



شبكة المعلومات الجامعية
التوثيق الإلكتروني والميكرو فيلم

بسم الله الرحمن الرحيم



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جامعة عين شمس

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Relation of Lactobacilli Acidophilus To Obesity in Egyptian Population

Thesis

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إِنَّمَا إِلَهُكُمُ اللَّهُ الَّذِي لَا إِلَهَ إِلَّا

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هُوَ وَسِعَ كُلَّ شَيْءٍ عِلْمًا

سُورَةُ طٰهٍ



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List of Abbreviations

<i>Abbrev.</i>	Full term
<i>4AAP</i>	4-chlorophenol and 4-aminoantipyrine
<i>ACVD</i>	Atherosclerotic cardiovascular disease
<i>ALT</i>	Alanine aminotransferase
<i>AMPk</i>	Adenosine monophosphate kinase
<i>ANOVA</i>	Analysis of variance
<i>ARC</i>	Arcuate nucleus
<i>ASD</i>	Autism Spectrum Disorder
<i>AST</i>	Aspartate aminotransferase
<i>AUC</i>	Area under the curve
<i>BAT</i>	Brown adipose tissue
<i>BBB</i>	Blood-brain barrier
<i>BMI</i>	Body mass index
<i>CART</i>	Cocaine and amphetamine regulated transcript
<i>CD</i>	Crohn's disease
<i>CE</i>	Cholesterol esterase
<i>CHD</i>	Coronary heart disease
<i>ChREBP</i>	Carbohydrate responsive element-binding protein
<i>CKD</i>	Chronic kidney disease
<i>CLA</i>	Conjugated linoleic acid
<i>COX</i>	Cholesterol oxidase
<i>CRC</i>	Colorectal cancer
<i>ct</i>	Cycle Threshold
<i>CVD</i>	Cardiovascular disease
<i>DAP</i>	Dihydroxyacetone phosphate
<i>EASO</i>	European Association for the Study of Obesity
<i>ELISA</i>	Enzyme-linked immunosorbent assay
<i>EOSS</i>	Edmonton Obesity Staging System
<i>FIAF</i>	Fasting induced adipocyte factor
<i>FISH</i>	Fluorescence in situ hybridization
<i>FMO3</i>	Flavin monooxygenases
<i>FMT</i>	Faecal microbiota transplantation

<i>Abbrev.</i>	Full term
<i>FT3</i>	Free serum tri-iodothyronin
<i>GALT</i>	Gut associated lymphoid tissues
<i>GF</i>	Germ-free
<i>GHb</i>	Glycosylated Haemoglobin
<i>GI</i>	Gastrointestinal
<i>GWAS</i>	Genomewide association studies
<i>Hb A1c</i>	Hemoglobin A1c
<i>HC</i>	Hip circumference
<i>HFD</i>	High-fat diet
<i>HRP</i>	Horseradish peroxidase
<i>HTGL</i>	Hepatic triglyceride lipase
<i>IBD</i>	Inflammatory bowel disease
<i>IBS</i>	Irritable bowel syndrome
<i>IL- 6</i>	Interleukin -6
<i>IR</i>	Insulin resistance
<i>LCAT</i>	Lecithin-cholesterol acyltransferase
<i>LCP</i>	Lactobacillus containing probiotics
<i>LDL</i>	Low density lipoproteins
<i>LFY</i>	low-fat yogurt
<i>LMIC</i>	Low and middle income countries
<i>LPL</i>	Lipoprotein lipase
<i>LPS</i>	Lipopolysaccharides
<i>MRS</i>	Man Rogosa Sharp agar
<i>MS</i>	Metabolic syndrome
<i>NAFLD</i>	Non-alcoholic fatty liver disease
<i>NLR</i>	NOD-like receptors
<i>NPY</i>	Neuropeptide Y
<i>nTS</i>	Nucleus tractus solitarii
<i>OSA</i>	Obstructive sleep apnoea
<i>OTUs</i>	Bacterial operational taxonomic units
<i>PAMPs</i>	Pathogen-associated molecular patterns
<i>PCOS</i>	Polycystic Ovarian Syndrome
<i>PCR</i>	Polymerase chain reaction
<i>POMC</i>	Pro-opiomelanocortin

<i>Abbrev.</i>	Full term
<i>PRRs</i>	Pattern recognition receptors
<i>PY</i>	Probiotic yogurt
<i>qPCR</i>	Quantitative PCR
<i>rRNA</i>	Ribosomal RNA gene
<i>SCFAs</i>	Short-chain fatty acids
<i>SREBP1</i>	Sterol regulatory element-binding transcription factor 1
<i>T1DM</i>	Type 1 diabetes mellitus
<i>T2DM</i>	Type 2 diabetes mellitus
<i>TGs</i>	Triacylglycerols
<i>TLRs</i>	Toll-like receptors
<i>TMA</i>	Trimethylamine
<i>TMAO</i>	Trimethylamine-N-oxide
<i>TMB</i>	Tetramethylbenzidine
<i>TNF-α</i>	Tumor necrosis factor- α
<i>UC</i>	Ulcerative colitis
<i>VLDL</i>	Very low density lipoproteins
<i>WAT</i>	White adipose tissue
<i>WC</i>	Waist circumference
<i>WHO</i>	World Health Organization
<i>WHR</i>	Waist-to-hip ratio
<i>WHtR</i>	Waist-to-height ratio

ABSTRACT

Background: Current considerations are existed about the sharing role of gut microbiota in the enhancement of obesity and its allied comorbidities

Objective: The aim of this observational case-control study was to assess the possible relation of *Lactobacilli acidophilus* to obesity in a sample of Egyptian population by real-time PCR of *Lactobacilli acidophilus* in stool.

Subjects and methods: The present study enrolled 20 healthy slim subjects and 40 subjects who had BMI >25 kg/m². Routine laboratory analysis and identification of stool *Lactobacillus acidophilus* by quantitative real time PCR technique was performed for all enrolled subjects.

Results: *Lactobacillus acidophilus* was expressed in 21 out of 40 (52.5%) faecal samples of obese cases and 16 out of 20 (80%) of faecal samples of non-obese cases. In rest of samples in both studied groups, the expression was below the detection limit. The results showed that the mean CT at which *Lactobacilli* were expressed in the obese cases was (38.89±2.57) compared to (36.08±4.63) in non-obese cases and this indicated that the expression of *Lactobacilli* was statistically higher in non-obese subjects compared to obese cases (P =0.04).

Conclusion: *Lactobacillus acidophilus* was significantly lowered in obese Egyptian patients. The argument about the significance of correlation between imbalance in gut microbiota and obesity is considered one of the hottest open topics in medicine.

Key words: Obesity, Gut Dysbiosis, *Lactobacilli acidophilus*.

Introduction

The prevalence of obesity has risen steeply over the past two decades, and it has become a significant global health issue (*Arroyo-Johnson et al 2016*).

The proper management of obesity is critical to prevent the development of obesity-associated metabolic disorders, including insulin resistance, diabetes, and cardiovascular disease, which increase patient mortality (*Gallagher et al., 2015; Bastien et al., 2014*).

Lipid accumulation and increased systemic inflammation in obesity is known to trigger an imbalance of energy homeostasis and abnormal cellular responses to insulin, leading to insulin resistance and type 2 diabetes (*Samuel and Shulman, 2012*).

Although a number of therapies have been developed to treat them, the disease remains largely irreversible, with many patients failing to respond satisfactorily to treatment, underlining the importance of prevention at the early stages of obesity and insulin resistance (*Alberti et al., 2007*).

The gut microbiome is composed of a thousand of bacterial species that are encoding approximately 3.3 million genes and largely shared 160 species individually (*Arumugam et al 2010*). It is also known to have a profound impact on host physiology and pathology. The diversity and stability of the gut microbiome in host organisms can, in turn, be affected by diverse environmental factors, including food consumption, which ultimately influences host metabolism (*David et al., 2014*).

Changes to the gut microbiota are associated with the development of obesity and type 2 diabetes. Furthermore, targeting the gut microbiome using