. Action is needed to resolve these inequalities. Countries, and even industry, might help with this through multilateral processes. However, levying fees or royalties from products incorporating DSI is unlikely to generate sufficient funding. This issue needs to be explored, and appropriate measures put in place to maximize output from science that generates DSI for

the public good but equally to find mechanisms and resources to fund the delivery of the CBD objectives of conservation, sustainable use and the fair and equitable sharing of benefits that arise from use.

Regarding current discussions within the CBD to find a common approach to DSI with respect to fair and equitable benefit-sharing, a number of requirements need to be addressed. First, any common approach must provide certainty and legal clarity for providers and users of DSI so as not to hinder the research and innovation that improves our ability to feed the global population and meet the SDGs. It must retain open access to data, available through a common gateway, to enable ready comparison of new NSD with known sequences. The system must be compatible with international legal obligations and recognize that the monetary and non-monetary benefits arising from the use of DSI should be used to support the conservation and sustainable use of biodiversity. The continuing discussions require further information and analysis of the outstanding unresolved issues and options, including assessment of the potential consequences of different policy approaches. Areas to be explored include options or modalities for benefit-sharing, legal feasibility in implementation, and options for addressing the challenges of tracking and tracing. Countries already implementing their own approaches need ways to integrate them into a global system, for example hybrid approaches. Following COP 15, a global multilateral benefit-sharing mechanism for monetary benefits is being considered.

The key messages that arise from this study are:

1. There are many different existing and potential applications of DSI that are highly relevant to GRFA, including applications of DSI that is not itself derived from GRFA.

2. The current and potential applications of DSI show that its generation, storage, accessibility and use are fundamental to the characterization of GRFA and important to efforts to make agriculture more sustainable.

3. Access to and use of DSI face serious obstacles in many countries. There is an urgent need to address the root causes of these problems, which include lack of technical infrastructure, financial and human resources, educational and training opportunities, scientific collaboration, computing infrastructure, reliable electricity and high-speed internet, and may in the future possibly include prohibitive charges for database use.

4. There is a need for a regulatory environment that facilitates access to DSI and the fair and equitable sharing of benefits arising from its use.

References

AHTEG (Ad Hoc Technical Expert Group). 2020. *Report of the Ad Hoc Technical Expert Group on Digital Sequence Information on Genetic Resources, Montreal, Canada, 17–20 March 2020*. CBD/DSI/AHTEG/2020/1/7. Montreal, Canada. https://www.cbd.int/doc/c/ba60/7272/3260b5e396821d42bc21035a/dsi-ahteg-2020-01-07-en.pdf

Ambavaram, M.M.R., Ali, A., Ryan, K.P., Peoples, O., Snell, K.D. & Somleva, M.N. 2018. Novel transcription factors PvBMY1 and PvBMY3 increase biomass yield in greenhouse-grown switchgrass (*Panicum virgatum* L.). *Plant Science*, 273: 100–109. https://doi.org/10.1016/j.plantsci.2018.04.003

Antonelli, A., Fry, C., Smith, R.J., Simmonds, M.S.J., Kersey, P.J., Pritchard, H.W., Abbo, M.S. *et al.* 2020. *State of the world's plants and fungi*. Kew, UK, Royal Botanic Gardens. https://doi.org/10.34885/172

Arita, M., Karsch-Mizrachi, I. & Cochrane, G. 2021. The international nucleotide sequence database collaboration. *Nucleic Acids Research*, 49(D1): D121–D124. https://doi.org/10.1093/nar/gkaa967

Bagley, M., Karger, E., Ruiz Muller, M., Perron-Welch, F. & Thambisetty, S. 2020. *Fact-finding study on how domestic measures address benefit-sharing arising from commercial and non-commercial use of digital sequence information on genetic resources and address the use of digital sequence information on genetic resources for research and development. Convention on Biological Diversity, Montreal*. Annex. Ad Hoc Technical Expert Group on Digital Sequence Information on Genetic Resources, Montreal, Canada, 17–20 March 2020. CBD/DSI/AHTEG/2020/1/5. Montreal Canada, Secretariat of the Convention on Biological Diversity. https://www.cbd.int/doc/c/428d/017b/1b0c60b47af50c81a1a34d52/dsi-ahteg-2020-01-05-en.pdf

Beagrie, N. & Houghton, J. 2021. *Data-driven discovery: The value and impact of EMBL-EBI managed data resources*. Salisbury, UK, Charles Beagrie, Ltd. https://www.embl.org/documents/wp-content/uploads/2021/10/EMBL-EBI-impact-report-2021.pdf

Benson, D.A., Karsch-Mizrachi, I., Lipman, D.J., Ostell, J. & Sayers, E.W. 2011. GenBank. *Nucleic Acids Research*, 39(Database issue): D32–D37. https://doi.org/10.1093/nar/gkq1079.

Blackwell, M. 2011. The Fungi: 1, 2, 3 … 5.1 million species? *American Journal of Botany*, 98(3): 426–438. https://doi.org/10.3732/ajb.1000298

Boamah, G.A., Huang, Z., Shen, Y., Lu, Y., Wang, Z., Su, Y., Xu, C., Luo, X., Ke, C. & Yu, W. 2022. Transcriptome analysis reveals fluid shear stress (FSS) and atherosclerosis pathway as a candidate molecular mechanism of short-term low salinity stress tolerance in abalone. *BMC Genomics* 23: 392. https://doi.org/10.1186/s12864-022-08611-8

Bonanomi, G., De Filippis, F., Zotti, M., Idbella, M., Cesarano, G., Al-Rowaily, S. & Abd-ElGawad, A. 2020. Repeated applications of organic amendments promote beneficial microbiota, improve soil fertility and increase crop yield. *Applied Soil Ecology*, 156: 103714. https://doi.org/10.1016/j.apsoil.2020.103714

CABI (CAB International). 2022a. *CABI centres*. Cited 12 December 2022. https://www.cabi.org/what-we-do/cabi-centres/

CABI. 2022b. *How we work*. Cited 12 December 2022. https://www.cabi.org/what-we-do/how-we-work/

CABI. 2022c. *Projects*. Cited 12 December 2022. https://www.cabi.org/what-we-do/cabi-projects/

CABI. 2022d. *CABI ABS policy*. https://www.cabi.org/wp-content/uploads/PDFs/AboutCABI/Cabi-Abs-Policy-Draft-For-Website-May2018.pdf

Calderini, D.F., Castillo, F.M., Arenas-M, A., Molero, G., Reynolds, M.P., Craze, M., Bowden, S. *et al.* 2021. Overcoming the trade-off between grain weight and number in wheat by the ectopic expression of expansin in developing seeds leads to increased yield potential. *New Phytologist*, 230(2): 629–640. https://doi.org/10.1111/nph.17048

Cantelli, G., Bateman, A., Brooksbank, C., Petrov, A.I., Malik-Sheriff, R.S., Ide-Smith, M., Hermjakob, H. *et al.* 2022. The European Bioinformatics

Institute (EMBL-EBI) in 2021. *Nucleic Acids Research*, 50: D11–D19. https://doi.org/10.1093/nar/gkab1127

CBD (Secretariat of the Convention on Biological Diversity). 2011. *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: text and annex*. Montreal, Canada. http://dx.doi.org/10.25607/OBP-789

CBD. 2016. *Decision 2/5. Cooperation with other international organizations, conventions and initiatives.* Conference of the Parties to the Convention on Biological Diversity Serving as the Meeting of the Parties to the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization. Second meeting Cancun, Mexico, 4–17 December 2016. CBD/NP/MOP/DEC/2/5. Montreal, Canada. https://www.cbd.int/doc/decisions/np-mop-02/np-mop-02-dec-05-en.pdf

CBD. 2018. *Decision14/20. Digital sequence information on genetic resources.* CBD/COP/DEC/14/20 30 November 2018. Conference of the Parties to the Convention on Biological Diversity Fourteenth meeting Sharm El-Sheikh, Egypt, 17-29 November 2018. Montreal, Canada. https://www.cbd.int/doc/decisions/cop-14/cop-14-dec-20-en.pdf

CBD. 2021. *Policy options for access and benefit sharing and digital sequence information.* Summary of webinar held on line April 2021. Montreal, Canada. https://www.cbd.int/abs/DSI-webinar/DSIPolicyOptions2021.pdf

CBD. 2022. *Decision 15/9 Digital sequence information on genetic resources.* CBD/COP/DEC/15/9, 19 December 2022. Conference of the Parties to the Convention on Biological Diversity, Fifteenth meeting – Part II, Montreal, Canada, 7–19 December 2022. Montreal, Canada. https://www.cbd.int/doc/decisions/cop-15/cop-15-dec-09-en.pdf

Chen, J.H., Chen, S.T., He, N.Y., Wang, Q.-L., Zhao, Y., Gao, W. & Guo, F.-Q. 2020. Nuclear-encoded synthesis of the D1 subunit of photosystem II increases photosynthetic efficiency and crop yield. *Nature Plants*, 6: 570–580. https://doi.org/10.1038/s41477-020-0629-z

Chen, Q., Chai, Y., Zhang, W., Cheng, Y., Zhang, Z., An, Q., Chen, S., Man, C., Du, L., Zhang, W. *et al.* 2022. Whole-genome sequencing reveals the genomic characteristics and selection signatures of Hainan black goat. *Genes*, 2022, 13: 1539. https://doi.org/10.3390/genes13091539

Chibeba, A.M., Kyei-Boahen, S., de Fátima Guimarães, M., Nogueira, M.A. & Hungria, M. 2017. Isolation, characterization and selection of indigenous *Bradyrhizobium* strains with outstanding symbiotic performance to increase soybean yields in Mozambique. *Agriculture, Ecosystems & Environment*, 246: 291–305. https://doi.org/10.1016/j.agee.2017.06.017

Chowhan, L.B., Mir, M.I., Sabra, M.A., El-Habbab, A.A. & Kumar, B.K. 2023. Plant growth promoting and antagonistic traits of bacteria isolated from forest soil samples. *Iranian Journal of Microbiology*, 15: 278–289. https://doi.org/10.18502/ijm.v15i2.12480

CNCB-NGDC (China National Center for Bioinformation - National Genomics Data Center). 2022. Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2022. *Nucleic Acids Research*, 50(D1): D27–D38. https://doi.org/10.1093/nar/gkab951

Cochrane, G. 2022. Genomic data for biodiversity – a global challenge**,** an exploration of where in the world genomics methods are applied and where the data are used. In: *EMBL-EBI*, Hinxton, UK. Cited 13 December 2022. https://www.ebi.ac.uk/about/news/perspectives/genomic-data-for-biodiversity-a-global-challenge/

Cook, C.E., Stroe, O., Cochrane, G., Birney, E. & Apweiler, R. 2020. The European Bioinformatics Institute in 2020: building a global infrastructure of interconnected data resources for the life sciences, *Nucleic Acids Research*, 48(D1): D17–D23. https://doi.org/10.1093/nar/gkz1033

Cowell, C., Paton, A., Borrell, J.S., Williams, C., Wilkin, P., Antonelli, A., Baker, W.J. *et al*. 2022. Uses and benefits of digital sequence information from plant genetic resources: lessons learnt from botanical collections. *Plants People Planet*, 4(1): 33–43. https://doi.org/10.1002/ppp3.10216

de los Ríos-Pérez, L., Nguinkal, J.A., Verleih, M. Rebl, A., Brunner, R.M., Klosa, J., Schäfer, N. *et al.* 2020. An ultra-high density SNP-based linkage map for enhancing the pikeperch (*Sander lucioperca*) genome assembly to chromosome-scale. *Science Reports*, 10: 22335. https://doi.org/10.1038/s41598-020-79358-z

DSI Network. 2022. *The CBD DSI Matrix: how do the DSI policy options measure up?* Cited 6 June

2023. https://www.dsiscientificnetwork.org/dsi-policy-options-for-benefit-sharing-by-dsi-scientific-network-2/

Duy, N.D., Dao, D.T.H., Dung, N.H., Nhung, V.T.T., Vu, P.A., Loan, L.Q., Diep, H.T. *et al.* 2022. Isolation and characterization of novel *Rhodobacter* spp. with the sodium removal ability from mangrove forest sediment in Southeast Vietnam. *Asian Journal of Agriculture and Biology*, 2022(1): 202012575. DOI: https://doi.org/10.35495/ajab.2020.12.575

Ebenezer, T.E., Muigai, A.W.T., Nouala, S., Badaoui, B., Blaxter, M., Buddie, A.G., Jarvis, E.D. *et al.* 2022. Africa: sequence 100,000 species to safeguard biodiversity. *Nature*, 603(7901): 388–392. https://doi.org/10.1038/d41586-022-00712-4

Edwards, D. & Batley, J. 2009. Plant genome sequencing: applications for crop improvement. *Plant Biotechnology Journal* 8(1): 2–9. https://doi.org/10.1111/j.1467-7652.2009.00459.x

Ellison, C.A., Pollard, K.M. & Varia, S. 2020. Potential of a coevolved rust fungus for the management of Himalayan balsam in the British Isles: first field releases. *Weed Research*, 60(1): 37–49. https://doi.org/10.1111/wre.12403

EMBL-EBI (European Molecular Biology Laboratory - European Bioinformatics Institute). 2022a. *Improving metadata for genomic sequences.* Cited 12 December 2022. https://www.ebi.ac.uk/about/news/technology-and-innovation/ena-new-metadata/

EMBL-EBI. 2022b. *European Nucleotide Archive (ENA) and International Nucleotide Sequence Databases (INSDC) Policies.* Cited 12 December 2022. https://www.ebi.ac.uk/ena/browser/about/policies

FAO. 2021. *Digital sequence information on genetic resources for food and agriculture: innovation opportunities, challenges and implications.* Commission on Genetic Resources for Food and Agriculture Eighteenth Regular Session 27 September – 1 October 2021. CGRFA-18/21/5. Rome. https://www.fao.org/3/ng847en/ng847en.pdf

Fleischmann, R.D., Adams, M.D., White, O., Clayton, R.A., Kirkness, E.F., Kerlavage, A.R., Bult, C.J. *et al.* 1995. Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd. *Science*, 269(5223): 496–512. https://www.science.org/doi/10.1126/science.7542800

Forin, N., Nigris, S., Voyron, S., Girlanda, M., Vizzini A., Casadoro, G. & Baldan, B. 2018 Next generation sequencing of ancient fungal specimens: the case of the Saccardo Mycological Herbarium. *Frontiers in Ecology and Evolution*, 6: 129. https://www.frontiersin.org/article/10.3389/fevo.2018.00129

GBA (Global Biofoundry Alliance). 2022. *Global Biofoundry Alliance.* Cited 12 December 2022. https://biofoundries.org/

GBC (Global Biodata Coalition). 2022. *Global Biodata Coalition.* Cited 12 December 2022. https://globalbiodata.org/

Gupta, S., Schillaci, M. & Roessner, U. 2022. Metabolomics as an emerging tool to study plant–microbe interactions. *Emerging Topics in Life Sciences*, 6(2): 175–183. https://doi.org/10.1042/ETLS20210262

Halewood, M., Lopez Noriega, I., Ellis, D., Roa, C., Rouard, M. & Hamilton, R.S. 2017. *Potential implications of the use of digital sequence information on genetic resources for the three objectives of the Convention on Biological Diversity. A submission from CGIAR to the Secretary of the Convention on Biological Diversity.* Rome, Bioversity International. https://cgspace.cgiar.org/handle/10568/92049

Hawksworth, D.L. & Lücking, R. 2017. Fungal diversity revisited: 2.2 to 3.8 million species. *Microbiology Spectrum*, 5(4): FUNK-0052-2016. https://doi.org/10.1128/microbiolspec.FUNK-0052-2016

Hayes, B.J. & Daetwyler, H.D. 2019. 1000 Bull Genomes Project to map simple and complex genetic traits in cattle: applications and outcomes. *Annual Review of Animal Biosciences*, 7: 89–102. https://www.annualreviews.org/doi/abs/10.1146/annurev-animal-020518-115024

HBC (Harvard Chan Bioinformatics Core). 2022. *Accessing public NGS sequencing data. Tutorials on accessing public reference and genomic data.* Cited 12 December 2022. https://hbctraining.github.io/Accessing_public_genomic_data/lessons/accessing_public_experimental_data_odyssey.html

Heinemann, J.A., Coray, D.S. & Thaler, D.S. 2018. *Exploratory fact-finding scoping study on "Digital Sequence Information" on genetic resources for food and agriculture.* Commission on Genetic Resources for Food and Agriculture: Background Study Paper No. 68. Rome. FAO.

https://www.fao.org/3/CA2359EN/ca2359en.pdf

Hillson, N., Caddick, M., Cai, Y. Carrasco, J.A., Chang, M.W., Curach, N.C., Bell, D.J. *et al.* 2019. Building a global alliance of biofoundries. *Nature Communications*, 10: 2040. https://doi.org/10.1038/s41467-019-10079-2

Hong, Z., He,W., Liu, X., Tembrock, L.R., Wu, Z., Xu, D. & Liao, X. 2022. Comparative analyses of 35 complete chloroplast genomes from the genus *Dalbergia* (Fabaceae) and the identification of DNA barcodes for tracking illegal logging and counterfeit rosewood. *Forests*, 13: 626. https://doi.org/10.3390/f13040626

Hotaling, S., Kelleya, J.L. & Frandsen, P.B. 2021. Toward a genome sequence for every animal: where are we now? *Proceedings of the National Academy of Sciences of the United States of America*, 118 (52): e2109019118. https://doi.org/10.1073/pnas.2109019118

Hotaling, S. Sproul, J.S., Heckenhauer, J., Powell, A., Larracuente, A.M., Pauls, S.U., Kelley, J.L. & Frandsen, P.B. 2021a. Long reads are revolutionizing 20 years of insect genome sequencing, *Genome Biology and Evolution*, 13(8): evab138. https://doi.org/10.1093/gbe/evab138

Hurgobin, B. & Lewsey, M.G. 2022a. How 'omics technologies can drive plant engineering, ecosystem surveillance, human and animal health. *Emerging Topics in Life Sciences*, 6(2): 137–139. https://doi.org/10.1042/ETLS20220020

Hurgobin, B. & Lewsey, M.G. 2022b. Applications of cell- and tissue-specific 'omics to improve plant productivity. *Emerging Topics in Life Sciences*, 136(2): 163–173. https://doi.org/10.1042/ETLS20210286

Javal, M., Terblanche, J.S, Conlong, D.E., Delahaye, N., Grobbelaar, E., Benoit, L., Lopez-Vaamonde, C. & Haran J.M. 2021. DNA barcoding for bio-surveillance of emerging pests and species identification in Afrotropical Prioninae (Coleoptera, Cerambycidae). *Biodiversity Data Journal*, 9: e64499. https://doi.org/10.3897/BDJ.9.e64499

John, J. 2016. Experts hack away at portable DNA barcode scanner to fight timber and wildlife trafficking. In: *Mongabay*. Cited 16 June 2023. https://wildtech.mongabay.com/2016/09/experts-hack-away-portable-dna-barcode-scanner-fight-timber-wildlife-trafficking/

Kalaitzidou, M.P., Alvanou, M.V., Papageorgiou, K.V., Lattos, A., Sofia, M.; Kritas, S.K., Petridou, E. & Giantsis, I.A. 2022. Pollution indicators and HAB-associated halophilic bacteria alongside harmful cyanobacteria in the largest mussel cultivation area in Greece. *International Journal of Environmental Research and Public Health*, 19: 5285. https://doi.org/10.3390/ijerph19095285.

Kates, H.R., Doby, J.R., Siniscalchi, C.M., LaFrance, R., Soltis, D.E., Soltis, P.S., Guralnick, R.P. & Folk, R.A. 2021. The effects of herbarium specimen characteristics on short-read NGS sequencing success in nearly 8000 specimens: old, degraded samples have lower DNA yields but consistent sequencing success. *Frontiers in Plant Science*, 12: 669064. https://doi.org/10.3389/fpls.2021.669064

Kong, X., Lv, L., Ren, J., Liu, Y., Lin, Z. & Dong, Y. 2022. Comparative transcriptome analyses unravel the response to acute thermal stress in the razor clam, *Sinonovacula constricta*. *Aquaculture Reports*, 23: 101079, ISSN 2352-5134, https://doi.org/10.1016/j.aqrep.2022.101079.

Korkuć, P., Neumann, G.B., Hesse, D., Arends, D., Reißmann, M., Rahmatalla, S., May, K. *et al.* 2023. Whole-genome sequencing data reveal new loci affecting milk production in German Black Pied cattle (DSN). *Genes*, 14: 581. https://doi.org/10.3390/genes14030581

Land, M., Hauser, L., Jun, S.R. Nookaew, I., Leuze, M.R., Ahn, T-H, Karpinets, T. *et al.* 2015. Insights from 20 years of bacterial genome sequencing. *Functional & Integrative Genomics*, 15(2): 141–161. https://doi.org/10.1007/s10142-015-0433-4

Lange, M., Alako, B.T.F., Cochrane, G., Ghaffar, M., Mascher, M., Habekost, P-K., Hillebrand, U. *et al.* 2021. Quantitative monitoring of nucleotide sequence data from genetic resources in context of their citation in the scientific literature. *GigaScience*, 10(12): giab084, https://doi.org/10.1093/gigascience/giab084

Lattos, A., Papadopoulos, D.K., Feidantsis, K., Karagiannis, D., Giantsis, I.A. & Michaelidis, B. 2022. Are marine heatwaves responsible for mortalities of farmed *Mytilus galloprovincialis*? A pathophysiological analysis of *Marteilia* infected mussels from Thermaikos Gulf, Greece. *Animals*, 12: 2805. https://doi.org/10.3390/ani12202805

Lewin, H.A., Robinson, G.E., Kress, W.J., Baker, W.J., Coddington, J. Crandall, K.A., Durbin, R. *et al.* 2018. Earth BioGenome Project: sequencing

life for the future of life. *Proceedings of the National Academy of Sciences of the United States of America*, 115(17): 4325–4333. https://doi.org/10.1073/pnas.1720115115

Lewin, H.A., Richards, S., Aiden, E.L., Archibald, J.M., Bálint, M., Barker, K.B., Baumgartner, B. *et al.* 2022. The Earth BioGenome Project 2020: starting the clock. *Proceedings of the National Academy of Science U.S.A.*, 119(4): e2115635118. https://doi.org/10.1073/pnas.2115635118

Li, B. & Xue, D. 2019. Application of digital sequence information in biodiversity research and its potential impact on benefit sharing. *Journal of Biodiversity Science*, 27(12): 1379–1385. DOI: 10.17520/biods.2019242. https://www.biodiversity-science.net/EN/10.17520/biods.2019242

Li, F., Zhao, X., Li, M., He, K., Huang, C., Zhou, Y., Li, Z. & Walters, J.R. 2019. Insect genomes: progress and challenges. *Insect Molecular Biology* 28, 739–758. https://doi.org/10.1111/imb.12599

Li, Y., Lu, X., Gao, W., Yu, L., Wen, H., Jiang, M., Tian, J. & Wu, F. 2022. The effect of dietary paeonol on growth performance, antioxidant enzyme activities and gene expressions of genetic improvement of farmed tilapia juveniles (*Oreochromis niloticus*). *Aquaculture Reports*, 26, 2022, 101302, ISSN 2352-5134. https://doi.org/10.1016/j.aqrep.2022.101302.

Louca, S., Mazel, F., Doebeli, M. & Parfrey, L.W. 2019. A census-based estimate of earth's bacterial and archaeal diversity. *PLoS Biology*, 17(2): e3000106. https://doi.org/10.1371/journal.pbio.3000106.

Lyal, C.H.C. 2022. Digital sequence information on genetic resources and the convention on biological diversity. In: E. Chege Kamau, ed. *Global transformations in the use of biodiversity for research and development*. Ius Gentium: Comparative Perspectives on Law and Justice, 95, pp. 589–619. Cham, Switzerland, Springer.

Mark Cigan, A. & Knap, P.W. 2022. Technical considerations towards commercialization of porcine respiratory and reproductive syndrome (PRRS) virus resistant pigs. *CABI Agriculture and Bioscience* 3: 34. https://doi.org/10.1186/s43170-022-00107-5

Matthes, N., Pietsch, K., Rullmann, A. Näumann, G., Pöpping, B. & Szabo, K. 2020. The Barcoding Table of Animal Species (BaTAnS): a new tool to select appropriate methods for animal species identification using DNA barcoding. *Molecular Biology Reports*, 47: 6457–6461. https://doi.org/10.1007/s11033-020-05675-1

Morand, S. 2018. Advances and challenges in barcoding of microbes, parasites, and their vectors and reservoirs. *Parasitology*, 145(5): 537–542. https://doi.org/10.1017/S0031182018000884

Muhich, A.J., Agosto-Ramos, A. & Kliebenstein, D.J. 2022. The ease and complexity of identifying and using specialized metabolites for crop engineering. *Emerging Topics in Life Sciences*, 6(2): 153–162. https://doi.org/10.1042/ETLS20210248

Nature. 2022. *Data repository guidance*. Cited 12 December 2022. https://www.nature.com/sdata/policies/repositories

Nayan, V., Singh, K., Iquebal, M.A., Jaiswal, S., Bhardwaj, A., Singh, C., Bhatia, T. *et al.* 2022. Genome-wide DNA methylation and its effect on gene expression during subclinical mastitis in water buffalo. *Frontiers in Genetics*, 13: 828292. https://doi.org/10.3389/fgene.2022.828292

NCBI (National Center for Biotechnology Information). 2022. National Center for Biotechnology Information. In: *National Library of Medicine*. Bethesda, USA. Cited 12 December 2022. www.ncbi.nlm.nih.gov/genbank/

NHGRI (National Human Genome Research Institute). 2020. *DNA sequencing fact sheet*. Cited 12 December 2022. https://www.genome.gov/about-genomics/fact-sheets/DNA-Sequencing-Fact-Sheet

NHGRI. 2022. *DNA sequencing costs: data*. Cited 12 December 2022. https://www.genome.gov/about-genomics/fact-sheets/DNA-Sequencing-Costs-Data

Niu, Q., Zhang, T., Xu, L., Wang, T., Wang, Z., Zhu, B., Gao, X. *et al.* 2021. Identification of candidate variants associated with bone weight using whole genome sequence in beef cattle. *Frontiers in Genetics*, 12:750746. doi: 10.3389/fgene.2021.750746. https://www.frontiersin.org/articles/10.3389/fgene.2021.750746/full

Nucleic Acids Research. 2017. Nucleic acid sequence, structure, and regulation. *Nucleic Acids Research*, 45: D1 (Database Issue). https://academic.oup.com/nar/issue/45/D1

Octaviana, S., Primahana, G., Mozef, T., Borges, L.G.A., Pieper, D.H. & Wink, J. 2023. Diversity of Myxobacteria isolated from Indonesian mangroves and their potential for new antimicrobial sources. *Current Microbiology*, 80: 46. https://doi.org/10.1007/s00284-022-03066-2

OEWG (Open-Ended Working Group). 2021a. *Digital sequence information on genetic resources. Note by the Executive Secretary*. OEWG on the Post-2020 Global Biodiversity Framework, third meeting (online), 23 August – 3 September 2021. CBD/WG2020/3/4. Montreal, Canada. https://www.cbd.int/doc/c/afd4/4df3/d2d62f-5f6a1bfe367c7448f4/wg2020-03-04-en.pdf.

OEWG. 2021b. *Information from the Commission on Genetic Resources for Food and Agriculture related to digital sequence information on genetic resources.* Open-Ended Working Group on the Post-2020 Global Biodiversity Framework, third meeting (resumed), Geneva, Switzerland, 12–28 January 2022. CBD/WG2020/3/INF/9. Montreal, Canada. https://www.cbd.int/doc/c/986f/cb0e/07d17d0f56a7fac64bffc90f/wg2020-03-inf-09-en.pdf

OEWG. 2021c. *Digital sequence information on genetic resources. Addendum: Note by the Executive Secretary*. Open-Ended Working Group (OEWG) on the Post-2020 Global Biodiversity Framework, third meeting (resumed), Geneva, Switzerland, 12–28 January 2022. CBD/WG2020/3/4/Add.1. Montreal, Canada. https://www.cbd.int/doc/c/1081/7ad0/05a4577d6c756e8d2f6cb22f/wg2020-03-04-add1-en.pdf

Onyia, C.O., Ilo, O.P., Obih, C.E., Ugbogu, O., Ojiego, B.O., Rufai, S.S., Onyemaechi, P.S. & Chukwuma, E.C. 2022. DNA barcoding of Nigeria's forest species listed in CITES and other endangered plant species of national interest. *American Journal of Plant Sciences* 13: 1335–1346. https://doi.org/10.4236/ajps.2022.1311090

Palminteri, S. 2017. DNA barcoding helps identify endangered species from market specimens of sharks and rays. In: *Mongabay*. Cited 12 December 2022. https://news.mongabay.com/2017/09/dna-barcoding-helps-identify-endangered-species-from-market-specimens/

Pedris, L. 2017. Scanning the barcode of wildlife. In: *Mongabay*. Cited 12 December 2022. https://news.mongabay.com/2017/02/scanning-the-barcode-of-wildlife/

Peng, W., Zhang, Y., Gao, L., Feng, C., Yang, Y., Li, B., Wu, L. *et al.* 2022. Analysis of world-scale mitochondrial DNA reveals the origin and migration route of East Asia goats. *Frontiers in Genetics*, 13: 796979. https://doi.org/10.3389/fgene.2022.796979

Qin, H., Gu, Q., Zhang, J., Sun, L., Kuppu, S., Zhang, Y., Burow, M. *et al.* 2011. Regulated expression of an isopentenyltransferase gene (IPT) in peanut significantly improves drought tolerance and increases yield under field conditions. *Plant and Cell Physiology*, 52(11): 1904–1914. https://doi.org/10.1093/pcp/pcr125

Richardson, S.M., Mitchell, L.A., Stracquadanio, G., Yang, K., Dymond, J.S., Dicarlo, J.E., Lee, D. *et al.* 2017. Design of a synthetic yeast genome. *Science*, 355(53223): 1040–1044. https://www.science.org/doi/10.1126/science.aaf4557

Rigden, D.J. & Fernández, X.M. 2022. The 2022 Nucleic Acids Research database issue and the online molecular biology database collection, *Nucleic Acids Research*, 50: D1–D10. https://doi.org/10.1093/nar/gkab1195

Rohden, F., Huang, S., Dröge, G. & Scholz, A.H. 2020. *Combined study on digital sequence information in public and private databases and traceability.* Annex 1. Ad Hoc Technical Expert Group on Digital Sequence Information on Genetic Resources, Montreal, Canada, 17–20 March 2020. CBD/DSI/AHTEG/2020/1/4. Montreal, Canada, Secretariat of the Convention on Biological Diversity. https://www.cbd.int/doc/c/1f8f/d793/57cb114ca40cb6468f479584/dsi-ahteg-2020-01-04-en.pdf

Rotter, A., Gaudêncio, S.P., Klun, K., Macher, J.-N., Thomas, O.P., Deniz, I., Edwards, C. *et al.* 2021. A new tool for faster construction of marine biotechnology collaborative networks. *Frontiers in Marine Science*, 8: 685164. https://doi.org/10.3389/fmars.2021.685164

Royal Entomology Society. 2023. *Facts and figures.* Cited 13 June 2023. https://www.royensoc.co.uk/understanding-insects/facts-and-figures/

Ruiz Muller, M. 2018. *Access to genetic resources and benefit sharing 25 years on: progress and challenges.* Issue Paper No. 44. Geneva, Switzerland, International Centre for Trade and Sustainable Development (ICTSD). https://www.voices4biojustice.org/wp-content/uploads/2018/12/Access-to-Genetic-Resources-and-Benefit-Sharing-25-Years-On-Progress-and-Challenges.pdf

Samuel, B., Mengistie, D., Assefa, E., Kang, M., Park, C., Dadi, H. & Dinka, H. 2022. Genetic diversity of DGAT1 gene linked to milk production in cattle populations of Ethiopia. *BMC Genomic*

Data, 23: 64. https://doi.org/10.1186/s12863-022-01080-8

Sayers, E.W., Cavanaugh, M., Clark, K., Pruitt, K.D., Schoch, C.L., Sherry, S.T. & Karsch-Mizrachi, I. 2022a. GenBank, *Nucleic Acids Research*, 50: D161–D164. https://doi.org/10.1093/nar/gkab1135

Sayers, E.W., Bolton, E.E., Brister, J.R., Canese, K., Chan, J., Comeau, D.C., Connor, R. *et al.* 2022b. Database resources of the National Center for Biotechnology Information, *Nucleic Acids Research*, 50: D20–D26. https://doi.org/10.1093/nar/gkab1112

Schilling, R.K., Marschner, P., Shavrukov, Y., Berger, B., Tester, M., Roy, S.J. & Plett, D.C. 2013. Expression of the Arabidopsis vacuolar H+-pyrophosphatase gene (AVP1) improves the shoot biomass of transgenic barley and increases grain yield in a saline field. *Plant Biotechnology Journal*, 12(3): 378–386. https://doi.org/10.1111/pbi.12145

Scholz, A.H., Lange, M., Habekost, P., Oldham, P., Cancio, I., Cochrane, G. & Freitag, J. 2021. Myth-busting the provider-user relationship for digital sequence information, *GigaScience*, 10(12): giab085. https://doi.org/10.1093/gigascience/giab085

Si, T., Chao, R., Min, Y., Wu, Y., Ren, W. & Zhao. H. 2017. Automated multiplex genome-scale engineering in yeast. *Nature Communications*, 8: 15187. https://doi.org/10.1038/ncomms15187

Silvestri, L., Sosa, A., McKay, F., Diniz Vitorino, M., Hill, M., Zachariades, C. & Hight, S. 2019. The Nagoya Protocol and its implications for classical weed biological control. In: H.L. Hinz, M.-C. Bon, G. Bourdôt, M. Cristofaro, G. Desurmont, D. Kurose & H. Müller-Schärer, eds. *Proceedings of the XV International Symposium on Biological Control of Weeds, Engelberg, Switzerland*, pp. 304–309. https://bugwoodcloud.org/resource/files/15115.pdf

Singh, R. & Goodwin, S.B. 2022. Exploring the corn microbiome: a detailed review on current knowledge, techniques, and future directions. *PhytoFrontiers*, 3(2): 158–175. https://doi.org/10.1094/PHYTOFR-04-21-0026-RVW

Smith, D., Hinz, H., Mulema, J., Weyl, P. & Ryan, M.J. 2018. Biological control and the Nagoya Protocol on access and benefit sharing – a case of effective due diligence. *Biocontrol Science and Technology*, 28(10): 914–926. https://doi.org/10.1080/09583157.2018.1460317

Smith, D., Ryan, M.J., Luke, B., Djeddour, D., Seier, M.K., Varia, S., Pollard, K.M. *et al.* 2021. *CABI UK and Nagoya Protocol triggered benefit sharing*. CABI Working Paper 25. Egham, UK, CABI. https://www.cabi.org/wp-content/uploads/Working-Paper-25.pdf

Sohn, H.B., Lee, H.Y., Seo, J.S., Jung, C., Jeon, J.H., Kim, J.H., Lee, Y.W. *et al.* 2011. Overexpression of jasmonic acid carboxyl methyltransferase increases tuber yield and size in transgenic potato. *Plant Biotechnology Reports*, 5: 27–34. https://doi.org/10.1007/s11816-010-0153-0

Sun, X., Wu, B., Tu, K., Zhou, L., Yang, A. & Liu, Z. 2022b. Transcriptome and metabolome analyses provide insights into the salinity adaptation of clam *Ruditapes philippinarum*, *Aquaculture Reports*, 27: 101368, ISSN 2352–5134. https://doi.org/10.1016/j.aqrep.2022.101368.

Sun, Y., Shang, L., Zhu, Q-H., Fan, L. & Guo, L. 2022a. Twenty years of plant genome sequencing: achievements and challenges. *Trends in Plant Science*, 27: 391–401. https://doi.org/10.1016/j.tplants.2021.10.006

Supple, M.A. & Shapiro, B. 2018. Conservation of biodiversity in the genomics era. *Genome Biology*, 19: 131. https://doi.org/10.1186/s13059-018-1520-3

Vallarino, J.G., Kubiszewski-Jakubiak, S., Ruf, S., Rößner, M., Timm, S., Bauwe, H., Carrari, F. *et al.* 2020. Multi-gene metabolic engineering of tomato plants results in increased fruit yield up to 23%. *Science Reports*, 10: 17219. https://doi.org/10.1038/s41598-020-73709-6

Vogel, J.H., Muller, M.R., Angerer, K., Delgado-Gutiérrez, D. & Ballón, A.G. 2022. Bounded openness: a robust modality of access to genetic resources and the sharing of benefits. *Plants People Planet*, 4(1): 13–22. doi.org/10.1002/ppp3.10239

Whitfield, J. 2003. DNA barcodes catalogue animals. *Nature*. https://doi.org/10.1038/news030512-7

Wiryawan, A., Eginarta, W. S., Hermanto, F. E., Ustiatik, R., Dinira, L. & Mustafa, I. 2022. Changes in essential soil nutrients and soil disturbance directly affected soil microbial community structure – a metagenomic approach. *Journal of Ecological Engineering*, 23: 238–245. https://doi.org/10.12911/22998993/149972

WHO (World Health Organization). 2017. *Comments by the World Health Organization on the draft factfinding and scoping study "The emergence*

and growth of digital sequence information in research and development: implications for the conservation and sustainable use of biodiversity, and fair and equitable benefit sharing" dated 9 November 2017. Geneva, Switzerland. https://www.cbd.int/abs/DSI-peer/WHO.pdf

WiLDSI (Wissenschaftsbasierte Lösungsansätze für Digitale Sequenzinformation). 2020. *Finding compromise on ABS & DSI in the CBD: requirements & policy ideas from a scientific perspective*. WiLDSI White Paper. https://www.dsmz.de/fileadmin/user_upload/C

Wilkinson, M., Dumontier, M., Aalbersberg, I., Appleton, M., Axton, A., Baak, N., Blomberg, *et al.* 2016. The FAIR Guiding Principles for scientific data management and stewardship. *Science Data*, 3: 160018. https://doi.org/10.1038/sdata.2016.18

Yang, W., Liu, Z., Zhao, Q., Du, H., Yu, J., Wang, H., Liu, X., *et al.* 2022 Population genetic structure and selection signature analysis of Beijing Black pig. *Frontiers in Genetics*, 13: 860669. https://doi.org/10.3389/fgene.2022.860669

Yu, N., Zeng, W., Xiong, Z. & Liu, Z. 2022a. A high efficacy DNA vaccine against Tilapia lake virus in Nile tilapia (*Oreochromis niloticus*). *Aquaculture Reports*, 24: 101166. https://doi.org/10.1016/j.aqrep.2022.101166.

Yu, X., Mengistu, S.B., Mulder, H.A., Palstra, A.P., Benzie, J.A.H., Trinh, T.Q. Groenen, M.A.M., Komen, H. & Megens, H.-J. 2022b. Quantitative trait loci controlling swimming performance and their effect on growth in Nile tilapia (*Oreochromis niloticus*). *Aquaculture*, 560: 738522. https://doi.org/10.1016/j.aquaculture.2022.738522.

Zhang, S., Peng, G. & Xia, Y. 2010. Microcycle conidiation and the conidial properties in the entomopathogenic fungus *Metarhizium acridum* on agar medium. *Biocontrol Science and Technology*, 20(8): 809–819. https://doi.org/10.1080/09583157.2010.482201

Zhang, Z., Wang, J., Wang, J., Wang, J. & Li, Y. 2020. Estimate of the sequenced proportion of the global prokaryotic genome. *Microbiome*, 8: 134. https://doi.org/10.1186/s40168-020-00903-z

Zhang, Y., Li, W., Lu, P., Xu, T. & Pan, K. 2022a Three preceding crops increased the yield of and inhibited clubroot disease in continuously monocropped Chinese cabbage by regulating the soil properties and rhizosphere microbial community. *Microorganisms*, 10(4): 799. https://doi.org/10.3390/microorganisms10040799

Zhang, Y., Andrews, H., Eglitis-Sexton, J., Godwin, I., Tanurdžić, M. & Crisp, P.A. 2022b. Epigenome guided crop improvement: current progress and future opportunities. *Emerging Topics in Life Sciences*, 6(2): 141–151. https://doi.org/10.1042/ETLS20210258

Zhou, Y., Li, Y., Qi, X., Liu, R., Dong, J., Jing, W., Guo, M. *et al.* 2020. Overexpression of V-type H+ pyrophosphatase gene EdVP1 from *Elymus dahuricus* increases yield and potassium uptake of transgenic wheat under low potassium conditions. *Scientific Reports*, 10: 5020. https://doi.org/10.1038/s41598-020-62052-5

Zhou, Z, Tran, P.Q., Breister, A.M., Liu, Y., Kieft, K., Cowley, E.S., Karaoz, U. & Anantharaman, K. 2022. METABOLIC: high-throughput profiling of microbial genomes for functional traits, metabolism, biogeochemistry, and community-scale functional networks. *Microbiome*, 10: 33. https://doi.org/10.1186/s40168-021-01213-8

Appendix I. CAB Abstracts literature survey

CABI has been gathering data on agriculture for over 100 years, and much of this is presented via CAB Direct.[1] The CAB Abstracts bibliographic database is part of this resource and covers applied life sciences, including agriculture, plant sciences, animal sciences and related subjects. It includes over 10.9 million records dating from 1973 to the present (and an archive covering the period from 1912 to 1973). It is searchable on several platforms, including CAB Direct, which was used in this study. Our search strategy extracted the DSI-related studies from CAB Abstracts and grouped these into various categories, such as dominant crops in FAO regions, various types of terminology used to describe DSI, and examples of actual and potential applications of DSI in food and agriculture.

Original literature survey

The search (carried out at end March 2022) resulted in 1 180 915 hits, which represents the core dataset (DSI data pool) used for further analysis. The majority of the publications concerned plant genetic resources. The results demonstrate the extent and nature of the uses to which DSI is put in the food and agriculture sector. The study presents trends in the growth and use of DSI and looks at the level of publications in each of the identified areas of use of DSI on GRFA. The searches enabled the selection of examples that demonstrate the impact and importance of DSI studies in the food and agriculture sector. The results of these searches showed that DSI on genetic material directly relevant to food and agriculture is of actual or potential value beyond the food and agriculture sector and, conversely, that much DSI originating from other sectors is of relevance to food and agriculture. Thus, DSI might also present scope-related issues.

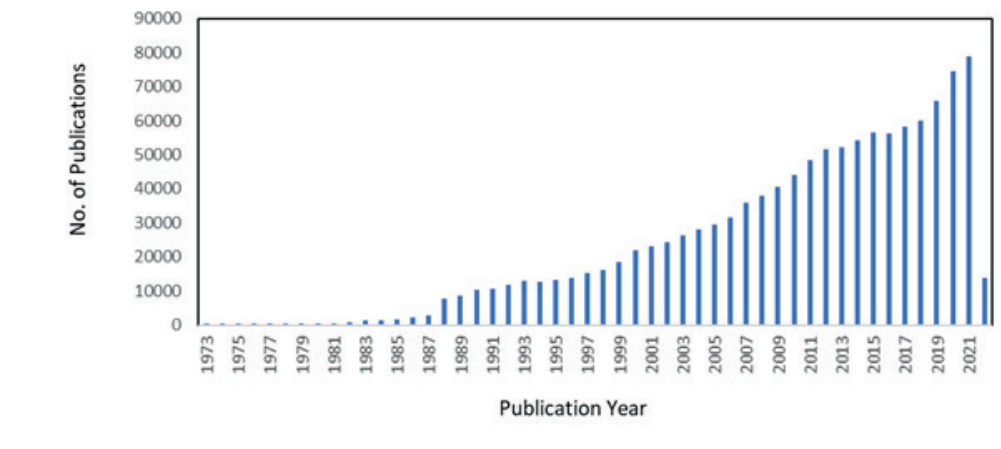
Figure 1 shows the number of records in the database that cite DSI by publication year, reflecting the growth in DSI studies over the years, from the first citation in 1973 to 2022. The first 20 years, from 1973 to 1993, saw publications in the CAB Abstracts database rise to around 10 000 per year, and the number rose eight-fold between 1993 and 2021, with almost 80 000 publications addressing DSI in the latter year. The total of 1 180 915 hits represents almost 11 percent of the papers in CAB Abstracts.

Table 1 compares the FAO regions of the world for the number of publications on five crops (wheat, maize, rice, soybean and potato) that cite DSI as having impact. Asia and the Pacific has by far the greatest number of publications on DSI, followed by Europe and North America. The figures demonstrate the extent to which DSI is reaching into crop improvement and agriculture.

Analysing the content of 1.18 million publications citing gene, protein and metabolite content in the CAB Abstracts database/Food Agriculture/ would be a huge task. Narrowing the analysis by including search parameters related to improved yield, gene technologies and cellular processes and to targeted crops, such as wheat, rice and potato, and livestock, reduced the number of hits considerably, as shown below. However, the task of reading thousands of papers to select examples of use meant that further targeting was needed. Including only records that had “yield increase” in the title, while also limiting the search to the last 11 years, resulted in 287 records. A review of these revealed how genomics and metabolomics have helped improve yields and resistance to disease, drought and increased temperature. Specifically, it showed that genomics has provided a greater understanding of how crop plants function and how DSI can enable interventions in areas such as in photosynthesis (40 papers), nitrogen metabolism (44 papers) and phosphate uptake (11 papers). Additionally, many of the papers were concerned with how DSI enables the exploration of different traits that could contribute to climate-change adaptation, such as drought resistance (29 papers) and heat-

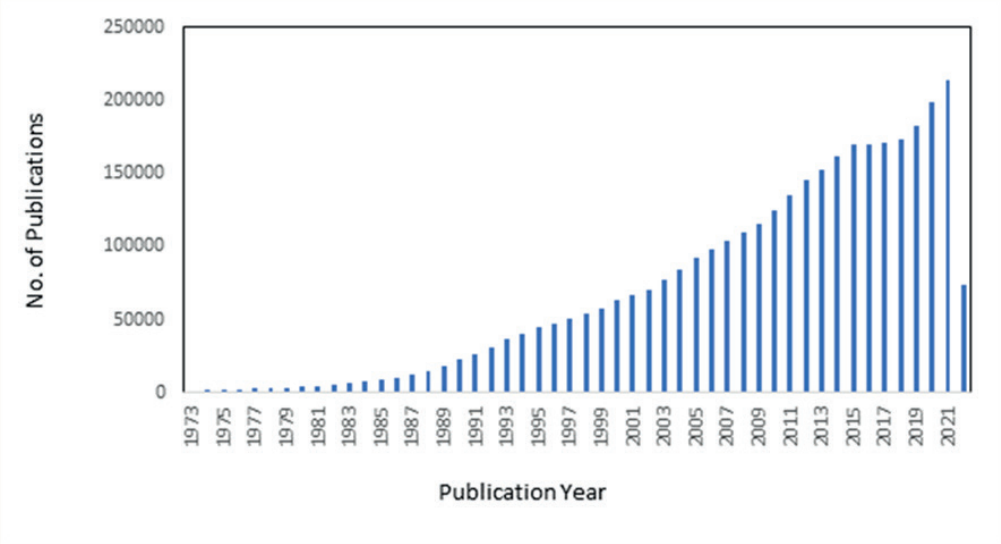
[1] https://www.cabdirect.org

Figure 1. Number of publications in the CAB Abstracts database from 1973 to 2022 that address DSI



Source: Output from CAB Abstracts - Authors elaboration for this background study.

Figure 2. Number of publications in PubMed from 1973 to 2022 that mention DSI



Source: Output from CAB Abstracts database - Authors elaboration for this background study.

stress resistance (50 papers). The types of GRFA addressed in these papers were crops (129 papers) (e.g. wheat [40], rice [86], maize [30], potato [7], yam [5] and tomato [12]), livestock (13) (e.g. cattle [6]), bacteria (28) fungi (15) and viruses (8). Examples were selected to show how generation, analysis and use of DSI are contributing to the improvement of yields and to the future-proofing of food and agriculture with traits that increase drought and heat resistance and hence contribute to climate change adaptation and help improve food security.

Table 1. Number of hits for the top crops in the FAO regions

FAO Regions	Number of hits in DSI pool	Top crops [common name] (no. of hits)
Africa	26 981	*Triticum* [wheat] (967) *Zea mays* [maize] (743) *Oryza sativa* [rice] (313) *Glycine* [soybean] (266) *Solanum tuberosum* [potato] (245)
Asia and the Pacific	128 783	*Oryza sativa* [rice] (8 841) *Triticum* [wheat] (5 945) *Glycine* [soybean] (2 906) *Zea mays* [maize] (1 840) *Solanum tuberosum* [potato] (925)
Europe	53 811	*Triticum* [wheat] (2 179) *Zea mays* [maize] (1 193) *Solanum tuberosum* [potato] (730)
Latin America and the Caribbean	28 438	*Glycine* [soybean] (1 403) *Zea mays* [maize] (1 005) *Triticum* [wheat] (791) *Solanum tuberosum* [potato] (389)
Middle and Near East	22 166	Triticum [wheat] (1792) Oryza sativa [rice] (227) Solanum tuberosum [potato] (217)
North America	45 946	Triticum [wheat] (2 562) Glycine [soybean] (2 173) Zea mays [maize] (1 931) Solanum tuberosum [potato] (630)

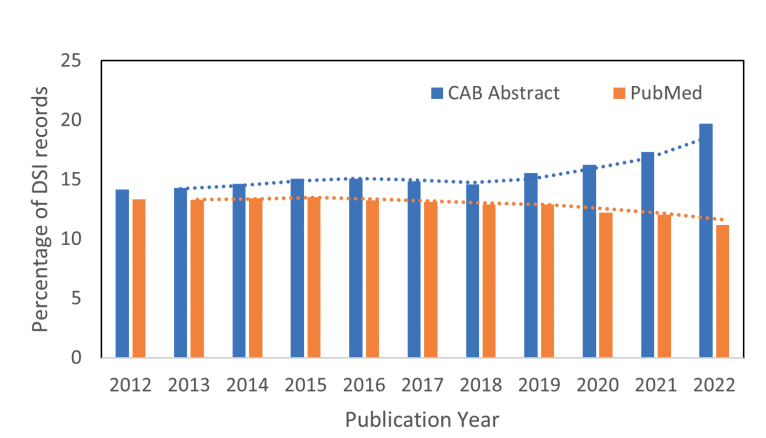
Comparing CABI data with other sources

The analysis focused on the validated and comprehensively indexed CABI databases. The CABI team ruled out simple searches in Google to compare results but attempted to perform searches using the same search terms in PubMed and Google Scholar. Unfortunately, the string length for searches in Google Scholar did not allow the use of the terms used to compile the data pool on DSI from CAB Abstracts. Using a narrower set of terms for DSI in Google Scholar returned far fewer hits. The PubMed returns are presented in Figure 2.

Figure 3 shows the percentage of total records over the years from 2012 to 2022 in CAB Abstracts and PubMed that cite DSI. The moving-average trendlines illustrate the growth pattern of records citing DSI. A steady growth is seen in the predominantly agriculture-focused CAB Abstracts from 14.2 percent of the records in 2012 to 19.7 percent of the records in 2022 (up to the time of the analysis).

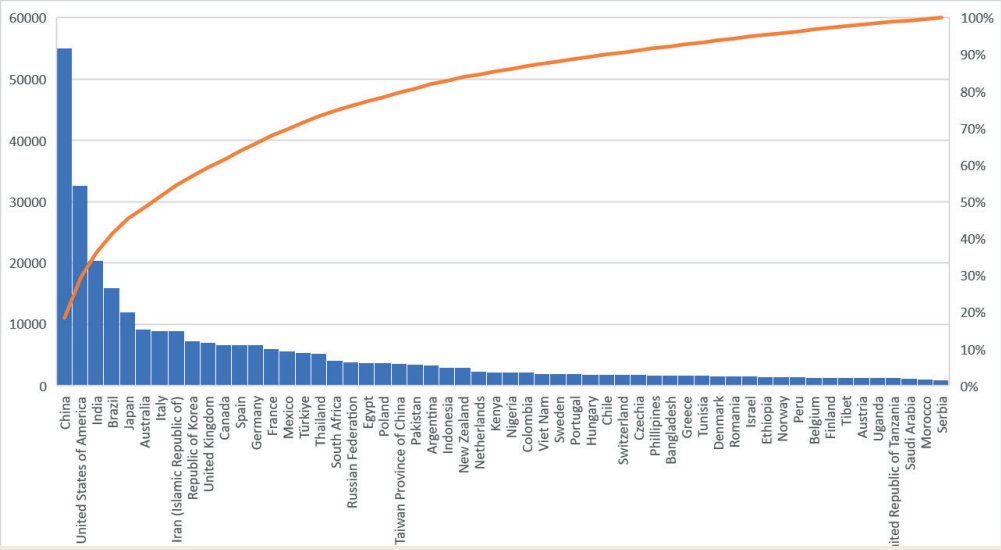
Figure 4 shows the distribution of publications related to DSI for 97 locations, with most publications coming from authors in China (over 55 000), the United States (just under 35 000) and India (approximately 20 000). As with the WiLDSI data, it is difficult to determine where the work was carried out, and again there were many North–South collaborations. Although there are many publications from LMICs, there remains an imbalance in these countries' capacity to take full advantage of DSI technology.

Figure 3. Percentage of publications citing DSI among the total records added per year (2012 to 2022) in CAB Abstracts and PubMed



Source: Output from CAB Abstracts database - Authors elaboration for this background study.

Figure 4. Distribution of DSI-related publications from different geographical locations



Source: Output from CAB Abstracts database - Authors elaboration for this background study.

Search results April 2022 to June 2023

In June 2023, the opportunity was taken to carry out a follow-up literature survey on records added to the CAB Abstracts database since the initial study was undertaken and hence to compare trends in DSI publication. 658 945 records had been added to the CAB Abstracts database between 1 April 2022 and 2 June 2023, and of these 99 149 were literature records citing DSI (15 percent of the records added). Table2 lists the number of records for different types of GRFA.

Table 2. DSI publication records in CAB Abstracts for different types of genetic resources for food and agriculture

Type of genetic resource	Literature records added 1 April 2022 to 2 June 2023	
	Number	**Percentage**
Animal	56 672	45.9%
Aquatic	6 668	5.4%
Forest	5 533	4.5%
Plant	48 126	39%
Microorganism	6 419	5.2%
Total	123 418 (in 99 149 literature records)*	15% (of literature records added)

**Some publications mentioned more than one type of genetic resource.*
Source: Authors elaboration for this background study.

The number of literature records citing DSI for each type of genetic resource exceeds the total number of publications citing DSI because some publications mentioned more than one type of genetic resource. The proportion of records of DSI increased from a baseline of almost 11 percent for the period up to March 2022 to 15 percent for the period from April to June 2023. Additionally, more papers in the latter period covered animal genetic resources than plant genetic resources, and there was a much lower proportion of papers on microorganisms.

Appendix II. CABI centre survey of obstacles to access and use of DSI

CABI centres[1] provided information on the generation and use of DSI in their host countries and regions, drawing both on their project work and on the experiences of the scientists at the centres and their partners. Where possible, the CABI centres contacted the national authorities of their host countries for input. The centres contributing are listed below and the information they provided is summarized in Section 5 of the main paper along with a table of commonalities. The full details are provided here (the contributors of this information are listed in the acknowledgements section of the main paper).

Bahamas

The Bahamas Agricultural Health and Food Safety Agency (BAHFSA) fully understands the importance of DSI to sustainable agriculture. One of BAHFSA's core objectives is to establish diagnostic laboratories with DNA-sequencing and molecular-biology capacity to access and utilize NSD to detect and identify pests and diseases. In the Bahamas, several obstacles, including a lack of human and financial resources to facilitate the establishment of the required technical infrastructure, prevent the widespread adoption and use of DSI. However, BAHFSA notes that scientific collaboration with local and regional research institutions could facilitate greater use of DSI.

Brazil

CABI's centre in São Paulo, Brazil, operates across the whole of Latin America, providing scientific knowledge, information and expertise to the Latin American nations. CABI engages in projects that address agriculture in this region, investigating climate change, biodiversity and highly sensitive environments where a wide range of crops and livestock are farmed and traded, particularly coffee and cocoa. As in all regions, CABI works with a wide range of partners and has sourced information regarding the generation and use of DSI in their research in food and agriculture. At state level, a large number of public and private institutions generate and use DSI: EMBRAPA Cenargen is one of the key public institutions doing so. There are clear rules in Brazil that provide legal clarity to users of genetic resources and the DSI associated with them (CBD, 2019a; CEUB, 2022). There is consensus in Brazil that legal measures that facilitate and foster research and development will generate more benefits that can be channelled to biodiversity conservation and sustainable use, fulfilling the objectives of the international agreements on ABS.

DSI is generated locally, especially by research institutions, but it is difficult to estimate the exact extent. It is generated mainly by researchers and postgraduate students in both public- and private-sector institutions. Brazilian genetic heritage can be freely accessed, but the results and products of its utilization are regulated by a registration or notification procedure. It is the national understanding that access, including through DSI, must be facilitated to generate the benefits that will fund biodiversity conservation and sustainable use.

DSI is easy to access for research institutions and researchers in Brazil, following the SisGen requirements (da Silva and Ribeiro de Oliveira, 2018). A facilitated mechanism exists for access to genetic resources, with a focus on control of the economic exploitation of products or reproductive materials arising from access. An online registration system for tracing, tracking and overseeing access to genetic resources and associated traditional knowledge activities is in place, and the SisGen electronic system facilitates a procedure for the use of DSI within the framework of the CBD.

[1] https://www.cabi.org/what-we-do/cabi-centres

Despite all this being in place, there are problems that restrict the use of DSI. For instance, access to proper infrastructure and resources varies from place to place. The north of Brazil has limited resources, thus limiting the full use of DSI. Training, budget and resource limitations also constrain the development and maintenance of information databases.

Caribbean

CABI's office in Trinidad and Tobago[2] works with local partners in a region rich in natural resources, particularly commodity crops, which remain economically important for the area. The centre works across the whole of the Caribbean and Central America, carrying out work that is significant not just to the region but globally. Projects have a focus on finding sustainable ways to manage crop pests and invasive species, conserve or enhance biodiversity and support the commodity chains that flow from farmer to consumer. In executing and supporting projects in the region (CABI, 2022a) the centre works with several partners, some of whom provided feedback on the generation and use of DSI.

The Cocoa Research Centre under the Faculty of Science and Agriculture (FSA) of the University of the West Indies (UWI) was established in the 1930s, with a mandate to conserve, characterize, evaluate, utilize and distribute material from its internationally recognized germplasm collection (International Cocoa Germplasm, Trinidad). Research activities include germplasm conservation, morphological and molecular characterization of cacao accessions, screening of germplasm for resistance to diseases, germplasm enhancement (prebreeding for desirable traits), and quality and flavour assessment (TTBCH, 2022). DSI generated is stored in the International Cocoa Germplasm Database, maintained by the University of Reading in the United Kingdom. The DSI in this database is freely accessible (Gillian Bidaisee, Genebank Characterization, personal communication, 2022).

In the late 1990s, the genetic basis for resistance to bacterial blight disease in anthurium was investigated. Most of the 60 anthurium cultivars grown in the Caribbean have been genotyped and their level of resistance to bacterial blight determined at the foliar and systemic levels using a two-stage screening method. The screening method developed and the knowledge obtained on the genetics of resistance allow targeted hybridizations between anthurium genotypes to obtain higher levels of resistance. The principles are being put into practice in the breeding programme at Kairi Cut-flowers Ltd. A number of novel varieties that combine resistance to bacterial blight with other horticultural characteristics have been developed. The Caribbean Agricultural Research and Development Institute (CARDI) has capacity but no equipment and needs to upgrade its facilities to house polymeric chain reaction (PCR) and related equipment that can be used to genetically analyse Caribbean agrobiodiversity (Fayaz Shaw, personal communication, 2022).

UWI is working on crosses and selection in minor crops, such as UWI F7 field maize and pigeon pea, but no materials have yet been sequenced. The crop-pathology team uses part- or whole-genome sequencing and data processing of microorganisms, including soil microbes and plant pathogens. They note that interest in and use of DSI has increased in recent times at UWI, St. Augustine. The interest at St. Augustine is mostly related to ITS and/or 16S rRNA gene (as appropriate) sequencing, whole genome sequencing of microbes and genome-wide association studies in crops such as cocoa. However, UWI lacks a database or centre for storing and processing their DSI data. DSI is used at UWI for reference purposes and to study similarity. However, limitations to technical capacity, computing infrastructure and logistics restrict its use. The situation is possibly the same across the Caribbean in all the few cases where DSI data are generated or used. Crop pathologists usually submit their sequences to databases such as NCBI and access DSI data from open databases.

The main conclusion for Trinidad and Tobago to date is that capacity and actual work on DSI are limited to the sequencing of the Cocoa Germplasm Collection, which is ongoing in collaboration with the University of Reading University, United Kingdom. In addition, some work was carried out in the 1990s on about 60 varieties of anthuriums found in the Caribbean to investigate resistance to fungal and bacterial diseases.

China

The CABI Chinese centre consulted Chinese experts working in research fields related to DSI and reviewed relevant Chinese literature. This indicated that the generation and use of DSI is common in China and

[2] https://www.cabi.org/what-we-do/cabi-centre/trinidad-and-tobago

represents an important part of daily scientific research work. In the food and agriculture sector, this mainly involves sequence analysis of crop genome, transcriptome and protein groups and comparison with public databases. One expert reported that DSI is generated and used in 80 percent of their research. Sequencing data are generated locally, often through domestic contracted services, with the cost varying greatly each year depending on the sequencing type, the number of samples and developments in sequencing technology. Simple RNA samples CNY 700-1100 (USD 100-1700) to sequence. These costs increase if bioinformatic analysis is also provided. Chinese researchers use data from other countries once they are released on a public database, as do researchers worldwide (e.g. GenBank,[3] RefSeq,[4] SRA[5]) (Wu *et al.*, 2021).

Despite the extensive generation and use of DSI in China demonstrated by the figures available from the WiLDSI portal (see Section 3.1 of the main paper) researchers report limitations with regard to data accessibility, basic hardware conditions (such as network facilities and computers), data quality and format, data background information, and data analysis and utilization abilities. There is concern that researchers will not fully release the DSI data they generate after publishing their papers. Other concerns include the following: DSI data generated from a large number of enterprise/private-sector grants are not released to the public; the public database storing DSI data is not being maintained; download speed is too slow or easy to interrupt in the case of access from China; and source information for released DSI data material is incomplete. Access to some databases is restricted, and some are no longer open to the public: often they can only be accessed if purchased by institutions. There are also a few databases with restricted access in China. DSI generation and use are extensively published in China by local researchers on local biodiversity in the fields of biotechnology, food and agricultural science, medical sciences and life sciences (Wu *et al.*, 2021; Li and Xue, 2019; Liu, 2021; Sun, Li and Zhao, 2021; Zhang, 2021).

Ghana

CABI's centre in Ghana[6] serves West Africa, representing 15 countries with a combined population of about 300 million and where agriculture is of huge importance but not without significant challenges. The centre received two contributions on Ghana's ability to generate, access and use DSI. The first was from the Council for Scientific and Industrial Research (CSIR), Oil Palm Research Institute,[7] which is a division under Ghana's Crops Research Institute. This organization reported that, although its researchers rely on DSI to a large extent, resource limitations mean that it is not able to generate and use DSI extensively. Researchers depend on external resources, which are expensive and not readily available or accessible. The problems affecting access and use include lack of technical infrastructure, financial and human resources, educational and training opportunities, scientific collaboration, computing infrastructure, reliable electricity, high-speed internet, capacity to store data and computing capacity, as well as the cost of data charges. DSI generated externally is used mainly as reference material. Examples of this are the genome sequencing of an African oil palm (*Elaeis guineensis*) (fruit type Dura) and whole-genome resequencing of 72 oil palms from the African continent and Southeast Asian countries, which were performed on the Pacbio sequel II and Illumina sequencing platforms (NCBI, 2022a) by Temasek Life Sciences Laboratory, Singapore. Three of the Dura genotypes were from Ghana (NCBI, 2022b, 2022c, 2022d). However, because of the lack of computing infrastructure, high-speed internet, technical infrastructure, and financial and human resources, the raw data were not analysed.

The second contribution came from the CSIR Crops Research Institute, which is an agriculture-based institution working on all food crops. This organization reported that the use of DSI is critical to its work but that researchers are not able to extensively generate and use it. They rely on platforms that produce results at a fee, which is not affordable for their resource-challenged systems. The CSIR Crops Research Institute currently has a 3730 genome sequencer, which was purchased as part of a project. However, the installation was not completed, and staff were not trained in its use. Their ambition is to set it up as a hub to resource scientists in the subregions. Researchers in the institute generate as well as use DSI or data (both RNA and DNA). They use it for genetic analysis, including classification of plant viruses, bacteria, fungi and crop genotypes/varieties. This DSI is not generated locally, but rather it is generally generated by and sourced from international companies in the United States, Europe, South Africa or Australia. DSI is very important for the

[3] https://ngdc.cncb.ac.cn/databasecommons/database/id/460
[4] https://www.ncbi.nlm.nih.gov/refseq
[5] https://ngdc.cncb.ac.cn/databasecommons/database/id/460
[6] https://www.cabi.org/what-we-do/cabi-centre/ghana
[7] https://opri.csir.org.gh

organization's research work. However, because of difficulty accessing it, its use is limited. DSI is available at websites such as NCBI, and with the right skills and internet availability it can be accessed when needed. Constraints to the availability of DSI include lack of technical infrastructure, financial and human resources, educational and training opportunities, scientific collaboration, computing infrastructure, reliable electricity, high-speed internet and capacity to store data, as well as the cost of charges.

The development of low-density single-nucleotide polymorphism (SNP) panels and cost-effective genotyping platforms holds great promise for resource-limited breeding programmes in Africa. Prempeh *et a*l. (2022) recommended the use of low-density SNP markers to characterize cassava accessions and for quality control in breeding activities. In crops such as rice and oil palm, different strategies have been employed to genotype large numbers of samples. SNP marker development through deep resequencing could provide all variation types on the resequenced region, but this is expensive (Xia *et al.*, 2019). However, low-density SNP microarrays are generated across known genes, and they therefore provide less-developed countries with a cost-effective option for analysing large sample data (Handyside and Wells, 2013). Using a high-density SNP panel, Bissah (2016) mapped quantitative trait loci for salt tolerance in rice and compared the identified loci with mapped genes in SNPSEEK. Other examples of collaborative work with DSI include the following: determining the genetic makeup of some *Musa* (banana) hybrids (Quain *et al.*, 2018a; Quain, Agyeman and Dzomeku, 2018); population studies of released and elite sweet potato (Quain *et al.*, 2018b); comparison of the performance pepper varieties (Boateng *et al.*, 2017); investigation of genetic relationships among genotypes of *Ceiba pentandra* (white silk-cotton tree) (Abengmeneng *et al.*, 2016); characterization of *Solanum* species (Oppong *et al.*, 2015a); investigation of genetic relationships among cassava cultivars (Twumasi *et al.*, 2014); soybean diversity studies (Appiah-Kubi *et al.*, 2014); mapping of the distribution of maize streak virus genotypes across the forest and transition zones of Ghana (Oppong *et al.*, 2015b); and studying the distribution and spread of cassava mosaic virus disease in Ghana (Oppong *et al.*, 2021).

India

The CABI centre in India[8] has been implementing programmes and working with partners to help improve the lives of people and communities in the region since 1948. It manages and contributes to agricultural projects across South Asia, where more than 50 percent of the population is engaged in agriculture as their primary occupation. The region produces some key food-security crops and is responsible for feeding a significant proportion of the world's population.

After consulting with partners in the region, the centre reports that various private and public institutions generate and use DSI. The Indian Council of Agricultural Research's National Bureau of Plant Genetic Resources,New Delhi, deals with various aspects of the germplasm of agricultural and horticultural crops. The Forest Research Institute, Dehradun, deals with the germplasm of forest species, and the Botanical Survey of India, Calcutta, deals with the germplasm of the remaining plant species. The National Biodiversity Authority,[9] established by the Central Government in 2003, implements India's Biological Diversity Act of 2002. There are five national bureaus for genetic resources. Of these (under ICAR), the National Bureau of Plant Genetic Resources, National Bureau of Agricultural Insect Resources, National Bureau of Forest Genetic Resources and National Bureau of Agriculturally Important Microbial Resources regularly generate DSI on plant, insect, animal and microbial genetic resources. Similarly, the Botanical Survey of India, Zoological Survey of India, Centre for Cellular and Molecular Biology, state agricultural universities and many other universities generate DSI, with a focus on DNA and RNA sequences. Many crop-based institutes, such as the Indian Institute of Rice Research, Indian Institute of Wheat and Barley Research, Indian Institute of Millets Research, Central Plantation Crops Research Institute, Indian Institute of Horticultural Research and many more, as well as private-sector players, such as the seed industry, generate DSI locally.

What started as a trickle in early 2000 is now a flood. ICAR itself has more than 60 institutes and universities, and most of the crop institutes and many of the universities under ICAR maintain small gene banks; some institutes have their own germplasm information databases. Examples include the Germplasm Registration Information System,[10] the Musa Transcriptome Simple Sequence Repeat Database[11] and the

[8] https://www.cabi.org/what-we-do/cabi-centre/india
[9] http://nbaindia.org/content/22/2/1/aboutnba.html
[10] http://www.nbpgr.ernet.in:8080/registration/AboutUs.aspx
[11] https://nrcb.icar.gov.in/nrcbbio/about.html

CottonGen – Cotton Database Resources.[12] NBPGR manages one of the world's largest genebanks, with >400,000 accessions (ICAR, 2022a). It reports the use of genome technologies to improve breeding stock and even cites a patent (2011 Patent No. 245749) on a technology/process enabling simultaneous detection of two transgenes in transgenic maize (ICAR, 2022b). Researchers have also accessed NSD from other countries for genetic improvement programmes. The response on DSI access and use indicated that some information is available to researchers, and indeed that some institutes provide training on how to use their databases (e.g. NBPGR). Some institutions have online databases, while others do not but are working to develop them. DSI information is also accessed by researchers in published literature. DSI is not available until it is published. Much of the DSI generated is for local use, and it is often not published or shared.

Partners in India explained that the use of DSI is constrained by a number of problems, including limited access to training. There are budget and resource constraints to the development and maintenance of information databases. Additionally, wide sharing of DSI can be constrained by exploitation of resources, others patenting useful sequential information and reverse engineering.

Singh *et al.* (2020) report on advances in sequencing technology and its outputs in their paper on the management and utilization of plant genetic resources in India. They explain that the "fundamental merit of an organized digital information system is that it provides fair and just opportunity for all to access. On-line portals, as a consequence of PGR Informatics, enable non-exclusive access to PGR information to a large number of users involved in overlapping research areas on PGR management."

Kenya

The CABI centre in Kenya[13] serves the African region and is based in Nairobi. CABI runs projects that are essential for agriculture and economic growth in sub-Saharan Africa, where average crop yields are among the lowest in the world. DSI is starting to have an impact on science and agriculture in the region, but most of the DSI generated in Africa in recent years has been in the medical field, with most of this related to epidemics/pandemics such as Ebola and COVID-19. The DSI generated in food and agriculture has mainly been associated with DNA barcoding in cases where species need to be identified. Estimates of use are based on how much has been published, and data from the WiLDSI Data Portal[14] demonstrate that DSI from Kenya has been used by only 953 authors from Kenya but by over 9 000 authors from other countries.

Nucleotide sequences are generated and used locally, both within CABI projects and by others, as demonstrated again by the data from the WiLDSI Data Portal, but not to the same extent as in countries and regions such as China, Europe and the United States. These data are most often generated by universities, government-led research organizations, CGIAR centres, other international research organizations (such as CABI and the International Centre of Insect Physiology and Ecology), national plant-protection organizations and the private sector. African capacity is low, mainly because of a lack of infrastructure and financial resources, but data are available from the major nucleotide sequence databases such as NCBI, EMBL-EBI and DDBJ, which are all open access. Using DSI requires skills and knowledge in molecular sciences, and these are still limited in most of Africa. The cost of internet access is also an issue. The data from the WiLDSI Data Portal indicate that access to, and usage of, DSI are still low.

Malaysia

The CABI centre in Malaysia[15] works across the whole of Southeast Asia, a region that is still largely dependent on agriculture and is very rich in biodiversity and environmentally fragile. Projects run through the centre focus on crops such as rice and fruit, invasive species and strengthening agricultural ecosystems (CABI, 2022b). DSI is used at significant levels to identify genetic resources and their traits. CABI works with many partners and local agencies in Malaysia. The Department of Agriculture stated that it does not have any countrywide system for access to and use of DSI and that there are no centralized DNA/RNA databases. However, MyGeneBankTM,[16] the genebank of Malaysian Agriculture Research and Development Institute (MARDI), has its own information

[12] https://www.cottongen.org
[13] https://www.cabi.org/what-we-do/cabi-centre/kenya
[14] https://apex.ipk-gatersleben.de/apex/wildsi/r/wildsi/home
[15] https://www.cabi.org/what-we-do/cabi-centre/malaysia
[16] http://mygenebank.mardi.gov.my

system called AgrobiS,[17] which has been developed by MARDI to provide the publi with direct access to data on all the genetic resources conserved at MARDI. The system, once fully operational, will contain germplasm information for more than 40 000 accessions of plant genetic resources for food and agriculture, including fruits, rice, vegetables and medicinal plants. The system also includes information on 2 500 isolates of microbial genetic resources and about 30 000 specimens of arthropods.

MARDI explained that DNA and RNA sequences are generated using a next-generation sequencing platform for non-model species or organisms in food and agriculture. The sequences are used to develop molecular markers for use in genetic and breeding studies and in work on genetic diversity, population genetics and analysis of quantitative trait loci. For bacterial genome sequencing, DNA and RNA sequences are used to harness beneficial microbes obtained from the soil microbiome to develop biofertilizers. For model organisms or species that are available in public sequence databases, MARDI researchers download and use sequences to mine molecular markers or genes of interest. To publish in high-impact scientific journals, the researcher(s) must deposit the sequence information in well-known databases (NCBI SRA, NCBI GenBank, ENA). This promotes reproducibility and transparency in the scientific community.

DSI is generated locally by MARDI for its projects: it could be as little as two to three organisms per year. The relevant molecular biologisit will send the samples (DNA/RNA/raw materials) to the sequencing provider. The bioinformatician will analyse the sequence data accordingly. Additionally, DSI generated by others is used extensively: for example, genome and transcriptome sequences in public databases are used to mine molecular markers or genes of interest, and in comparative genomics analysis. DSI is easy to access and use from public databases, as instructions are provided. Moreover, the owner of each public database publishes a peer-reviewed article so that other researchers can learn about the database's function and availability.

MARDI currently describes the problems that reduce access and ability to use DSI in Malaysia as "low risk". For example, a user may be unable to access DSI because of a network issue. Some countries impose restrictions on access to data, often requiring users to log in using their organization's email. For commercial companies, a subscription is needed to access some databases.

Pakistan

Pakistan has made tremendous progress in developing biotechnology by establishing over 50 institutes/centres in the public sector during the last five decades. Funding of over PKR 20 billion (more than EUR 88 million) was made available in the government sector under the Planning Commission of Pakistan, the Higher Education Commission (HEC) and the Pakistan Science Foundation, and through various international development partners, such as the Commission on Science and Technology for Development, the United States Department of Agriculture, the United States Agency for International Development and the International Centre for Genetic Engineering and Biotechnology.

As a result of these efforts, considerable human resources with sufficient scientific expertise have been developed. The country has therefore benefited from well-trained staff in this sector in the context of the mushrooming growth of PCR-based diagnostic tests for various diseases, especially hepatitis and recently COVID-19. Similarly, applications of modern biotechnology in forensic science have also made great strides, with a forensic laboratory in Punjab, Pakistan (PSFA, 2022). DNA marker studies are also carried out routinely in the food and agriculture sector in Pakistan, including studies of viruses, microbes, insects, plants and animals.

The response to the question "is DSI generated locally, if so can you estimate how much and by whom?" indicated that, with support from Japan, over 90 000 plant accessions are being conserved and maintained at the Plant Genetics Research Institute (PGRI) at the National Agriculture Research Centre (NARC) in Islamabad. In 2017, PGRI was restructured and renamed the Bio-resources Conservation Institute (BCI). Two new research programmes, the Microbial Genetic Resources Programme and the Animal Genetic Resources Programme, were established to extend the research activities from plant genetic resources to microbial and animal genetic resources. The progress is slow but is continuing in the right direction (PARC, 2022).

Pakistan Barcode of Life "offers a platform to the barcoding community in Pakistan and is a member of the International Bar Code of Life (iBOL)" (PakBOL, 2022). This enables countrywide collaboration to

[17] http://agrobis.mardi.gov.my/agrobis_v2/admin/what-is-agrobis

document and understand the country's biodiversity, building on DNA barcoding studies conducted in 2010. Collaboration is underway with research scientists at the Centre for Biodiversity Genomics at the University of Guelph, Canada, where iBOL's secretariat is located. To date, Pakistan's research community has generated around 50 000 barcode records from animals and 1 600 from plants. The country has also been actively participating in iBOL's Global Malaise Trap Programme (CBG, 2022), with arthropod sampling completed at nine sites already and ongoing at eleven (iBOL, 2022).

This forms a modest beginning, and further investment and work are needed. However, it illustrates that there is capacity and an impetus to enable more generation and use of DSI. The degree of effort needed is reflected in the state of microbial culture collections in Pakistan. Ahmed, Abbas and Tariq (2018) described the importance of microbes in biotechnological, agricultural and industrial applications in Pakistan. According to the World Data Centre for Microorganisms,[18] when consulted in 2018, there were five Culture Collection Centres registered from Pakistan, holding just over 3 500 strains. These include strains with plant-growth-promoting activity, strains that may have applications in bioremediation of heavy-metal polluted soils and water systems, strains useful in the food industry, pathogenic strains of bacterial blight from rice and citrus canker, and other extremophilic (e.g. salt-tolerant) strains for biotechnology. However, very few of these microbes have been truly identified at species level based on 16S ribosomal RNA gene sequence, and examples of new species of bacteria from the rich ecology of Pakistan are rare. Few of the holdings have been gene sequenced. Research collaborations with, for example, China and Saudi Arabia have made it possible to isolate and identify novel species of bacteria from Pakistan and sequence them (Amin *et al.*, 2016; Ali *et al.*, 2021). In addition to its use in the identification of microbial diversity, NSD is proving valuable in Pakistan for genome sequencing multidrug-resistant, novel candidate bacteria (Ali *et al.*, 2021). NSD is also used in barcoding and biochemical profiling of medical plants and in the study of genotypic variation for drought tolerance in cotton (Rahman *et al.*, 2008). It is also used for characterizing insects, for example revealing cryptic species complexes through DNA barcode analysis of thrip (Thysanoptera) diversity in Pakistan (Iftikhar *et al.*, 2016). A DNA barcode survey of insect biodiversity has been carried out in Pakistan (Ashfaq, *et al.*, 2022). DNA barcoding also has been used to identify edible fish species (Ghouri *et al.*, 2020) and to identify specimens in the control of the illegal wildlife trade (Rehman *et al.*, 2015).

Global data, especially data available in public databases, are frequently utilized by specific research groups in Pakistan in the study of viruses and bacteria, and in plant and animal research. Bioinformatics departments are active in many public and private universities in Pakistan. To enable facilitated access to and use of DSI, which is significant, the HEC has established a digital library for universities (more than 280) in the country (HECP, 2022). Additionally, G4/G5 connectivity to the internet is readily available in the country at a reasonable cost and speed. The use of sequence data in certain cases is mandatory, for example in ensuring the purity of basmati rice for export to European Union countries. Similarly, DNA fingerprinting is essential for approval/registration of a new plant variety by the Federal Seed Certification and Registration Authority. In order to comply with World Trade Organization and International Union for the Protection of New Varieties of Plants obligations, Pakistan established the Plant Breeders Registry and requirement for DNA fingerprinting of novel plant varieties. The courts in Pakistan now accept DNA/RNA sequencing data for any dispute on ownership, paternity, theft or any other criminal act. Furthermore, under Pakistan Biosafety Rules, 2005 (FAO, 2022), PCR-based testing using specific molecular markers to detect the presence of genetically modified organism material is mandatory. The Government of Pakistan Gazette notified four public research centres for this purpose.

Pakistan is making progress in pockets on NSD. A few elite centres among the 50 institutes of biotechnology are capable of carrying out reasonable quality work on DSI. Trained human resources and sufficient infrastructure are available. However, there is a strong need for more collaboration and sustainability in DSI-related programmes.

Zambia

CABI's Zambia office[19] serves the Southern African region, where agriculture is the main employer and source of income for the majority of the population. The office oversees projects and improves knowledge-sharing to address agricultural and environmental challenges encountered by Southern African smallholder farmers. The

[18] http://www.wfcc.info/ccinfo
[19] https://www.cabi.org/what-we-do/cabi-centre/zambia

office received feedback from Dr Paul W. Kachapulula, Head of Department, Department of Plant Sciences, School of Agricultural Sciences, and Dr Evans Kaimoyo, UNZA School of Natural Sciences, both at the University of Zambia (UNZA), and from Dr Rabson Mulenga, Zambia Agricultural Research Institute (ZARI), Plant Pathology Department, Mount Makuru.

In his response, Dr Kachapulula estimated that about 20 percent of the members of staff at UNZA generate and use DSI. This is mostly sequencing of microorganisms (mainly fungi and bacteria) and genotyping as part of species identification, and research on gene expression and the qualities of new cultivars. Scientists normally extract DNA/RNA, ship it out of the country for sequencing and receive electronic sequences for further analyses. Such analyses normally require online access to databases such as NCBI and several others. Sequencing is normally conducted abroad at places such as INQABA, University of Cape Town (South Africa) and BECA (Kenya). The School of Veterinary Medicine at UNZA has sequencing capabilities, but the centre is not yet optimized for commercial use. Dr Kaimoyo indicated that relatively little DSI is generated in the country and that it is mostly limited to universities, and medical and agricultural research institutes, which are few in number. Research scientists at the Schools of Veterinary Medicine, Natural Sciences, Agriculture Sciences and Health and Medical Sciences and at local and internationally affiliated research institutes are generating sizeable amounts of sequence data, equivalent to 40–50 percent of what is downloaded from sequence databases. Dr Mulenga, reporting on the generation and use of DSI at ZARI, explained that the institute generated and used DSI regularly to detect and characterize pathogens that infect crops, and used the data to generate technologies that reduce crop yield loss caused by pathogens. He reported that about 30 percent of the DSI used is generated locally. Data generated locally are deposited in public databases.

At UNZA, as with all university and research institutes in Zambia, staff are able to access DSI from publicly available online resources: internet facilities and quality are fairly good. However, access to databases often needs a subscription, and for high-throughput computations, the facilities at UNZA need upgrading. Dr Kaimoyo (UNZA) indicated that use of nucleotide and polypeptide sequence information is to some extent dependent on the availability of sequencing services in the country. It is still relatively hard to find local gene-sequencing services in Zambia, let alone genome-sequencing and polypeptide-sequencing facilities. Most of the work carried out by UNZA depends on sequencing services from abroad, where DNA samples are typically sent for sequencing at a relatively high cost. Dr Mulenga (ZARI) reported that the main problem is the actual generation of reliable DSI, mainly because of a lack of computing capacity and the complexity of bioinformatics. It is reported that DSI on Zambian biodiversity has been generated almost entirely in collaboration with the United States (Cowan *et al.*, 2022) and other countries, such as Australia (Mulenga *et al.*, 2015a, Mulenga *et al.*, 2015b, Mulenga *et al.*, 2018; Mulenga *et al.*, 2020; Mulenga *et al.*, 2022).

References

Abengmeneng, C.S., Ofori, D.A., Kumapley, P., Akromah, R., Jamnadass, R. & Quain, M. 2016. Genetic relationships among 36 genotypes of *Ceiba pentandra* (L.) as revealed by RAPD and ISSR markers. *American Journal of Agriculture and Forestry*, 4(4): 86–96. https://www.sciencepublishinggroup.com/journal/paperinfo?journalid=218&doi=10.11648/j.ajaf.20160404.13

Ahmed, I., Abbas, S. & Tariq, H. 2018. Importance of microbial culture collection in Pakistan: challenges and opportunities. *Bulletin of the BISMiS*, 7(2): 44–48. https://www.bismis.net/files/BulletinofBISMIS_7-2.pdf

Ali, A., Tariq, H., Abbas, S., Arshad, M., Li, S, Dong, L., Li., L., Li, W.J. & Ahmed, I. 2021. Draft genome sequence of a multidrug-resistant novel candidate *Pseudomonas* sp. NCCP-436 isolated from faeces of a bovine host in Pakistan. *Journal of Global Antimicrobial Resistance*, 27: 91–94. https://doi.org/10.1016/j.jgar.2021.08.011

Amin, A., Ahmed, I., Habib, N., Abbas, S., Hasan, F., Xiao, M., Hozzein, W.N. & Li, W.J. 2016. *Microvirga pakistanensis* sp. nov., a novel bacterium isolated from desert soil of Cholistan, Pakistan. *Archives of Microbiology*, 198(10): 933–939. https://doi.org/10.1007/s00203-016-1251-3

Appiah-Kubi, D., Asibuo, J.Y., Quain, M.D., Oppong, A. & Akromah, R. 2014. Diversity studies on soybean accessions from three countries. *Biocatalysis and Agricultural Biotechnology*, 3(2): 198–206. http://dx.doi.org/10.1016/j.bcab.2013.11.008

Ashfaq, M., Khan, A.M., Rasool, A., Akhtar, S., Nazir, N., Ahmed, N., Manzoor, F. *et al.* 2022. A DNA barcode survey of insect biodiversity in Pakistan. *PeerJ*, 10: e13267. https://doi.org/10.7717/peerj.13267

Bissah, M.N. 2016. *A study of genetic variability and quantitative trait loci (QTL) for salinity tolerance in rice (*Oryza sativa *L.)*. Accra, University of Ghana. PhD Thesis.

Boateng, S.K., Aboagye L.M., Egbadzor, K.F., Gamedoagbao, D.K., Allotey, L.N. & Quain, M.D. 2017. The performance of five selected pepper accessions in comparison with two local varieties. *Agricultural and Food Science Journal of Ghana*, 10(1): 795–802. https://www.ajol.info/index.php/afsjg/article/view/162905

CABI. 2022a. What we do, Projects, Central America and the Caribbean. Cited 12 December 2022. https://www.cabi.org/what-we-do/cabi-projects?section=1&region=central-america-and-the-caribbean&order=text-asc

CABI. 2022b. CABI Centres / Malaysia. Cited 12 December 2022. https://www.cabi.org/what-we-do/cabi-centre/malaysia/

CBD. (Secretariat of the Convention on Biological Diversity). 2019a. *Brazil´s position on DSI (Notification 2019-012) - 03 June 2019*. Cited 12 December 2022.

https://www.cbd.int/abs/DSI-views/2019/Brazil-DSI.pdf

CBD. 2019b. *India's submission on Digital Sequence Information on Genetic Resources in response to CBD notification 2019-012 dated 5 February 2019 pursuant to decisions 14/20 and NP-3/12*. Cited 12 December 2022. https://www.cbd.int/abs/DSI-views/2019/India-DSI.pdf

CBG (Centre for Biodiversity Genomics). 2022. *Global Malaise Trap Program*. Cited 12 December 2022. https://biodiversitygenomics.net/projects/gmp/

CEUB (Centro Universitário de Brasília - University Center of Brasília). 2022. The inclusion of the Digital Sequence Information (DSI) in the scope of the Nagoya Protocol and its consequences. *International Law Magazine. History of International Law in Brazil*, 19(3).

Cowan, D., Lebre, P., Amon, C., Becker, R.W., Boga, H.I., Boulangé, A., Chiyaka, T.L., Coetzee, T. *et al.* 2022. Biogeographical survey of soil microbiomes across sub-Saharan Africa: structure, drivers, and predicted climate-driven changes. *Microbiome*, 10: 131. https://doi.org/10.1186/s40168-022-01297-w

da Silva, M. & Ribeiro de Oliveira, D. 2018. The new Brazilian legislation on access to the biodiversity (Law 13,123/15 and Decree 8772/16), *Brazilian Journal of Microbiology*, 49: 1–4. https://doi.org/10.1016/j.bjm.2017.12.001.

FAO. 2022. Pakistan Biosafety Rules, 2005. *Gazette of Pakistan Extraordinary*, 26 April 2005: 975–989. https://www.fao.org/faolex/results/details/en/c/LEX-FAOC053471

Ghouri, M.Z., Ismail, M., Javed, M.A., Khan, S.H., Munawar, N., Umar, A.B., Nisa, M. *et al.* 2020. Identification of edible fish species of Pakistan through DNA barcoding. *Frontiers in Marine Science*, 7: 554183. https://doi.org/10.3389/fmars.2020.554183

Handyside, A.H. & Wells, D. 2013. Single nucleotide polymorphisms and next generation sequencing. In: D. Gardner, D. Sakkas, E. Seli & D. Wells, eds. *Human gametes and preimplantation embryos*, pp. 135–145. New York, USA, Springer.

HECP (Higher Education Commission Pakistan). 2022. *HECP*. Cited 12 December 2022. http://www.hec.gov.pk

iBOL (International Barcode of Life). 2022. *Scientific community in Pakistan announces the launch of Pakistan Barcode of Life (PakBOL)*. Cited 12 December 2022. http://ibol.org/site/wp-content/uploads/2019/04/iBOL-PR-PakBOL.pdf

ICAR (Indian Council of Agricultural Research). 2022a. *National Genebank*. Cited 12 December 2022. http://genebank.nbpgr.ernet.in

ICAR. 2022b. *Institute Technology Management Unit (ITMU) Database*. Cited 12 December 2022. http://www.nbpgr.ernet.in/Technologies_and_IPRs.aspx

Iftikhar, R., Ashfaq, M., Rasool, A. & Hebert, P.D.N. 2016. DNA barcode analysis of thrips (Thysanoptera) diversity in Pakistan reveals cryptic species complexes. *PLoS ONE*, 11(1): e146014. https://doi.org/10.1371/journal.pone.0146014

Li, B. & Xue, D. 2019. Application of digital sequence information in biodiversity research and its potential impact on benefit sharing. *Journal of Biodiversity Science*, 27(12): 1379–1385. https://www.biodiversity-science.net/EN/10.17520/biods.2019242

Liu, Q. 2021. The development status and the China's choice on the issue of digital sequence information of genetic resources. *Journal of Ecology and Rural Environment*, 37(9): 1109–1114. [in Chinese with English abstract]. https://doi.org/10.19741/j.issn.1673-4831.2021.0326

Mulenga, R.M., Legg, J. P., Ndunguru, J., Miano, D.W., Mutitu, E.W., Chikoti, P.C. & Alabi, O.J. 2015a. Survey, molecular detection and characterization of geminiviruses associated with cassava mosaic disease in Zambia. *Plant Disease*, 100(7): 1379–1387. https://doi.org/10.1094/PDIS-10-15-1170-RE

Mulenga, M.R., Miano, D.W., Chikoti, P.C., Ndunguru, J., Legg, J.P. & Alabi, O.J. 2015b. First report of *East African cassava mosaic Malawi virus* in plants affected by cassava mosaic disease in Zambia. *Plant Disease*, 99(9): 1290. https://doi.org/10.1094/pdis-03-15-0264-pdn

Mulenga, R.M., Boykin, L.M., Chikoti, P.C., Suwilanji, S., Ng'uni, D. & Alabi, O.J. 2018. Cassava brown streak disease and Ugandan cassava brown streak virus reported for the first time in Zambia. *Plant Disease*, 102(7): 1410–1418. https://doi.org/10.1094/PDIS-11-17-1707-RE.

Mulenga, R.M., Miano, D.W., Kaimoyo, E., Akello, J., Nzuve, F.M., Simulundu, E. & Alabi, O.J. 2020. First report of Ethiopian tobacco bushy top virus and its associated satellite RNA infecting common bean (*Phaseolus vulgaris* L.) in Zambia. *Plant Disease*, 105(2): 516. https://doi.org/10.1094/PDIS-03-20-0596-PDN

Mulenga, R.M., Miano, D.W., Al Rwahnih, M., Kaimoyo, E., Akello, J., Nzuve, F.M., Simulundu, E., *et al.* 2022. Survey for virus diversity in common bean (*Phaseolus vulgaris*) fields and the detection of a novel strain of *Cowpea polerovirus 1* in Zambia. *Plant Disease*, 106(9): 2380–2391. https://doi.org/10.1094/PDIS-11-21-2533-RE

NCBI (National Center for Biotechnology Information). 2022a. *Genome sequencing of the African oil palm* (Elaeis guineensis*)*. Cited 12 December 2022. https://www.ncbi.nlm.nih.gov/bioproject/841085

NCBI. 2022b. *Ghana oil palm Gha07*. Cited 12 December 2022. https://www.ncbi.nlm.nih.gov/sra/DRX281513

NCBI. 2022c. *Ghana oil palm Gha05*. Cited 12 December 2022. https://www.ncbi.nlm.nih.gov/sra/DRX281512

NCBI. 2022d. *Ghana oil palm Gha*. Cited 12 December 2022. https://www.ncbi.nlm.nih.gov/sra/DRX281514

Oppong L.A., Quain M.D., Oppong, A., Doku, H.A., Agyemang, A. & Bonsu, O.K. 2015a. Molecular characterization of *Solanum* species using EST-SSRs and analysis of their zinc and iron contents. *American Journal of Experimental Agriculture*, 6(1): 30–44. https://doi.org/10.9734/AJEA/2015/6337

Oppong, A., Offei, S.K., Ofori, K., Adu-Dapaah, H., Lamptey, J.N.L., Kurenbach, B., Walters, M. *et al.* 2015b. Mapping the distribution of maize streak virus genotypes across the forest and transition zones of Ghana. *Archives of Virology*, 159: 1–10. https://doi.org/10.1007/s00705-014-2260-7

Oppong, A., Prempeh, R.NA, Abrokwah, L.A., Annang, E.A., Marfo, E.A., Appiah Kubi, Z., Danquah, N.A.O. *et al.* 2021. Cassava mosaic virus disease in Ghana: distribution and spread, *Journal of Plant Physiology and Pathology*, 9(8): 258. https://www.scitechnol.com/peer-review/cassava-mosaic-virus-disease-in-ghana-distribution-and-spread-6D2O.php?article_id=16864

PakBol (Pakistan Barcode of Life). 2022. *Pakistan Barcode of Life. IBOL*. Cited 12 December 2022. https://www.

ibol.org/phase1/category/country/pakistan/

PARC (Pakistan Agricultural Research Council). 2022. *Bio-Resources Conservation Institute (BCI)*. Cited 12 December 2022. http://www.parc.gov.pk/Detail/ZmVhYzQ4MDktMTQzNS00OWIyLTlkMTUtYWUzNTRhNWNhYmMz

PSFA (Punjab Forensic Science Agency). 2022. *Punjab Forensic Science Agency*. Cited 12 December 2022. https://pfsa.punjab.gov.pk/

Prempeh, R., Oppong, A., Amankwaah, V., Akomeah, B., Abrokwah, L., Allotey, L., Annang, E., *et al.* 2022. Characterization of cassava germplasm using a low-cost SNP panel. In: *Report of the Second Conference of the African Plant Breeding Association Conference (APBA) 25–29 October 2021, Kigali, Rwanda*, pp 43–44. APBA.

Quain, M.D., Agyeman, A. & Dzomeku, B.M. 2018. Assessment of plantain (*Musa sapientum* L.) accessions genotypic groups relatedness using simple sequence repeats markers. *African Journal of Biotechnology*, 17(16): 541–551. https://doi.org/10.5897/AJB2017.16363

Quain, M.D., Agyeman, A., Okyere E. & Dzomeku, B.M. 2018a. Unravelling genetic makeup of some *Musa* hybrids and selected *Musa* accessions using molecular and morphological characterization. *International Journal of Genetics and Molecular Biology*, 10(1): 1–13. https://doi.org/10.5897/IJGMB2018.0161

Quain, M.D., Adofo, K., Appiah-Kubi, D., Prempeh, R.N., Asafu-Agyei, J., Akomeah, B. & Dapaah, H. 2018b. Use of expressed sequence tags-derived simple sequence repeat (SSR) markers for population studies of released and elite sweet potato. *International Journal of Genetics and Molecular Biology*, 10(2): 14–25. https://doi.org/10.5897/IJGMB2017.0159

Rahman, M., Ullah, I., Ashraf, M. & Zafar, Y. 2008. A study of genotypic variation for drought tolerance in cotton. *Agronomy for Sustainable Development*, 28: 439–447. https://doi.org/10.1051/agro:2007041

Rehman, A., Jafar, S., Raja, N. A. & Mahar, J. 2015. Use of DNA barcoding to control the illegal wildlife trade: a CITES case report from Pakistan. *Journal of Bioresource Management*, 2(2): 19–22. DOI: 10.35691/JBM.5102.0017

Singh, K., Gupta, K., Tyagi, V. & Rajkumar, S. 2020. Plant genetic resources in India: management and utilization. Вавиловский журнал генетики и селекции [*Vavilov Journal of Genetics and Breeding*], 24(3): 306–314. https://doi.org/10.18699/VJ20.622

Sun, M., Li, Y. & Zhao, F. 2021. 生物遗传资源保护、获取与惠益分享现状和挑战 [Current status and challenges of protection, access to and benefit sharing of bio-genetic resources of China]. 环境保护[*Environmental Protection*], 49(21): 30–34. doi: 10.14026/j.cnki.0253-9705.2021.21.002

TTBCH (Trinidad & Tobago Biosafety Clearing House). 2022. *Trinidad & Tobago Biosafety Clearing House, Biodiversity in Trinidad & Tobago*. Cited 12 December 2022. http://tt.biosafetyclearinghouse.net/0010.shtml

Twumasi, P., Acquah, E.W., Quain, M.D. & Parkes, E.Y. 2014. Use of simple sequence repeat (SSR) markers to establish genetic relationships among cassava cultivars released by different research groups in Ghanaian. *International Journal of Genetic and Molecular Biology*, 6(3): 29–36. https://doi.org/10.5897/IJGMB2014.0097

Wu, L., Shi, L., Gao, M. & Ma, J. 2021. Analysis on the status and suggestions for the development of digital sequence information of genetic resources. *China Science & Technology Resource Review*, 53(2): 36–43. [in Chinese with English abstract]. https://doi: 10.3772/j.issn.1674-1544.2021.02.005

Xia, W., Luo, T., Zhang W., Mason A.S., Huang D., Huang X., Tang W. *et al.* 2019. Development of high-density SNP markers and their application in evaluating genetic diversity and population structure in *Elaeis guineensis*. *Frontiers in Plant Science*, 10: 130. https://doi.org/10.3389/fpls.2019.00130

Zhang, X. 2021. Rules challenges and countermeasures of sharing of pathogens in the context of the implementation of the Nagoya Protocol. *Journal of Ecology and Rural Environment*, 37(9), 1098-1103.

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9 789251 383469

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