

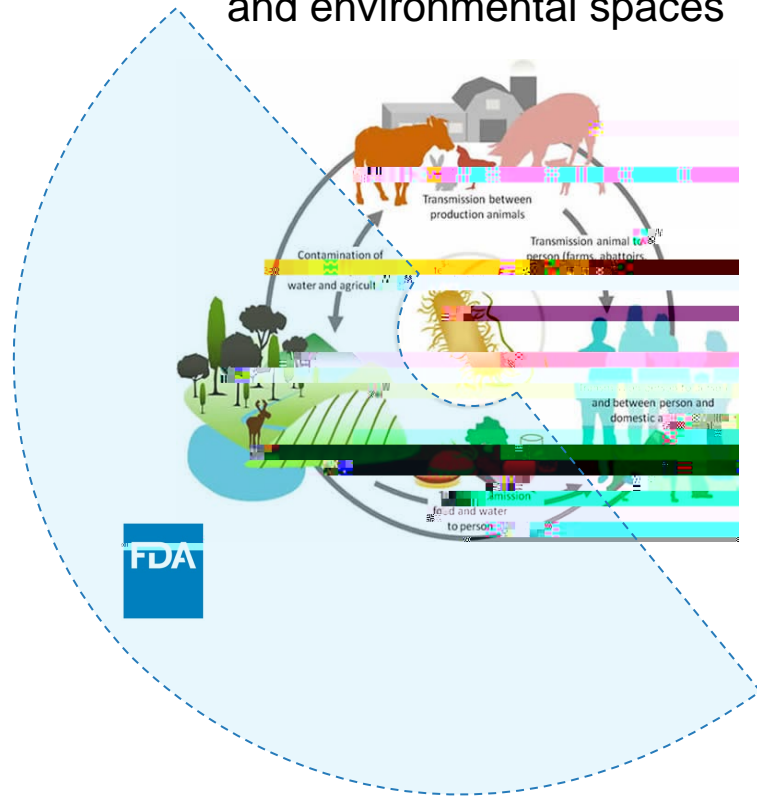


GenomeTrakr: FDA's Genomic epidemiology program for enteric pathogens



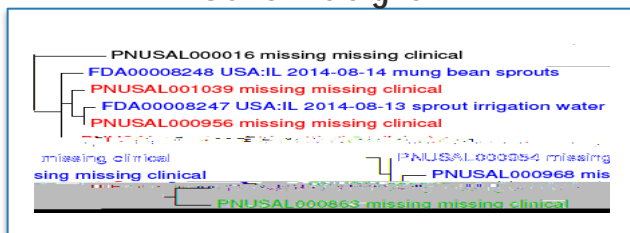
One Health
CSFAN focus on surveillance of food
and environmental spaces

46 Directly Funded Labs:



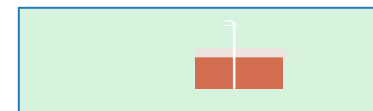
The Balanced (all - encompassing) Approach:

Genomic Signal



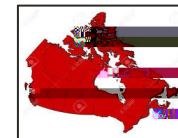
Epidemiological Signal

Traceback



Listeriaenoki mushroom event cluster highlights global NGS contribution

103,465 Clusters currently tracked.





WGS: Direct Industry Application

Current Testing is Effective and Supportive: BUT Can we achieve additional value?

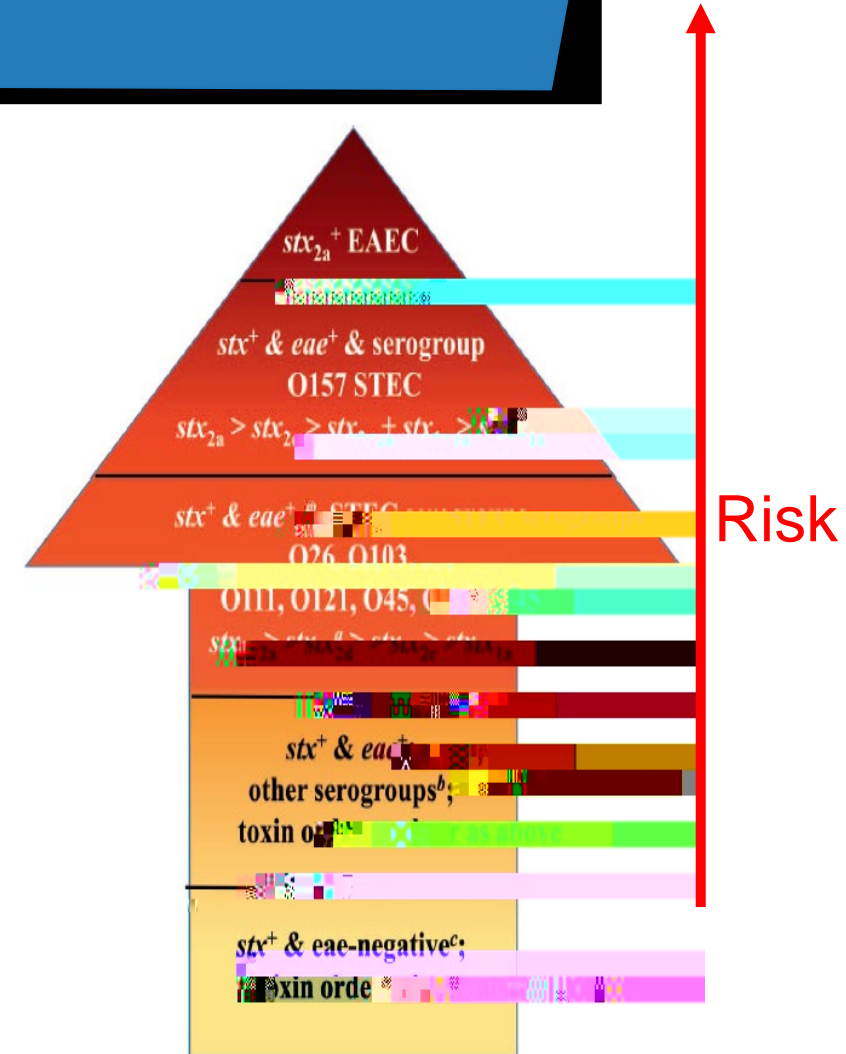


- That is, is there additional information that could drive a public health investigation, a risk assessment, or a compliance event further and/or faster by answering follow-up questions such as:
 - ¾ Is it possible to use genomic technology to predict a pathogen's risk and public health impact earlier and faster?
 - ¾ Is it possible to enhance identification of pathogen reservoirs and routes of transmission by applying environmental metagenomics as a complementary approach to longitudinal environmental microbiology studies?
 - ¾ Is it possible to employ genomic technologies to look deeper into microbiological sample enrichments to characterize strain diversity and specific population make-up of a pathogen (ie, not only to find Salmonella in an env sample but to find the Salmonella that caused a specific contamination event)?
 - ¾ It is possible to achieve precision food safety by using genomic tools to identify specifically acquired



(1) Predicting a pathogen's risk and public health impact earlier and faster.

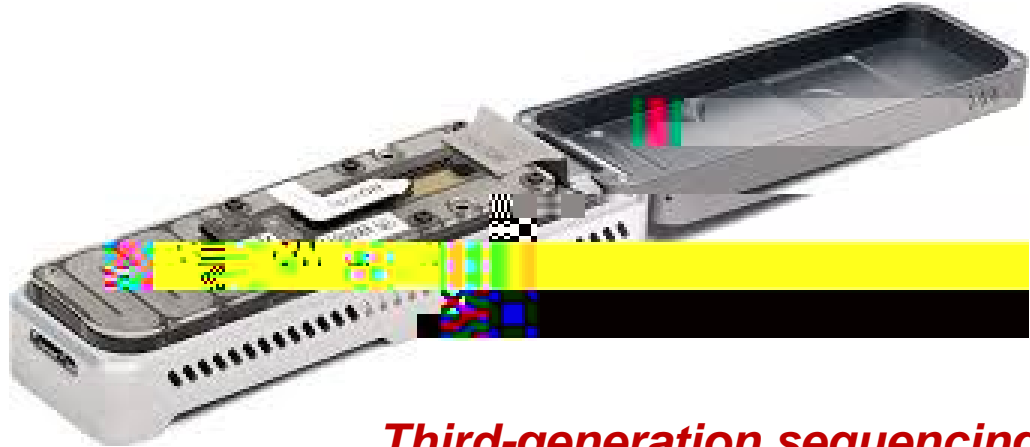
- > 400 STEC serotypes
- ~100 cause illness in humans
- Shiga toxin genes (stx1 and stx2)
- Intimin (eae) and/or adherence gene (aggR)
- We need to determine stx and eae genes, serotype and virulotype



Detection AND Identification

National Advisory Committee on Microbiology Criteria for Foods. J Food Prot. 2019;82(5):724-767.

Determining pathogenicity of *E. coli*



Third-generation sequencing (also known as long-read sequencing) is a class of DNA sequencing methods currently under active development....this sequencing works by reading the nucleotide sequences at the single molecule level, in contrast to existing methods that require breaking long strands of DNA into small segments then inferring nucleotide sequences by amplification and synthesis.



In silico characterization of the genomes of the STECs - serotype and virulence genes

Applications of metagenomic sequencing in longitudinal studies

Metagenomics for Produce Safety

- Overall health of the various environmental sources and how that changes over time or with agricultural impacts
- How the localized geography, environmental factors, or activities impact water sources and whether this is correlated with pathogen presence or persistence.
- “Indicator” microbiomes that may be indicative of pathogen presence (co-associated) or may be inhibitory for pathogen growth.
- How sample collection methods influence information gained and best method for a particular application.



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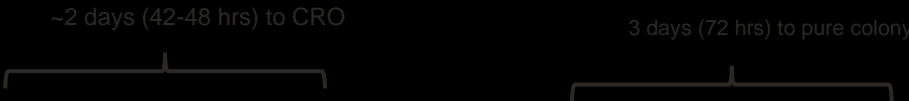
Biocontrols identified from agroecology

Enriched *Paenibacillus* spp.

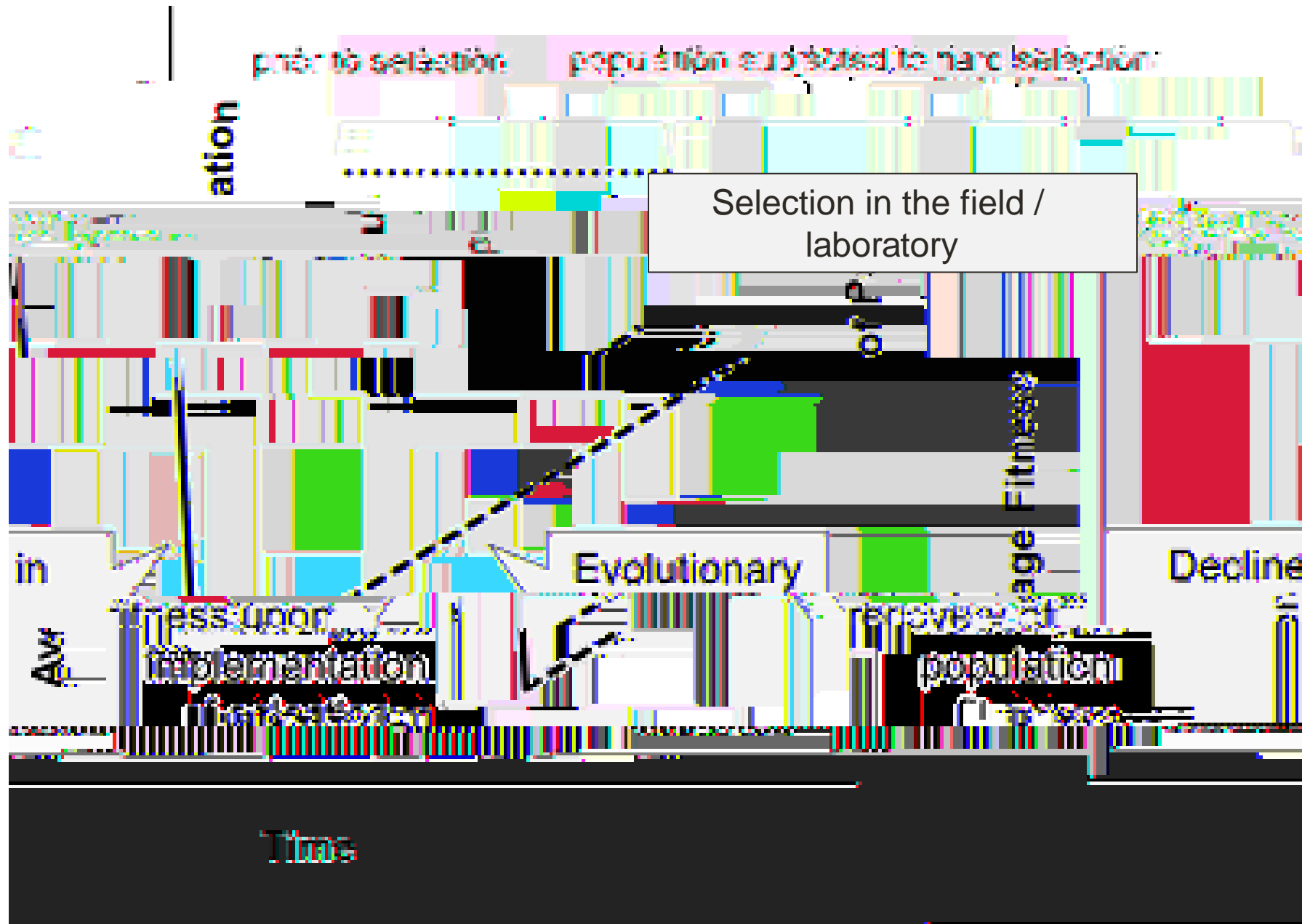


Bacterial Pathogen Workflow

FDA



FDA
(STEC/EHEC/
SALMO)

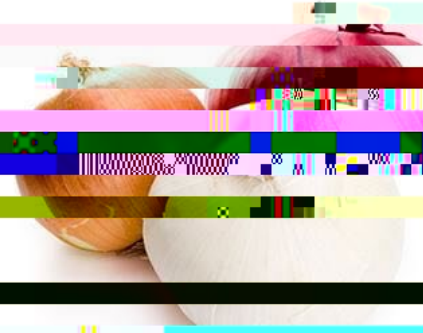


Salmonella Outbreak: Link Established to Onions



Food Safety Alert

Posted October 20, 2021



Fast Facts

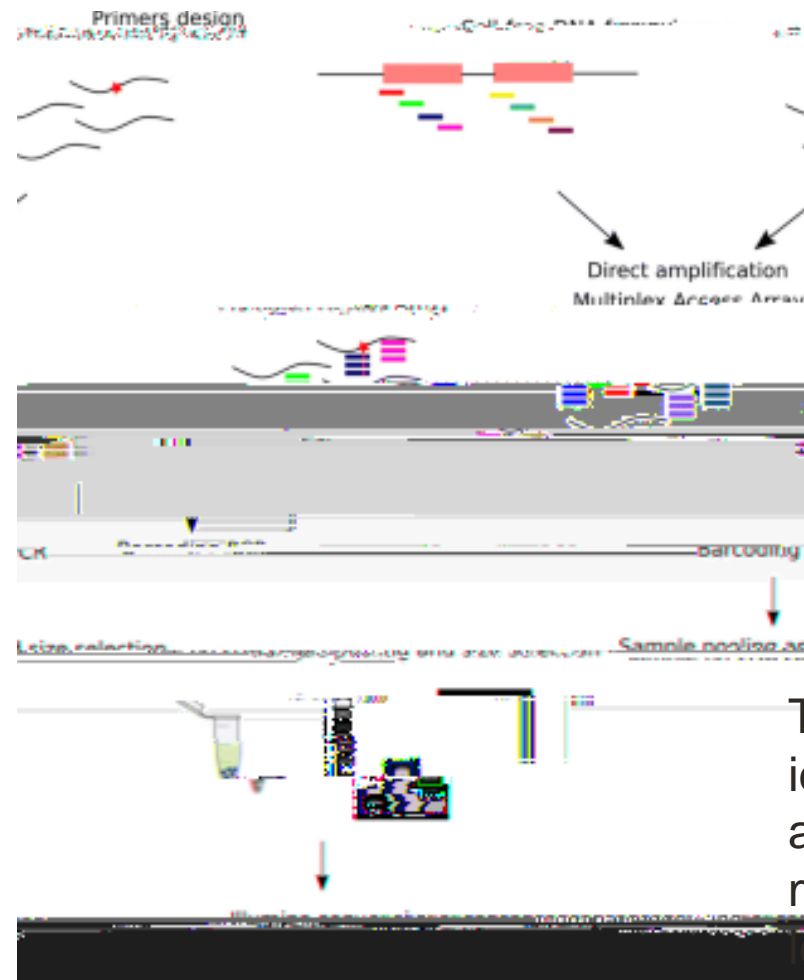
- Illnesses: 652 (60 new)
- Hospitalizations: 129 (13 new)
- Deaths: 0
- States: 37 (1 new)
- Recall: No
- Investigation status: Active

targeted amplicon sequencing : how does it work?

Targeted amplicon sequencing is a next-generation sequencing (NGS) method that uses polymerase chain reaction (PCR) to amplify specific DNA fragments, or amplicons, from a genome.

The process involves the following steps:

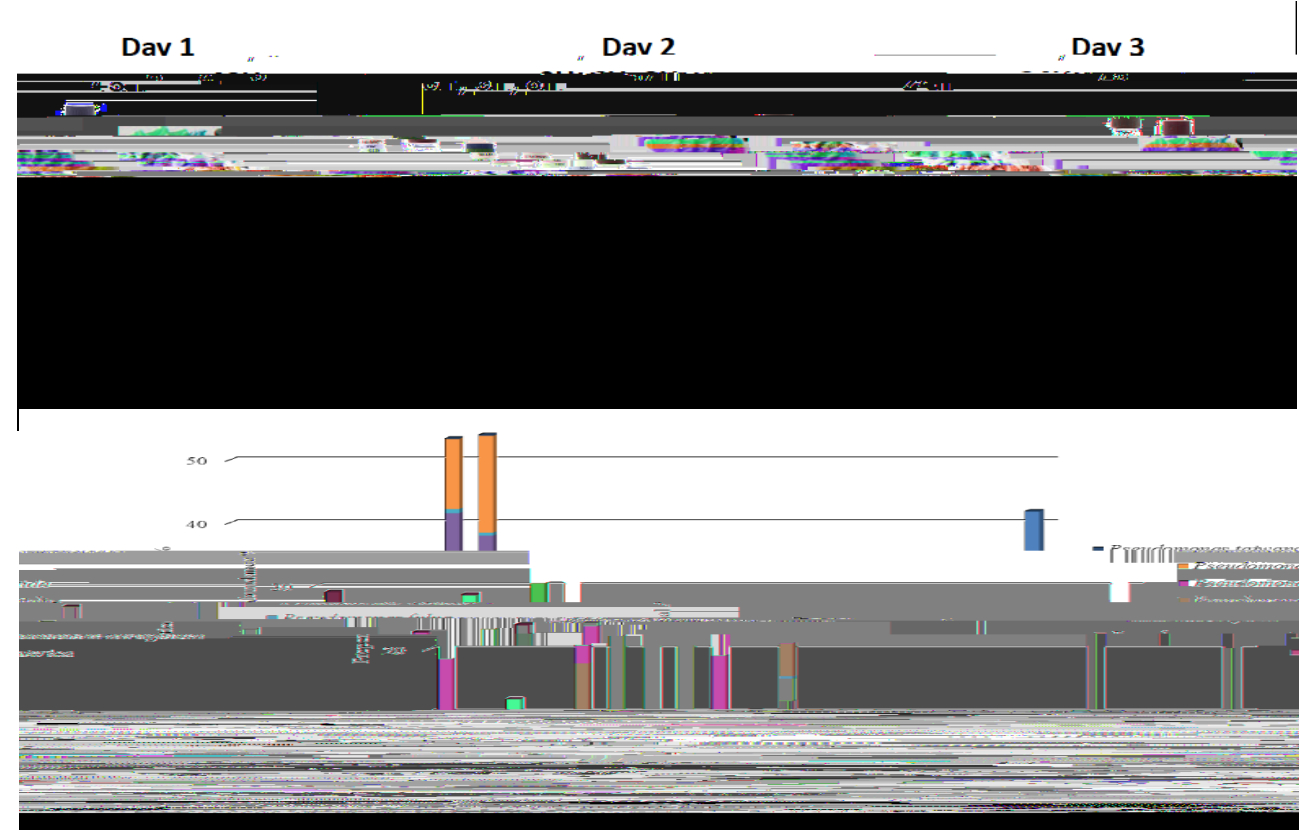
1. Design primers
2. Transform samples into libraries
3. Amplify DNA
4. Multiplex samples
5. Sequence amplicons



Targeted amplicon sequencing can identify individual strains in a population and characterize them down to a molecular epidemiologically relevant level.

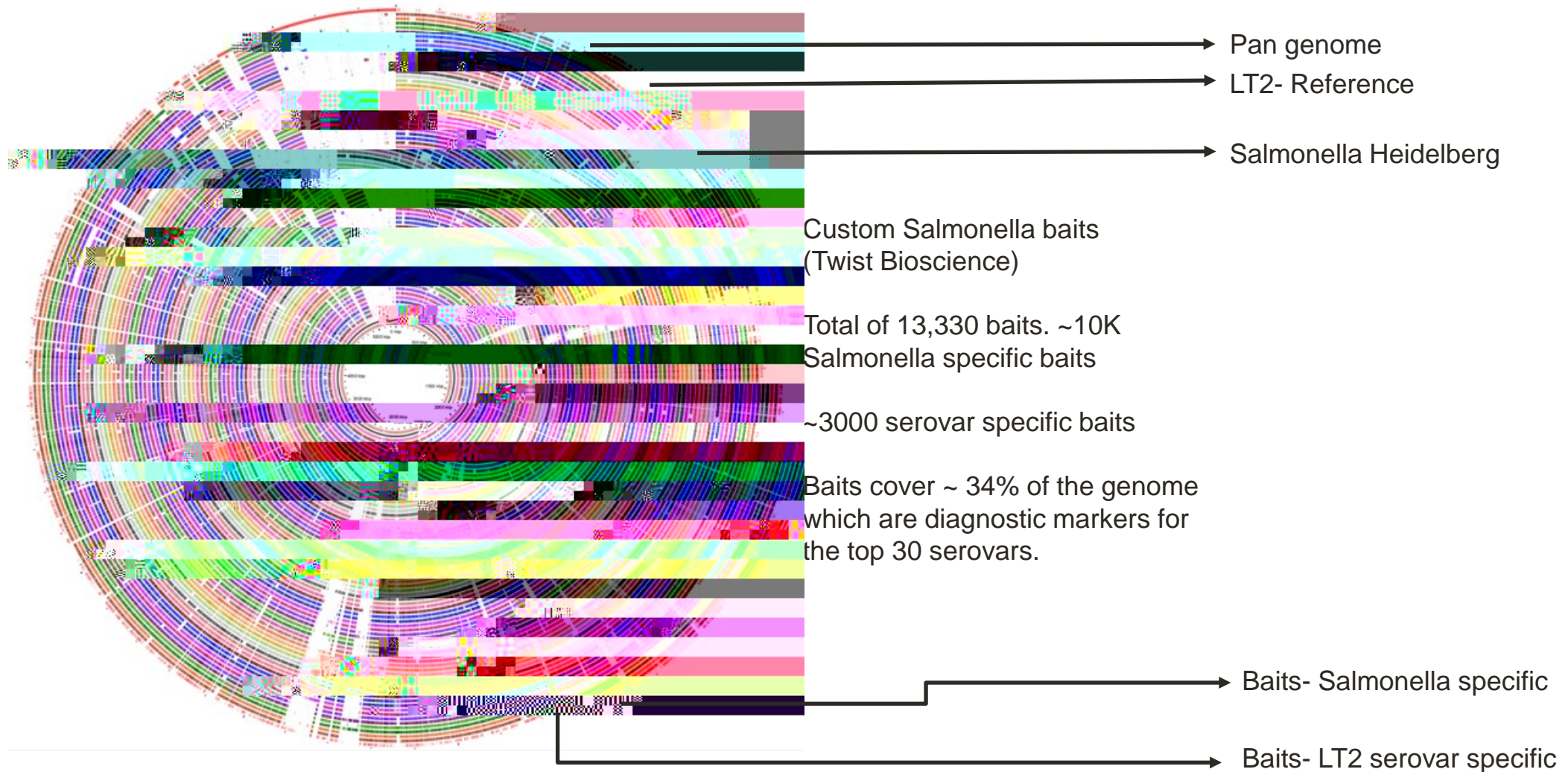
TOWARDS A CULTURE INDEPENDENT FOOD TESTING PROGRAM

Lm enrichment (BAM) – characterized every 4 hours to describe genomic coverage of Lm and describe co-enriching microbiota



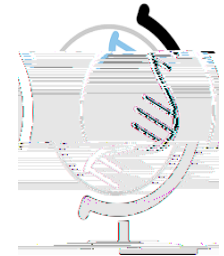
METAGENOMICS

Salmonella Baits Panel (SBP) Design (v0.07)

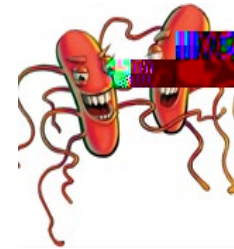


Functional Genomics

④ The study of how genes and intergenic regions of the genome contribute to different biological processes or environments



④ Represent links between genotype (genome wide) and phenotype, or metagenome and community phenotype



Food Safety Questions





Research Paper...

...tion of Pan-Asian Sources... Survival of salmonella on Endive, Pumpkin, Sunflower, and Chia Seeds Dried for

...Direct Consum



research Paper

...Arising from the Consumption of Almonds in the United S



Increasing occurrences of outbreaks associated with low moisture food (LMFs)

2012 - 2020

- 54 outbreaks

