Special Event on Genomics Information

Genomic information: technological & institutional dimensions

Scoping study:
Technological Landscape

Todd Kuiken, North Carolina State University
Eric Welch, Arizona State University
Margo Bagley, Emory University
Selim Louafi, CIRAD

ASU center for science, technology and environmental policy studies
ARIZONA STATE UNIVERSITY

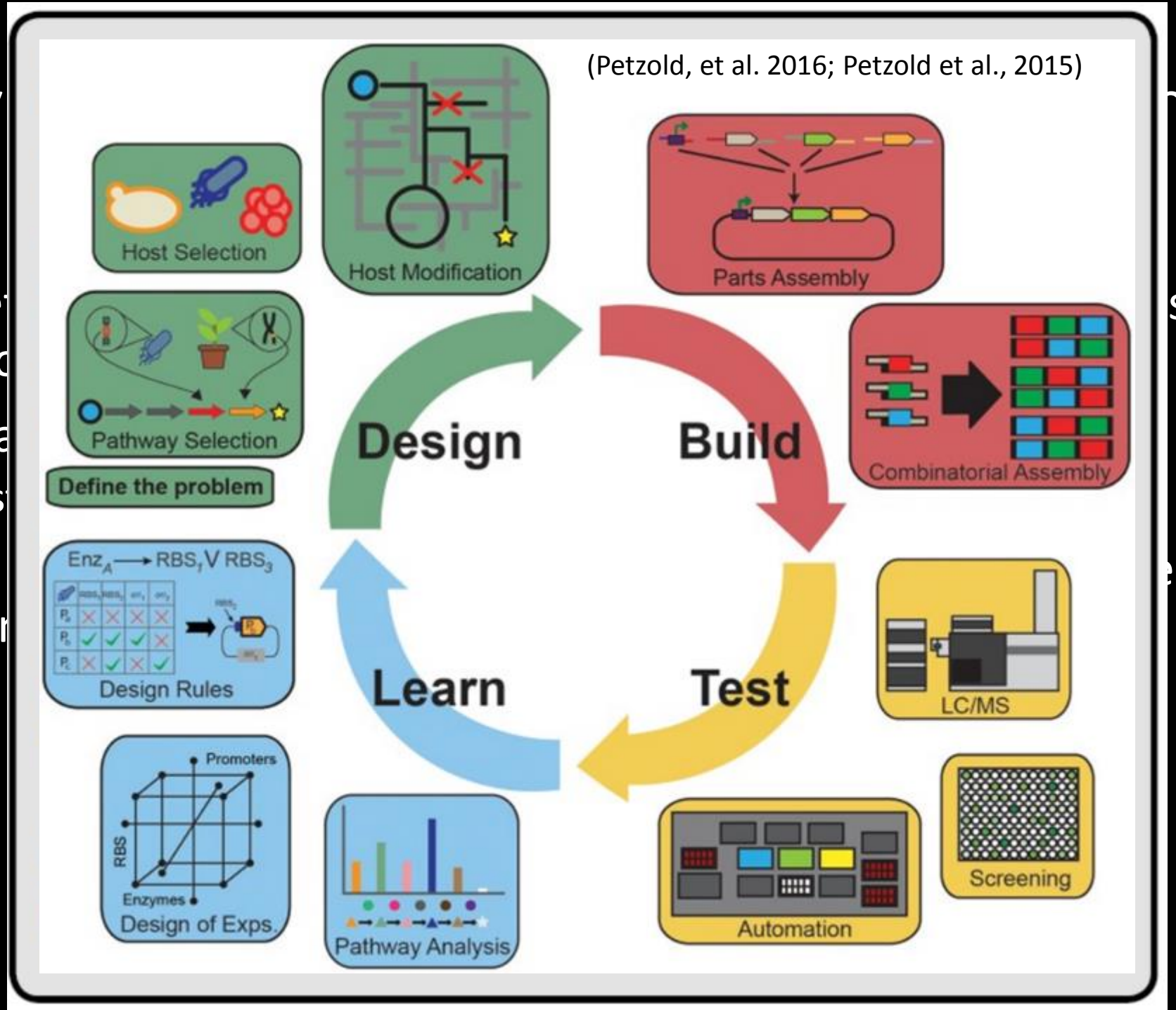
EMORY LAW

NC STATE UNIVERSITY

cirad

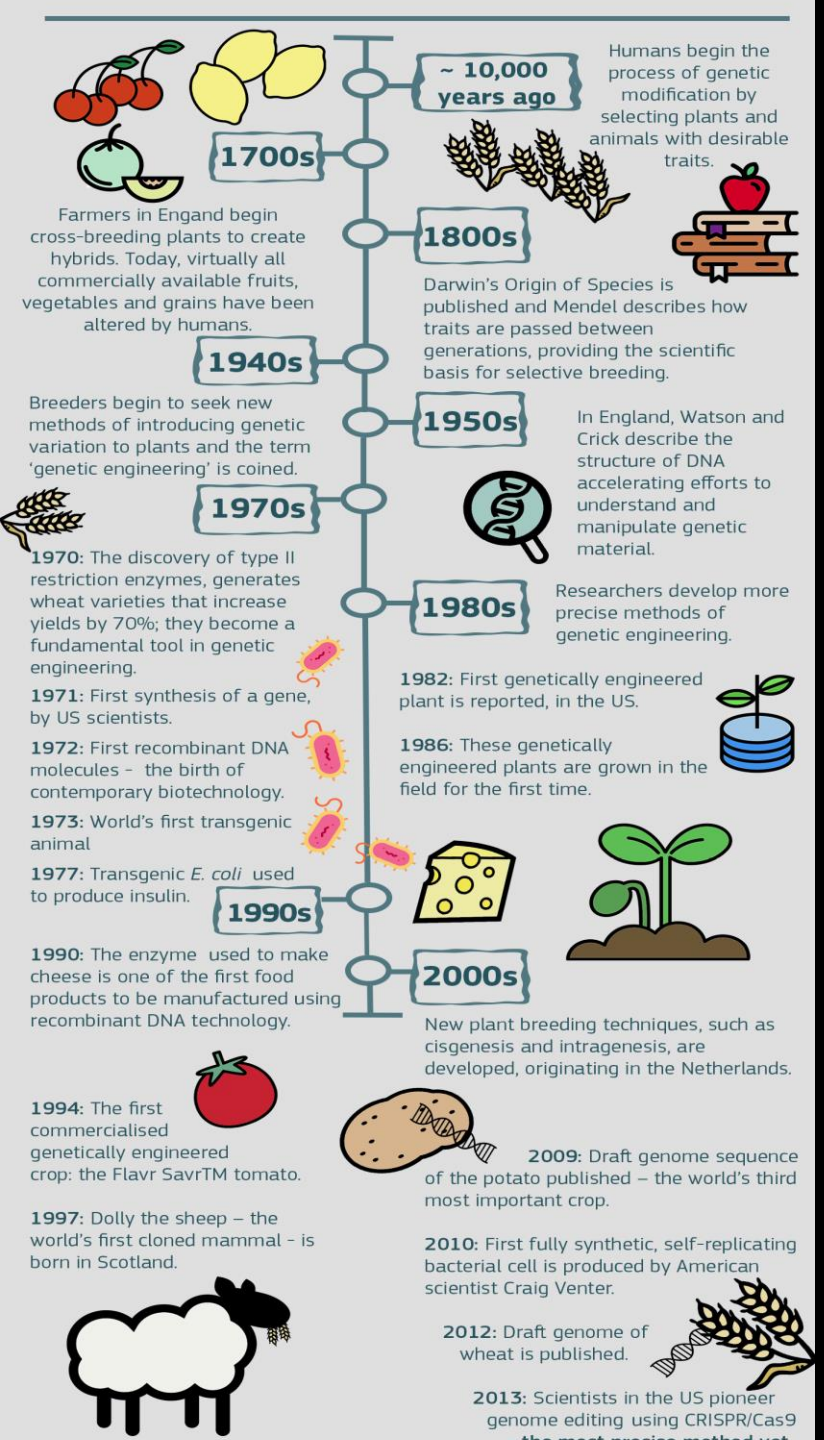
Sy

- Synthe
  incorpo
- There a
  - Most
- Unless
  changi



s that

rapidly



- Many elements are entirely novel
- Involves designing and constructing new biological "parts", "devices" and "systems"
- Can involve much larger-scale interventions
- Pace of change is increasing

European Commission Future Brief, Synthetic Biology and biodiversity:
http://ec.europa.eu/environment/integration/research/newsalert/pdf/synthetic_biology_biodiversity_FB15_en.pdf

Moving from physical to digital

- Prior to DSI technologies a researcher interested in an organisms genetic information would need to obtain the organism and then have it sequenced
  - Today its possible to download an organisms sequence information from a database or academic journal and have it synthesized by a DNA synthesis company (or increasingly synthesize it themselves)
  - Breeders and researchers have characterized numerous alleles (or mutations) associated with plant domestication and improvement, and have identified the genes and phenotypic differences between crops and their wild relatives.
  - According to some researchers, these mutations are the “raw material on which selection can operate making species adaptation and long-term evolution possible” (Nogue et al., 2016).
  - This ‘raw material’ is equivalent to computer codes that can be analyzed, reprogrammed and theoretically used either within the plant it was obtained from, or within a different species of plant.
  - This type of description or abstraction of the plant’s genetic make-up is part of the scientific/engineering philosophy surrounding synthetic biology
- However many factors determine whether its possible to build living material from DSI and whether it will function in a living system:
  - Cost
  - Time available
  - Ease of access to and quality of DNA synthesis and construction
  - Quality of the DNA libraries and digital sequence information in them
  - Quality of the “parts” (if in physical format)

Proliferation and decentralization of data (material)

- In the past physical material was accessed through collections held in gene banks, botanical gardens or private/public collections
- Fueled by decreasing costs and improvements in computer software (AI) we have seen a shift towards digital collections that include complete genomes and “parts” registries
  - Some are public databases (iGEM registry), some are public/private partnerships and others are individual researchers collections
  - Some of the databases also include the physical “parts” along with the digital file (iGEM)
- There has been a push (in part) towards open data and open exchange of data across the globe
  - This is driven by the need to access different data sets in order to understand and utilize the “parts” or functionalities that are encoded in the genomes of organisms
  - It’s not clear whether these databases will remain “open” as our understanding and utilization of these parts increases
- The field seems to be moving towards a highly distributed service oriented model in which foundries and DNA synthesis companies build their own collections of sequence data and then produce the physical constructs based on those digital files

Monitoring DSI?

- As discussed vast amounts of DSI are being collated in different databases and repositories (Genbank, Adgene, NCBI, iGEM and others)
- While some interviewees mentioned data sharing and use agreements there was no indication that such agreements are widespread or imposed by all database operators
- In theory database access could be tracked
  - some interviewees suggested that some database operators have been and will continue to be resistant to implementing such tracking
- It’s not clear what you should track
  - Many ways that partial sequence information (parts) can be combined
  - The same sequence (or part) could be present in multiple organisms

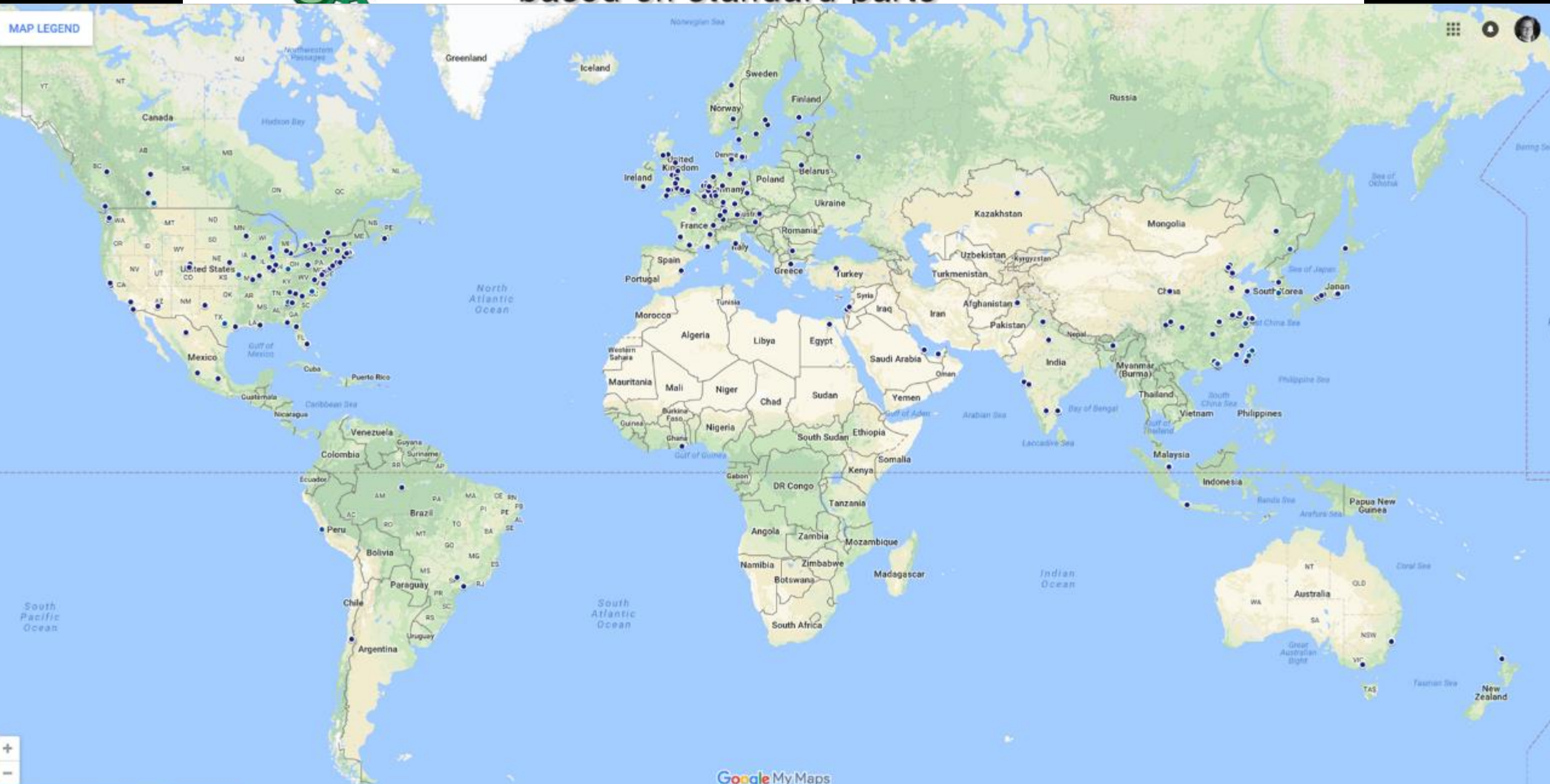
“New” technologies and plant breeding

- Advances in genetic technologies, machine learning (AI), and growing databases of DSI could impact plant breeding
  - The rise of DNA construction and genome editing technologies (i.e. CRISPR/Cas9) could facilitate the construction of multiple variants that involve alterations to multiple genes across an organism (National Academies of Sciences, 2017)
  - Many of these technologies are still young and will depend on our understanding of the plant species, complexity of the traits of interest and how they interrelate
- Researchers are increasingly able to scan DSI and identify traits of interest across multiple species
  - Need access to digital libraries of DNA sequence data
  - Do not (necessarily) need access to the physical material
    - Once the traits are identified they can be synthesized
  - Many researchers we spoke with suggested they still need/prefer to go back to the physical material from which the trait was identified in
    - This could present a problem for both research and ABS if that origin information is not tracked with the DSI
      - We found that this origin information varies by DSI database/collections

Deskilled/Democratized/Decentralized

Synthetic Biology

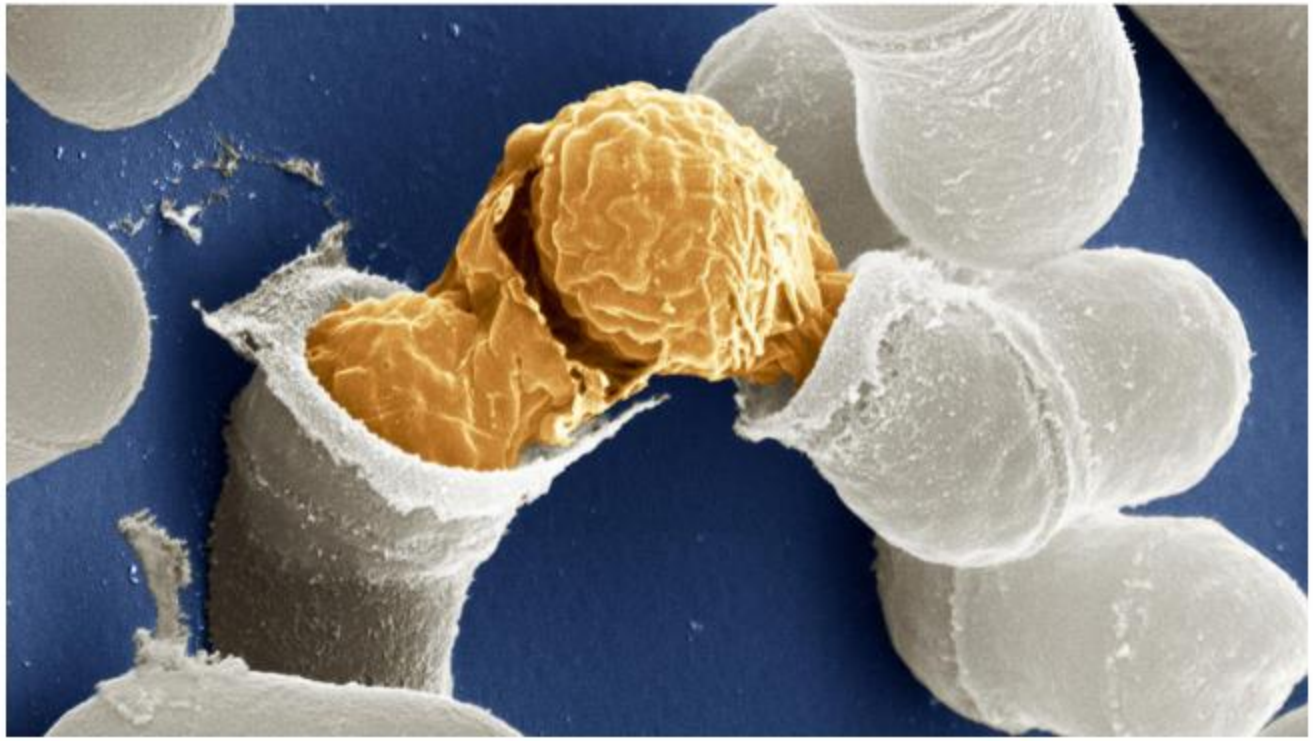
based on standard parts



IN THE LAB

College students try to hack a gene drive — and set a science fair abuzz

By IKE SWETLITZ @ikeswetlitz / DECEMBER 14, 2016



College students worked with yeast cells like these, attempting to insert a "gene drive."
JUERGEN BERGER/MARIA LANGEGGER VIA NIH

May 2008 – 1st DIYbio meet-up

global community bio summit

september 22, 2017 - september 24, 2017

community biotechnology initiative @ mit media lab

APPLICATION CLOSED

Final Thoughts….

1. The digitization era is producing large amounts of sequence data that is widely available and easily exchanged
    1. High throughput and automation of screening has enabled researchers to “screen thousands to billions of variants of an organism for function or phenotype” (National Academies of Sciences, 2017)
    2. Mining plant genomic information (data) for gene editing purposes in agriculture
    3. Mining for plant genomic information (data) for use outside of agriculture
2. While many researchers we spoke with still require or prefer the physical material for their work, there was a suggestion that the separation between material and data (DSI) is increasing
3. Demand for screening technologies is increasing and moving towards “omics approaches that are agnostic to the type of organism being tested
4. There is a community building dimension to “synbio”
    1. Most people know each other
    2. They also need each other (both in terms of data and techniques)
    3. De-skilling/Democratization
        1. iGEM
        2. DIYbio

Thank You....

Todd Kuiken, Ph.D.
tkuiken@ncsu.edu
@drtoddoliver
+1-919-515-2593