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Evaluation of the Faecal Microbiota and its Metabolites in Obese Pet Owners and their Obese Pets

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Introduction

One of the most significant healthcare issues facing the human population, and shared by small companion animals, is the growing problem of obesity[1]. Defined as an accumulation of excessive amounts of adipose tissue in the body, obesity is related to the development of other metabolic disorders such as type 2 diabetes[2].

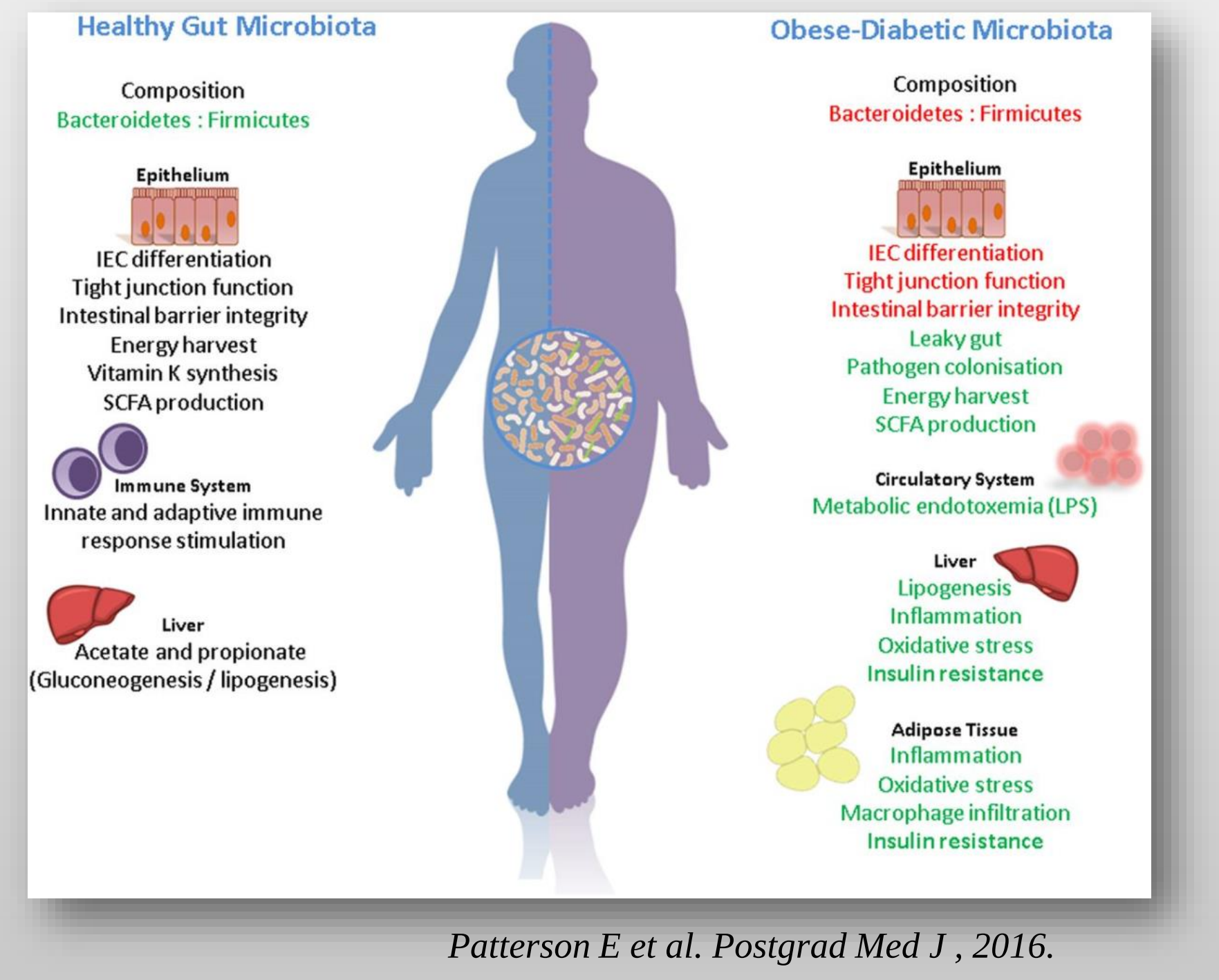
Despite decades of research into causes and risk factors, obesity remains a serious concern for people and companion animals. The quality and composition of diet and an individual's genetic endowments may impact on the types of microbes that exist in the gastrointestinal tract, which are directly implicated in food absorption, and can alter energy utilization[3].

Studies in animal models and humans revealed a different gut microbiota pattern between obese and lean groups[4-6], showing that obesity may affect the diversity of the gut microbiota. However, other studies, both in humans and dogs, did not support these findings, not clarifying the relationship between this pathology and the microbiota[7, 8]. These discordant results stand out the necessity of studying better the microbial composition, as well as the role of its metabolites in obese humans and companion animals.

Objective

Since prevalence of obesity in pets is rising during the last years, the purpose of this project is, by taking a "One Health" perspective, to study the possible role of the microbiota and its metabolites in this disease. To accomplish it, we will evaluate the faecal microbiota and metabolome of obese and healthy companion animals as well as their owners, analysing also relevant factors as lifestyle and diet.

Considering that no studies have been performed to compare faecal microbiota of both obese pet and owners, we expect be able to report valuable information about the intestinal microbiota interaction with this disease, which could be useful for new perspectives of research, treatment, diagnosis and prevention.



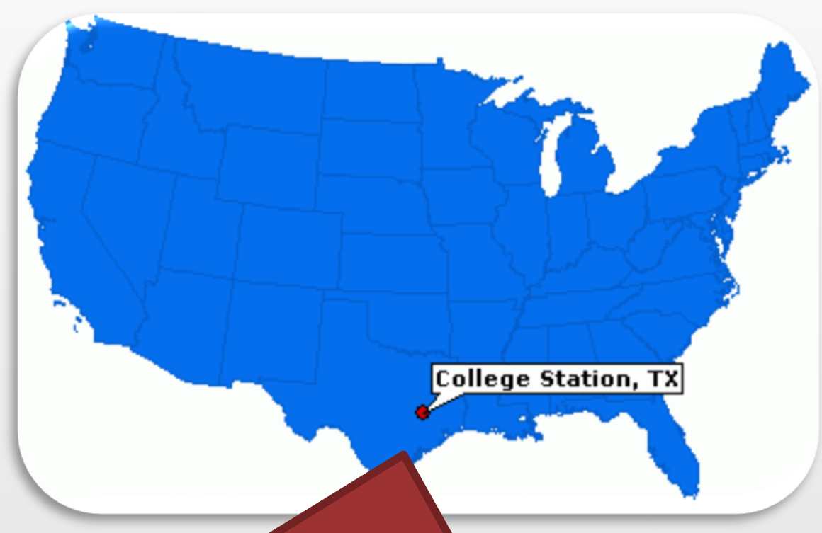
Patterson E et al. Postgrad Med J , 2016.

Method

Animal and human enrollment. Sample collection
The recruitment of participants for the project is being carried out in the Abruzzo region (Italy). The check-up of the animals is being effectuated at the Veterinary Hospital of the University of Teramo, whereas for the owners is being realised at Sani Medical Center.

DNA isolation
DNA from faecal samples will be extracted with MoBio Power soil DNA isolation kit (MoBio Laboratories, USA).

Sequencing of 16S rRNA genes
Bacterial pyrosequencing targeting the V4–V6 region of the 16S rRNA gene will be performed at MR DNA Laboratory, Shallowater, TX, USA.



Metabolomics
Metabolome analysis of stool samples will be achieved by GS-MS equipment.

Bioinformatics and Statistical Analysis
Differences in bacterial communities between groups of individuals will we analyzed with the bioinformatics tool QIIME 2.

References

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Main Research Questions

I. Do specific faecal microbiota and/or metabolome profiles exist in healthy, obese, and obese-diabetic individuals?
II. Are there similarities between faecal microbiota and/or metabolome composition of pets and owners?
III. Is the gastrointestinal microbiota a good target for the treatment of obesity and diabetes?
IV. Are the gut microbial metabolites possible targets for metabolic disorders treatment?
V. Could be the gastrointestinal microbiota and/or metabolome a non-invasive biomarker to detect obesity and diabetes?