بسم الله الرحمن الرحيم

MONA MAGHRABY

شبكة المعلومات الجامعية

التوثيق الالكتروني والميكروفيلم

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التوثيق الإلكتروني والميكروفيلم

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MONA MAGHRABY

STUDY OF RELATIONSHIP BETWEEN STOOL LACTOBACILLUS ACIDOPHILUS AND GRAVE'S DISEASE IN A SAMPLE OF EGYPTIAN POPULATION

Thesis

Submitted for partial fulfillment of Master Degree in Internal Medicine

By

Aya Madboly Helmy

MBBCh, Faculty of Medicine, Ain Shams University, 2015

Under supervision of

Prof. Inas Mohammed Sabry

Professor of Internal Medicine & Endocrinology

Faculty of Medicine, Ain Shams University

Dr. Laila Mahmoud Ali Hendawy

Assistant Professor of Internal Medicine & Endocrinology

Faculty of Medicine, Ain Shams University

Dr. Hanan Mahmoud Ali

Lecturer of Internal Medicine & Endocrinology

Faculty of Medicine, Ain Shams University

Faculty of Medicine

Ain Shams University

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Aya Madboly Helmy

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LIST OF ABBREVIATIONS

Abb.	Full Term

BMI …….. body mass index

CTLA4 …….. cytotoxic T-lymphocyte associated antigen 4

EMP …….. Embden Meyerhof Parnas

IQR …….. interquartile range

LAB …….. lactic acid bacteria

MMI …….. methimazole

PCR …….. polymerase chain reaction

PTU …….. propylthiouracil

RAI …….. radioactive iodine

T3 …….. triiodothyronine

T4 …….. thyroxine

TNF …….. tumor necrosis factor

TPO …….. thyroid peroxidase

TSH …….. thyroid stimulating hormone

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INTRODUCTION

INTRODUCTION

Graves' disease is an autoimmune disorder in which the thyroid is activated by antibodies to the thyrotropin receptor. The hyperthyroidism that develops is one of many somatic and psychiatric manifestations of the disease that can affect the quality and length of life. **(Terry et al., 2016)**

The annual incidence of the disease is about 20 to 50 cases per 100,000 persons. The incidence peaks between 30 and 50 years of age, but people can be affected at any age. The lifetime risk is 3% for women and 0.5% for men. **(Zimmermann et al., 2015)**

Unambiguous identification of the factors underlying Graves' disease has not yet been accomplished. Genetic and epigenetic determinants are leading candidates for these factors. Large-scale genetic analyses have identified several genes conferring susceptibility. These include genes encoding thyroglobulin, thyrotropin receptor, HLA-DRβ-Arg74, the protein tyrosine phosphatase nonreceptor type 22 (PTPN22), cytotoxic T-lymphocyte–associated antigen 4 (CTLA4), CD25, and CD40. **(Limbach et al., 2016)**

Gut microbiota are trillions of bacterial strains per gram faeces. Their genome, also known as the microbiome,

contains a 100-fold greater number of genes than the human genome. **(Qin et al., 2010)**

Majority of which are obligate anaerobes. Every study reporting the human gut microbiota underlined its uniqueness as highly inter-individual specific. **(Arumugam et al., 2011)**

The intestinal microbiota play a key function in metabolism, absorption, immune functioning along with defense mechanism against pathogen. **(Kamada et al., 2013) (Walsh et al., 2014)**

The regulation of gut microbiota configuration has been compromised in a variety of disorders like inflammatory bowel disease, Crohn's disease, colitis, type II diabetes, Hashimoto's thyroiditis, and asthma. **(Ishaq et al., 2018)**