

The impact of environmental pollution on the gut microbiome of Tanzanian goats

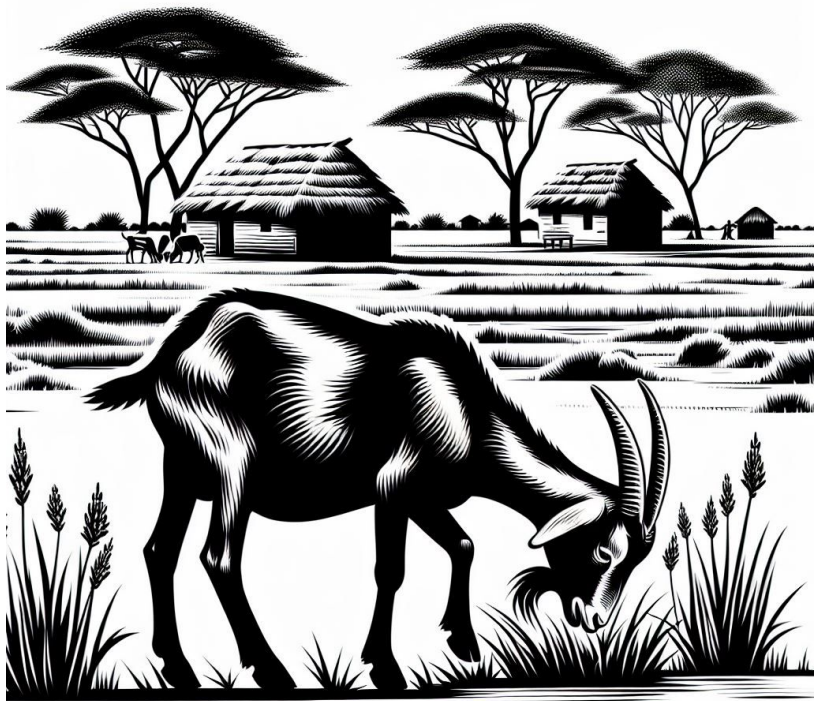
Emilie Egholm Bruun Jensen

Sample collection

19 road goats



15 rural goats



Generated with AI

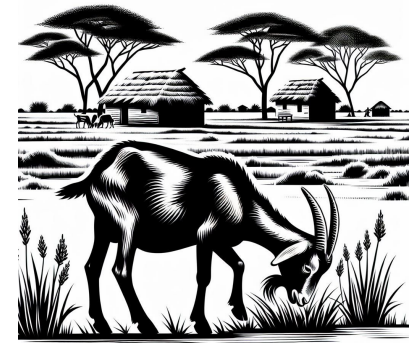
Sample collection

- How does environmental pollutants affect the gut microbiome?
 - Airborne pollutants (particulate matter, nitrogen oxides, sulphur dioxide, carbon monoxide and volatile organic compounds)
 - Gasoline, oil, rubber
 - Heavy metals
 - (Micro)plastic

19 x



15 x



Generated with AI

Sequencing and quality control

Sequencing

- QIAamp Fast DNA stool mini kit (Qiagen)
- PCR-free Kapa Hyper Prep Kit (Roche)
- Illumina Novaseq 6000 S4 (2 × 150 bp) platform

Quality control

- FoodQCPipeline

Read mapping with KMA

How much can we explain?

	Perc Aligned (%)	Perc Mapped (%)
Genomic db	6.93%	7.12%

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MAGs

SPAdes version 3.14.0 (--meta)
MetaBat version 2.12.1 (Contigs with length >1500)
checkM version 1.0.18
dRep version 2.6.2 (798 HQ and 1,452 MQ bins)

Result: 1,468 MAGs

Read mapping with KMA

How much can we explain?

	Perc Aligned (%)	Perc Mapped (%)
Genomic db	6.93%	7.12%

MAG databases

Goat MAGs + bacteria + bacteria_draft (from genomic db)

Goat padMAGs + bacteria + bacteria_draft (from genomic db)

Read mapping with KMA

AAGCGACATGGCGCGCTTAAGGCCAATGCCGCGACACATGCGCAGGCGCGACAGGTGCT
CTCCACAAGCCCCACAAGCGAGCCGAGAAGCTCTTAAGCAGCTCCTCGCCATGACAAG
GGCGCGATCATCGGTTGCAGTGTGCGCAACAGCAGAGCCACAAGCTCAACATCACTCAA
CGCTCCGACCACGCGAGAGCAGTTTATCTGTGAGATTTTTCATTGTTTACGGATTTAA
GTACGAAGGTACAAAACAATTATCAAGAGCAAAGAAAACGGCTCTTTTTTGTGTCAG
CAACACCGACAACTAACTTGATGGGCGCAGGGCGGTAGGAGCAGGCGGTAGGCGCAGG
CGGTAGGCGCAGTCAATAGGATTTGATAGGACTGAATAGGACTTAATAGGATTAAGCGCG
GCCGACATTTACCGGTGGCAGTGTGCTATCCCTAATCTTCCCATCTCTTCCCATCTCTT
CCCATCTCTTCCCATCTCTTCTATCTTGTGTTTTCTAAAATAGGTTGACTCGTTGCAC
CTTATTAACGGATAAAAGAAAGACTCTGGTTAGATAATAAACTGATAGATGTTTACT

GCTATTTCCCGTATTTCGAGATTTTCCGTGTAATGCATTTATAGTCAGTGAAAAATGCA
CTATTATTCGATTTTCAGTTGATTATTCAGCGTTTTTTCGTAACTTTGCATCTATTTG
AAACAATAACAGTTAACTATAACCCGCATGAACAAATTAATTAACCTTACCGTTATGGGA
TTTATGGCACTTACAGCATGTGCTACGGCTGCAACACCCGAGCAGCCCTGGGTCTAGAC
CGCTTTGACGATATCAAGGTA CTGCGCTATGAGGTACCCGGCTTCGAGAAGCTGTGCTG
CGCGAGAAGGAGCTTATCTACTACCTCTCGGAGGCTGCAAAGTGTGGCCGCGACATCCTC
TTCGACCAGAACTTCAAGTACAACCTCGCCGTGCGTCGCACGCTCGAGACCATCTACTCG
TCGGTACCCGGCAAGGAGCGCAAGAGCGAGGAGTTTGTAGCCATGGAGAAGTACCTCAAG
AAGGTGTGGTTCGCCAACGGCATACACCACCACTACTCGAACGACAAGTTCGACCCGAG
TTCTCGGAGGCATGGTTCGCGACCAGCTCAAGGCCATACATCAACGACTCTAACCGTCAG

Database padded with 800 characters of lowercase n to optimise conclave scoring for resolving multiple template matches.

Read mapping with KMA

Number of unique species:

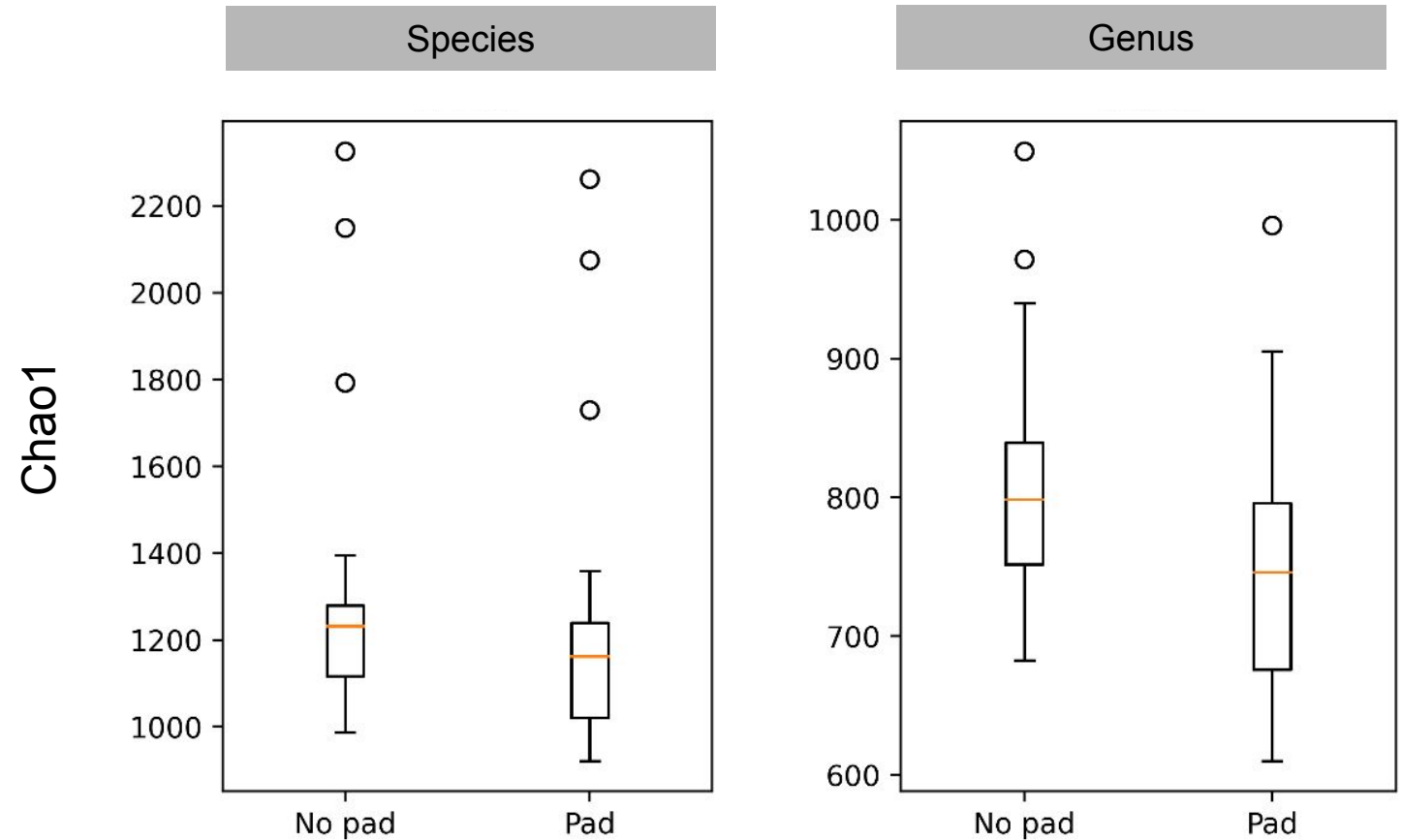
No pad: 4180

Pad : 4146

Number of unique genera:

No pad: 1611

Pad : 1580



Read mapping with KMA

How much can we explain?

	Perc Aligned (%)	Perc Mapped (%)
Genomic db	6.93%	7.12%

MAGs

Goat MAGs + bacteria + bacteria_draft (from genomic db)

Goat padMAGs + bacteria + bacteria_draft (from genomic db)

Read mapping with KMA

How much can we explain?

	Perc Aligned (%)	Perc Mapped (%)
Genomic db	6.93%	7.12%
Goat MAGs	45.94%	78.30%
Goat MAGs + bacteria + bacteria_draft	52.01%	64.66%
Goat padMAGS + bacteria + bacteria_draft	51.83%	75.53%

Bacterial community

CLR transformation

Reference length-adjusted abundance table

Bacterial community

Bacterial community

Resistome differences

- Read mapping to:
 - ResFinder
 - ResFinderFG
 - ResFinderNG
 - BacMet

Resistome differences

A

B

Functional differences

Method

- Prediction of proteins with Prodigal version 2.6.3 (-p meta)
- Functional annotation with eggNOG-mapper tool version 2.1.12
 - Mapping of trimmed reads to the predicted gene products with BBMap version 38.90
 - Abundance tables created with samtools idxstats from BBMap

Level A	Level B	Level C	ko	Sample	#query	Location	Length	mapped
Metabolism	Carbohydrate metabolism	Citrate cycle (TCA cycle) [PATH:ko00020]	K01681	Road_19	NODE_13022_length_4970_cov_2.489017_2	Road	2700.0	161.0
Metabolism	Carbohydrate metabolism	Glyoxylate and dicarboxylate metabolism [PATH:...	K01681	Road_19	NODE_13022_length_4970_cov_2.489017_2	Road	2700.0	161.0
Metabolism	Energy metabolism	Other carbon fixation pathways [PATH:ko00720]	K01681	Road_19	NODE_13022_length_4970_cov_2.489017_2	Road	2700.0	161.0
Metabolism	Carbohydrate metabolism	Citrate cycle (TCA cycle) [PATH:ko00020]	K01681	Road_19	NODE_499_length_62951_cov_3.502784_38	Road	2664.0	229.0
Metabolism	Carbohydrate metabolism	Glyoxylate and dicarboxylate metabolism [PATH:...	K01681	Road_19	NODE_499_length_62951_cov_3.502784_38	Road	2664.0	229.0



Functional analysis

Method

- Prediction of proteins with Prodigal version 2.6.3 (-p meta)
- Functional annotation with eggNOG-mapper tool version 2.1.12
 - Mapping of trimmed reads to the predicted gene products with BBMap version 38.90
 - Abundance tables created with samtools idxstats from BBMap
- Curated db: PlasticDB (219 enzymes described to break down plastics)

Plastic-degrading capability

Xenobiotic biodegradation and metabolism

Road

Rural

Functional adaptation

Linking gene product to genomes

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=> None of them were present in the MAGs

- To do:
 - Blast contigs to do taxonomic annotation of the contigs

