TERAMO

ISTITUTO
ZOOPROFILATTICO
SPERIMENTALE
DELL'ABRUZZO
E DEL MOLISE
"G. CAPORALE"

OH and Funding-Italy

Alessio Lorusso, Isabella Monne

IZS TERAMO

ISTITUTO ZOOPROFILATTICO SPERIMENTALE
DELL'ABRUZZO
E DEL MOLISE
"G. CAPORALE"

National and International Ref Labs

Veterinary Public Health in Italy

- Veterinary services fall under the Ministry of Health.
  - Located within the One Health Department.
  - Integration of animal health, food safety, and public health.

- Department for One Health.
  - **DGSAF:** national plans, surveillance, regulations.
  - Coordination with EU/WOAH/ECDC.

IZS Network

- 11 Istituti Zooprofilattici Sperimentali.
  - Diagnostics, epidemiology, research.
  - National & international reference labs.

Regional Level

- Regions manage veterinary systems.
  - Implement national plans.
  - Coordinate ASL activities and emergencies.

One Health Implementation

- Strong structure
  - Veterinary sector leads zoonoses & arbovirus surveillance.
  - Further integration with human prevention desirable.

Ministero della Salute

Direzione Generale della Prevenzione Sanitaria

Piano Nazionale della Prevenzione 2020-2025

1. Prevention of chronic diseases

Promotion of healthy lifestyles, physical activity, proper nutrition, and reduction of smoking, alcohol consumption, overweight and obesity.

2. Vaccination prevention

Improving vaccination coverage, recovering unvaccinated individuals, and strengthening immunisation programs for adults and vulnerable populations.

3. Environmental prevention and safety in living and working environments

Protection of air and water quality, monitoring of environmental and climate-related risks, food safety, and workplace health and safety.

4. Prevention of infectious diseases and preparedness for health emergencies

Strengthening epidemiological surveillance, rapid response to outbreaks, enhancing laboratory capacity, and implementing a One Health approach to emerging threats.

National Arbovirus Surveillance Plan

- Italy’s best operational One Health example.
  - IZS network leads surveillance in wild birds and mosquito vectors.
  - Animal/vector detection triggers public health actions (blood donor restrictions, enhanced surveillance).
  - Demonstrates strong integration between veterinary and human health sectors.

Genomic Surveillance & Viral Evolution

- Veterinary laboratories perform extensive genomic sequencing of arboviruses.
  - Genomic data allow early detection of variants and reassortant strains.
  - Supports risk assessment for human and animal health.
  - A cornerstone of Italy’s One Health surveillance capacity.

From Structure to Practice

- Italy has a robust institutional foundation for One Health.
  - Practical implementation can still be improved, especially in cross-sector coordination.
  - Greater synergy between veterinary services, public health, and prevention units would increase effectiveness.
  - Future adjustments could bring Italy closer to a fully operational One Health system.

One Health funding from the IZS Network

- Most One Health funding across the IZS Network originate from IZS-driven research and field activities.
- Key funded initiatives of IZSAM include:
  - **MedNet 4 OH** – funded by AICS, supporting Tunisian hospital authorities to strengthen infectious disease diagnostics.
  - **PROVNA/PROVBA** – funded by WOAH, improving surveillance and laboratory capacity for priority pathogens.
  - **ECOSURV** – funded by EFSA, enhancing integrated surveillance and risk assessment frameworks.
  - **INF-ACT-** funded by Italy’s National Recovery and Resilience Plan (NextGenEU)

INF-ACT

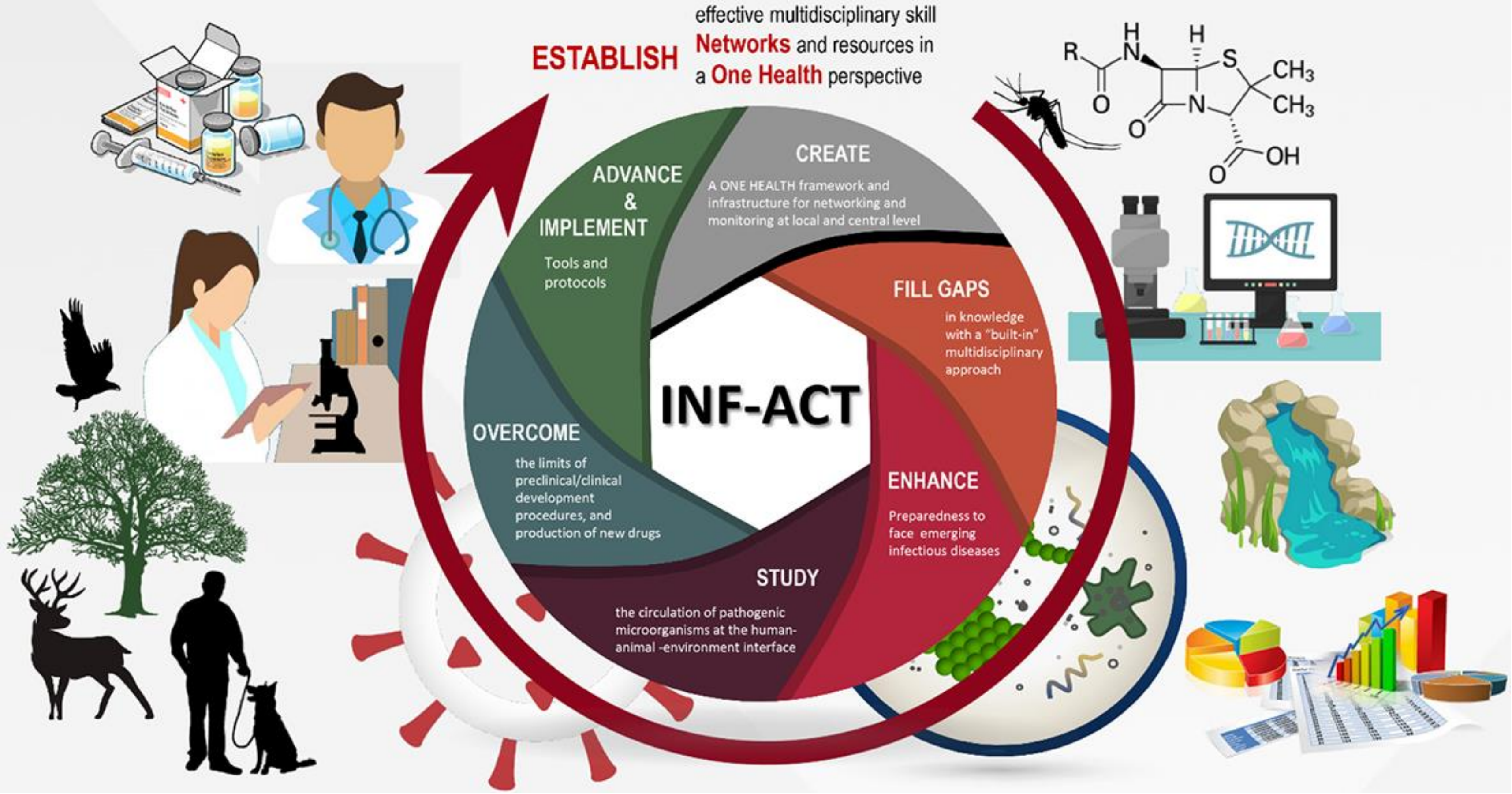
EPI-MOD

Finanziato dall'Unione europea
NextGenerationEU

Ministero dell'Università e della Ricerca

Italiadomani
PIANO NAZIONALE DI RIPRESA E RESILIENZA

One Health basic and translational actions addressing unmet needs on emerging infectious diseases



ESTABLISH effective multidisciplinary skill **Networks** and resources in a **One Health** perspective

CREATE A ONE HEALTH framework and infrastructure for networking and monitoring at local and central level

FILL GAPS in knowledge with a "built-in" multidisciplinary approach

ENHANCE Preparedness to face emerging infectious diseases

STUDY the circulation of pathogenic microorganisms at the human-animal -environment interface

OVERCOME the limits of preclinical/clinical development procedures, and production of new drugs

ADVANCE & IMPLEMENT Tools and protocols

INF-ACT
EPI-MOD

UNIVERSITÀ DI PAVIA
UNIVERSITÀ DEGLI STUDI DI PADOVA
Università di Catania
ISTITUTO SUPERIORE DI SANITÀ
Consiglio Nazionale delle Ricerche
UNIVERSITÀ DEGLI STUDI DI MILANO

SAPIENZA UNIVERSITÀ DI ROMA
UNIVERSITÀ DEGLI STUDI DI NAPOLI FEDERICO II
ALMA MATER STUDIORUM UNIVERSITÀ DI BOLOGNA
UNIVERSITÀ DI SIENA 1240
UNIVERSITÀ DEGLI STUDI DI BARI ALDO MORO

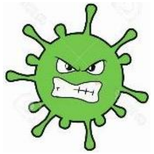
UNICA UNIVERSITÀ DEGLI STUDI DI CAGLIARI
UNIVERSITÀ DI TORINO
UNIVERSITÀ CATTOLICA del Sacro Cuore
HU HUMANITAS UNIVERSITY
UniSR Università Vita-Salute San Raffaele
IZS

FONDAZIONE BRUNO KESSLER
INGM ISTITUTO NAZIONALE GENETICA MOLECOLARE "Romeo ed Enrica Invernizzi"
FONDAZIONE POLICLINICO UNIVERSITARIO CAMPUS BIO-MEDICO
ISTITUTO DI RICERCHE FARMACOLOGICHE MARIO NEGRI · IRCCS
Istituto Don Calabria IRCCS Ospedale Sacro Cuore Don Calabria Presidio Ospedaliero Accreditato - Regione Veneto

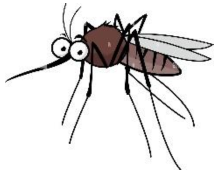
ISMETT Istituto di Ricovero e Cura a Carattere Scientifico
Bambino Gesù OSPEDALE PEDIATRICO
IRBM passionate about science

Malattie infettive emergenti nell’uomo con approccio *One Health*

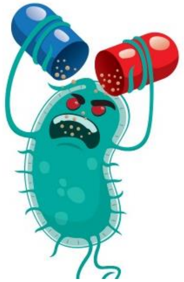
5 Nodi di Ricerca



3 verticali



1. Minacce virali emergenti e riemergenti (focus su virus respiratori e zoonosi)
2. Malattie trasmesse da vettori
3. Malattie causate da agenti patogeni resistenti ad antibiotici (focus sui meccanismi di AMR)



2 trasversali

1. Epidemiologia integrata in chiave One Health: monitoraggio e modelli matematici
2. Sviluppo nuove strategie terapeutiche

Scopo del Nodo 1

Creazione network nazionale per affrontare futuri virus emergenti o riemergenti dal punto di vista medico e biologico

4 WPs

1.1 nuovi approcci diagnostici per monitoraggio delle infezioni virali respiratorie

1.2 interazione virus-ospite e immunoediting

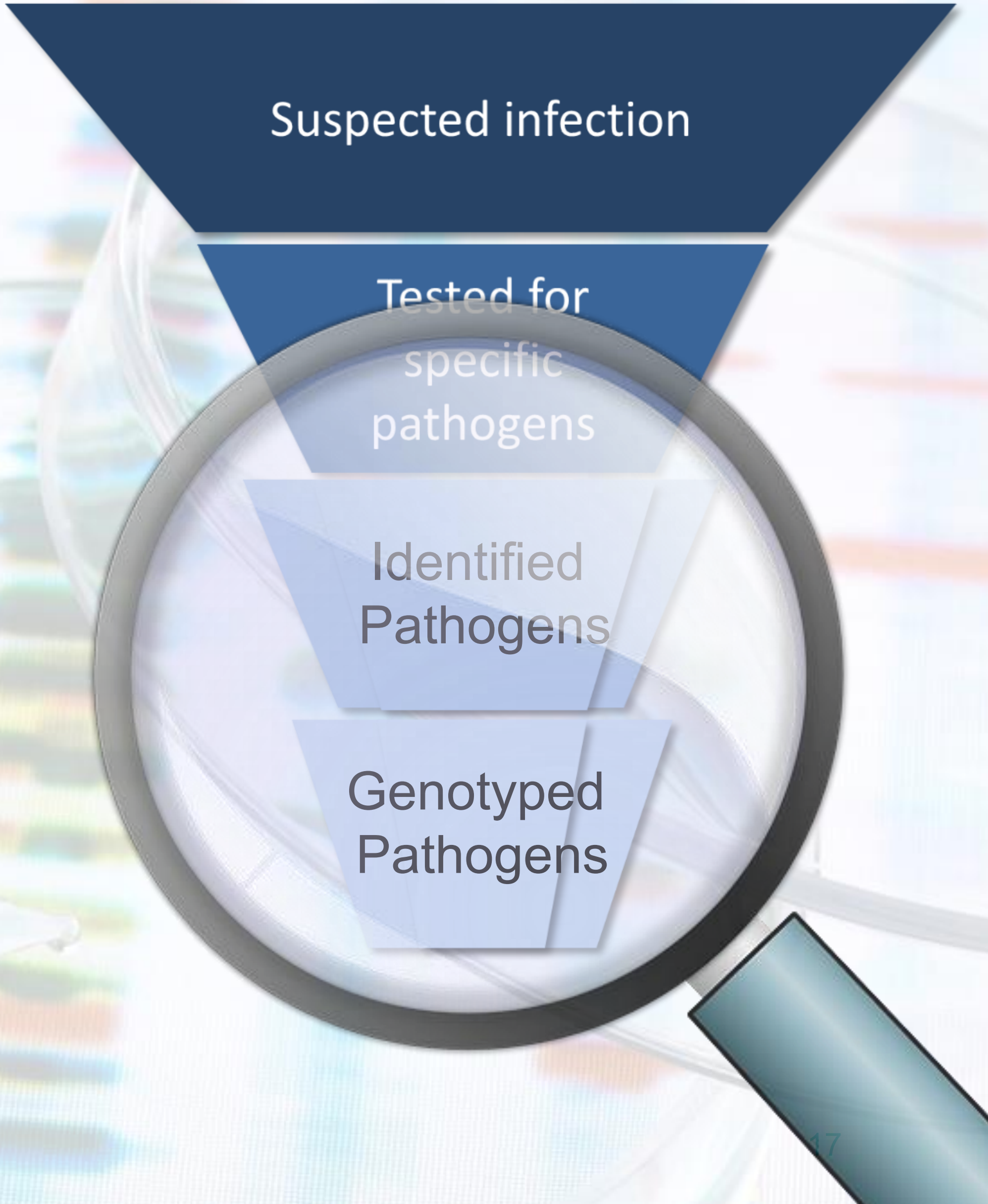
1.3 monitoraggio della comparsa di nuovi virus nell'interfaccia uomo-animale

1.4 manifestazioni cliniche di virus emergenti e riemergenti e sviluppo di vaccini e terapie

Why Genomic Capacity Matters

Addressing Diagnostic Gaps through Genomic Surveillance

- Significant number of infections remain unexplained due to limitations in diagnostics
- Standard PCRs focus on limited number of pathogens
- Lack of genotyping limits epidemiological understanding and diagnostic improvements



Suspected infection

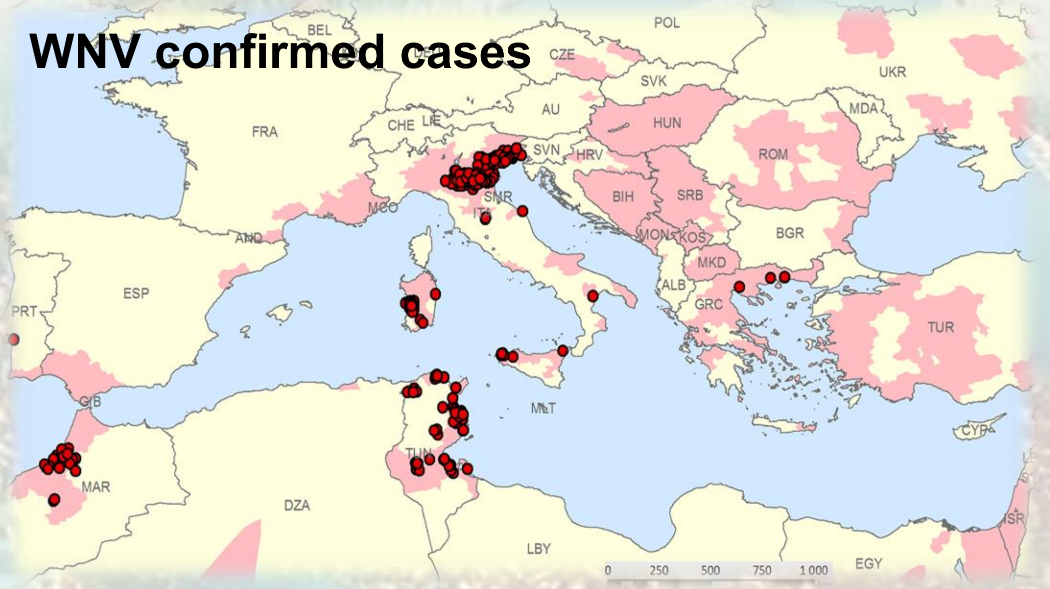
Tested for specific pathogens

Identified Pathogens

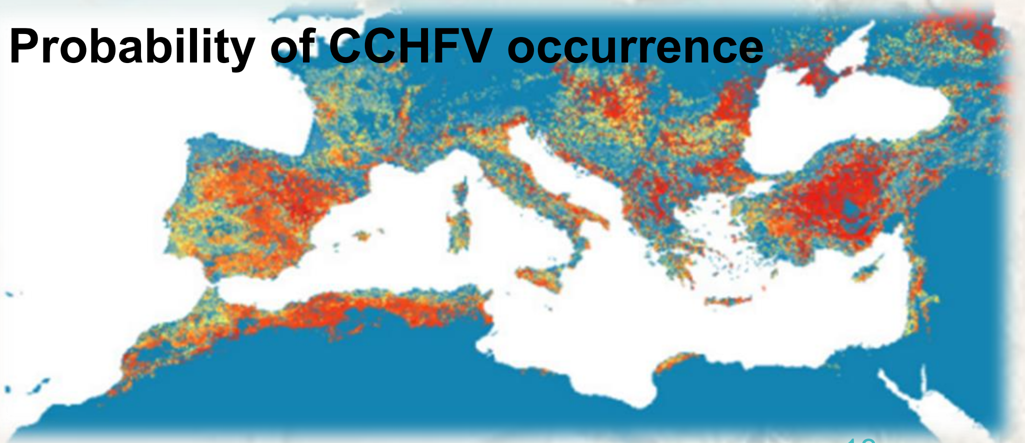
Genotyped Pathogens

One Health Challenge in the Mediterranean Region

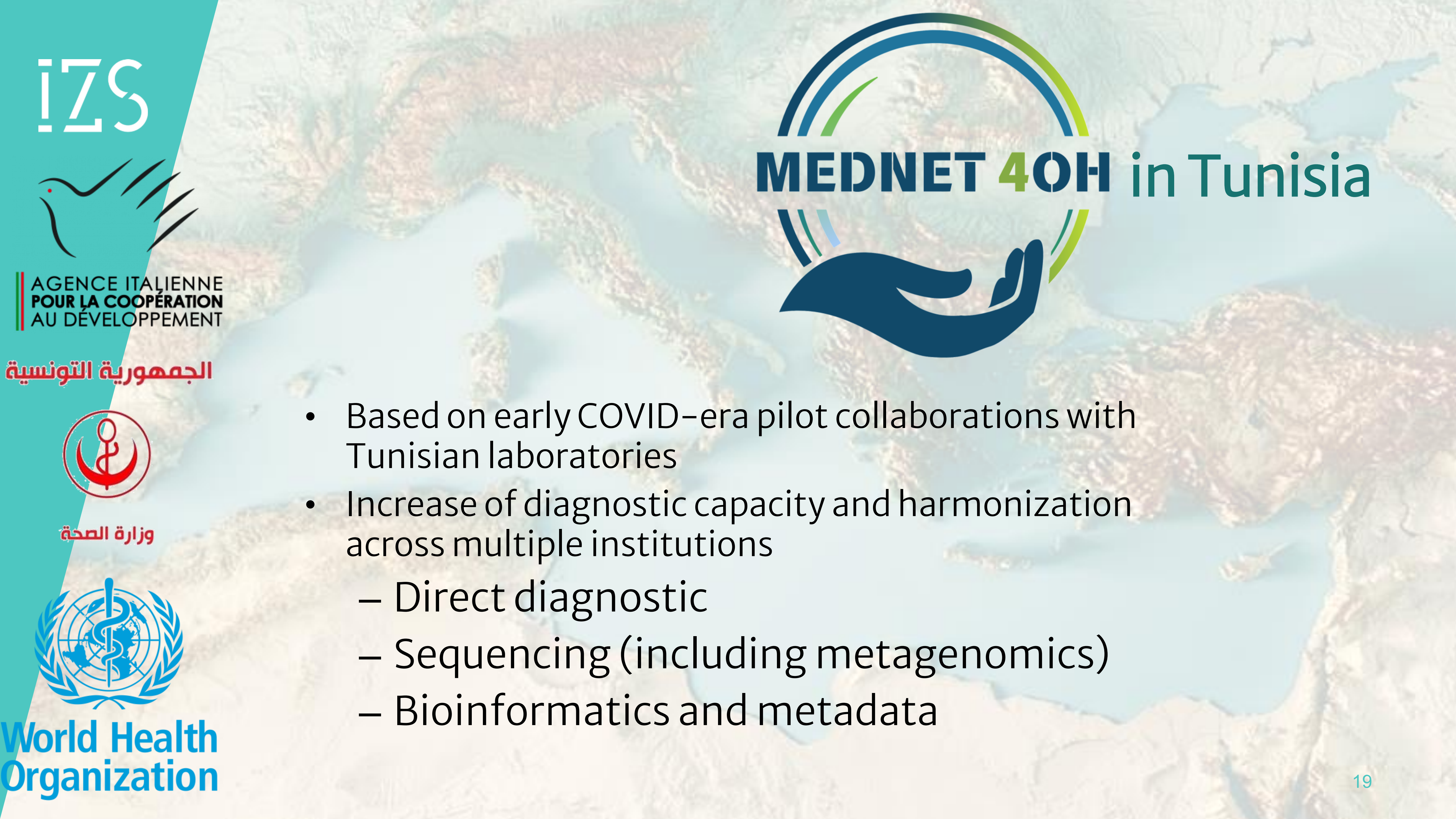
- Zoonotic threats are rising in frequency and complexity
- Migration, climate change, and trade impact cross-border disease dynamics
- Fragmented coordination between human, animal, and environmental sectors
- Surveillance systems often limited to a few known pathogens with underreporting of emerging diseases
- High density of domestic animals, wildlife interfaces, and intensive agriculture increase risk of spillover


WNV confirmed cases

Conte (2015) PLOS One


Probability of CCHFV occurrence

ECDC (2023) CCHFV technical report



MEDNET 4OH in Tunisia

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AU DÉVELOPPEMENT

الجمهورية التونسية

وزارة الصحة

World Health
Organization

- Based on early COVID-era pilot collaborations with Tunisian laboratories
- Increase of diagnostic capacity and harmonization across multiple institutions
  - Direct diagnostic
  - Sequencing (including metagenomics)
  - Bioinformatics and metadata

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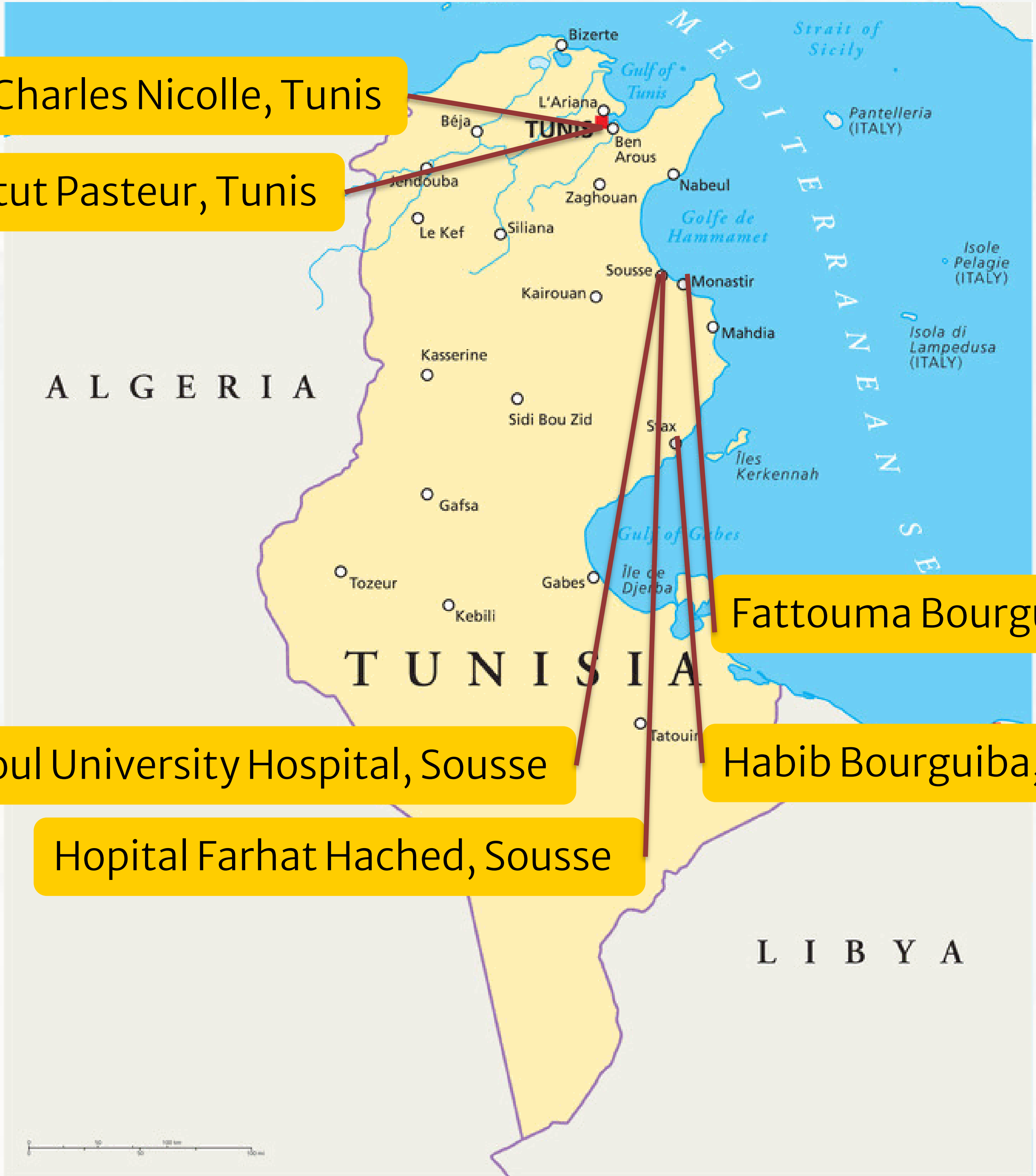
World Health
Organization

MEDNET 4OH



Hopital Charles Nicolle, Tunis

Institut Pasteur, Tunis

Fattouma Bourguiba University Hospital, Monastir

Sahloul University Hospital, Sousse

Habib Bourguiba, SfaxHospital

Hopital Farhat Hached, Sousse

What We Sequence and Why

Neurological Infections

(meningitis, encephalitis, and neuro-fever syndromes)

- West Nile virus
- *Haemophilus influenzae*
- Meningococcal Disease

Respiratory Infections

Supporting Severe Acute Respiratory Infection (SARI) and Influenza-like illness (ILI) surveillance

Integrating Sequencing in Key Surveillance Systems

Neurological Infections

Respiratory Infections

Metagenomics for undiagnosed cases

Targeted sequencing for pathogens of interest

Identifying new target to be included in routine surveillance

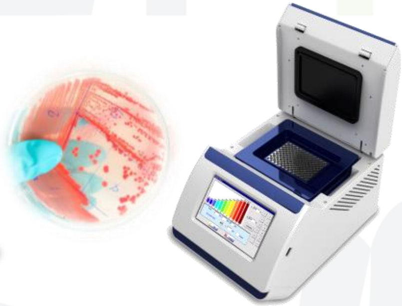
Optimizing current assays used in routine surveillance based on detected genomic changes

From Equipment to Expertise

Workflow Overview

- Providing harmonized direct diagnostic, NGS platform and consumables
- Training scientists on sample preparation, library building, bioinformatics

- Hopital Charles Nicolle, Tunis
- Institut Pasteur, Tunis
- Sahloul University Hospital, Sousse
- Hopital Farhat Hached, Sousse
- Hospital Habib Bourguiba, Sfax
- Fattouma Bourguiba University Hospital, Monastir
- Ministry of Health
- National Observatory of New and Emerging Diseases (ONMNE)



1. Standard Diagnostic

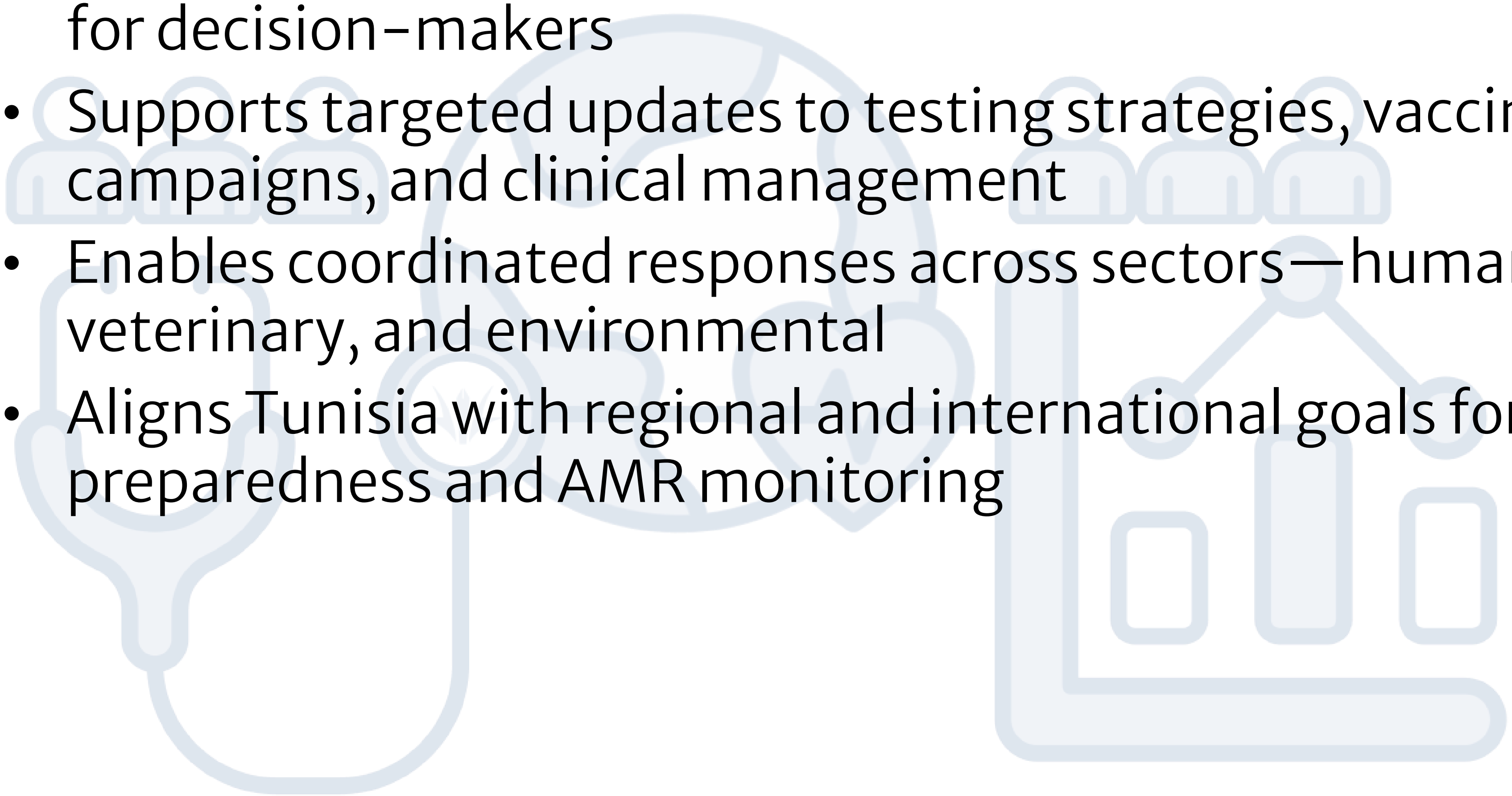
2. BioFire Filmarrays

3. AmpliSequ and Metagenomics

Piattaforma GenPat

Evidence for Better Public Health Decisions

Supporting Public Health Decision-Making



- Genomic surveillance provides real-time, locally relevant evidence for decision-makers
- Supports targeted updates to testing strategies, vaccination campaigns, and clinical management
- Enables coordinated responses across sectors—human health, veterinary, and environmental
- Aligns Tunisia with regional and international goals for epidemic preparedness and AMR monitoring

PROVNA project

World Organisation
for Animal Health
Founded as OIE

2022-2024

Main objective: ECOREGIONS IN NORTH AFRICA

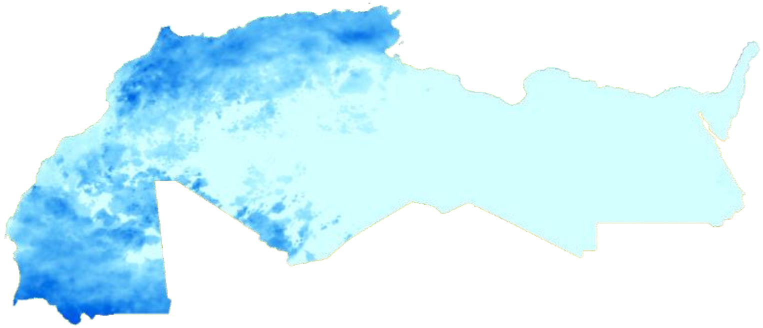
To define the “**ecoregions**” of the North African territory (Mauritania, Morocco, Algeria, Tunisia, Libya, and Egypt), each one **characterized by distinct environmental and climatic factors.**

Assumption: similar areas (in space and/or time) are subject to similar diseases (especially vector–borne diseases)

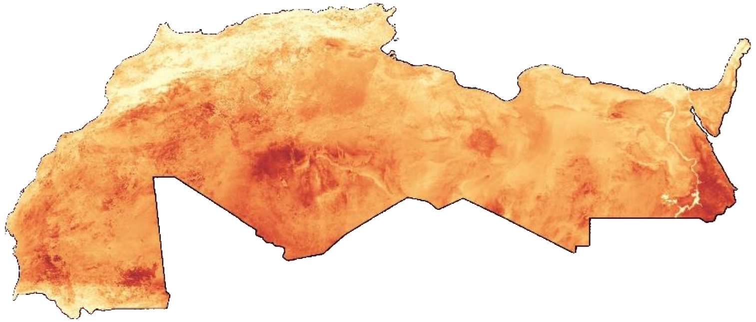
ECOREGIONALIZATION in North Africa

Selected Earth Observation data (2018-2022)

Rainfall



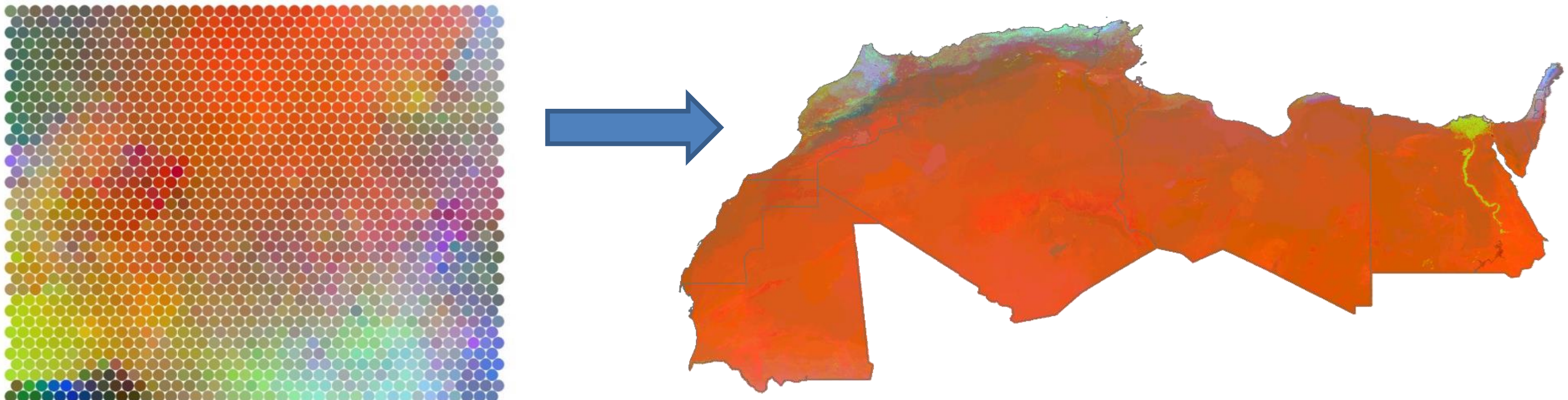
250 mt spatial resolution
16 days temporal resolution



- Land Surface Temperature Day and Night - LSTD and LSTN,
- Normalised Difference Vegetation Index - NDVI,
- Soil moisture - SM,
- Normalised Difference Water Index - NDWI,
- Rainfall - RF

- Collected
- Aggregated
- Standardised at a seasonal/year level

ECOREGIONALIZATION in North Africa



Emerging VBDs could benefit from the approach:

1. Definition of ecoregions
2. Mapping the climatic and environmental similarity
3. Inform in **which areas** a specific VBD can potentially spread/persist

→ How can we identify these areas?

NA phase 2

PROVNA2

World Organisation
for Animal Health
Founded as OIE

Given the work done, it is crucial to combine the decision-making tools based on eco-regionalization with data from in-field surveillance.

Ecoregions in NA

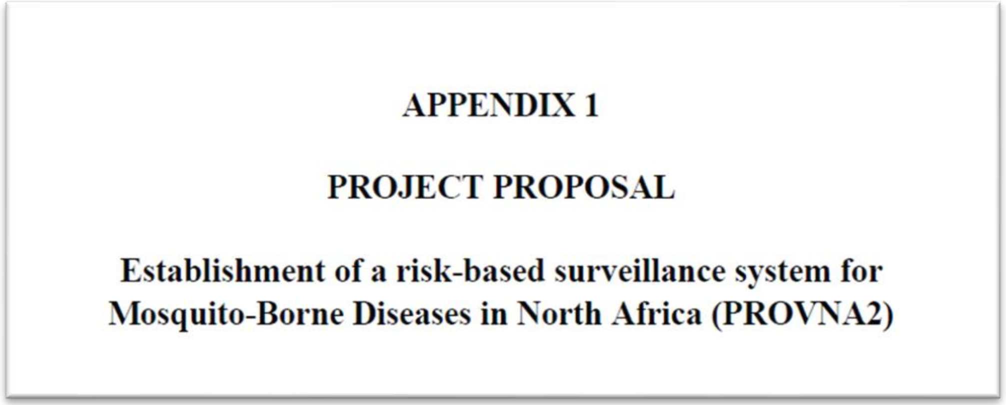
Suitability for RVF

→ Essential to strengthen the capacity of the National Veterinary Authorities to effectively prevent, predict, detect and respond to diseases – with the optimisation of the available resources.

PROVNA phase 2

Duration (months):

18 months



APPENDIX 1

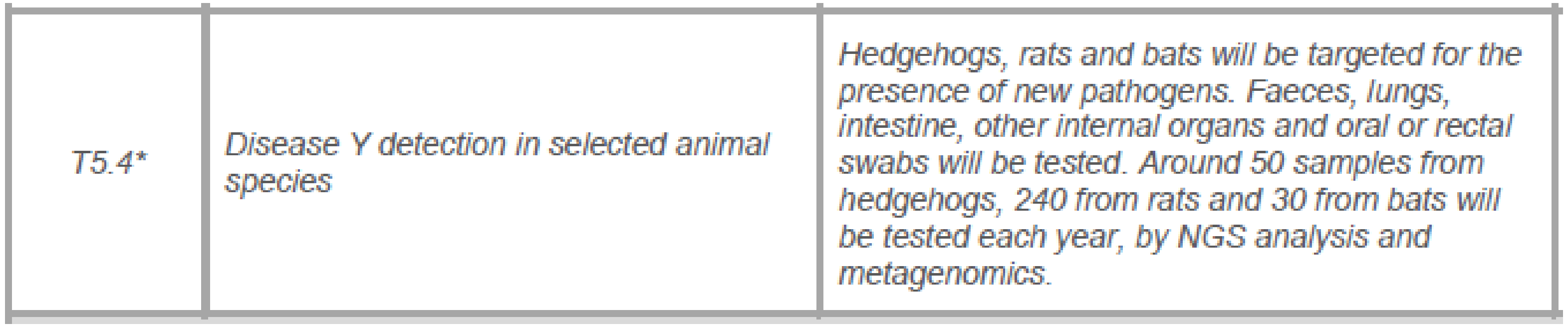
PROJECT PROPOSAL

Establishment of a risk-based surveillance system for
Mosquito-Borne Diseases in North Africa (PROVNA2)

General Objective

To establish a **risk-based surveillance system** across the six North African countries, using the eco-regionalization method, **to monitor the emergence and spread of key animal and zoonotic diseases** transmitted by mosquitoes.

Work Package 5: Surveillance activities on wild and synanthropic mammals



*T5.4**	*Disease Y detection in selected animal species*	*Hedgehogs, rats and bats will be targeted for the presence of new pathogens. Faeces, lungs, intestine, other internal organs and oral or rectal swabs will be tested. Around 50 samples from hedgehogs, 240 from rats and 30 from bats will be tested each year, by NGS analysis and metagenomics.*

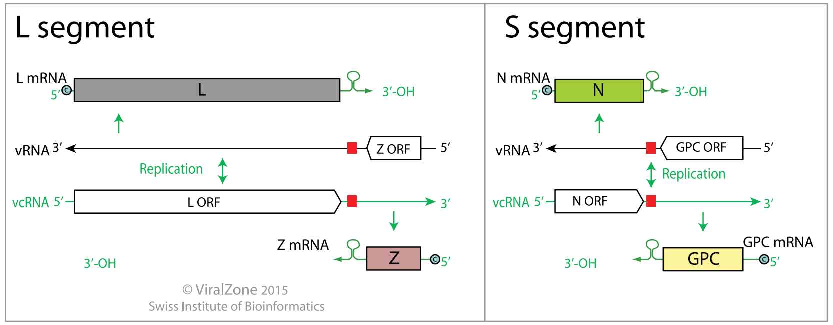
Disease Y

An unknown disease that can affect any animal species and may pose a threat to humans

Rodents

- Rodents have historically been associated with major pandemics, including the medieval plague (Yersinia pestis).
- Reservoirs of pathogens relevant to livestock, such as PEDV, Aujeszky’s disease virus, PCV2, and Influenza A virus.
- Involved in the spread of Leptospira, Salmonella, and antibiotic-resistant bacteria.
- Reservoirs of zoonotic agents, including members of the genus Hantavirus (HFRS, Hantavirus Pulmonary Syndrome).

Roditori



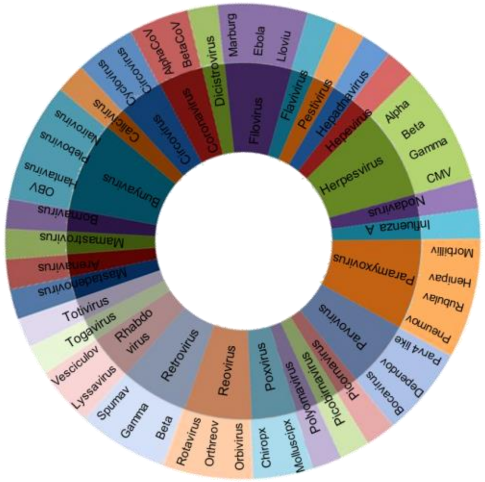
© ViralZone 2015
Swiss Institute of Bioinformatics

- **Reservoirs of zoonotic agents such as viruses belonging to the genus *Mammarenavirus***
- **Lassa virus**
  - **Disease:** Lassa fever
  - **Symptoms:** The infection may begin with fever and general malaise, followed by gastrointestinal symptoms and, in severe cases, shock and multi-organ failure.
  - **Transmission:** Believed to be transmitted to humans through contact with infected rodents.
- **Lymphocytic choriomeningitis virus (LCMV)**
  - **Disease:** Lymphocytic choriomeningitis
  - **Symptoms:** It may present as an influenza-like illness that can progress to meningitis or meningoencephalitis.
  - **Transmission:** Transmission to humans occurs through contact with secretions from infected rodents.

Pipistrelli

Istituto Zooprofilattico Sperimentale delle Venezie

- **Numerous new RNA viruses identified**, associated with diseases of potential pandemic concern.
- **Over 1,400 bat species** exist worldwide, hosting a vast and largely unexplored viral diversity with zoonotic potential.
- **Risk factors favoring the spread of new viruses:**
- Habitat loss
- Food scarcity
- Exposure to toxic substances
- **Zoonotic viruses detected in European bats:**
- *Lyssavirus*, *Filovirus*, *Coronavirus*, *Astrovirus*, *Orthoreovirus*



EcoSurv

Rentokil
100 ANNI

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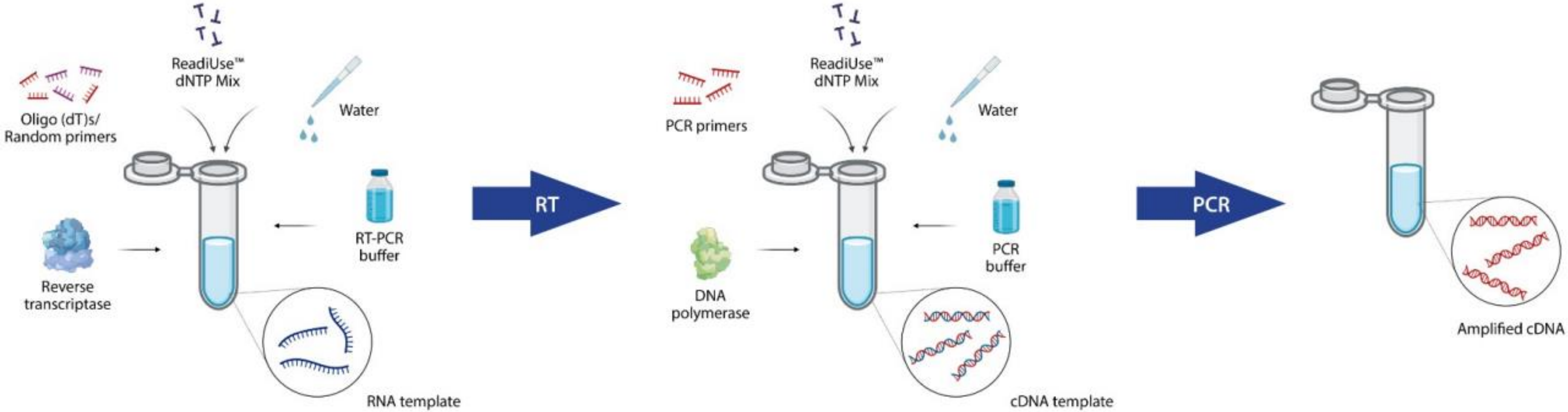
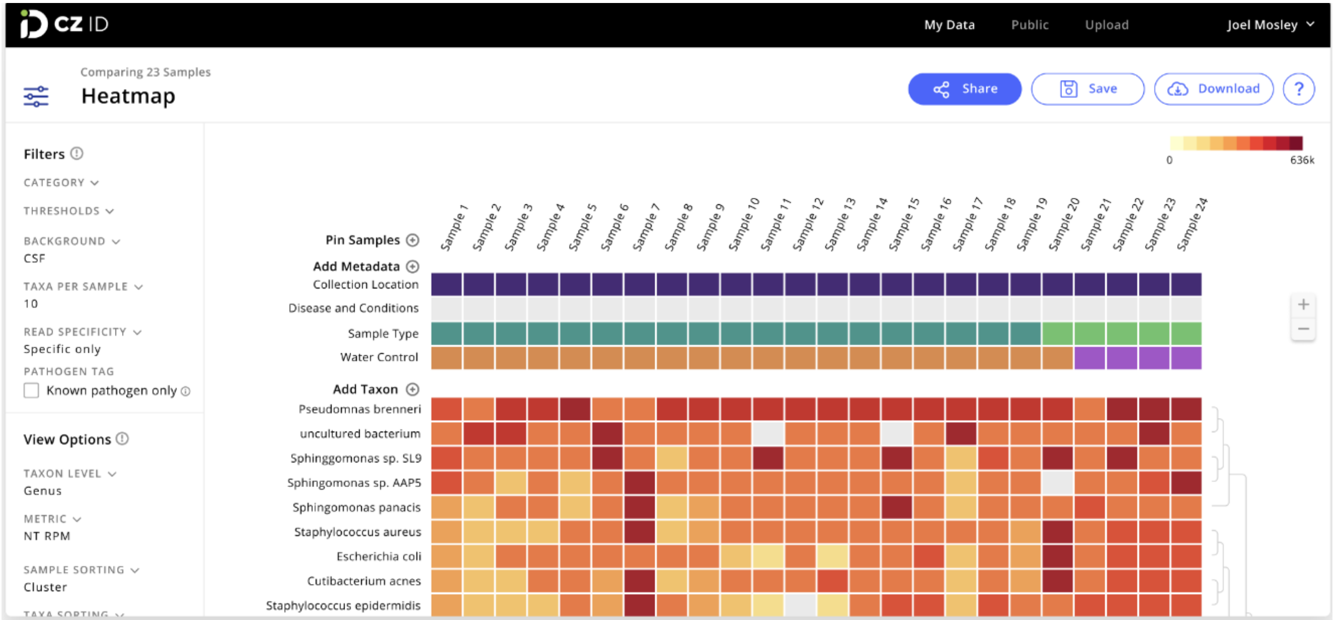
Workflow- Retrotrascrizione e amplificazione dell'RNA virale con random primers



Analisi Metagenomica con CZ ID



BACKGROUND
CSF

TAXA PER SAMPLE
10

READ SPECIFICITY
Specific only

PATHOGEN TAG
☐ Known pathogen only

TAXON LEVEL
Genus

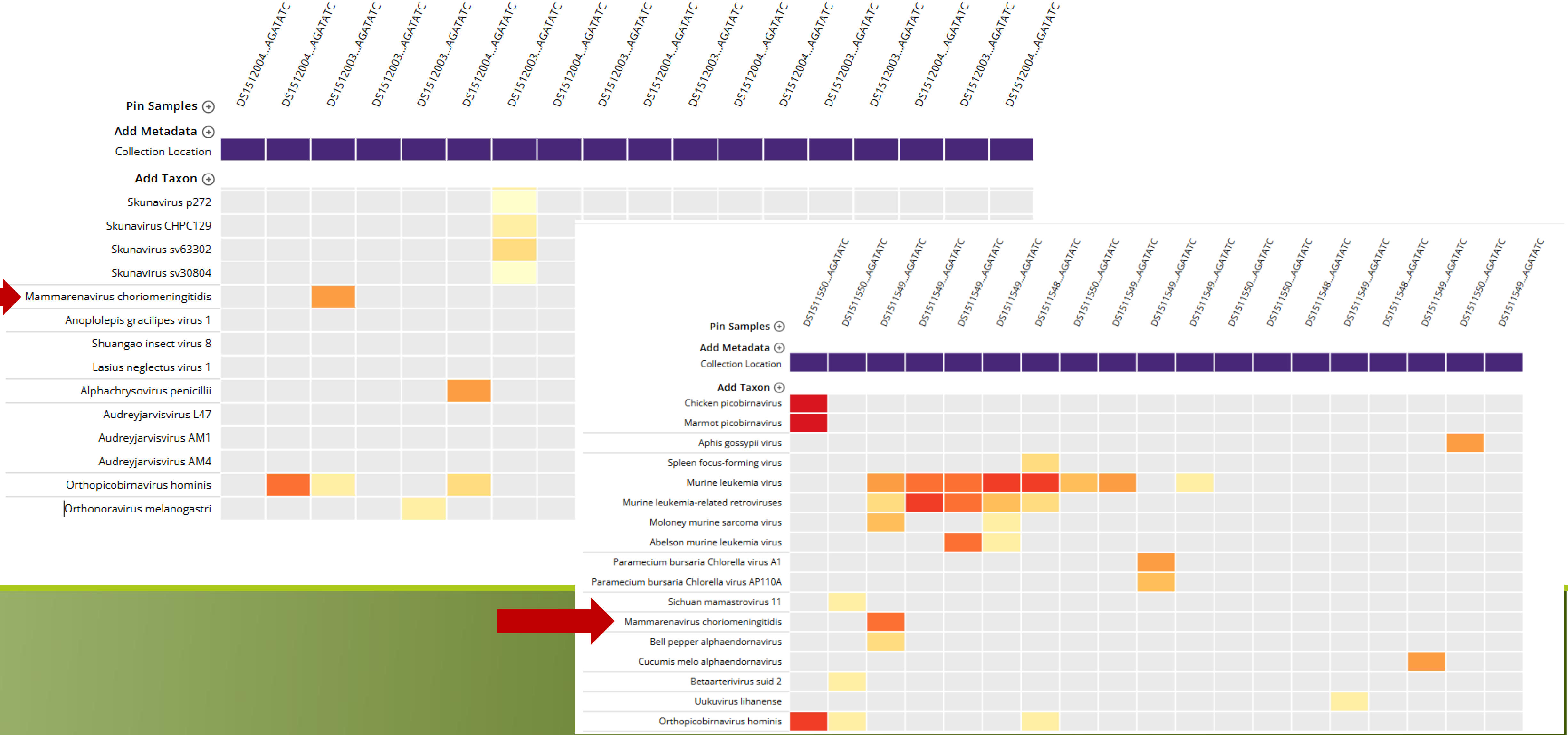
METRIC
NT RPM

SAMPLE SORTING
Cluster

TAXA SORTING

- **Classificazione tassonomica delle reads (NCBI database)**
- **Visualizzazione dei risultati con Heatmap**

Rodents from Camerun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Pin Samples ⊕
Add Metadata ⊕
Collection Location
Add Taxon ⊕
Skunavirus p272
Skunavirus CHPC129
Skunavirus sv63302
Skunavirus sv30804
Mammarenavirus choriomeningitidis
Anoplolepis gracilipes virus 1
Shuangao insect virus 8
Lasius neglectus virus 1
Alphachrysovirus penicillii
Audreyjarvisvirus L47
Audreyjarvisvirus AM1
Audreyjarvisvirus AM4
Orthopicobirnavirus hominis
Orthonoravirus melanogastri
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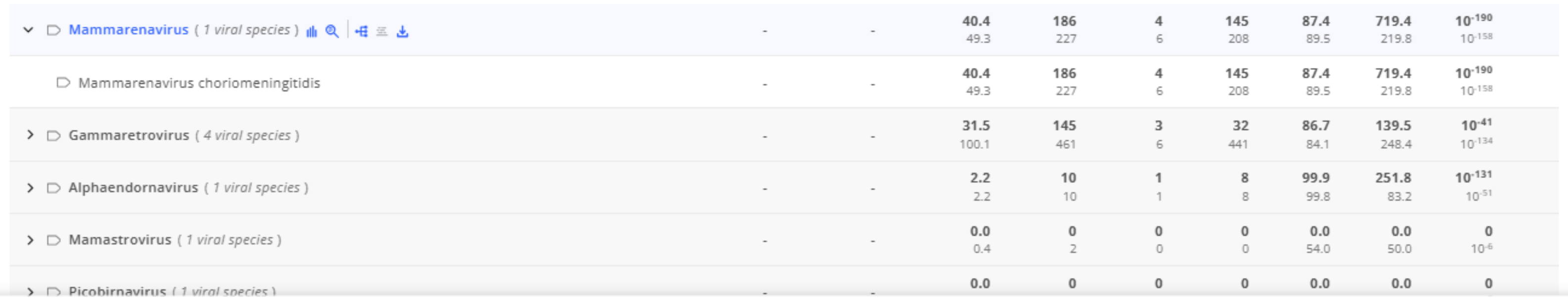
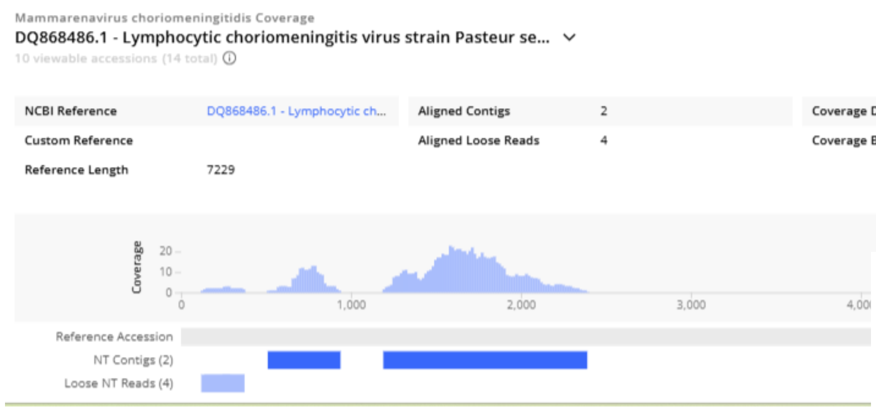
DS1511549...AGATATC
Pin Samples ⊕
Add Metadata ⊕
Collection Location
Add Taxon ⊕
Chicken picobirnavirus
Marmot picobirnavirus
Aphis gossypii virus
Spleen focus-forming virus
Murine leukemia virus
Murine leukemia-related retroviruses
Moloney murine sarcoma virus
Abelson murine leukemia virus
Paramecium bursaria Chlorella virus A1
Paramecium bursaria Chlorella virus AP110A
Sichuan mamastrovirus 11
Mammarenavirus choriomeningitidis
Bell pepper alphaendornavirus
Cucumis melo alphaendornavirus
Betaarterivirus suid 2
Uukuvirus lihanense
Orthopicobirnavirus hominis



Mammarenavirus (*1 viral species*)	-	-	40.4 49.3	186 227	4 6	145 208	87.4 89.5	719.4 219.8	10^{-190} 10^{-158}
Mammarenavirus choriomeningitidis	-	-	40.4 49.3	186 227	4 6	145 208	87.4 89.5	719.4 219.8	10^{-190} 10^{-158}
Gammaretrovirus (*4 viral species*)	-	-	31.5 100.1	145 461	3 6	32 441	86.7 84.1	139.5 248.4	10^{-41} 10^{-134}
Alphaendornavirus (*1 viral species*)	-	-	2.2 2.2	10 10	1 1	8 8	99.9 99.8	251.8 83.2	10^{-131} 10^{-51}
Mamastrovirus (*1 viral species*)	-	-	0.0 0.4	0 2	0 0	0 0	0.0 54.0	0.0 50.0	0 10^{-6}
Picobirnavirus (*1 viral species*)	-	-	0.0	0	0	0	0.0	0.0	0

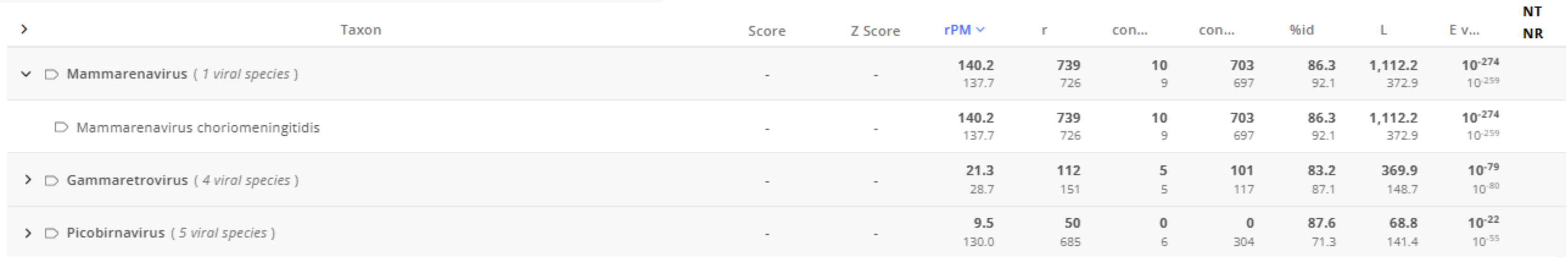


Mammarenavirus choriomeningitidis Coverage

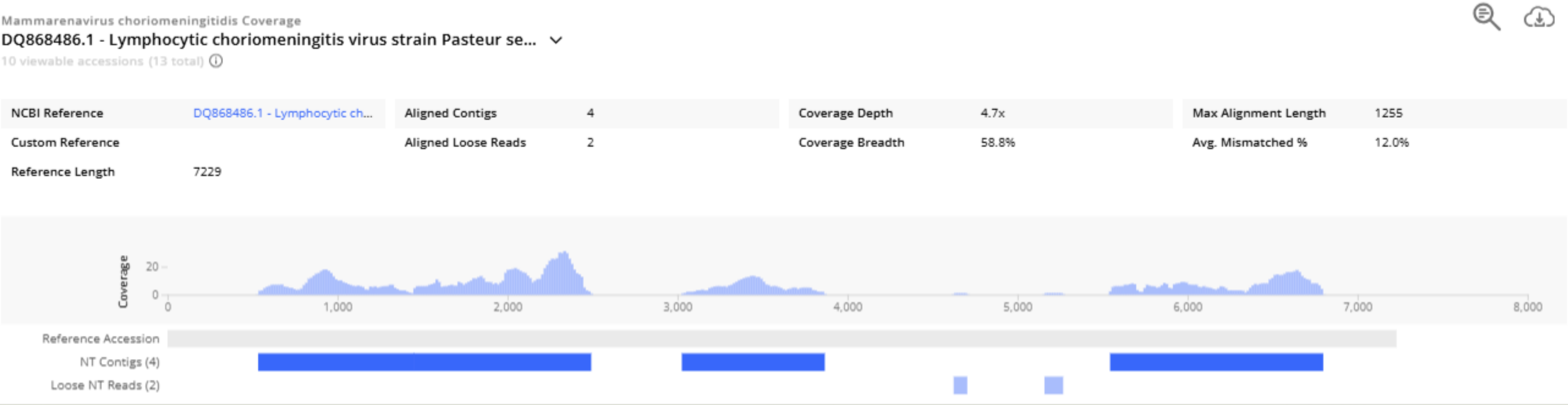
DQ868486.1 - Lymphocytic choriomeningitis virus strain Pasteur se...

10 viewable accessions (14 total)

NCBI Reference	DQ868486.1 - Lymphocytic ch...	Aligned Contigs	2	Coverage Depth	2.1x	Max Alignment Length	1201
Custom Reference		Aligned Loose Reads	4	Coverage Breadth	26.1%	Avg. Mismatched %	14.3%
Reference Length	7229						



Taxon	Score	Z Score	rPM	r	con...	con...	%id	L	E v...	NT NR
Mammarenavirus (*1 viral species*)	-	-	140.2 137.7	739 726	10 9	703 697	86.3 92.1	1,112.2 372.9	10^{-274} 10^{-259}	
Mammarenavirus choriomeningitidis	-	-	140.2 137.7	739 726	10 9	703 697	86.3 92.1	1,112.2 372.9	10^{-274} 10^{-259}	
Gammaretrovirus (*4 viral species*)	-	-	21.3 28.7	112 151	5 5	101 117	83.2 87.1	369.9 148.7	10^{-79} 10^{-80}	
Picobirnavirus (*5 viral species*)	-	-	9.5 130.0	50 685	0 6	0 304	87.6 71.3	68.8 141.4	10^{-22} 10^{-55}	



Mammarenavirus choriomeningitidis Coverage

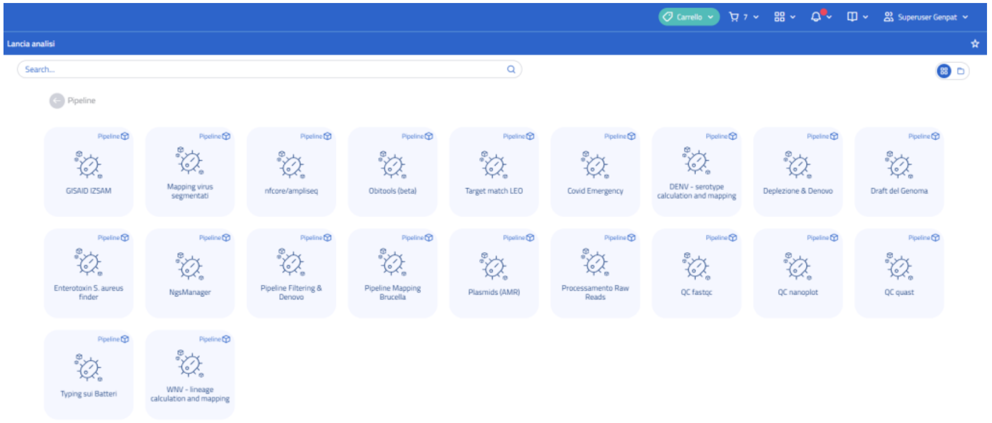
DQ868486.1 - Lymphocytic choriomeningitis virus strain Pasteur se...

10 viewable accessions (13 total)

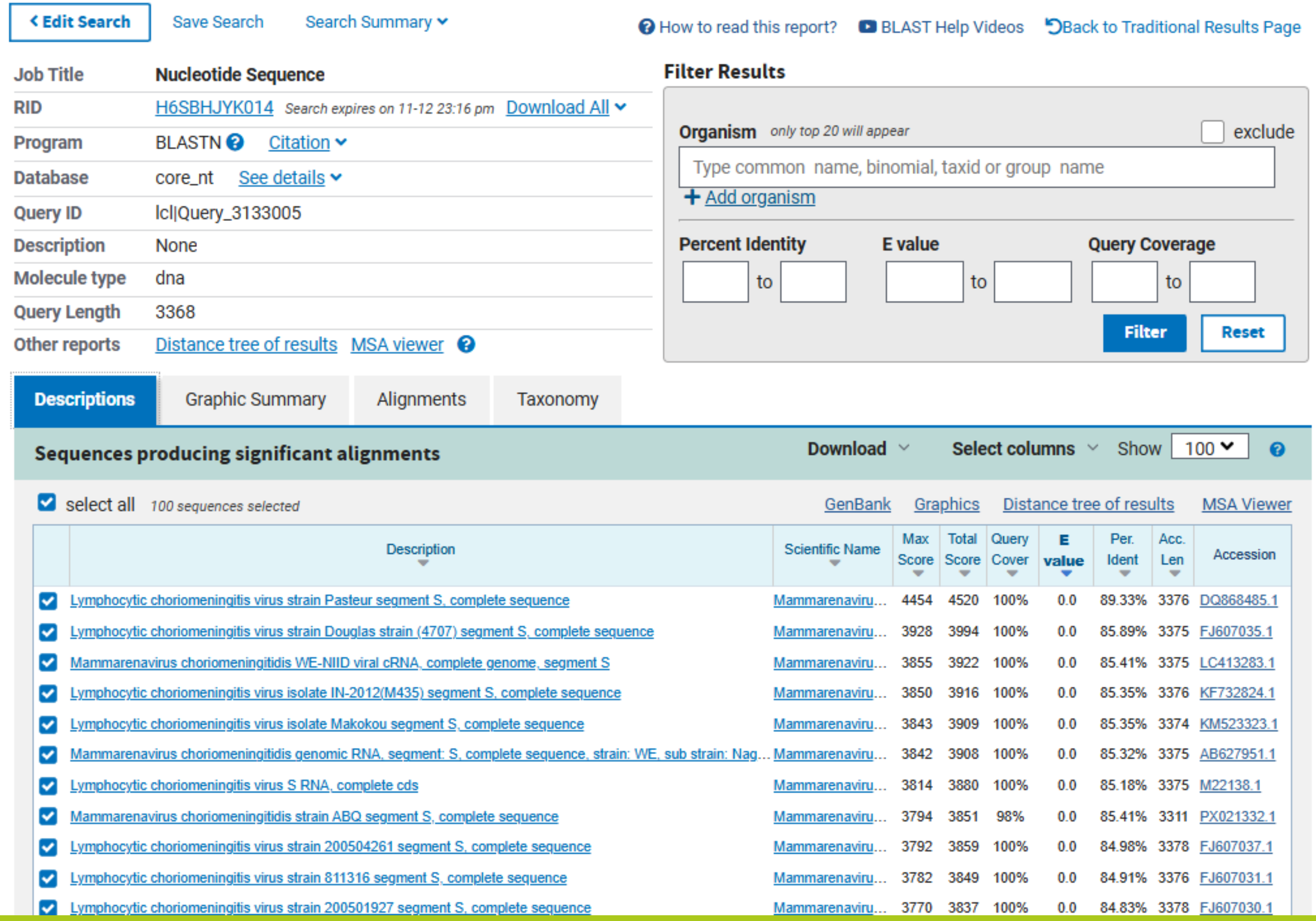
NCBI Reference	DQ868486.1 - Lymphocytic ch...	Aligned Contigs	4	Coverage Depth	4.7x	Max Alignment Length	1255
Custom Reference		Aligned Loose Reads	2	Coverage Breadth	58.8%	Avg. Mismatched %	12.0%
Reference Length	7229						

GenPat Platform

BLAST analysis



ID Sample	Vcov (x)	Hcov (%)	Numero di read mappate	% IUPAC	% Ns	Lunghezza consensus (bp)
2025.TE.10245.1.2	964	99,7	22 108	0.03	0	3368
2025.TE.10125.1.1	3 628	100	87 699	0	0	3376
2025.TE.10245.1.2	2 423	97,4	124 298	0	2	7201
2025.TE.10125.1.1	1 823	95,7	87 428	0	4	7228



Job Title	Nucleotide Sequence
RID	H6SBHJYK014 *Search expires on 11-12 23:16 pm* Download All
Program	BLASTN Citation
Database	core_nt See details
Query ID	lcl|Query_3133005
Description	None
Molecule type	dna
Query Length	3368
Other reports	Distance tree of results MSA viewer

Sequences producing significant alignments

☑ select all *100 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	Lymphocytic choriomeningitis virus strain Pasteur segment S, complete sequence	Mammarenaviru...	4454	4520	100%	0.0	89.33%	3376	DQ868485.1
☑	Lymphocytic choriomeningitis virus strain Douglas strain (4707) segment S, complete sequence	Mammarenaviru...	3928	3994	100%	0.0	85.89%	3375	FJ607035.1
☑	Mammarenavirus choriomeningitidis WE-NIID viral cRNA, complete genome, segment S	Mammarenaviru...	3855	3922	100%	0.0	85.41%	3375	LC413283.1
☑	Lymphocytic choriomeningitis virus isolate IN-2012(M435) segment S, complete sequence	Mammarenaviru...	3850	3916	100%	0.0	85.35%	3376	KF732824.1
☑	Lymphocytic choriomeningitis virus isolate Makokou segment S, complete sequence	Mammarenaviru...	3843	3909	100%	0.0	85.35%	3374	KM523323.1
☑	Mammarenavirus choriomeningitidis genomic RNA, segment: S, complete sequence, strain: WE, sub strain: Nag...	Mammarenaviru...	3842	3908	100%	0.0	85.32%	3375	AB627951.1
☑	Lymphocytic choriomeningitis virus S RNA, complete cds	Mammarenaviru...	3814	3880	100%	0.0	85.18%	3375	M22138.1
☑	Mammarenavirus choriomeningitidis strain ABQ segment S, complete sequence	Mammarenaviru...	3794	3851	98%	0.0	85.41%	3311	PX021332.1
☑	Lymphocytic choriomeningitis virus strain 200504261 segment S, complete sequence	Mammarenaviru...	3792	3859	100%	0.0	84.98%	3378	FJ607037.1
☑	Lymphocytic choriomeningitis virus strain 811316 segment S, complete sequence	Mammarenaviru...	3782	3849	100%	0.0	84.91%	3376	FJ607031.1
☑	Lymphocytic choriomeningitis virus strain 200501927 segment S, complete sequence	Mammarenaviru...	3770	3837	100%	0.0	84.83%	3378	FJ607030.1

Genus	Taxon	DS1499476...678.1.7	DS1503012...45.1.12	DS1503012...45.1.13	DS1503012...45.1.14	DS1503012...45.1.15	DS1503012...45.1.16	DS1503012...45.1.17	DS1503012...45.1.18	DS1503012...45.1.19	DS1503012...45.1.20	DS1503012...45.1.21	DS1503013...45.1.2
Cardiovirus	Cardiovirus B	0	0	NA	31226	0	273	NA	0	0	174	0	34
Cardiovirus	Rodent Cardiovirus	0	0	0	21	0	NA	0	0	0	0	0	14
Cardiovirus	Marmot cardiovirus	0	0	0	11	0	0	0	0	0	0	0	0
Chaphamaparvovirus	Chaphamaparvovirus rodent1	0	0	NA	24	0	0	0	18	0	0	0	NA
Chapparvovirus	Murine chapparvovirus	0	0	0	2502	0	0	0	NA	0	0	0	0
Deltapartitivirus	Plant associated deltapartitivirus 5	0	0	0	0	1177	0	0	0	0	0	0	0
Dependoparvovirus	Anser anser dependoparvovirus	0	0	0	0	0	0	0	0	0	0	0	0
Gammaretrovirus	Murine leukemia-related retroviruses	0	0	0	0	0	0	0	NA	NA	0	0	0
Gammaretrovirus	Murine leukemia virus	0	0	0	0	0	0	0	65	NA	0	0	0
Hunnivirus	Hunnivirus sp.	0	0	0	0	0	0	48	0	0	0	0	NA
Hunnivirus	Hunnivirus A	0	0	0	0	0	NA	4937	0	0	0	309	NA
Hunnivirus	Rattus tanezumi hunnivirus	0	0	0	0	0	NA	3648	0	0	0	22	NA
Jeilongvirus	Jeilongvirus myodesis	0	0	0	0	0	0	0	0	0	0	0	0
Jeilongvirus	Eothenomys eva jeilongvirus	0	0	0	0	0	0	0	0	0	0	0	0
Jeilongvirus	Jeilongvirus apodemi	0	0	0	0	0	0	0	0	0	0	0	0
Jeilongvirus	Apodemus draco jeilongvirus	0	0	0	0	0	0	0	0	0	0	0	0
Jeilongvirus	Longquan Niviventer fulvescens jeilongvirus 2	0	0	0	0	0	0	0	0	0	0	0	0
Jeilongvirus	Jeilongvirus queenslandense	0	0	0	0	0	0	0	0	0	0	0	0
Jeilongvirus	Jeilongvirus beilongi	0	0	0	0	0	0	0	0	0	0	0	0
Jeilongvirus	Jingmen Apodemus agrarius jeilongvirus 2	0	0	0	0	0	0	0	0	0	0	0	0
Jeilongvirus	Mus musculus jeilongvirus	0	0	0	0	0	0	0	0	0	0	0	0
Mamastrovirus	Rodent astrovirus	0	0	0	0	0	681	838	0	0	36	0	1872
Mupivirus	Mupivirus A	0	0	0	62	0	0	0	0	0	0	0	0
Orbivirus	Attungu rodent orbivirus	0	0	0	10	0	101	0	0	0	52	48	0
Orbivirus	Mulberry orbivirus	0	0	0	NA	0	NA	0	0	0	17	NA	0
Orthoreovirus	Mammalian orthoreovirus	0	0	NA	0	0	35	34840	0	0	0	0	0
Parechovirus	Rattus tanezumi parechovirus	0	0	117	NA	0	0	0	0	0	0	0	0
Picobirnavirus	Picobirnavirus sp.	NA	0	7216	0	0	10	19	0	0	NA	NA	0
Picobirnavirus	Porcine picobirnavirus	0	0	2585	0	NA	NA	NA	0	0	0	NA	0
Picobirnavirus	Marmot picobirnavirus	0	0	83	0	0	NA	25	0	0	0	0	0
Picobirnavirus	Chimpanzee picobirnavirus	0	0	0	0	0	0	0	0	0	0	0	0
Picobirnavirus	Rat picobirnavirus	0	0	299	0	0	0	20	0	0	0	0	0
Picobirnavirus	Chicken picobirnavirus	0	0	97	0	0	0	NA	0	0	0	0	0
Picobirnavirus	Fox picobirnavirus	0	0	427	0	0	0	0	0	0	0	0	0
Picobirnavirus	Porcine picobirnavirus group II	0	0	20268	0	0	0	0	0	0	0	0	0
Picobirnavirus	Mongoose picobirnavirus	0	0	1462	0	0	0	NA	0	0	0	0	0
Picobirnavirus	Microtus picobirnavirus V-111/USA/2008	0	0	237	0	0	0	0	0	0	0	0	0
Picobirnavirus	Picobirnavirus 504	0	0	NA	0	0	NA	0	0	0	0	0	0
Picobirnavirus	Turkey picobirnavirus	0	0	NA	0	0	0	NA	0	0	0	0	0
Protoparvovirus	Protoparvovirus rodent1	0	0	0	0	0	0	0	0	0	0	0	0
Protoparvovirus	Hamster parvovirus	0	0	0	0	0	0	0	0	0	0	0	0
Rosavirus	Rosavirus B	0	0	0	0	0	0	150	0	0	0	0	0
Rosavirus	Rosavirus C	0	0	0	0	0	0	33	0	0	0	0	0