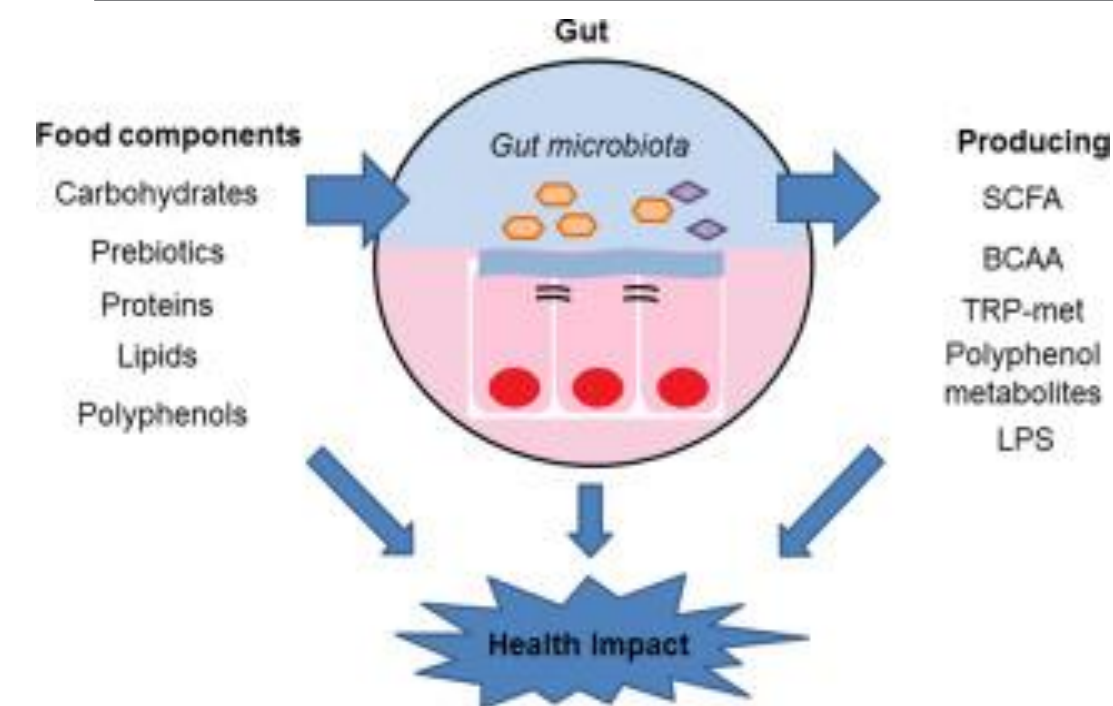


Characterizing the Gut Microbiome of Colorectal Cancer Patients in Mali by Disease Stage.

Diakité Mahamane Talphi 1,3,4; Palanisamy Nisha 2; Diallo Dramane 1,3; Camara Issiaka 1; Koné Amadou 1,3; Diakité Bréhima 1; Traore Cheick Boukadari 1,4; Maiga Mamoudou 1,2; Lifang Hou 2

¹University of Sciences Techniques and Technologies of Bamako, ²Northwestern University Center for Global Health, ³University Clinical Research Center, ⁴Point G University Hospital Center of Bamako

Background



It has been demonstrated that the microbiota is associated with the development of many types of cancer including colorectal cancer. Furthermore, the microbiota has been shown to play an essential role in the efficacy of cancer chemotherapy and immunotherapy by modulating the tumor microenvironment, thus, suggesting its direct involvement not only in the development but equally in the propagation of cancer.

The specific aims of this project are to Evaluate the impact of colorectal cancer stage on gut microbiome biodiversity and Assess the impact of colorectal cancer (CCR) on gut microbiome-related metabolic pathways.

<https://www.sciencedirect.com/science/article/abs/pii/S0963996918305829>

Question

Do patients with colorectal cancer have a typical gut microbiota profile by stage of disease?

Methods

This particular study will analyze the gut microbiome in colon cancer patients in Mali by cancer stage, which may clarify the differences from the prior studies.

we will use the whole genome sequencing, for the analysis of the complete genome of the gut microbiota, and measure the concentration of inflammatory cytokines from CCR and healthy by flow cytometry.

Non-parametric Wilcoxon test, Metaphlan and Kraken softwares will be used to analyze metagenomic data.

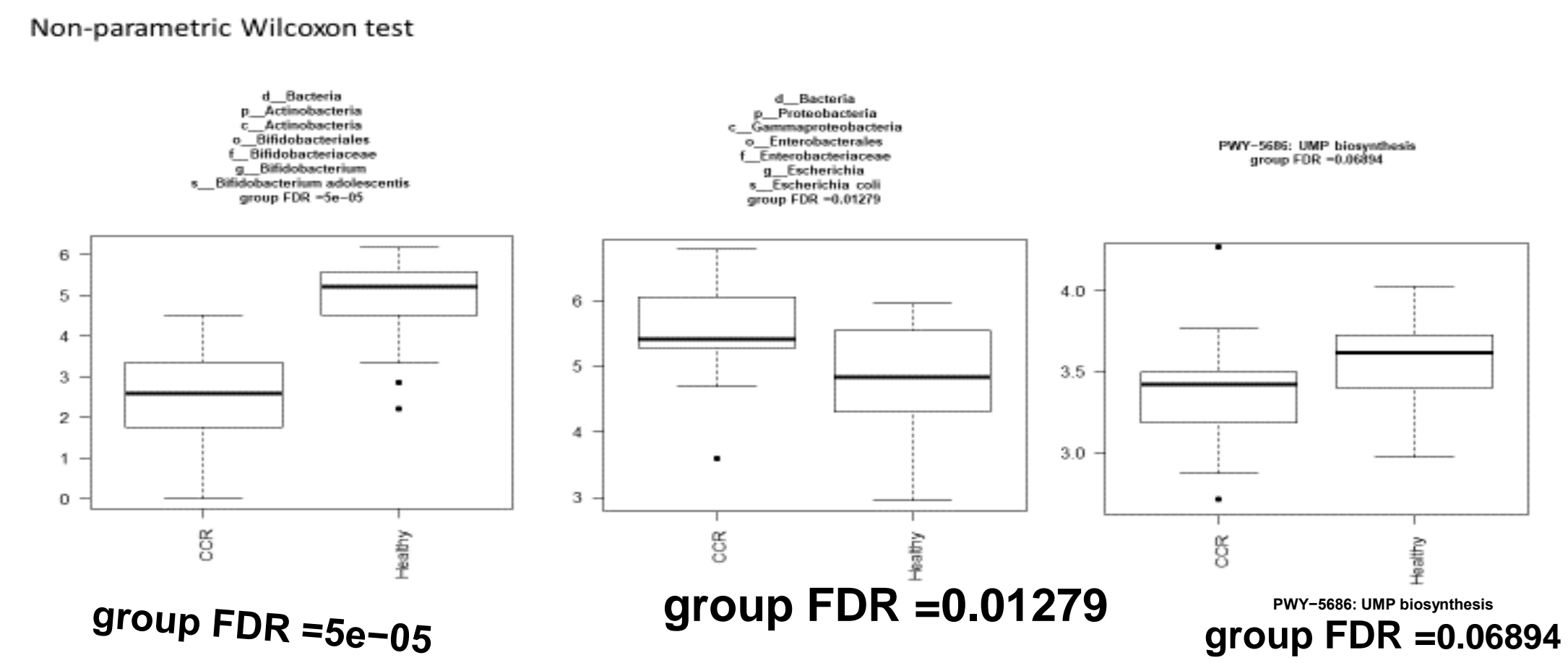


Fig.1 Analysis of gut microbial composition from healthy control and CCR

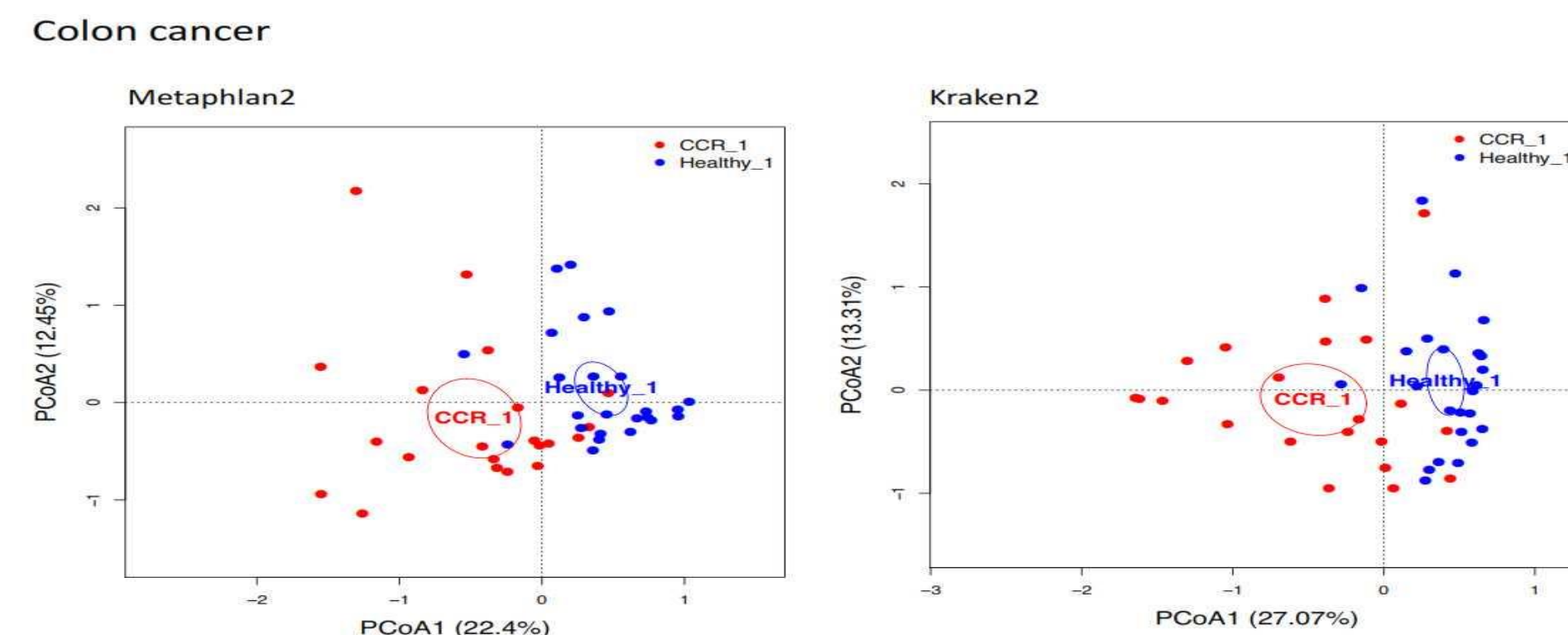


Fig.2: Quantitative taxonomic profiling of microbial communities

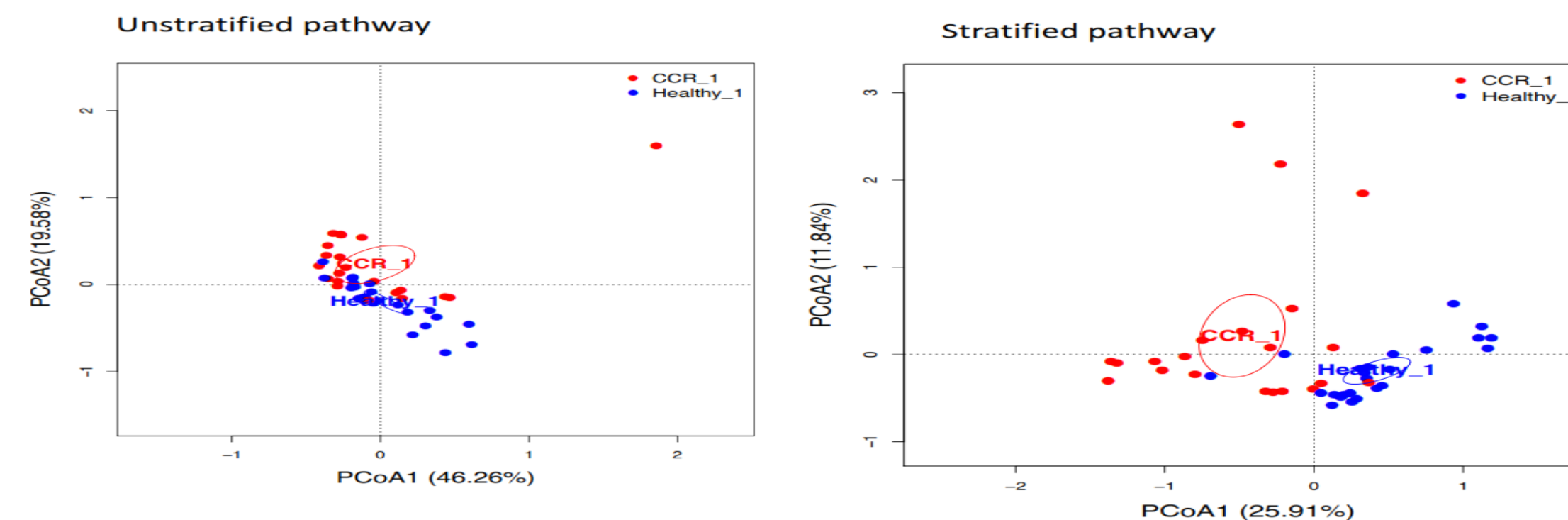


Fig.3: Metagenomic stratified and unstratified analysis from CCR and healthy control

Results

Early studies have shown significant changes in the gut microbiome during colorectal cancer, but the types of changes reported in microbial populations are not consistent in these studies. This may be due to differences in disease stages within the studied population.

We found that for the same disease stage, the gut microbiome diversity is well-conserved and significantly different from healthy controls in terms of both microbial composition and metabolic pathways, including inflammation pathways.

Conclusions

The preliminary results of this study generally show a difference between healthy control and colorectal cancer patients in terms of microbial composition (phylogenetic and taxonomic).

This study may have implications for microbiome-based prevention and treatment strategies, such as probiotics, prebiotics and fecal transplants; thanks to this knowledge of the difference in terms of composition of the microbiota between healthy control and colorectal cancer patients.

How would you describe the importance of your work to a lay person with no background in population health?

A good knowledge of the composition of the gut microbiota during colorectal cancer is an important step for the implementation of prevention and treatment strategies against the disease, such as probiotics, prebiotics and fecal transplants.

