GENOMIC SURVEILLANCE OF FOODBORNE PATHOGENS: CHANGING THE PARADIGM AFTER COVID-19

Unidad Operativa
Centro Nacional de Genómica
y Bioinformática

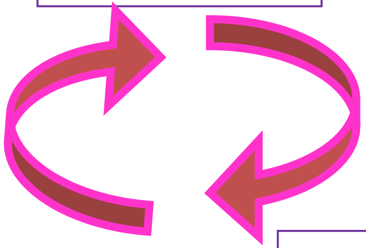
JOSEFINA CAMPOS

ANLIS
MALBRÁN
ADMINISTRACIÓN NACIONAL DE LABORATORIOS
E INSTITUTOS DE SALUD "DR. CARLOS G. MALBRÁN"

NATIONAL REFERENCE LABORATORY FOR MOH

GENERATE EVIDENCE FOR PUBLIC HEALTH MEASURES

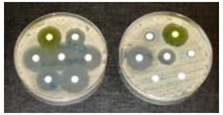
ANLIS “Dr. Carlos G. Malbrán”



Epi Data

SNSV

Lab data

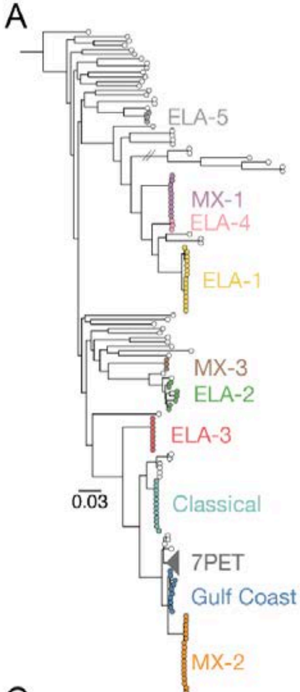


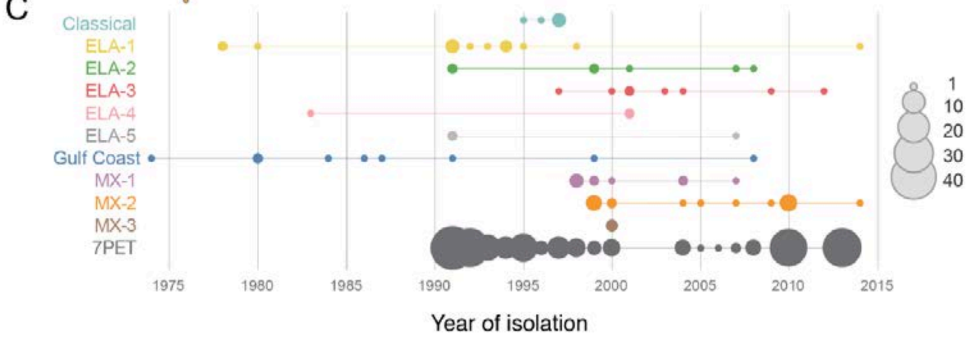
Data analysis and interpretation

REPORTS with interpreted data

PUBLIC HEALTH ACTIONS

Alerts, POLICIES CHANGE





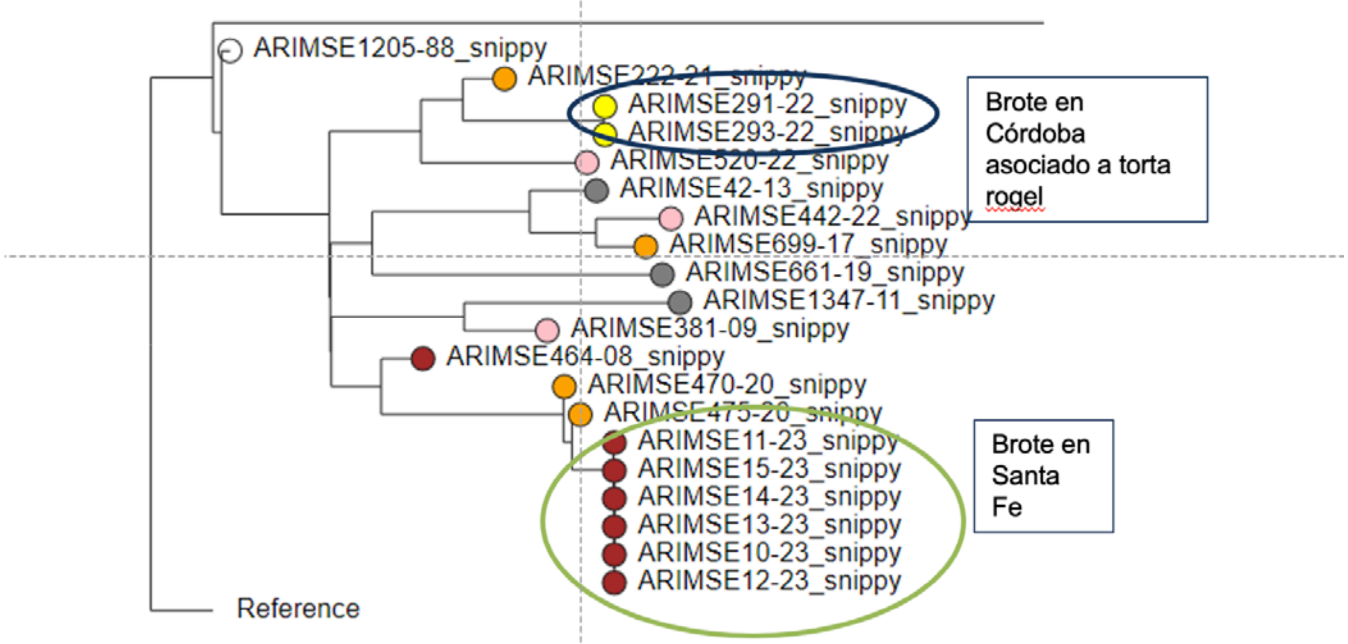
RESEARCH

CHOLERA

Integrated view of *Vibrio cholerae* in the Americas

Salmonella enterica ser. Enteritidis

Fine tuning for outbreak confirmation



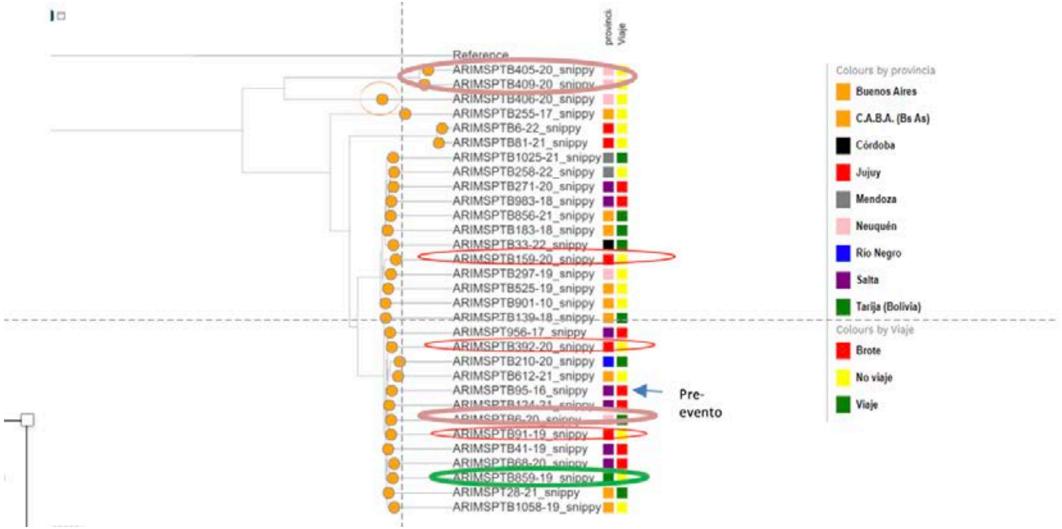
Brote en Córdoba asociado a torta rogel

Brote en Santa Fe

Phylogenetic tree of hqSNPs using Snippy and Salmonella_enterica_subsp_enterica_serovar_Enteritidis_str_P125109 as reference by Miriam Moroni

Salmonella enterica ser. Paratyphi B

Study of endemic diseases trough time (2017-2022) and it's travel associated cases in different provinces



Philogenetic tree of hqSNPs using Snippy and by Miriam Moroni

2020

COVID-19 has opened up new possibilities

Alberto Fernández visitó el Malbrán y felicitó a sus profesionales: "Están haciendo historia"

El Presidente ponderó a los científicos que lograron secuenciar de forma exitosa el genoma en pacientes argentinos y explicó a Página12 por qué los hallazgos son importantes para el desarrollo de la vacuna y para determinar por qué algunos virus son más feroces que otros.

Por Romina Calderaro

Científicos argentinos lograron secuenciar el genoma completo del coronavirus

Por Perfil | 8 abril, 2020 | 6:18 pm | Lectura: 3 minutos

OUTCOME

NEW SEQUENCING FACILITY

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- Scale from 900 genomes/week to 6000 genomes/week
- New sequencing platform: NovaSeq 6000, 2 Miseq (Illumina), 4 MinIon (Nanopore)
- Robotic Plataform to scale up sequencing capacity National Level
- New IT infrastructure

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FEDERAL GENOMIC NETWORK

Aim:

To generate sequencing capacity across the 24 public health jurisdictions in the country, using various available technologies to respond to the COVID-19 pandemic.

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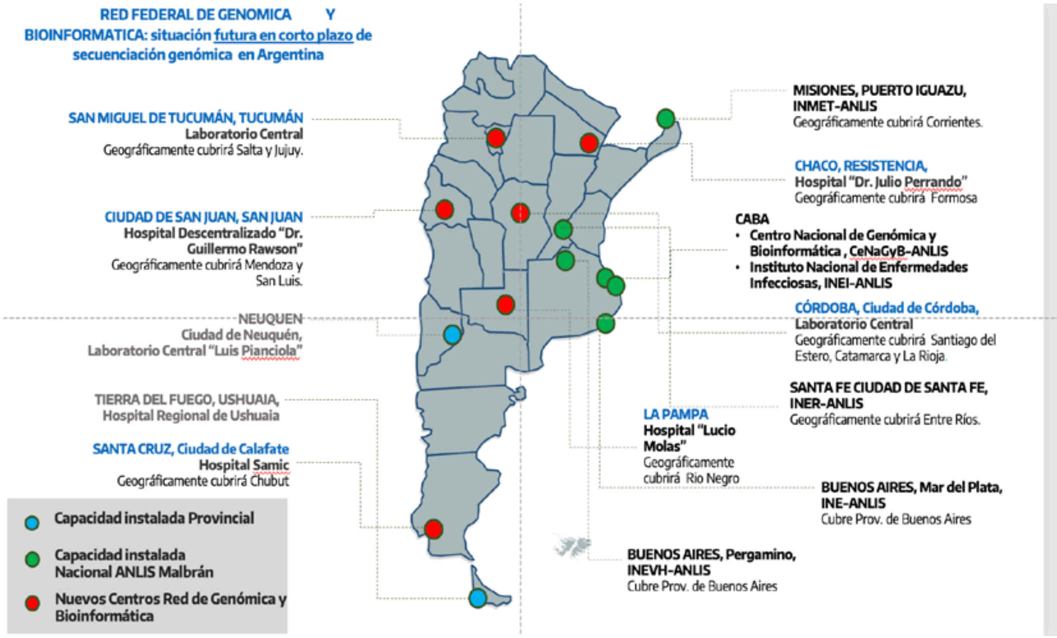
- All 24 jurisdictions have sequencing capacity at the Public Health labs (MinIon-Nanopore)
- 8 new public health laboratories have Illumina sequencing capacity (MiSeq plus all accesory equipment). Total:12
- National standarized lab and bionformatics protocols and dataa sharing (working together with WTSI) and data visualization reports for COVID-19



RED FEDERAL DE GENOMICA Y BIOINFORMATICA: situación futura en corto plazo de secuenciación genómica en Argentina

SAN MIGUEL DE TUCUMÁN, TUCUMÁN
Laboratorio Central
Geográficamente cubrirá Salta y Jujuy.

CIUDAD DE SAN JUAN, SAN JUAN
Hospital Descentralizado "Dr. Guillermo Rawson"
Geográficamente cubrirá Mendoza y San Luis.

NEUQUEN
Ciudad de Neuquén,
Laboratorio Central "Luis Pianciola"

TIERRA DEL FUEGO, USHUAIA,
Hospital Regional de Ushuaia

SANTA CRUZ, Ciudad de Calafate
Hospital Samic
Geográficamente cubrirá Chubut

- 🔵 Capacidad instalada Provincial
- 🟢 Capacidad instalada Nacional ANLIS Malbrán
- 🔴 Nuevos Centros Red de Genómica y Bioinformática

MISIONES, PUERTO IGUAZU,
INMET-ANLIS
Geográficamente cubrirá Corrientes.

CHACO, RESISTENCIA,
Hospital "Dr. Julio Perrando"
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- **Instituto Nacional de Enfermedades Infecciosas, INEI-ANLIS**

CÓRDOBA, Ciudad de Córdoba,
Laboratorio Central
Geográficamente cubrirá Santiago del Estero, Catamarca y La Rioja.

SANTA FE CIUDAD DE SANTA FE,
INER-ANLIS
Geográficamente cubrirá Entre Ríos.

LA PAMPA
Hospital "Lucio Molas"
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BUENOS AIRES, Mar del Plata,
INE-ANLIS
Cubre Prov. de Buenos Aires

BUENOS AIRES, Pergamino,
INEVH-ANLIS
Cubre Prov. de Buenos Aires

A new pathogen genomic strategy has been developed to prepare for pandemic and epidemic response to pathogens with a federal character TO address clinical needs considering the provinces capacity, the large-scale sequencing center and the established laboratory surveillance

FIRST

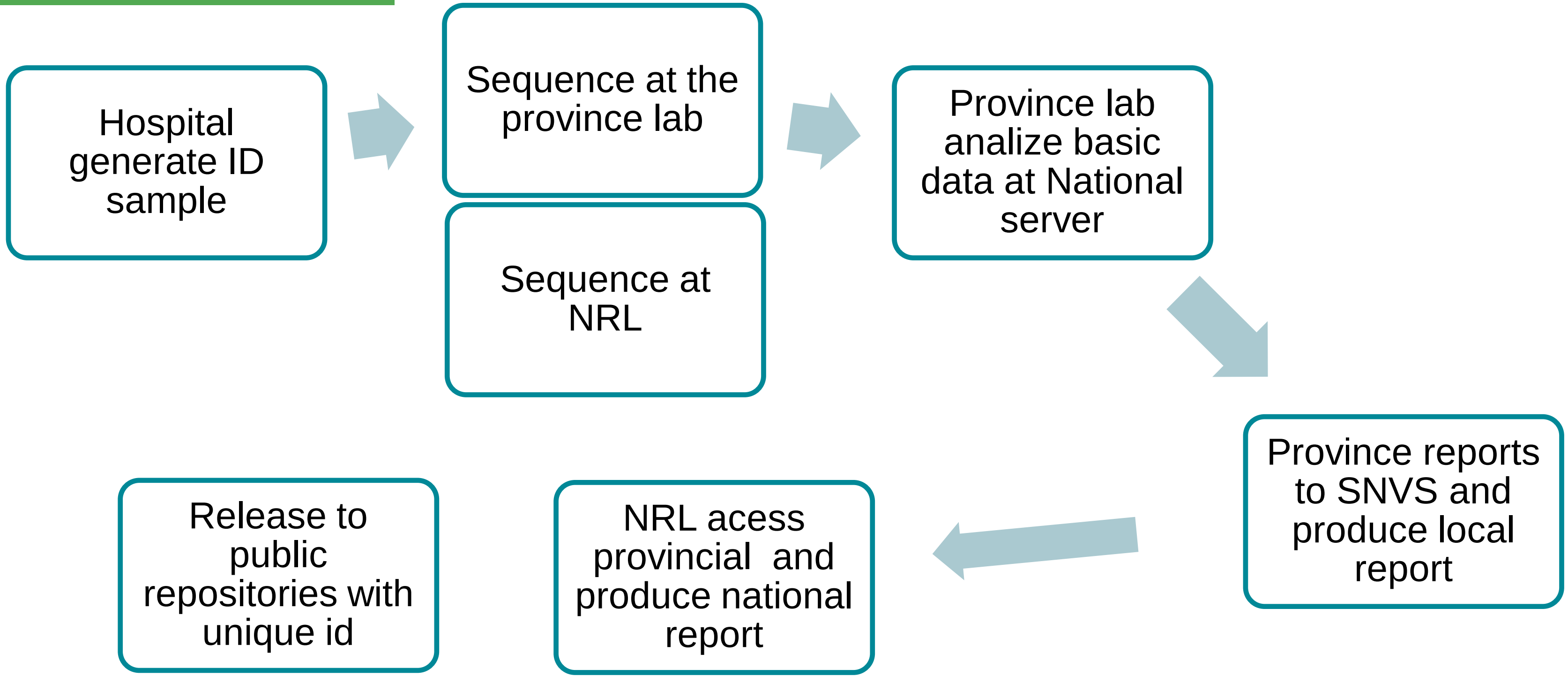
Pathogens:

- Virus with high prevalence: Influenza, RSV, Norovirus, Rotavirus, Dengue, Chikungunya
- Bacteria: the group with longer experience and larger datasets: PulseNet

Salmonella and *E. coli*

ARCHITECTURE

New model for data sharing



Hospital generate ID sample

Sequence at the province lab

Sequence at NRL

Province lab analize basic data at National server

Province reports to SNVS and produce local report

NRL acess provincial and produce national report

Release to public repositories with unique id

QA PROGRAMME

PulseNet flavour:

- Certification per pathogen for wet lab and data analysis
- Annual PT
- Dataset prepared with the NRL, only genetic material will be sent.
- Linked to the microbiology QA

SUSTAINABILITY

- Central purchases process to keep lower price
- Centralized strategy for large scale sequences for emergencies: Legionella metagenomics, Human genetics
- Using sequencing investment for service delivery, strengthening relationships with non-traditional public health partners across academic and commercial sectors will be crucial

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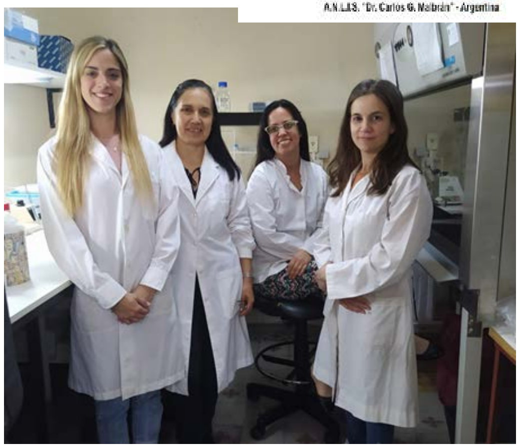

THANKS

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Laboratorios de la Red Nacional de Diarreas (RND)
Servicio Enterobacterias, Bacteriología INEI- “Dr Carlos. G. Malbrán”