
Heightening Awareness of WGS

Jennifer McEntire,
VP Food Safety & Technology
United Fresh Produce Association

What's WGS?

- Familiarity with PFGE?
- Understanding of Whole Genome Sequencing on a scale of 1 (never heard of it) to 5 (I'm an expert)
- Human Genome Project
 - Early 2000s

What it means

Pre-1995

- Gray Hyundai Sonata

1995-
2015

- MD license plate 6ay1??

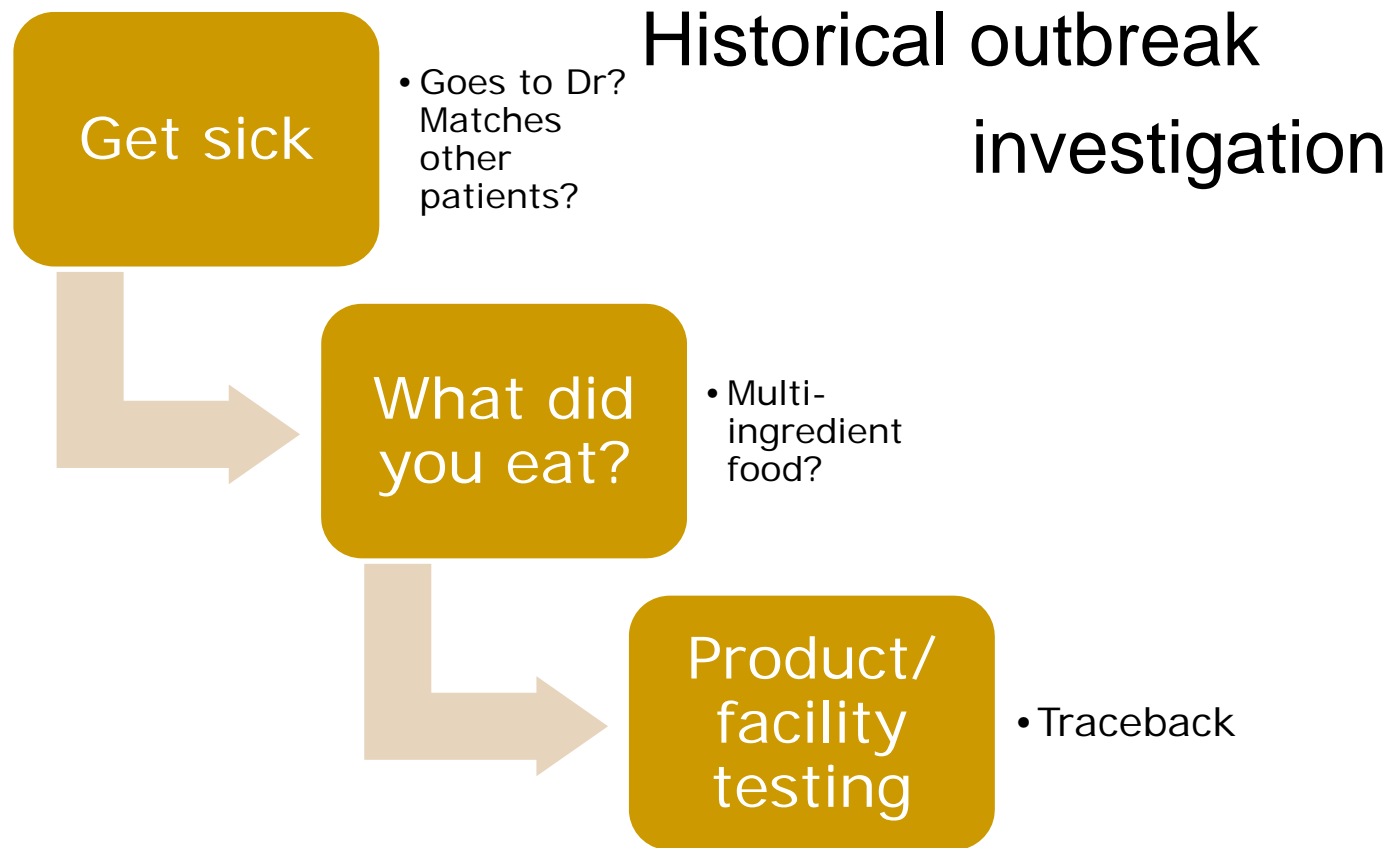
Present

- VIN ABC123DEF456

PFGE shows a yes/no match

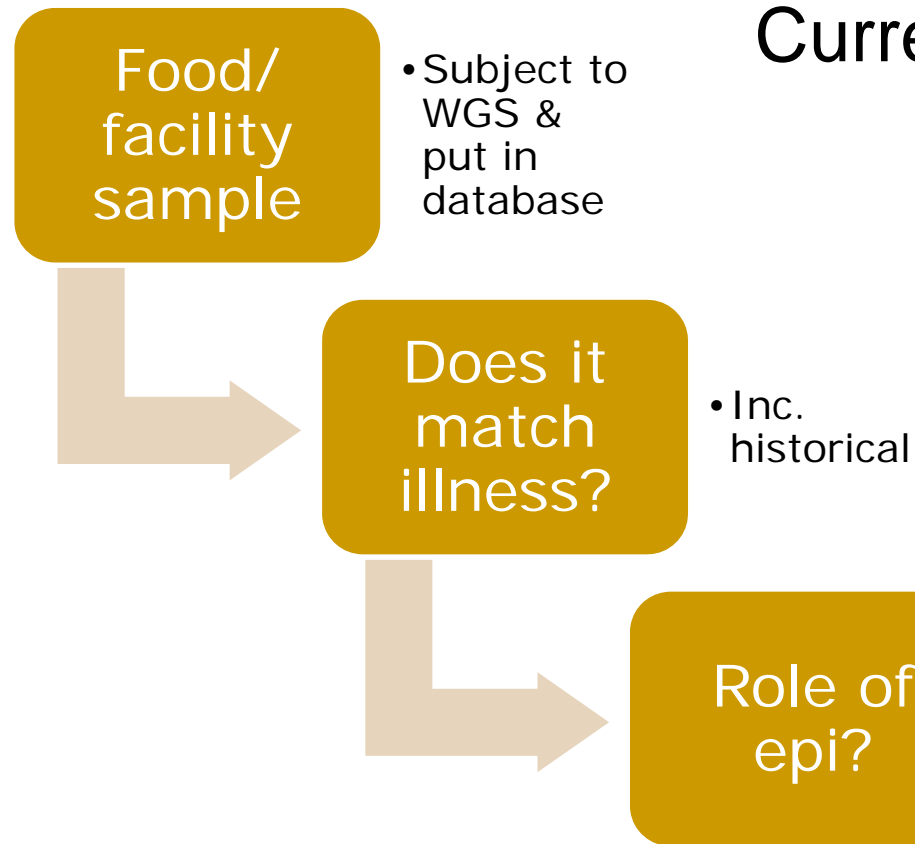
WGS shows a familial relationship

WGS relevance to food safety



WGS relevance to food safety

Current approach

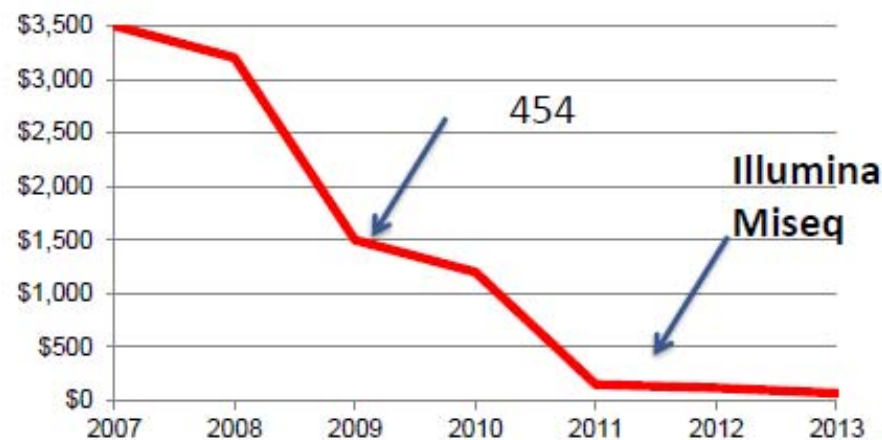




Is WGS a viable solution?

- Cost
- Increasing ease of operation
- Database longevity
- Comparable times to conventional pipelines
- Sample prep
 - Identical for all pathogens
- Cost savings
 - Resistance, subtyping, virulence factors, more...
- New applications
 - tracking, regulatory/compliance actions, historical trends, more...

Cost per bacterial genome



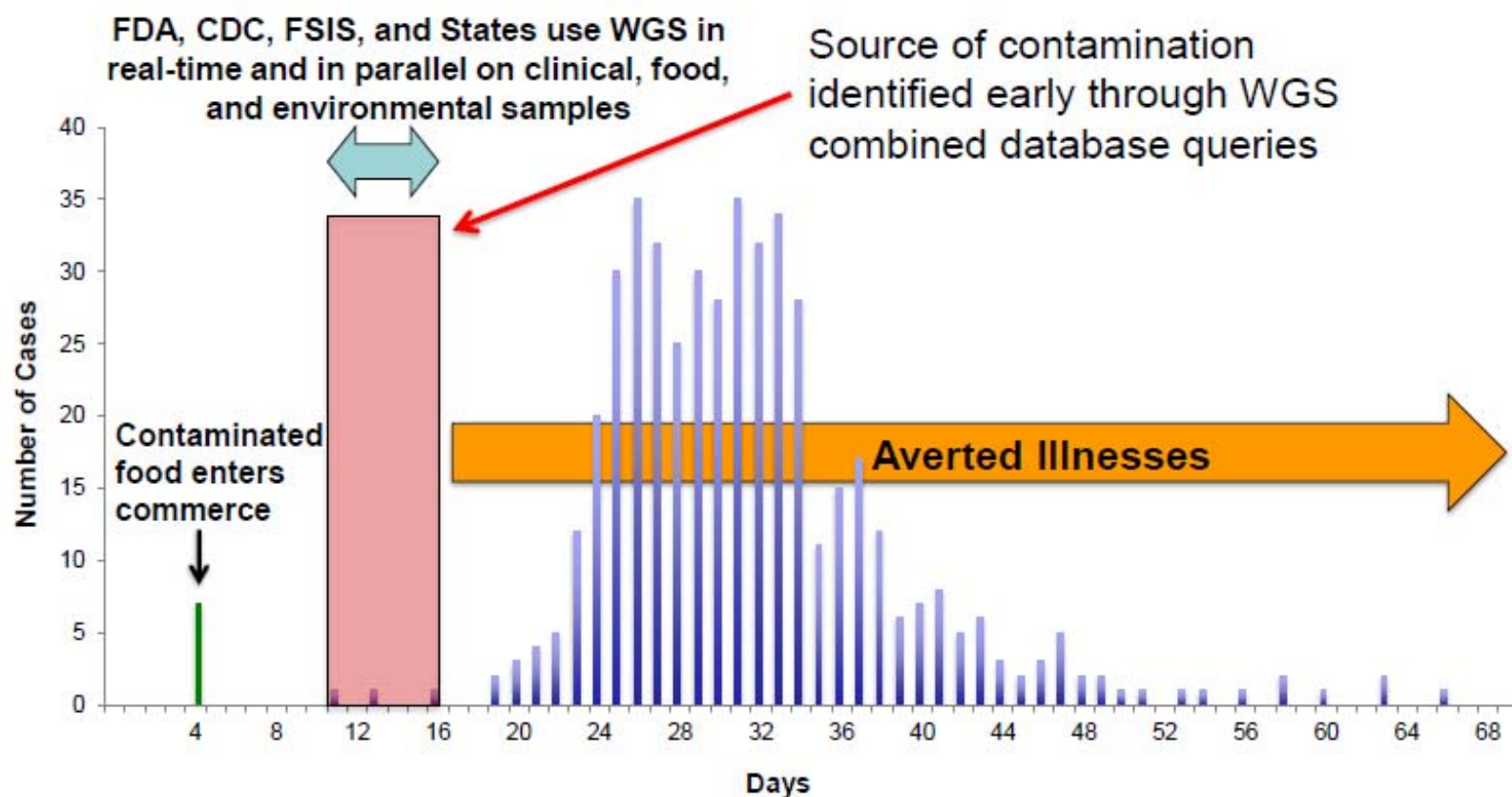
\$70/genome
in 2015

\$40/genome
in 2016 w/
Illumina NextSeq Technology

Illumina NextSeq Technology



TARGET: Timeline for Foodborne Illness Investigation Using Whole Genome Sequencing



Opportunities

- Characterizing relatedness of strains to assist with source attribution
- Understanding factors that contribute to distribution/movement in the environment
- Understanding factors that impact persistence
 - Resistance to sanitizing agents
 - Strategies for hygienic design
- Factors that impact survival
 - Development and validation of control measures

Root of the Concern

- What industry heard a few years ago

WGS is the greatest thing ever (and we won't need epi anymore).

WGS match between a food and clinical isolate **doesn't** mean food caused illness. Epi and traceback critical

Present Day, CDC



Fear of warning letters

“The WGS phylogenetic analysis of these five (5) isolates finds that they comprise two (2) strains of *L. monocytogenes*. **Comparing** these five (5) strains to the larger **WGS database** shows that four (4) of the isolates are virtually identical to twenty eight (28) isolates from sample [abc] and [xyz] collected in January of 2016 from the same facility. This demonstrates a **resident strain** of *L. monocytogenes* has maintained its presence in your facility since at least January of 2016. The presence of a resident strain of *L. monocytogenes* in your facility is significant in that it demonstrates your sanitation efforts are inadequate to effectively control pathogens in your facility to **prevent contamination of food.**”



FAX: 559 526 4696 | 12133 AVENUE 408 | CUTLER, CALIFORNIA 93615 USA

Voluntary Recall 07/19/2014



(WGS) analysis by whole-genome multilocus sequence typing showed that isolates cultured from the Massachusetts and Minnesota patients were highly related (<10 allele differences and <10 high-quality single nucleotide polymorphism differences) to the isolates from recalled fruits

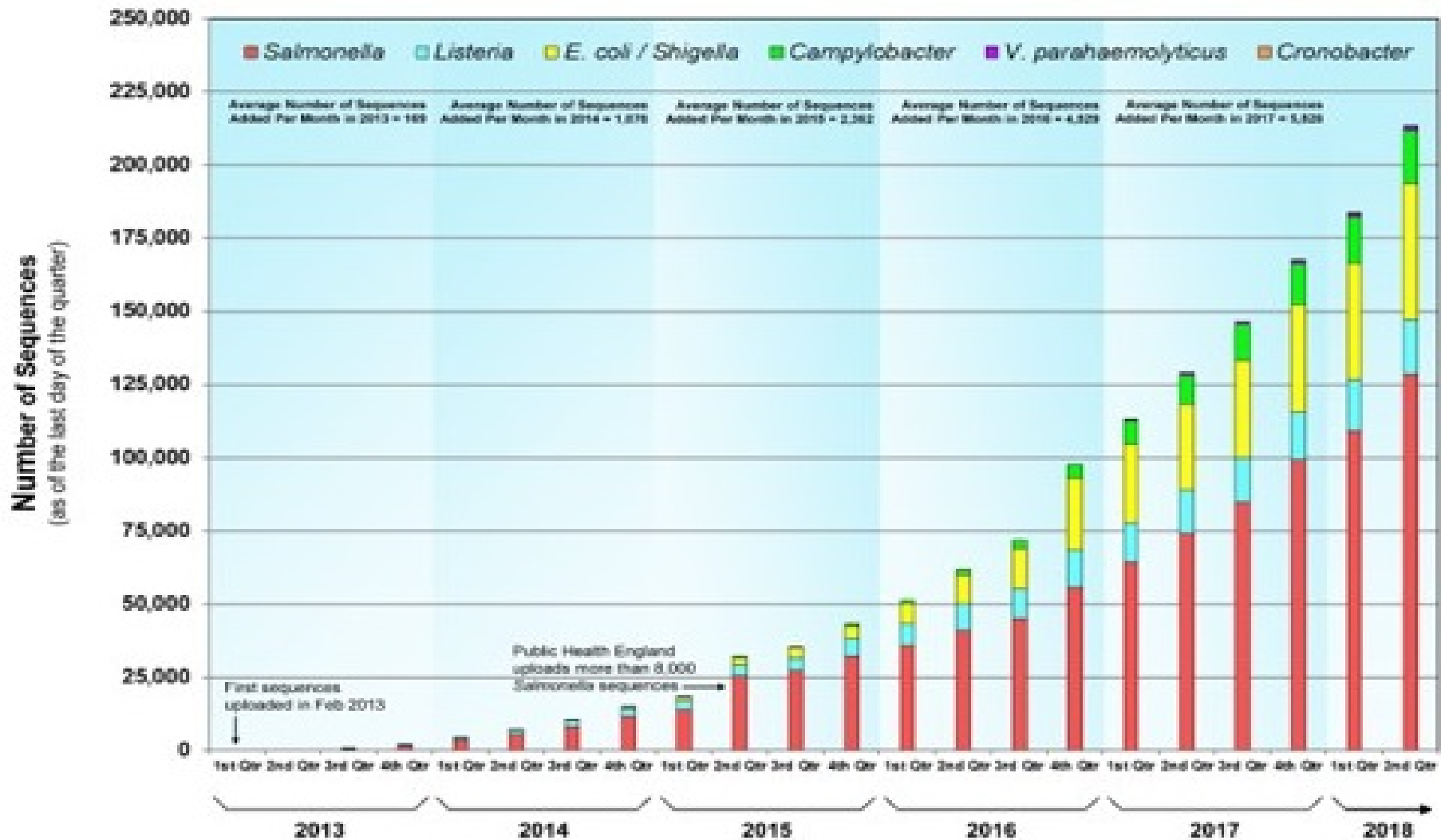
9
illnesses
over 2.5
yrs

WGS showed that the *Listeria monocytogenes* isolated from the frozen corn was closely related genetically to eight bacterial isolates from ill people... This close genetic relationship provides additional evidence that the people in this outbreak became ill from eating frozen vegetables produced by CRF Frozen Foods. ...environmental samples collected by FDA from Oregon Potato Company, located in Pasco, WA, were found to be closely related genetically to eight of the isolates of ill people associated with this outbreak.

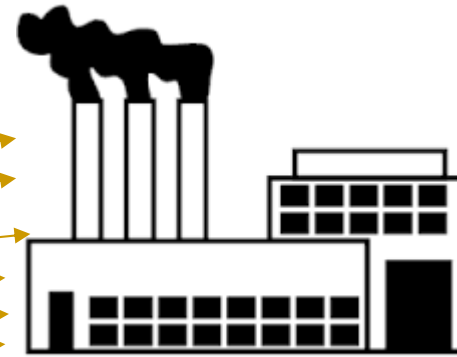
UNITED FRESH
PRODUCE ASSOCIATION

GenomeTrakr

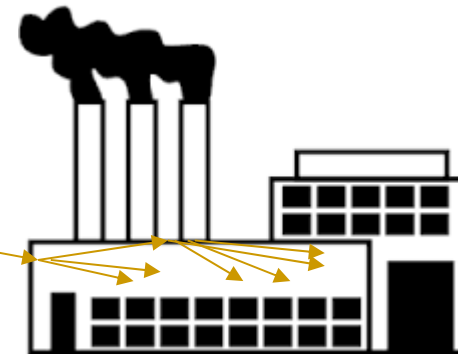
Total Number of Sequences in the GenomeTrakr Database



Resident or Repeat Transient?



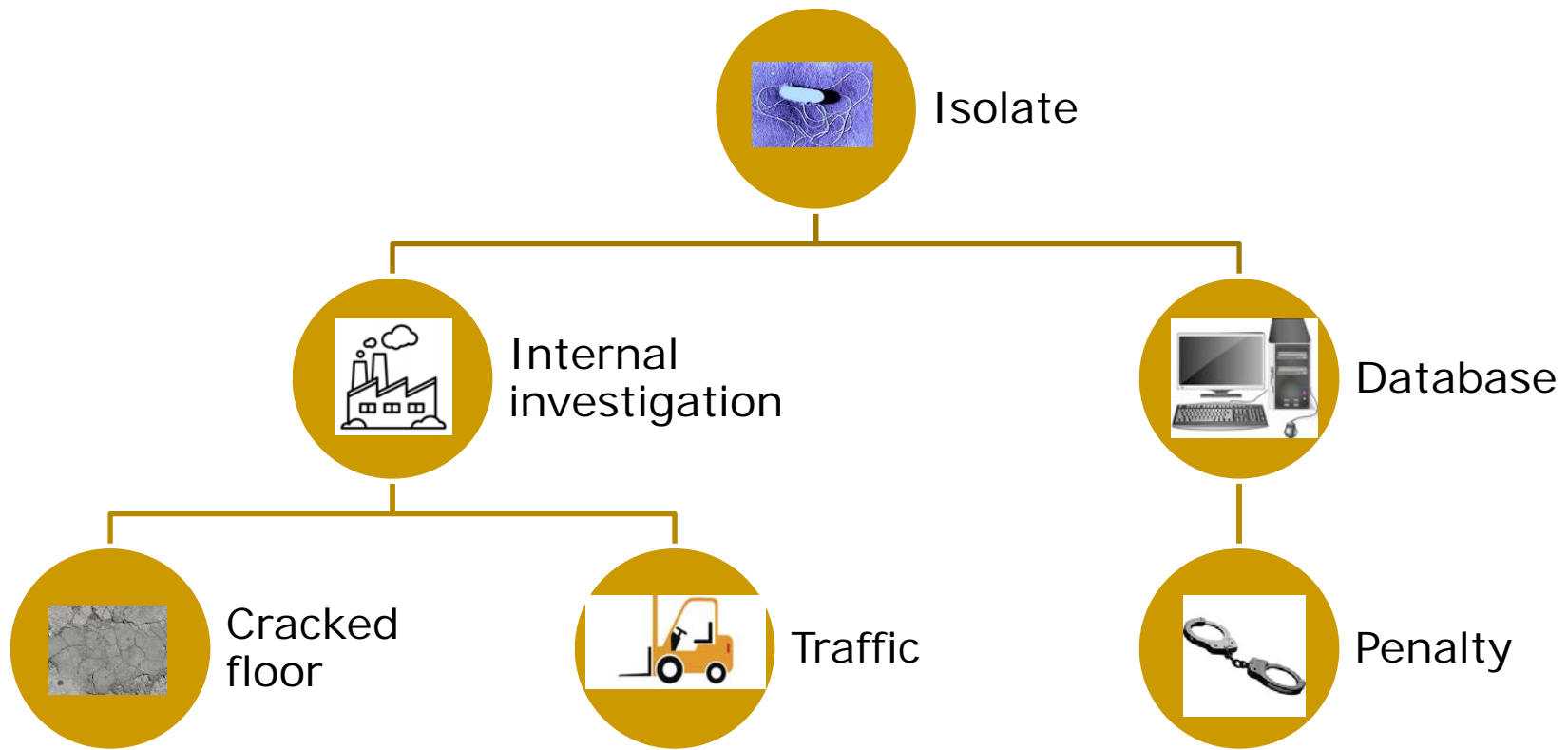
Resident in orchard,
transient in facility



Resident in facility

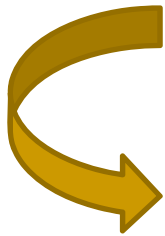
-what is the true ubiquity of sequences?

Should Industry do WGS?



Retrospective Investigations

- If you collect WGS data must you share it?
 - Are blinded data really safe?
 - Metadata: friend or foe?
- Once in the database it's there forever
- What do we know about ubiquity, genetic drift?



Role of epi, traceback,
etc.

Summary

- WGS is here to stay
 - High fidelity method
 - Still gathering more data & understanding how to interpret it
 - Salmonella and Lm evolve differently
- Outstanding questions
 - Role in an investigation
 - Quantitative methods
 - Live/dead; dose response; gene expression/virulence
 - Retrospective analyses
 - What guides regulatory use of WGS?

Questions?

Jennifer McEntire, Ph.D.
VP Food Safety & Technology
jmcentire@unitedfresh.org