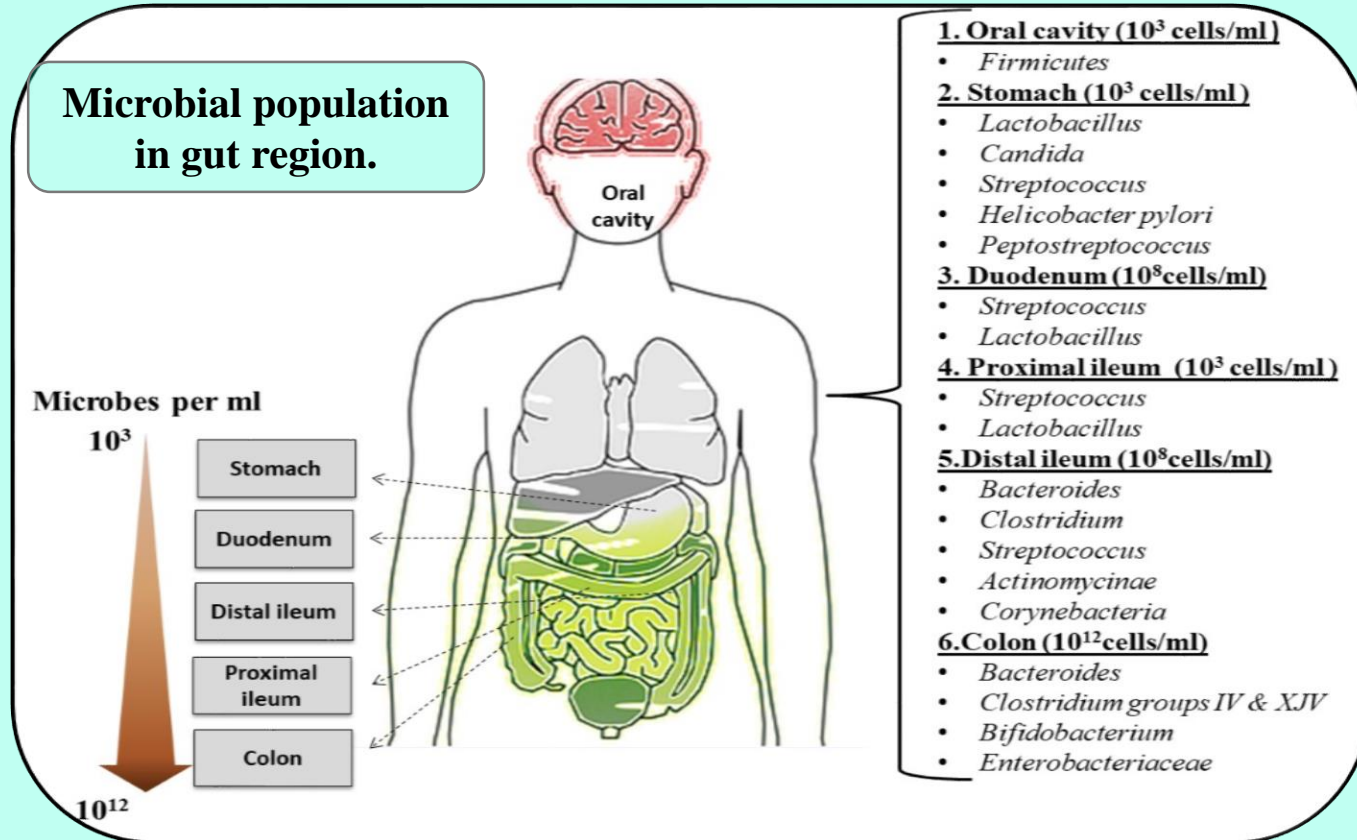


Faculty and Postdoc
Population, Health & Wellness

Introduction

Obesity is the major metabolic disorder that affects more than 2 billion people worldwide. Gut microbiota comprises of abundant species of bacteria and their diversity significantly contributes to Good health; whereas, changes in their composition to the development of diseases. Diet is one of the main factors contributes to the change in the gut microbiota. Microbiota specific to different regions of the gut influence the metabolism of the various diets. We investigate the taxonomical abundance present in the fecal & cecum samples from the cafeteria (CAF) diet fed Sprague Dawley (SD) rats compared with normal chow diet fed rats. We highlight the behavior, phenotype and metabolic activities of the CAF and normal chow diet fed animals.

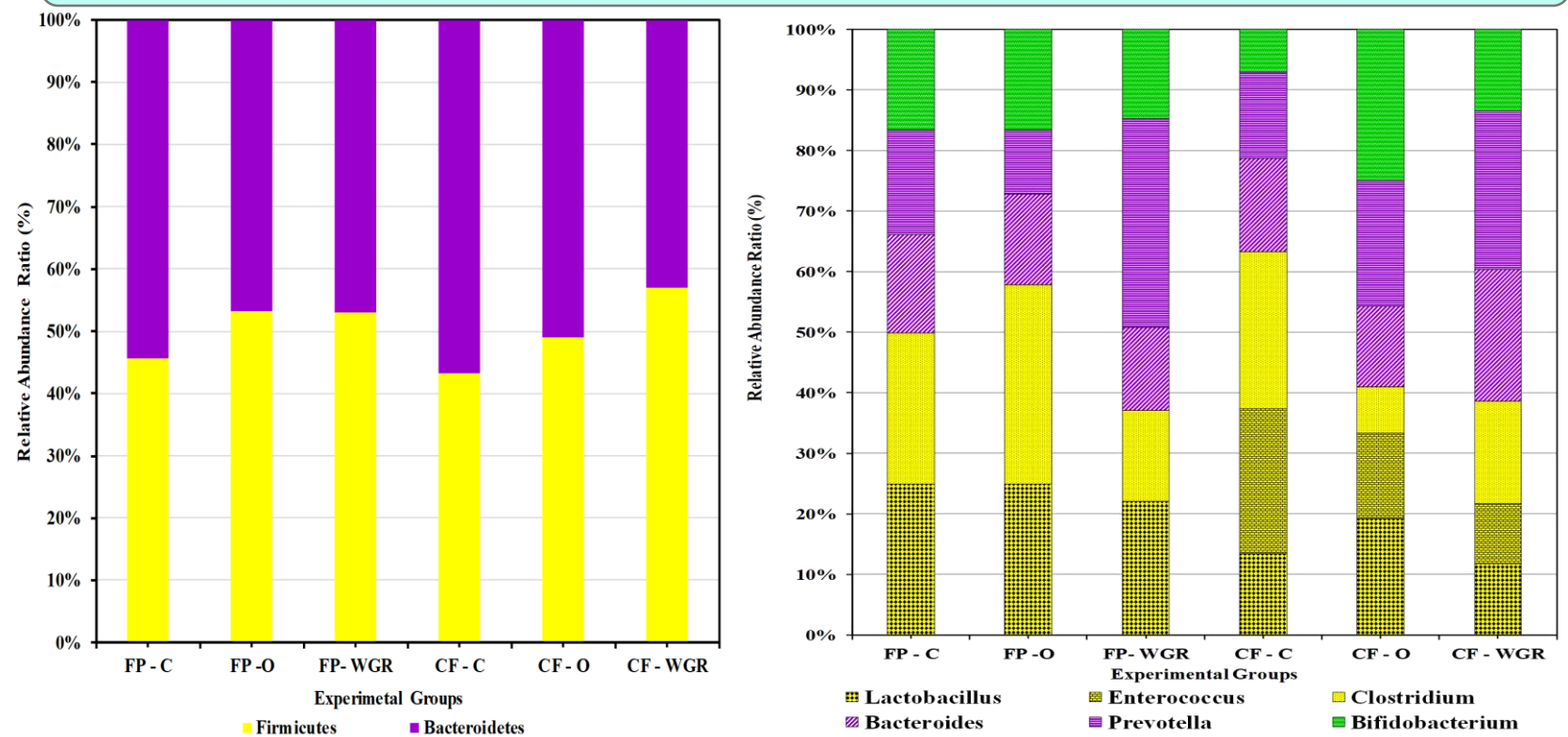


Experiments

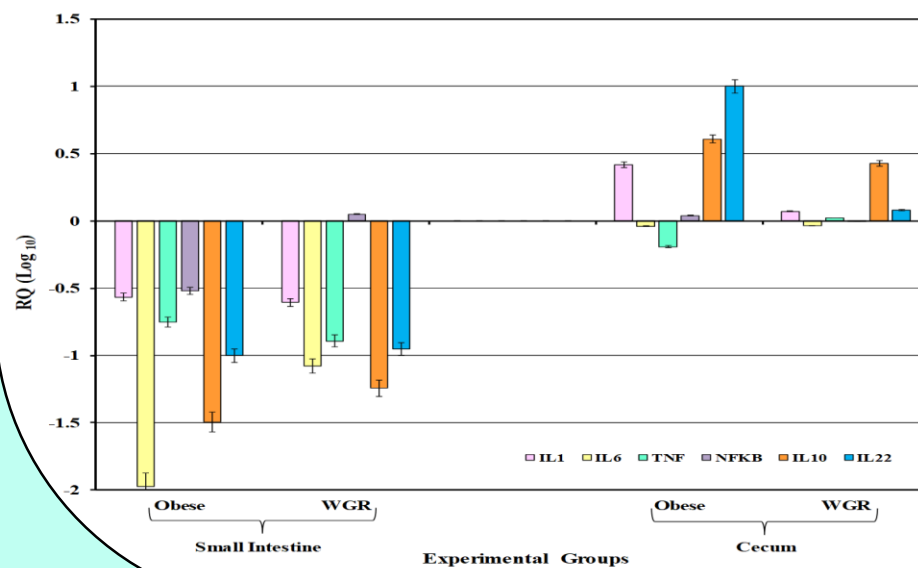
- ❖ SD rats are separated into two different groups. Control group with normal chow diet, the obese group with cafeteria (CAF) diet. Body weight, food and water intake are recorded for 8 weeks.
- ❖ The phenotype of the experimental SD rats are closely observed and changes noted accordingly
- ❖ After necropsy, the cecum stool samples are collected under aseptic conditions from all experimental groups Fresh fecal samples (2 - 4 pellets) from each group are also collected before necropsy and stored immediately at -80 °C.
- ❖ Genomic DNA extracted from fecal pellet and cecum stool samples using QIAamp DNA kit.
- ❖ PCR experiments were done using specific primer for the respective gut microbiome analysis and quantified the relative abundance of the Phylum and genera.

Results

Relative abundance of gut microbial population in CAF fed SD rats

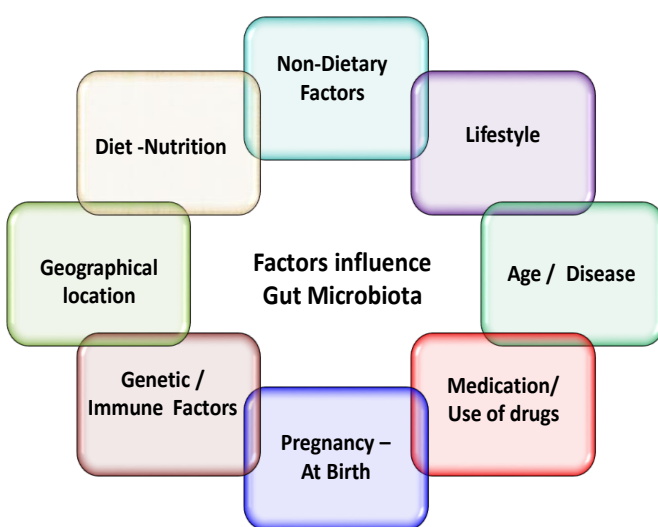


Gene expression analysis of Inflammatory markers



- ❖ The results showed significant up-regulation of IL-1 β , IL-10 & IL-22 in both WGR & obese compared to the control groups whereas most of them are downregulated in small intestine samples irrespective of diet regime..
- ❖ CAF diet alters gut microbiota that might produce signaling components causing up-regulation of chemokines at the tissue level that might contribute in low-grade systemic inflammation related to CAF-diet induced obesity

Factors affecting the gut microbial diversity



Conclusion

- ❖ Based on our study outcome, we conclude that focus on strain dependent metabolic pathway and metabolite analysis may significantly reveal the dynamic mechanism behind the diet induced obesity and the weight gain resistant phenotypes.
- ❖ If all these parameters are satisfied, then certainly a study of this kind might reveal the mechanism in detail with more clarity for further therapeutic approach.

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Research Outcomes: This work published in "Advances in Microbiology" Journal as a research article and Food and Nutrition Science as a Review article