

Cross-talk between Folic acid and MMP2 /Leptin genes Methylation in Childhood Obesity, Nutrigenomics approach

Thesis

Submitted for partial fulfillment of M.D in Medical Biochemistry & Molecular Biology
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العلاقة بين حمض الفوليك واضافة مجموعة الميثيل لجينات الميتالوبروتيناز ٢ و الليبتين في السمنة في الاطفال. نهج المورثات الغذائية

توطئة للحصول على درجة الدكتوراه في العلوم الطبيث الاساسية (كيمباء حيوبة طبية)

مقدمةمن

الطبيبة /سارة السيد عبد الرحمن ابراهيم ماجستير الكيمياء الحيوية الطبية والبيولوجيا الجزيئية كلية الطب- جامعة عين شمس

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First of all, thanks to Allah, for his great care and guidance in every step of my life and for giving me the ability to complete this work.

I would like to express my deepest appreciation, respect and thanks to Dr. Samar Kamal Kassim, Professor of Medical Biochemistry & Molecular Biology, faculty of Medicine, Ain Shams University, for her great support, helpful advice and patience. It has been a great honor for me to work under her generous supervision.

I would like also to express my deepest gratitude to Dr. Eman Khairy Farhat, Lecturer of Medical Biochemistry & Molecular Biology, faculty of Medicine, Ain Shams University, for her hard work, guidance and support she gave me throughout the whole work.

My appreciation is expressed to Dr. Ayman Ragaa Basheer, Lecturer of Medical Biochemistry & Molecular Biology, Faculty of Medicine, Ain Shams University, for his big effort, experience and guidance during completing this work.

Special thanks to Dr. Gihan Fouad Ahmad, Fellow of Pediatrics, National Nutrition Institute, for her help and valuable advice.

Many thanks to **Dr. walid Said Zaki**, Lecturer of Medical Biochemistry & Molecular Biology, Faculty of Medicine, Ain Shams University, for his help and support.

This work was supported by Ain Shams University Faculty of Medicine Grants Office, Grant No. 37/2017

Last but not least I wish to express my sincere gratitude to My Family for their continuous encouragement and spiritual support.

Sara Elsayed

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List of Abbreviations

ARCArcuate nucleus

AgRP.....agouti-related protein

BATbrown adipose tissue

BBBblood brain barrier

DHF.....Dihydrofolate

FTOFat mass and obesity associated gene

GWASThe genome-wide association studies

HFD.....high fat diet

Jak-2.....Janus kinase-2

LEP.....leptin

LEPRleptin receptor

MC4RMelanocortin receptor-4

MMPs.....Matrix metalloproteinases

MMP-2.....Matrix metalloproteinase-2

NPC-1Niemann-Pick C1 gene

POMCPro-opiomelanocortin

SAM.....S adenosyl methionine

SNPssingle nucleotide polymorphisms

THFTetrahydrofolate

WAT.....white adipose tissue

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Abstract

Introduction: Over the last few decades there has been a worldwide increase in pediatric obesity affecting both developed and developing countries (*Popkin*, 2006). Obese children are at increased risk of a number of health problems including diabetes, sleep problems, joint problems, early puberty or menarche, asthma and other respiratory problems.

Aim: To correlate between MMP2 /leptin genes expression and folic acid levels in sera of obese children in order to study the effect of folic acid on methylation of these genes.

Patients and methods: This case control study was conducted on 80 children and adolescents (37 boys and 43 girls), children age range (2-16 years), with simple obesity recruited from National Nutrition Institute, the nutrition clinic. The study was initiated and completed in the period from the June 2015 till October 2016.

Results: The present study included (80) children. They were stratified into (4) groups: Group (I): Obese children (12 boys and 18 girls) before starting special diet regimen or folic acid intake (n=30). Group (II): Obese children (17 boys and 13 girls) after completing a special diet regimen for 3 months but without folic acid intake (n=30). Group (III): Some of group I children who completed folic acid intake and the same diet regimen for 3 months (n=15). Group (IV): Age and sex matched children (12 girls and 8 boys) as control group (n=20). No age or sex significant differences were found when we compared the three groups of included children (groups I, II and IV).

Conclusion: Depending on the previous information, MMP-2 and leptin methylation could be important source of information about pathogenesis and complications of childhood obesity.

Keywords: Cross-talk between Folic acid and MMP2 / Leptin genes Methylation in Childhood Obesity, Nutrigenomics approach

INTRODUCTION

Over the last few decades there has been a worldwide increase in pediatric obesity affecting both developed and developing countries (*Popkin*, 2006). Obese children are at increased risk of a number of health problems including diabetes, sleep problems, joint problems, early puberty or menarche, asthma and other respiratory problems (*Lee*, 2009).

The prevalence and severity of obesity have been increased in children and adolescents, as well as in adults (*Wang and Beydoun, 2007*), in the United States, as reported by (*Ogden, 2014*), the prevelance of obesity among children (2- 19 years) is 16.9% and that is referred to complex interactions between genetic and environmental factors.

In recent years, epigenetic modifications such as DNA methylation and histone modifications have been highlighted in chronic non-communicable diseases as obesity due to their role in chromatin structure and gene expression and their potential use as markers for disease onset, progression, diagnosis and prognosis was considered (*Garver et al, 2013*).

DNA methylation is the only known modification that targets the DNA itself. Compared to histones, which undergo a variety of post-translational modifications under different conditions, DNA methylation is relatively stable over a longer period. The methylation of cytosine residues at CpG dinucleotides in gene promoters or CpG islands is well described and known to have profound effects on the regulation of gene expression (*Burdge and Lillycrop*, 2010; *Choi and Friso*, 2010). Thus, the role of epigenetic modifications in obesity is a fruitful area for research.

AIM OF THE WORK

- 1. To estimate serum folic acid in obese children
- 2. To evaluate methylation state of MMP2 /leptin genes before and after folic acid supplementation.
- 3. To correlate between MMP2 /leptin genes expression and folic acid levels in sera of obese children in order to study the effect of folic acid on methylation of these genes.
- 4. To validate these biomarkers as contributors in pathogenesis of childhood obesity.

Obesity

Obesity is the excessive accumulation of fat which results in an increased risk of developing associated pathologies, including mortality. Childhood obesity is defined as a BMI of 95th percentile or greater on standardized age-based growth charts (*Davila et al.*, 2017). It is a disease state resulting from an imbalance between energy intake and energy expenditure Excess calories create a positive energy balance with the excess energy stored in the body (*Mraz and Haluzik*, 2014).

Child obesity has been progressively increasing over the last few decades, being considered a worldwide epidemic by the World Health Organization (WHO). Worldwide, it is estimated that 43 million children under 5 years are overweight and obese, 35 million in developing countries and 8 million in developed countries (WHO, 7 · 10).

Although reduced energy expenditure and increased consumption of highly caloric foods are important factors contributing to the current epidemic of obesity, studies suggest that the development of obesity and associated metabolic disorders involves complex interactions between genetic and environmental factors, which are underpinned by epigenetic mechanisms (*Kuehnen et al., 2012*).