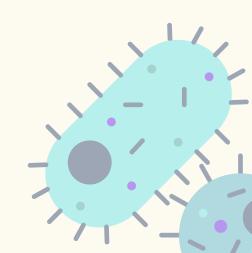


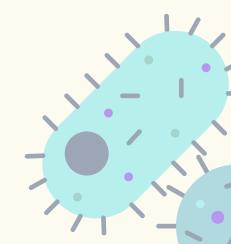
What is Pseudomonas aeruginosa?

- Microbiological characteristic; Gram-negative
- Commonly found in soil and water
- Disease symptoms;
 - o infection in blood, lungs, etc.
- Infection numbers (US, 2017);
 - 32,600 hospitalized patients
 - 2,700 estimated deaths
- Spreads through;
 - o contaminated water/soil, hands, equipment, surfaces



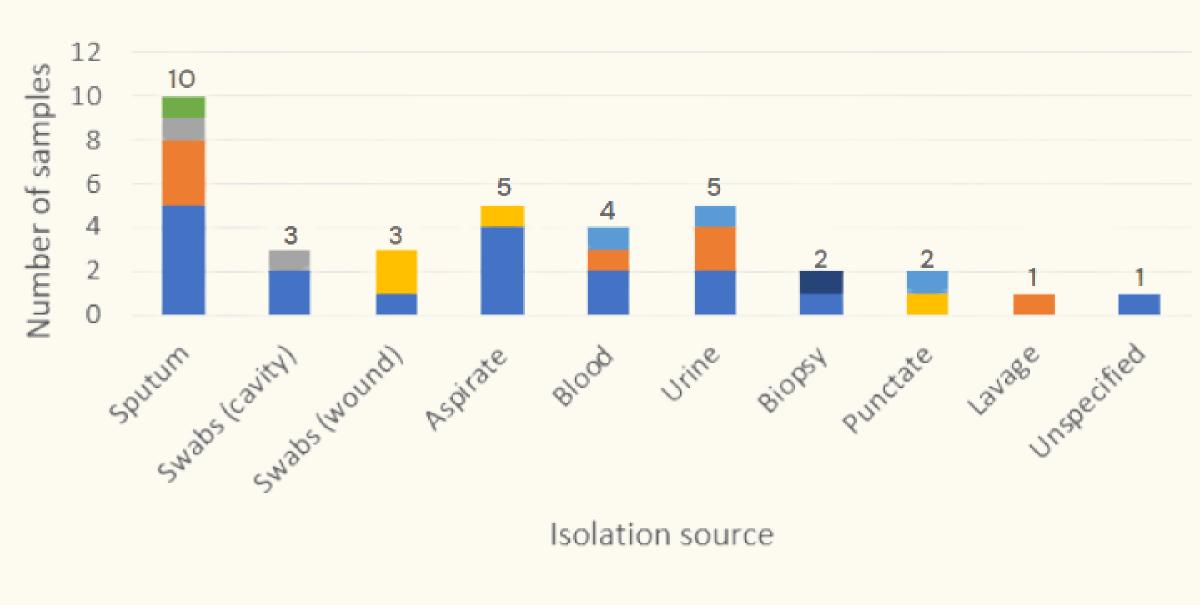
What is Pseudomonas aeruginosa?

- Treatment;
 - Antibiotics
- Drug resistance;
 - ESKAPE Highly virulent / antibiotic resistant
 - Multi-drug resistance
 - Advanced antibiotic resistance mechanism
- Genome;
 - Relatively large (5.5 7 Mb)
 - High GC content (65–67%)



What data were we working with?





■ Europe Asia North America South America Africa Oceania Eurasia

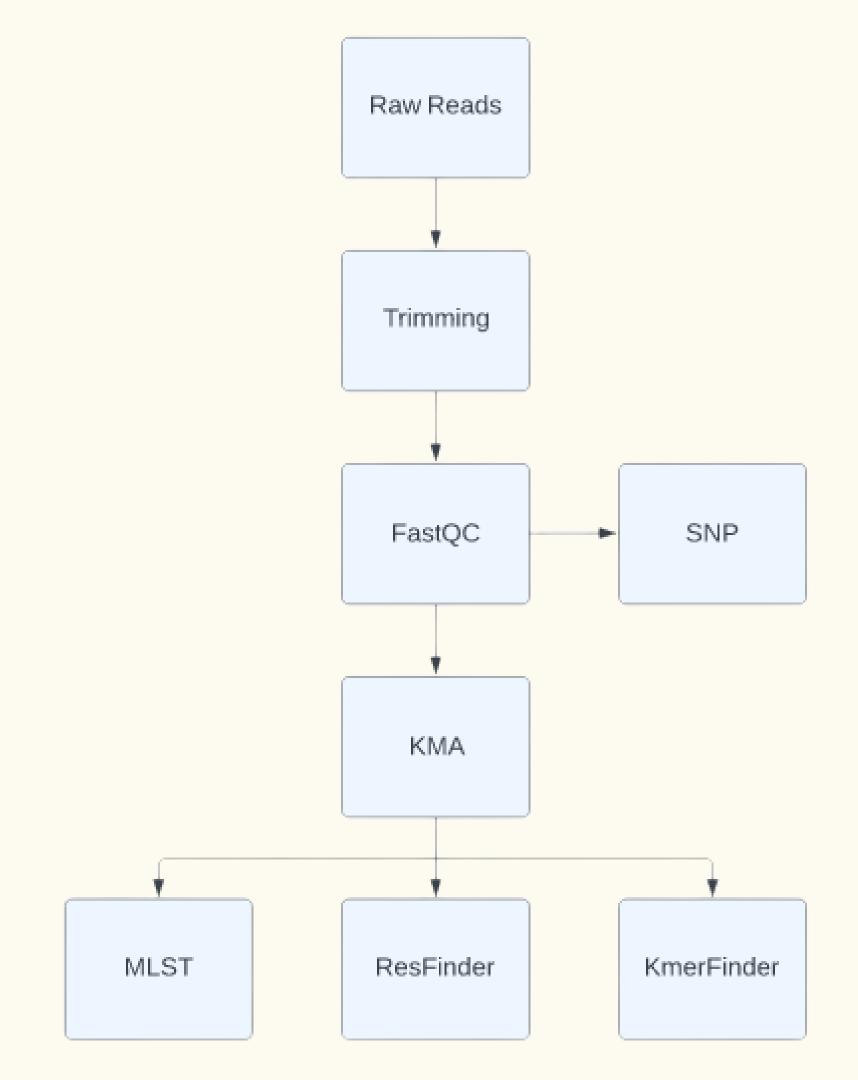
- Data from Two Weeks in The World (TWIW)
- 36 samples
- 25 different countries (from all continents)
- Samples coming from hospitals (humans)
- Sampled between
 26/02/2020 09/12/2020



HOW DO ANTIMICROBIAL RESISTANCE PROFILES DIFFER ACROSS COUNTRIES?

HOW DOES DEMOGRAPHICS INFLUENCE THE GENETIC MAKEUP OF P. AERUGINOSA?

Workflow

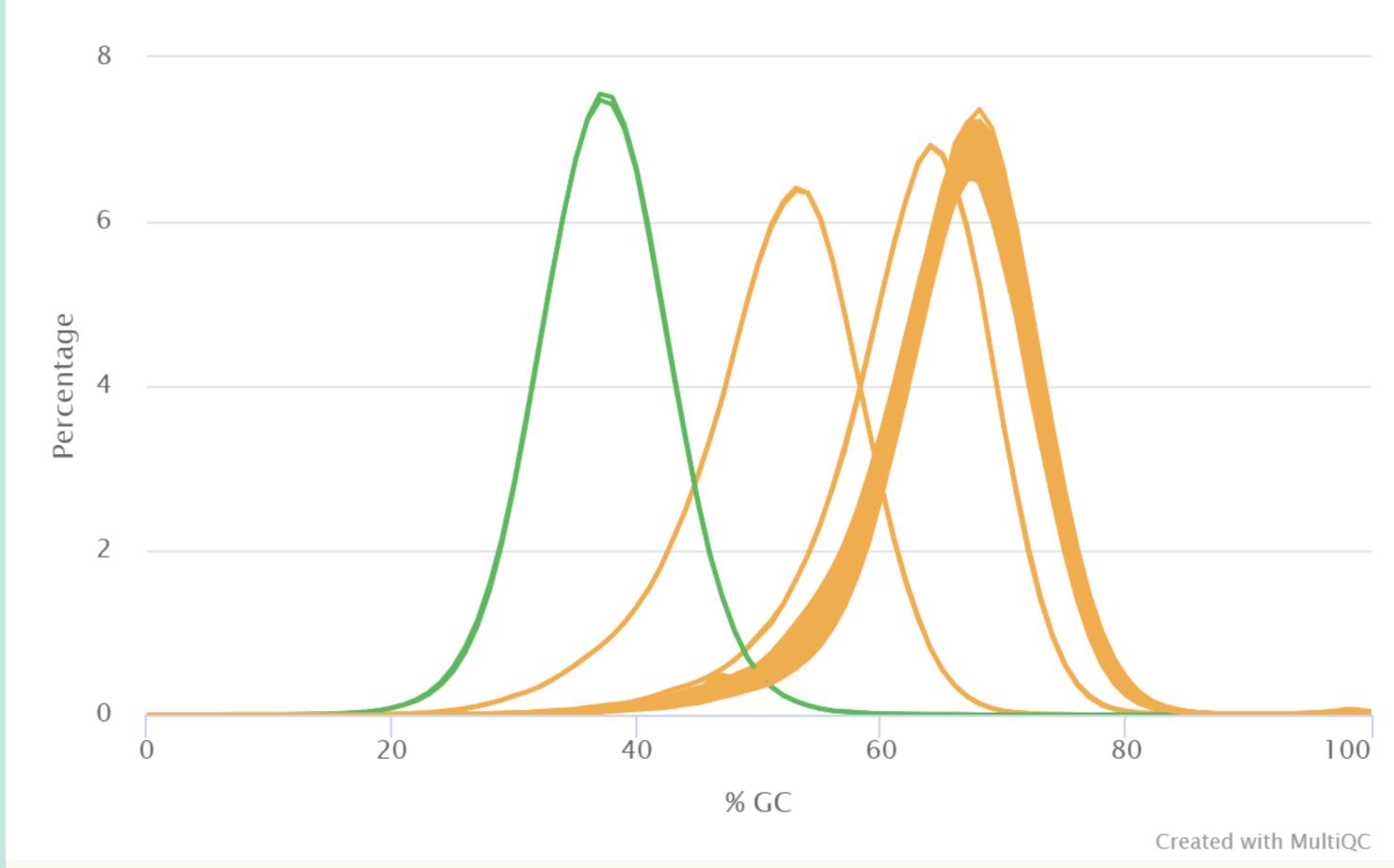


Read Trimming and Quality Control

Samples	% Dups	% GC	M Seqs
DTU_2020_1000469	27.7%	50%	01.06
DTU_2020_1001615	6.2%	62%	00.03
DTU_2021_1002458	29.2%	37%	01.05
DTU_2020_1000925	57.2%	64%	12.04
DTU_2021_1002653	16.4%	65%	01.00
DTU_2020_1000631	24.5%	65%	02.01
DTU_2020_1000674	16.4%	65%	01.01

Read Trimming and Quality Control

FastQC: Per Sequence GC Content



Species	Samples	Template_Coverage	Depth	TAXID	TAXID Species
Escherichia coli	DTU_2020_1000469	95,61	77,54	562	562
Pseudomonas asiatica	DTU_2020_1001615	85,45	10,59	2219225	2219225
Elizabethkingia anophelis	DTU_2021_1002458	79,26	65,11	1117645	1117645
Pseudomonas aeruginosa	DTU_2020_1000925	257,34	324,54	287	287
Pseudomonas aeruginosa	DTU_2021_1002653	85,13	30,95	381754	287
Pseudomonas aeruginosa	DTU_2020_1000631	90,72	63,13	287	287
Pseudomonas aeruginosa	DTU_2020_1000674	82,52	29,77	287	287

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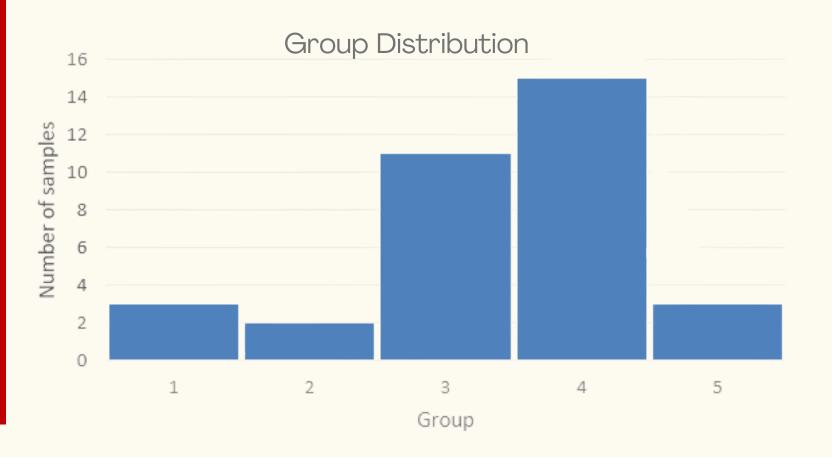
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	Group 1	Group 2	Group 3	Group 4	Group 5
amoxicillin	+	+	+	+	-
ampicillin	+	+	+	+	-
butiromycin	+	+	-	-	-
cefepime	+	+	+	+	-
ceftazidime	+	+	+	+	-
chloramphenicol	+	+	+	+	-
fosfomycin	+	+	+	+	-
gentamicin	+	+	-	-	-
kanamycin	+	+	-	-	-
meropenem	+	-	+	-	-
neomycin	+	+	-	-	-
paromomycin	+	+	-	-	-
ribostamycin	+	+	-	-	-

- Resistance gene detection
- 5 different groups

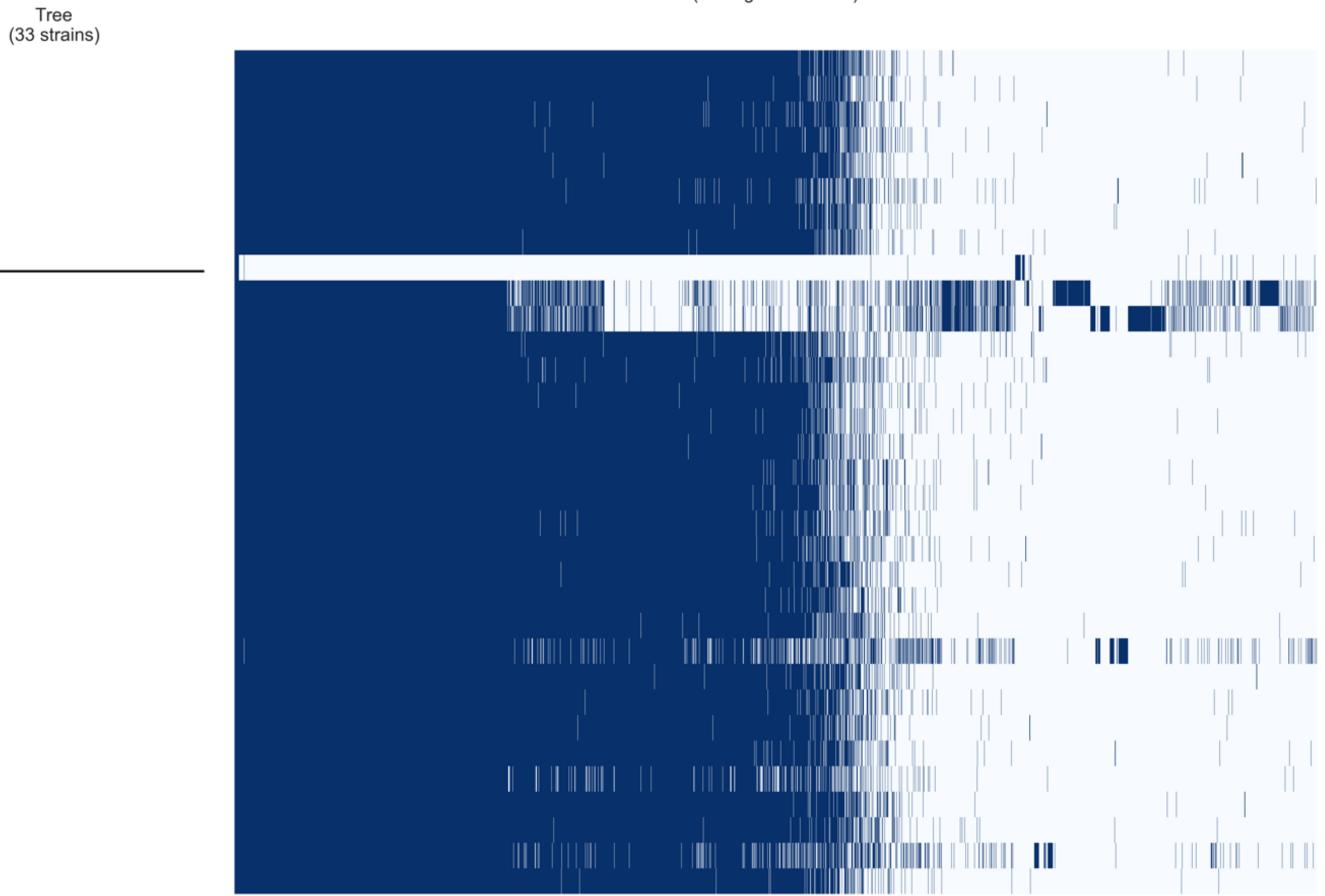




Phylogeny (ResFinder tree)

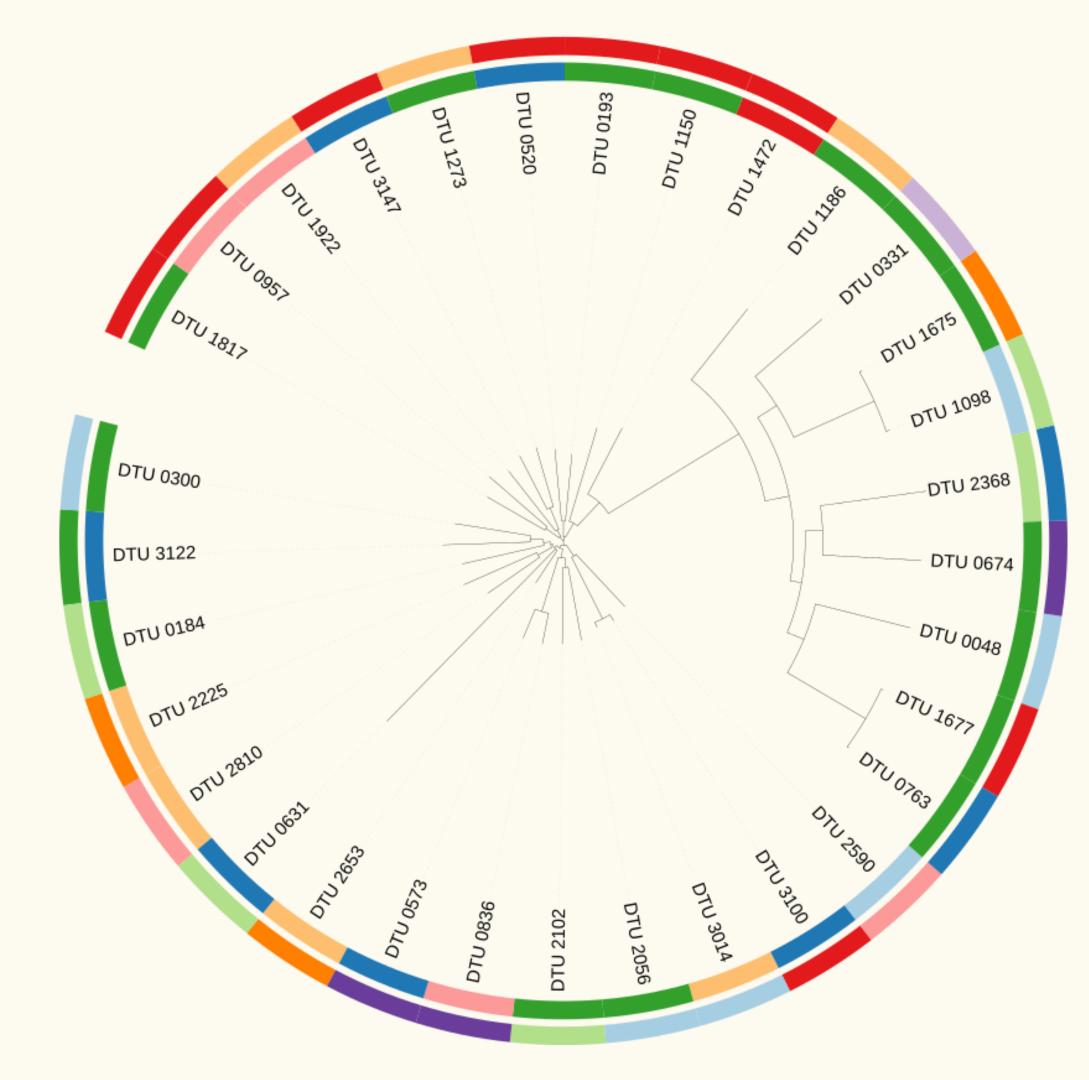
Roary matrix (9619 gene clusters)



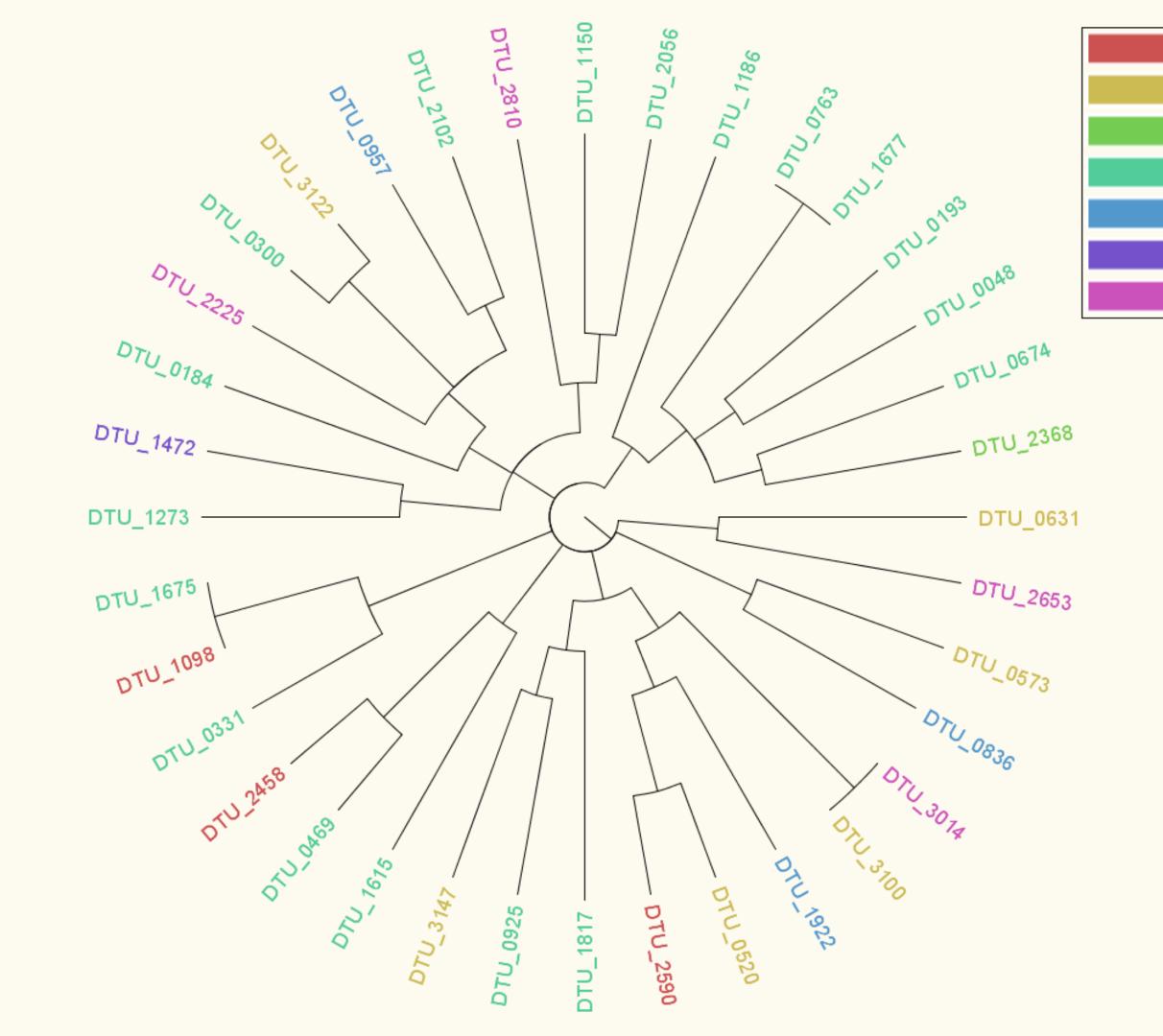


Tree scale: 0.1 ⊢ Continent (inner) Africa Asia Eurasia Europe North America Oceania South America Isolation source (outer) aspirate biopsy blood lavage punctate sputum swab (cavity) swab (wound) unspecified diagnostic sample urine





Phylogeny (MLST tree)



Africa

Eurasia

Europe

Oceania

North America

South America

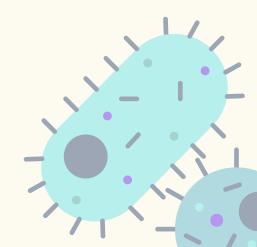
Asia

What is our final thoughts?

- Sample size too small (N = 36)
- No clustering

What could future steps be?

- More samples
- Continue in the future to monitor





Thankyou

ANY QUESTIONS?

