

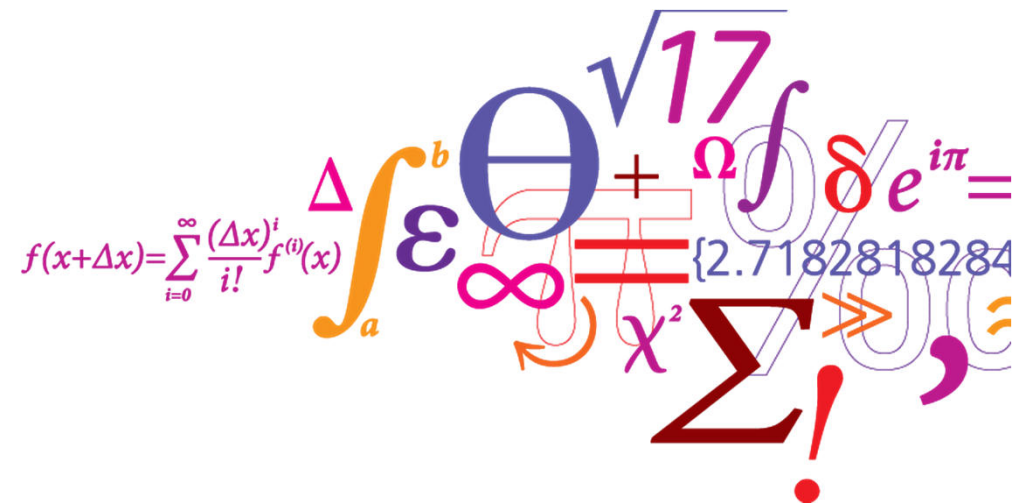


Whole genome sequencing of foodborne *Listeria* in Denmark: Pilot project for implementation in routine surveillance

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Some of the partners involved in outbreak investigations and surveillance of Listeria in Denmark



- Typing of human isolates
- Patient interviews



Ministry of Food, Agriculture and Fisheries
Danish Veterinary and Food Administration

- Control food producing companies
- Take samples and isolate Listeria

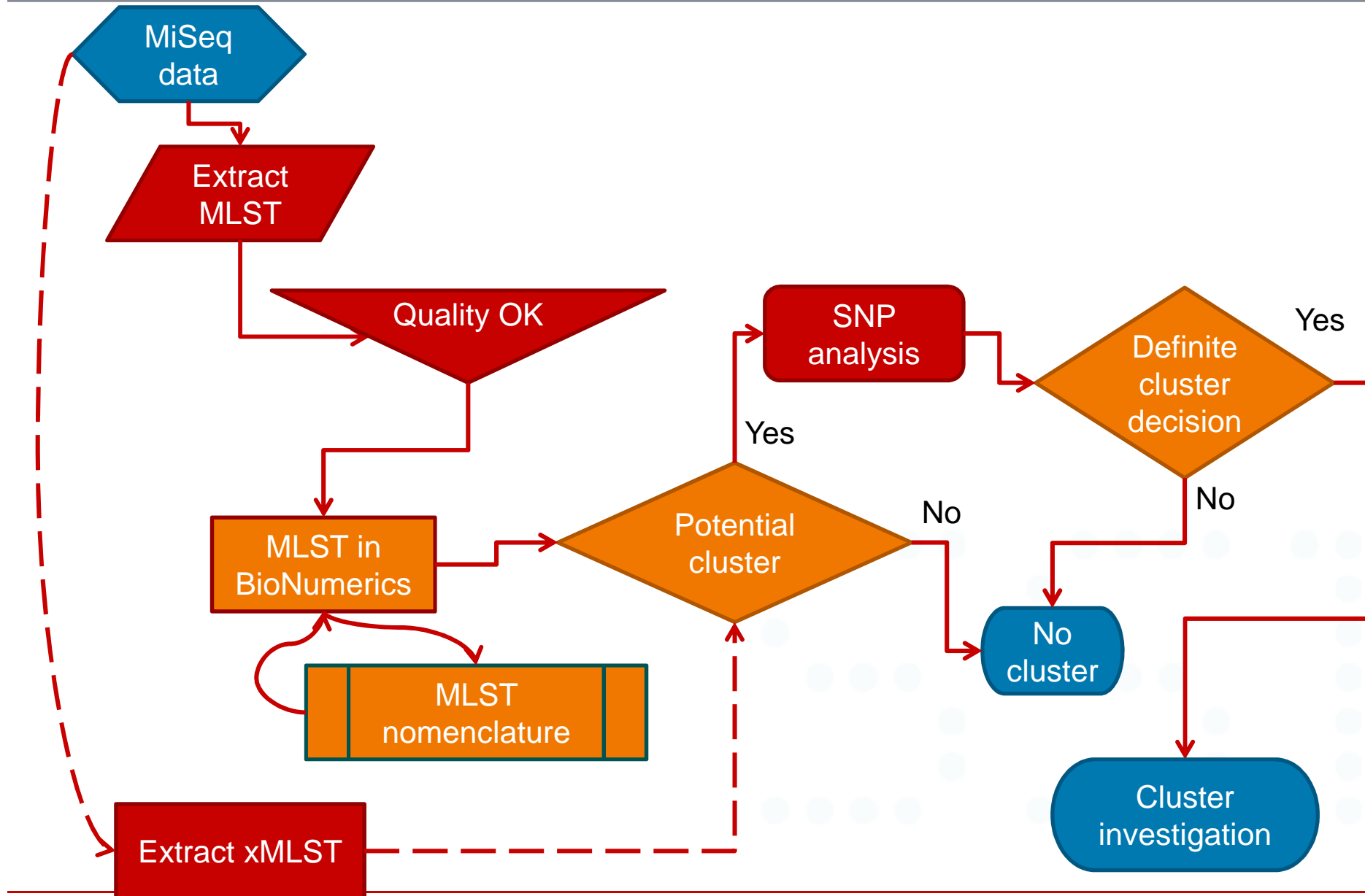
DTU Food
National Food Institute

- Typing of food and veterinary isolates

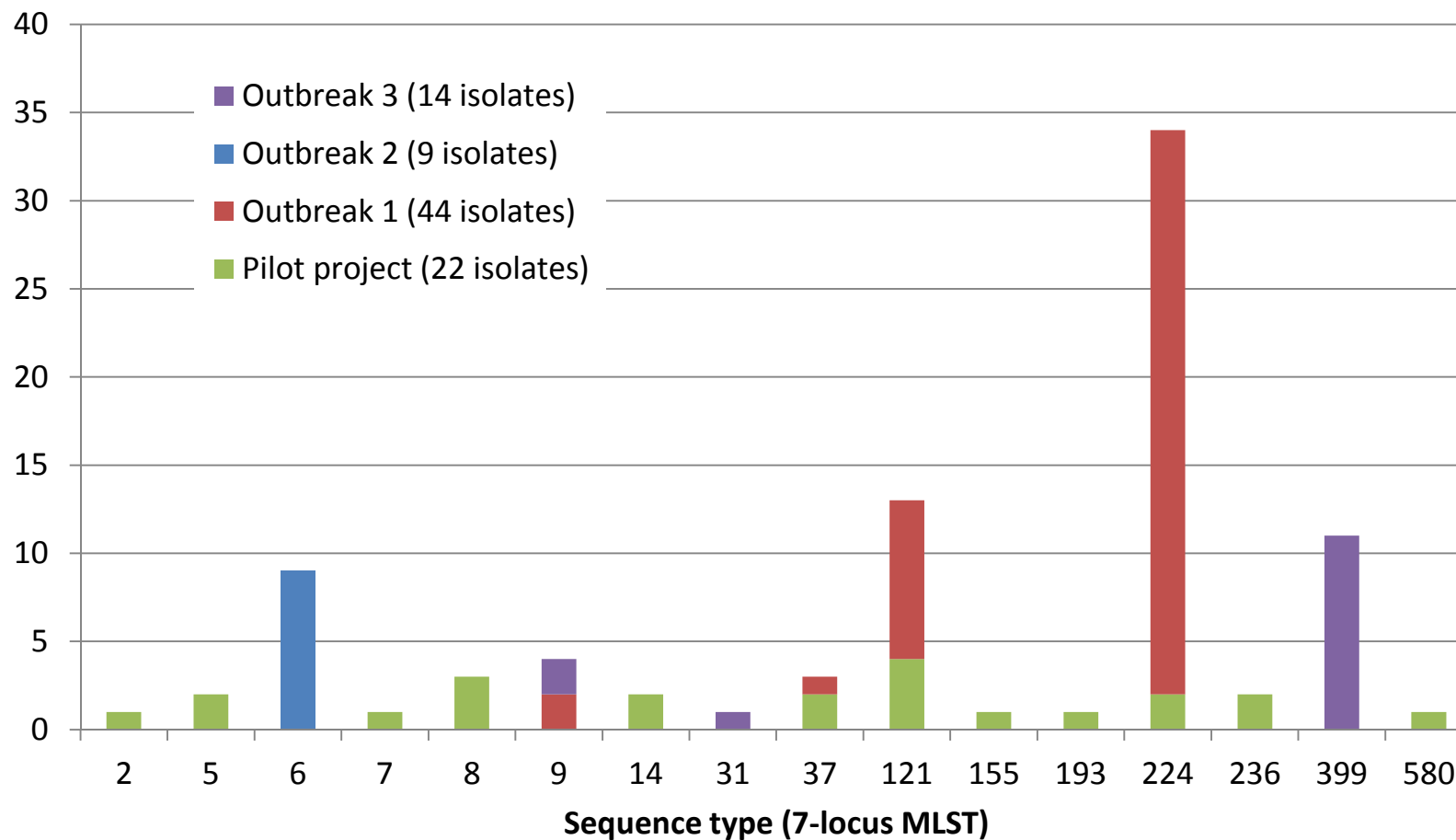
Pilot project WGS: collaboration DTU, SSI and DVFA

- April 2014, approx. 1 year
- From May 2014 food isolates from official control undergo WGS
- SSI performs interviews with all patients
- Can WGS be used for “real-time” surveillance of Listeria?
 - Human and food isolates

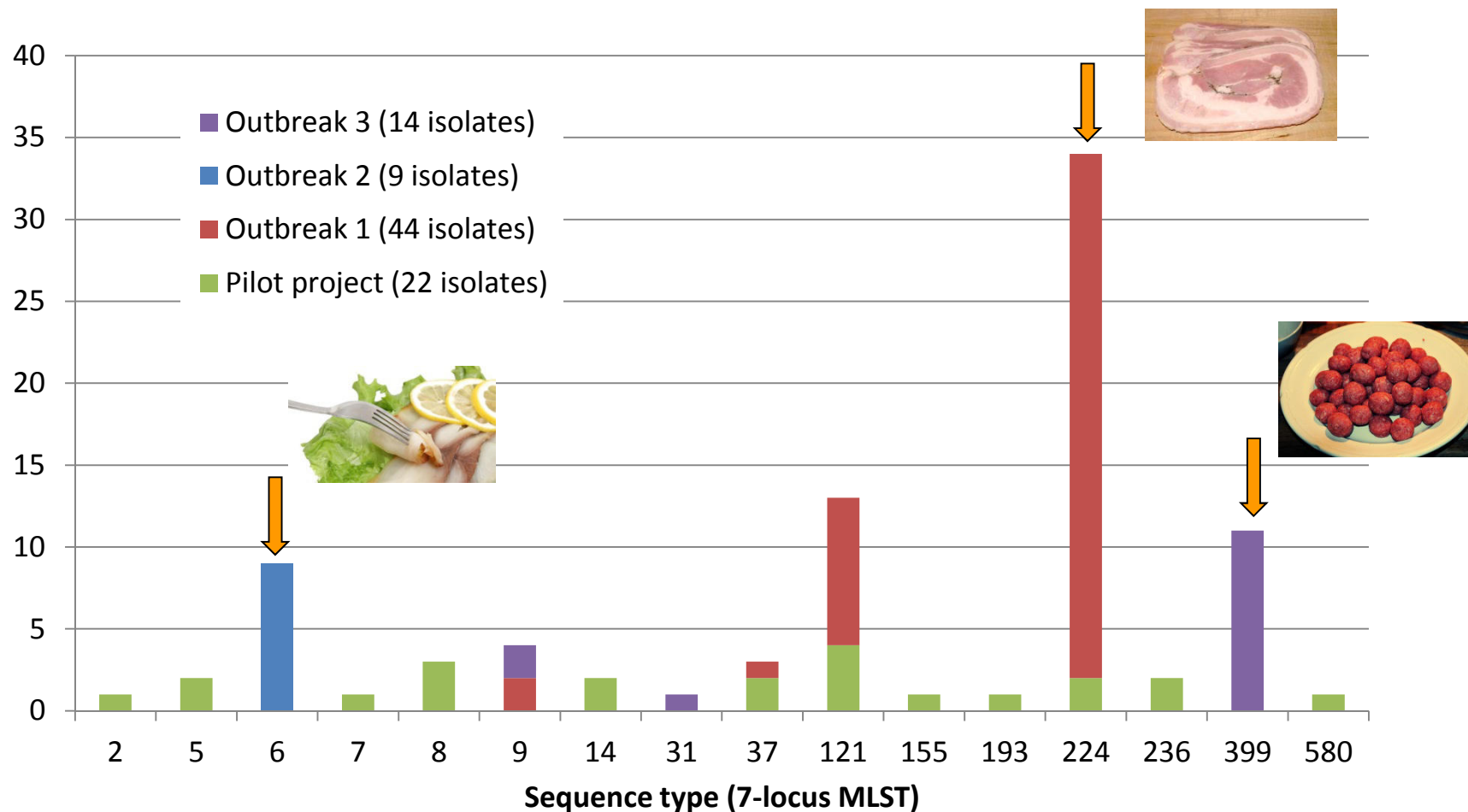
LISTERIA – DATA ANALYSIS WORK FLOW WGS



Results food isolates from the pilot project



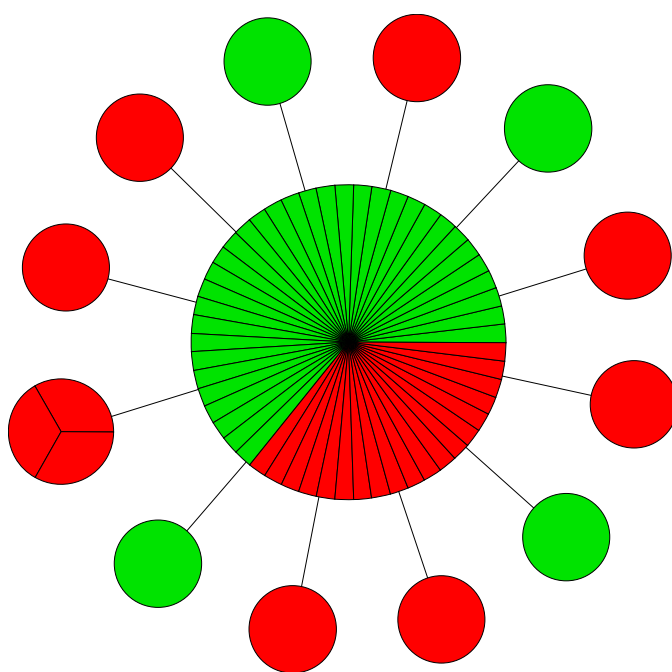
Results food isolates from the pilot project



Match to human cases:

WGS typing of isolates reason for finding link

ST-224 outbreak Summer 2014



● Isolates from 38 patients

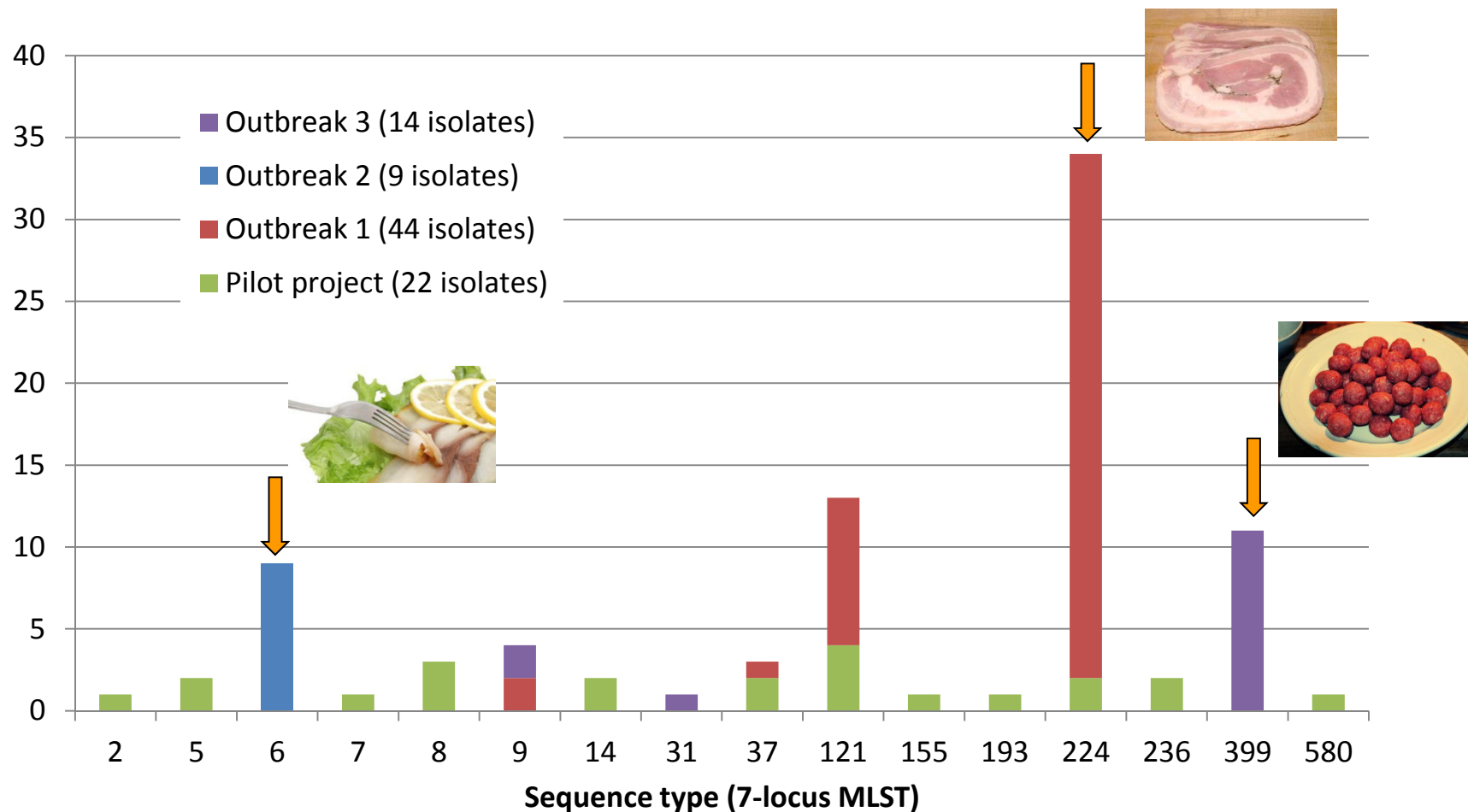
● Isolates from 29 samples of food from producer A and several packaging and slicing companies



All cases and all food isolates (ST-224) linked to the outbreak had a max of 2 SNPs difference

—
1 SNP

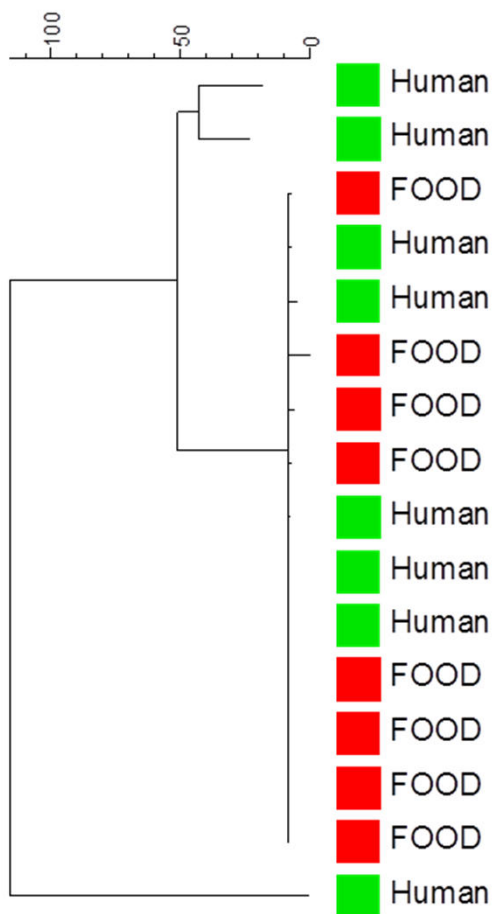
Results food isolates from the pilot project



Match to human cases:

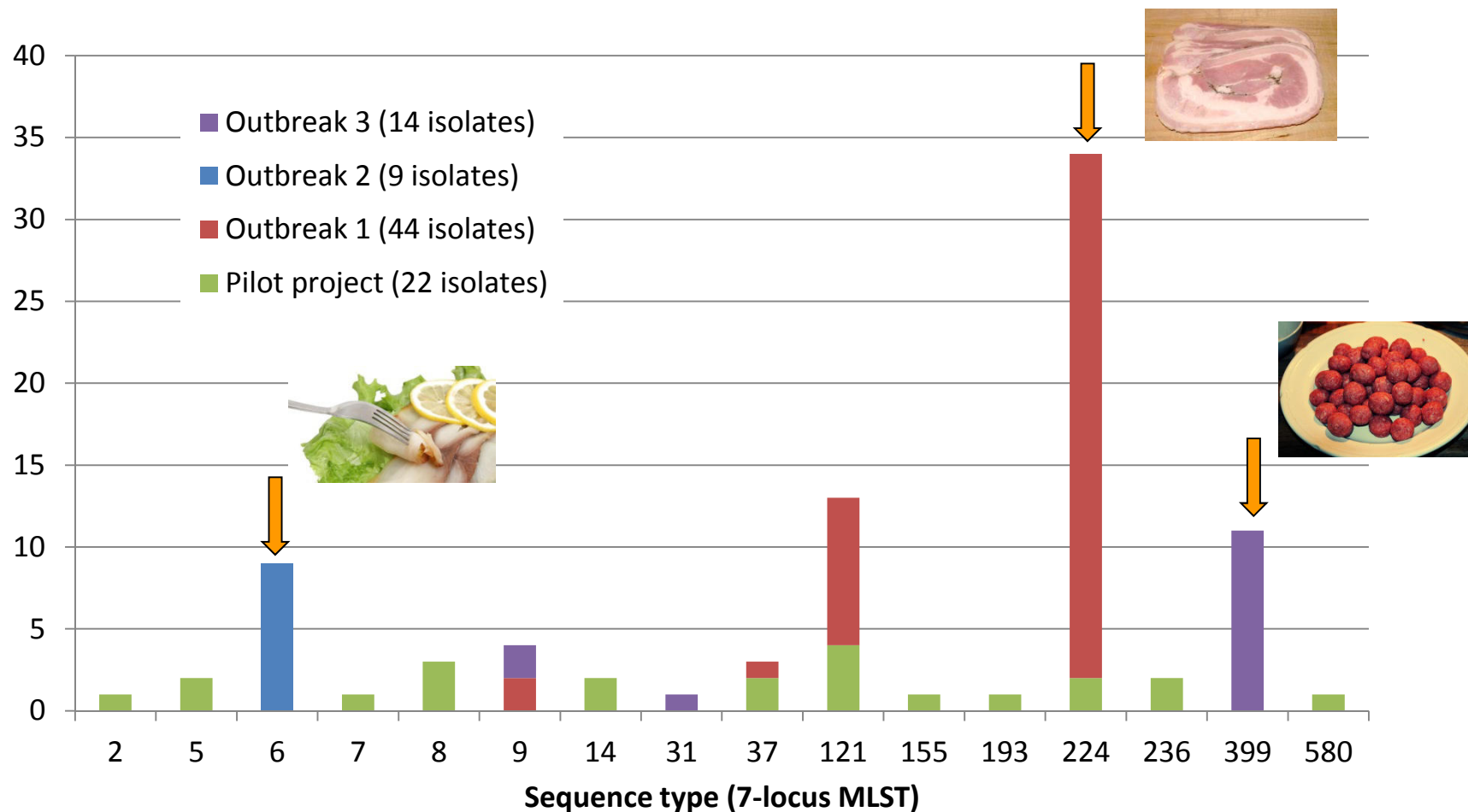
WGS typing of isolates reason for finding link

SNP analysis of ST6 group



- Link patients and smoked fish products
- Few SNPs difference between food and human isolates within the outbreak

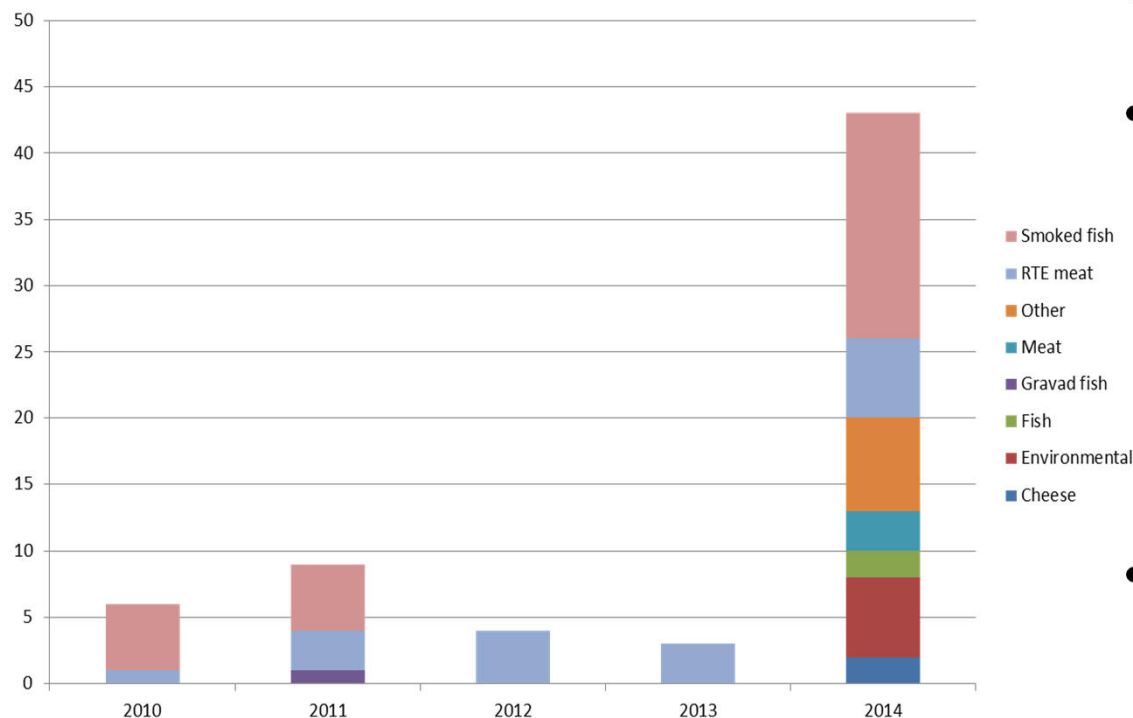
Results food isolates from the pilot project



Match to human cases:

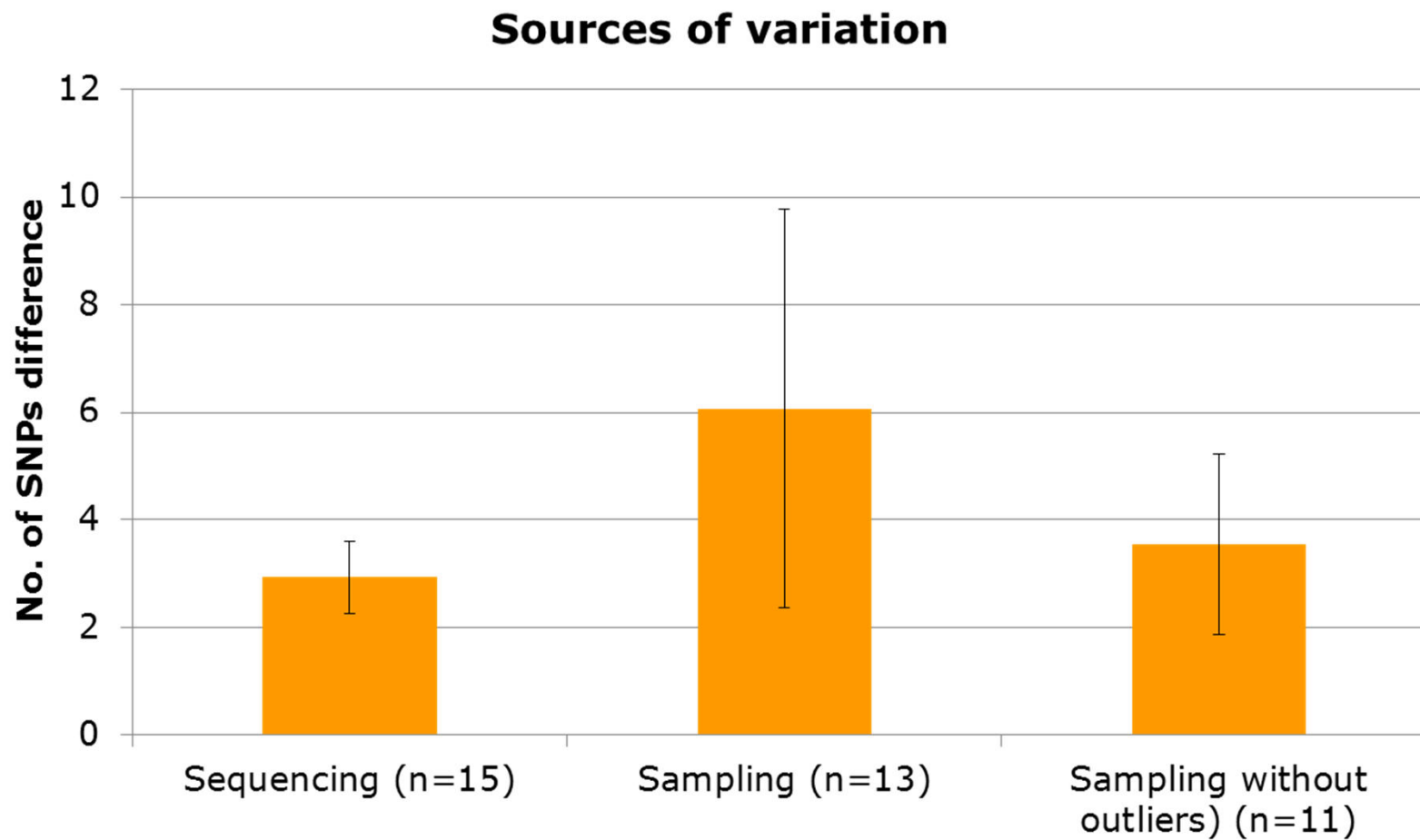
WGS typing of isolates reason for finding link

WGS typing of background food isolates

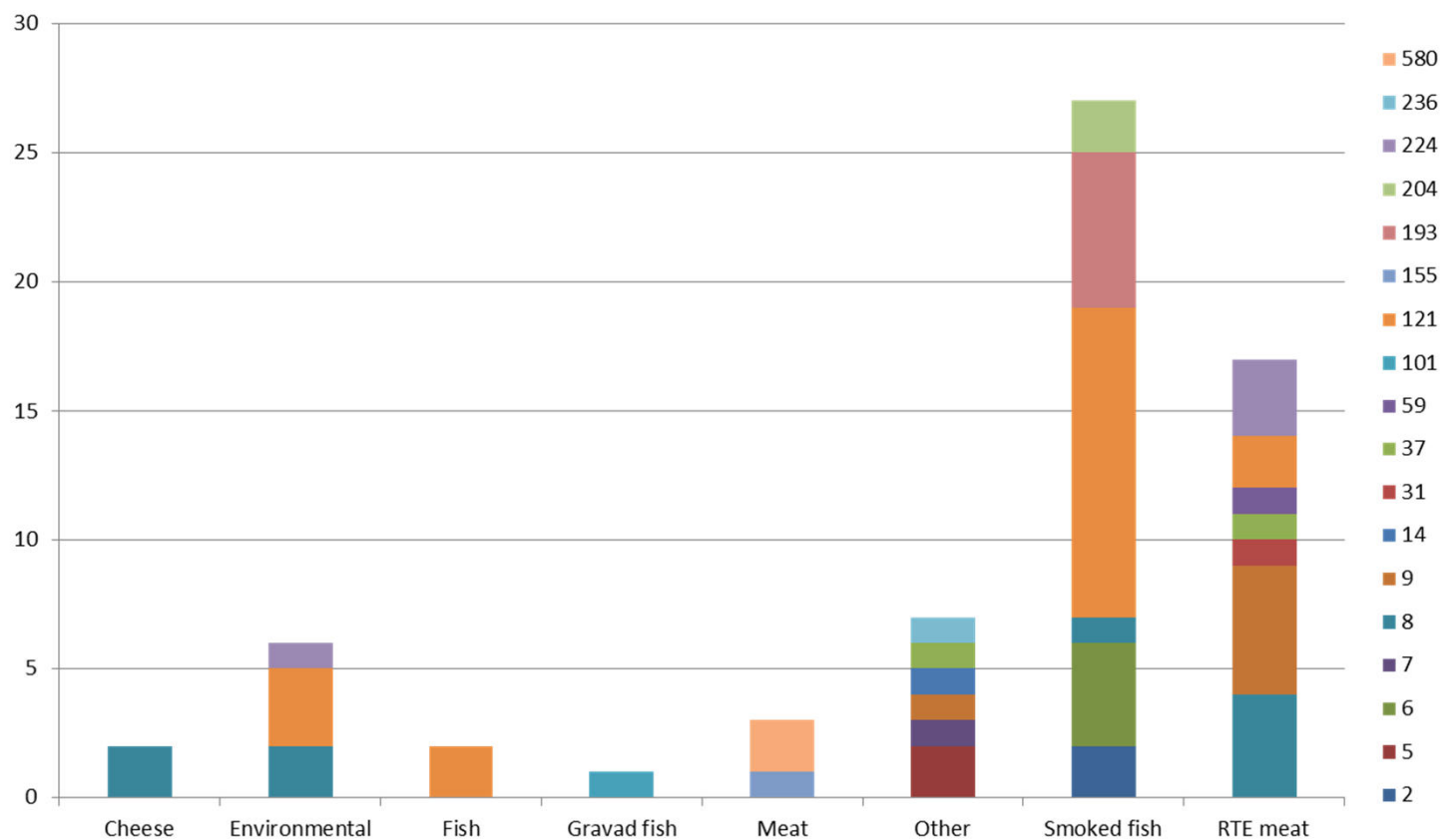


- n = 65, 2010-2014
- Diversity of Listeria:
 - From same food batch
 - From same production line, but different sample sites
 - From same company over a longer period of time
- Possible sources of SNP differences:
 - Sequencing errors
 - Different sequencing platforms
 - Data analysis pipelines

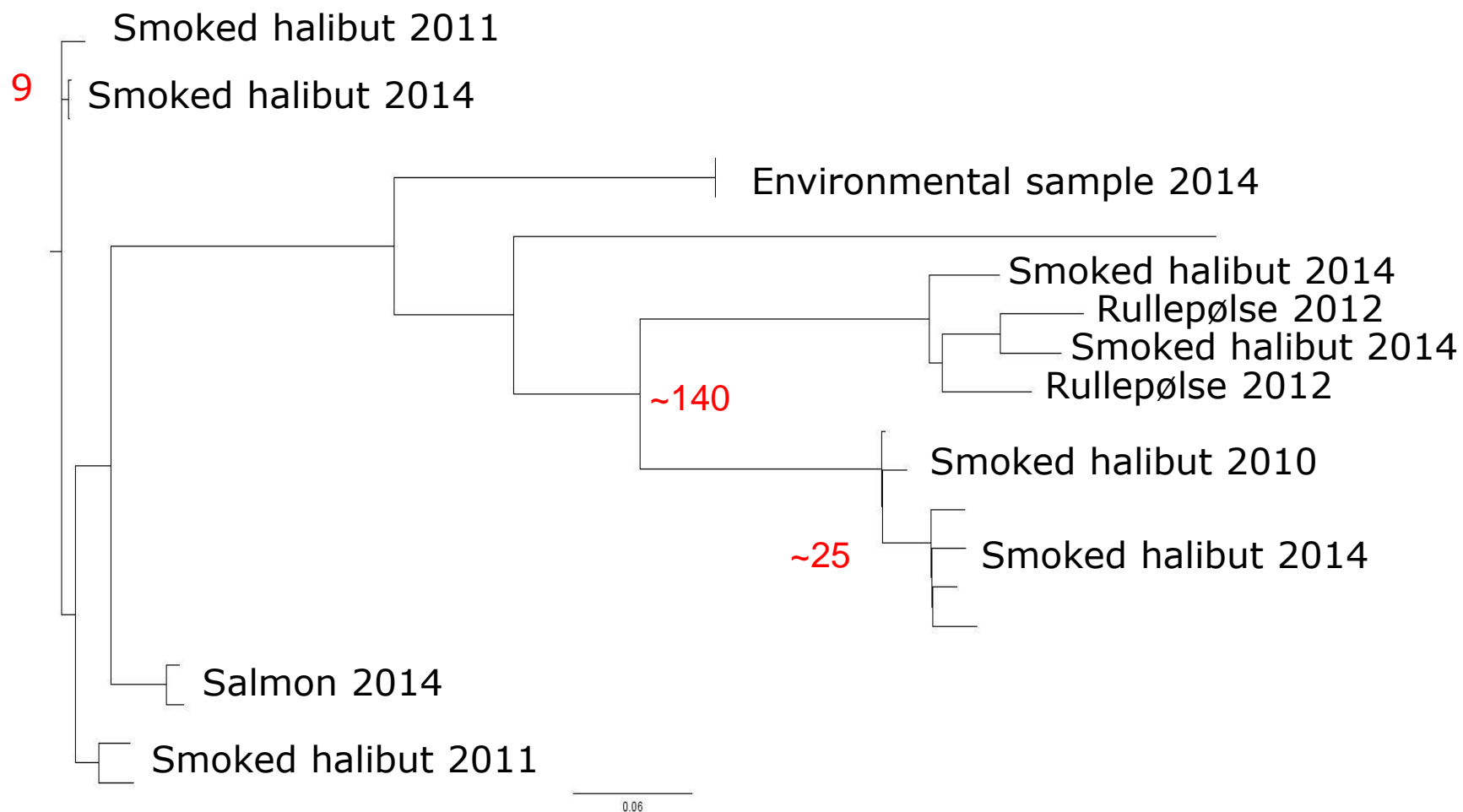
Variation due to repeated sequencing and sampling



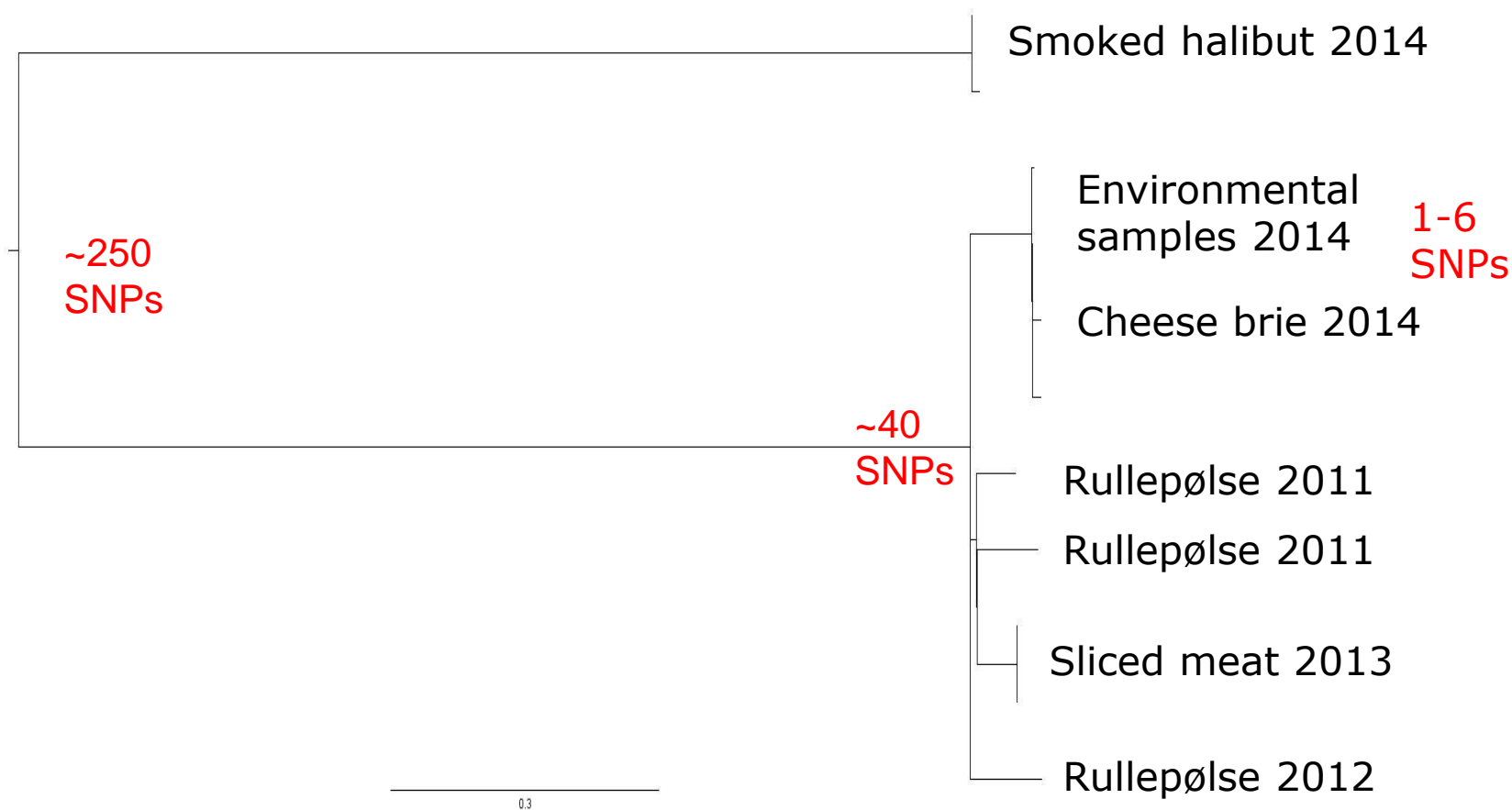
WGS analysis of Danish food isolates



Most common types: ST121



Most common types: ST8

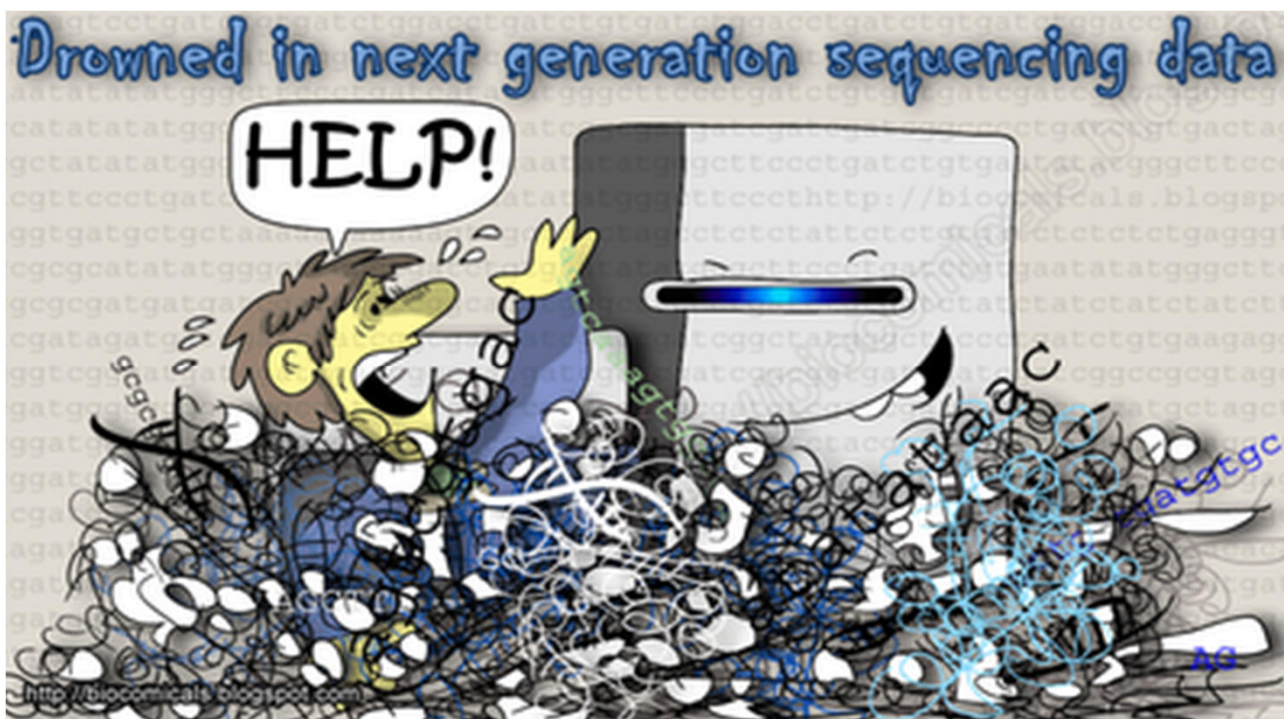


Future plans and challenges

- Implementation of WGS routinely
 - SOPs
 - Quality of WGS data
- Sharing of WGS data between partners
 - MLST types to screen for common sources
 - SNP types to find links between human and food isolates
 - Storage and transfer challenges
- Further studies on diversity of foodborne Listeria
 - From same food batch
 - From same production line, but different sample sites
 - From same company over a longer period of time

Thanks for your attention!

- Questions?



Source: www.biocomicals.com, Alper-Uzun, PhD