

PROJECT PROGRESS REPORT

Jana Robeyst Trust Fund (JRTF)

Comparative gut microbiome and antimicrobial resistance (AMR) surveillance in wild baboons and roan antelope of Ruma National Park, Kenya: implications for conservation and One Health

1. Project and grantee information

Grantee	Michael Wasonga Opere
Affiliation	Kibabii University, Kenya
Project location	Ruma National Park, Homa Bay County, Kenya
Funding programme	Jana Robeyst Trust Fund (JRTF)
Grant amount	€1,500
Reporting period	September 2026

2. Project overview and objectives

The project set to investigate gut-associated microbial communities and potential antimicrobial-resistance (AMR) concerns in wild baboons and roan antelope in Ruma National Park, Kenya. The work aimed to generate baseline evidence relevant to wildlife health, conservation management and One Health surveillance through a combination factor including wildlife faecal sampling, culture-based microbiology and molecular approaches. The project is intended to improve understanding of microbial communities associated with these wildlife hosts and to establish a basis for investigating organisms of potential public-health or conservation significance.

3. Activities undertaken and progress

3.1 Field and sample preparation

From our field sampling and sample processing we were able to generate wildlife-associated biological material for microbiological and molecular investigation (Figure 1) The samples collected in specific sampling sites are as tabulated in Table 1:

Table 1: Samples

Site	Baboon fecal	Water samples	Roan Antelope	Other opportunistic samples
Ruma National Park	15	15	5	5





Figure 1: Field work photos (Photo credit: Thomas Adino)

3.2 Culture-based microbiology

The laboratory work established and refined culture-based workflows, including serial dilution, colony isolation, sub-culturing and preservation of representative microbial isolates for downstream characterization. Culturing of 3rd, 4th and 5th Dilutions gave between 1-5 colonies per sample per plate as tabulated in Tabel 2.

Tabel 2. Serial dilutions

Lab no	3 rd Dilution	4 th Dilution	5 th dilution
N1	2	4	4
N2	4	2	3
N3	3	4	3
N4	3	3	4
N5	3	4	4
N6	4	4	5
N7	2	2	2

N8	1	3	4
N9	4	3	3
N10	2	2	3
N11	3	3	4
N12	3	4	3
N13	3	2	2
N14	2	3	2
N15	2	3	3
N16	4	4	4
N17	4	4	3
N18	4	3	4
N19	3	3	3
TOTALS	56	60	63

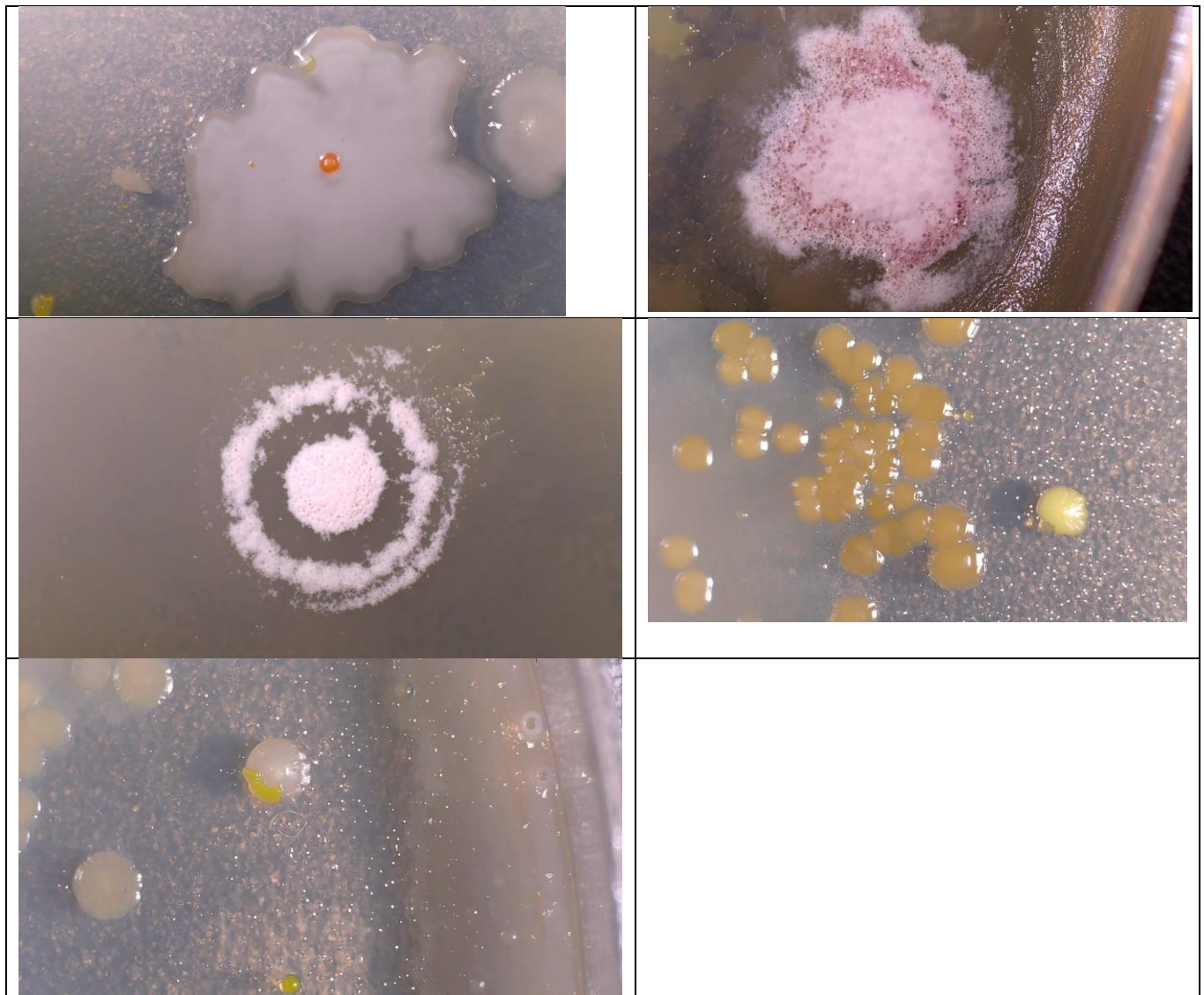


Figure 2: Some of the photos of some of the recordings

3.3 DNA extraction, PCR and sequencing

We documented DNA extraction from 12 selected samples using the Zymo Quick-DNA Fecal/Soil Microbe MiniPrep Kit, followed by PCR amplification, library preparation and an Oxford Nanopore MinION sequencing run lasting 48 hours. More than 113 preliminary sequence reads were reported

as generated, with bioinformatic analysis ongoing. Preliminary BLAST searches returned candidate taxonomic matches, including entries provisionally labelled as Parvimonas pharyngis and Leptospira barantonii, alongside unclassified and fungal sequence matches (Table 3).

Table 3. DNA extraction and PCR amplification results

Sample ID	Sample description	DNA concentration	PCR concentration
M1	Baboon faeces	65.8	6.9
M2	Roan antelope	32.2	57.6
M3	Roan antelope	13.2	337.7
M4	water	14.1	201.7

Figure 3. PCR gel electrophoresis showing amplification of representative samples prior to library preparation.



Oxford Nanopore sequencing

PCR products were pooled, cleaned, and prepared for sequencing using the Oxford Nanopore Rapid PCR Barcoding Kit (SQK-RPB114.24). Sequencing was performed on the MinION platform over a 48-hour run.

Table 4. Summary of sequencing outputs

Parameter	Result
Samples sequenced	12
Sequencing platform	Oxford Nanopore MinION
Library preparation	Completed
Sequencing duration	48 hours
Preliminary sequences generated	>113
Bioinformatic analysis	Ongoing

Preliminary microbial identification

Initial BLAST searches of representative sequence reads identified microorganisms belonging to diverse bacterial, fungal and other taxonomic groups. These preliminary identifications are currently undergoing quality filtering and taxonomic verification before ecological interpretation.

Table 5. Representative sequence reads and preliminary BLAST identifications

Sequence ID	Representative nucleotide sequence (5'–3')*	Preliminary identification	Status
M1a	TTTGTA CTTTAGCCCTCTTTGTTTTGCTG CAAAACCAAAATACAAAGAATCAGTTCCA TAACTATGACAATAACTATTTAAACAAGCT TCATTTGTAGTAT...	Parvimonas pharyngis	Under verification
M1b	TTTGTTAACCCTACTTCGTTGCGTTGTGA AGCCGTAGAGGAAAATCGCCTACCGTGA CAAAGTTGTGCGGGTGTCTTTGTGCGTTTT TCGTGCGCCGCTTC...	Leptospira barantonii	Under verification
M1c	GTCCTCTTACTTCGTTTCAGTTATATGCCA AAAGCGATATTAACGGAAAATCTTCATAA AGAAAGTTGTGCGTCTGTTACGTTTCGT CACCGCTTCACC...	Unclassified sequence	BLAST analysis ongoing
Representative sequence	—	Candida jiufengensis	Preliminary
Representative sequence	—	Candida pseudojiufengensis	Preliminary
Representative sequence	—	Additional bacterial, fungal and environmental taxa	Under analysis

* Only the initial portion of representative sequence reads is shown for presentation purposes. Complete sequence datasets are retained for downstream bioinformatic analyses.

Table 6. Overall outputs achieved during this reporting period

Research Output	Achievement
Representative samples selected for metabarcoding	12
DNA extractions completed	12
PCR amplifications completed	12
Oxford Nanopore sequencing run completed	✓
Preliminary sequence reads generated	>113
Representative microbial taxa identified	✓
Culture-based bacterial isolation	✓
Microscopy	In progress
Bioinformatic analyses	Ongoing

4. Key achievements to date

- i. Established and refined workflows for processing wildlife faecal material and recovering representative microbial isolates.
- ii. Completed DNA extraction and PCR amplification for a 12-sample sequencing batch
- iii. Completed library preparation and an initial Oxford Nanopore MinION sequencing run.
- iv. Generated more than 113 preliminary sequence reads and initiated bioinformatic and taxonomic analyses.
- v. Built on collaborations and laboratory capacity established.

5. Publications and dissemination

No manuscript arising directly from this project has yet been published or submitted. A manuscript is in preparation and is currently pending completion of the remaining sequence quality control, taxonomic verification and interpretation. The intended publication will communicate the findings once they are sufficiently validated.

6. Relevance to conservation

The project is developing baseline evidence on microbial communities associated with wildlife in Ruma National Park. Once analyses are complete, the findings may help identify microbial patterns and concerns relevant to wildlife health and ecosystem management.

7. Financial summary

Budget category	Amount spent (€)	Notes / supporting record
Fieldwork / travel	500	Transport to and within Ruma National Park for field sampling
Sampling and consumables	200	Purchase of sample collection and preservation materials and other field consumables
Laboratory analysis	300	For processing of wildlife faecal samples, including microbiological culture, serial dilution, colony isolation and sample preparation
Sequencing / molecular reagents	500	DNA extraction, PCR amplification, library preparation and molecular sequencing
TOTAL	1500	consumables used in the project

Compiled:

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