

Oxidative Stress and 3243 A/G Mitochondrial Dna Mutation In Maternally Inherited Type 2 Diabetes Mellitus

Utpal J. Dongre¹, Virendra G. Meshram², Shailesh Pitale³

¹Assistant Professor, Department of Biochemistry, Dr. Ambedkar College, Deeksha Bhoomi, Nagpur 440010, Maharashtra, India

²Professor, University Department of Biochemistry, RTM Nagpur University, Nagpur 440033, Maharashtra, India

³Diabetes Hospital, Dhantoli, Nagpur 440012, Maharashtra, India.

Abstract: Aims: The imbalance between the activities of antioxidant enzymes and free radicals gives rise to oxidative stress. Increased oxidative stress can induce other serious complications in diabetic patients. Mutations in mitochondrial DNA can cause oxidative stress and type 2 diabetes mellitus. Hence, the present study was undertaken to evaluate the levels of antioxidant enzymes, lipid peroxidation and mitochondrial DNA 3243 A/G mutation in families with a history of maternally inherited type 2 diabetes mellitus. Method: This study included two diabetic families and one normal healthy family. The level of catalase, Mn/Fe SOD, Cu/Zn SOD, nitric oxide and malonaldehyde formation were studied via various biochemical standard methods. DNA isolation and mutation analysis were done as per standard protocols and methods. Result: As compared to control samples, a significant decrease in the activities of catalase (family 1 $p < 0.01$, family 2 $p < 0.01$), Mn/Fe SOD (family 1 $p < 0.01$, family 2 $p < 0.05$), Cu/Zn SOD (family 1 $p < 0.001$, family 2 $p < 0.01$) was observed. Significantly increased concentrations of malonaldehyde (family 1 $p < 0.05$, family 2 $p < 0.05$) and nitric oxide (family 1 $p < 0.05$, family 2 $p < 0.05$) was also observed. Both diabetic families represent altered antioxidant enzymes status. This study corroborates an absence of the mutation. Conclusion: High oxidative stress was shown in both the families with diabetes, but we did not find a mutation in mitochondrial DNA.

Keywords: Oxidative stress, Antioxidant Enzymes, Free Radicals, Mitochondrial DNA.

1. Introduction

Diabetes mellitus is now prevalent everywhere around the world. In the year 2000 the prevalence of the diabetes in the world was 171 million, which is expected to rise up to 366 million in the year 2030 [1,2]. Mitochondria are dynamic organelles and found almost in every cell and play a central role in ATP generation via oxidative phosphorylation. [3]. Oxidation of glucose generates reducing equivalents like FADH₂ and NADH, which transfer their electron to the electron transport chain. But the electron transport chain found to be leaked sometimes which gives rise to an electron leakage during its passage from complex I to complexes IV. These leaked electrons can form free radicals like ONOO⁻, OH⁻ ion, O⁻ superoxide anion, H₂O₂ etc; referred as ROS (reactive oxygen species), which are chemically highly reactive and can react with various cellular organelles, proteins, DNA (deoxyribonucleic acid), cell membranes etc. and damage them. This intracellular damage initiates the cascade of cellular non functioning [4,5,6].

Aerobic animals have generated a defence mechanism against free radicals through various antioxidant enzymes, including Catalase, Superoxide dismutase (SOD), Glutathione peroxidase etc. [7]. Among these, Cu/Zn SOD is a cytoplasmic enzyme, whereas Mn/Fe SOD found in mitochondria [8]. Mitochondria are the main site for respiration and inherited maternally by their offspring's. Mitochondrial DNA with nuclear DNA codes for the polypeptides of the electron transport chain (ETC). Mutated mitochondrial DNA generates an aberrant ETC and reported as a causative agent for type 2 diabetes mellitus. Inheritance

of such defective mitochondria could increase the oxidative stress in families [9, 10, 11, 12,13].

Lipid peroxidation is a chain process; generated due to leakage of electrons. It determines the free radicals attack and the cell damage by them [14]. Nitric oxide is a potent free radical which is formed from the conversion of L-Arginine to L Citrulline via nitric oxide synthase enzyme. Excess concentration of NO plays a key role in cardiovascular and other cell damages [15]. In diabetes mellitus oxidative stress is generated by an imbalance between free radicals and its scavenging systems. An aberrant activity of an antioxidant enzyme accelerates oxidative stress in diabetes patients, which can cause serious complications [16,17,18].

A mitochondrial DNA mutation at position 3243 A/G transcribes the aberrant tRNA Leucine, which may code, the defective polypeptide of an electron transport chain [19]. Mitochondrial DNA mutation A/G at position 3243 in mitochondrial DNA is not only associated with type 2 diabetes mellitus but also it can cause Mitochondrial Encephalopathy Lactic Acidosis and Stroke like Syndrome (MELAS) [20]. Many studies manifest the involvement of mitochondrial DNA 3243A/G mutation in maternally inherited type 2 diabetes mellitus. Because of high frequency rate amongst the worldwide population, we selected this mutation for study [21,22,23].

2. Material and Method

Sample Collections and family History

This study included eighteen samples from three families; family 1 and family 2 are diabetic whereas family 3 is non diabetic (healthy control) between the age group of 18 to 70 years. Samples were collected after taking a signed consent form from the patients. All the samples and family history of patients were taken from "Diabetes Hospital" located at, Nagpur, Maharashtra, India.

Inclusion Criteria: Families with a history of maternally inherited diabetes.

Exclusion Criteria: Any kind of paternal history of type 2 diabetes mellitus, type 1 diabetes mellitus, Juvenile diabetes mellitus.

Sample Preparation

2 ml blood samples were collected in EDTA vacutainer tubes; from each tube 0.3 ml of blood sample was used to isolate DNA immediately and the remaining blood sample was centrifuged at 3000×g for 15 minutes for the collection of plasma. The plasma samples were recentrifuged at 3000×g for the same time and were collected in new vials to avoid the carryover of blood cells. All the samples were stored at -20°C until further analysis.

Enzymatic Analysis

All standard methods were used to determine the concentration of various antioxidant enzymes. Catalase was estimated according to the method of Aebi et. al. (1983) [24]. In plasma samples, the addition of 2mM cyanide inhibited Cu/Zn SOD and MnSOD were unaffected by it, whereas the addition of 50 micro L ice cold Chloroform/Ethanol inactivated Mn/Fe SOD [25,26]. Both Cu/Zn SOD and Mn/Fe SOD were assayed as per Marklund and Marklund (1974) [27]. TBARS (Thio Barbituric Acid Reactive Substances) was measured according to J. Stocks et. al. (1971) [28]. The concentration of Nitric Oxide was measured as per Green's et al (1982) [29]. And the concentration of protein was estimated according to Lawery O.H. et. al. (1951) [30].

Isolation of Mitochondrial DNA

DNA was isolated by using whole blood DNA isolation Kit (Ge Nei catalogue No: 612102300011730)

Identification of Mutation:

Total 581 nucleotides containing DNA amplification were carried out using ready to use Master Mix Bioline (Catalogue No.BIO-33057) by PCR (Polymerase Chain Reaction) method. Mutation analysis was done according to

the method given by Ouweland J.M.W. [31]. The 20 nucleotides containing each forward and reverse primers were taken from nucleotide sequence 3029 to 3048 as FORWARD 5' AAGGTTTCGTTTGTTC AACGA 3' and from 3591 to 3610 as REVERSE 5' GGCCTAGGTTGAGGTTGACC 3' as per revised Cambridge Reference sequence (rCRS) of the human mitochondrial DNA (MITOMAP) and performed pBLAST online tool, using NCBI (National Centre for Biotechnology Information) gene sequences. Primers were synthesized through IDT scientific technologies. PCR reactions were carried out in the 12 µL reaction mixture consisting of 1 µL of DNA template (100ng), 2µL Forward primer (100ng), 2µL reverse primer (100ng) and 7µL of the Bioline master mix. Protocol condition consisted, incubation at 94°C for 3 minutes, followed by 94°C for 30 seconds, 55°C for 30 seconds, 72°C for 45 seconds and a final incubation at 72°C for 5 minutes in Biorad Thermal Cycler (USA). Amplified samples were then preceded by RFLP (Restriction Fragment Length Polymorphism); digested by Restriction Enzyme ApaI GeNei at 37°C for approximately 24 hours. Resultant amplicons were subsequently electrophoresed using 2% agarose gel and visualized by ethidium bromide, with DNA ladder (100 to 1000 bp) GeNei (Catalogue No. GeNei 612652671001730) in the Gel-Doc system (Bio-Rad USA). The digested amplicons will give 367 bp and 214 bp containing DNA fragments if A/G mutation is present at position 3243 in mitochondrial DNA. A single 581 bp DNA band represents an absence of the mutation.

Statistical Analysis:

Med Calc statistical software was used for statistical analysis of oxidative stress. All results were expressed in Mean ± SD. The two tailed probability student's T test was used to differentiate between the two diabetic families assuming unequal variance. P< 0.05 was a standard for significance difference.

3. Result

Table 1 shows the general data about the diabetic family 1 and 2 and normal control samples selected for the study. Oxidative stress markers are represented in table 2.

This study demonstrates that, as compared to normal control subjects, the activity of catalase is significantly decreased not only in family 1 (p<0.01) but also in family 2 (p<0.01) [Table 2, Fig (A)]. Likewise the significant decrease in Mn/Fe SOD activity has been reported in family 1 (p<0.01) and family 2 (p<0.05) [Table 2, Fig (B)]. In addition to this the activity of Cu/Zn SOD was significantly lower in family1 (p<0.001) as well as in family 2 (p< 0.01) [Table 2, Fig (C)]. The levels of MDA were significantly increased in both familiy1 (p<0.05) and family 2 (p<0.05) [Table 2, Fig (D)]. The concentration of nitric oxide was found significantly increased in family1 (p<0.05) and family 2 (p<0.05) [Table 2, Fig (E)].

Table 1: General Data of Selected Families.

PARAMETERS	TOTAL Obs.	CONTROL MEAN±SD (No. Obs. 6)	FAMILY1 MEAN±SD (No. Obs. 6)	FAMILY2 MEAN±SD (No. Obs. 6)
AGE (YEARS)	18	43.16±11.99	43.83±15.99	46.66±16.07
ONSET	12		39.83±9.94	39.83±9.17
WEIGHT (Kg)	18	60.33±6.59	75.83±9.23	71.50±15.43
FPGU (Mg/dL)	18	81.00±12.93	189.00±18.31	195.33±28.07

Obs. = Observations, No.Obs. = Number of observations,
 FPGU = Fasting Plasma Glucose.

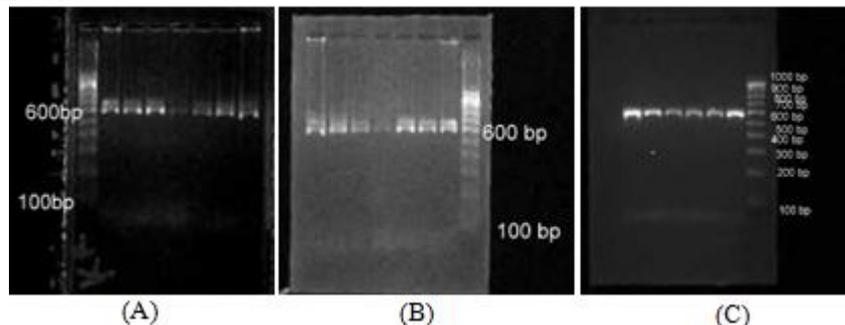


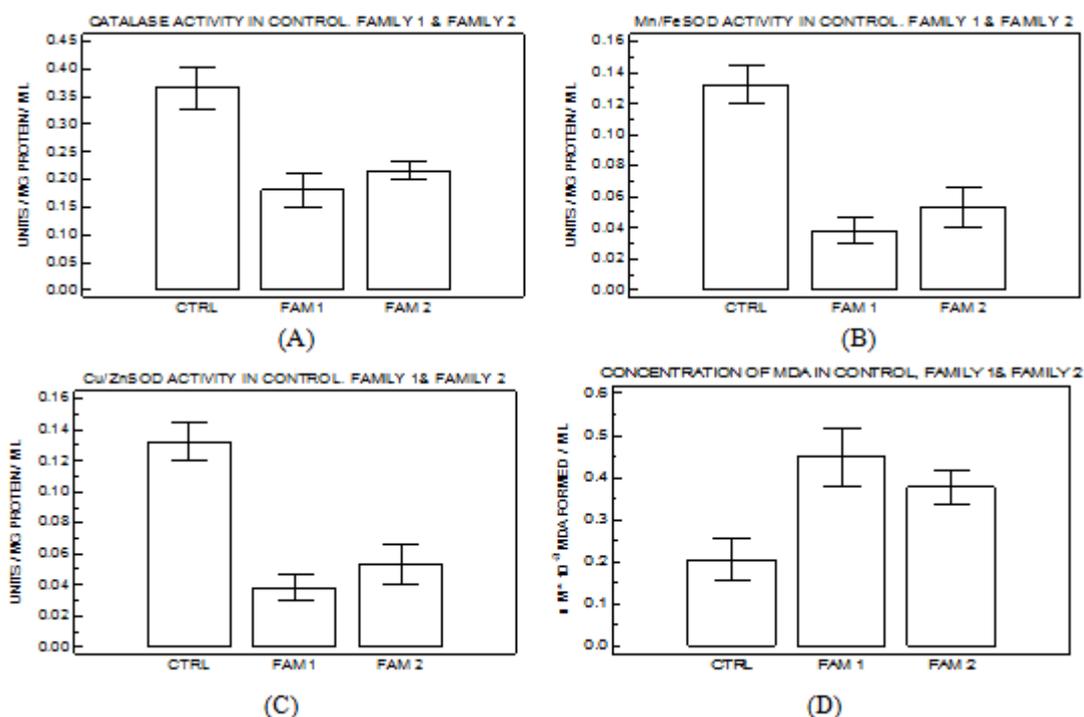
Figure 1: A 3243 A/G mutation analysis in Family 1(A), family 2 and in control healthy subjects (C). The intact 581 bp containing DNA bands were observed. In panel A, first well contains DNA ladder and from well 2 to 8 contains patient's amplified DNA samples except well number 5. In panel B, last well contains DNA ladder and from well 1 to 7 contains patient's amplified DNA samples except well number 4. In panel C, last well contains a DNA ladder and from well 2 to 7 contains patient's amplified DNA samples.

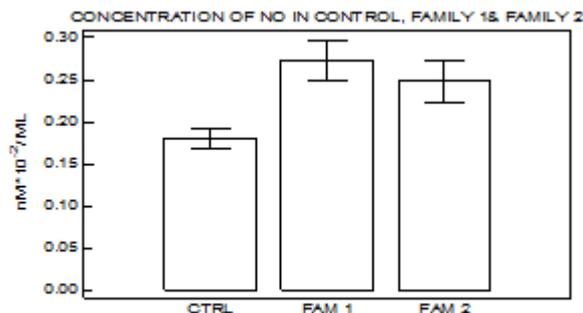
Figure 1 represents the 3243A/G mutation analysis in both diabetic family 1, 2 and in control samples. Electrophoresis showed 581 bp containing DNA bands when they were compared to control DNA ladder. This showed that there was no 3243A/G mutation in mitochondrial DNA of maternally inherited type 2 diabetes mellitus.

4. Discussion

Mutated mitochondria can generate more free radicals. The free radicals are highly reactive in nature due to its

unsatisfied valencies [32] and hence it can act as a potent source in the pathogenesis of diabetes mellitus [33,34]. The various antioxidant enzymes and other antioxidants like vitamin E, vitamin C, carotene, etc. play a vital role in free radicals scavenging mechanism [35,36]. Oxidative stress is an imbalance between the free radicals and antioxidant enzymes. Many studies revealed that oxidative stress in diabetes mellitus gives rise to an increase concentration of free radicals and diminishes the activity of antioxidant enzymes [37-39].





(E)

Figure 2: The activity of various antioxidant enzymes, including catalase represented by a graph (A), the Mn/FeSOD and Cu/Zn SOD represented by (B) and (C) respectively; similarly the concentration TBARS shown by (D) and the concentration of Nitric Oxide shown by (E) in normal control subjects and in patients with diabetes of family 1 and family 2.

We evaluated the levels of antioxidant enzymes in maternally inherited type 2 diabetes mellitus and in a healthy control subjects. The results of this study, clearly corroborates the oxidative stress in both family 1 and family 2. Catalase is the important antioxidant enzyme found nearly in all cells [40] which converts hydrogen peroxide into water molecule and oxygen [41]. Hydrogen peroxide if not removed from the biological samples it may convert into hydroxyl radicals, which may impart more oxidative stress. Hydroxyl radicals are the potent free radical, which is reported as the deadliest free radical which has ever been found. Hence catalase plays an important role in free radical scavenging [42]. Statistical analysis affirms that not only in family 1 but also in family 2 there is a significant decrease in the activity of catalase enzyme in both the diabetic families. This is in accordance with various other studies [43,44]

Like the catalase enzyme, Manganese/ Iron Superoxide Dismutase and Copper/ Zinc containing Superoxide Dismutase also plays a central role in the defence mechanism against the free radicals damage [45]. The main function of the Superoxide Dismutase enzyme is to eradicate superoxide anion which can cause damage to cells, cellular membranes, DNA and other biological organelles. Superoxide Dismutase converts superoxide anion radical into the hydrogen peroxide molecule [46,47]. Many studies showed that there is decreased activity of Mn/Fe SOD and Cu/Zn SOD in type 2 diabetes mellitus than normal control samples [48]. This study also shows a significant decrease in the activity of Mn/Fe SOD and Cu/Zn SOD in patients with type 2 diabetes.

Malonaldehyde formation is an indication of increased lipid peroxidation in diabetes mellitus [49]. It is used to determine the oxidative stress through determining the balance between free radicals and antioxidant enzymes [50]. We analysed the significant increase in the concentration of malonaldehyde in both diabetic families. The increased concentration of malonaldehyde indicates an oxidative stress in patients with diabetes. Various other studies showed an increase in oxidative stress in diabetes mellitus [43,51,52].

Statistics showed somewhat similar results for the concentration of nitric oxide to those of malonaldehyde. Nitric oxide may react with superoxide anion and can form peroxynitrite molecules, which can harm cellular mechanism. Hence, it is very essential to maintain the concentrations of

free radicals like nitric oxide and superoxide radicals [53]. Although, the life span of nitric oxide is very less, increased concentration can induce an oxidative stress and may play a pivotal role in diabetes mellitus [54]. The present study, exhibited significant increase in the concentration of nitric oxide in both the families of diabetic patients. Certain other studies have also demonstrated an increase concentration of nitric oxide in patients with diabetes than control [55,56].

Table 2 : A Statistical analysis of various antioxidant enzymes, lipid peroxidation and nitric oxide.

ENZYMES	GROUPS	MEAN±SD	P-VALUE
CATALASE (Units/Mg protein/ML)	CONTROL	0.3659±0.0931	
	FAMILY1	0.1805±0.0752	<0.01
	FAMILY2	0.2160±0.0400	<0.01
Mn/Fe SOD (Units/Mg protein/ML)	CONTROL	0.0376±0.0074	
	FAMILY1	0.0244±0.0064	<0.01
	FAMILY2	0.0215±0.0115	<0.05
Cu/Zn SOD (Units/Mg protein/ML)	CONTROL	0.1325±0.0308	
	FAMILY1	0.0379±0.0203	<0.001
	FAMILY2	0.0532±0.0305	<0.01
MDA (nM × 10 ⁻³ /ML)	CONTROL	0.2048±0.1247	
	FAMILY1	0.4487±0.1656	<0.05
	FAMILY2	0.3767±0.1022	<0.05
NO (nM × 10 ⁻² /ML)	CONTROL	0.1800±0.0303	
	FAMILY1	0.2483±0.0611	<0.05
	FAMILY2	0.2733±0.0592	<0.05

Mitochondrial DNA lacks histone proteins and DNA repair mechanisms, which increases the chances of its damage by free radicals [57]. Colossal work on mitochondrial DNA exhibited its role in maternally inherited type 2 diabetes mellitus [21,22,23]. For last few decades, researchers have been working on mitochondrial DNA to identify the various mitochondrial DNA mutations, which can play a pivotal role in the pathogenesis of type 2 diabetes mellitus. Over more than 40 different mitochondrial DNA mutations associated with type 2 Diabetes Mellitus have been identified yet [58]. In this study, the absence of 3243 A/G mutation has been observed in the selected families (Fig: 2), this was according to the study of Naveed AK et.al. [59].

5. Conclusion

This study cogitated on oxidative stress and 3243 A/G mitochondrial DNA mutation in two families with a history of maternally inherited type 2 diabetes mellitus. Decrease activities of various antioxidant enzymes like catalase, Mn/Fe SOD, Cu/Zn SOD with increase concentration of nitric oxide and lipid peroxidation providing a straight forward evidence of oxidative stress in both diabetic families. Increased oxidative stress can cause other complications like DNA and cellular damage in the patients. Therefore, monitoring oxidative stress in patients with maternally inherited type 2 diabetes mellitus could be of utmost importance to prevent these complications. The undertaken study did not observe a 3243A/G mutation in patients with a history of maternally inherited type 2 diabetes mellitus, other mutations might be present in selected families.

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