# Study of the Effect of Probiotics on Serum IndoxylSulphate in Haemodialysis Patients

# Thesis

Submitted For Partial Fulfillment of MD Degree in *Nephrology* 

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2018



- All praise are to **Allah** and all thanks. He has guided and enabled me by his mercy to fulfill this thesis, which I hope to be beneficial for people.
- I would like to express my deepest gratitude and sincere appreciation to **Prof Dr. Gamal El-SayedMady,**Professor of Internal Medicine and Nephrology, Faculty of Medicine, Ain Shams University for his encouragement, his kind support and appreciated suggestions that guided me to accomplish this work.
- SarhanProfessor of Internal Medicine and Nephrology, Faculty of Medicine, Ain Shams University, who freely gave her time, effort and experience along with continuous guidance throughout this work.
- A lot of thanks are extended to **Prof. Dr. Sahar Mahmoud Shawky,** Professor of Internal Medicine and Nephrology, Faculty of Medicine, Ain Shams University for her effort, constant encouragement and advice whenever needed.
- I also wish to introduce my deep respect and thanks to **Dr. AberHalimBaki**, Assistant Professor of Internal Medicine and Nephrology, Faculty of Medicine, Ain Shams University, for her great assistance and supervision.
- I would like to express my scincere gratitude to **Prof. Dr. Nayra Shaker Mehanna**, Professor of Dairy and Food Microbiology National Research Center, for supervising this work with great interest and gaving me unlimited support throughout the work.
- I would like to express my thanks for **Dr.Mohammed TawfikFouad**,Researcher in Dairy and Food
  MicrobiologyNational Research Center for his help, support
  and effort during the work.
- Finally, I would like to express my endless thanks to my dear small family, my lovely wife and for her endless support, And never to forget the great efforts of my parents to reach this moment, God blesses you all.

Mahmoud Abdallah Mahmoud Amer





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## <u>Abstract</u>

Chronic kidney disease (CKD) is a worldwide health problem that has many clinical outcomes and affecting the patients due to accumulation of uremic toxins. Many classifications for uremic toxins based on different aspects specially bounding to plasma proteins and molecular size are well known now and affect the mechanism and module of replacement therapy that fit End stage renal disease (ESRD) patients. Indoxyl sulphate (IS) is a protein bound uremic toxin that has many deleterious effects on cardiovascular system with deterioration of kidney functions, It is believed that gut kidney axis has main role for production of IS and so targeting gut microbiota and modifying the dysbiotic content in CKD patients can help in decreasing IS. Probiotics are emerging strategy in clinical life and appear to be effective in targeting IS.

Methodology: Study conducted on 92 ESRD patients on regular HD from January/2017 to March/2017 and patients divided to two groups: intervention group receiving probiotics regimen for 6 weeks while control group receiving placebo for the same period.

Results show reduction of IS (14±22.71 µg/ml vs 3.6±14.33 µg/ml,Pvalue 0.02) in intervention group vs control group respectively,reduction in serum phosphorus,CRP,lipid profile was recorded.

conclusion : Probiotics cause reduction in IS with reduction in phosphorus, CRP, lipid profile with no reported side effects

#### **Key Words:**

Chronic kidney disease(ckd),indoxyl sulphate, probiotics, protein bound uremic toxins

### List of Abbreviations

**AHL** : Acetyl homoserine lactone

**AHR** : Aryl hydrocarbon receptor

**cAMP** : Adenosine 3',5'-cyclic monophosphate

**CKD** : Chronic Kidney Disease

**COX-2**: Cyclooxygenase 2

**CREB**: camp response element binding protein

**CVD** : Cardio-Vascular Disease

**DCM**: Dilated cardiomyopathy

**DNA** : Deoxyribonucleic acid

ERK1/2: Extracellular Signal-Regulated Kinases 1 and 2

Extracellularly-Regulated Kinase-1 and -2

**FAO** : Food and Agriculture Organization

**FGF23**: Fibroblast growth factor 23

**FOXP3**: Forkhead box p3

**GFR** : Glomerular filtration rate

**GPR** : G protein–coupled receptors

**GIT** : Gastrointestinal tract

**GABA**: Gamma-aminobutyric acid

**GALT**: Gut-associated lymphoid tissue

**IS** : IndoxylSulphate

**IBD** : Inflammatory bowel disease

#### List of Abbreviations

**IgA** : Immunoglobulin A

**IBD**: Irritable bowel disease

**KDIG**: Kidney Disease Intiative Global Outcome

 $\mathbf{O}$ 

**Keap1**: Kelch-like ECH protein-1

**LVH** : Left ventricular hypertrophy

**MAPK**: Mitogen-activated protein kinase

**MAMPs**: Microbeassociated molecular patterns

**NADPH**: Nicotinamide Adenine Dinucleotide Phosphate

Hydrogen

(NF)- : Nuclear factor

к**В** р65

**Nox4** : NADPH oxidase-4

Nrf2 : NF erthroid-2-derived factor-2

**NOD1**: Nucleotide-Binding Oligomerization Domain 1

**NF-B**: Nuclear Factor- B

**OAT** : Organic anion transporters

**PCS**: P-CresylSulphate

**PTC**: Proximal tubular epithelial cells

**PTH** : Parathyroid hormone

**PBUTs**: Protein bound uremic toxins

**PWV**: Pulse wave velocity

**PRR** : Pattern recognition receptors

#### List of Abbreviations

**ROS** : Reactive oxygen species

**RAS** : Renin-angiotensin system

**RRT** : Renal replacement therapy

**SULT** : Sulphotransferase

**SLCO4**: A gene on chromosome 5q21.2 that encodes a protein w

C1 hich mediates Na+-independent transport

**SCFAs**: short-chain fatty acids

**TGF**: Transforming growth factor

UC : Ulcerative colitis

**WHO** : World health organization

**1,25-D3** : 1,25-dihydroxyvitamin D3

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#### Introduction

In recent years, an appreciation for the role of the gut microbiota in health and disease has gained momentum, with microbial modulating therapies emerging mainstream medicine. Within the discipline of Nephrology, the evidence supporting the role of the kidney-gut axis in uremia is building. In fact, it is now clear that the dysbiotic gut microbiota observed in chronic kidney disease (CKD)produce key nephrovascular toxins, indoxylsulphate (IS) and p-cresol sulphate (PCS). There is convincing evidence demonstrating dose dependent nephro- and cardiovascular toxicities of IS and PCS in both in vitro and animal studies (Vaziri et al., 2013).

Uremic patients show greatly increased counts of both aerobic (approximately 10<sup>6</sup> bacteria/ml) and anaerobic (approximately10<sup>7</sup> bacteria/ml) organisms in the duodenum and jejunum, normally not colonized heavily by bacteria in healthy persons. Lower intestinal colonic microbial flora which counts (approximately 10<sup>12</sup>) has also been shown to be altered in patients with CKD (*Vaziri et al.*, 2013).

Hida et al., 1996 studied the colonic composition of microbiota in healthy controls and hemodialysis patients. Analysis of the fecal microbiota revealed a disturbed

composition of the microbiota characterized by an overgrowth of aerobic bacteria. Although this study did not show a significant difference in the total number of bacteria, the number of aerobic bacteria, such as Enterobacteria and Enterococci species, was approximately 100 times higher in hemodialysis patients.

The gastrointestinal system is at the interphase between the blood and the potentially toxic contents of the gut. Histologic changes, including reduction of villous height, elongation of the crypts, and infiltration of lamina propria with inflammatory cells are noted in CKD. Uremia increases intestinal permeability in patients with CKD. The disruption of colonic epithelial tight junction could subsequently lead to translocation ofbacteriaacross the intestinal wall. Hemodialysis induced systemic circulatory stress and recurrent regional ischemia may also damage the mechanical barrier of the gut that promote intestinal dysbiosis contributing to the leaky gut in CKD (Wang et al., 2012).

Certain intestinal bacteria can generate uremic toxins that are absorbed into the blood and are normally cleared by the kidney. Proteinfermentation by gut microbiota results in the generation of different metabolites, including phenols and indoles (*Macfarlane and Macfarlane*, 2012).

Aronov et al., (2011)compare plasma from hemodialysis patients with and without colon and confirmed the colonic origin of indoxyl sulfate and p-cresol. These are prototype members of a large group of protein bound uremic toxins that are resistant to clearance by dialysis.

Barreto et al., (2009) showed that an elevated level of indoxyl sulfate is associated with vascular stiffness, aortic calcification, and higher cardiovascular mortality. Indoxyl sulfate is a potential vascular toxin that induces oxidative stress in endothelial cells, increases shedding of endothelial microparticles, impairs endothelial cell repair mechanism, and increases vascular smooth muscle cell proliferation.

A number of therapeutic opportunities for targetingIS and Pcs have been proposed, including inhibition of colonic bacterial biosynthesis (protein restriction and microbial modulating therapies), suppression of absorption (oral adsorbents), augmentation of clearance (enhanced dialysis) and modulation of cellular pathways (organic anion transporters and antioxidants). Many of these therapies remain limited to experimental studies, have unfavourable

side effects or a high cost burden preventing their translation to clinical research. In particular, oral adsorbents have been extensively studied, with promising improvements in both cardiovascular risk and kidney functionfollowing reductions in serum IS (*Rossi et al.*, 2013).

Probiotics are defined by the United Nations Food and Agriculture Organization and the World Health Organization as live microorganisms which when administered in adequate amounts confer a health benefit on the host. It exerts its effect through

- Acid and bile resistance to ensure survival through the uppergastrointestinal tract.
- Competitive exclusion ofindoxyl sulphate and p-cresol sulphate producing bacteria (through competition for essential nutrients and luminal and epithelial binding sites).
- Direct bacterial antagonism via inhibitory substance production (such as biosurfactants, hydrogen peroxide, and bacteriocins).
- Immunomodulation via immune cell activation resulting in indirectinhibition of pathogenic bacteria (Food and Agriculture Organsization: Guidelines for the evaluation of probiotics in food, 2002).