

Assessing (biotechnology) capacity development needs for the use of DSI – Overview about DSI users and use

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Content

DSI users and use

 Origin of DSI in and DSI users of the International Nucleotide Sequence Database Collaboration

(slides adapted from Amber Scholz, DSMZ, Germany and Guy Cochrane, EMBL-EBI, UK, presented at 1st Global Dialogue on DSI, Nov 2019 and the Webinar "Understanding DSI: a technical overview of its production, distribution and use", Dec 2020, resp.)

- Sequencing of African cattle genomes and providing DSI to databanks
- African bioremediation research and use of DSI from Databanks
- Synthetic biology approaches to bioremediation and biosafety implications



International Nucleotide Sequence Database Collaboration (INSDC) Scale

- Rate: 1 new dataset every 6 minutes
- Data: 2x10⁹ sequences and 1x10¹⁶ base pairs of read data across 2x10⁶ taxa
- **Usage**: 2,000 submitters; 10x thousands monthly consumers; 10x millions of monthly hits, many times this globally
- **Support**: 46 tickets per day and in-person training delivered to more than 350 users per annum
- Infrastructure: includes 100s of petabytes of storage, ~\$50 USD mil./year
- Biodiversity data
 - 7.2 million records point to natural history museums, culture collections and biobanks
 - 7.9 million sequences with geographical coordinates
 - 2.1 million sequences have place name annotation
 - 1 million raw sequencing data sets have coordinates



http://www.insdc.org/



There are 10-15 million total users of INSDC. They live in every country in the world.





Where does the original GR for these NSD come from?

What is the country of origin for non-human NSD?

1.	China	18.23 %
2.	United States	17.39 %
3.	Canada	9.10 %
4.	Japan	7.24 %
5.	India	3.46 %
ć.	Australia	2.66 %
7.	Mexico	2.54 %
8.	Brazil	2.30 %
g.	Germany	1.83 %
10.	Spain	1.58 %

52% of NSD comes from 4 countries





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The mosaic genome of indigenous African cattle as a unique genetic resource for African pastoralism

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Creating DSI from African cattle

DSI used for characterising cattle breeds

- Sequencing genomes of 114 individuals of 12 indigenous African cattle breeds from Ethiopia, Kenya, Sudan and Uganda
- ~3.50 terabytes of sequences, uploaded to GenBank
- Comparison with 217 publicly available genomes
- Statistical analysis revealing mosaic genome structure and evolutionary developments
 Bos indicus (zebu cattle)

Accession: PR

African cattle raw sequence reads

Raw sequence reads for 12 indigenous African cattle breeds (114 individuals) and African buffalo (2 individuals)

Accession	PRJNA574857
Data Type	Raw sequence reads, Genome sequencing
Scope	Multiisolate
Organism	Bos indicus [Taxonomy ID: 9916] Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Artiodactyla; Ruminantia; Pacora; Bovidae; Bovinae; Bos; Bos indicus
Submission	Registration date: 29-Sep-2019 Seoul National University
Relevance	Agricultural

- Goal: publicly available genome data to "open the door to sustainable crossbreeding programs combining local environmental adaptation and increased exotic productivity"
- Sources: Kim et al. (2020). Nature Genetics 52: 1099; GenBank Acc. No. PRJNA574857



DSI for African bioremediation research

SCIENTIFIC REPORTS

OPEN

Received: 14 December 2017 Accepted: 2 May 2018 Published online: 15 May 2018 Metagenomic profiling for assessing microbial diversity and microbial adaptation to degradation of hydrocarbons in two South African petroleumcontaminated water aquifers

Leonard Kachienga¹, Keshri Jitendra² & Maggy Momba¹

DSI for African bioremediation research

Methods applied / DSI used for characterising microbes

- Extraction of metagenomic DNA
- Amplification of 18 S rRNA by PCR
 18 S rRNA sequences are used in taxonomic research for identification of taxonomic groups as genus or family in, e.g., a sample of environmental DNA
- Sequencing of genomic DNA performed by a commercial DNA sequencing company
- Analysis of sequence data
 BLAST-Analysis (using DSI stored in databanks) and statistical analysis based on standard software
 Second site
- Goals: Isolation, selection and use of microbes



Figure 3. Different genera of the microbes observed in the first and second sites in petroleum-polluted water.

Source: Kachienga et al. (2018). Scientific Reports 8: 7564





Synbio approaches to bioremediation



REVIEW published: 19 May 2020 doi: 10.3389/fmicb.2020.00808



Alternative Strategies for Microbial Remediation of Pollutants via Synthetic Biology

Shweta Jaiswal and Pratyoosh Shukla**

Enzyme Technology and Protein Bioinformatics Laboratory, Department of Microbiology, Maharshi Dayanand University, Rohtak, India

Synbio approaches to bioremediation

Methods suggested / DSI also used for engineering microbes



- Synthetic microbial biosensor systems
- Metabolic engineering
- Genome editing
- Data mining
- Developing synthetic microbial communities
- Goals: Production of GM microbes
- Biosafety risk assessments, depending on national laws



FIGURE 1 | The strategies of synthetic biology applicable for bioremediation.