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OGG1 enzyme and its effect on some biochemical variables in the serum of patients with type 2 diabetes

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Abstract
The term diabetes defines a group of chronic metabolic disorders characterized by high blood sugar (Hyperglycemia) in the absence of treatment, and occurs as a result of a defect in the secretion of the hormone insulin (Insulin), its function, or both. Or as a result of metabolic disorders of carbohydrates, fats, and proteins (1). Diabetes is one of the most common chronic conditions with multiple devastating complications for the body's systems. Diabetes is among the top ten causes of death in adults (2). Glucose is the vital element of the body that provides the body with the necessary energy. Glucose enters the cells through the hormone insulin, which acts as a main key for glucose to enter the cells, which is secreted from the beta cells in the pancreas. If there is an imbalance, such as in diabetes, glucose will accumulate in the bloodstream and be excreted through the urine (3). The current study was conducted on the effect of the OGG1 enzyme and knowing its level in the serum of people suffering from type 2 diabetes. (64) blood samples were obtained from people with type 2 diabetes whose ages ranged between (26-80) years. Both genders (35 males - 29 females), where samples were collected from Tikrit Teaching Hospital and their condition was diagnosed by specialized doctors. As for the control group, samples were collected from healthy people through routine examinations and blood donors in the hospital, where the number of samples for the control group was (36) A sample of people aged between (30-75) years of both sexes. The study also included finding a correlation between the OGG1 enzyme and some biochemical variables in patients with diabetes.

Keywords: Diabetes, OGG1 enzyme, some biochemical variables

Introduction
The OGG1 enzyme is a bi-functional glycolase that has the ability to break the glycosidic bond of the lesion causing the damage and the occurrence of mutation. The lesions caused by (ROS) are repaired mainly through the base excision repair (BER) pathway, where the first step of excision is by a specific DNA glycosylase, which is OGG1 [4]. These enzymes are distributed in tissues and have specific substrates that characterize damage resulting from lesions. It has become increasingly clear that beta cell failure plays a crucial role in the pathogenesis of type 2 diabetes [5]. It has long been recognized that free radicals (Such as superoxide dismutases, hydroxyl radicals, nitric oxide, and peroxynitrite) are a key component of cellular dysfunction that is central to the pathogenesis of many aspects of diabetes. In type 1 diabetes, inflammatory cytokines have been shown to play a major role in beta cell destruction producing insulin, which leads to the production of free radicals derived from oxygen, which stimulate DNA damage and tissue cell death in both rodent and human beta cells. The role of free radicals for both types in diabetes has been studied, and accumulating evidence has shown that oxidative DNA damage is mediated by free radicals. It plays a major role in beta cell dysfunction and loss, which contributes to the development of type 2 diabetes. The increase in free radical production is probably due to increased mitochondrial oxidative metabolism that is secondary to high intracellular glucose concentration. Glucose also leads to advanced glycation end products. While free radicals play a major role in the pathogenesis of many aspects of diabetes and it is known that free radicals can cause DNA damage, there is little direct evidence of DNA damage in causing diabetes. Beta cells in type 2 diabetes. An exception is a study in which it was reported that DNA derived from the oxygen radical 7, 8-dihydro-8-oxoguanosine (8-OH-dG) is present in the islets of diabetic rats, after introduction in this study, it was reported that the number of positive islet cells (8-OH-Dg) was increased in the pancreas of people with type 2 diabetes

[6]. In that study, an increased number of cells with DNA damage was associated with a decrease in cell mass [7].

Some biochemical variables

1. Glucose: It is a hexadecane sugar and is considered a monosaccharide. It represents a source of energy for tissues. The surplus is stored in the form of glycogen in the liver and muscles and triglycerides in adipose tissue. It has a direct relationship with many metabolic processes within the body, as any defect in the glucose metabolism process leads to damage and many changes in the body. These metabolic processes [9, 8]. It is obtained from the digestion and absorption of disaccharides and polysaccharides. During a state of hunger and fasting, that is, when the level of glucose decreases, the liver releases glucose into the blood from the glycogen stored in it, and when fasting continues for a long period, it begins to manufacture it from non-sugar substances such as amino acids. Glucose is considered a main food for the brain. For red blood cells and the retina, it can be obtained in the absence of oxygen, as well as in cells that do not contain mitochondria [10]. Many studies have shown an increase in the concentration of glucose in the blood serum of patients with diabetes of both types compared to its level in normal people [11]. This relationship between diabetes and the level of glucose is an established fact, as a high level of glucose in the blood is one of the most important clinical symptoms for people with diabetes, as glucose enters the cells through special protein carriers called glucose transporters, where the hormone insulin is secreted to activate the metabolic processes that lead to a reduction in Blood sugar, which is the only hormone that works to lower blood sugar. Other hormones, such as glucocorticoid and adrenaline, work to raise blood sugar levels.

2. Cholesterol and lipoproteins: Cholesterol is the intermediate compound in the formation of all steroid hormones, bile salts, and vitamin D. Cholesterol is built in the liver and transported in the blood by special carrier molecules, which are lipoproteins, including lipoproteins that transport cholesterol from the original tissues to the target, and any defect in protein metabolism. Fatty foods may lead to an increase in cholesterol, as many studies have indicated an increase in the concentration of cholesterol in the blood serum of diabetic patients, in addition to its increase in patients with heart disease and high blood pressure [13, 14].

While lipoproteins are a group of biomolecules resulting from the combination of fats with proteins to form protein fats, as the fatty part consists of (Triacylglycerol, phosphorylated fat, and free cholesterol), which combine in certain proportions with protein. Proteins are considered a means of transporting fats from the small intestine to the liver, then from the liver to the targeted tissue to store fat in it.

They can be classified according to their fat density into

1. **High-density lipoproteins (HDL):** HDL is one of the smallest and densest lipoprotein molecules. It is high in protein, approximately equal amounts of cholesterol and phospholipids, and small amounts of triglycerides. It consists of 50% proteins and 50% fats [15].
2. **Low density lipoproteins (LDL):** They are molecules composed of 80% fat and 20% protein, and cholesterol constitutes approximately 50% of the fat percentage, and it is smaller in size than VLDL and denser than it, which is a small molecule. The size ranges in diameter from about (18 to 25 nanometers) [16]. And it is the main carrier of cholesterol, as it works to transfer it from the liver to other tissues [17].
3. **Very Low Density Lipoprotei (VLDL):** They are large molecules ranging in diameter from 30 to 80 nanometers and are considered one of the largest proteins Fatty in size, it is very rich in triglycerides and a small amount of cholesterol and protein It is formed mainly in the liver and to a lesser extent in the mucosal tissue of the intestine and is excreted into the blood plasma from these two sites [18]. Very low-density lipoproteins transport both triglycerides and cholesterol formed in the liver to other tissues in the body, and most of the VLDL particles are excreted into the plasma. By hepatocytes, and VLDL represents endogenous hepatic synthesis of it is increased when there is an increased synthesis of triglycerides, that is there is an increased transfer of free fatty acids to the liver [19].

3. Total proteins: Proteins are the basic components of life, as they constitute about 50% of the dry cell weight. They are partial polymers of alpha-amino acids linked to each other by peptide bonds and have high molecular weights.

4. Proteins in blood serum are classified into two types

1. Albumin: It is built in the liver and is one of the most abundant proteins in the blood. Its percentage ranges from 75-80% and the total amount of kidney proteins in the blood serum. Its molecular weight is 69,000 Daltons and has a half-life estimated at 20 days. It consists of 580 amino acids. Most of the albumin (60%) is present some of it is in body fluids outside blood vessels, while the remaining 40% is found in blood serum. The concentration of intact albumin in the blood serum is 3.5-5.5 gm/dL and the total protein level in the serum is 5.5-9.0 gm/dL. Albumin plays an important role in preserving body fluids and preventing their leakage from blood vessels by maintaining osmotic pressure inside the cell [20]. It also contributes to nourishing tissues and also works to transport many substances through different tissues in the body with hormones, vitamins, calcium, and other chemical elements. It is considered an important antioxidant in the body that protects tissues from oxidation and the formation of free radicals that lead to damage to cell components. Albumin binds to most free radicals, in addition to its ability to reduce the formation of free radicals by binding to some substances such as iron and copper, thus reducing the process of oxidation occurs and protects the body from diseases [21].

2. Globulin: It is the second necessary component of blood, as it consists of four parts.

1. Alpha globulins (α2, α1) as globulin-α1 is the main transporter of steroids and phospholipids, while globulin-α2 transports fats and hemoglobin broken down from red blood cells, as well as transporting copper.
2. β-globulins, which are formed in the liver and include both beta-lipoprotein and transferrin, which transports iron.

3. Gamma globulin γ, which is synthesized by lymphocytes [22] which are the largest part of blood serum globulins. Which are called antibodies, as they perform defensive and immune functions against foreign bodies such as viruses and bacteria because they contain different antibodies called immune proteins (Immunoglobulin (Ig), the most important types of which are (IgA, IgM, IgN, IgG, IgE, IgD), which are present in low concentrations. Different types of tissues in the body depend on many factors, including genetics, age, breed, and gender [23].

4. Magnesium: Magnesium is present in more than 300 enzyme systems, and contributes to carbohydrate metabolism. Amino acids, proteins, and nucleic acids, and participates in the metabolism of fatty acids and phosphorylated fats. It also helps in regulating the levels of calcium, potassium, zinc, copper, and vitamin D in the body [24]. Magnesium comes in the second degree, depending on its concentration inside the cell compared to other positive ions. Its percentage in a normal adult person is approximately (20-28 grams), and 66% of it is concentrated in the bone, 34% inside the cells, and the majority of it is in muscle tissue, while 1% of it is present in the fluid outside the cells [25]. Magnesium deficiency is linked to many reasons, including its lack of presence in the foods we eat, malabsorption, and the use of some medications, such as diuretics used in patients with kidney failure, which lead to its depletion and the loss of the regulatory role of the kidney. As well as the result of diabetes, as frequent diuresis is one of the main symptoms of people with diabetes, it can have significant effects on the magnesium balance within the body [26].

5. Vitamin D3: Also called (calcitriol), it is a fat-soluble vitamin and is one of the important and necessary elements for bone mineral metabolism because it participates in calcium and phosphorus metabolism and skeletal homeostasis, as well as a wide range of non-skeletal vital processes. It is also classified as a prohormone and not a true vitamin because it exhibits hormone-like effects [27]. The primary source of vitamin D is cholecalciferol or vitamin [25(OH)D3], which is generated by sunlight (specifically ultraviolet rays). On the skin of the precursors of cholesterol (7-dehydrocholesterol). Vitamin D is also found in animal foods in the form of cholecalciferol and in plant foods in the form of ergocalciferol or vitamin D2 [28]. Vitamin D, as well as other steroid hormones, is transported through the bloodstream if it binds to binding protein (DBP), which is a specific protein belonging to the albuminoid family and has binding sites for all vitamin D receptors and a high affinity for 25OH and 1,25OH D2, thus creating a large pool of circulating cells that prevents Rapid deficiency of vitamin D. It also binds to albumin and carrier lipoproteins in small amounts [29].

Materials and Methods

Determination of the concentration of the enzyme oxoguanine DNA glycosylase 1 (OGG1)-8 by ELISA method.

Determination of (OGG1) by Enzym link Immunosorbent Assay (ELIZA)

The concentration of the enzyme (OGG1) in the serum was estimated using the Elisa device kit manufactured by the company (BT LAB). The basis is the prior addition of the antibody to the wells on the plate, where the antigen present in the sample (The substance to be measured, OGG1) is added and it binds to the antibodies coated on the plate. Drilling. The method is based on the use of a plate containing holes containing the antibody specific to the substance to be measured. Standard solutions and samples are added to the hole if the antigen combines with the biotin bound to the antibody (Biotin-conjugated antibode for the required test (Biotinylated) present in the hole and then Avidin, which is bound to Horseradish Peroxidase (HRP), is added to each hole for a period of time. After completing the washing, the base material Substrate Solution is added to the hole. A change in color will appear, and then the reaction is stopped by adding Stop Solution. It is measured at a wavelength of 450 nm, and its concentration in the sample is determined by Compare the absorbance of the sample with the standard solution by drawing a curve between them.

Reagent Preparation

1. Place the components of the measuring kit at room temperature (18-28C0) before use.
2. Standard solution: (120 µl) of concentrated stock solution (48ng/ml) was prepared with (120 µl) diluted solution to form (24ng/ml) of diluted standard solution and left for 10 minutes at room temperature, then shaken carefully (Take care not to form foam.)
3. I prepared 5 tubes containing 0.5 ml of the diluted solution of the standard solution, as in the ftable1 and figure1.

Table 1: Reagent Preparation

24 ng/ml	Standard No. 5	120 µl original standard + 120 µl standard Diluent
12 ng/ml	Standard No. 4	120 µl standard No.5 + 120 µl standard Diluent
6 ng/ml	Standard No. 3	120 µl standard No.4 + 120 µl standard Diluent
3 ng/ml	Standard No. 2	120 µl standard No.3 + 120 µl standard Diluent
1.5 ng/ml	Standard No. 1	120 µl standard No.2 + 120 µl standard Diluent

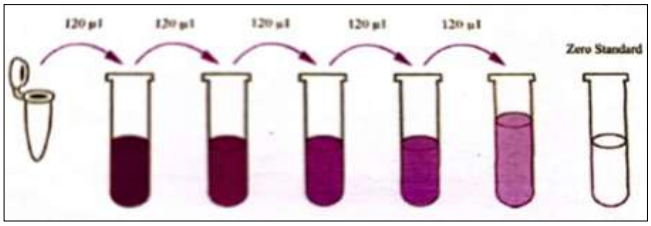

Fig 1: Reagent Preparation

Assay Procedure

1. All solutions were kept at room temperature.
2. The pits for standard solutions, efficient solutions, and samples were identified. I identified 7 holes for standard solutions and one hole for the efficient solution.
3. Add 50 µl of the standard solution to each hole in sequence from highest to lowest concentration.
4. Add 40 µl of serum (sample) to each hole except the eight holes for standard solutions. 10 µl of antibodies were added to all the wells except the standard solutions containing antibodies.
5. Add 50 µl of HRB binder to all drilled samples and standard solutions.
6. Place the lid on all the pits containing the standard solutions and samples, then place them in the incubator for 60 minutes at a temperature of 37 CO.
7. Wash all the holes five times with the washing solution for a minute, then remove the solution and dry it through a filter paper.
8. 50 µl of Substrate solution (A) and 50 µl of Substrate solution (B) were added to all the holes containing the standard solutions and samples, and then they were placed in the incubator for 10 minutes at a temperature of 37C0 in the dark.
9. Add 50 µl of the solution. The reaction will change the color from blue to yellow.
10. Turn on the reader and measure at a wavelength of 450nm over a period of 10 minutes the accounts

I took the average readings for the standard solutions, subtracted the average optical density of the efficient solution, and created a measurement curve of absorbance versus concentration for each standard solution as in the figure 2.

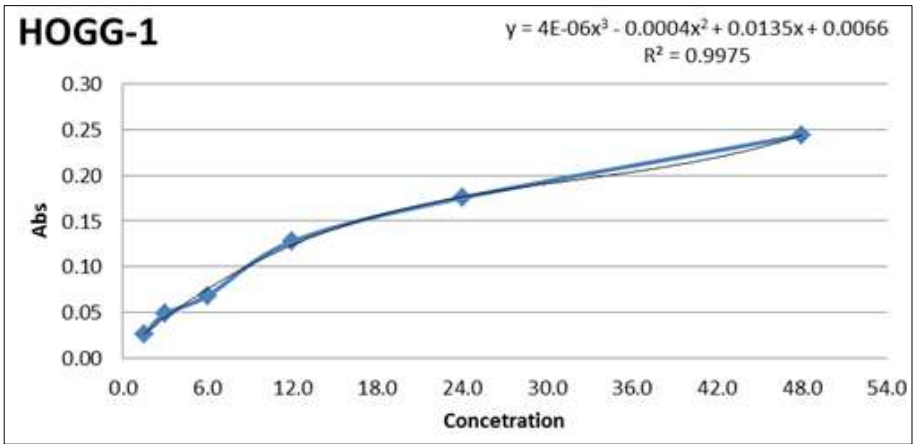

Fig 2: Standard curve for estimating enzyme concentration

Measuring the level of glucose in blood serum

Basic Principle

The concentration of glucose in blood serum was estimated by using the enzymatic calorimetric method using the ready-made kit manufactured by the Italian company AMS. This method relies on the enzymatic oxidation of glucose (Trinder reaction mediated by the enzyme Glucose Oxidase - GOD to gluconate and hydrogen peroxide, then In the presence of the enzyme Peroxidase-POD to the colored compound Quinonimin, as shown in the following equations:

$$\text{Glucose} + O_2 + H_2O \xrightarrow{\text{Glucose oxidase}} \text{Gluconate} + H_2O_2$$

$$2H_2O_2 + \text{phenol} + \text{4-amino-antipyrine} \xrightarrow{\text{Peroxidase}} \text{red quinonimine} + 4$$

Calculations

Calculations of glucose (mg/dl) =Atest /Astandard x1000
Normal Values (FPG) =65-110 mg/dl

Estimation of cholesterol concentration in serum

Basic Principle

The concentration of cholesterol in blood serum was estimated based on the enzymatic method and according to the colorimetric method (CHOD-POD). This method depends on the enzymatic oxidation of free cholesterol and esterified cholesterol, which gives a pink color. It is explained by the following equations:

$$\text{Cholesteryl esters} \xrightarrow{\text{Cholesterol esterase (CE)}} \text{Cholesterol} + \text{Fatty acids}$$

$$\text{Cholesterol} + O_2 \xrightarrow{\text{Cholesrol oxidase (CO)}} \text{Cholestenone} + H_2O$$

$$\text{4-AA} + \text{Phenol} \xrightarrow{\text{H2O2 / Peroxidase (POD)}} \text{Quinoneimine} + 4H_2$$

Calculation

Conc. of cholesterol (mg/dl)=Abs(sample)/Abs(standard) × Standard conc.

Determination of High density lipoproteins (HDL-Ch) in Blood Serum

Basic Principle

Estimate the level of HDL-Ch in blood serum by using the diagnostic kit manufactured by the Egyptian company Spectrum. The principle of the method is based on the enzymatic method in which chylomicrons and lipoproteins LDL-Ch and VlDL-Ch are precipitated by adding Phosphotungstic acid and in the presence of magnesium ions. Only HDL-Ch remains in the blood serum after centrifugation.

Calculation

Conc. of HDL_C (mg/dL) = (Abs (sample) / Abs (standard)) × Standard conc.

Determination of low Density lipoprotein-cholesterol (LDLCh.) Concentration in serum

Basic Principle

The concentration of low-density lipoprotein cholesterol was calculated according to the following relationship:

LDL_C=Total cholesterol- (Tri glyceride/5)-HDL

Determination of very Low density lipoproteins (VLDL-Ch) in Blood serum

The VLDL-Ch level was calculated according to the Friedwald equation:

VLDL-Ch=Triglyceride/5

Determination of Total Protein (TP) in Blood Serum

Basic Principle

The amount of quantitative protein was estimated using the Biuret Reagent method, which involves reacting a blood serum sample containing the protein with a Biuret Reagent solution to give a blue-violet complex with the protein binding with copper (Cu) in a basic medium, the intensity of which depends on the number of The peptide bonds present in the protein present in the sample, and its intensity can be measured at a wavelength of (546nm) with a spectrometer.

Calculations

Conc. of Total Protein (g/dL) = Abs(sample)/Abs(standard) × Conc. Standard (g/dl).

Determination of Albumin (ALB) in Blood Serum:

Basic Principle

Albumin was estimated using the Bromocresol Green method, which depends on the amount of albumin that binds with the reagent (3,3,5,5-tetrabromo-metacresol phthalene sulfate), which is called Bromocresol Green, in an acidic medium (pH=) 3.8 The green albumin-bromocresol complex (CC Complex Albumin-B) is green in color and the intensity of this color is proportional to the albumin concentration in the sample, and its intensity is measured at a wavelength of 628nm in the optical spectrometer.

Calculation

Serum Albumin (g/dL) = (Abs(sample)/Abs(standard)) ×Standard (g/dl).

Determination of Globulin (GLUB) in Blood Serum

Globulin was estimated after calculating the value of quantitative protein and albumin according to the following equation:

Total protein = albums + Globulin

Globulin = total protein - albums

Determination of magnesium concentration in blood Serum

Basic Principle

Magnesium ions and blue xylidyl ions react in an alkaline medium to form a purple-coloured kidney complex dissolved in water. The intensity of the color is proportional to the concentration of magnesium ions present in the sample. Usually, the xylidyl blue ions that cause absorbance decrease with the formation of the total complex, so magnesium is estimated by measuring the optical density of the increase in the formation of the total complex or the decrease in the optical density of xylidyl blue.

Calculations

Magnesium (mg/dL) = (Abs (sample)/ Abs (standard)) ×Standard (mg/dl).

Estimation of the concentration of vitamin D in the blood serum

Basic Principle

The level of vitamin D was estimated using an Enzyme Linked Immunosorbent Assay (ELISA) test kit manufactured by the German company. The method relies on using a plate containing wells containing the antibody for the vitamin. Standard solutions or samples are added to the wells. The antigen combines with biotin bound to the biotin-conjugated antibody to vitamin D present in the hole. In the first analysis step, calibrators and patient samples were diluted with 25-OH biotin-labeled vitamin D and added to microplate etches coated with an anti-vitamin D monoclonal antibody. During incubation, an unknown amount of vitamin D (25-OH) was extracted into the sample. The patient and a known amount of biotin-labeled vitamin D (25-OH) are applied to the antibody binding site in a microwell plate, and unbound vitamin D is then removed by washing with washing fluid. In the second analysis step, vitamin D (25-OH) is detected through a second incubation with streptavidin called peroxidase. On a third incubation with the peroxidase substrate tetramethylbenzidine (TMB), the bound peroxidase enhanced the color reaction as the color intensity was inversely proportional to the vitamin D concentration in the sample. The sample result was calculated directly using the standard curve figure 3.

Calculations

Standard curve from which 25-OH vitamin D concentrations in serum samples were taken and obtained by dot plotting the measured value of 6 calibrated serums against the corresponding units (linear/logarithmic).

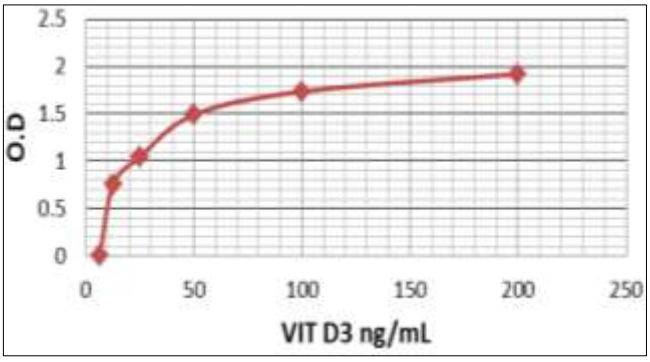

Fig 3: Standard curve for Vit D

Results and Discussion

Measurement of the level of oxoguanine DNA glycosylase 1 (OGG1)-8 for diabetic patients and control groups. Table (2) and Figure (4) show the concentration of the OGG1 enzyme in the blood serum of both patients and the control group, where a highly significant increase was observed at the level

of probability ≤0.0001 (P) for the patient group compared to the control group.

Table 2: Diabetic patients and control groups

Test	Group	Mean ± SD	SE	Min-Max	T-test	P-value
OGG1	Case	10.19±3.93	0.65	4.05-18	9.12	≤0.0001
	Control	3.47±1.63	0.33	1.45-7.62		

The OGG1 enzyme is one of the important and necessary enzymes in repairing oxidative stress and the formation of free radicals. In general, oxidative stress leads to the development of the disease. Free radicals play an essential role in causing many aspects of diabetes through damage to many cells, causing damage to proteins, fats, and nucleic acids through various mechanisms, which also causes damage to mitochondrial DNA, mutations, and weakness in the function of beta cells [30]. It is one of the most important metabolically active cells, which leads to a decrease in insulin secretion in general or its complete loss or absence, and this is consistent with the study conducted by Farook Thameem [31]. Therefore, it is necessary to have repair materials and mechanisms to avoid diseases caused by ROS) [32]. Therefore, a high enzyme concentration is a clear indicator of an increase in free radicals, which may be the main cause of type 2 diabetes, and this is consistent with the study conducted by Sakuraba on Goto-Kakizaki rats with type 2 diabetes, in which the presence of 7,8-dihydro-8-oxoguanosine radical-derived nuclear enzyme was reported [33].

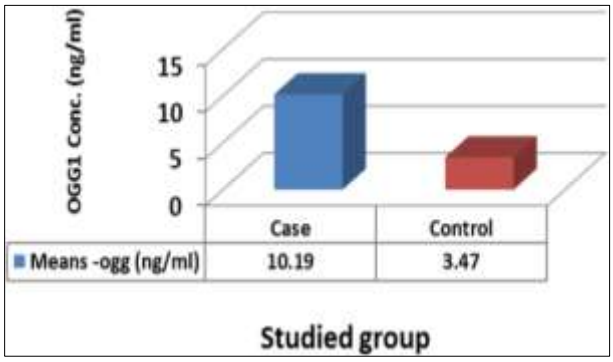

Fig 4: OGG1 enzyme level for diabetic patients and the control group

The OGG1 enzyme was studied in the serum of diabetic patients with a difference in genders and compared with the control group, as in Table (3) and Figure (5) below.

Table 3: Effect genders on OGG1 enzyme

Test (M ± SD)	Groups	Male	Female	P-value
Ogg (UI\ml)	Case	9.55±3.97	10.90±3.89	0.31
	Control	3.05±1.51	3.97±1.69	0.17

It was found that there were no significant differences between the sexes at the probability level (P<0.O5). This indicates that the enzyme is not affected by any difference between the sexes.

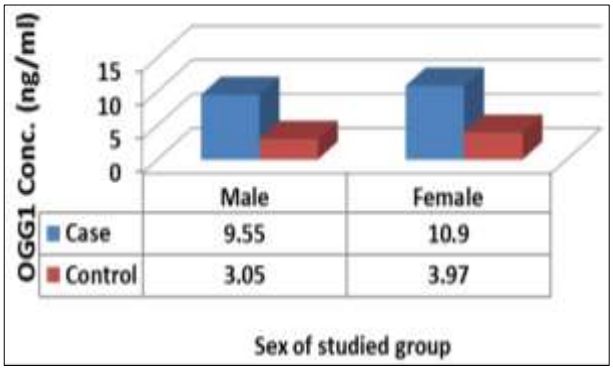

Fig 5: Sex differences in OGG1 enzyme levels in diabetic patients

The enzyme was studied by weight and it was found that there were significant differences when it was divided into three groups as shown in Table (4) and Figure (6)

Table 4: Effect Weight on enzyme

Weight (Kg)	Mean± SD	P-value
(50-70)	7.83±3.10	0.11 (N.S)
(71-90)	10.83±3.77	
>90	11.31±4.49	

The results in Table (5) and Figure (6) show a significant increase in OGG1 enzyme levels with weight gain for diabetic patients, where the highest value is recorded at 90 kg (11.31±4.49), then followed by 10.83±3.77) for patients whose weight was between Between (71-90 kg), the lowest value was recorded in patients whose weight ranged between (50-70 kg) at a value of 7.83±3.10), and this is consistent with the study conducted on mice, which showed an increase in the levels of the OGG1 enzyme when the weights of those mice increased. The study demonstrated a new role for the DNA repair enzyme (OGG1) in reducing the risk of obesity, as the results conducted by (Natalie Burchat *et al*. 2021 showed that enhanced expression of the OGG1 gene makes mice more resistant to obesity. This resistance occurs through an increase in receiving energy from the entire body, increasing the content of mitochondria in tissues, and increasing the respiratory process works to protect mice from insulin resistance and fatty tissue infections. The study also proved that the genetic enzyme gives mice resistance to genetically induced obesity through a study between male and female mice, and it was shown that the gene may be transmitted through the mother. To children, they gain resistance to obesity, as the study also proved that the OGG1 enzyme has a crucial role in modifying energy balance through changes in the function of adipose tissue [34].

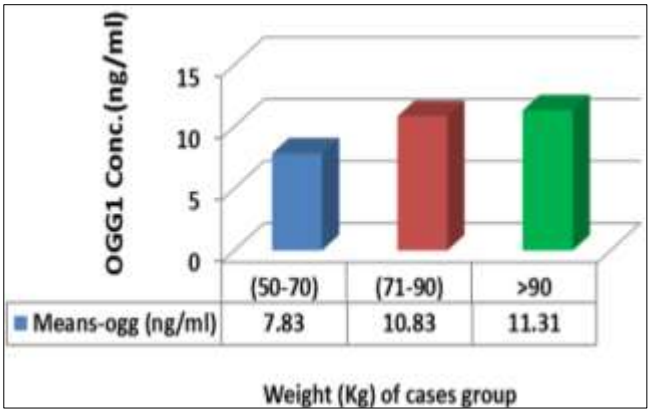

Fig 6: Weight differences in OGG1 enzyme levels for patients with diabetes

The concentration of the enzyme (OGG1) was measured in the serum of diabetic patients and the control group according to the different age groups, which were divided into three categories (25-49 years, 50-60 years, 61-80 years). The results in Table (5) below showed that there were differences. Significant at the probability level (≤0.0001 P) in enzyme levels between the age groups of the patient group.

Table 5: Effect age on Enzyme

Age range (Years)	M ± SD	P-value
(25-49)	8.46±2.71	0.01
(50-60)	10.16±4.12	
(61-80)	14.45±2.71	

The results in Table (5) and Figure (7) showed an increase in the level of OGG1 enzyme concentration with an increase in age groups, where the highest value was recorded at the average age (61-80 years) with a value of (14.45±2.71, then followed by a value of (10.16±4.12). At age (50-60 years) then the lowest value was recorded at age (27-49 years) (with a value of 8.46±2.71)), this was confirmed by the study conducted by (Manuela Dittmar. 2023) as it confirmed that with aging we increase levels of oxidative stress, which leads The most common damage to mitochondrial DNA is oxidation-induced DNA damage, which leads to an increase in the repair enzyme (OGG1) by base excision.

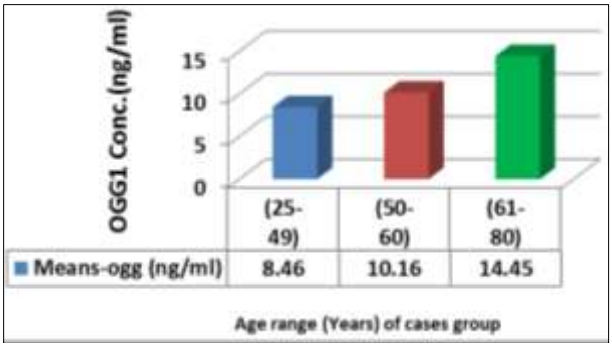

Fig 7: Age differences in OGG1 enzyme levels in patients with diabetes

Linear correlation between the level of the OGG1 enzyme and the clinical variables studied in diabetes patients and the control group.

The correlation coefficient is defined as a measure of the relationship and the extent of association between two variables for the same sample. The Pearson coefficient takes a value between (1+ and 1-). The sign indicates the side of the relationship that is positive, meaning direct, and negative, meaning inverse. The association of the OGG1 enzyme with the rest of the clinical variables was also studied. The correlation coefficient between the enzyme and age and weight is as shown in Table (6) below:

Table 6: Shows a relationship between the enzyme and clinical variables for patients with diabetes

Teset	r	P-value	Sig	Correlation score
Age	0.035	0.790	N.S	Weak positive
Weight	0.104	0.432	N.S	Weak positive
Glu	0.51**	0.0001	H.S	Moderate positive
Chol	0.640**	0.0001	H.S	Moderate positive
LDL	0.575**	0.0001	H.S	Moderate positive
VLDL	0.130	0.322	N.S	Weak positive
HDL	-0.237	0.069	N.S	Weak negative
Total protien	-0.171	0.190	N.S	Weak negative
Albumin	0.245	0.05	S	Weak positive
Globulin	-0.282	0.029	S	Weak negative
Mg	0.309-	0.06	S	Weak negative
Vit-D	-0.130	0.323	N.S	Weak negative
**. Correlation is significant at the 0.01 level (2-tailed).				
*. Correlation is significant at the 0.05 level (2-tailed).				

The results shown in Table (6) show that there is a weak, non-significant positive correlation between the enzyme concentration level and both age and weight at a correlation value (r=0.035, 0.104), respectively, at a probability level (p<0.05). There is also a weak, non-significant correlation between the enzyme concentration level and the VLDL value, at a correlation coefficient value (r=0.130). The table also shows that there is a high positive significant correlation between the level of enzyme concentration and the level of Glu, Chol, and LDL, with a correlation value (r=0.51, o.640, o.575) at a probability level of p<0.001), and the results also show the existence of a relationship A weak, non-significant negative correlation between low enzyme levels and high levels of HDL, Mg, and Total protein at a correlation value of r=-0.237,-0.171,-0.309), and the results also show that there is a significant positive correlation between the enzyme level and Albumin. At a correlation value of (r = 0.245), respectively, the results in the table also showed that there was a negative significant correlation between a low enzyme level and an increase in globulin levels at a correlation value of r = -0.282). The results also showed that there was a non-significant negative correlation between a low The enzyme in the blood serum of diabetics and high levels of Vit D3 reaches a correlation value (r=-o.130).

Conclusion

Based on the data presented, it is evident that the OGG1 enzyme plays a critical role in responding to oxidative stress and repairing DNA damage caused by free radicals, particularly in the context of diabetes. The study revealed a significant increase in OGG1 enzyme levels in diabetic patients compared to the control group, underscoring its association with oxidative damage and disease progression. This enzyme's elevated presence indicates heightened oxidative stress, which is implicated in the pathogenesis of diabetes, specifically type 2 diabetes.

Furthermore, the findings suggest that various factors such as weight and age can influence OGG1 enzyme levels. For

instance, obese diabetic patients exhibited higher OGG1 levels compared to those with lower body weights, aligning with studies demonstrating a link between increased OGG1 expression and resistance to obesity-related complications. Similarly, age also proved to be a significant factor, with older diabetic patients showing higher OGG1 enzyme concentrations, reinforcing its role in age-related metabolic changes.

The study highlights the crucial role of OGG1 in mitigating oxidative DNA damage, which is implicated in the pathophysiology of diabetes. Further research into the mechanisms underlying OGG1's regulation and its potential as a therapeutic target could offer new insights and strategies for managing diabetes and related complications effectively.

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