



INTERNATIONAL YEAR OF
CAMELIDS
2024

THE RELEVANCE OF CAMEL RESEARCH AND DEVELOPMENT FOR ONE HEALTH

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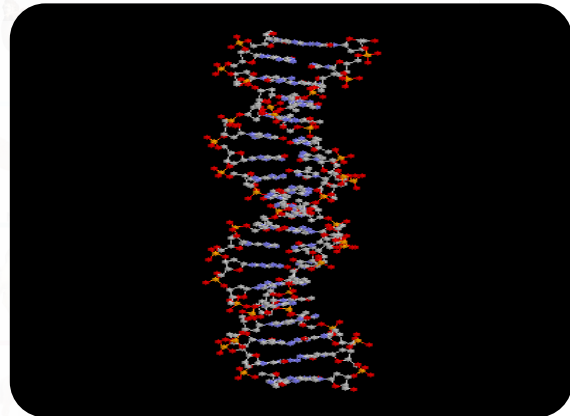
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Genetics and camel populations

- One Health principle
- metagenomic NGS
 - ❖ One Health genomics
 - ❖ screening for pathogens
- Importance of camel (immune) diversity
 - ❖ adaptation
 - ❖ evolutionary arms race
 - ❖ production
 - ❖ camels in the One Health context



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Importance of camelid biodiversity for ONE HEALTH

“ONE HEALTH is an integrated, unifying approach that aims to sustainably balance and optimize the health of people, animals, and ecosystems.”

(OHHLEP 2022)



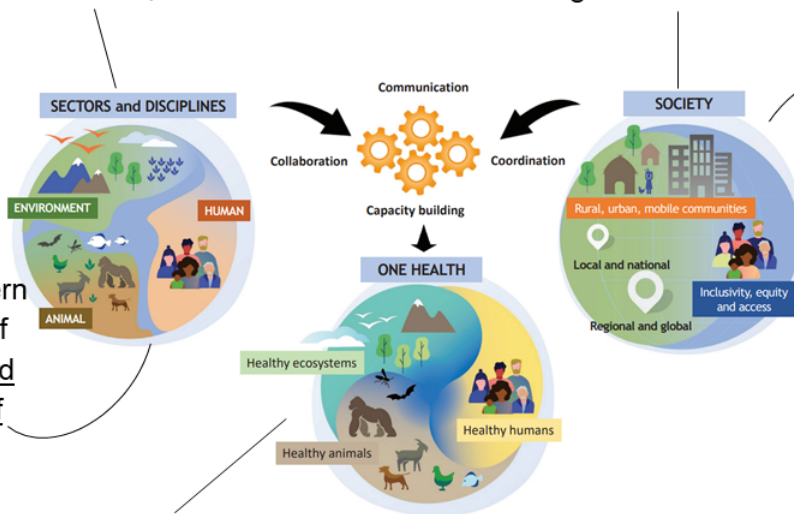
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1. **equity** between sectors and disciplines.

2. sociopolitical and multicultural **parity** and **inclusion** and engagement of communities and marginalized voices.

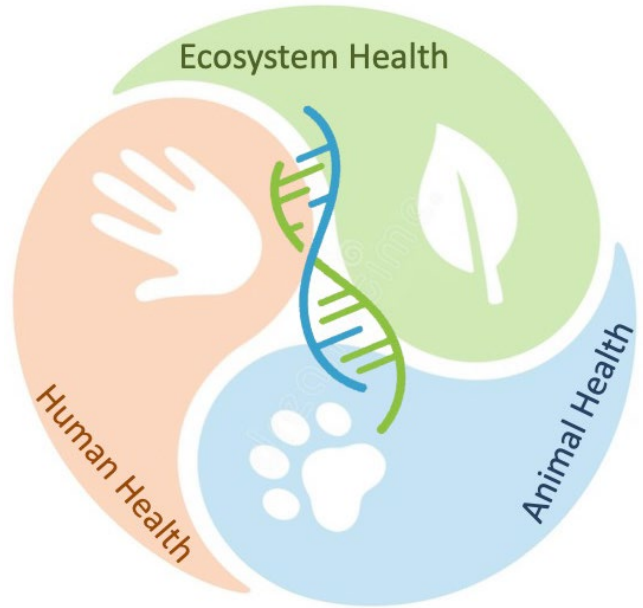
4. **stewardship** and the responsibility of humans to change behavior and adopt sustainable solutions that recognize the importance of animal welfare and the integrity of the whole ecosystem, thus securing the well-being of current and future generations



3. **socioecological equilibrium** that seeks a harmonious balance between **human-animal-environment interaction** and acknowledging the importance of biodiversity, access to sufficient natural space and resources, and the intrinsic value of all living things within the ecosystem.

One Health Genomics

Real-time genomic (metagenomic NGS) data retrieved from the three subsystems provide information for creating sustainable One Health outcomes.

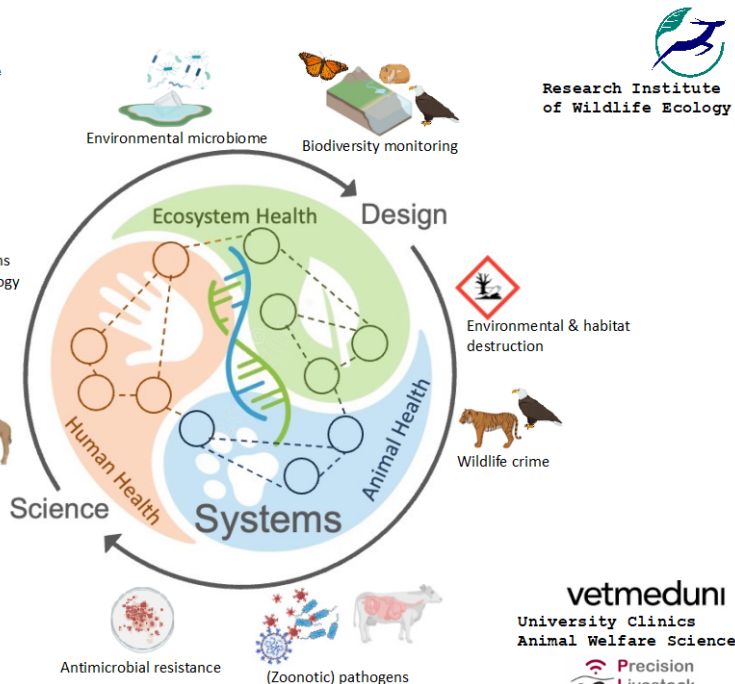


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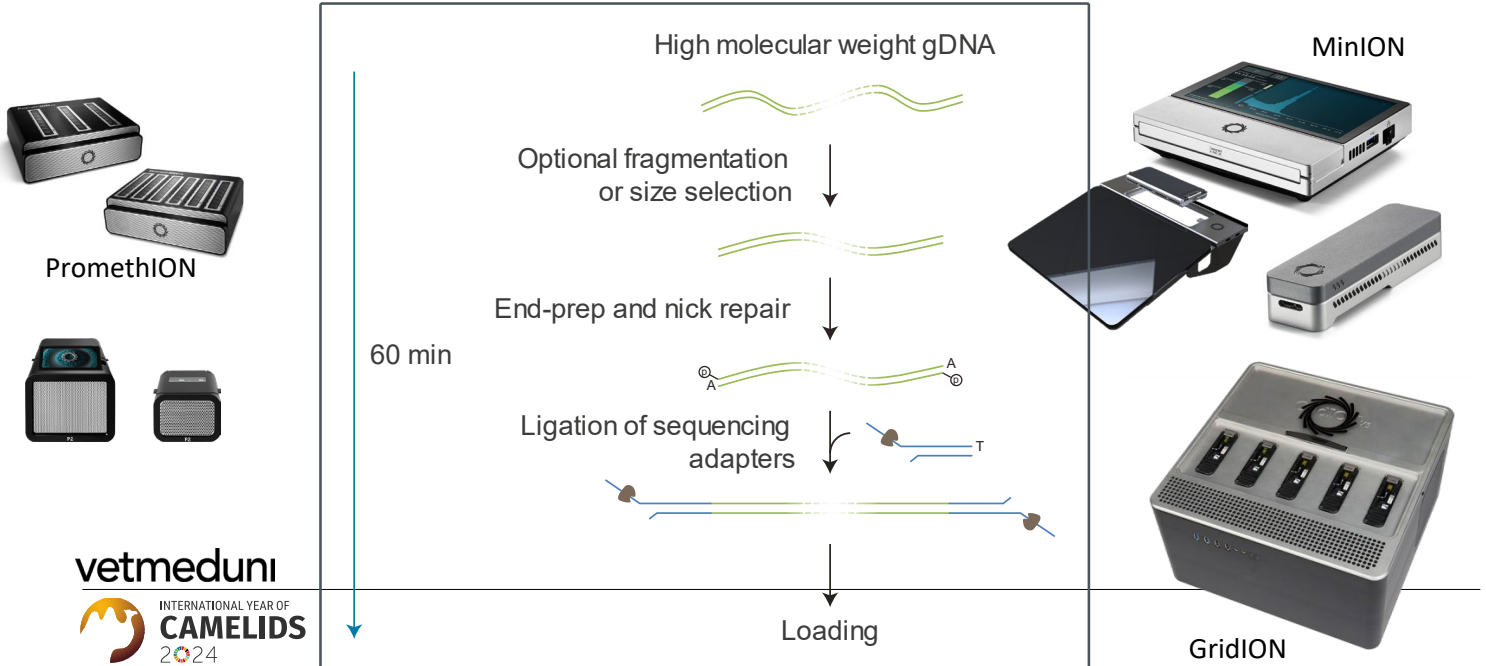
One Health Genomics

Real-time genomic (metagenomic NGS) data retrieved from the three subsystems provide information for creating sustainable One Health outcomes.



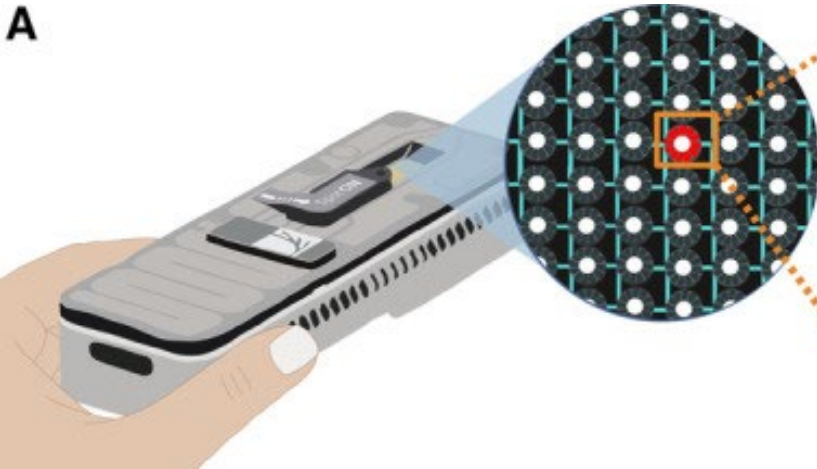
Real-time Genomics

NANOPORE SEQUENCING – METAGENOMIC NEXT GENERATION SEQUENCING

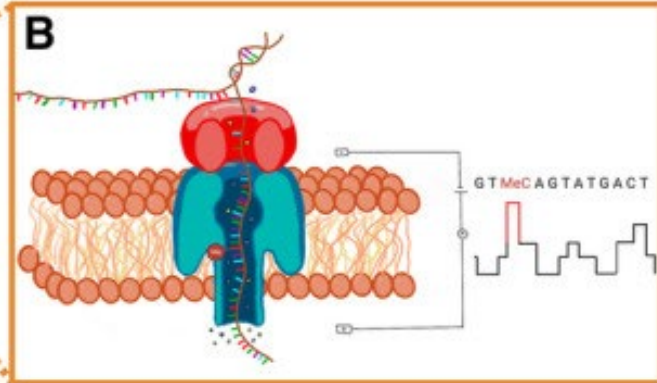


Real-time Genomics

A



B



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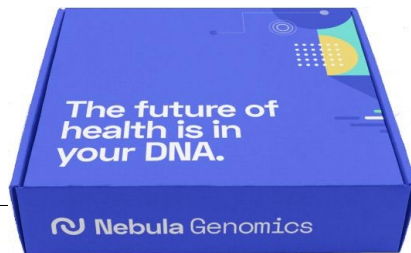
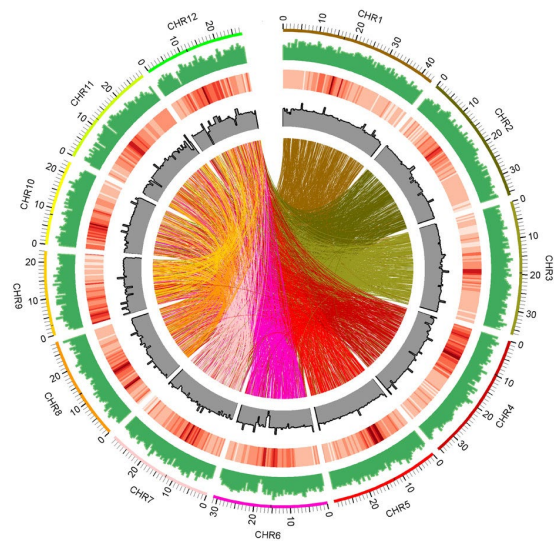
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One Health Genomics



One Health Genomics

- Whole-genome sequencing
 - ❖ Medical applications (cancer, rare disease detection, personalized medicine)
 - ❖ Animal and Plant breeding (pan-genomes)
 - ❖ Evolutionary genomics
 - ❖ Population and conservation genomics
 - ❖ One Health genomics



One Health Genomics in camels

Real-time genomic (metagenomic NGS) data retrieved from the three subsystems provide information for creating sustainable One Health outcomes.



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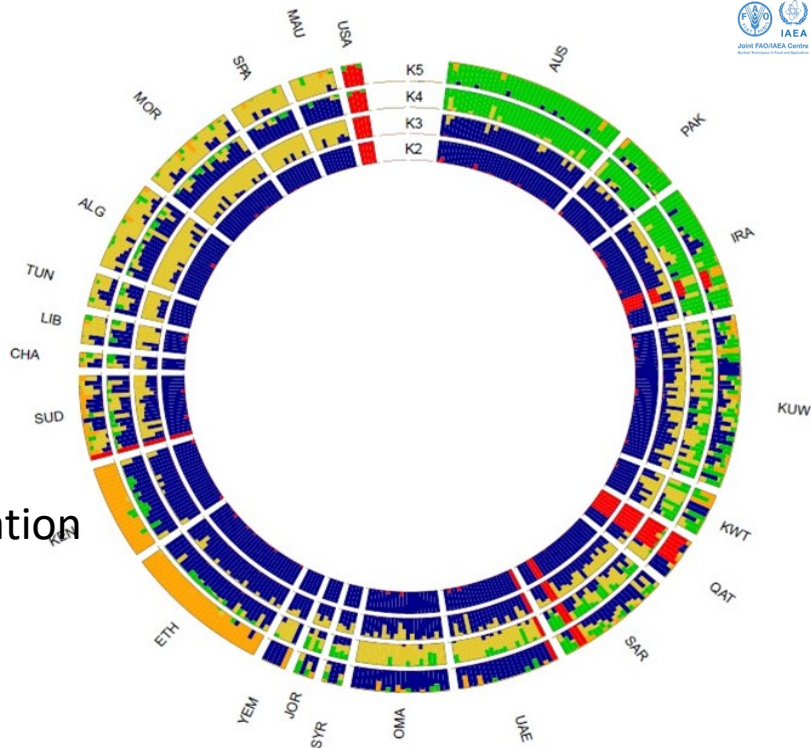




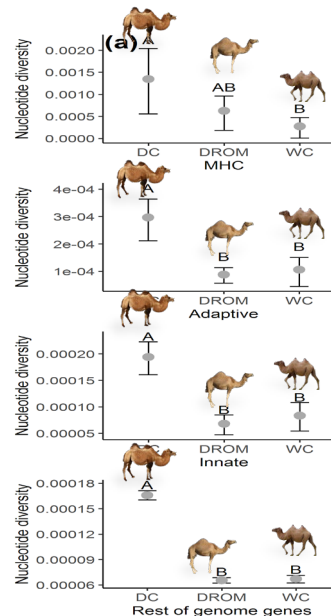
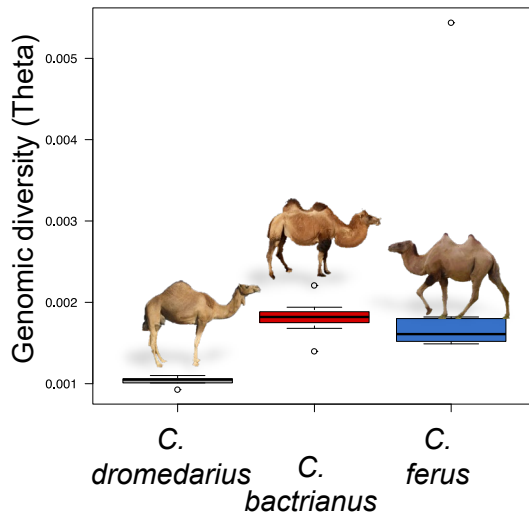
Genome-wide genetic diversity in dromedaries



- ❖ low genetic differentiation
- ❖ demographic contraction (bottleneck) during domestication
- ❖ Lower genetic diversity even before domestication



Empirical studies in immune response genes (Immune genomic variation in camels)



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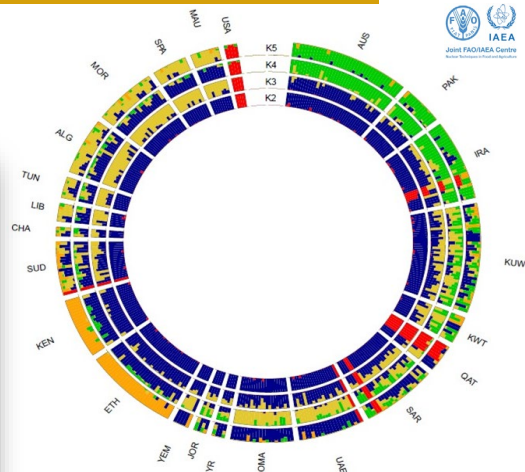
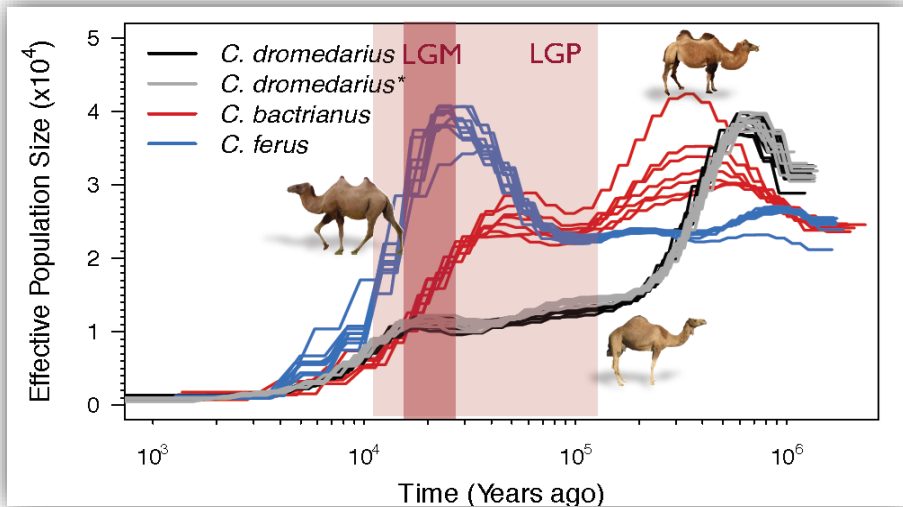


Genome-wide genetic diversity in dromedaries

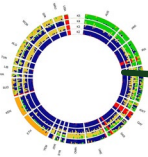
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- ❖ low genetic differentiation
- ❖ demographic contraction (bottleneck)



Screening for pathogens using CZID database



Preliminary screening of the whole genomes from Algerian and Kenyan dromedaries (Illumina reads)

Algeria: Drom1359 tested negative for *Trypanosoma* sp.

Drom1373 tested positive for *Trypanosoma evansi*



CZ ID

<https://czid.org>

Chan Zuckerberg ID - Detect & Track Infectious Diseases

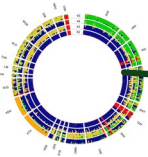
CZ ID: a free, cloud-based metagenomic platform for researchers, empowers global pathogen and outbreak detection and monitoring.

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Screening for pathogens using CZID database



Preliminary screening of the whole genomes from Algerian and Kenyan dromedaries (Illumina reads)

Algeria: Drom1359 tested negative for *Trypanosoma* sp.

Drom1373 tested positive for *Trypanosoma evansi*



CZ ID

<https://czid.org>

➤ Silvia Bruno

Chan Zuckerberg ID - Detect & Track Infectious Diseases

CZ ID: a free, cloud-based metagenomic platform for researchers, empowers global pathogen and outbreak detection and monitoring.

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Screening for pathogens using CZID database



Metagenomics



Upload Data

- ❖ Upload short- or long-read metagenomic data.



Explore Results

- ❖ View interactive reports summarizing identified taxa and associated QC metrics based on alignments against nucleotide and protein NCBI databases.



Analyze and Visualize Results*

- ❖ Use models to distinguish microbial signals from background contamination.
- ❖ Generate consensus genomes for viruses of interest.
- ❖ Generate heatmaps and phylogenetic trees to compare and visualize identified taxa across samples.

* Not available for Nanopore data



Antimicrobial Resistance



Upload or Select Data

- ❖ Upload short-read metagenomic or whole genome sequence data. Alternatively, select metagenomic data already on your account.



Explore Results

- ❖ View interactive reports summarizing identified AMR genes from the Comprehensive Antibiotic Resistance Database (CARD) and associated QC metrics.



SARS-CoV-2 and Viral Consensus Genomes



Upload Data

- ❖ Upload short-read data. SARS-CoV-2 pipeline also accepts long-read data.



Explore Results

- ❖ View coverage plots for assembled consensus genomes.



Analyze Genomes

- ❖ Analyze the quality of assembled genomes (e.g., mapped reads, missing bases, coverage).
- ❖ Download VCF files for downstream variant analysis.



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Screening for pathogens using CZID database

 My Data Public Upload Pamela Burger

dromedary_WGS VV-Drom1373_L003 metagenomic Share Download ...

Taxon name Name Type: Scientific Background: None Categories Threshold filters Read Specificity: All Annotation Pathogen Flags

Trypanosoma (genus) X

Report values are computed from 2,067,354 reads (2,000,000 unique reads) subsampled randomly from the reads that passed host and quality filters.

3 rows passing the above filters, out of 3167 total rows CLEAR FILTERS

	Taxon	Score	Z Score	rPM	r	con...	con...	%id	L	E v...	NT NR
▼	Trypanosoma (2 eukaryotic species)	-	-	0.3 5.1	1 15	0 2	0 8	91.7 54.5	36.0 58.8	10 ⁻⁸ 10 ⁻¹³	
▼	Trypanosoma evansi	-	-	0.3 0.0	1 0	0 0	0 0	91.7 0.0	36.0 0.0	10 ⁻⁸ 0	
	Trypanosoma congolense	-	-	0.0 5.1	0 15	0 2	0 8	0.0 54.5	0.0 58.8	0 10 ⁻¹³	

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Screening for pathogens using CZID database

 CZ ID

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dromedary_WGS

VV-Drom1373_L004

Illumina mNGS Pipeline v8.3 | NCBI Index Date: 2024-02-06 | processed 6 days ago | [SAMPLE DETAILS](#)

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Metagenomic

Taxon name

Name Type: Scientific

Background: None

Categories

Threshold filters

Read Specificity: All

Annotation

Pathogen Flags

Trypanosoma (genus) X

Report values are computed from 2,084,874 reads (2,000,000 unique reads) subsampled randomly from the reads that passed host and quality filters.
3 rows passing the above filters, out of 3279 total rows [CLEAR FILTERS](#)

	Taxon	Score	Z Score	rPM	r	con...	con...	%id	L	E v...	NT NR
	Trypanosoma (2 eukaryotic species: 1)	-	-	0.3 1.7	1 5	0 0	0 0	83.6 40.7	55.0 67.4	10 ⁻¹³ 10 ⁻¹¹	
	Trypanosoma brucei Known Pathogen	-	-	0.3 0.0	1 0	0 0	0 0	83.6 0.0	55.0 0.0	10 ⁻¹³ 0	
	Trypanosoma congolense	-	-	0.0 1.7	0 5	0 0	0 0	0.0 40.7	0.0 67.4	0 10 ⁻¹¹	

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Screening for pathogens using CZID database

 CZ ID

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< dromedary_WGS

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VV-Drom1373_L003

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Metagenomic

Name Type: Scientific

Background: None

Categories

Threshold filters

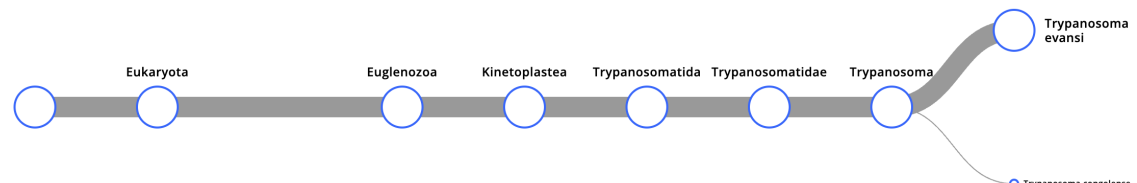
Read Specificity: All

Tree Metric: NT r (total reads)

Trypanosoma (genus) X

Report values are computed from 2,067,354 reads (2,000,000 unique reads) subsampled randomly from the reads that passed host and quality filters.

3 rows passing the above filters, out of 3167 total rows CLEAR FILTERS



```
graph LR; Eukaryota --- Euglenozoa; Euglenozoa --- Kinetoplastea; Kinetoplastea --- Trypanosomatida; Trypanosomatida --- Trypanosomatidae; Trypanosomatidae --- Trypanosoma; Trypanosoma --- Trypanosoma_evansi[Trypanosoma evansi]; Trypanosoma --- Trypanosoma_congolense[Trypanosoma congolense]
```

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Screening for pathogens using CZID database

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**Metagenomic**

Taxon name



Name Type: Scientific

Background: None

Categories

Threshold filters

Read Specificity: All

Annotation

Pathogen Flags

Trypanosoma (genus)

Report values are computed from 2,077,644 reads (2,000,000 unique reads) subsampled randomly from the reads that passed host and quality filters.

2 rows passing the above filters, out of 3764 total rows **CLEAR FILTERS**

	Taxon	Score	Z Score	rPM	r	con...	con...	%id	L	E v...	NT NR
	Trypanosoma (1 eukaryotic species)	-	-	0.0 13.0	0 37	0 2	0 8	0.0 52.4	0.0 65.0	0 10 ⁻¹²	
	Trypanosoma congolense	-	-	0.0 13.0	0 37	0 2	0 8	0.0 52.4	0.0 65.0	0 10 ⁻¹²	

Screening for pathogens using CZID database

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**Metagenomic**

Taxon name

Name Type: Scientific

Background: None

Categories

Threshold filters

Read Specificity: All

Annotation

Pathogen Flags

Trypanosoma (genus)

Report values are computed from 2,085,898 reads (2,000,000 unique reads) subsampled randomly from the reads that passed host and quality filters.

5 rows passing the above filters, out of 3719 total rows [CLEAR FILTERS](#)

	Taxon	Score	Z Score	rPM	r	con...	con...	%id	L	E v...	NT NR
	Trypanosoma (4 eukaryotic species: ● 1)	-	-	1.1 0.4	3 1	0 0	0 0	85.1 55.6	43.3 45.0	10 ⁻⁸ 10 ⁻⁴	
	Trypanosoma rangeli	-	-	0.4 0.0	1 0	0 0	0 0	83.3 0.0	48.0 0.0	10 ⁻⁹ 0	
	Trypanosoma evansi	-	-	0.4 0.0	1 0	0 0	0 0	91.9 0.0	37.0 0.0	10 ⁻⁹ 0	
	Trypanosoma brucei Known Pathogen	-	-	0.4 0.0	1 0	0 0	0 0	80.0 0.0	45.0 0.0	10 ⁻⁶ 0	
	Trypanosoma congolense	-	-	0.0 0.4	0 1	0 0	0 0	0.0 55.6	0.0 45.0	0 10 ⁻³	

Screening for pathogens using CZID database

[My Data](#)[Public](#)[Upload](#)[Pamela Burger](#) ▾[< dromedary_WGS](#)Illumina mNGS Pipeline v8.3 | NCBI Index Date: 2024-02-06 | processed 6 days ago | [SAMPLE DETAILS](#)**VV-Drom1359_L002** ▾[Share](#)[Download](#) ▾**Metagenomic**

Name Type: Scientific ▾

Background: None ▾

Categories ▾

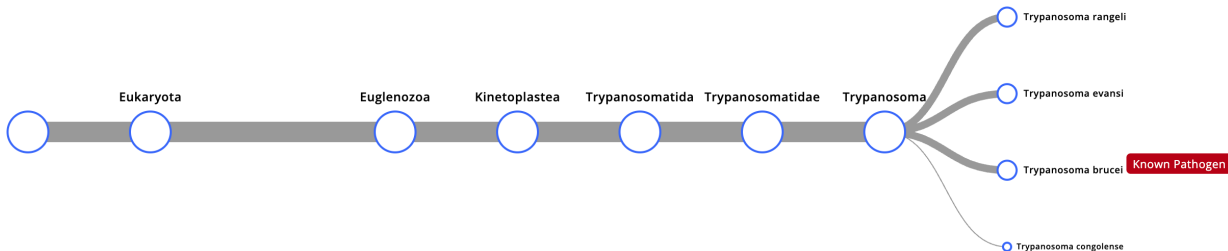
Threshold filters ▾

Read Specificity: All ▾

Tree Metric: NT r (total reads) ▾

[Trypanosoma \(genus\)](#) ✕

Report values are computed from 2,085,898 reads (2,000,000 unique reads) subsampled randomly from the reads that passed host and quality filters.

5 rows passing the above filters, out of 3719 total rows [CLEAR FILTERS](#)

Screening for pathogens using CZID database

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dromedary_WGS
VV-Drom1779_S15 ▾

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Metagenomic

Taxon name



Name Type: Scientific ▾

Background: None ▾

Categories ▾

Threshold filters ▾

Read Specificity: All ▾

Annotation ▾

Pathogen Flags ▾

Report values are computed from 2,085,490 reads (2,000,000 unique reads) subsampled randomly from the reads that passed host and quality filters.

27759 rows



		Taxon	Score	Z Score	rPM ▾	r	con...	con...	%id	L	E v...	NT NR
>	▢	Moraxella (41 bacterial species: ● 3)	-	-	129,833.0 149,316.8	314,204 361,356	6,484 10,244	266,756 300,867	91.6 91.9	2,586.8 321.2	10 ⁻²²³ 10 ⁻¹⁹⁰	
>	▢	Rothia (56 bacterial species: ● 1)	-	-	129,065.2 131,428.0	312,346 318,064	2,667 3,839	289,507 297,466	86.1 82.7	1,450.2 397.4	10 ⁻¹⁷⁸ 10 ⁻²¹⁰	
>	▢	Neisseria (94 bacterial species: ● 2)	-	-	47,954.1 45,499.2	116,052 110,111	1,804 1,854	104,568 101,077	93.9 92.4	3,713.5 420.5	10 ⁻²³⁸ 10 ⁻²⁴¹	
>	▢	Streptococcus (260 bacterial species: ● 16)	-	-	12,486.0 26,681.5	30,217 64,571	632 2,355	19,484 50,280	86.4 81.2	720.5 246.7	10 ⁻¹²⁸ 10 ⁻¹⁴⁰	
>	▢	Mannheimia (12 bacterial species)	-	-	7,879.1 9,069.2	19,068 21,948	1,062 1,364	10,286 11,690	87.0 89.4	496.4 109.6	10 ⁻¹⁰⁵ 10 ⁻⁶³	
>	▢	Corynebacterium (291 bacterial species: ● 4)	-	-	5,508.1 5,129.2	13,330 12,413	137 225	6,780 3,694	88.5 83.5	147.7 114.3	10 ⁻⁴⁶ 10 ⁻⁴⁸	
>	▢	Mammaliicoccus (27 bacterial species)	-	-	4,336.3 3,292.1	10,494 7,967	605 449	3,837 2,727	98.8 97.6	324.1 80.3	10 ⁻¹⁵⁵ 10 ⁻⁴⁷	

Screening for pathogens using CZID database

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Metagenomic

Taxon name



Name Type: Scientific ▾

Background: None ▾

Categories ▾

Threshold filters ▾

Read Specificity: All ▾

Annotation ▾

Pathogen Flags ▾

Report values are computed from 2,078,168 reads (2,000,000 unique reads) subsampled randomly from the reads that passed host and quality filters.

4043 rows



>	Taxon	Score	Z Score	rPM ▾	r	con...	con...	%id	L	E v...	NT NR
>	Stenotrophomonas (133 bacterial species: ● 1)	-	-	74,958.3 70,538.1	208,432 196,141	3,981 3,849	195,244 185,076	97.4 97.3	4,226.3 481.9	10 ⁻²⁷³ 10 ⁻²⁵¹	
>	Variovorax (92 bacterial species)	-	-	47,352.1 45,765.0	131,669 127,256	6,035 6,142	118,643 118,732	89.5 94.0	1,135.5 256.5	10 ⁻²²³ 10 ⁻¹⁷³	
>	Roseateles (51 bacterial species)	-	-	16,656.2 26,687.4	46,315 74,208	2,409 4,370	35,122 57,509	87.8 97.7	820.9 199.3	10 ⁻¹⁷⁰ 10 ⁻¹³¹	
>	Klebsiella (51 bacterial species: ● 3)	-	-	11,321.1 9,847.4	31,480 27,382	1,959 1,778	12,523 11,623	99.7 96.8	307.0 88.2	10 ⁻¹⁶⁴ 10 ⁻⁵²	
>	Delftia (30 bacterial species)	-	-	2,022.2 1,424.1	5,623 3,960	159 67	1,729 875	97.7 93.9	305.3 109.4	10 ⁻¹³⁵ 10 ⁻⁴⁷	
>	all taxa with neither family nor genus classification (81 species)	-	-	1,181.4 3,018.4	3,285 8,393	40 89	2,432 1,661	95.9 95.8	3,616.0 87.1	10 ⁻²²² 10 ⁻⁴⁶	
>	Pseudomonas (150 bacterial species: ● 3)	-	-	707.4 1,208.4	1,967 3,360	75 122	1,449 2,745	92.3 93.9	748.3 354.0	10 ⁻¹⁴⁵ 10 ⁻¹⁷⁶	

Screening for pathogens using CZID database

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Chromedary_WGS

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**Metagenomic**

Taxon name



Name Type: Scientific ▾

Background: None ▾

Categories ▾

Threshold filters ▾

Read Specificity: All ▾

Annotation ▾

Pathogen Flags ▾

Stenotrophomonas (genus) ✕

Report values are computed from 2,075,626 reads (2,000,000 unique reads) subsampled randomly from the reads that passed host and quality filters.

90 rows passing the above filters, out of 3738 total rows [CLEAR FILTERS](#)

▼	Taxon	Score	Z Score	rPM ▾	r	con...	con...	%id	L	E v...	NT NR
▼ ▾	Stenotrophomonas (89 bacterial species: ● 1)	-	-	72,095.7 68,623.5	204,272 194,434	1,263 1,245	202,793 193,231	97.9 97.7	7,428.3 659.4	10 ⁻²⁸⁹ 10 ⁻²⁹²	
▾	Stenotrophomonas maltophilia Known Pathogen	-	-	70,597.1 54,750.1	200,026 155,126	1,224 1,008	198,641 154,133	98.0 97.9	7,503.3 641.3	10 ⁻²⁹⁰ 10 ⁻²⁹¹	
▾	Stenotrophomonas sp. ASS1	-	-	372.4 1,298.1	1,055 3,678	7 21	1,046 3,673	88.7 97.5	3,838.8 870.0	10 ⁻²⁵² 10 ⁻³⁰⁰	
▾	Stenotrophomonas acidaminiphila	-	-	371.6 31.8	1,053 90	5 2	1,043 90	99.3 90.1	5,328.1 225.6	10 ⁻³⁰⁰ 10 ⁻¹²⁶	
▾	Stenotrophomonas sp. WZN-1	-	-	165.9 749.3	470 2,123	6 6	468 2,119	90.8 99.0	2,594.8 990.4	10 ⁻¹⁰¹ 10 ⁻³⁰⁵	
▾	Stenotrophomonas sp. CW117	-	-	161.6 0.0	458 0	2 0	455 0	98.8 0.0	6,302.5 0.0	10 ⁻³⁰⁶ 0	

Screening for pathogens using CZID database

Introduction

Go to: 

Stenotrophomonas maltophilia is a gram-negative bacillus, initially called *Bacterium bookeri*, when it was first identified in 1943 from a specimen of human pleural fluid.[1] It was later classified as *Pseudomonas maltophilia* in 1961, then reassigned to the gammaproteobacteria class as *Xanthomonas maltophilia* in 1983, and eventually classified as a *Stenotrophomonas* in 1999.[2][3][4] The name has Greek roots meaning “The narrow feeder - that loves malt.” The whole-genome sequence of representative isolate K279a genome sequence was published in 2008.[5][6]

S. maltophilia can be considered a “newly emerging pathogen of concern” that is being isolated more frequently.[7][8][9] It is also recognized as one of the underestimated important multi-drug resistant organisms in hospitals by the World Health Organization (WHO).[10][11] It was ranked as the ninth most important one per British microbiologists and one of the challenging pathogens in the infectious disease community and studies.[12][2] It is widely known as an opportunistic organism associated with high morbidity and mortality rates among immunocompromised patients.

Stenotrophomonas Maltophilia

Mina S. Said; Ekta Tirthani; Emil Lesho.

► [Author Information and Affiliations](#)

Last Update: June 12, 2023.

<https://www.ncbi.nlm.nih.gov/books/NBK572123/>

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Screening for pathogens using CZID database

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ORIGINAL ARTICLE

Food Science & Nutrition

Open Access

WILEY

Microorganisms in the rumen and intestine of camels have the ability to degrade 2-amino-3-methylimidazo[4, 5-f]quinoline

Jialing Lin^{1,2,3} | Chuanhui Zeng¹ | Xueli Li^{1,2}  | Qin Tang⁴ | Jing Liao⁵ | Yan Jiang¹ |
Xianchun Zeng¹

- ❖ IQs belong to heterocyclic amines (HA) -> cancerogenic
- ❖ Camels are able to digest HAs in foods
- ❖ camel rumen and intestinal microbiota used to degrade IQ
- ❖ Four main strains with good IQ clearance, including *Ochrobactrum*, *Pseudomonas*, *Bacillus*; also *Stenotrophomonas*

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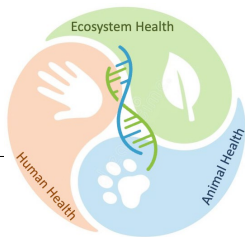


INTERNATIONAL YEAR OF
CAMELIDS
2024

Summary | bits to take home...

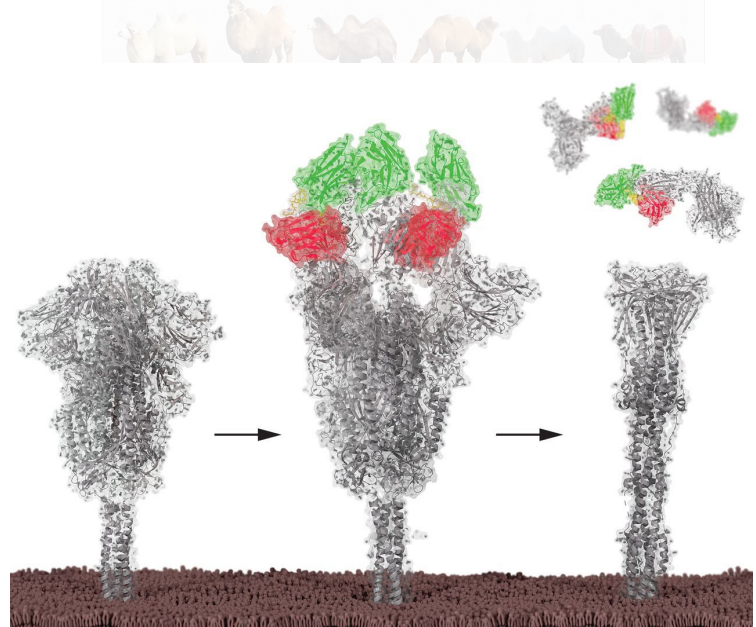
- One Health (meta)genomic sequencing allows retrieving
 - ❖ population-wide information
 - ❖ individual genomic information (IR genes)
 - ❖ pathogen information
 - ❖ microbiome information
- Identify emerging pathogens or beneficial microorganisms
- Important functions for camel, human and ecosystem health

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Importance of immune genomic diversity in camelids

- ❖ Neutralizing nanobodies block receptor binding domains (RBD) of the SARS-CoV spike glycoprotein against ACE2
- ❖ Immune response genes associated to MERS-CoV infection in dromedaries are similar to those identified in humans

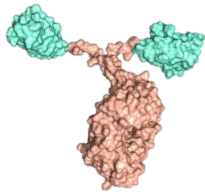


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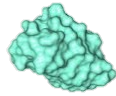


Lado et al. 2021, *Cells*; Koenig et al. 2021, *Science*; Wrapp et al. 2021, *Cell*

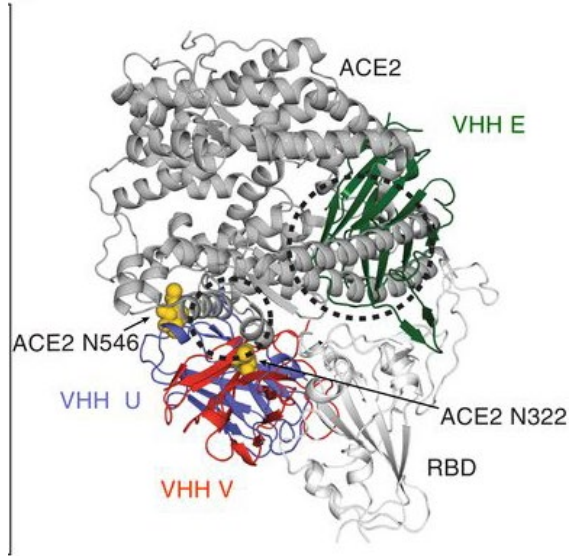
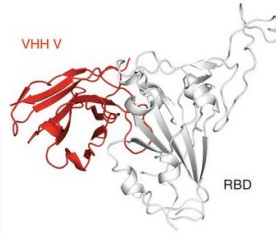
Facts: Camelid nanobodies block SARS-CoV-2



classical
antibody



nanobody



Neutralizing nanobodies block receptor binding domains of the SARS-CoV spike glycoprotein against ACE2 (host cell receptor)

Key messages



- ❖ Camel welfare is important for animal and human health.
- ❖ Camel zoonotic disease
- ❖ Camel immune system



Camelids contribute to the sustainable use of terrestrial ecosystems and build resilience to climate change.

- ❖ Camelids are of strong social and cultural importance
- ❖ Many livelihoods depend on camelid products and services
- ❖ Greater support to the camelid sector can accelerate progress towards achieving Zero Hunger and the SDGs

Excellent achievements in the International Year of Camelids 2024



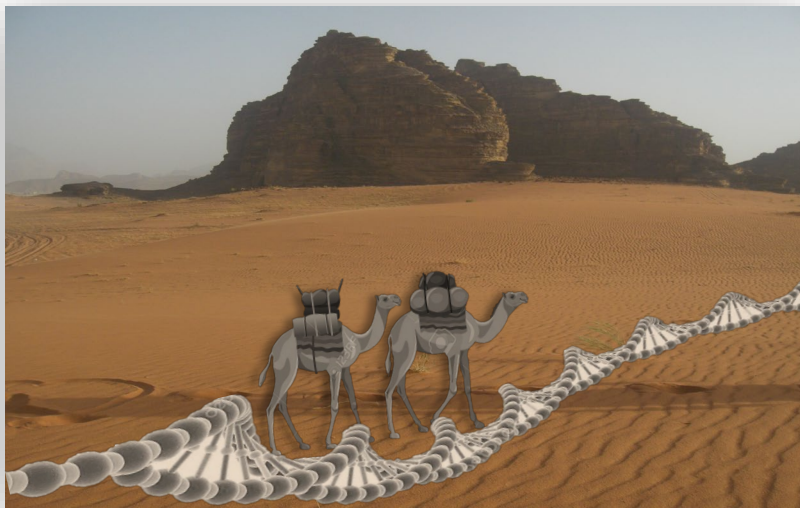
Screening for pathogens using CZID database



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Sustainable livestock species in arid regions



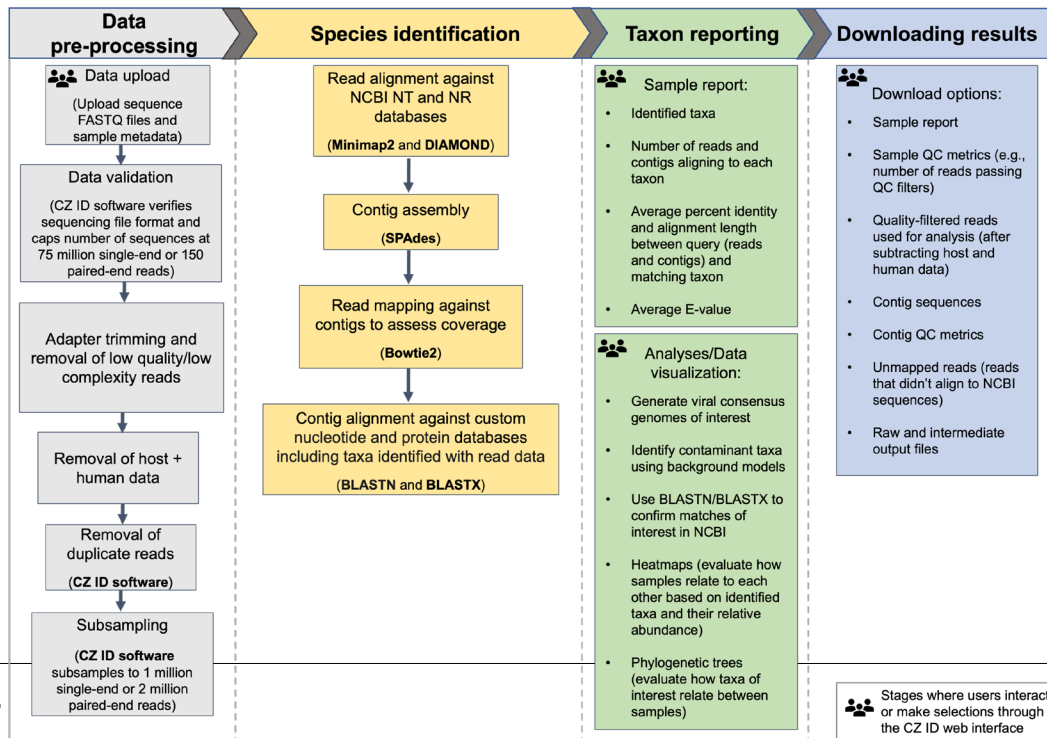
2 ZERO HUNGER



2

End hunger, achieve food security and improved nutrition and promote sustainable agriculture

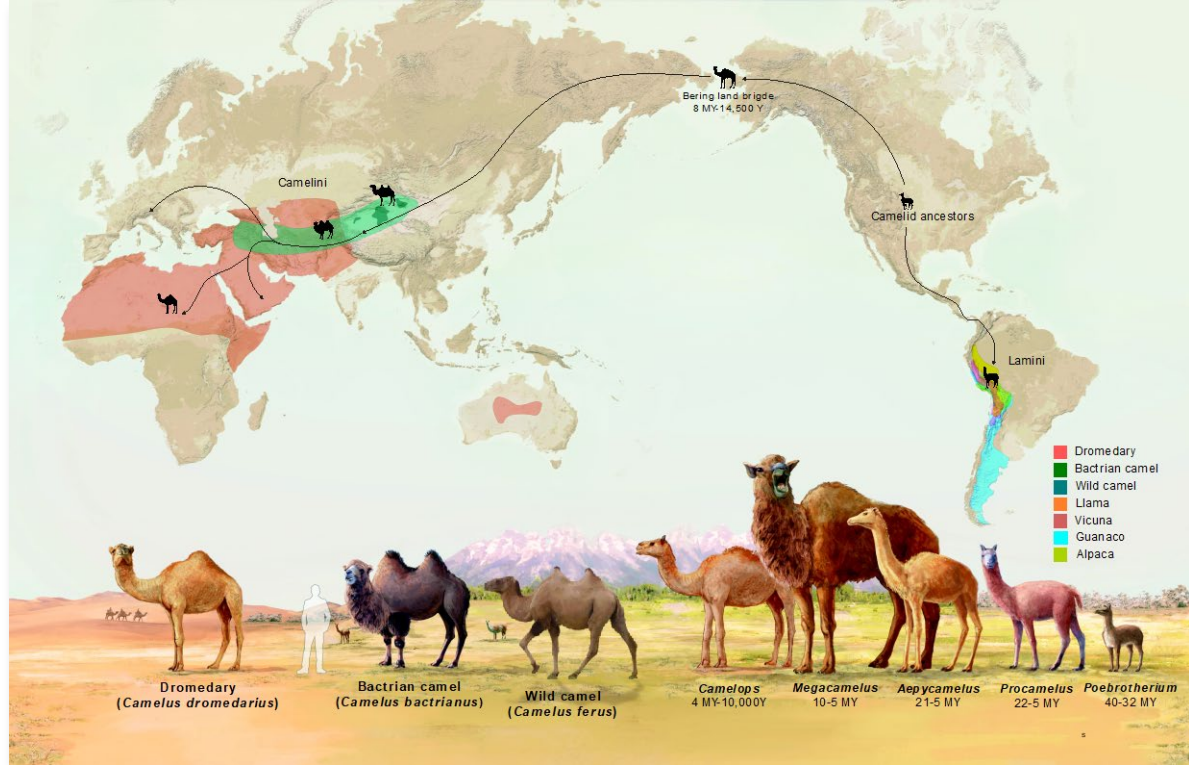
Screening for pathogens using CZID database



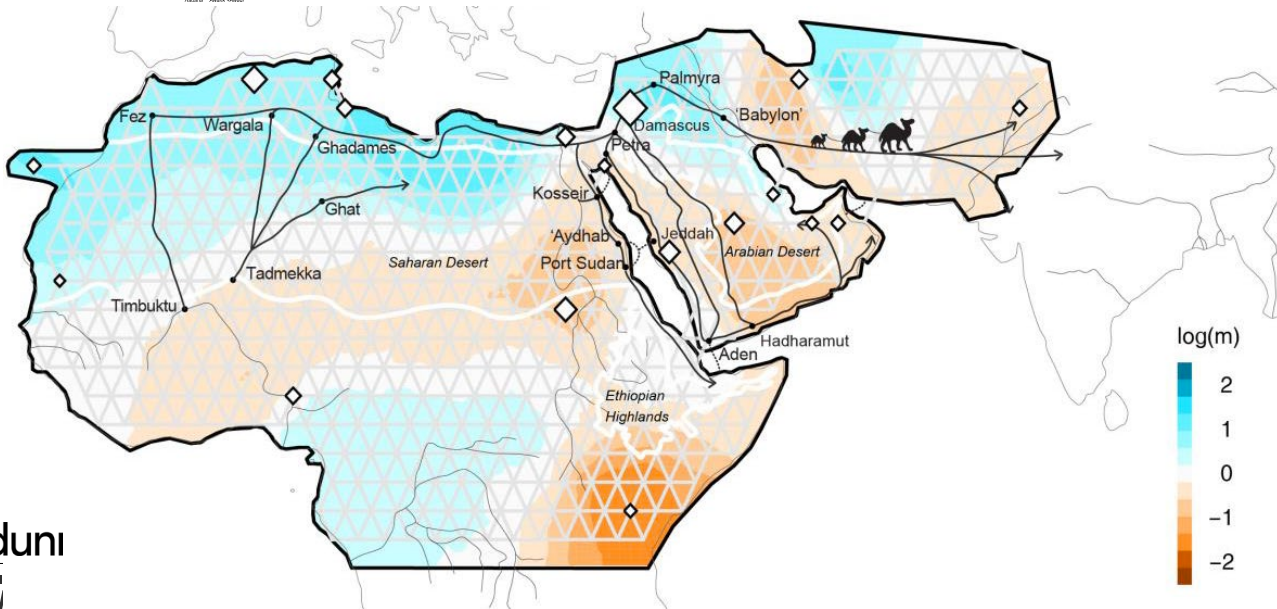
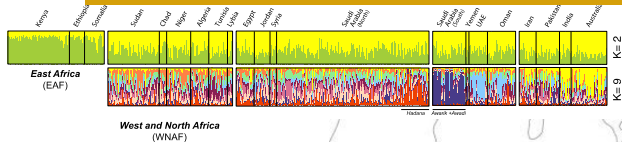
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Evolutionary history



Modern dromedary populations share genetic diversity

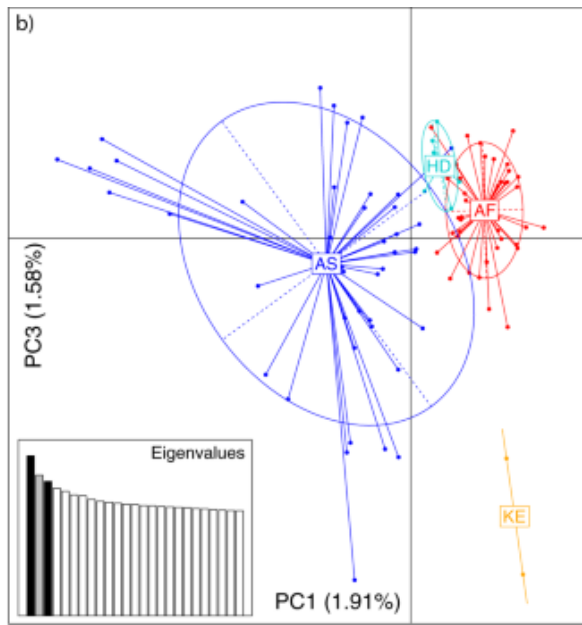
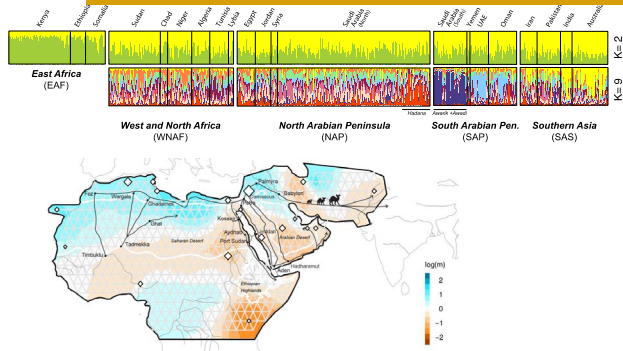


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Almathen, Charruau et al. & Burger 2016, PNAS; Lado et al. & Burger 2020, *Comms Biol*

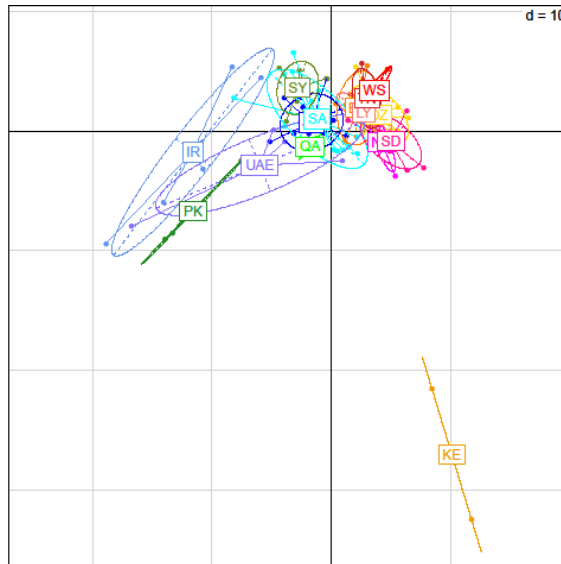
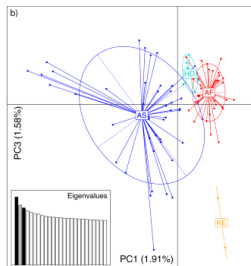
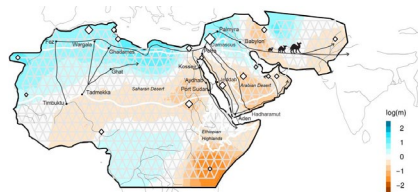
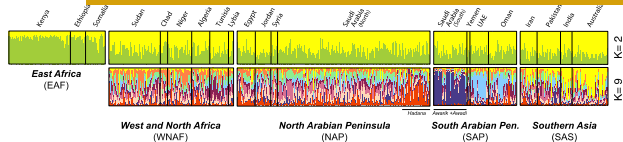
Modern dromedary populations share genetic diversity



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Modern dromedary populations share genetic diversity

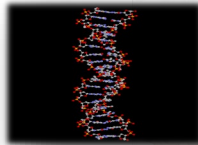


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Importance of camelids biodiversity in the world

- ❖ Maintaining (immuno)genetic diversity
- ❖ Co-evolution of pathogens and immune response genes
- ❖ Adaptive potential of the species
- ❖ Productive potential of the species



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