Gut Bacterial Metataxonomic Analysis of Elderly from Algarve

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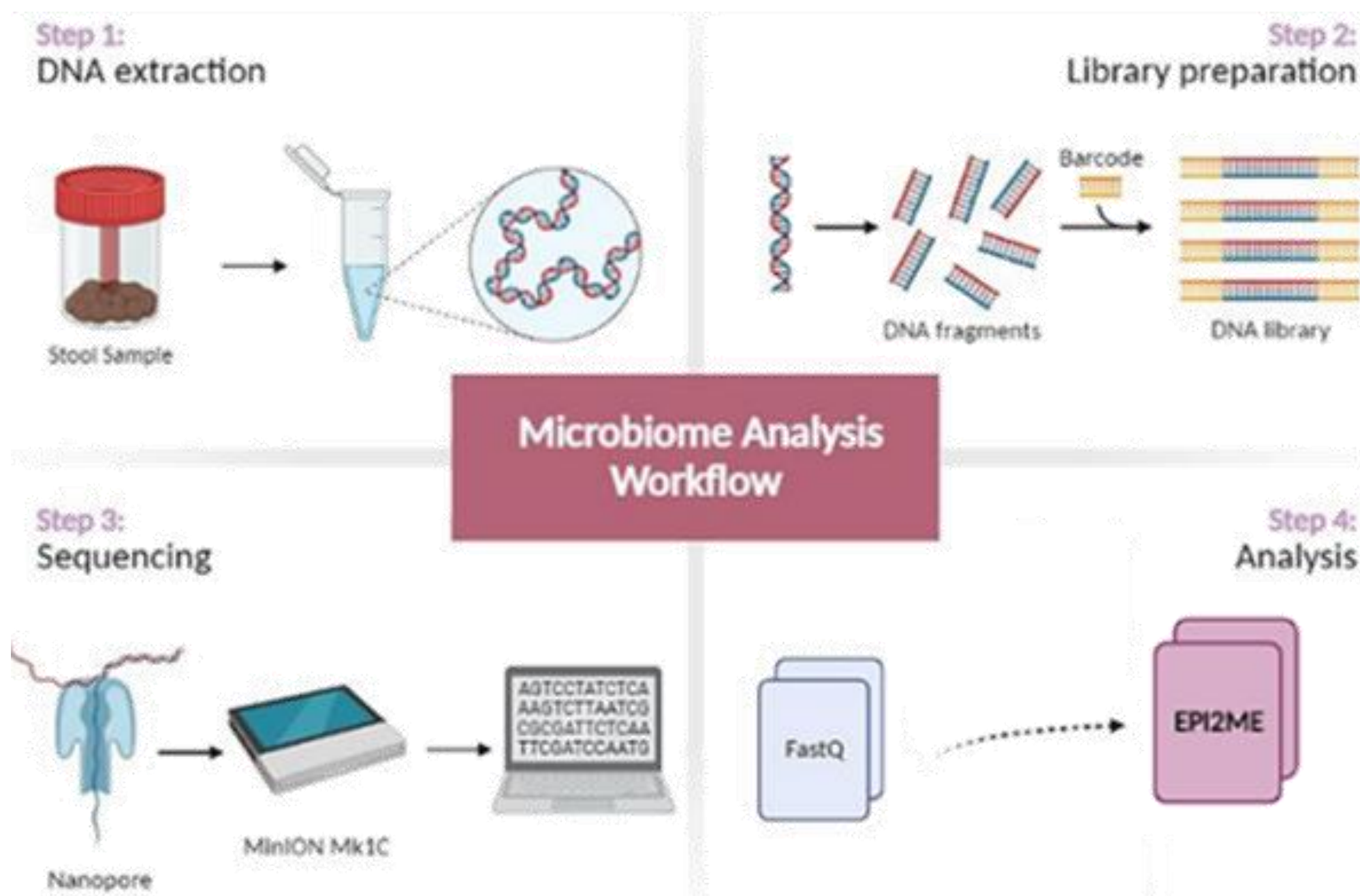
Introduction

Ageing is characterized by a progressive loss of homeostasis, impaired function, and susceptibility to death[1]. The microbiome of the elderly suffers variation, and geography is one of the factors that contribute to this variation[1]. Our goal is to evaluate the intestinal bacteriome of elderly individuals from Algarve. To achieve this, the intestinal bacterial metataxonomic analysis of the elderly from Algarve was performed by sequencing the *16S rRNA* gene using the Oxford Nanopore MinION system.
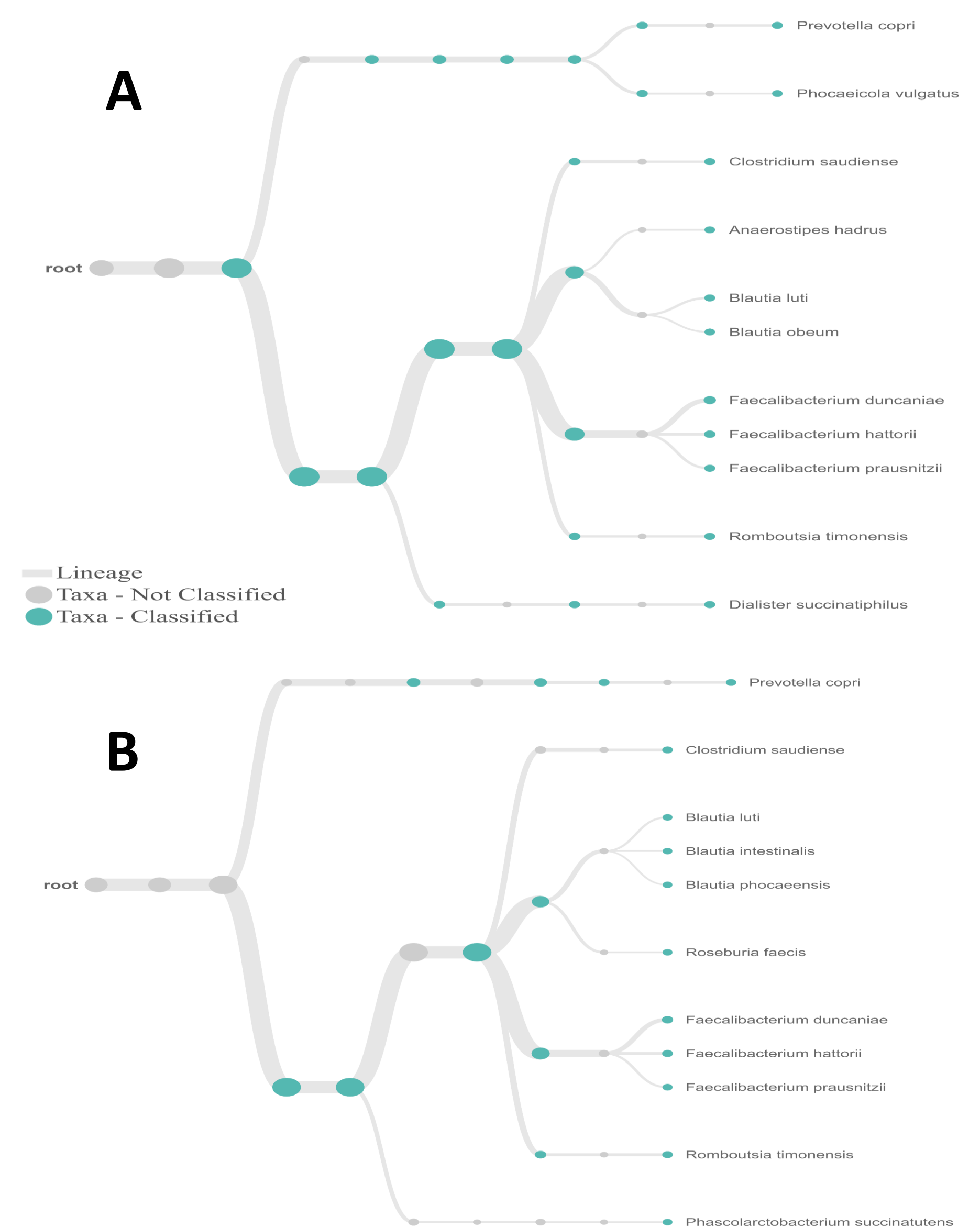
Methodology

- 3 main phyla: **Bacillota**, **Pseudomonadota** and **Bacteroidota**

- Bacterial species **cluster** the individuals by location **Rural** or **Urban**.

- *R. champanellensis*, *B. obeum*, *G. tenuis* and *P. vulgatus* was present in **Rural** , whereas *P. copri*, *D. succinatiphilus*, *R. timonensis* and *P. dorei* was present in **Urban** among the ten most abundant bacterial species.
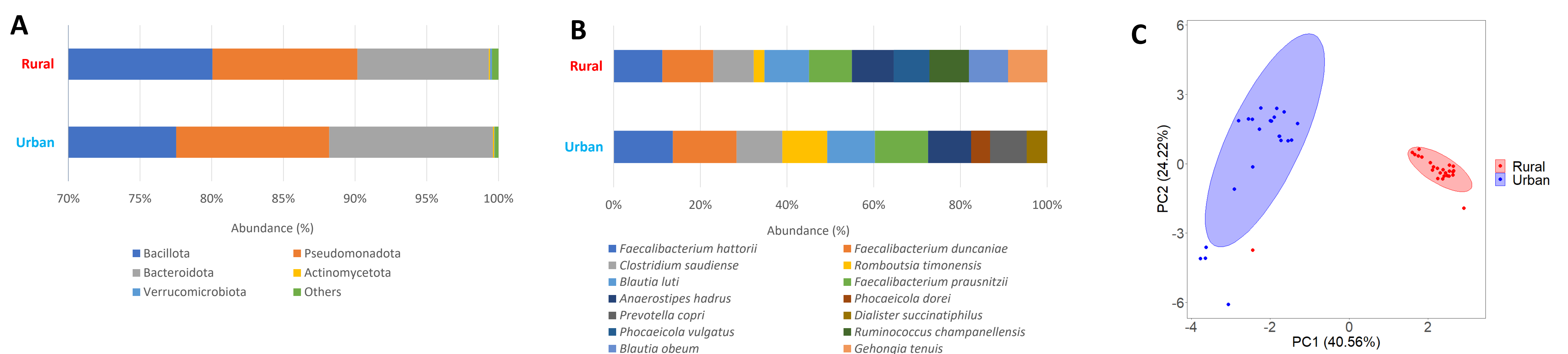
Results

Figure 2. Phylogenetic representation of the bacterial species identified in **A) Rural** and **B) Urban** faecal samples. Relative abundance is represented by the thickness of each branch. Minimum abundance cut off 0.5% and 10 top abundance taxa. Data obtained with the EPI2ME platform.

Figure 1. The most abundant phyla and species in the analysed faecal samples of elderly people from Algarve region, Portugal. Comparison of the phyla **(A)** and species **(B)** abundancy between **Urban** (n=25) vs **Rural** (n=23) samples. **C)** Principal component analysis (PCA) on Hellinger transformed species abundance data.

Conclusion

Differences in intestinal bacteriome of the enrolled old people, Rural vs Urban were observed, This study expands the knowledge on the intestinal bacterial community between rural and urban individuals from Algarve that can impact their health status.

References

1. DeJong, E. N., Surette, M. G., & Bowdish, D. M. E. (2020). The Gut Microbiota and Unhealthy Aging: Disentangling Cause from Consequence. Cell host & microbe, 28(2), 180–189.

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