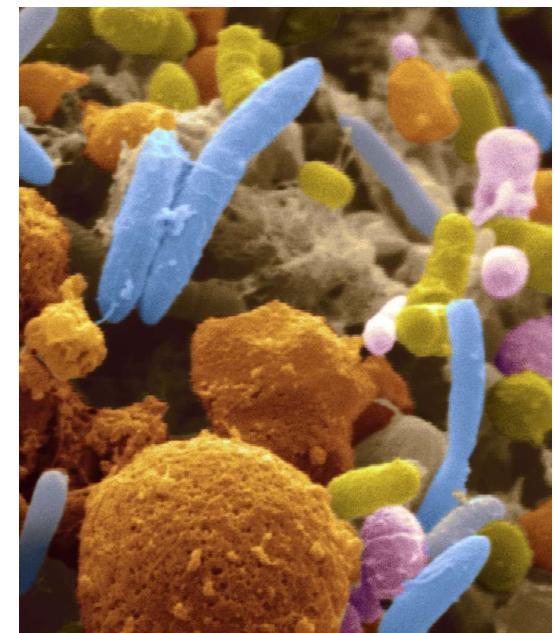
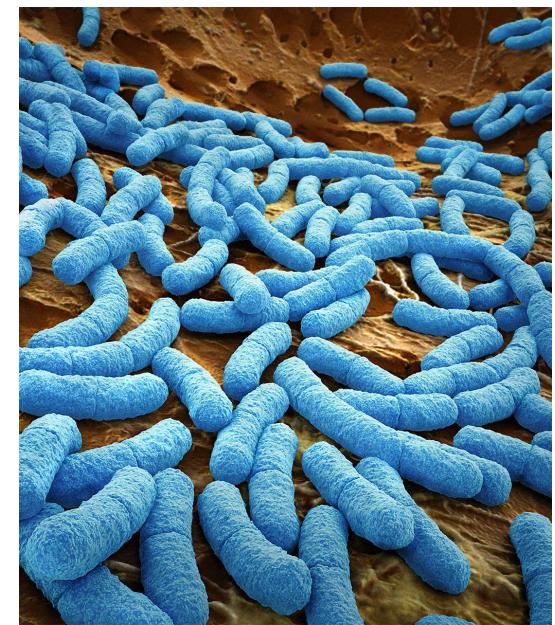




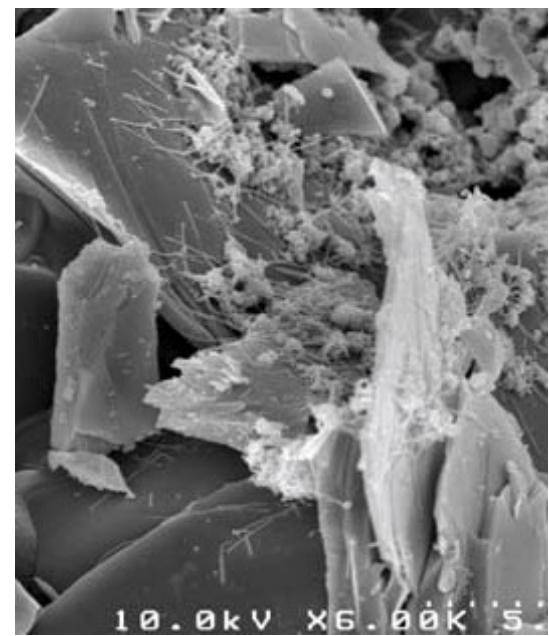
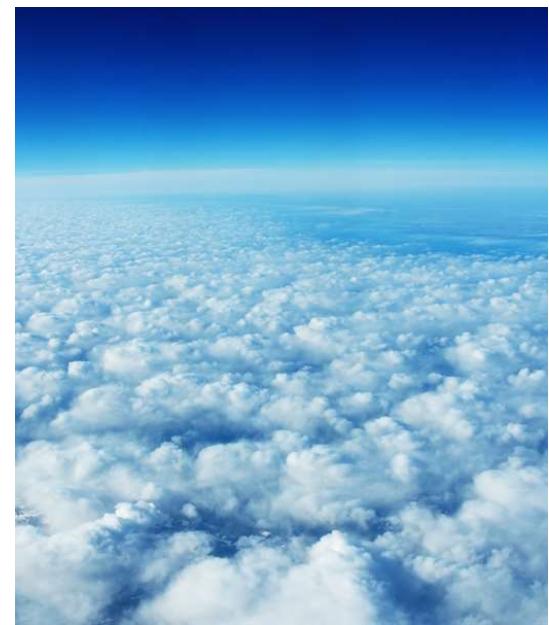
Phylogenetics for Outbreak Investigations

Midwest AR Lab Network Regional Meeting
Dr. Kelly F. Oakeson
July 25, 2019





We are living in a microbial world!



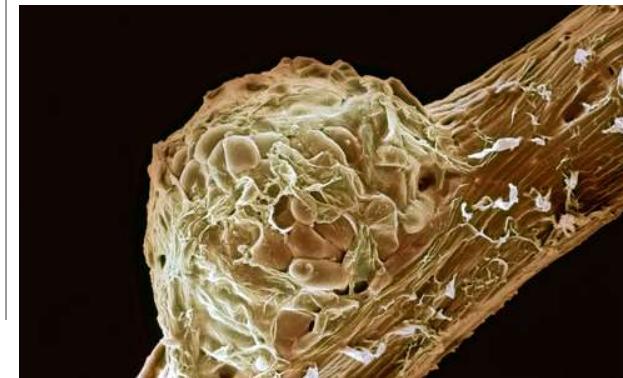
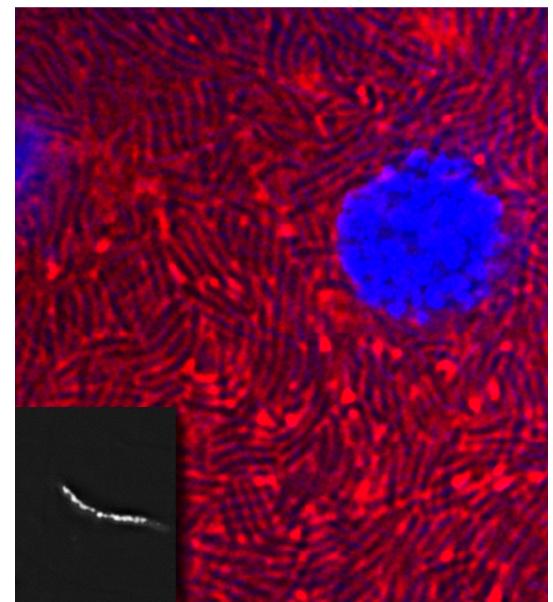
Microbes are everywhere



Microbes are everywhere

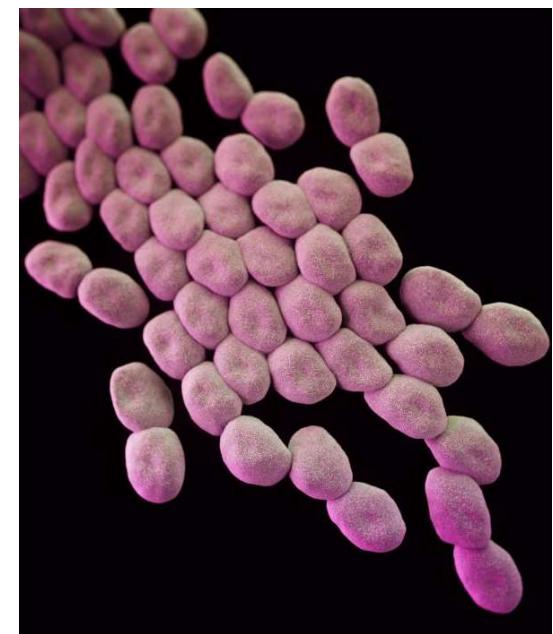
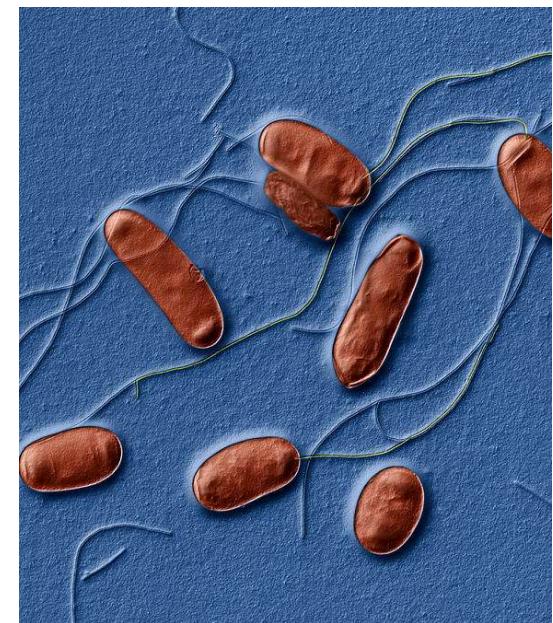


Beneficial microbes





Human Microbiome



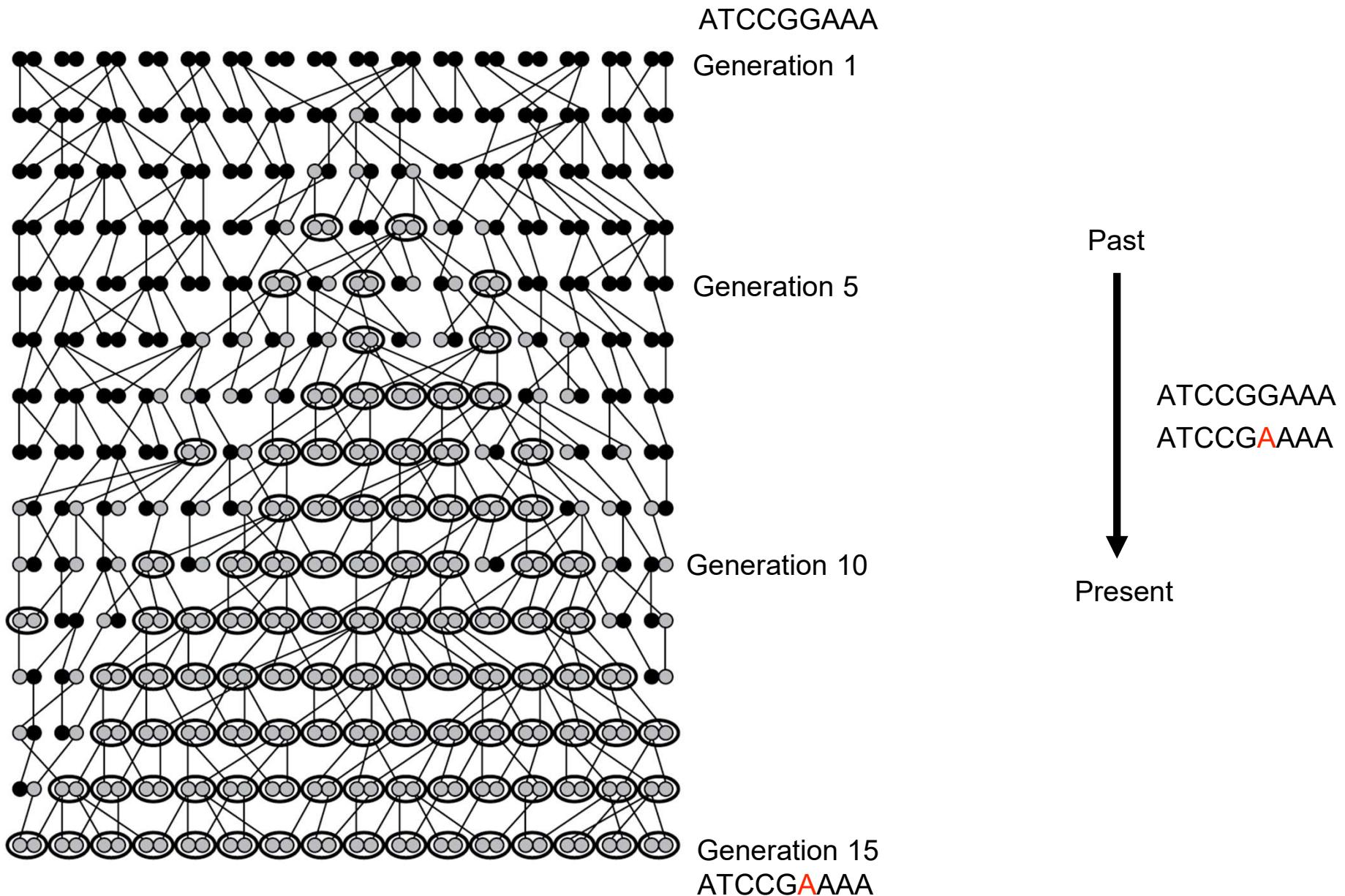
Pathogenic microbes

**“Nothing in Biology
Makes Sense Except
in the Light of
Evolution”**

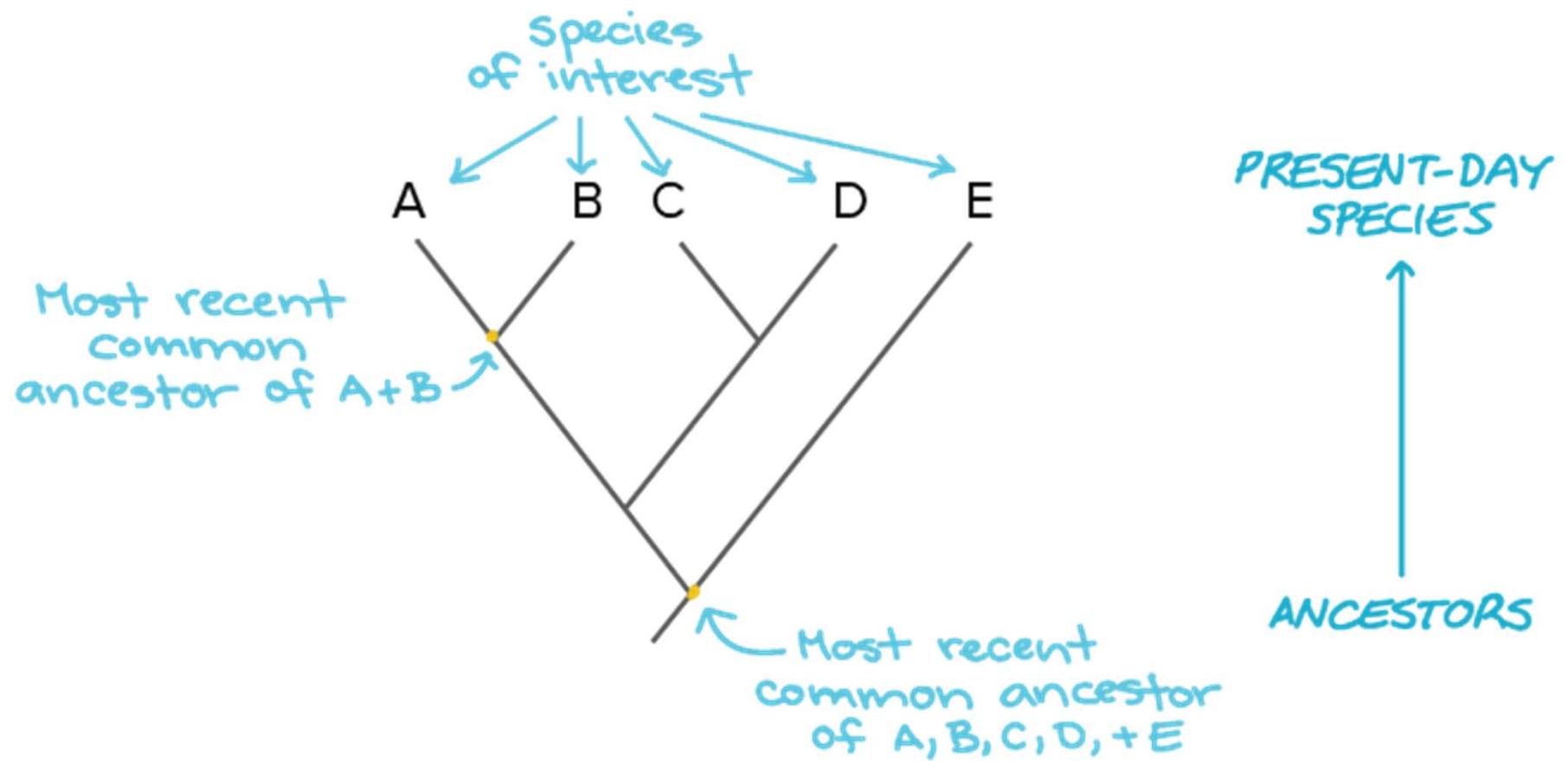
Theodosius Dobzhansky



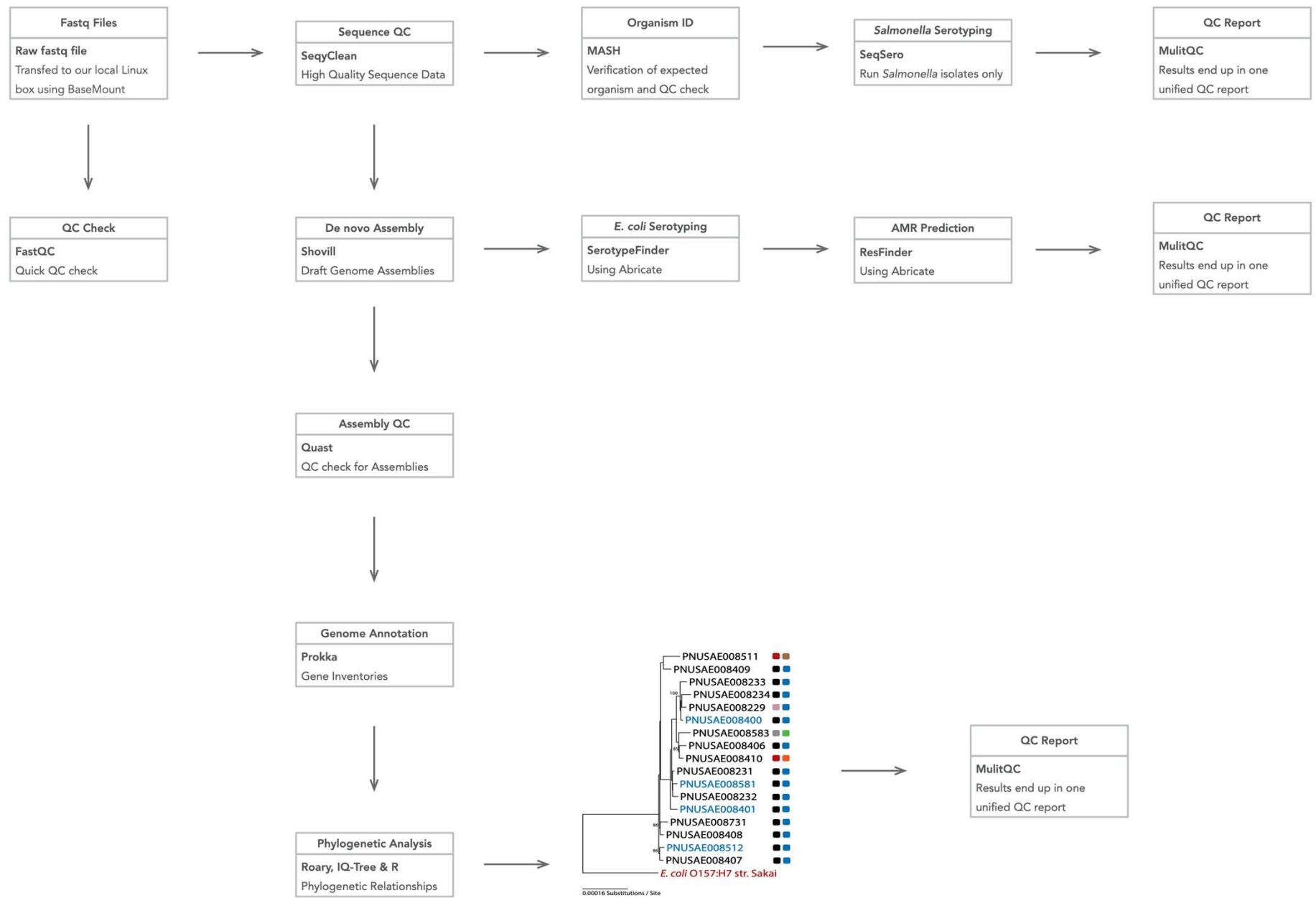
Descent with Modification



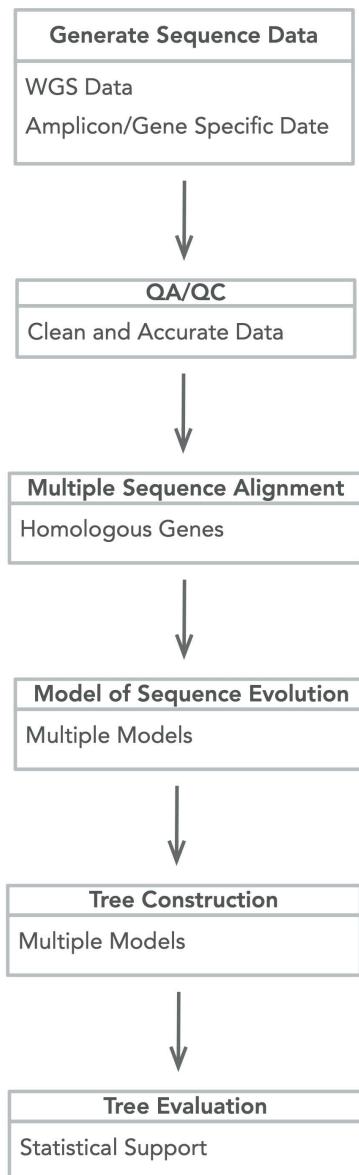
Phylogenetics



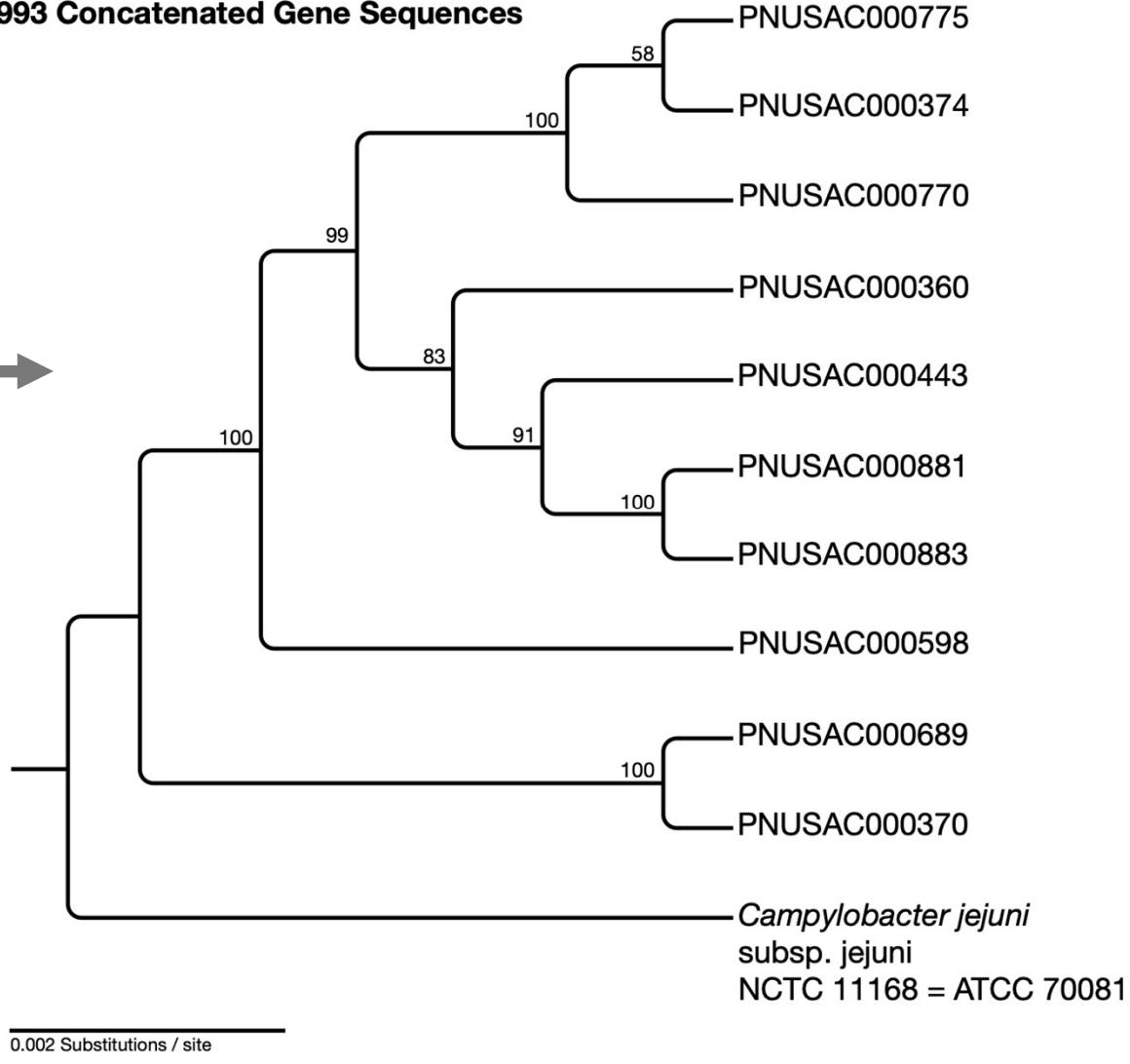
Reference Free WGS Analysis (URF)



Reference Free WGS Analysis (URF)



Maximum Likelihood Tree of 993 Concatenated Gene Sequences



Reference Free WGS Analysis (URF)



BACTERIOLOGY



Whole-Genome Sequencing and Bioinformatic Analysis of Isolates from Foodborne Illness Outbreaks of *Campylobacter jejuni* and *Salmonella enterica*

Kelly F. Oakeson,^a Jennifer Marie Wagner,^a Andreas Rohrwasser,^a Robyn Atkinson-Dunn^a

^aUtah Department of Health, Utah Public Health Laboratory, Salt Lake City, Utah, USA

Bioinformatic Analyses of Whole-Genome Sequence Data in a Public Health Laboratory

Kelly F. Oakeson, Jennifer Marie Wagner, Michelle Mendenhall, Andreas Rohrwasser, Robyn Atkinson-Dunn

Morbidity and Mortality Weekly Report

Outbreak of *E. coli* O157:H7 Infections Associated with Exposure to Animal Manure in a Rural Community — Arizona and Utah, June–July 2017

Sarah Luna, PhD¹; Vikram Krishnasamy, MD¹; Louise Saw, MPH^{2,4}; Lori Smith³; Jennifer Wagner, MS³; Jenna Weigand, MPH⁴; Mackenzie Tewell, MA⁵; Marilee Kellis⁵; Roumen Penev, PhD⁵; Laine McCullough, MPH²; Jeffrey Eason, MPH²; Keegan McCaffrey; Cindy Burnett, MPH²; Kelly Oakeson, PhD³; Melissa Dimond, MPH²; Allyn Nakashima, MD²; Deidre Barlow⁶; Anna Scherzer, MS⁶; Melanie Sarino, MPH⁷; Morgan Schroeder, MPH^{8,9}; Rashida Hassan; MSPH^{8,9}; Colin Basler, DVM⁹; Matthew Wise, PhD⁹; Laura Gieraltowski, PhD⁹

Morbidity and Mortality Weekly Report

Sepsis Attributed to Bacterial Contamination of Platelets Associated with a Potential Common Source — Multiple States, 2018

Sydney A. Jones, PhD^{1,2}; Jefferson M. Jones, MD³; Vivian Leung, MD²; Allyn K. Nakashima, MD⁴; Kelly F. Oakeson, PhD⁵; Amanda R. Smith, PhD⁴; Robert Hunter, MS⁶; Janice J. Kim, MD⁶; Melissa Cumming, MS⁷; Eileen McHale⁷; Pampee P. Young, MD, PhD⁸; Joy L. Friley, MD⁹; Walter E. Kelley, DO¹⁰; Susan L. Stramer, PhD¹¹; Stephen J. Wagner, PhD¹²; F. Bernadette West, MD¹³; Ross Herren, MD⁹; Edward Snyder, MD¹⁴; Jeanne E. Hendrickson, MD¹⁴; David R. Peaper, MD, PhD¹⁴; Adi V. Gundlapalli, MD, PhD^{15,16}; Charles Langelier, MD, PhD^{17,18}; Steve Miller, MD, PhD¹⁷; Ashok Nambiar, MD¹⁷; Morvarid Moayeri, MD, PhD¹⁷; Jack Kamm, PhD¹⁸; Heather Moulton-Meissner, PhD³; Pallavi Annambhotla, DrPH³; Paige Gable³; Gillian A. McAllister³; Erin Breaker, MS^{3,19}; Erisa Sula, MS^{3,19}; Alison Laufer Halpin, PhD³; Sridhar V. Basavaraju, MD³

Morbidity and Mortality Weekly Report

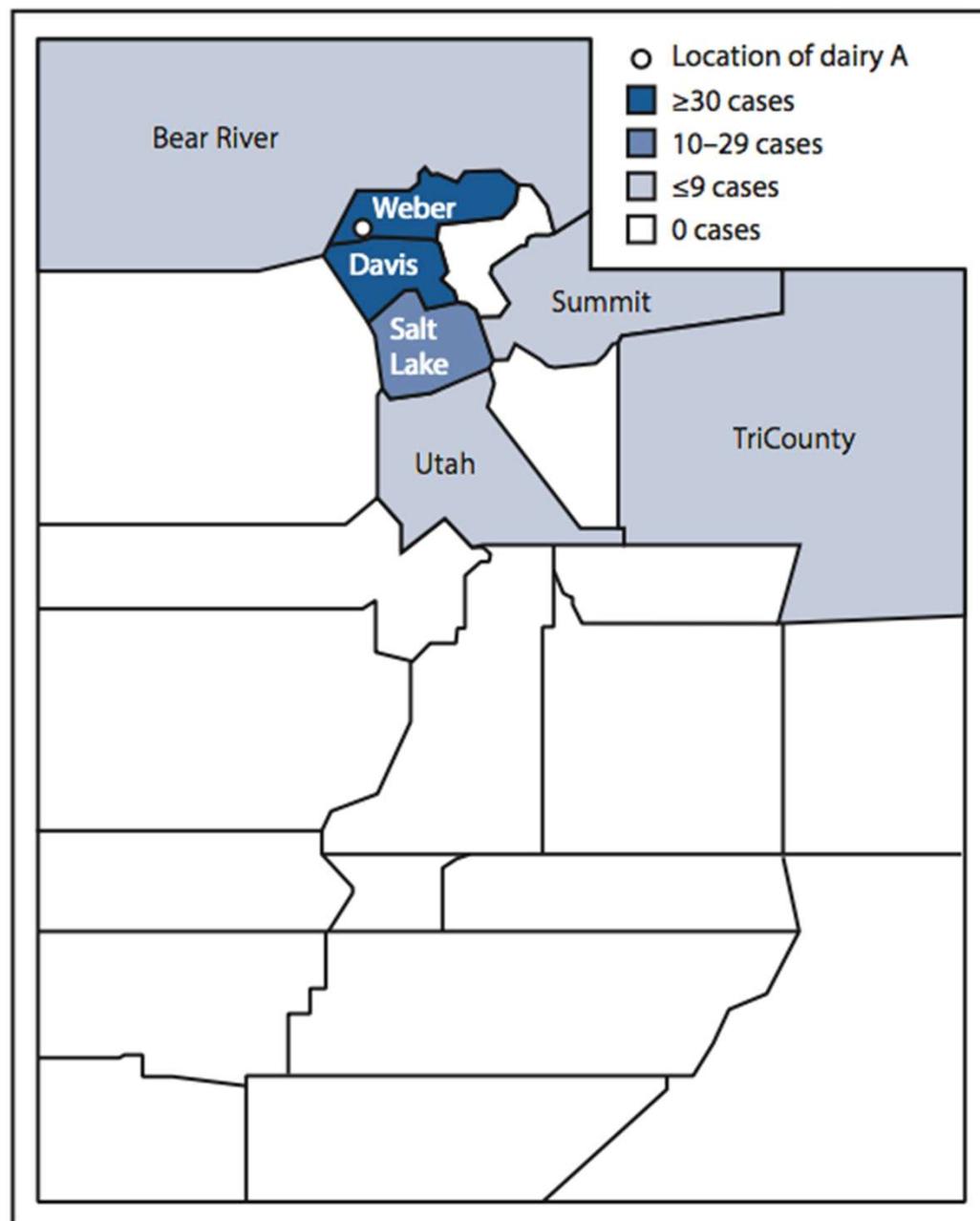
Fatal Sepsis Associated with Bacterial Contamination of Platelets — Utah and California, August 2017

Roberta Z. Horth, PhD^{1,2,3}; Jefferson M. Jones, MD⁴; Janice J. Kim, MD⁵; Bert K. Lopansri, MD⁶; Sarah J. Istrup, MD⁶; Joy Friley, MD⁷; Walter E. Kelley, DO⁸; Susan L. Stramer, PhD⁹; Ashok Nambiar, MD¹⁰; Lynn Ramirez-Avila, MD¹⁰; Amy Nichols, MBA¹⁰; Wendy Garcia¹¹; Kelly F. Oakeson, PhD¹²; Nicholas Vlachos, MS⁴; Gillian McAllister⁴; Robert Hunter, MS⁵; Allyn K. Nakashima, MD³; Sridhar V. Basavaraju, MD³

Campylobacter jejuni

- May 2014, three confirmed cases of *C. jejuni* infections
- Identical PFGE patterns
- All patients reported raw milk consumption from dairy “A”
- Additional cases identified during May and June
- Outbreak investigation initiated June 10, 2014
- Total of 99 cases

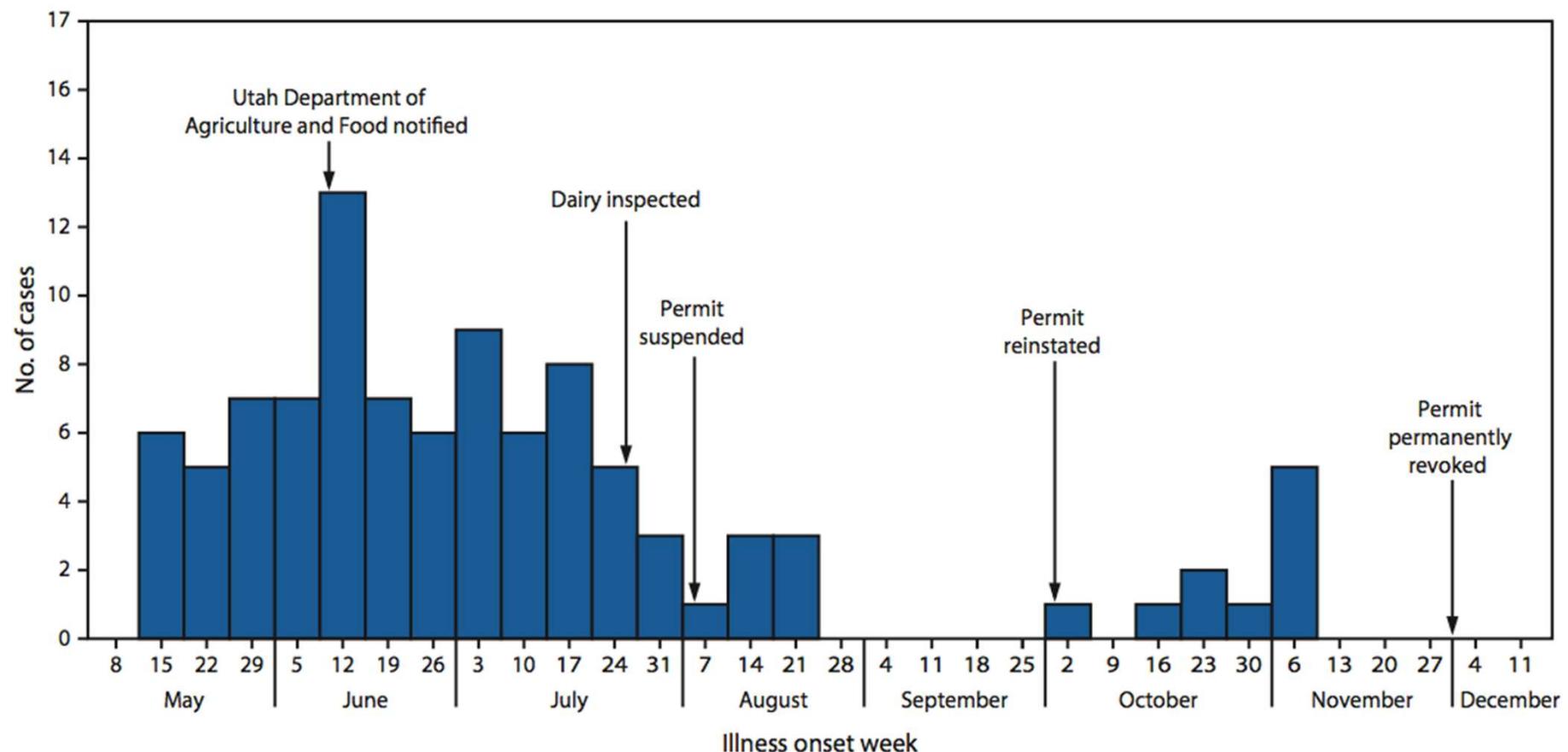
FIGURE 1. Location of dairy A and distribution of *Campylobacter jejuni* cases, by local health department district — Utah, May–November 2014



Davis KR, Dunn AC, Burnett C, McCullough L, Dimond M, Wagner J, et al. *Campylobacter jejuni* Infections Associated with Raw Milk Consumption—Utah, 2014. MMWR Morb Mortal Wkly Rep. 2016 Apr 1;65(12):301–5.

Campylobacter jejuni

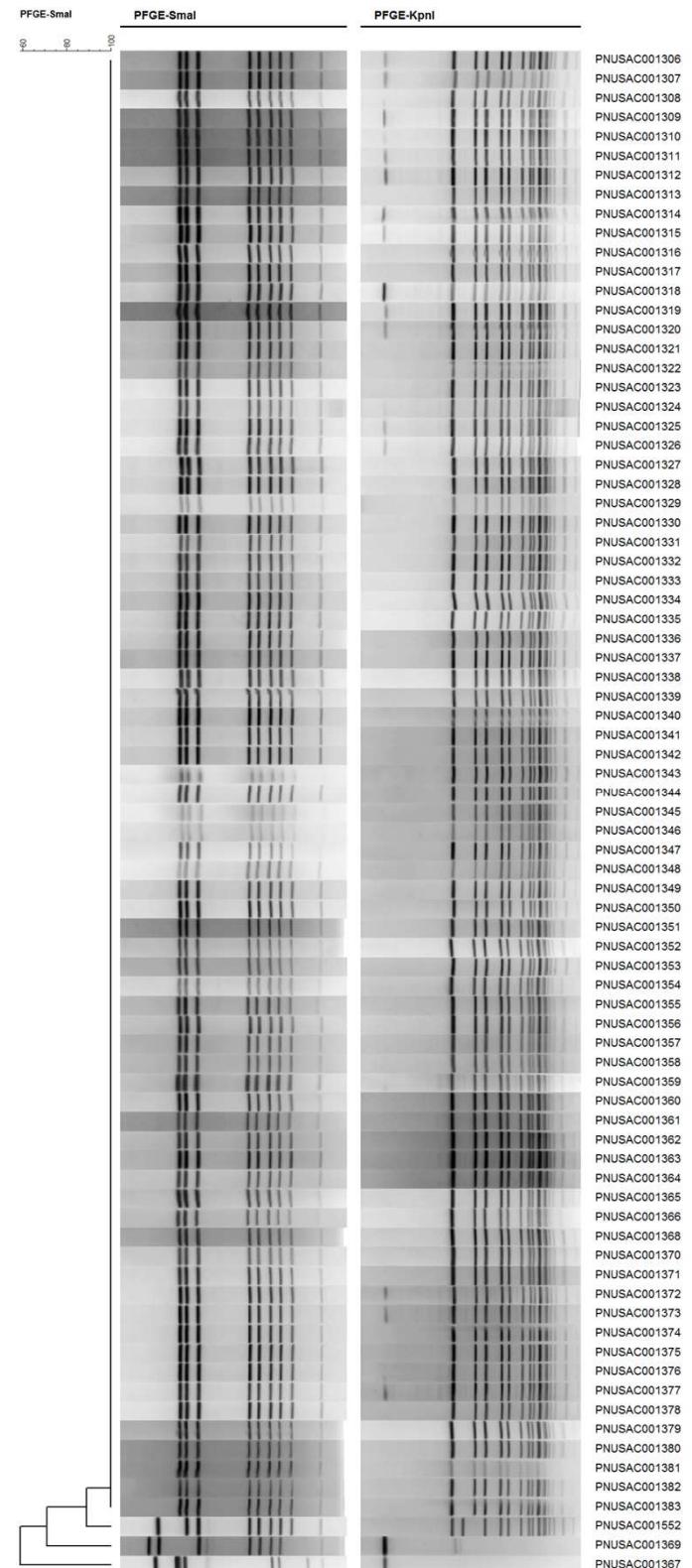
FIGURE 2. Week of illness onset among patients (N=99) with probable and confirmed *Campylobacter jejuni* infection associated with consumption of raw milk from a dairy — Utah, May–November 2014



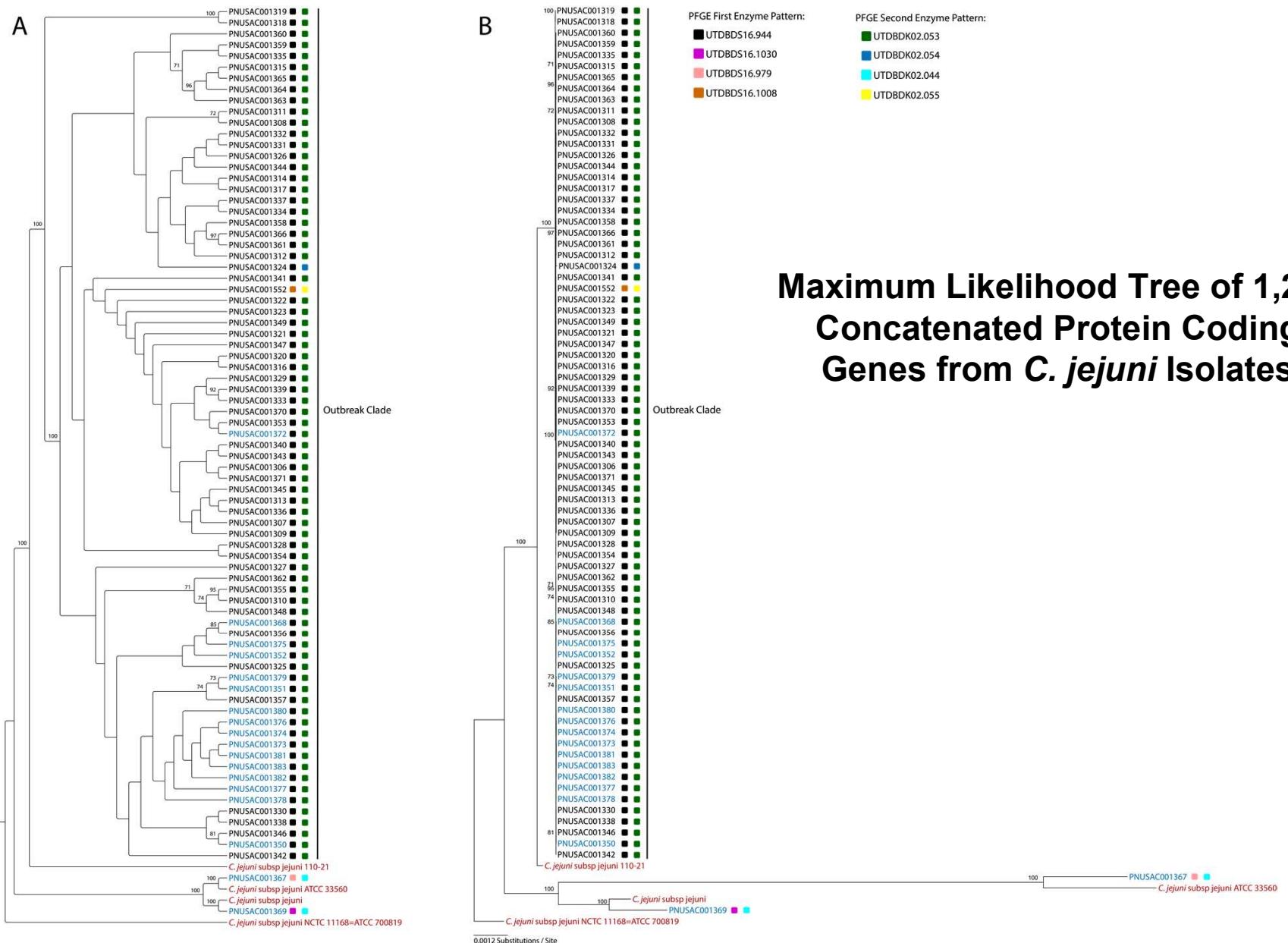
Davis KR, Dunn AC, Burnett C, McCullough L, Dimond M, Wagner J, et al. *Campylobacter jejuni* Infections Associated with Raw Milk Consumption—Utah, 2014. MMWR Morb Mortal Wkly Rep. 2016 Apr 1;65(12):301–5.

Campylobacter jejuni PFGE

- PFGE performed on 79 isolates
- 61 patient derived isolates
- 18 isolates derived from bulk milk storage tanks
- 76 of 79 isolates have indistinguishable Smal PFGE patterns



Reference Free WGS Analysis (URF)

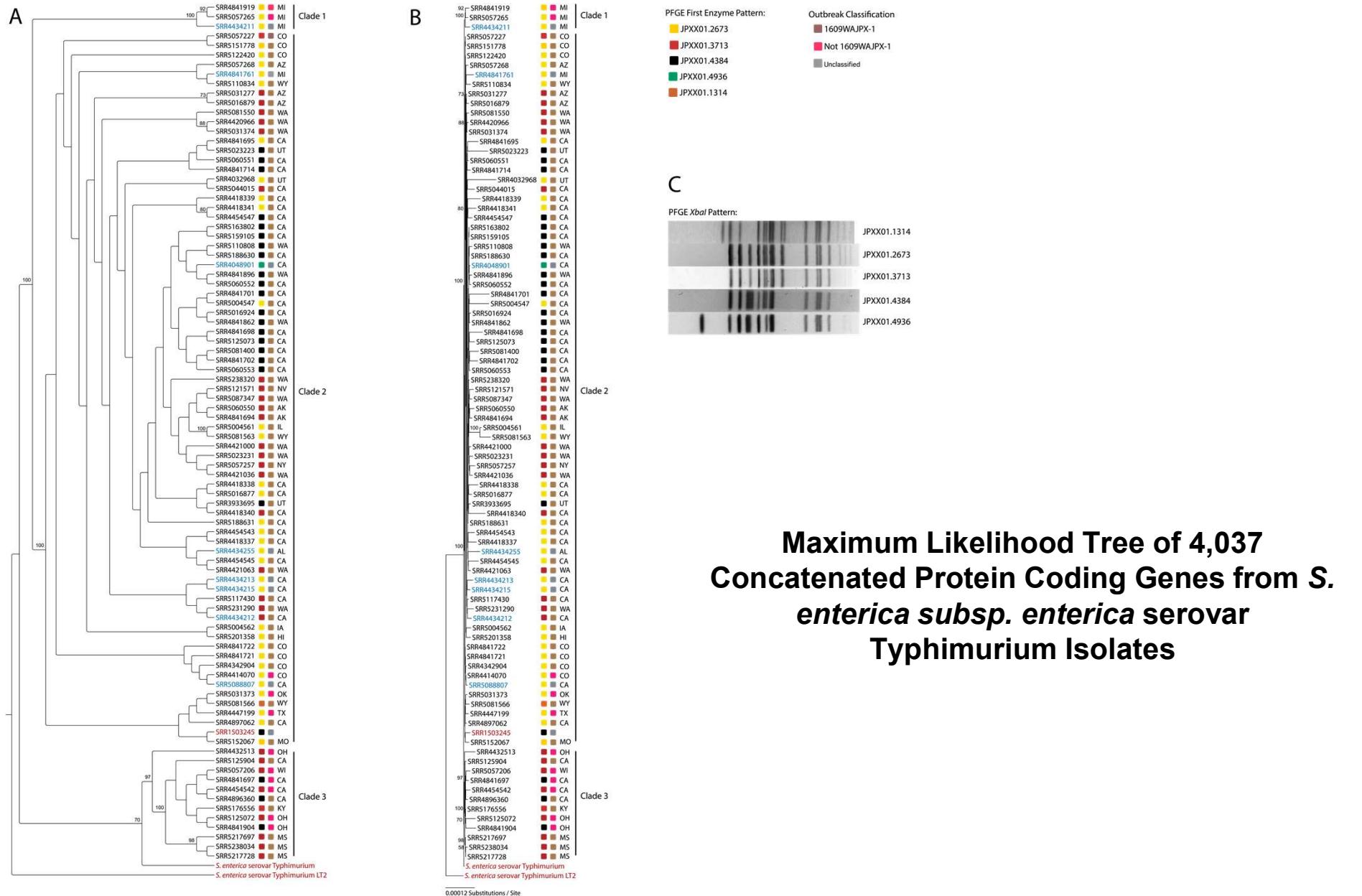


Salmonella enterica

- Complex Multi-state Outbreak
- Associated with Rotisserie Chicken
- Five Distinct PFGE Patterns
- 88 Isolates in Total
- 80 Patient Derived Isolates
- 8 Environmental Isolates
- Sequence Data Obtained From SRA



Reference Free WGS Analysis (URF)





Escherichia coli O157:H7

Hilldale, Utah 2017

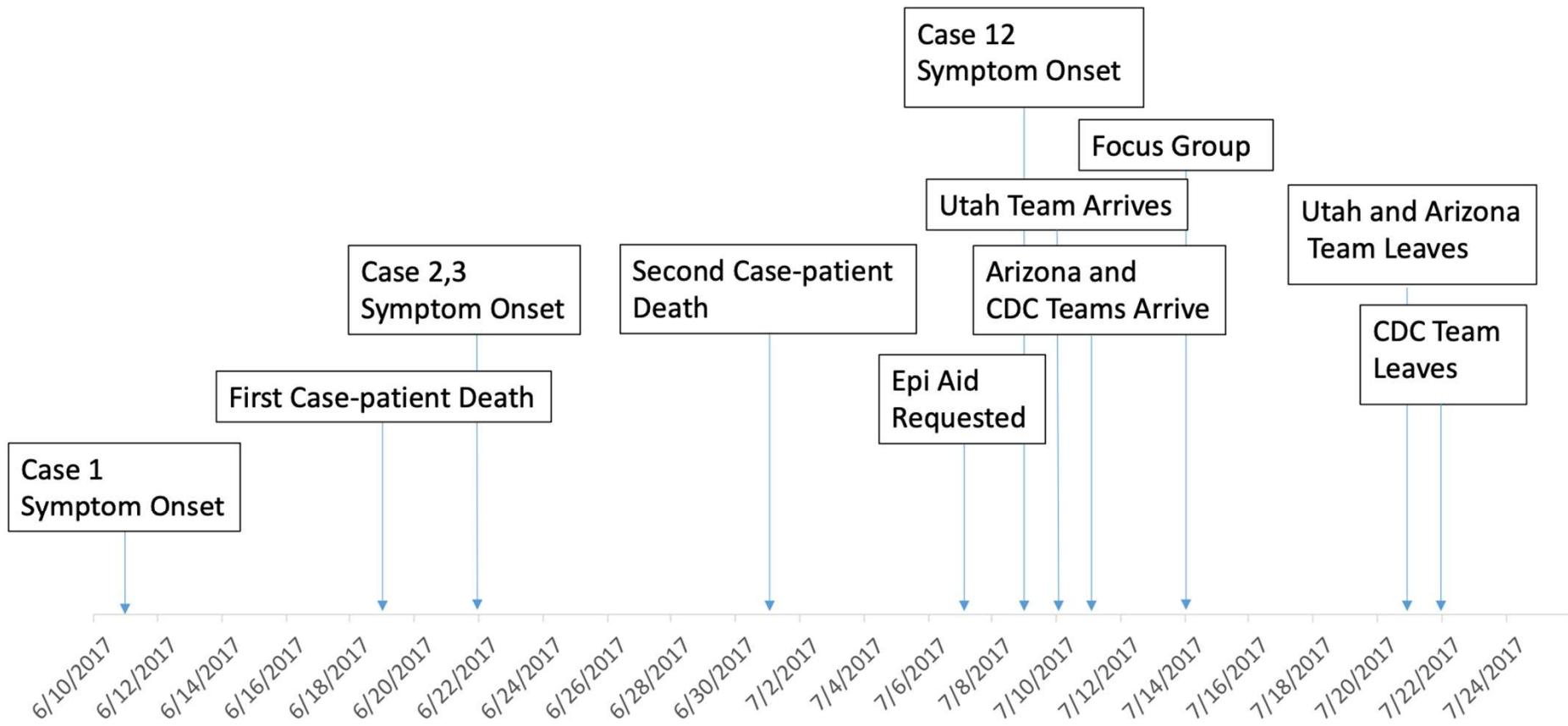
Escherichia coli O157:H7

- Twin cities splitting the Utah and Arizona boarder
- Population of 7,700
- Diverse religious affiliations
- 12 cases total
- Age range from 1-28
- Median age of 3

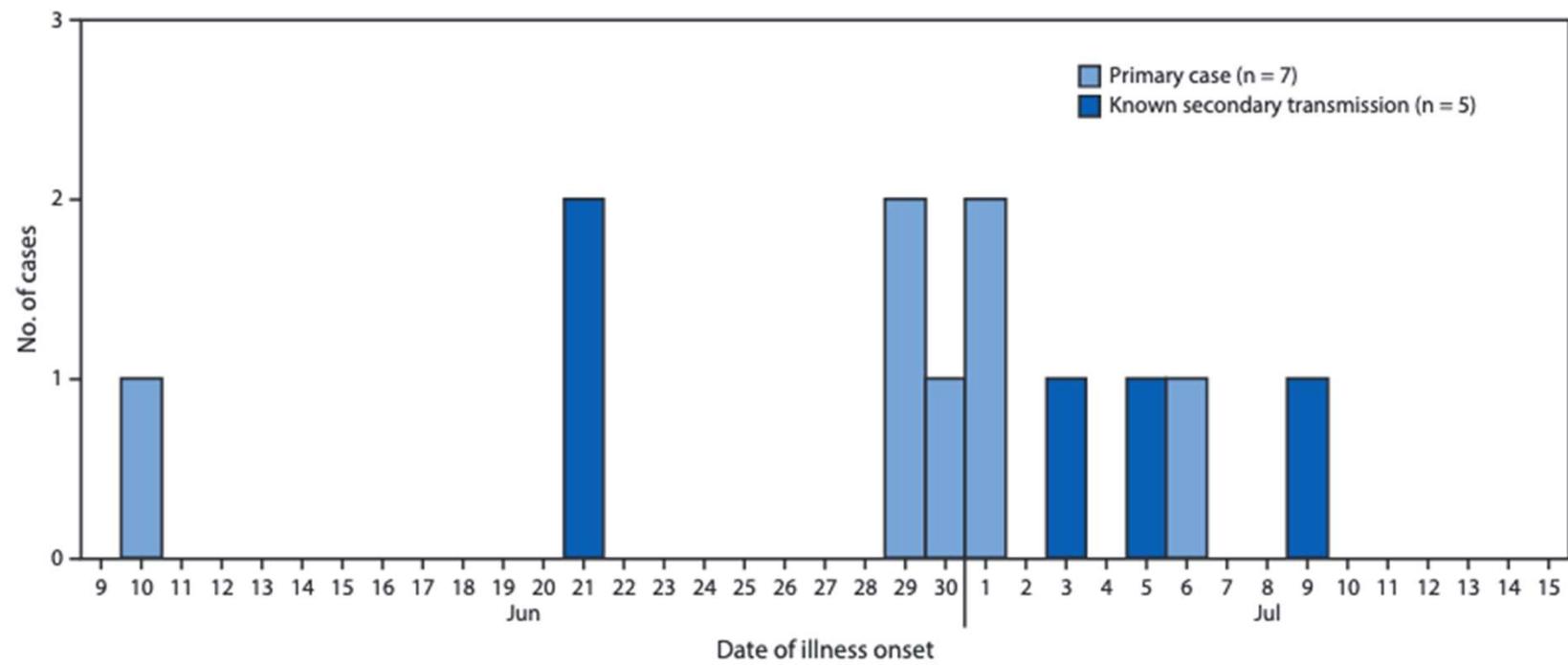


Escherichia coli O157:H7

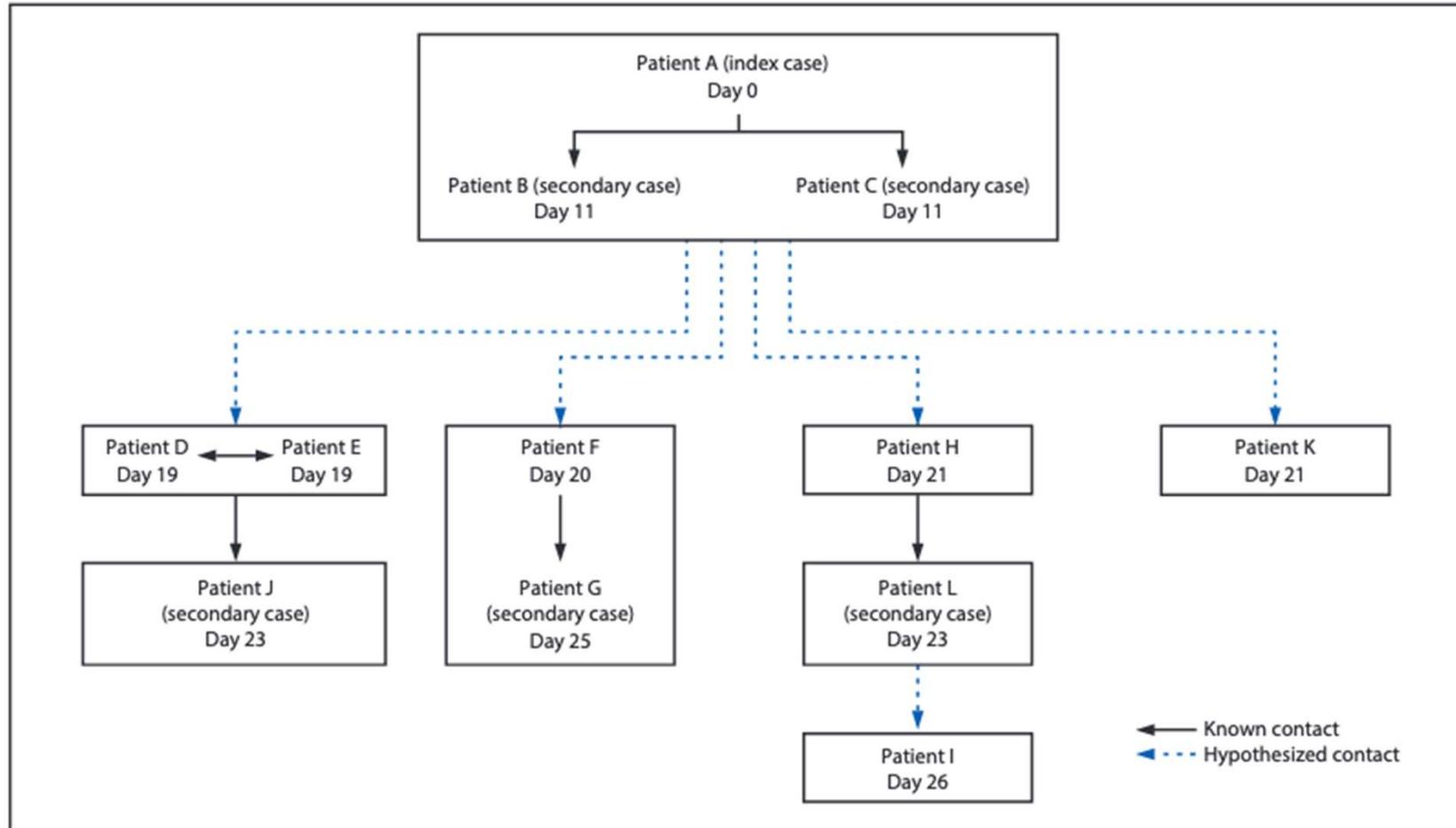
Timeline



Escherichia coli O157:H7

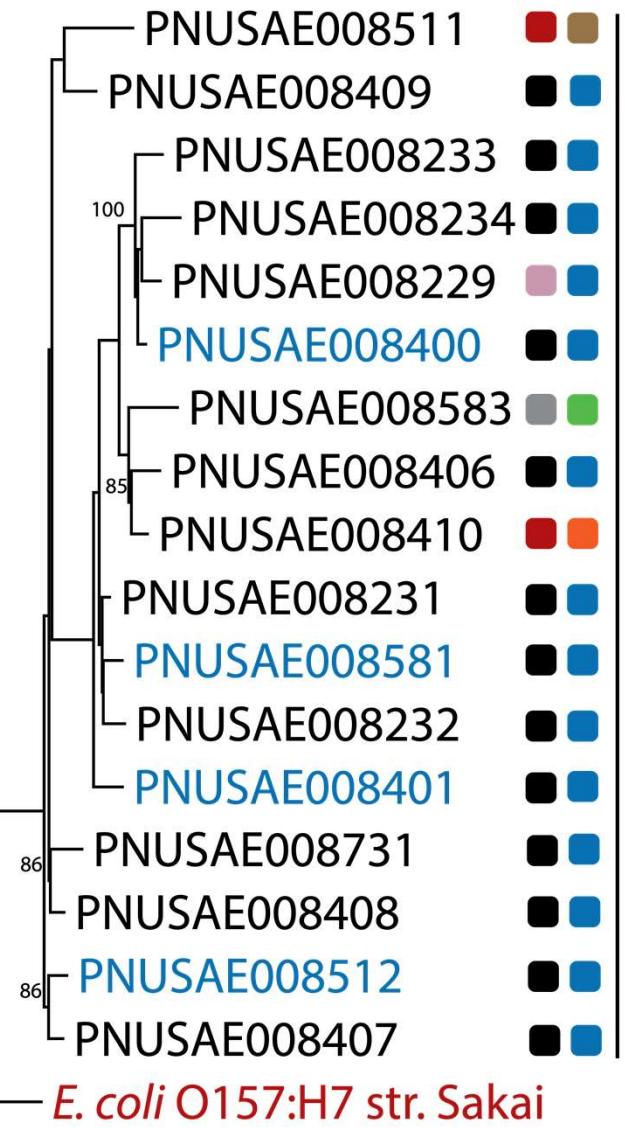


Escherichia coli O157:H7

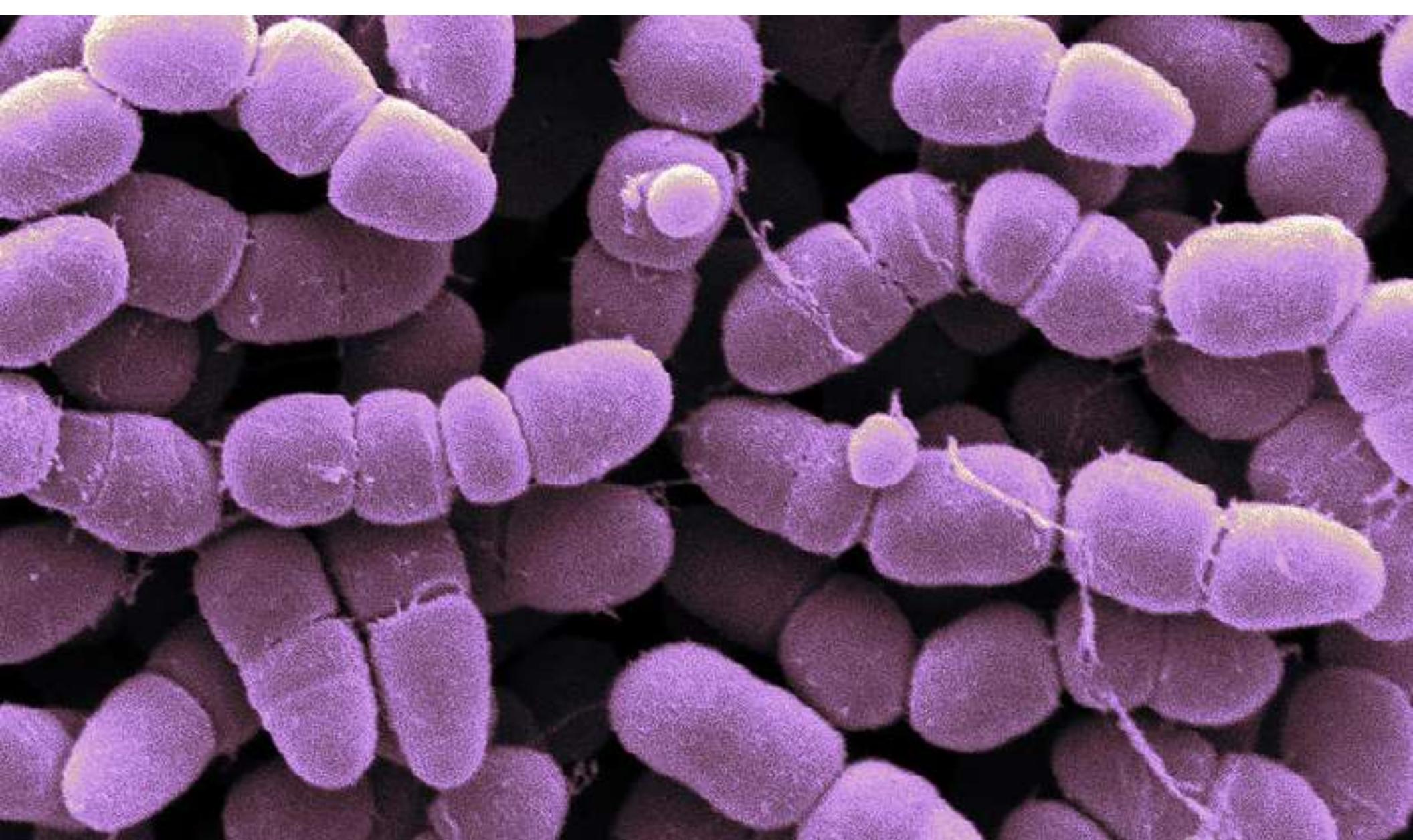


* Boxes represent households.

Escherichia coli O157:H7 URF Result



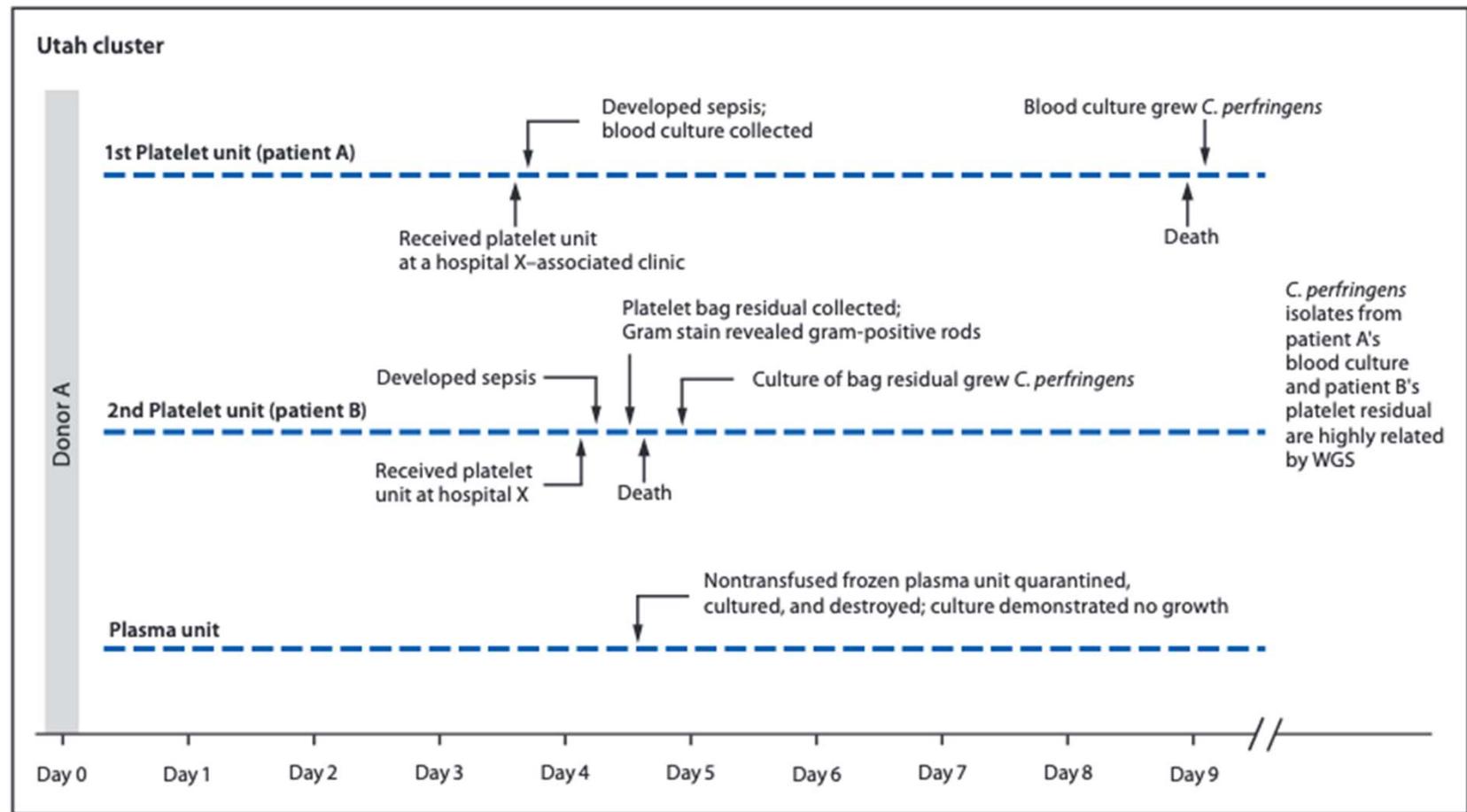
Maximum Likelihood Tree of 4,467 Concatenated Protein Coding Genes



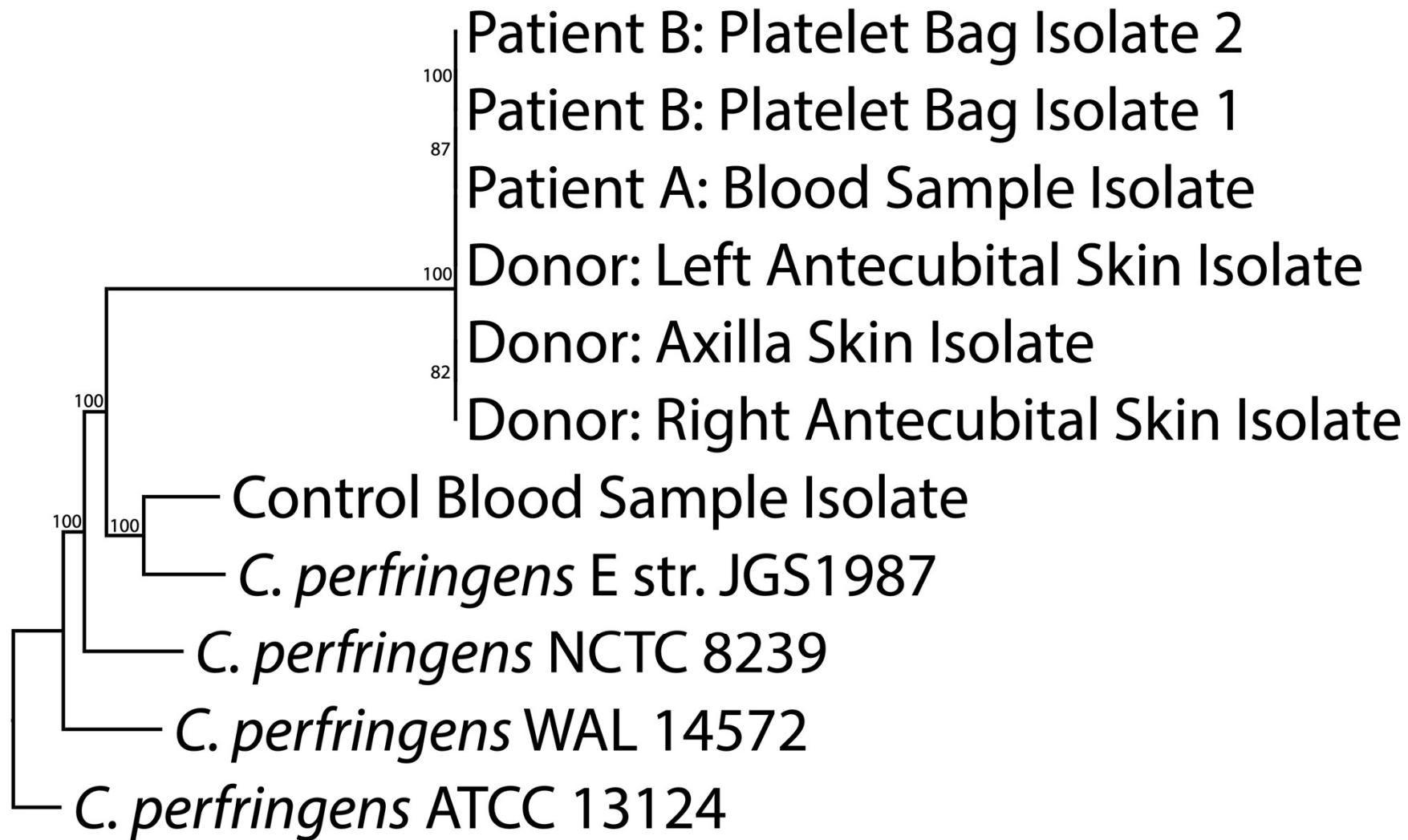
*Clostridium
perfringens*

2017

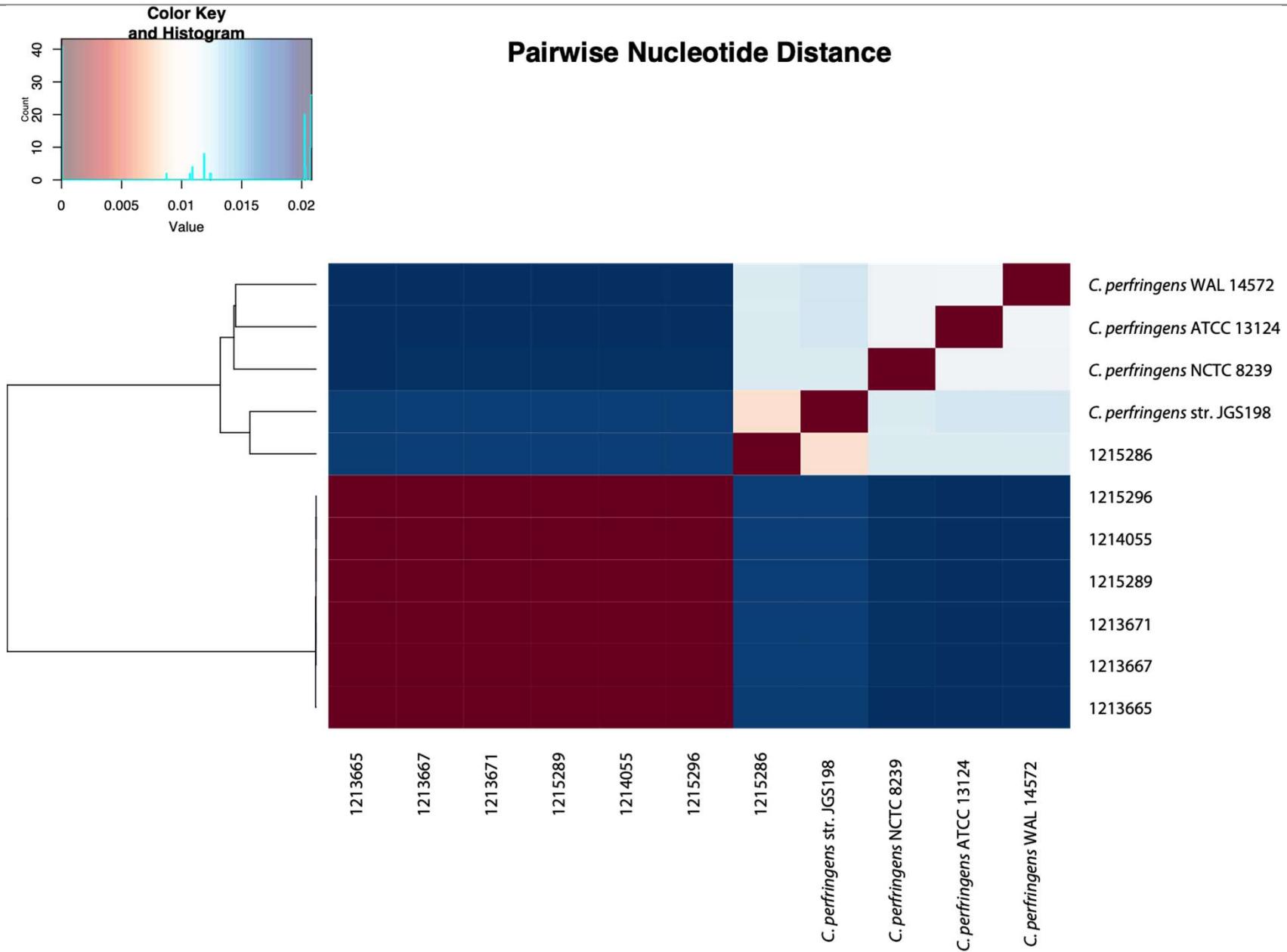
Clostridium perfringens

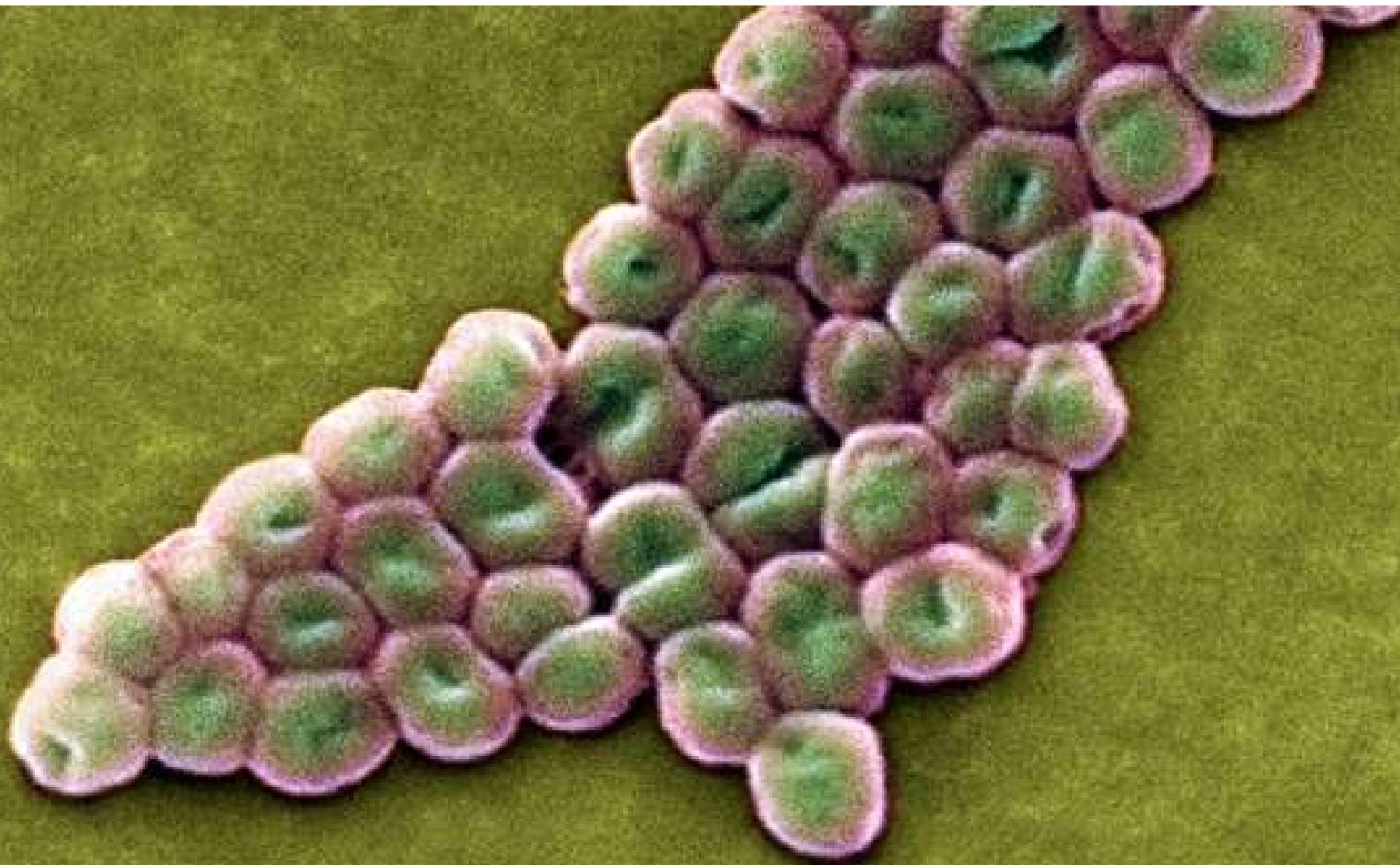


Clostridium perfringens URF Result



Clostridium perfringens URF Result

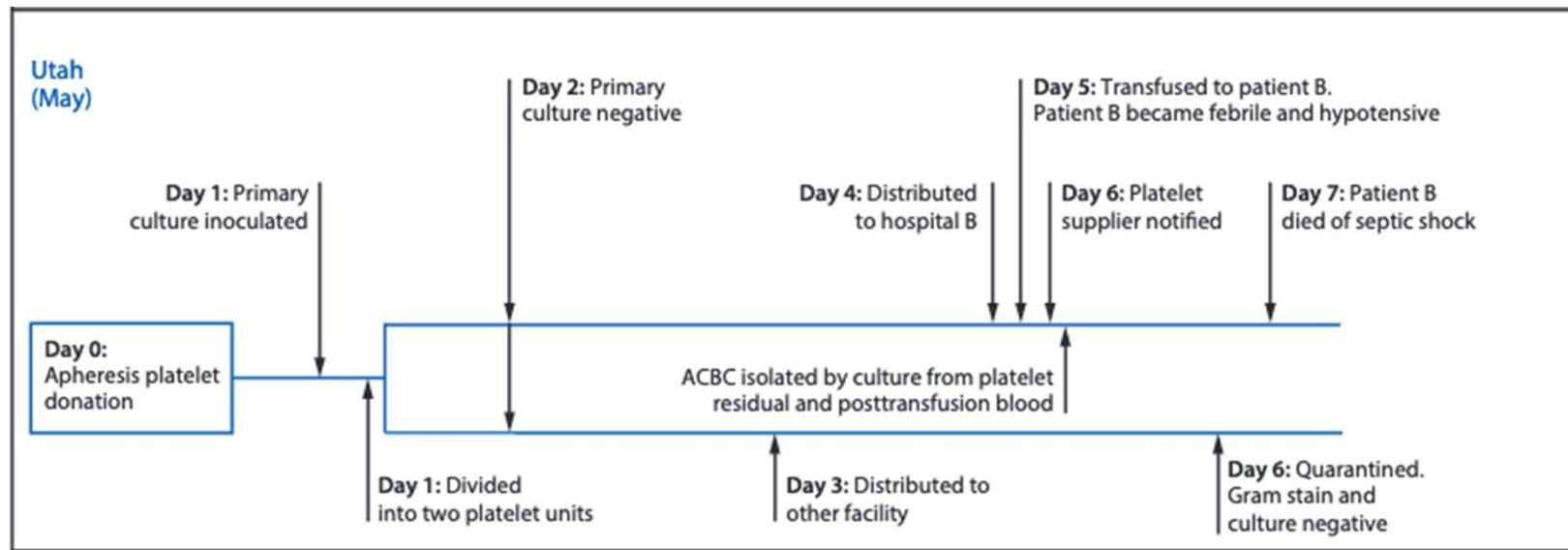




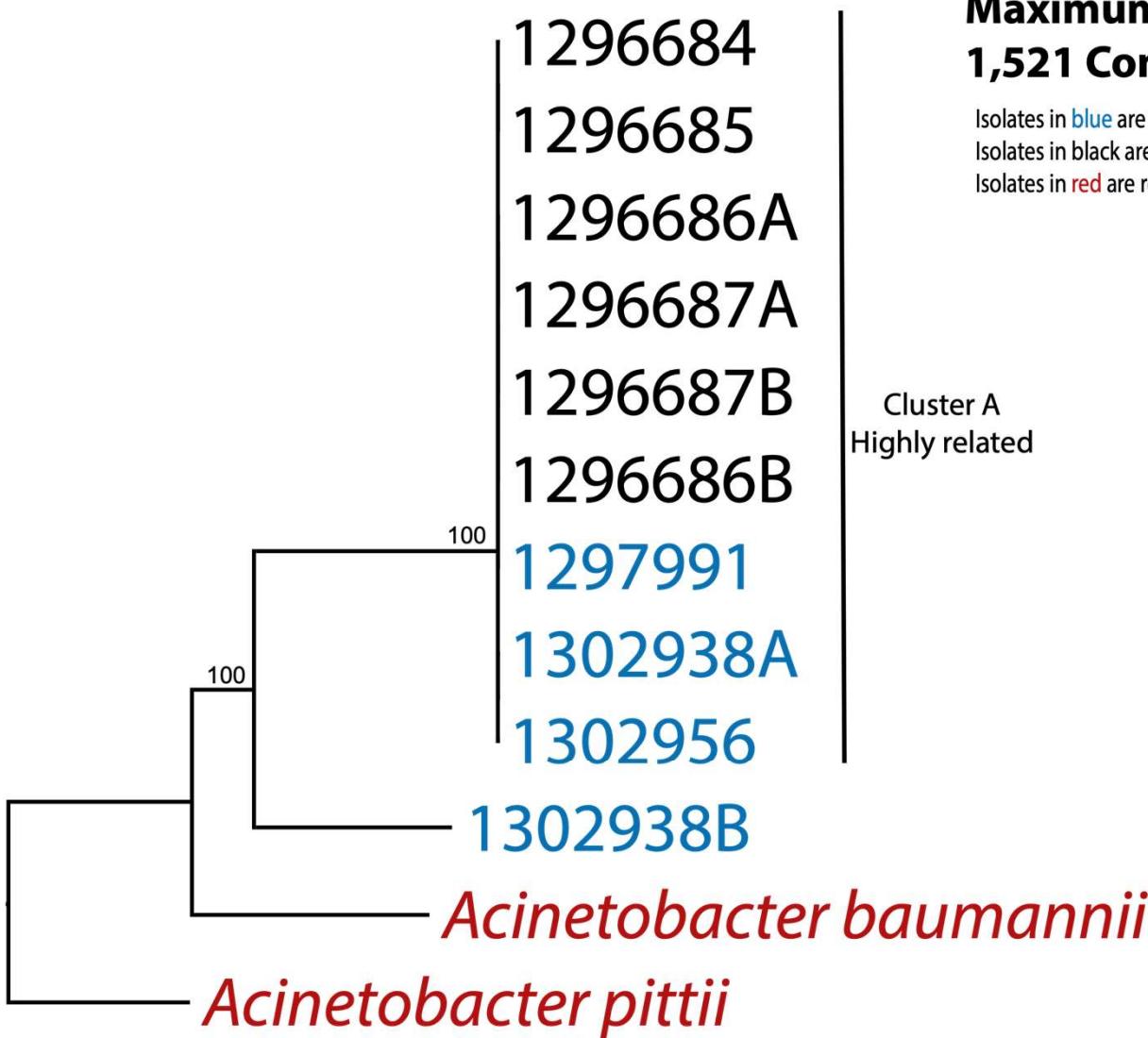
*Acinetobacter
baumannii*

2018

Acinetobacter baumannii



Acinetobacter baumannii



Maximum Likelihood Phylogenetic Tree of 1,521 Concatinated Protein Coding Genes

Isolates in **blue** are from environmental sources

Isolates in **black** are from clinical sources

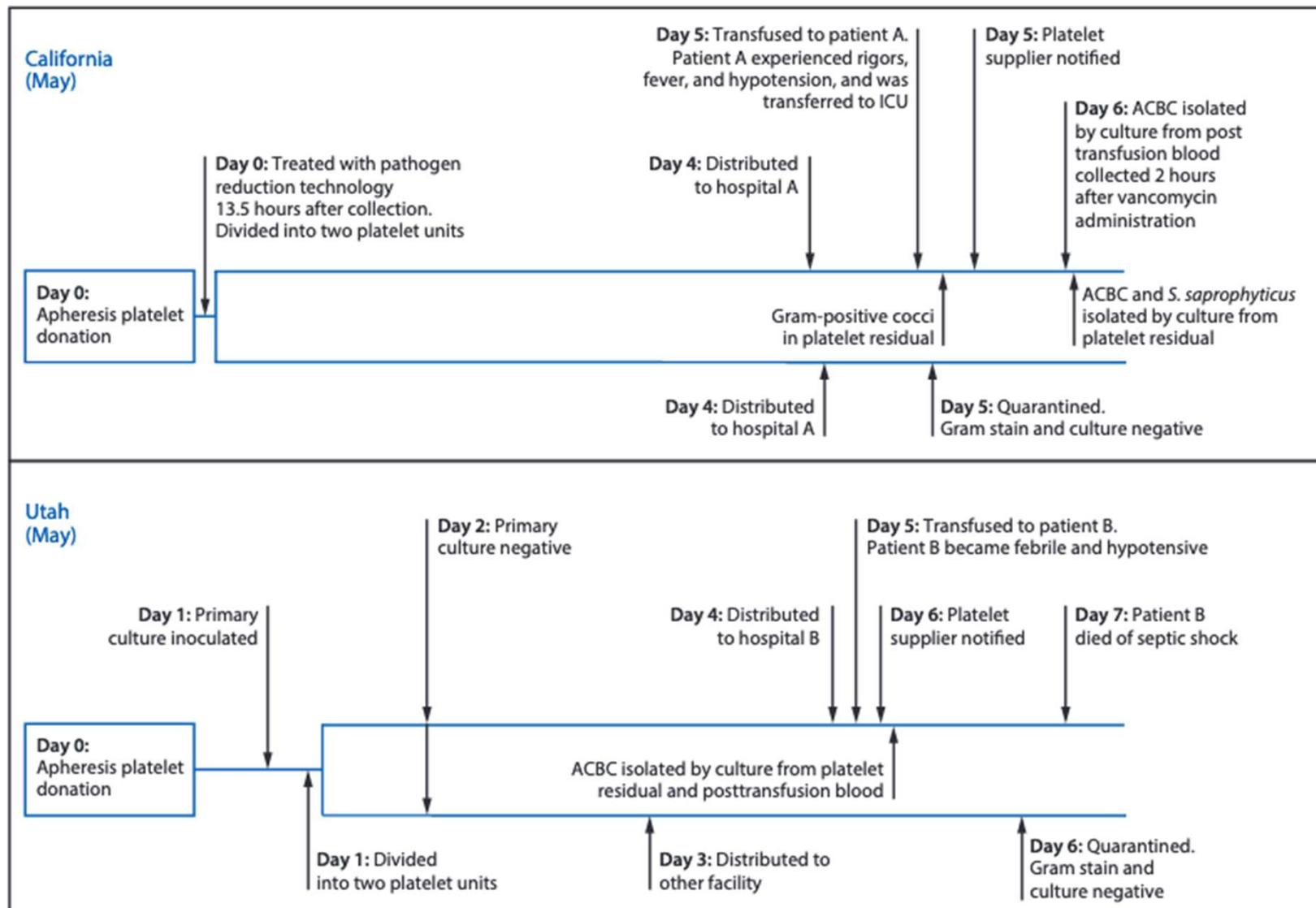
Isolates in **red** are reference sequences

Cluster A
Highly related

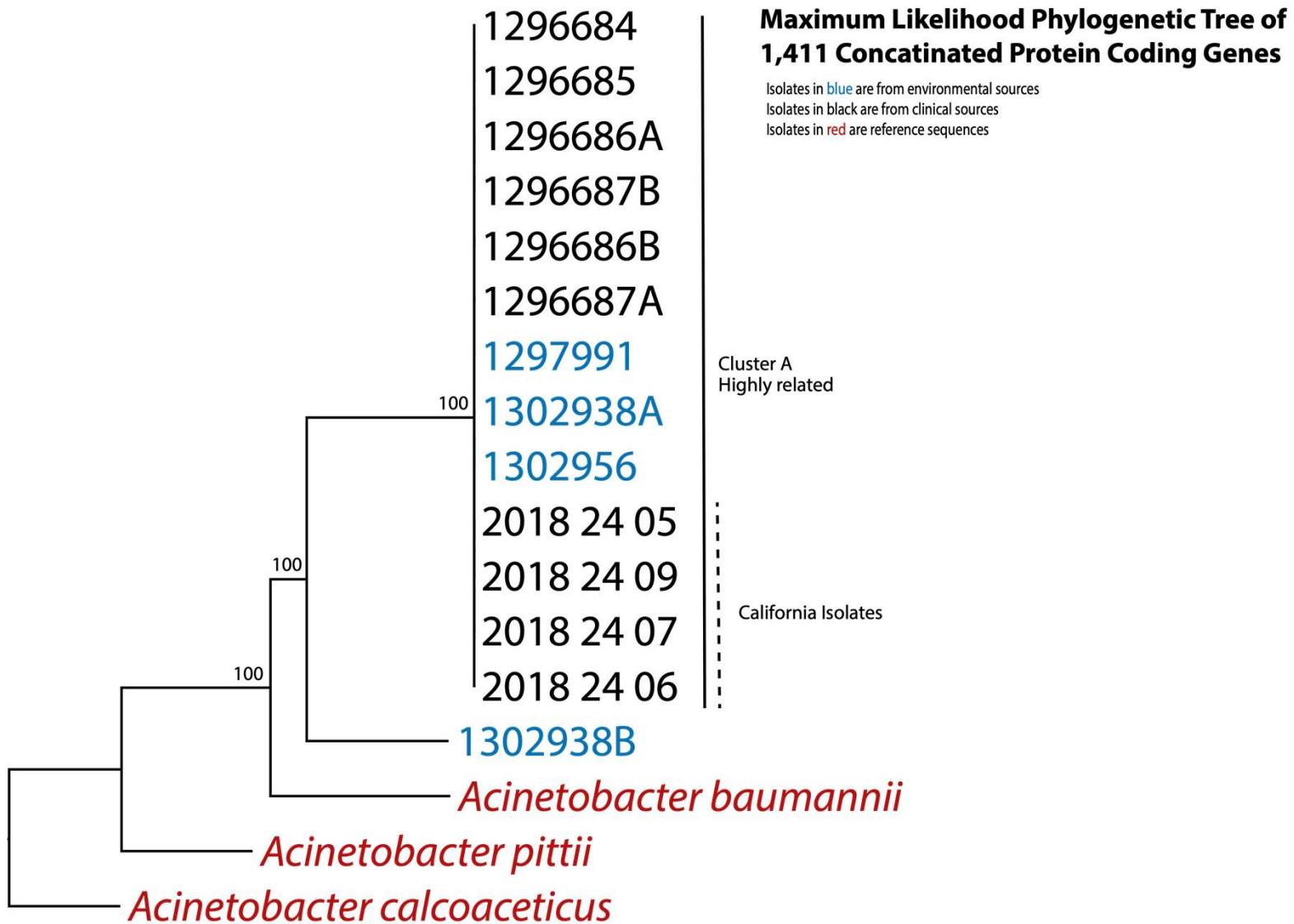


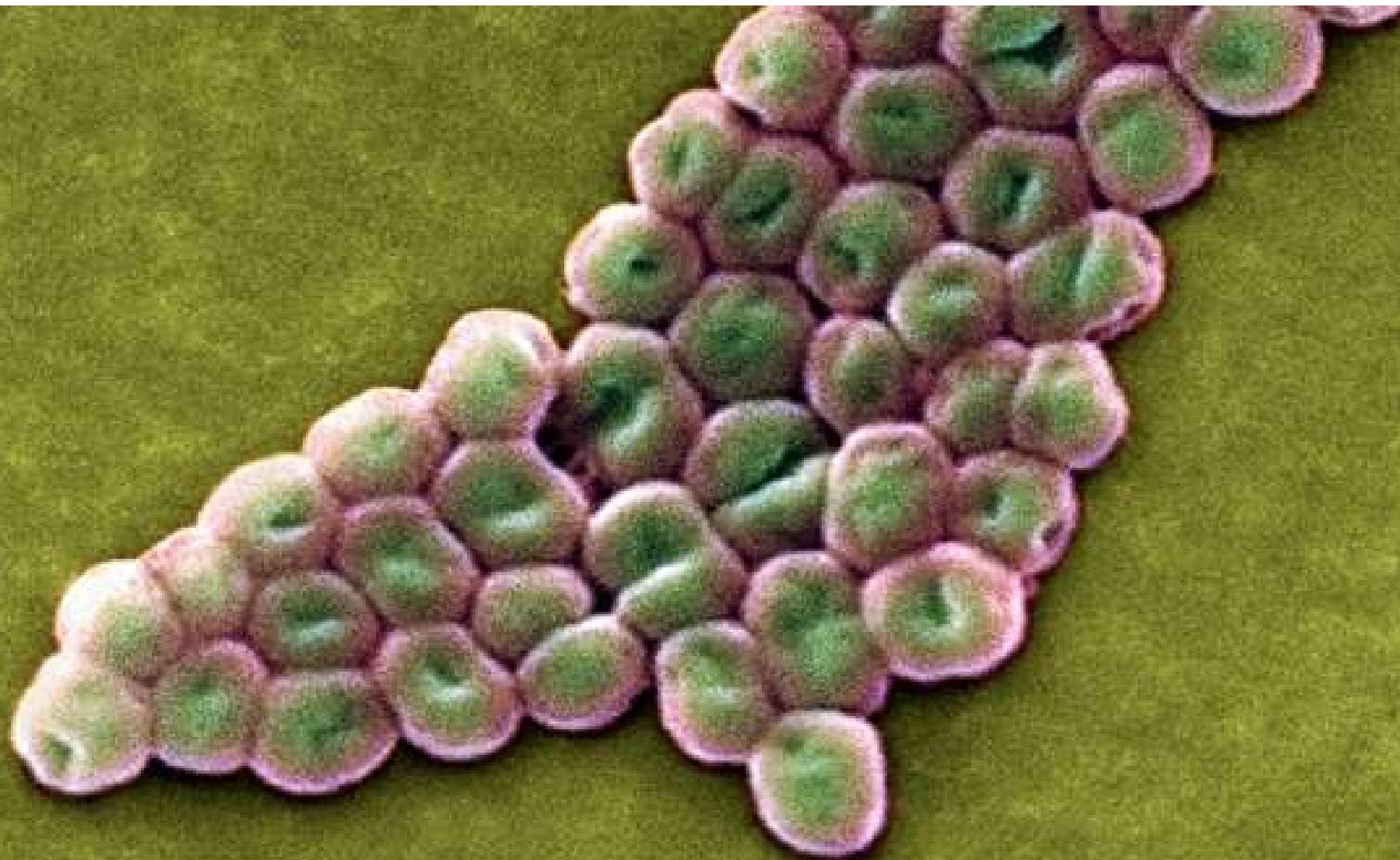
Microbes are everywhere

Acinetobacter baumannii



Acinetobacter baumannii



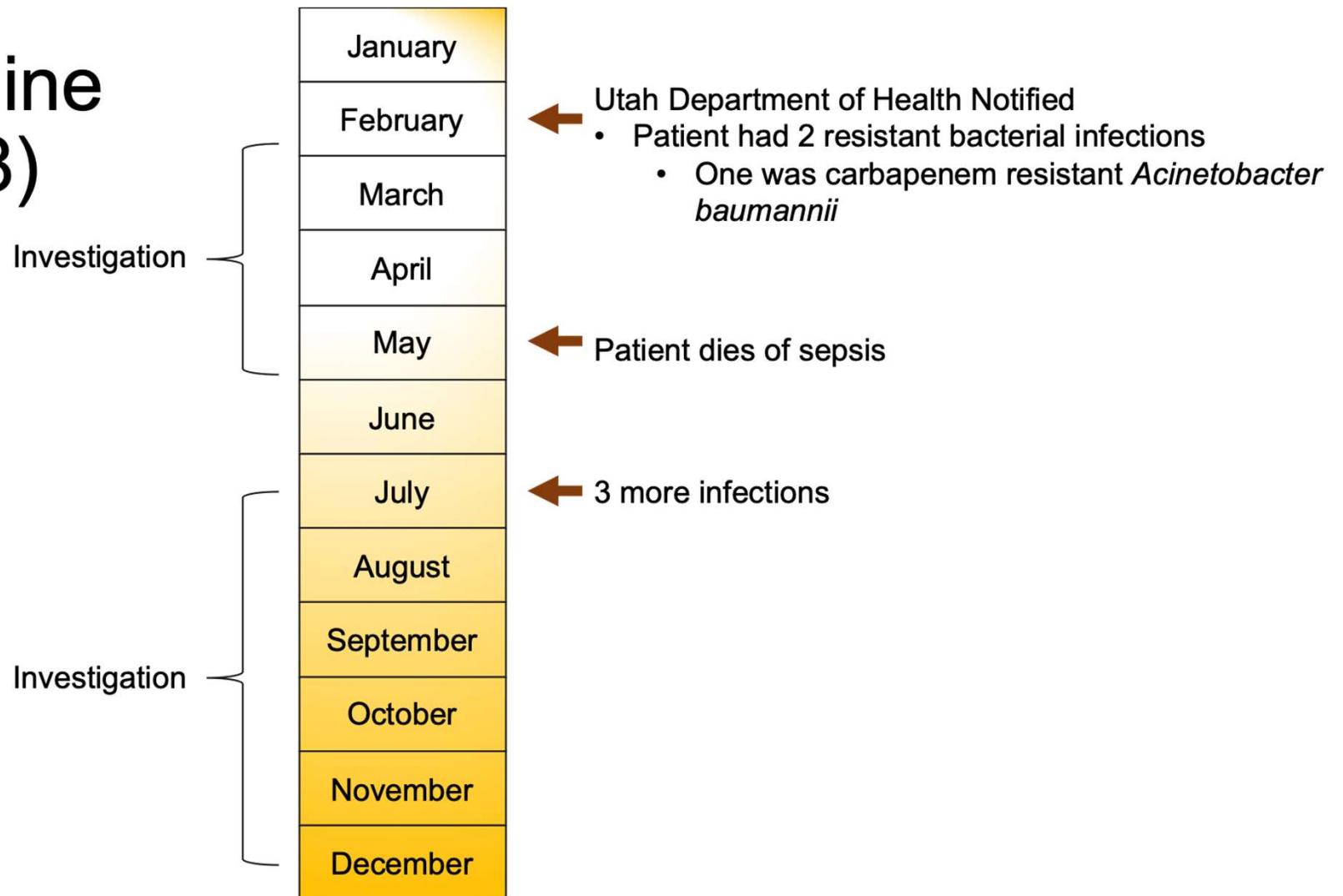


*Acinetobacter
baumannii*

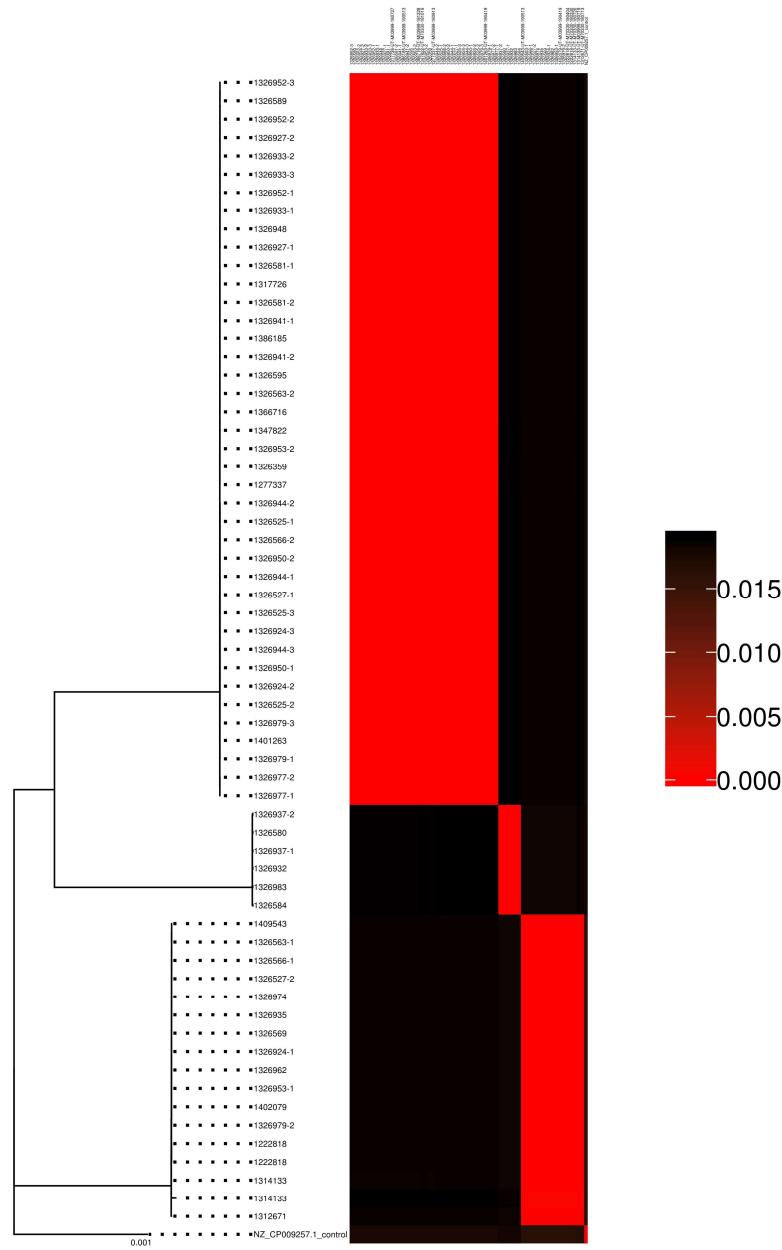
OXA-23

Acinetobacter baumannii OXA-23

Timeline (2018)



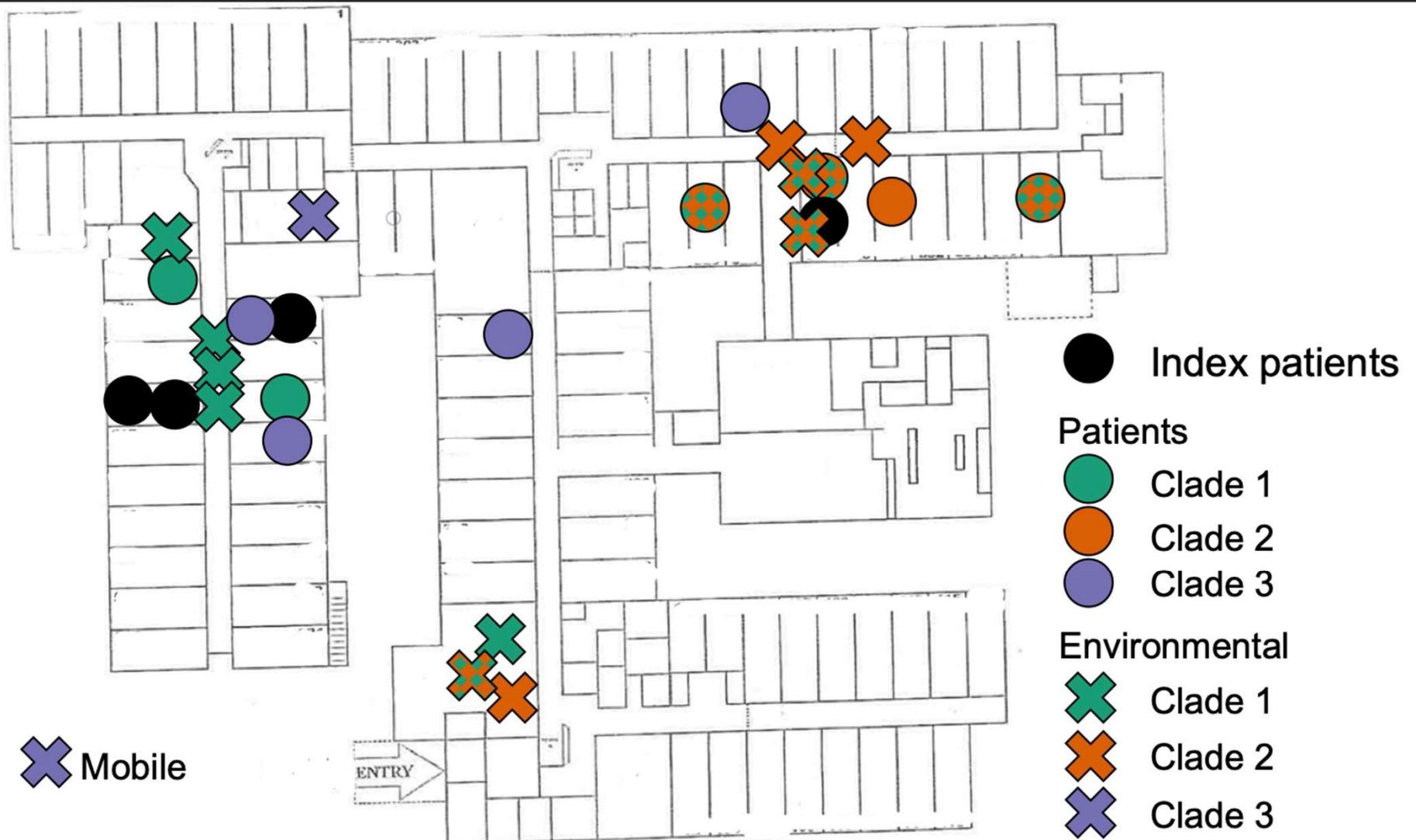
Acinetobacter baumannii OXA-23



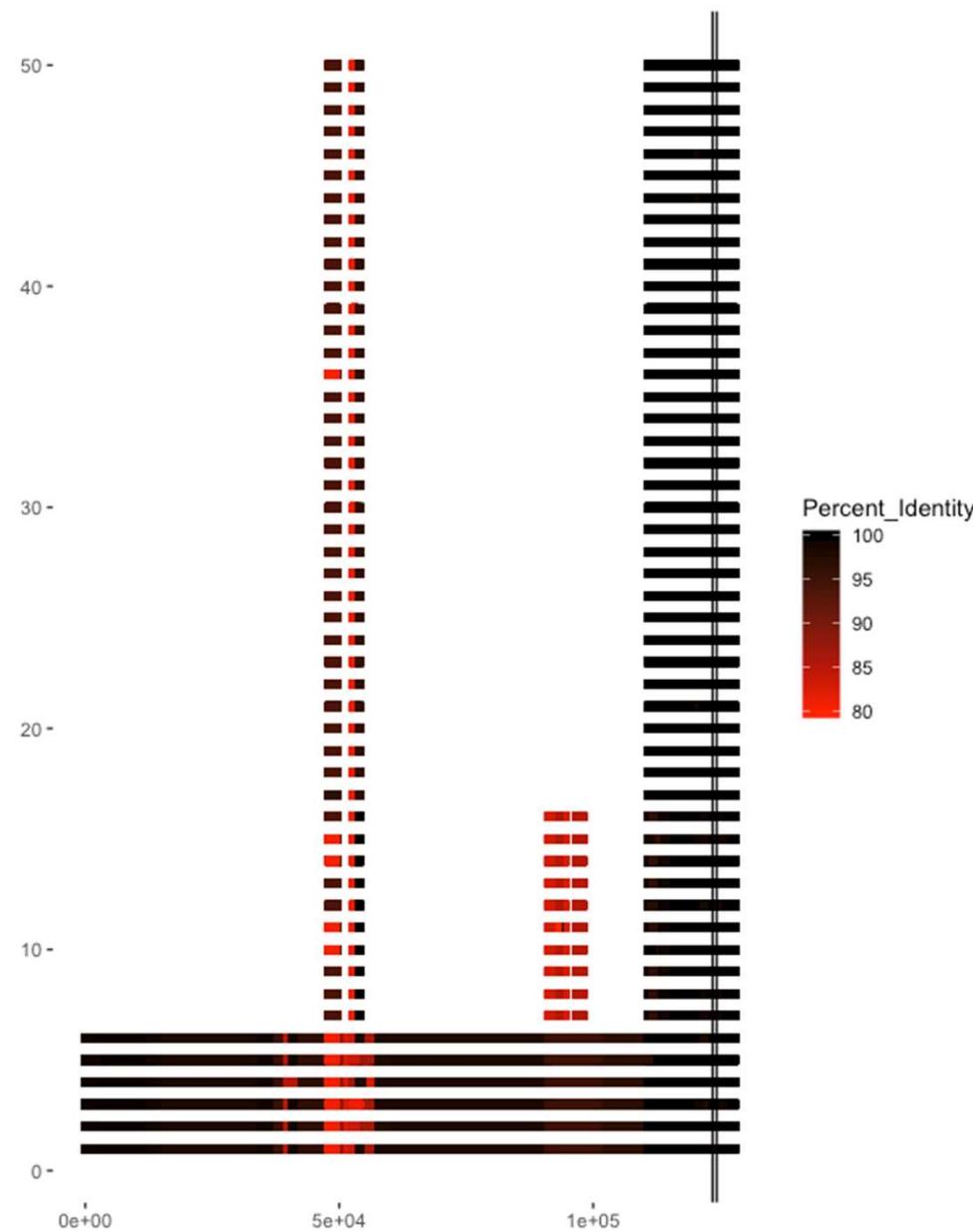
Acinetobacter baumannii OXA-23



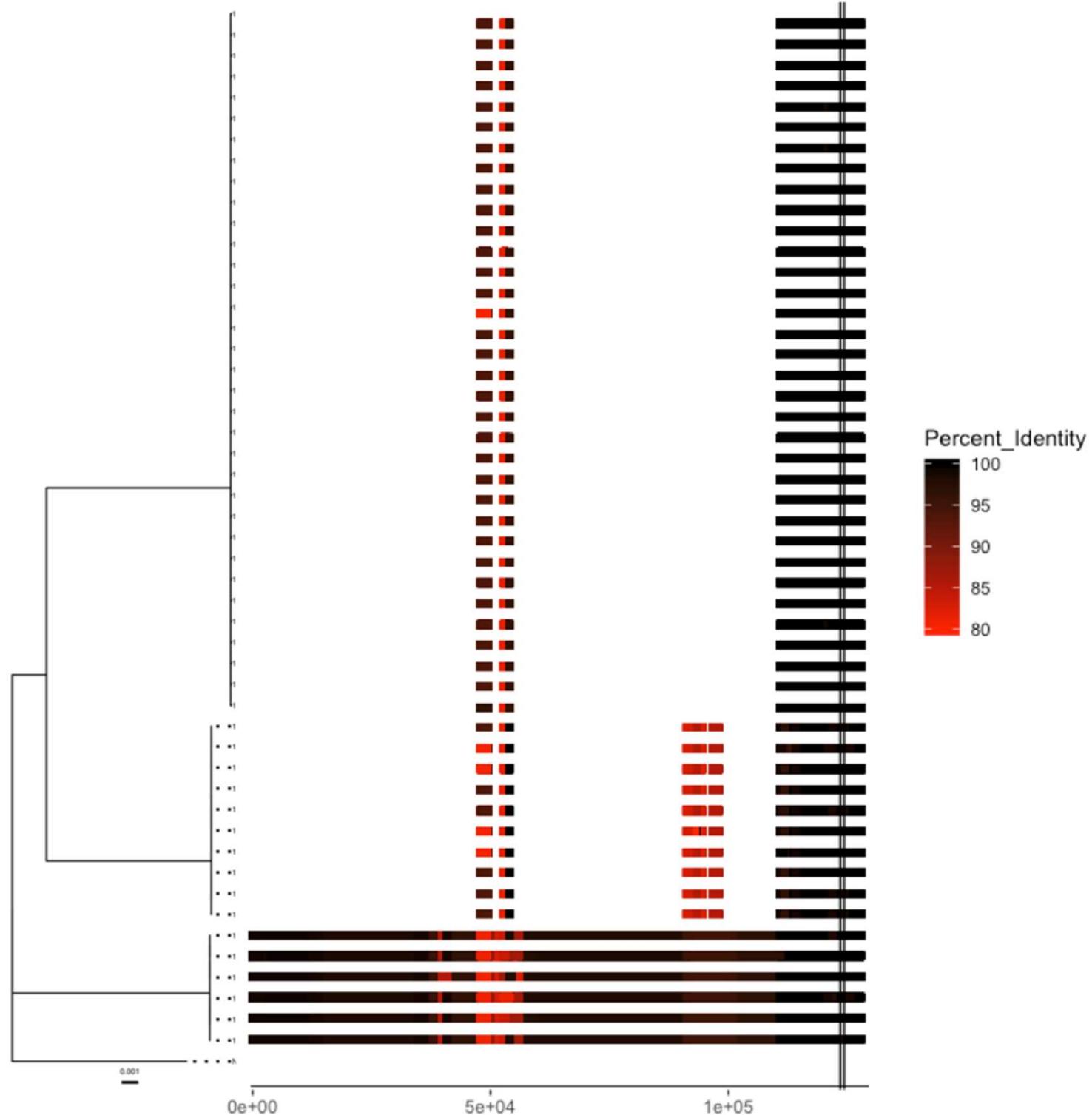
Acinetobacter baumannii OXA-23



Acinetobacter baumannii OXA-23



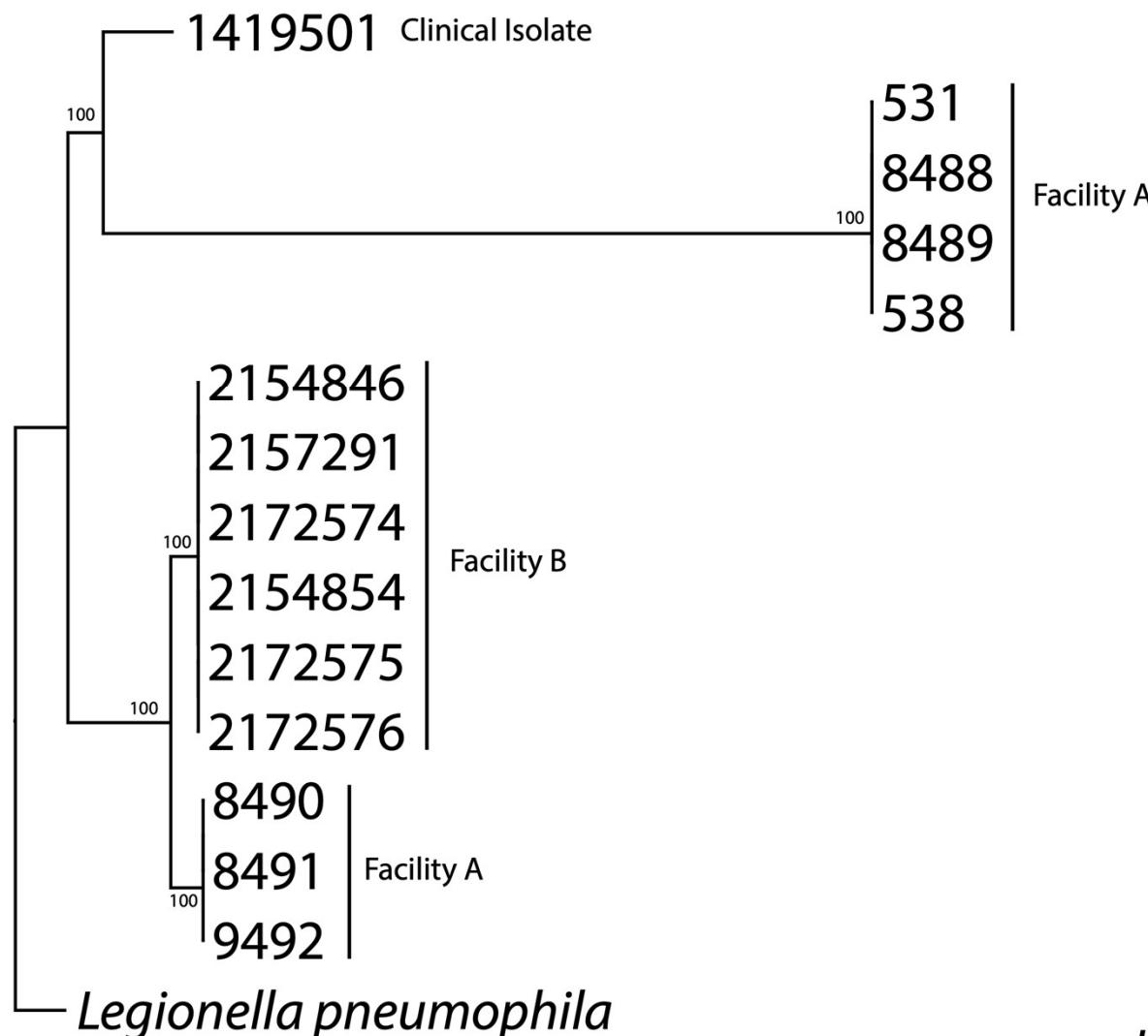
OXA-23





Legionella pneumophila

Reference Free WGS Analysis



Legionella pneumophila
Phylogenetic Tree Based on 1,356
Concatenated Protein Coding Genes

Laboratory Epidemiology Communication

docs.google.com

Save to Mendeley MediaLab Altmetric it! Harmons Pharmacy GalaxyTrakr The Illumina Community EdgeOS Syndromic Trends SciQuest PulseNet_SharePoint AIMS HealthNet IDGenomics_NAS Download NC...anPhlAn FAQ > +

Lab/Epi WGS Sample Result Tracker Share

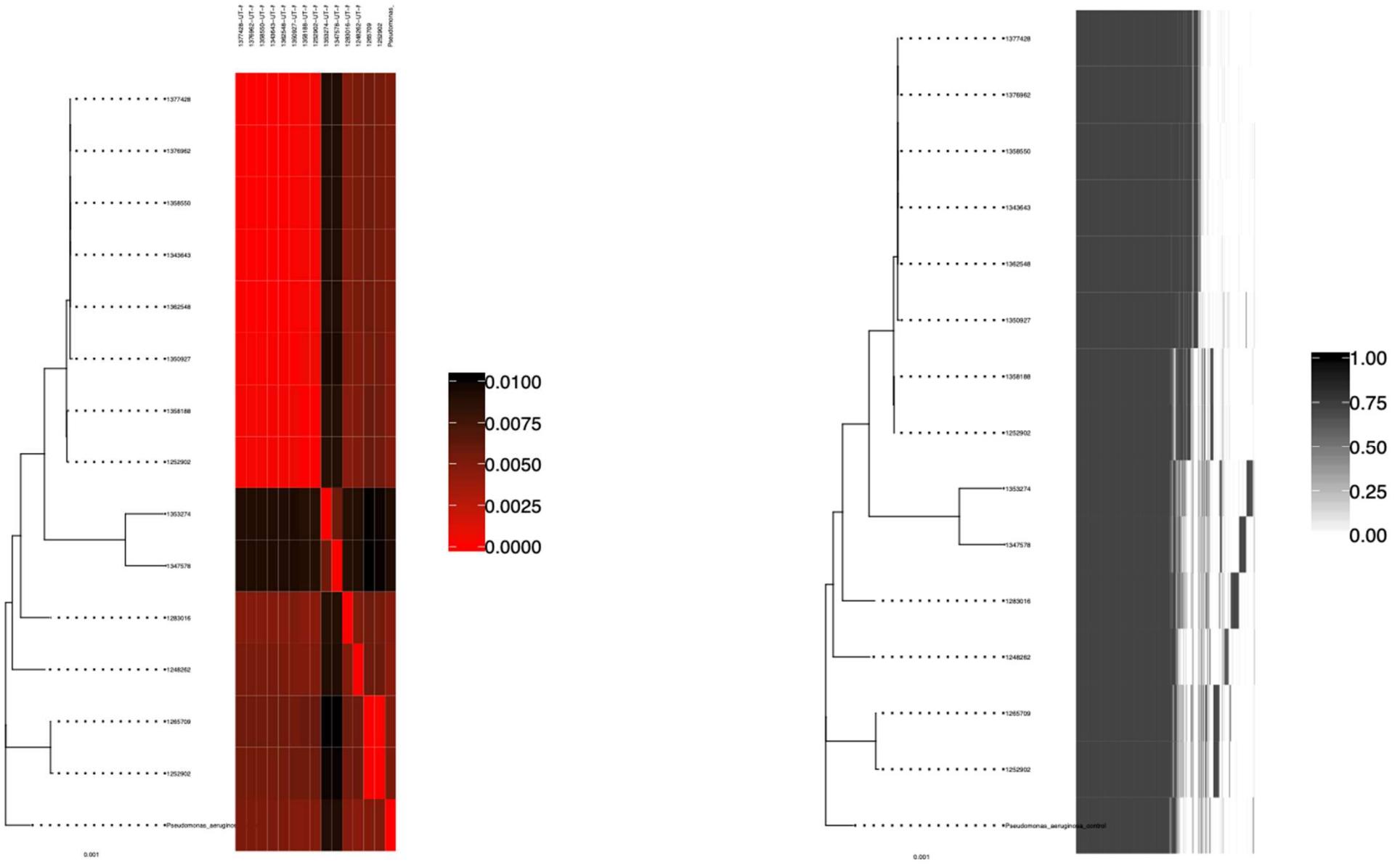
File Edit View Insert Format Data Tools Help All changes saved in Drive

A B C D E F G

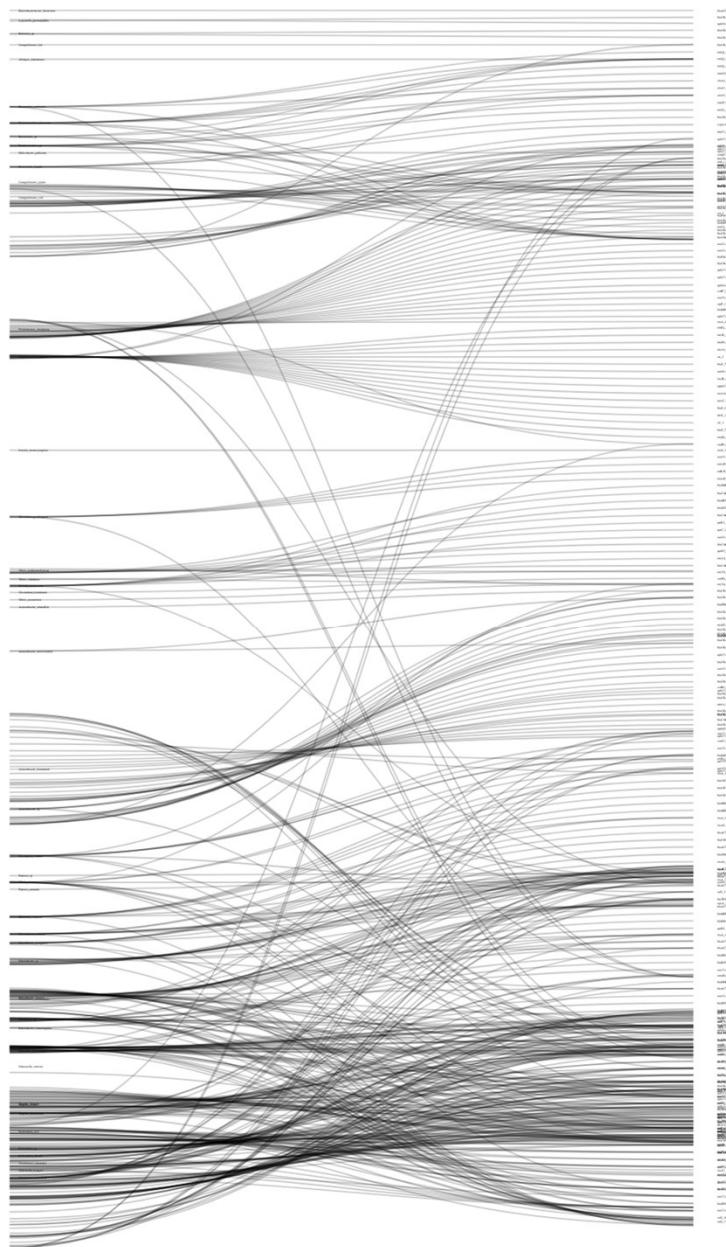
1	Lab Accession	Collection Date	Organism	Run Name	Run Date	Link to Tree	Notes
2	1415961	05/13/2019	Campylobacter coli	UT-M03999-190712	07/12/2019	?id=1ifZq9m9Rw&	
3	1425162	6/10/2019	Campylobacter jejuni	UT-M03999-190712	07/12/2019	?id=1hVcJb0EUb&	Possible cluster with 1425170, 1416214, 1408326, PNUSAC008889, 1387699, 8
4	1425170	6/7/2019	Campylobacter jejuni	UT-M03999-190712	07/12/2019	?id=1hVcJb0EUb&	Possible cluster with 1425162, 1416214, 1408326, PNUSAC008889, 1387699, 8
5	1425171	6/8/2019	Campylobacter coli	UT-M03999-190712	07/12/2019	?id=1ifZq9m9Rw&	
6	1425172	6/8/2019	Campylobacter jejuni	UT-M03999-190712	07/12/2019	?id=1hVcJb0EUb&	
7	1425530	6/13/2019	Campylobacter jejuni	UT-M03999-190712	07/12/2019	?id=1hVcJb0EUb&	
8	1425601	6/10/2019	Campylobacter jejuni	UT-M03999-190712	07/12/2019	?id=1hVcJb0EUb&	Possible cluster with 1350070, PNUSAC008729, PNUSAC008728, 1369979, 13425601, PNUSAC008720, 1351861, 1388102A, 1393944, 1415050, PNUSAC008727
9	1425602	6/9/2019	Campylobacter jejuni	UT-M03999-190712	07/12/2019	?id=1hVcJb0EUb&	
10	1425603	6/8/2019	Campylobacter jejuni	UT-M03999-190712	07/12/2019	?id=1hVcJb0EUb&	
11	1425604	6/8/2019	Campylobacter jejuni	UT-M03999-190712	07/12/2019	?id=1hVcJb0EUb&	
12	1425605	6/11/2019	Campylobacter jejuni	UT-M03999-190712	07/12/2019	?id=1hVcJb0EUb&	
13	1425607	6/10/2019	Campylobacter jejuni	UT-M03999-190712	07/12/2019	?id=1hVcJb0EUb&	
14	1425609	6/12/2019	Campylobacter jejuni	UT-M03999-190712	07/12/2019	?id=1hVcJb0EUb&	
15	1426454	6/8/2019	Campylobacter jejuni	UT-M03999-190712	07/12/2019	?id=1hVcJb0EUb&	
16	1426480	6/14/2019	Campylobacter upsaliensis	UT-M03999-190712	07/12/2019	?id=1p604GIYN6	
17	1427231	6/18/2019	Escherichia coli O121:H19	UT-M03999-190712	07/12/2019	N/A	Too few samples in past 120 days
18	1428520	6/23/2019	Escherichia coli O26:H11	UT-M03999-190712	07/12/2019	?id=1KSXuJX87Y_	
19	1428655	6/16/2019	Escherichia coli O26:H11	UT-M03999-190712	07/12/2019	?id=1KSXuJX87Y_	
20	1431069	6/27/2019	Salmonella enterica serovar Widemarsh or IIIa_35:z29:-	UT-M03999-190712	07/12/2019	N/A	Too few samples in past 120 days
21	1431071	6/27/2019	Escherichia coli O157:H7	UT-M03999-190712	07/12/2019	?id=1QWUcSrxITC	
22	1431974	6/27/2019	Escherichia coli O111:H8	UT-M03999-190712	07/12/2019	?id=1gqb-iW6N9C	
23	1431996	6/28/2019	Escherichia coli O26:H11	UT-M03999-190712	07/12/2019	?id=1KSXuJX87Y_	
24	1432125	6/30/2019	Salmonella enterica serovar Infantis	UT-M03999-190712	07/12/2019	n?id=1xLYIIKRAI	
25	1432435	6/28/2019	Shigella flexneri	UT-M03999-190712	07/12/2019	?id=1AHT8_EIE4I	Possible cluster with sample 1416743
26	1432901	7/4/2019	Salmonella enterica serovar Enteritidis	UT-M03999-190712	07/12/2019	?id=1W2BLauQ1el	Possible cluster with sample PNUSAS067208
27	1432908	7/1/2019	Salmonella enterica serovar Newport	UT-M03999-190712	07/12/2019	?id=1DaIAvCaeTG	Possible cluster with samples 1430758 & 1403890
28	1433284	6/26/2019	Salmonella enterica serovar Newport	UT-M03999-190712	07/12/2019	?id=1DaIAvCaeTG	Possible cluster with samples PNUSA072077, 1373362, 1367889, 1426478 & 1403890

Run Result Summary Explore

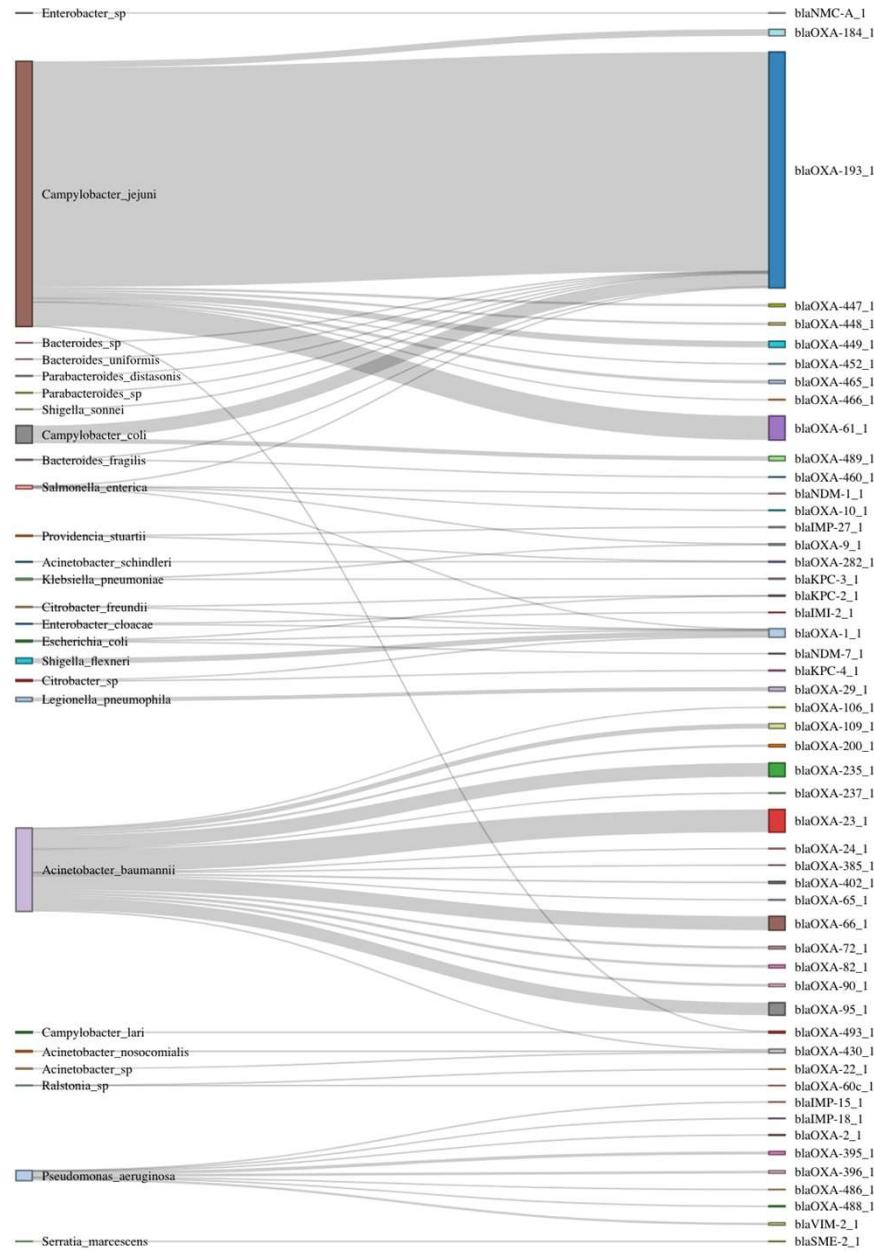
Laboratory Epidemiology Communication



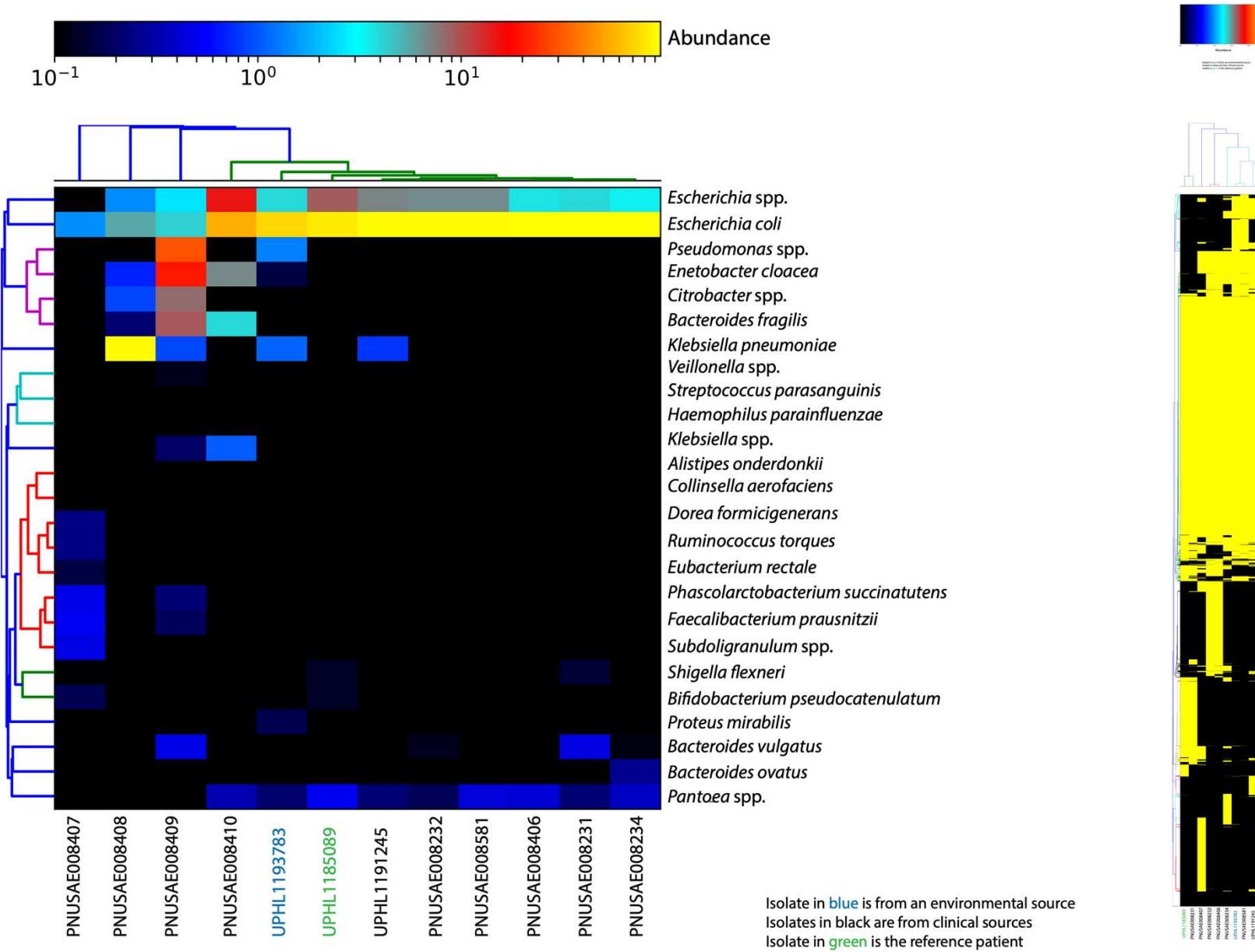
Antimicrobial Resistance Gene Flow



Antimicrobial Resistance Gene Flow



WGS & Metagenomics



Questions/Discussion



Thank You

Utah Public Health Laboratory

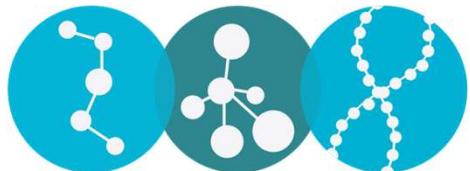
Robyn Atkinson-Dunn

Andy Rohwasser

Jenni Wagner

Anna Sangster

Erin Young



StaPH-B
State Public Health Bioinformatics

