

Effect of long-term oral glutathione supplementation on gut microbiome of type 2 diabetic individuals.



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Introduction

Diabetes is a complex metabolic syndrome characterized by insulin dysfunction and abnormalities in glucose and lipid metabolism

Factors affecting diabetes: Host genetics, oxidative stress, environmental factors, diatery habits, sedentary lifestyle, host metabolism and microbiome.

It is known that oxidative stress is involved in development of type 2 diabetes.

Among various parameters of oxidative stress examined, Glutathione (GSH) was the best co variate of glucose recovery.

Objective: Dysbiosis of gut microbiome is known to be associated with diabetes. Thus, this study aims to understand whether glutathione supplementation would have any effect on gut microbiome of T2D individuals.



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Results: Effect of GSH supplementation on blood biochemical parameters and microbial diversity

► Fasting Glucose, HbA1c, decreased significantly and GSH increased significantly in T2D individuals on glutathione supplements.

► HOMA- β , an indicator of insulin secretion, significantly increased while, 8-OHdG, an oxidative DNA damage marker, decreased significantly in DG gamma compared to DG alpha, and remained unchanged in D gamma versus D alpha.

Simpson diversity was analyzed based on dominant taxa, it was found to be increased significantly in DG gamma compared to DG alpha.

Fig. 1 Longitudinal changes in concentration of serum biomarkers in different groups.



Fig. 2 Comparison of alpha diversity and beta-diversity between four study groups



Intra-individual differences measured by beta diversity using generalized UniFrac distance method were found to be different between T2D with & without GSH supplementation.

Differentially abundant taxa among study groups

A)

1.00

Relative

0.00

Six months of glutathione supplementation resulted in an increased abundance of Bacteroidetes and Firmicutes, while there was a significant decrease in the abundance of Proteobacteria.

Genus Bacteroides, Megasphaera, Megamonas was found to be significantly abundant with increasing trend while genus Escherichia-Shigella exhibited decreasing trend in subjects with glutathione supplementation.

In individuals with GSH supplementation ASV1 from Escherichia decreased while ASV2 from Megasphaera increased significantly in almost all individuals.

Fig. 3 Comparison of differentially abundant significant phyla

Fig. 4 Comparison of differentially abundant A) significant genera and B) response of GSH on ASV's at individual levels



► Thus, glutathione supplementation led to decrease in fasting glucose and HbA1c and increase in body stores of GSH in diabetic individuals.

► Overall, the GSH supplementation in addition to antidiabetic treatment helped in altering dominant taxa in the T2D individuals, which subsequently leads to enrichment in beneficial bacteria and reduction in pathogenic bacteria in diabetic gut.

Reference: Effect of long-term oral glutathione supplementation on gut microbiome of type 2 diabetic individuals Akshay H. Gaike et. al. 2023

Key Message

GSH supplementation can be used as an adjuvant therapy to T2D individuals for restoration of healthy gut.

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