

# Evaluation of the Intestinal Microbiota in Obese Pet Owners and their Obese Pets

*S Bermúdez Sanchez<sup>1,2</sup>, J Suchodolski<sup>2</sup>, A Gramenzi<sup>1</sup>, F Marsilio<sup>1</sup>.*

*1.Faculty of Veterinary Medicine, Università degli Studi di Teramo, Località Piano D'Accio, Teramo, Italy.*

*2.Gastrointestinal Laboratory, Department of Small Animal Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, Texas, United States of America*

REP-eat

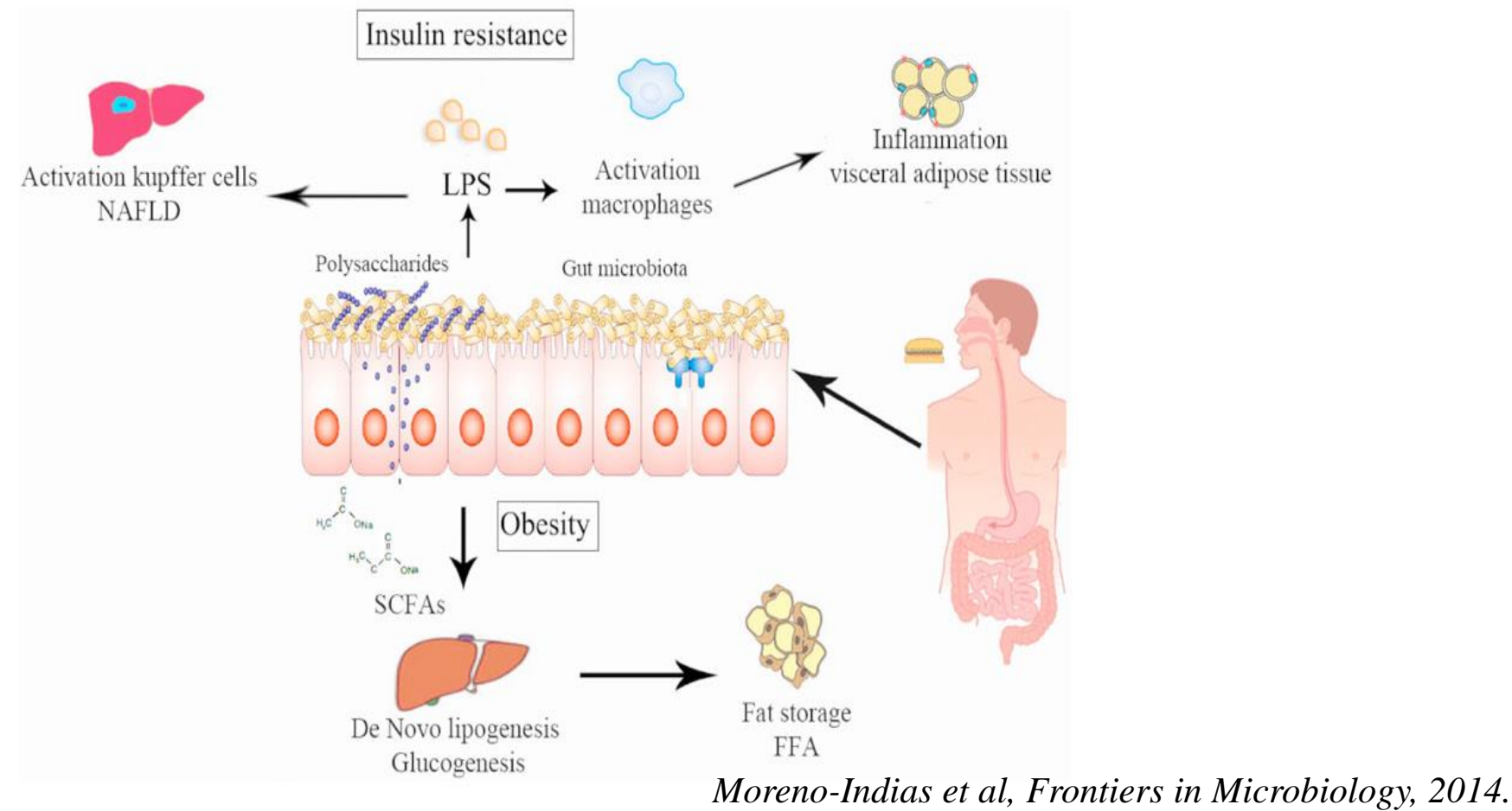
REP-eat

## Introduction

The prevalence of obesity is rapidly increasing worldwide, constituting an important health problem. Obesity is the result of a positive imbalance between energy intake and energy expenditure over a long period and is related to the development of other disorders such as type 2 diabetes (T2D), non-alcoholic fatty liver disease (NAFLD), metabolic syndrome (MetS) and cardiovascular disease (CVD)<sup>1</sup>.

Similarly as occurs in human, there is increasing the number of pets with obesity, being the most common nutritional disorder in companion animals <sup>2</sup>.

Despite decades of research into causes, risk factors and interventions for prevention and treatment, obesity remains a serious concern for people and companion animals. Apart from genetic susceptibility, sedentary lifestyle and increased food consumption<sup>3,4</sup>, environment factors such as changes in gut microbiota and gut metabolites pool seem to play a role in the development of metabolic disorders as obesity and diabetes <sup>5-10</sup>.



## Objective

The purpose of this project is implementing the knowledge about obesity and the possible implication of the gut microbiota and its metabolites in this disease. To accomplish it, we will evaluate the faecal microbiota and metabolome of obese non-diabetic, obese-diabetic, and healthy companion animals as well as their owners.

Considering the relevant environment factors; lifestyle and diet, through New-Generation sequencing (NGS) method and bioinformatics tools we will define the faecal microbiota profile and its metabolites in both pets and owners with different health conditions, and keeping in mind the term: One Health, we expect be able to report valuable information about this disease, which could be useful for new perspectives of research, treatment, diagnosis and prevention.

## References

- Després JP, Lemieux I. Abdominal obesity and metabolic syndrome. *Nature* 2006;444:881-887.
- German AJ. The growing problem of obesity in dogs and cats. *J Nutr* 2006;136:1940S-1946S.
- Mayer-Davis EJ, Costacou T. Obesity and sedentary lifestyle: modifiable risk factors for prevention of type 2 diabetes. *Curr Diab Rep* 2001;1:170-176.
- Hu FB. Sedentary lifestyle and risk of obesity and type 2 diabetes. *Lipids* 2003;38:103-108.
- Cox AJ, West NP, Cripps AW. Obesity, inflammation, and the gut microbiota. *Lancet Diabetes Endocrinol* 2015;3:207-215.
- Ley RE, Bäckhed F, Turnbaugh P, et al. Obesity alters gut microbial ecology. *Proc Natl Acad Sci U S A* 2005;102:11070-11075.
- Turnbaugh PJ, Ley RE, Mahowald MA, et al. An obesity-associated gut microbiome with increased capacity for energy harvest. *Nature* 2006;444:1027-1031.
- Greiner T, Bäckhed F. Effects of the gut microbiota on obesity and glucose homeostasis. *Trends Endocrinol Metab* 2011;22:117-123.
- Khan MT, Nieuwdorp M, Bäckhed F. Microbial modulation of insulin sensitivity. *Cell Metab* 2014;20:753-760.
- Fernandes J, Su W, Rahat-Rozenbloom S, et al. Adiposity, gut microbiota and faecal short chain fatty acids are linked in adult humans. *Nutr Diabetes* 2014;4:e121.

## Method

### • Animal and human enrollment. Sample collection

To describe the faecal microbiota and metabolome of pets and their owners in different health conditions, the stool samples collection is being carried out considering a questionnaire carefully elaborated.

### • DNA isolation

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

### • Sequencing of 16S rRNA genes

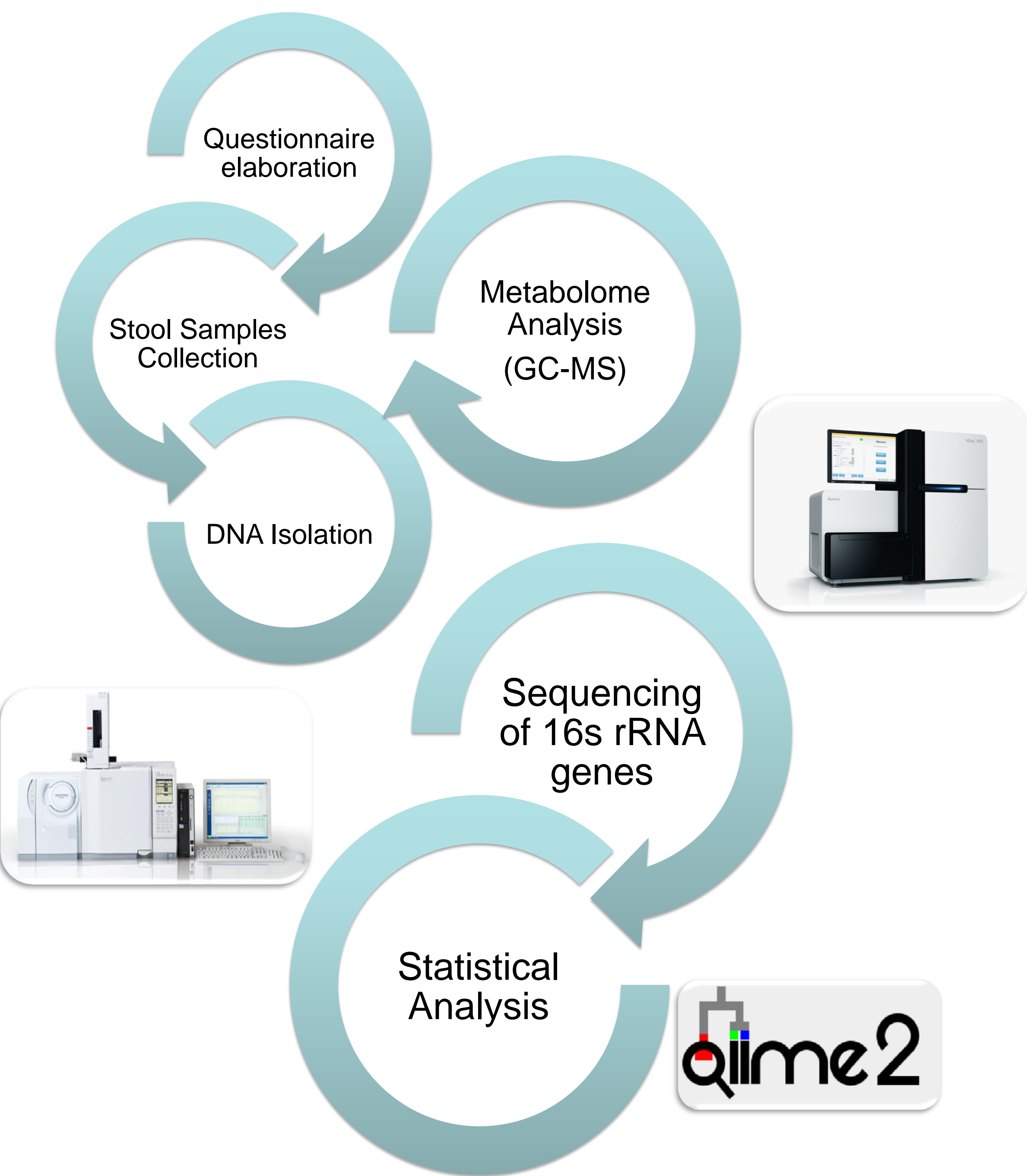
Bacterial pyrosequencing targeting the V4–V6 region of the 16S rRNA gene will be performed at MR DNA Laboratory, Shallowater, TX, USA.

### • Metabolomics

Metabolites analysis of stool samples will be achieved with the use of GS-MS equipment.

### • Bioinformatics and Statistical Analysis

Differences in bacterial communities between groups of individuals will we analyzed with the bioinformatics tool Qiime 2.



## Main Research Questions

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