A healthy human "scaffold" of Italian adults' microbiota: a proposal for reference intervals

👤 **Sisti D**, Amatori S , Piccini F, Pazienza V, Citterio B, Baffone W, Donati Zeppa S, Biavasco F, Prospero E, De Luca A, Artico M, Battistelli M, Minelli A, Perri F, Binda E, Pracella R, Santolini R, Sestili P, Gobbi P, Rocchi MBL.

INTRODUCTION

Several factors, from genetic background, age, lifestyle, dietary habits, contribute to microbiota heterogeneity in humans.

Understanding the variability of the "healthy microbiome" is a major challenge in microbiome research, studying the factors constituting the normal ranges of these features in healthy populations. To date, just a few data were reported about microbiota of healthy population.

AIMS

- To define the reference intervals of the gut microbiota of a healthy Italian people sample with relatively homogeneous physiological features.

METHODS

148 healthy subjects of seventeen Italian regions, (69M / 79F | 23-57 years old) were recruited.

A questionnaire has been administered to each participant to collect information regarding the demographic and anthropometric variables, dietary habits and physical activity. For 16SrDNA sequencing, the total microbial DNA of the samples was extracted.

K means clustering was performed, PERMANOVA was used on the Bray-Curtis distance matrix to assess if the gut microbiota structure differed between the two clusters.

The 90% C.I. relative to the 95% lower and upper limits of the reference intervals have been calculated using the bootstrap method.

RESULTS

Differences in phyla, families and genera among two clusters were observed (PERMANOVA, Bonferroni corrected; p<0.001 for all comparison).
Heatmap was used to represent the abundance of the nine more prevalent phyla.
Firmicutes and Bacteroidetes reached together about 85% of the total phyla abundance.

CONCLUSION

Our study may contribute to primarily identify the existence, within the healthy Italian population, of a commonly distributed, constantly present, main microbiological pattern, thus suggesting the presence of a short of a microbiological scaffold.
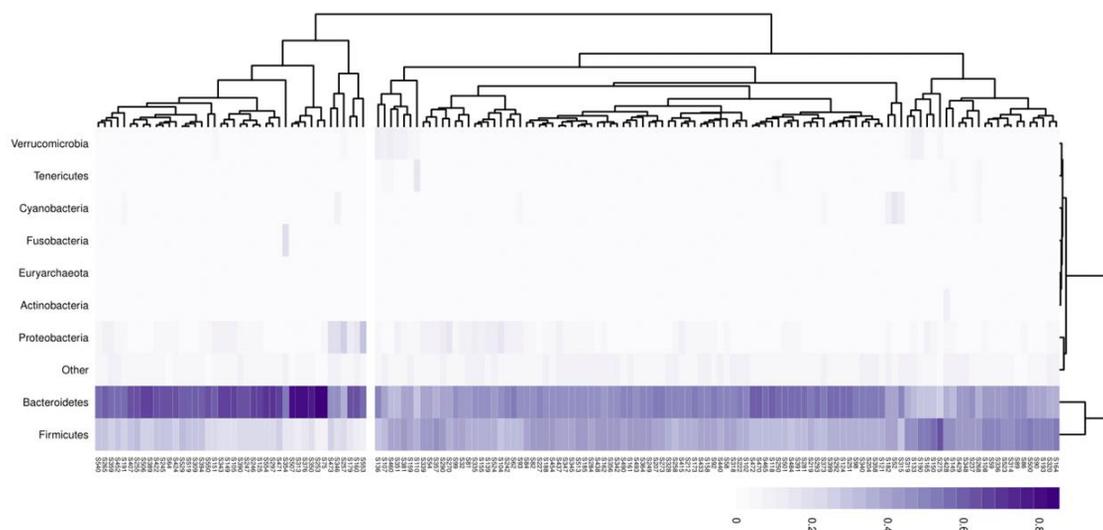

Figure caption

Heatmap of the most represented 9 phyla. Each row represents a single phylum, with each column representing a different subject. Bray-Curtis distance has been used as a clustering method.

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