



22 May 2025



# The microbiology of noma: insights from a pilot deep shotgun metagenomic project of patients presenting at the Noma Children's Hospital, Sokoto, Nigeria

Micheal Olaleye<sup>1</sup>, Angus More O'Ferrell<sup>2</sup>, Richard Goodman<sup>2</sup>, Deogracia Wa Kabila<sup>1</sup>, M. Peters<sup>3</sup>, Gregoire. Falq<sup>4</sup>, Moses Malual<sup>1</sup>, Joseph Samuel<sup>1</sup>, Donal Doyal<sup>4</sup>, Diana Gomez<sup>5</sup>, Gbemisola Oloruntuyi<sup>6</sup>, Shafi'u. Isah<sup>7</sup>, Adeniyi Semiyu Adetunji<sup>7</sup>, Elise Farley<sup>1,8</sup>, Mark Sherlock<sup>4</sup>, Adam Roberts<sup>2</sup>, Mohana Amirtharajah<sup>4</sup>, \***Stuart Ainsworth**<sup>8,9</sup>

<sup>1</sup>Médecins Sans Frontières (MSF), Sokoto, Nigeria; <sup>2</sup>Liverpool School of Tropical Medicine, Liverpool, UK; <sup>3</sup>MSF, Zamfara and Abuja, Nigeria; <sup>4</sup>MSF, Amsterdam, Netherlands; <sup>5</sup>MSF, Geneva, Switzerland; <sup>6</sup>MSF, Lagos, Nigeria; <sup>7</sup>Noma Children's Hospital, Sokoto, Nigeria; <sup>8</sup>International Noma Network, Cape Town, South Africa; <sup>9</sup>The University of Liverpool, Liverpool, UK

\* [stuart.ainsworth@liverpool.ac.uk](mailto:stuart.ainsworth@liverpool.ac.uk)

## Introduction

Noma is an oral-facial gangrene that primarily affects chronically malnourished children aged 2–6 years who live in conditions of extreme poverty. Supported by Médecins Sans Frontières (MSF) since 2014, the Noma Children's Hospital (NCH) in Sokoto, Nigeria, is one of only two facilities fully dedicated to treating noma in the country. Previous attempts to characterise the microbiology of noma have been hampered by limitations of technology. Here, we present data from the first deep shotgun metagenomics survey of the oral microbiome of patients with acute noma.

## Methods

Between October 2023 and February 2024, 20 patients with acute noma were recruited. Inclusion criteria consisted of patients who arrived at NCH and who: i) were diagnosed as having Stage 0–4 noma; ii) were aged 0–12 years; iii) had not had antibiotics in the last 7 days, and iv) provided assent (where applicable) and whose caregiver provided consent. Buccal swabs and saliva samples were collected, and total DNA was extracted and shotgun sequenced using Illumina NovaSeq X Plus. Healthy saliva metagenome data were compiled from existing publicly available data, consisting of 20 individuals from various countries. Taxonomic classification and relative abundance were determined using Kraken and Bracken, with differential genera analysis via DESeq2. Key microbial predictors were identified using random forests. Metagenome assembly was performed with metaSPAdes, and metagenome assembled genomes (MAGs) were classified using MetaBAT2 and GTDB-Tk.

## Ethics

This study was approved by the MSF Ethics Review Board (ERB), the Liverpool School of Tropical Medicine ERB, the Nigerian Federal ERB, the Usman Danfodiyo University Teaching Hospital Health Research and Ethics Committee, and the Sokoto Ministry of Health Ethics Department.

## Results

Of the 20 patients, 10 were female and 10 male, and 17 were aged 2–6 years, with three aged 7–10 years. All patients had stage 1–4 noma, with stage 2 (n=10) and stage 3 (n=7) being predominant. Differential analysis showed *Treponema*, *Porphyromonas*, *Bacteroides*, and *Selenomonas* species were more abundant in noma samples, while *Streptococcus*, *Veillonella*, *Gemella*, *Schaalia*, *Rothia*, *Actinomyces*, and *Haemophilus* were more abundant in the healthy metagenome dataset. Random Forest and Permanova analysis both identified presence of *Treponema* and absence of *Streptococcus* as key aspects of distinguishing noma metagenomes from healthy metagenomes. Analysis revealed over 40 determinants of antimicrobial resistance in the metagenomes of patients with noma, with resistance for tetracycline, lincosamide, beta-lactam, and aminoglycoside present in more than 50% of samples. Analysis of MAGs identified 14 novel uncultured *Treponema* species, one of which was particularly abundant (present in 50% of samples).

## Conclusion

The study highlights significant microbial alterations in noma oral microbiomes compared to healthy oral microbiomes, particularly the depletion of *Streptococcus* and enrichment of *Treponema* species. The discovery of a novel *Treponema* species possibly associated with noma suggests a potential target for future research.

## Conflicts of interest

All authors declare no competing interests.