

# PulseNet Latin America and the Caribbean. Towards a Regional Integration in Genome Analysis

Relavra 2019

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**PAHO**  
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# Contents



- Considerations regarding the epidemiology, surveillance, laboratory diagnosis and genomic epidemiology
- PulseNet Latin America and the Caribbean

# Genomic Surveillance



- Track epidemic origins and transmission hotspots
- Characterize genetic diversity to aid molecular diagnostics,
- Detect mutations associated with disease severity, and supports the characterization of antimicrobial resistant patterns
- Exclude the possibility that human cases are caused by vaccine reversion

# Genomic Surveillance

- The combination of genomic and epidemiological data from pathogen infections can give essential information:
  - Understanding the past and the future of an epidemic, its dynamics, making it possible to establish an effective surveillance framework
  - Tracking the spread of infections to other geographic regions
- PAHO has strategically strengthen the networking between
  - the national public health laboratories (NPHL),
  - the regional reference labs
  - PAHO/WHO Collaborating Centers (WHO-CC)
- To improve the epidemiological surveillance and response to outbreaks

## Arbovirus Diagnosis Laboratory Network of the Americas (RELDA)

Geographic distribution



Country				
Argentina	Costa Rica	French Guiana	Mexico	Puerto Rico-...
Bolivia	Cuba	Guatemala	Nicaragua	Suriname
Brazil	Dominican Re..	Haiti	Panama	Trinidad y Tob..
Chile	Ecuador	Honduras	Paraguay	Uruguay
Colombia	El Salvador	Jamaica	Peru	USA
				Venezuela

30 Labs in 26 countries

4 WHO CC (MEX, ARG, CUB, USA)

All labs have **molecular platforms** for at least 4 arboviral diseases (DENV, CHIKV, ZIKV, YFV)

At least 10 Mayaro PCR

All labs have ELISA platforms for at least 3 arboviral diseases (DENV, CHIKV, ZIKV); YFV in endemic countries

# PulseNet Latin America and the Caribbean

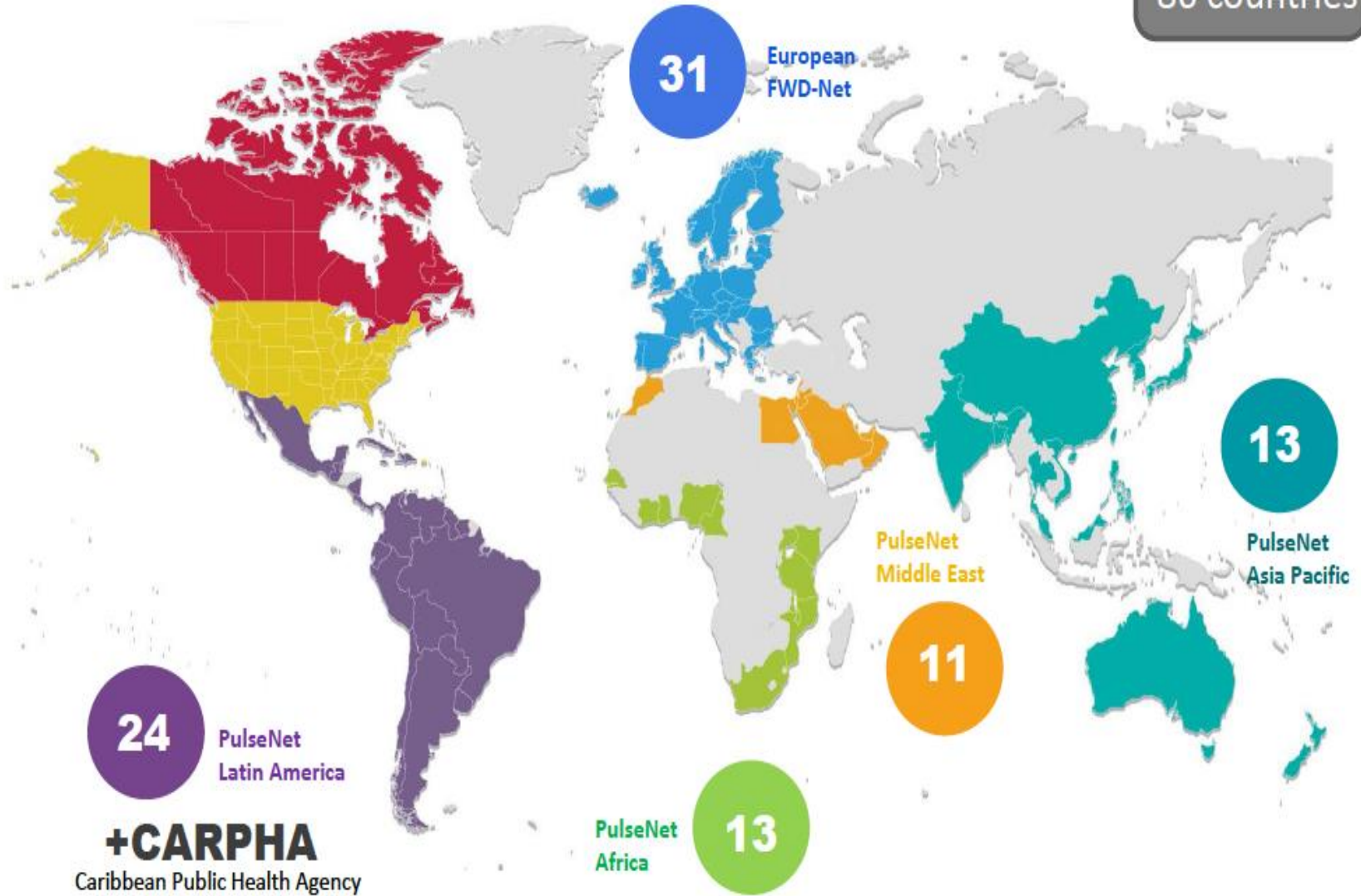


- PulseNet Latin America and Caribbean (PNLAC) was established in 2003 and is one of seven Regional networks within PulseNet International.
- The main objectives of the network are to strengthen national and regional laboratory-based foodborne disease surveillance for early detection and investigation of outbreaks to setup control and prevention strategies in contribution to Public Health



# PulseNet International

7 Regions  
86 countries





## Vision of PN International



- To use WGS in all PHL in the world to identify, characterize, and subtype foodborne bacterial pathogens, replacing the existing phenotypic and molecular methods in support of foodborne diseases preparedness and response to save lives and reduce global social and economic loss



# Genomic Epidemiology

**Pulsed Field Gel Electrophoresis**

## **Challenge**

- New paradigm
- Revolutionary



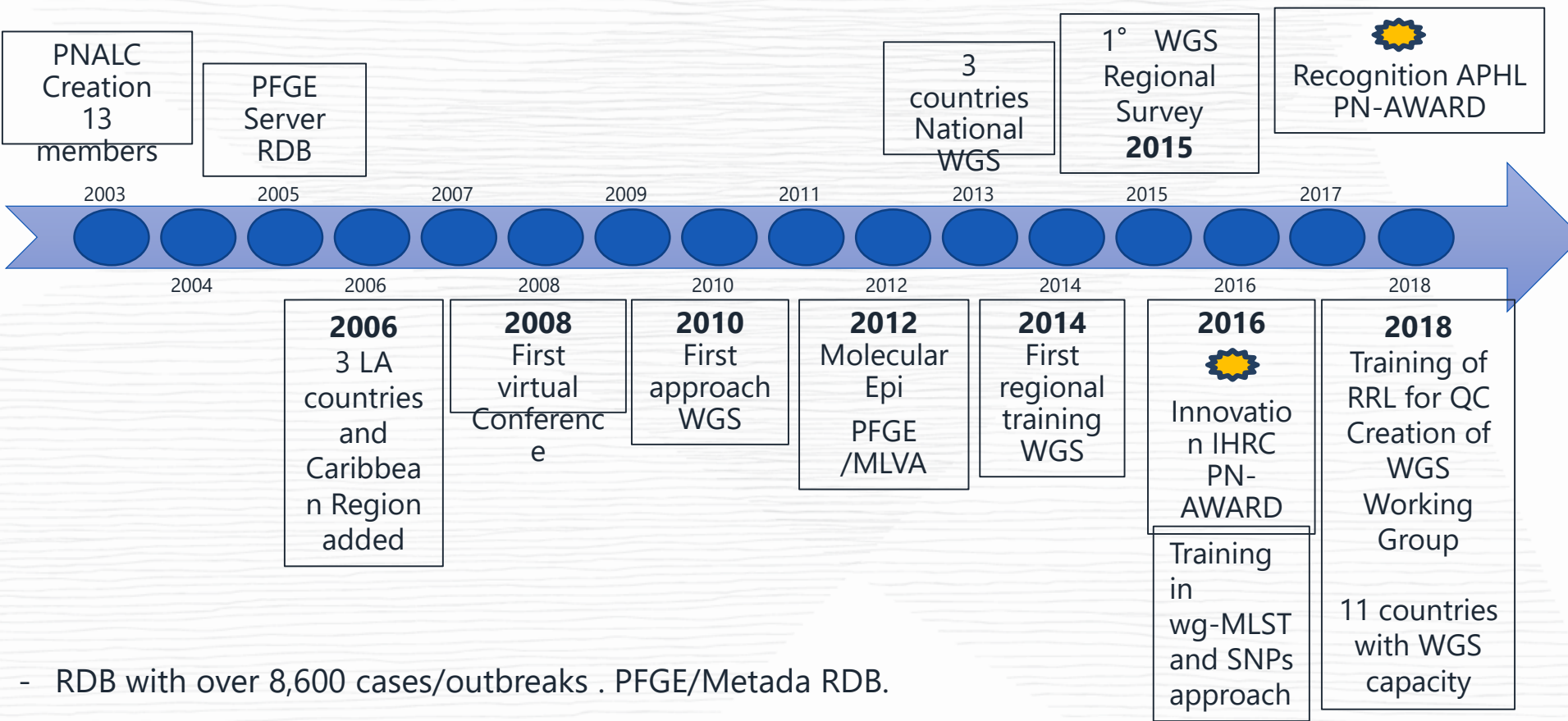
## **Political decision**

- Resources
- Priorities Public Health

**Whole Genome Sequencing (WGS)**

Diagnosis, characterization and genomic epidemiology

# Regional Network – 16 LA countries and Caribbean Region PulseNet Latin America and The Caribbean (PNLAC)



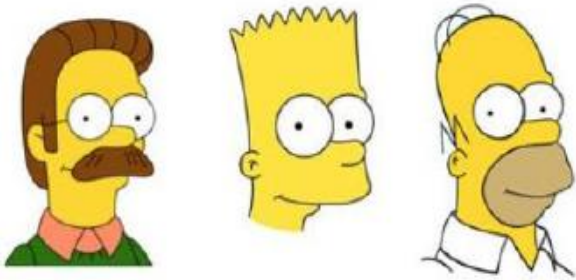
- RDB with over 8,600 cases/outbreaks . PFGE/Metada RDB.

# To use WGS in a laboratory network: the tools must be



- Simple
- Universal standardized methods
- Public health laboratorians are NOT bioinformaticians
- Use existing software
- Comprehensive
- All characterization in one workflow
- Work in all laboratories
- Free sharing and comparison of data between laboratories
- Central AND local databases
- “IF IT WORKS, FOR PUBLIC HEALTH IT IS GOOD ENOUGH”

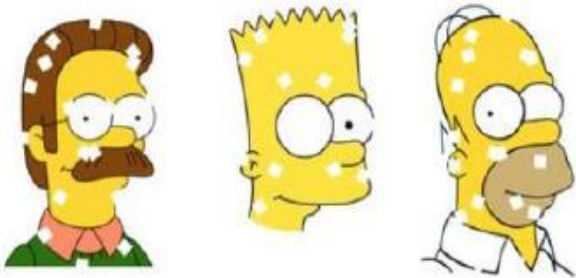
### Genomes



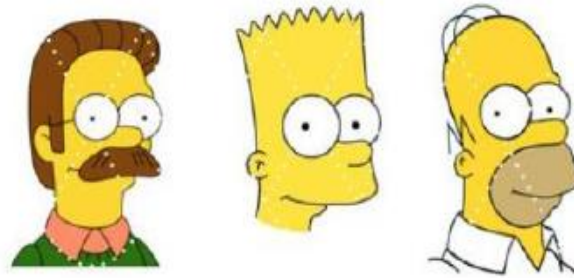
### Multi Locus Sequence Typing



### Core/Whole Genome MLST



### Whole genome SNPs



Source: Torsten Seeman, University of Melbourne Australia.



# 2019 Update

## WGS - Regional Status

	Seq Capacity	WGS analysis	Server
<b>N° Countries</b>	<b>12 (14 Lab)</b>	<b>9 BN 7.0-7.6 (10 Lab)</b>	<b>9 (10 Lab)</b>
<b>Description</b>	HiSeq	BioNumerics 7.6	Cloud
	Next Seq	BioNumerics 7.0	Server
	MiSeq	Other institutional, commercial or public tools (NML-Canada pipelines; WTSI pipelines; CGE)	Server-access
	MiniSeq		(NML-Canada ; WTSI )
	Ion Torrent		

Until 2017 - Mexico, Colombia, Chile, Argentina, Peru.

2017-2019 - Brazil AL (Sao Paulo), Brazil OC (Rio de Janeiro), Costa Rica, Panama, Ecuador, Paraguay, Venezuela, Uruguay.

2019-2020 – Bolivia, Cuba, CARPHA (en adquisicion)

# TECHNICAL / ANALYSIS: Challenges during the implementation process

- Availability of the reagents / suppliers
- On job training and/or assistance were required for:
  - WGS capacity installation
  - First steps implementation
- Electric power supply / Internet connectivity
- Use of commercial / free softwares

# Sequences in LA – updated to 2019



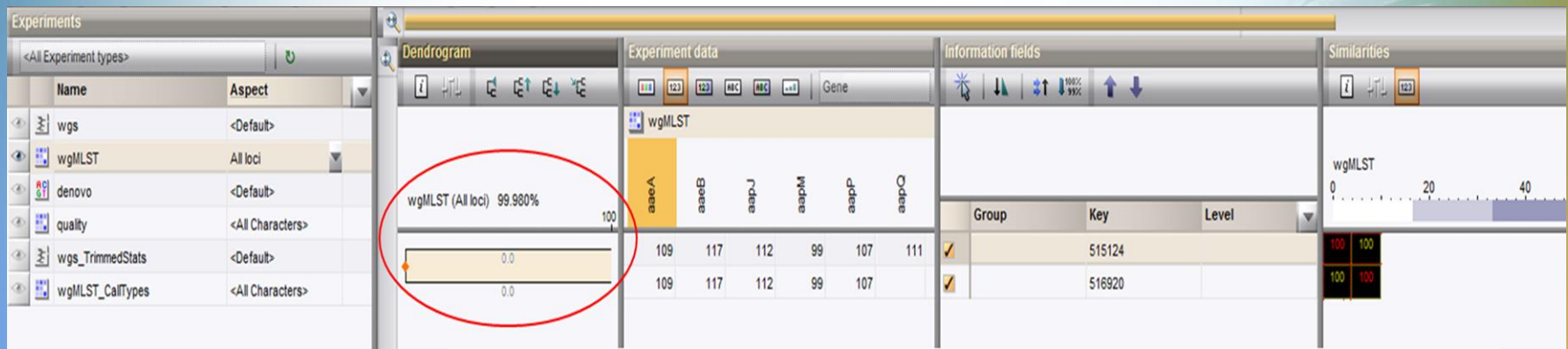
Country	N° sequences	Outbreaks
Argentina	163 <i>E. coli</i> (STEC; EAEC; EAEC-stx) 310 <i>Salmonella</i> ( <i>S. Enteritidis</i> , <i>S. Typhimurium</i> , <i>S. Typhi</i> , other serotypes) 48 <i>Shigella</i> ; 50 <i>V. cholerae</i> ; <i>Streptococcus pyogenes</i>	7
Chile	100 <i>Salmonella</i> , <i>Shigella</i> , <i>V. parahaemolyticus</i> , <i>E. coli</i> y <i>Listeria</i>	1
Colombia	704 <i>Salmonella</i> (6 <i>S. Infantis</i> , 404 <i>S. Enteritidis</i> , 252 <i>S. Typhimurium</i> , 96 <i>S. Typhi</i> ; 119 <i>S. Derby</i> , <i>S. Dublin</i> , <i>S. Javiana</i> , <i>S. Muenchen</i> , <i>S. Muenster</i> , <i>S. Newport</i> , <i>S. Panama</i> , <i>S. 1,4,5,12:i:-</i> , <i>S. 4,5,12:i:-</i> ); 31 <i>Shigella sonnei</i> , 14 <i>V. cholerae</i> ; <i>Campylobacter</i> , <i>Enterococcus</i>	1
México	946 <i>Salmonella</i> , <i>V. cholerae</i>	1
Costa Rica	46 <i>Salmonella</i> Parayphi B/Infantis /I 4,4,12:i:-/Typhi/Welbedere 14 <i>Shigella flexneri</i> /sonnei 22 <i>E. coli</i> 13 <i>Klebsiella pneumoniae</i> / 8 <i>S. liquefaciens</i> / 2 <i>Chronobacter Sakazakii</i>	10
Paraguay	14 <i>Salmonella</i> , <i>E. coli</i>	1
Perú	24 <i>Salmonella</i> , <i>Shigella</i> , <i>Vibrio</i>	--
Brazil AL	<i>Salmonella</i> , <i>Shigella</i> , <i>E. coli</i> y <i>Listeria</i> 96 (HiSeq); 24(IT)	1



# Foodborne case of *Cronobacter sakazakii* - 2018

Costa Rica INCIENSA. Francisco Duarte

fduarte@inciensa.ca



## Results:

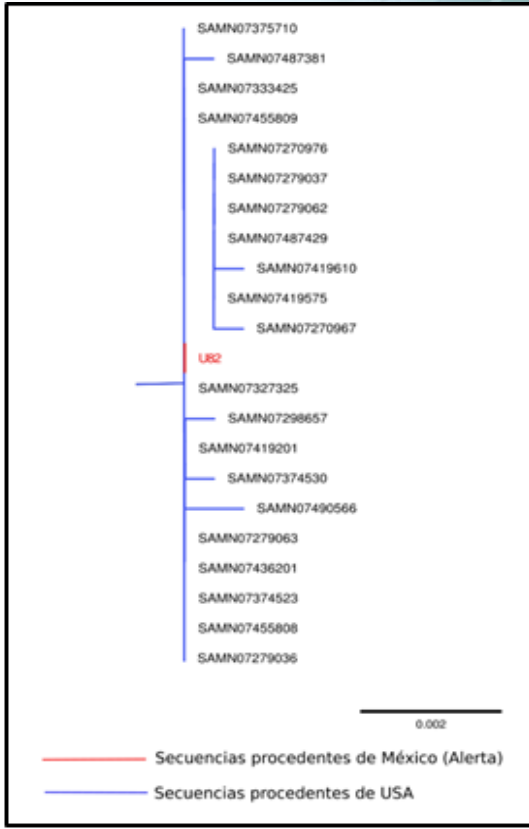
- Identical by PFGE and one allele difference by wg-MLST
- Sampling of infant formula by Ministry of health => **NEGATIVE**
- Contamination by manipulation of infant formula at home

## WGS Advantages

- Species confirmation
- Genetic similarity confirmation
- High resolution

# S. Kiambu Investigation in Papayas – México

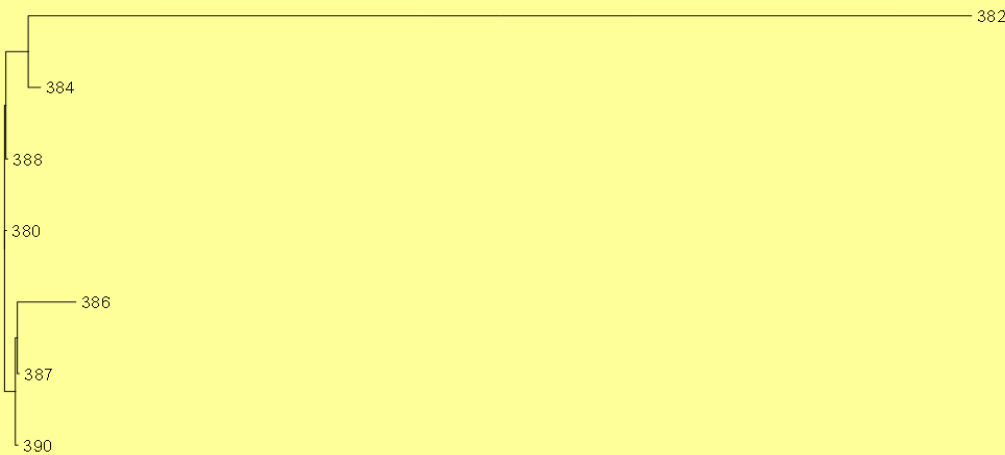
	SAMN07279036	SAMN07279037	SAMN07327325	SAMN07270967	SAMN07270976	SAMN07279062	SAMN07298657	SAMN07333425	SAMN07279063	SAMN07375710	SAMN07374523	SAMN07374530	SAMN07419575	SAMN07419610	SAMN07419201	SAMN07436201	SAMN07487381	SAMN07487429	SAMN07455809	SAMN07455808	SAMN07490566	U82
SAMN07279036	0	1	0	2	1	1	0	0	0	0	0	1	1	1	0	0	1	1	0	0	2	0
SAMN07279037	1	0	1	1	0	0	2	1	1	1	1	2	0	1	1	1	2	0	1	1	3	1
SAMN07327325	0	1	0	2	1	1	1	0	0	0	0	0	1	2	0	0	1	1	0	0	2	0
SAMN07270967	2	1	2	0	1	1	3	2	2	2	2	3	1	2	2	2	3	1	2	2	4	2
SAMN07270976	1	0	1	1	0	0	2	1	1	1	1	2	0	1	1	1	2	0	1	1	3	1
SAMN07279062	1	0	1	1	0	0	1	1	1	1	1	2	0	1	1	1	2	0	1	1	3	1
SAMN07298657	0	2	1	3	2	1	0	1	1	1	1	1	2	3	0	1	2	2	1	1	3	1
SAMN07333425	0	1	0	2	1	1	1	0	0	0	0	1	1	2	0	0	1	1	0	0	2	0
SAMN07279063	0	1	0	2	1	1	1	0	0	0	0	1	1	2	0	0	1	1	0	0	2	0
SAMN07375710	0	1	0	2	1	1	1	0	0	0	0	1	1	2	0	0	1	1	0	0	2	0
SAMN07374523	0	1	0	2	1	1	1	0	0	0	0	1	1	2	0	0	1	1	0	0	2	0
SAMN07374530	1	2	0	3	2	2	1	1	1	1	1	0	2	3	0	1	2	2	1	1	3	0
SAMN07419575	1	0	1	1	0	0	2	1	1	1	1	2	0	1	1	1	2	0	1	1	3	1
SAMN07419610	1	1	2	2	1	1	3	2	2	2	2	3	1	0	2	2	3	1	2	2	4	2
SAMN07419201	0	1	0	2	1	1	0	0	0	0	0	0	1	2	0	0	1	1	0	0	2	0
SAMN07436201	0	1	0	2	1	1	1	0	0	0	0	1	1	2	0	0	1	1	0	0	2	0
SAMN07487381	1	2	1	3	2	2	2	1	1	1	1	2	2	3	1	1	0	2	1	1	3	1
SAMN07487429	1	0	1	1	0	0	2	1	1	1	1	2	0	1	1	1	2	0	1	1	3	1
SAMN07455809	0	1	0	2	1	1	1	0	0	0	0	1	1	2	0	0	1	1	0	0	2	0
SAMN07455808	0	1	0	2	1	1	1	0	0	0	0	1	1	2	0	0	1	1	0	0	2	0
SAMN07490566	2	3	2	4	3	3	3	2	2	2	2	3	3	4	2	2	3	3	2	2	0	1
U82	0	1	0	2	1	1	1	0	0	0	0	0	1	2	0	0	1	1	0	0	1	0



PFGE – not conclusive data  
 0 a 2 hq-SNPs between Mexican Papayas (MARADOL) and USA cases/papayas  
 Red GenomeTrakr en 2018 → NCBI



# Foodborne outbreak of *Salmonella* Infantis Nariño, 2018. Colombia

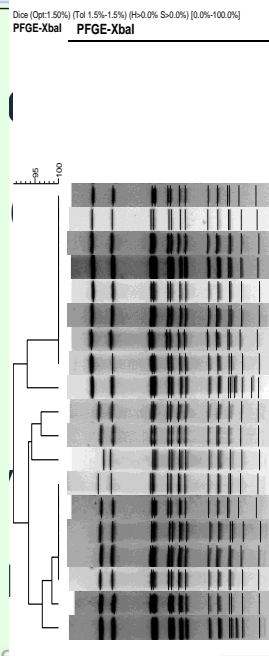
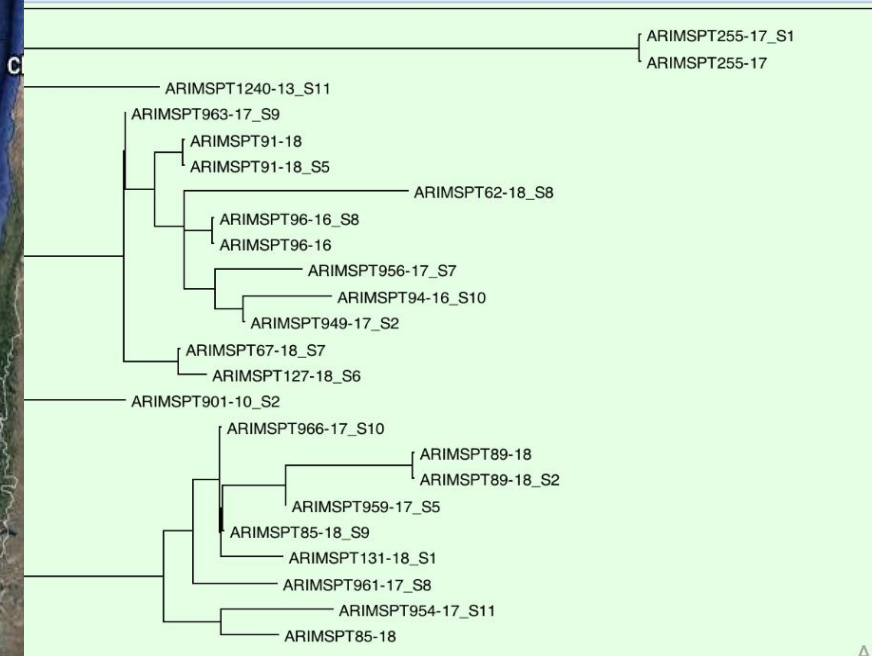


## WGS

- Serotype and AMR confirmation
- *bla*TEM-family, *sul2*, *floR*, *tetA*, *aac(6′)-Iaa* and *parC* and *gyrB*
- Plasmid families Inc1 and IncX4

Sources not detected

# Salmonella Paratyphi B Outbreak 2018-2019. Argentina



Strain ID	Location	Specimen Type	Date	Accession Number	Strain Name
● SPT131/18	Hospital Materno-Infantil Salta	Blood	2018-01-10	ARJXXX01.0004	Paratyphi B
○ SPT901/10	Hospital Piñero Capital Federal	vesical liq.	2010-03-31	ARJXXX01.0004	Paratyphi B
● SPT954/17	Hospital Materno-Infantil Salta	Blood	2017-12-04	ARJXXX01.0004	Paratyphi B
● SPT959/17	Hospital Materno-Infantil Salta	Líquido bili. MF del S.	2017-12-04	ARJXXX01.0004	Paratyphi B
★ SPT96/16	Hospital Materno-Infantil Salta	Blood	Enero 2016	ARJXXX01.0004	Paratyphi B
● SPT961/17	Hospital San Bernardo Salta	Blood	Dic. 2017	ARJXXX01.0004	Paratyphi B
● SPT85/18	Hospital San Bernardo Salta	Blood	Enero 2018	ARJXXX01.0004	Paratyphi B var. L(-)
● SPT89/18	Hospital San Bernardo Salta	Blood	Enero 2018	ARJXXX01.0004	Paratyphi B
● SPT966/17	Hospital San Bernardo Salta	Blood	Dic. 2017	ARJXXX01.0001	Paratyphi B
★ SPT67/18	Hospital Materno-Infantil Salta	Urine	2017-12-24	ARJXXX01.0008	Paratyphi B
○ SPT255/17	Hospital Fernández Capital Federal	Blood	Marzo 2017	ARJXXX01.0003	Paratyphi B var. L(-)
★ SPT94/16	Hospital Materno-Infantil Salta	Blood	Enero 2016	ARJXXX01.0005	Paratyphi B var. L(-)
○ SPT1240/13	Hospital Piñero Capital Federal	Partes blan.	2013-08-30	ARJXXX01.0006	Paratyphi B
★ SPT127/18	Hospital Materno-Infantil Salta	Blood	2018-01-12	ARJXXX01.0006	Paratyphi B
★ SPT949/17	Hospital Materno-Infantil Salta	Blood	2017-11-23	ARJXXX01.0006	Paratyphi B
★ SPT963/17	Hospital San Bernardo Salta	Blood	Dic. 2017	ARJXXX01.0006	Paratyphi B
● SPT91/18	Hospital San Bernardo Salta	Blood	Enero 2018	ARJXXX01.0006	Paratyphi B
★ SPT62/18	Hospital Materno-Infantil Salta	Blood	2017-12-20	ARJXXX01.0006	Paratyphi B
★ SPT956/17	Hospital Materno-Infantil Salta	Stool MF del S.	2017-11-23	ARJXXX01.0007	Paratyphi B

**WGS** not detected.

**PFGE**



# Shigella sonnei – Outbreaks 2010-2011 Argentina



# WGS

- Species confirmation
- Virulence genes detection
- AMR genes detection
  
- Phylogenetic relationship
  - Genetic similarity
  - High resolution

# USES

- Diagnostic (genus /species)
- Virulence Genes profile
- Resistance Genes profile
  
- Outbreak /cluster
  
- Foodborne cases
  
- Food safety
  
- Population studies

# PATHOGENS

*Chronobacter sakazakii*  
*E. coli* / *S. sonnei* / *S. Infantis* /  
*S. Paratyphi B* / *S. Kiambu*

*S. Infantis* / *S. Paratyphi B* /  
*S. sonnei* / *E. coli*

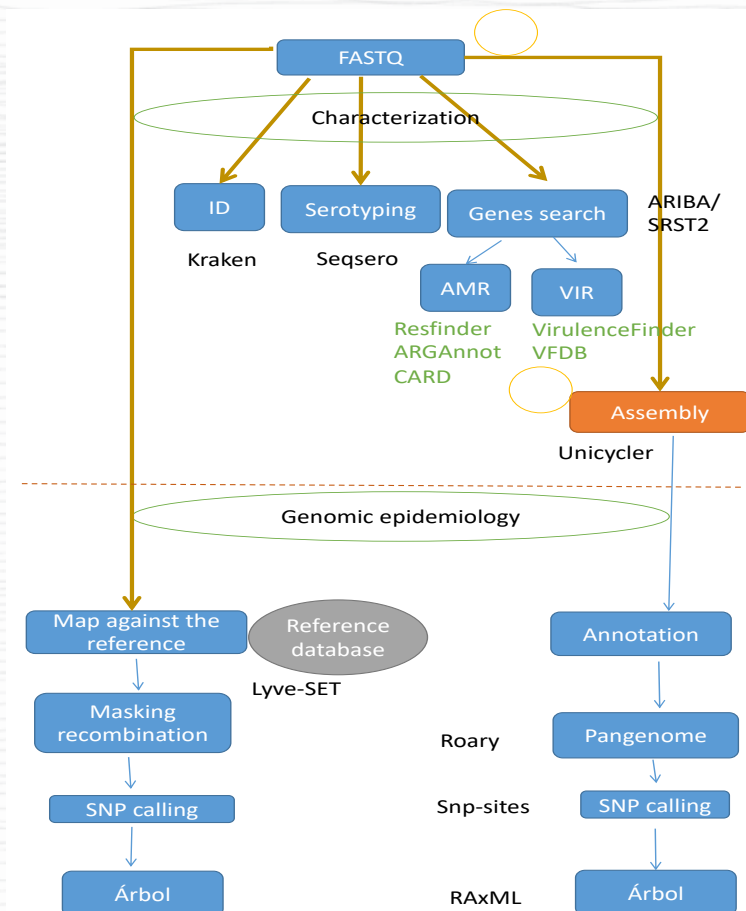
*Chronobacter sakazakii* / *E. coli*

*S. Kiambu*

*E. coli* / *S. Paratyphi B*

# REGIONAL WORKFLOW

## Diagnosis and outbreak investigation



# WGS for Public Health in LA

WGS for Public Health



National & International collaboration

WSG  
specific events/projects

✓ Visits

✓ Training on job

✓ Meetings

✓ Courses

✓ Technical Support

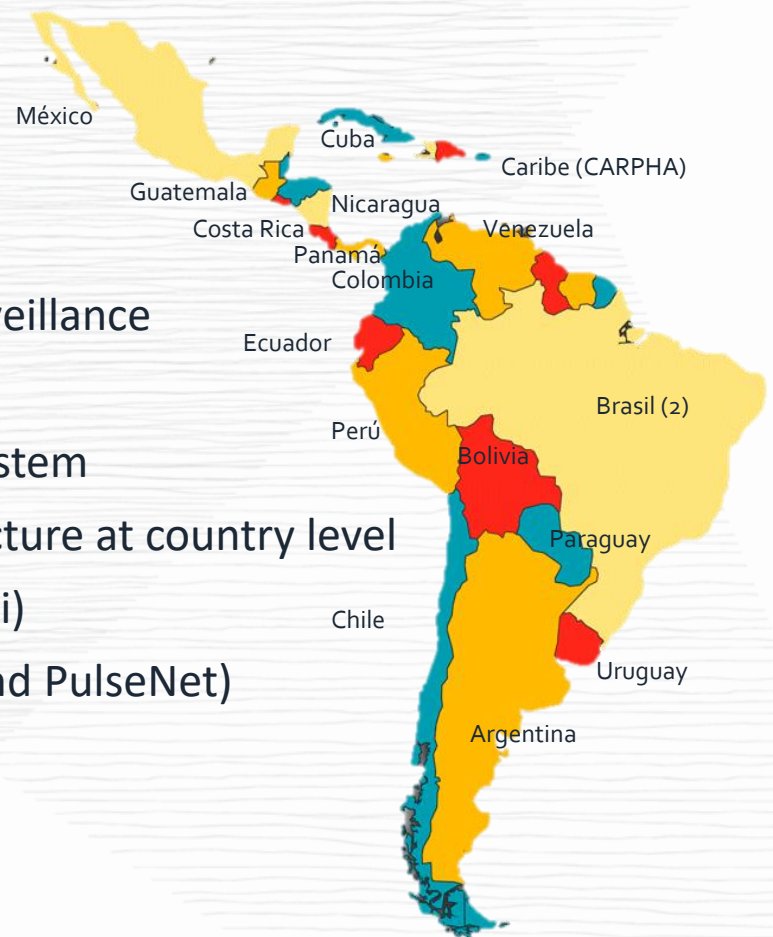
✓ Financial Support

✓ Informatic / Bioinformatic support

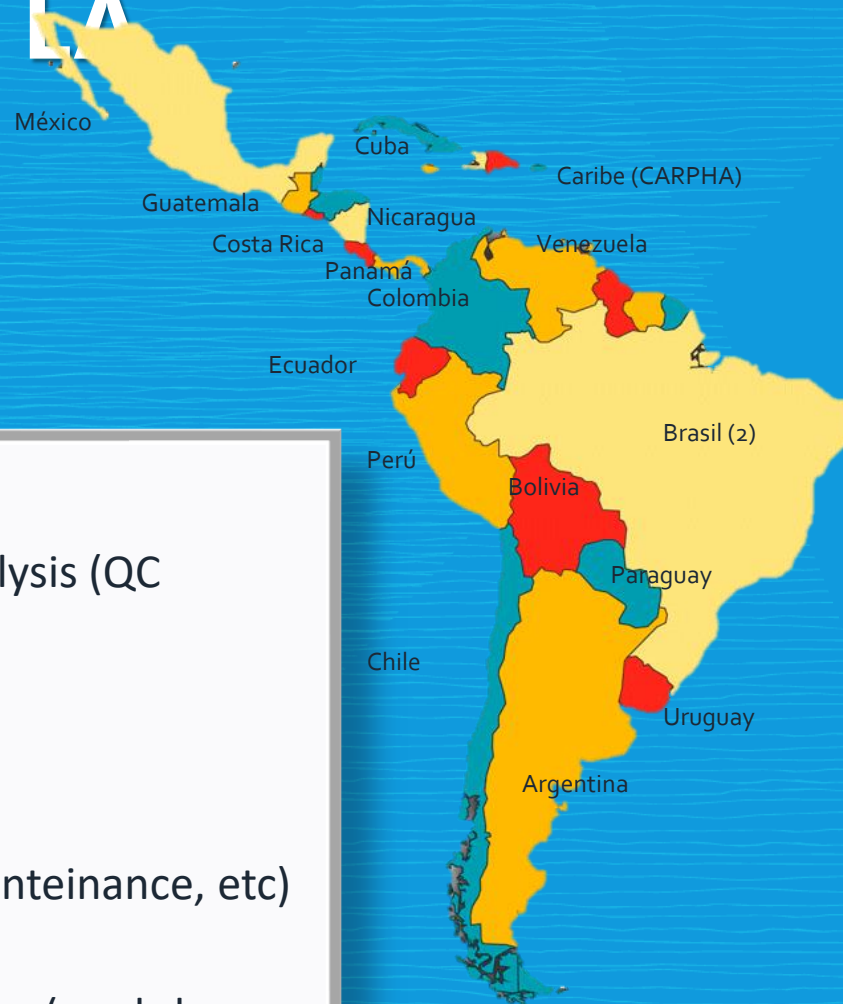


## Moving Forward

- Raise awareness at higher levels
- Acquire resources to fund its implementation
- Prove that WGS works for national real-time surveillance
- Identify/develop, test, and validate the pipelines
- Develop a QA/certification/proficiency testing system
- Insure availability of sequencers and IT-infrastructure at country level
- Train implementers and future users (lab AND epi)
- Implementing all network laboratories (RELDA and PulseNet)



# WGS Future Steps - LA



- ➡ Regional workflow
- ➡ Standardized protocols for Lab and analysis (QC metrics)
- ➡ Regional SERVER
- ➡ Regional Database
- ➡ WGS Certification/Proficiency Test
- ➡ Sustainability (reagents, installation maintenance, etc)
- ➡ Sharing of best practices
- ➡ Training/assistance to different countries (workshops, visits, virtual conferences)


- Training courses for lab & epi
- Lab & epi still need more training
- Explain everything (again) to managers
- Learn bioinformatics
- Figure out how to stop crashing the network
- Why aren't all these clusters being investigated?
- Revise all protocols, validate, and accredit
- How do I put the results into excel
- Write (another) grant proposal to fund this
- Get lab and epi to talk to each other
- Really must learn bioinformatics
- Reduce turnaround time due to batching
- Convince everyone to make the data public
- Get all metadata into single ontology (from multiple surveillance systems from different decades designed for different purposes)
- Design and administer national quality control program
- Ask for more money (again)
- Breathe

Nadon, PHAC




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**RELAVRA 2019. Genomic Epidemiology in the  
Region of the Americas Genomic Epidemiology**

**THANK  
YOU!**