



## **JATROPHA CURCAS REPAIRING EFFECT ON ADHESION MOLECULES, DNA DAMAGE AND GENE EXPRESSION ALTERATION IN STZ-INDUCED DIABETIC RATS**

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### **ABSTRACT**

The recent research converges on the evaluation of *Jatropha curcas* different extracts on some biochemical parameters in streptozotocin (STZ)-induced diabetic rats. Diabetes mellitus (DM) was induced using STZ (45 mg/kg b.w) while, *J. curcas* extracts were orally administered at a dose of 250mg/kg/day and glibenclamide (antidiabetic drug) at a dose of 10mg/kg/day for 30 days. Adhesion molecules; VCAM-1 and ICAM-1 were measured in blood serum of rats and the results showed that VCAM-1 and ICAM-1 levels were significantly increased in diabetic rats as compared to controls. The results showed that *J. curcas* extracts have reduced VCAM-1 and ICAM-1 high levels in diabetic rats. DNA fragmentation was determined using diphenylamine reaction as well as DNA gel electrophoresis laddering assays and the expression of diabetes related genes was determined by qRT-PCR. The results revealed that the administration of *J. curcas* extracts exhibited relatively the rates of DNA damage similar to those in the control group. Moreover, *J. curcas* extracts altered the expression of diabetes related genes and appeared similar to those in control group. Thus, *J. curcas* extracts might be a promising regulator supplement for hyperglycemia and the expression of genes related DM.

**KEYWORDS:** *Jatropha curcas*; streptozotocin; adhesion molecules; DNA damage; diabetes related genes.



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## INTRODUCTION

Adhesion molecules are important in cell-cell and cell-basement membrane interactions. Vascular cell adhesion molecule-1 (VCAM-1) and intercellular adhesion molecule-1 (ICAM-1) play a role in cell adhesion to the vascular endothelium. Type 2 diabetes mellitus (T2DM) is powerful and independent risk factors for coronary artery disease, stroke, and peripheral arterial disease. Accelerated atherosclerosis is the morbidity and mortality in this common metabolic disorder<sup>1</sup>. It was proved that, hyperglycemia in diabetic patients can trigger endothelial damage through increased oxidative stress and up-regulation of cellular adhesion molecules<sup>2</sup>. On the other hand, the increased production of reactive oxygen species (ROS) plays a key role in pathogenesis of DM complications where, ROS are generated by exogenous and endogenous factors such as during hyperglycemia ensued by oxidative stress<sup>3</sup>. The authors added that, oxidative stress induces DNA damage and when DNA damage exceeds the cellular capacity to repair it, the accumulation of errors can overwhelm the cell resulting in cell death or fixation of genome mutations that can be transmitted to future cell generations. Additionally, mutations can promote genome instability and directly lead to various human diseases such as cancer, neurological abnormalities, immunodeficiency, and premature aging<sup>4,5</sup>. Oxidative stress induced inflammatory responses cause damage to the vasculature and may play an important role in the development of many diseases. Activation of endothelial cells by oxidants may lead to a wide range of functional changes such as an increased expression of VCAM-1 and ICAM-1<sup>6</sup>. In addition, ROS can cause strand breaks in DNA and base modifications, including oxidation of guanine residues to 8-hydroxy-2'deoxyguanosine (8-OHdG) - an oxidized nucleoside of DNA that is the most frequently detected and studied DNA lesion<sup>7</sup>. Medicinal plants have been used to cure or prevent diseases leading to the promotion of good health. The benefit of these plants is related to the secondary metabolites that are produced by

the plants, even though plants produced these secondary metabolites for the benefits of the plant itself as defense against infection and injury, but it was found that the secondary metabolites have benefits to the human health and curing human diseases<sup>8</sup>. Secondary metabolites of medicinal plants produce a natural source of antioxidants. These natural antioxidants gained major attention and importance towards treatment of various free radical-related diseases such as cancer, asthma, atherosclerosis, arthritis, aging, and autoimmune disorders, several stress related diseases, including cataracts, cognitive dysfunction, myocardial infarction, and diabetes, and several cardiovascular and neurodegenerative diseases<sup>9,10</sup>. *J. curcas* (Euphorbiaceae family) is a shrub or small tree that gained its name from the Greek word *jatro's* (doctor) and *trophe'* (food), which connotes its medicinal uses. Several biological activities were reported to the plant throughout the amelioration of neuropathic pain and treating inflammatory diseases<sup>11</sup>. Different parts of the plant, including the leaves, fruits, latex and bark contain bioactive compounds such as glycosides, tannins, phytosterol, flavonoids and steroidal sapogenins with several medicinal properties<sup>12,13</sup>. So, the present research aims to evaluate the ameliorative effects of *J. curcas* extracts on increased levels of adhesion molecules as well as the DNA damage attributed to DM deadly disease.

## MATERIALS AND METHODS

### (i) Chemicals and reagents

All chemicals in the present study are of analytical grade, products of Sigma, Merck and Aldrich. All kits were the products of Biosystems (Alcobendas, Madrid, Spain), Sigma Chemical Company (St. Louis, MO, USA), Biodiagnostic Company (Cairo, Egypt).

**(ii) Collection and preparation of plant material**

*J. curcas* fresh leaves were collected from the farm of Aromatic and Medicinal Plant Department, Agriculture Research Centre, Egypt. The plant was kindly authenticated by Mrs Treas Labib, Herbarium section, El-Orman Botanical Garden, Giza, Egypt. The leaves were washed with tap water, then with distilled water to remove dust and dirt. Leaves were air dried under shade, then grinded and homogenized to coarse powder finally stored in opaque screw tight jars until use.

**(iii) Successive and crude extracts preparation**

About 2.5 kg powdered leaves were extracted successively by a cold maceration method with different solvents of increasing polarity on shaker (Heidolph) *i.e.* petroleum ether, ethyl acetate and methanol. The marc was dried each time before extraction with next solvent. After complete extraction the extracts were filtered by using Whatman grade No. 4 filter paper and Buchner. Filtrates were concentrated using Rotary evaporator (Heidolph) at 40°C under vacuum and stored in refrigerator (4°C) till biological assay and chemical analysis. While, the crude methanolic extract was prepared by cold maceration in methanol of 300 g of *J. curcas* powdered leaves on shaker. The extract was filtered by using Whatman grade No. 4 filter paper and Buchner. The filtrate was concentrated using Rotary evaporator at 40°C under vacuum and stored in refrigerator (4°C) till biological assay and chemical analysis.

**(iv) Biological experiment:**

**1. Animals**

Female albino rats (n=110) weighted (150-200 g), were used for the evaluation of anti-diabetic effects of *J. curcas* extracts and provided by the Animal House of the National Research Centre (NRC) and housed in a temperature-controlled environment (26-29°C) with a fixed light/dark cycle for one week as an adaptation period to acclimatize under normal combination with free access to water and food. The present study is approved by the Ethical Committee of the NRC,

Egypt, provided that the animals will not suffer at any stage of the experiment.

**2. Experimental design<sup>14-17</sup>**

One hundred and ten rats were selected for this study and divided into eleven groups of ten rats each as follows:

Group 1: Normal, healthy control rats, Groups 2-5: Normal rats treated orally with 250 mg/kg body of petroleum ether, ethyl acetate, successive and crude methanolic extracts for 30 days. Group 6: Is considered as diabetic group; where type2 diabetes was induced by intraperitoneally injection of a single dose of STZ (45 mg/kg body weight) dissolved in 0.01 M citrate buffer immediately before use. After injection, animals had free access to food, water and were given 5% glucose solution to drink overnight to encounter hypoglycaemic shock. Animals were checked daily for the presence of glycosuria. Animals were considered to be diabetic if glycosuria was present for 3 consecutive days. After 3 days of STZ injection fasting blood samples were obtained and blood sugar was determined ( $\geq 300$  mg/dl). Hyperglycemic rats were used for the experiment and classified as follows:

Groups 7-10: Diabetic rats oral administered 250 mg/kg body weight petroleum ether, ethyl acetate, successive and crude methanolic extracts for 30 days respectively, Groups 11: Diabetic rats administered orally antidiabetic glibenclamide reference drug 10 mg/kg body weight daily for 30 days.

**3. Sample preparations**

After 30 days of treatments, rats were fasted overnight (12-14 hours), anesthetized by diethyl ether and blood collected by puncture of the sublingual vein in clean and dry test tube, left 10 minutes to clot and centrifuged at 3000 r.p.m for serum separation. The separated serum was used for biochemical analysis of adhesion molecules (VCAM-1 and ICAM-1).

**4. Biochemical examination**

Estimation of serum adhesion molecules; VCAM-1 and ICAM-1 was performed by ELISA; a sandwich enzyme immunoassay.

**Calculation:**

$$\% \text{ change} = \frac{\text{Mean of control} - \text{mean of treated} \times 100}{\text{Mean of control}}$$

$$\% \text{ of improvement} = \frac{\text{Mean of treated} - \text{mean of disease} \times 100}{\text{Mean of control}}$$

**5. DNA Fragmentation Analysis****a- Diphenylamine reaction procedure**<sup>18</sup>

Rats liver and heart tissues were used to determine the quantitative profile of the DNA fragmentation. Liver and heart samples were collected immediately after sacrificing the animals. The tissues were lysed in 0.5 ml of lysis buffer containing, 10 mM tris-HCl (pH 8), 1 mM EDTA, 0.2% triton X-100, centrifuged at 10 000 rpm (Eppendorf) for 20 min at 4°C. The pellets were re-suspended in 0.5 ml of lysis buffer. To the pellets (P) and the supernatants (S), 0.5 ml of 25% tri-chloroacetic acid (TCA) was added and incubated at 4°C for 24 h. The samples were then centrifuged for 20 min at 10 000 rpm (Eppendorf) at 4°C and the pellets were suspended in 80 ml of 5% TCA, followed by incubation at 83°C for 20 min. Subsequently, to each sample 160 ml of DPA solution [150 mg DPA in 10 ml glacial acetic acid, 150 ml of sulfuric acid and 50 ml acetaldehyde (16 mg:ml)] was added and incubated at room temperature for 24 h. The proportion of fragmented DNA was calculated from absorbance reading at 600 nm wavelength using the formula:

$$\% \text{ Fragmented DNA} = \frac{\text{OD(S)}}{\text{OD(S)} + \text{OD(P)}} \times 100$$

**b- DNA gel Electrophoresis Laddering Assay**<sup>19</sup>

Apoptotic DNA fragmentation was qualitatively analyzed by detecting the laddering pattern of nuclear DNA. Briefly, liver tissues were homogenized, washed in PBS, and lysed in 0.5 ml of DNA extraction buffer (50 mM Tris-HCl, 10 mM EDTA, 0.5% Triton, and 100 µg/ml proteinase K, pH 8.0) for overnight at 37 °C. The lysate was then incubated with 100 µg/ml

DNase-free RNase for 2h at 37 °C, followed by three extractions of an equal volume of phenol/chloroform (1:1 v/v) and a subsequent re-extraction with chloroform by centrifuging at 15,000 rpm for 5 min at 4 °C. The extracted DNA was precipitated in 2 volume of ice-cold 100% ethanol with 1/10 volume of 3 M sodium acetate, pH 5.2 at -20 °C for 1h, followed by centrifuging at 15,000 rpm for 15 min at 4 °C. After washing with 70% ethanol, the DNA pellet was air-dried and dissolved in 10 mM Tris-HCl/1 mM EDTA, pH 8.0. The DNA was then electrophoresed on 1.5% agarose gel and stained with ethidium bromide in Tris/acetate/EDTA (TAE) buffer (pH 8.5, 2 mM EDTA, and 40 mM Tris-acetate). A 100-bp DNA ladder (Invitrogen, USA) was included as a molecular size marker and DNA fragments were visualized and photographed by exposing the gels to ultraviolet transillumination.

**6. Expression of diabetes related genes by qRT-PCR****a- Isolation of total RNA**

Total RNA was isolated from liver and heart tissues of male rats by the standard TRIzol® Reagent extraction method (Invitrogen, Germany). Briefly, tissue samples were homogenized in 1 ml of TRIzol® Reagent per 50 mg of the tissue. Afterwards, the homogenized sample was incubated for 15 minutes at room temperature. A volume of 0.2 ml of chloroform per 1 ml of TRIzol® Reagent was added. Then the samples were vortexed vigorously for 15 seconds and incubated at room temperature for 3 minutes. The samples were centrifuged for no more than 12,000 x g for 15 minutes at 4 °C. Following centrifugation, the mixture was separated into lower red, phenol-chloroform phase, an interphase, and a

colorless upper aqueous phase. RNA was remained exclusively in the aqueous phase. Therefore, the upper aqueous phase was carefully transferred without disturbing the interphase into a fresh tube. The RNA was precipitated from the aqueous phase by mixing with isopropyl alcohol. A volume of 0.5 ml of isopropyl alcohol was added per 1 ml of TRIzol® Reagent used for the initial homogenization. Afterwards, the samples were incubated at 15 to 30 °C for 10 minutes and centrifuged at not more than 12,000 x g for 10 minutes at 4 °C. The RNA was precipitated which was often invisible before centrifugation, formed a gel-like pellet on the side and bottom of the tube. The supernatant was removed completely. The RNA pellet was washed once with 1 ml of 75% ethanol. The samples were mixed by vortexing and centrifuged at no more than 7,500 x g for 5 minutes at 4 °C. The supernatant was removed and RNA pellet was air-dried for 10 minutes. RNA was dissolved in diethylpyrocarbonate (DEPC)-treated water by passing solution a few times through a pipette tip. Total RNA was treated with 1 U of RQ1 RNase-free DNase (Invitrogen, Germany) to digest DNA residues, re-suspended in DEPC-treated water. Purity of total RNA was assessed by the 260/280 nm ratio (between 1.8 and 2.1). Additionally, integrity was assured with ethidium bromide-stain analysis of 28S and 18S bands by formaldehyde-containing agarose gel electrophoresis. Aliquots were used immediately for reverse transcription (RT).

#### ***b- Reverse transcription (RT) reaction***

The complete Poly(A)<sup>+</sup> RNA isolated from male rat liver and heart tissues was reverse transcribed into cDNA in a total volume of 20 µl using RevertAid™ First Strand cDNA Synthesis Kit (MBI Fermentas, Germany). An amount of total RNA (5µg) was used with a reaction mixture, termed as master mix (MM). The MM was consisted of 50 mM MgCl<sub>2</sub>, 5x reverse transcription (RT) buffer (50 mM KCl; 10 mM Tris-HCl; pH 8.3; 10 mM of each dNTP, 50 µM oligo-dT primer, 20 U ribonuclease inhibitor (50 kDa recombinant enzyme to inhibit RNase

activity) and 50 U M- MuLV reverse transcriptase. The mixture of each sample was centrifuged for 30 sec at 1000 g and transferred to the thermocycler. The RT reaction was carried out at 25 °C for 10 min, followed by 1 h at 42 °C, and the reaction was stopped by heating for 5 min at 99 °C. Afterwards the reaction tubes containing RT preparations were flash-cooled in an ice chamber until being used for DNA amplification through semi-quantitative real time-polymerase chain reaction (qRT-PCR).

#### ***c- Quantitative Real Time-Polymerase Chain Reaction (qRT-PCR)***

QIAGEN's real-time PCR cycler (Rotor-Gene Q, USA) was used to determine the rat cDNA copy number. PCR reactions were set up in 25 µL reaction mixtures containing 12.5 µL 1x SYBR® Premix Ex Taq™ (TaKaRa, Biotech. Co. Ltd., Germany), 0.5 µL 0.2 µM sense primers, 0.5 µL 0.2 µM antisense primer, 6.5 µL distilled water, and 5 µL of cDNA template. The reaction program was allocated to 3 steps. First step was at 95.0°C for 3 min. Second step consisted of 40 cycles in which each cycle divided to 3 steps: (a) at 95.0°C for 15 sec; (b) at 55.0°C for 30 sec; and (c) at 72.0°C for 30 sec. The third step consisted of 71 cycles which started at 60.0°C and then increased about 0.5°C every 10 sec up to 95.0°C. At the end of each qRT-PCR a melting curve analysis was performed at 95.0°C to check the quality of the used primers. Each experiment included a distilled water control. the specific gene primer sequences and PCR cycling conditions are listed in (Table 1). The quantitative values of RT-PCR (qRT-PCR) of diabetes related genes (Insulin-like growth factor 1 receptor, IGF1R, Insulin-like growth factor binding protein 2, IGFBP2, Insulin-like growth factor binding protein 3, IGFBP3, Glutamate receptor, ionotropic, N-methyl D-aspartate 2C, GRIN2C and Vascular endothelial growth factor A, VEGFA) were normalized on the bases of β-actin expression. At the end of each qRT-PCR a melting curve analysis was performed at 95.0 °C to check the quality of the used primers.

**Table 1**  
**Oligonucleotide primers used for the analysis of diabetes related genes by qRT-PCR**

Gene name	Primer Sequence (5'-3')	Reference/ or Accession number	Annealing temp (°C)
β-actin	F: GTG GGC CGC TCT AGG CAC CAA R: CTC TTT GAT GTC ACG CAC GAT TTC	(Khalil and Booles) <sup>20</sup>	64.5
Insulin-like growth factor 1 receptor (IGF1R)	F: CCA ACA AGT TCG TCC ACA G R: AGT CCG TCT CGT AGA TGT C	NM_052807	59
Insulin-like growth factor binding protein 2 (IGFBP2)	F: GGG TCC TCT GGA ACA TCT C R: GTC CAT TCA GAG ACA TCT TGC	NM_013122	59
Insulin-like growth factor binding protein 3 (IGFBP3)	F: ACA GAC ACC CAG AAC TTC TC R: CAG CAC ATT GAG GAA CTT CAG	NM_012588	59
Glutamate receptor, ionotropic, N-methyl D-aspartate 2C (GRIN2C)	F: GGC CCA GCT TTT GAC CTT AGT R: CCT GTG ACC ACC GCA AGA G	U08259	59
Vascular endothelial growth factor A (VEGFA)	F: AGG AAA GGG AAA GGG TCA R: ACA AAT GCT TTC TCC GCT	NM_031836	57

F: Forward primers; R: Reverse primers

#### d- Calculation of Gene Expression

First the amplification efficiency (Ef) was calculated from the slope of the standard curve using the following formula found in the manufacturer's instruction pamphlet:

$$Ef = 10^{-1/\text{slope}}$$

$$\text{Efficiency (\%)} = (Ef - 1) \times 100$$

The relative quantification of the target to the reference was determined by using the  $2^{-\Delta\Delta CT}$  method if Ef for the target (IGF1R, IGFBP2, IGFBP3, GRIN2C and VEGFA) and the reference primers (β-Actin) as follows:

$$\Delta C_{T(\text{test})} = C_{T(\text{target, test})} - C_{T(\text{reference, test})}$$

$$\Delta C_{T(\text{calibrator})} = C_{T(\text{target, calibrator})} - C_{T(\text{reference, calibrator})}$$

$$\Delta\Delta CT = \Delta C_{T(\text{Test})} - \Delta C_{T(\text{calibrator})}$$

The relative expression was calculated by  $2^{-\Delta\Delta CT}$ .

#### 7. Statistical analysis

All data were subjected to one-way analysis of variance ANOVA and the significance of the differences between means was tested using co-state computer program and Tukey's HSD (Honestly Significant Difference) test ( $P <$

0.05). The software used was SAS, Version 9.1 (Statsoft Inc., Tulsa, USA). Values are expressed as means  $\pm$  standard error.

## RESULTS

### 1. Effect of successive extracts as well as crude methanolic extract of *J. curcas* on adhesion molecules

The effect of different extracts of *J. curcas* on adhesion molecules in STZ-induced diabetic rats and different therapeutic groups was showed in Table 2. The results demonstrated insignificant change in VCAM-1 and ICAM-1 levels with different extracts supplemented to normal rats as compared to untreated control one. Diabetic rats showed significant increase in both VCAM-1 and ICAM-1 levels with percentages 57.34 and 13.16%, respectively. VCAM-1 levels were markedly ameliorated in diabetic-treated groups with petroleum ether, ethyl acetate,

successive methanolic, crude methanolic extracts and glibenclamide as compared to untreated one with percentages of improvement 30.99, 34.12, 35.79, 38.65 and 38.36%, respectively. On the other hand, all extracts showed insignificant change in ICAM-1 levels. As shown in Table (2), the highest reduction in VCAM-1 and ICAM levels was obtained with crude methanolic extract followed by successive methanolic extract and petroleum ether

### Effect of *Jatropha curcas* extracts on rates of DNA fragmentation

The results of the DNA fragmentation assay revealed that treatment of diabetic rats with different extracts of *J. curcas* induced different rates of DNA fragmentation (Figure 1 and Table 3). The rate of DNA fragmentation in liver and heart tissues of control rats was observed at low rate of DNA damage (Table 3). However,

diabetic-female rats induced high rates of DNA fragmentation which were 34.6 and 31.2 in liver and heart tissues, compared with 9.8 and 9.6 in control rats, respectively. The different extracts of *J. curcas* exhibited low rates of DNA damage either in liver or heart tissues of non-diabetic rats, whereas the rate of DNA damage in groups treated with petroleum ether (PE), ethyl acetate (EA) and successive methanolic (SM) extracts were relatively similar to those in control group (Table 3). However, treatment of female rats with crude methanolic (CM) extract exhibited more DNA damage than the other extracts. On the other hand, treatment of diabetic rats with PEE, EAE and SME extracts revealed significantly low rates of DNA damage compared to DM rats. Moreover, treatment of female rats with CME decreased significantly the rate of DNA damage induced in DM rats, however, this decrease in the rate of DNA damage was higher than those induced by other extracts.

**Table 2**

**Effects of successive extracts and crude methanolic extract of *J. curcas* supplementation on adhesion molecules; VCAM-1 and ICAM-1 levels in normal, STZ-induced diabetic rats and different therapeutic groups**

Groups	Parameters	VCAM-1 (ng/ml)	ICAM-1 (ng/ml)
<b>Normal rats</b>	Mean± S.D.	12118.92±7.73 <sup>e</sup>	254.46±2.08 <sup>c</sup>
<b>Normal rats treated with petroleum ether extract (PEE)</b>	Mean ±S.D	13212.25±179.51 <sup>e</sup>	247.13±1.79 <sup>c</sup>
	% Change to control	9.02	2.88
<b>Normal rats treated with ethyl acetate extract (EAE)</b>	Mean ±S.D	13285.06±67.36 <sup>e</sup>	247.20±1.70 <sup>c</sup>
	% Change to control	9.62	2.85
<b>Normal rats treated with successive methanolic extract (SME)</b>	Mean ±S.D.	12978.48±265.16 <sup>e</sup>	245.65±3.30 <sup>c</sup>
	% Change to control	7.09	3.46
<b>Normal rats treated with crude methanolic extract (CME)</b>	Mean ±S.D.	13191.25±6.68 <sup>e</sup>	248.63±4.03 <sup>c</sup>
	% Change to control	8.84	2.29
<b>Diabetic rats (DM)</b>	Mean ±S.D.	19068.33±280.57 <sup>a</sup>	287.96±1.96 <sup>a</sup>
	% Change to control	57.34	13.16
<b>Diabetic rats treated with petroleum ether extract (DM+ PEE)</b>	Mean ±S.D.	15312.62±473.47 <sup>b</sup>	260.25±4.44 <sup>bc</sup>
	% Change to control	26.35	2.27
	% Of improvement	30.99	10.89
<b>Diabetic rats treated with ethyl acetate extract (DM+ EAE)</b>	Mean ±S.D.	14933.16±104.78 <sup>bc</sup>	255.12±1.34 <sup>bc</sup>
	% Change to control	23.22	0.26
	% Of improvement	34.12	12.90
<b>Diabetic rats treated with successive methanolic extract (DM+ SME)</b>	Mean ±S.D.	14730±464.11 <sup>c</sup>	257.42±0.54 <sup>bc</sup>
	% Change to control	21.54	1.16
	% Of improvement	35.79	12.00
<b>Diabetic rats treated with crude methanolic extract (DM+ CME)</b>	Mean ±S.D.	14383.35±125.50 <sup>c</sup>	248.13±1.45 <sup>c</sup>
	% Change to control	18.68	2.48
	% Of improvement	38.65	15.65
<b>Diabetic rats treated with antidiabetic drug (DM+ Glibenclamide)</b>	Mean ±S.D.	14419.19±511.76 <sup>c</sup>	246.55±2.53 <sup>c</sup>
	% Change to control	18.98	3.11
	% Of improvement	38.36	16.27

All values are means±SD of 10 rats in each group

-Data were analyzed using analysis of variance (ANOVA) combined with co-state computer program, where unshared letter is significant at  $p \leq 0.05$

Table 3

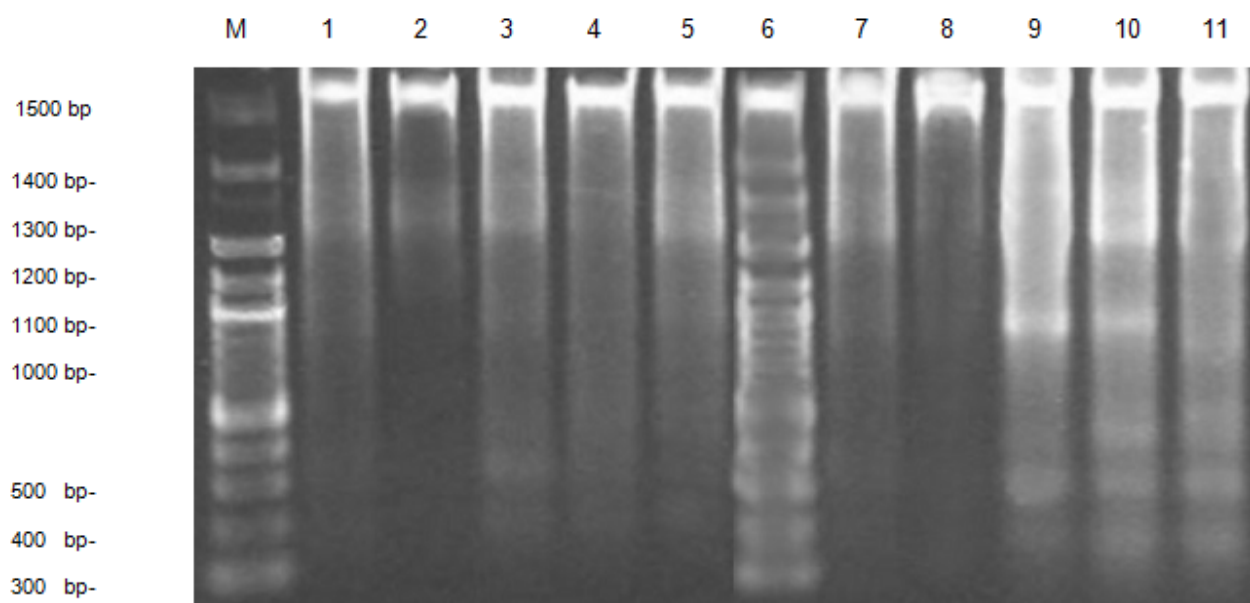
**DNA fragmentation in liver and heart tissues of male DM-rats treated with several extracts of *Jatropha curcas* analyzed by diphenylamine reaction procedure.**

Treatment	DNA Fragmentation (%)	
	Liver (Mean±SEM)	Heart (Mean±SEM)
Control	09.8±0.6 <sup>e</sup>	09.6±0.5 <sup>e</sup>
PEE	10.2±1.4 <sup>e</sup>	10.1±1.2 <sup>e</sup>
EAE	09.7±1.2 <sup>e</sup>	09.4±1.1 <sup>e</sup>
SME	11.6±1.1 <sup>de</sup>	11.2±1.3 <sup>de</sup>
CME	13.2±1.3 <sup>d</sup>	12.8±1.2 <sup>d</sup>
DM	34.6±3.7 <sup>a</sup>	31.2±3.1 <sup>a</sup>
DM+ PEE	18.3±1.5 <sup>c</sup>	17.7±1.4 <sup>c</sup>
DM+ EAE	17.4±1.6 <sup>c</sup>	16.3±1.3 <sup>c</sup>
DM+ SME	21.8±2.1 <sup>bc</sup>	20.2±1.7 <sup>bc</sup>
DM+ CME	23.6±2.3 <sup>b</sup>	22.3±2.1 <sup>b</sup>
DM+ Glibenclamide	19.1±1.3 <sup>c</sup>	18.2±1.3 <sup>c</sup>

PEE: Petroleum ether extract; EAE: Ethyl acetate extract; SME: Successive methanolic extract; CME: Crude methanolic extract; DM: Diabetes mellitus

Figure 1

**DNA fragmentation in liver tissues of male DM-rats treated with several extracts of *Jatropha curcas*. M: DNA marker. Lane 1 represents PCR products of untreated control samples; Lanes 2-5 represent rats treated with PEE, EAE, SME and CME extracts, respectively; lane 6 represents DM-rats; Lanes 7-10 represent DM-rats treated with PEE, EAE, SME and CME extracts, respectively; lane 6 represents DM-rats treated with glibenclamide drug.**



### 3. Effect of *J. curcas* extracts on the expression of diabetes related genes (IGF1R, IGFBP2, IGFBP3, GRIN2C and VEGFA)

The expression of diabetes-associated genes, in the STZ-induced diabetic rats treated with different extracts of *J. curcas* was determined using qRT-PCR (Figures 2-6). The results

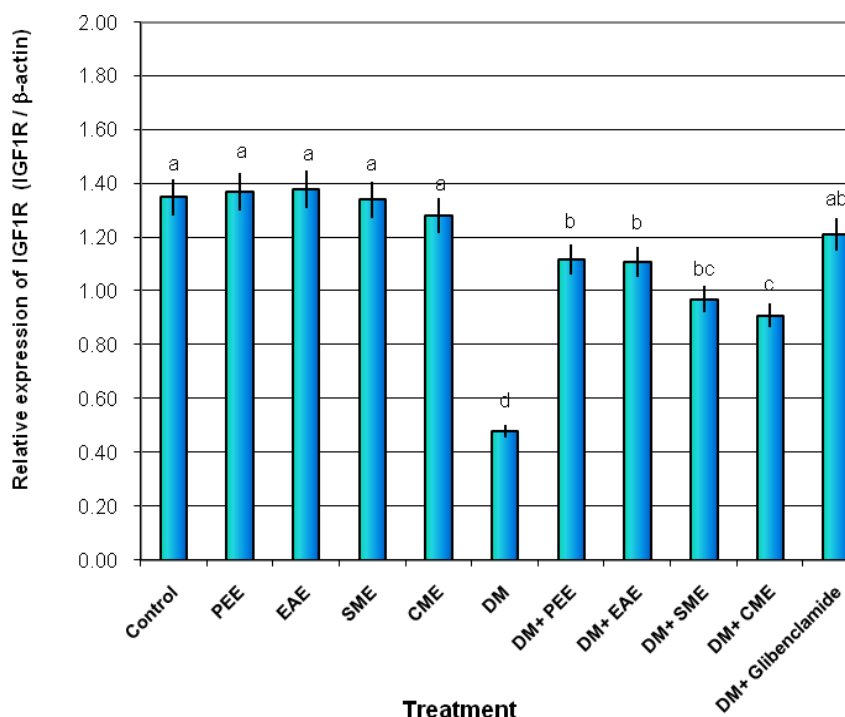


revealed that diabetic rats showed significantly low expression values of IGF1R, IGFBP2 and IGFBP3 (in liver) and VEGFA (in heart) comparing with the control rats (Figures 2, 3, 4 & 6). However, the expression of GRIN2C gene was increased significantly in heart tissues of diabetic rats as compared to control group (Figure 5). On the other hand, treatment of non-diabetic rats with PE; EA, SM and CM extracts exhibited expression values of IGF1R, IGFBP2, IGFBP3, GRIN2C and VEGFA genes relatively similar to those in control rats

(Figures 2-6). Moreover, treatment of diabetic rats with PE; EA, SM and CM extracts exhibited significantly higher expression values of IGF1R, IGFBP2, IGFBP3 (in liver) and VEGFA (in heart) and lower expression of GRIN2C gene (in heart) as compared to those in diabetic rats (Figures 2-6). Furthermore, PE and EA extracts exhibited more effective impact on the expression of IGF1R, IGFBP2, IGFBP3, GRIN2C and VEGFA genes as compared to other extracts.

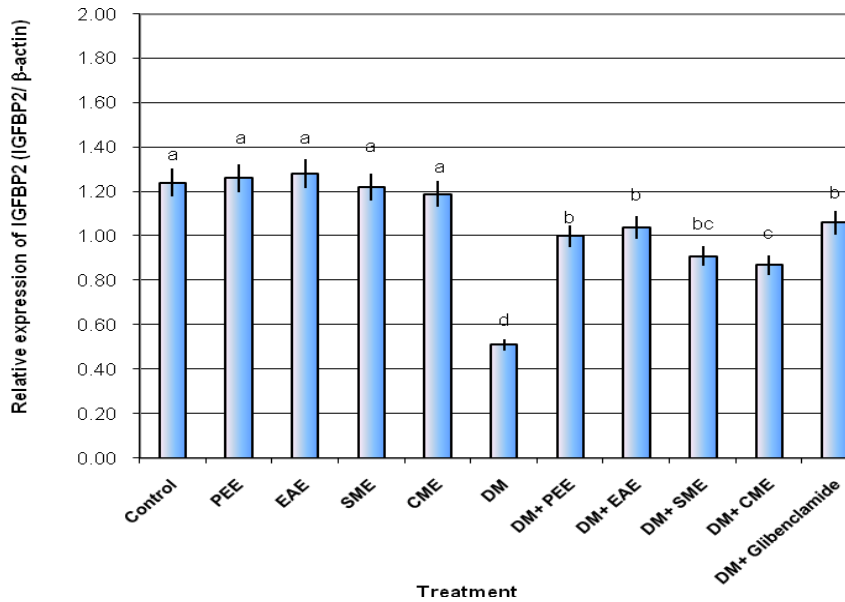
Figure 2

**The alterations of IGF1R mRNA in liver tissues isolated from male DM-rats treated with several extracts of *Jatropha curcas*. <sup>a,b,c</sup>Mean values within tissue with unlike superscript letters were significantly different ( $P < 0.05$ ).**



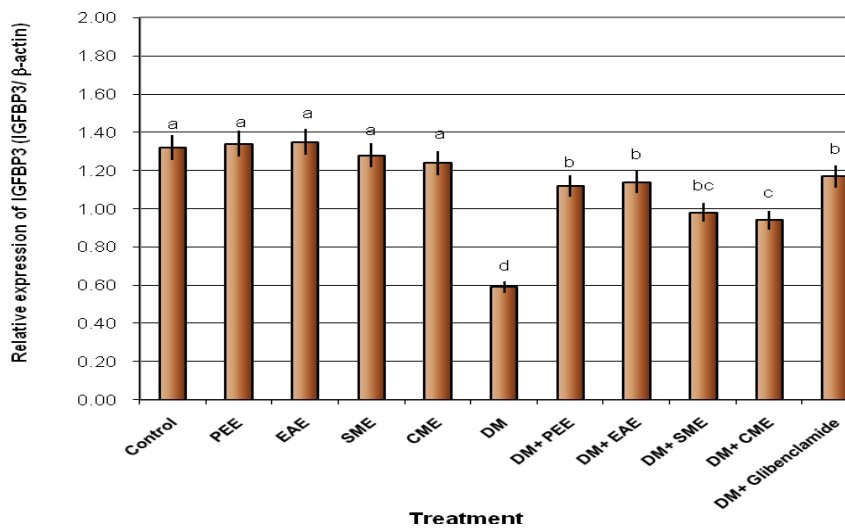
**Figure 3**

**The alterations of IGFBP2 mRNA in liver tissues isolated from male DM-rats treated with several extracts of *Jatropha curcas*. <sup>a,b,c</sup>Mean values within tissue with unlike superscript letters were significantly different ( $P<0.05$ ).**



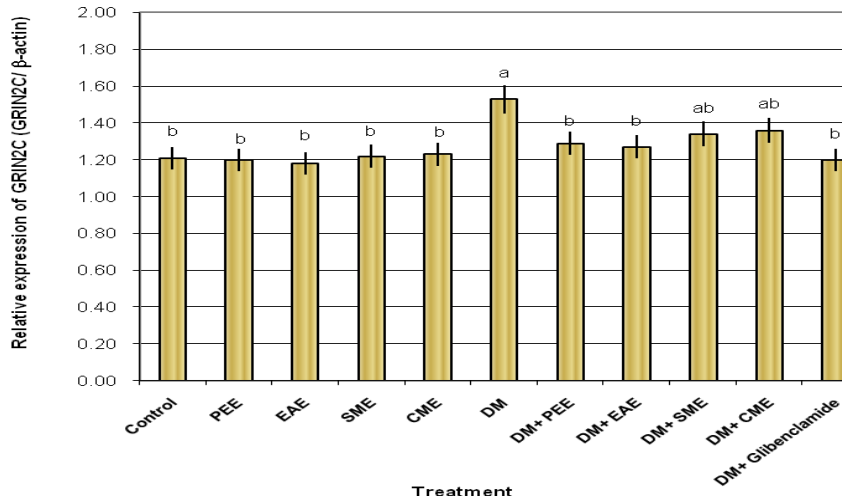
**Figure 4**

**The alterations of IGFBP3 mRNA in liver tissues isolated from male DM-rats treated with several extracts of *Jatropha curcas*. <sup>a,b,c</sup>Mean values within tissue with unlike superscript letters were significantly different ( $P<0.05$ ).**



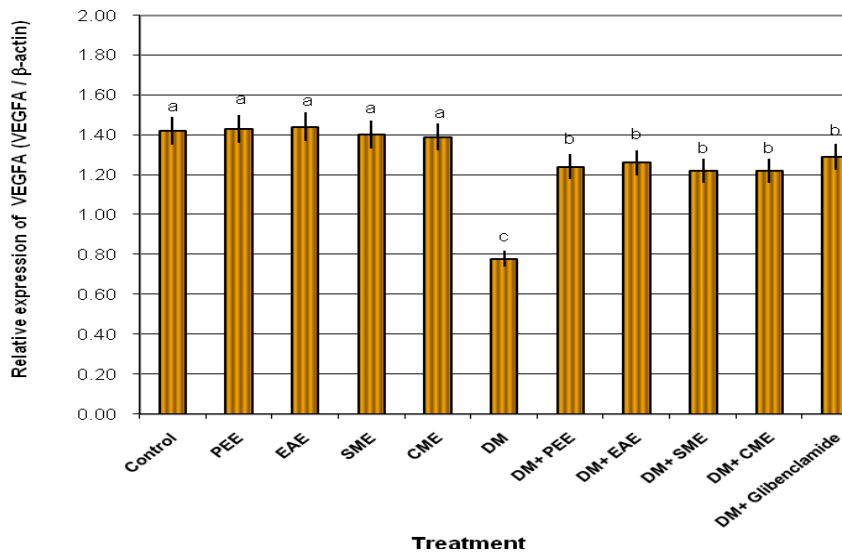
**Figure 5**

**The alterations of GRIN2C mRNA in heart tissues isolated from male DM-rats treated with several extracts of *Jatropha curcas*. <sup>a,b,c</sup>Mean values within tissue with unlike superscript letters were significantly different ( $P<0.05$ ).**



**Figure 6**

**The alterations of VEGFA mRNA in heart tissues isolated from male DM-rats treated with several extracts of *Jatropha curcas*. <sup>a,b,c</sup>Mean values within tissue with unlike superscript letters were significantly different ( $P<0.05$ ).**



## DISCUSSION

A single cell layer lining the vascular wall, called the vascular endothelium, plays an important role in maintaining the structure and function of vessels. Besides, being the vascular endothelium a mechanical barrier between blood and vessel wall, it is also the origin of production for different bioactive factors that regulate vascular tone, coagulation, cell proliferation, cell death, and inflammation<sup>21</sup>. The cytokines can be represented in two shapes including the anti-inflammatory markers such as IL-1 $\beta$ , IL-6 and TNF- $\alpha$ , the second shape is the adhesion molecules such as ICAM-1 and VCAM-1<sup>22</sup>. ICAM-1 and VCAM-1 belong to the Ig super family<sup>23</sup>. Where, ICAM-1 is widely distributed on leucocytes, endothelial cells, fibroblasts and epithelial cells and VCAM-1 is expressed on monocytes, endothelial cells and synovial cells<sup>24,25</sup>. Large evidence has shown strong associations of circulating levels of endothelial adhesion molecules with insulin resistance in non-diabetic individuals or with type 2 diabetic patients<sup>26</sup>. Besides, the concept that insulin resistance might be related to endothelial dysfunction<sup>27</sup>. This is may be due to insulin enhances nitric oxide production within the endothelial cells and nitric oxide modulates a number of endothelial functions, including the expression of adhesion molecules<sup>28</sup>. In a good connection with the present results, in type 2 diabetic patients there is an increase risk for developing infectious diseases and sepsis, and it may lead to mortality because of the ratio of infections can reach nearly twice when compared to non-diabetic patients<sup>29</sup>. The elevated levels of adhesion molecules in diabetic condition may be explained on the basis of, activation of macrophages can produce many of the cytokines known to stimulate endothelial VCAM-1 expression, the matter leading to macrophage accumulation and this consequently may leads to VCAM-1 expression<sup>30</sup>. In parallel results, ICAM-1 is one of the most important intercellular adhesion molecules involved in atherogenesis and noticed increased circulating ICAM-1 plasma levels in NIDDM patients that may be resulted from the

acute increase of plasma glucose which leads to produce an oxidative stress and induce cellular expression of ICAM-1<sup>31</sup>. In agreement with the present results, a significant increase in the immune histochemical expression of ICAM-1 and VCAM-1 proteins in diabetic patients that can reflect the inflammatory nature of this state and suggested a possible role for these adhesion molecules in the pathogenesis of diabetic micro angiopathy<sup>32</sup>. The present results clearly demonstrate amelioration with successive extracts as well as crude methanolic extract of *J. curcas* treatment to diabetic rats. To interpret the suppressing effect of plant extracts on adhesion molecules, the attenuation activity of VCAM-1 and ICAM-1 expression, and this effect was mediated by partial blockage of nuclear factor-kappa B (NF- $\kappa$ B) activation<sup>33</sup>. The antioxidant compounds have an inhibiting activity towards TNF- $\alpha$ -stimulated VCAM-1 and ICAM-1 expression *via* a mechanism involving NF- $\kappa$ B and activator protein-1 (AP-1)<sup>34,35</sup>. Methanolic extract of *J. curcas* leaves contained bioactive compounds including, steroids, phenolics and flavones<sup>36</sup>. Flavonoids can support health by strengthening capillaries and other connective tissue and some function as anti-inflammatory, antihistaminic and antiviral agents<sup>37</sup>. Endothelial dysfunction whether acute or chronic, can be counteracted by the administration of phenolic compounds<sup>38</sup>. So, it is probable that the enhancement of endothelial dysfunction effect of *J. curcas* extracts may be referred to its flavonoids and phenolics content. There is a correlation between diabetes and oxidative tissue damage arising from free radical release<sup>39</sup>. Diabetes causes increased free radical release which results in the alterations of liver tissue superoxide dismutase (SOD) and catalase (CAT)<sup>39</sup>. The administration of plant extract with antioxidant potentials was meant to create a balance between free radical release and free radical elimination<sup>39</sup>. Antioxidants are closely related to their bio-functionalities, such as the reduction of cellular abnormalities like DNA damage, mutagenesis, carcinogenesis and which is also associated with free radical

propagation in biological systems<sup>40</sup>. This study showed that different extracts of *J. curcas* were capable of scavenging hydroxyl and may have a stronger hydroxyl radical scavenging activity. The present study revealed that *J. curcas* extracts especially PE and EA extracts decreased significantly the rate of the DNA damage in diabetic rats induced by STZ treatment. The current results indicated that both the extracts of *J. curcas* had a prominent effect on hydroxyl radical/and or super oxide scavenging. These results were in agreement with those of Sundari et al.<sup>41</sup>. The authors reported that, *J. curcas* fractions decreased the DNA damage in human peripheral blood lymphocytes exposed to UVB-irradiation. In addition, the recent study revealed that detoxified *J. curcas* seed meal decreased the DNA fragmentation induced by benzene exposure in male rats<sup>42</sup>. Polyphenolic compounds present in these plant parts have been associated with anti-diabetic, antihypertensive effects and favorable to cardiovascular health<sup>43</sup>. Moreover, flavonoids, coumarins and other polyphenols present in the leaf, stem bark and root extracts of *J. curcas* are well known for their strong antioxidant properties which play important roles in protecting cells and organs from oxidative damage<sup>44</sup>. The free radical scavenging activity of the *J. curcas* fractions might be due to the presence of steroids and terpenoids as they are known to occur in *J. curcas* plant<sup>45</sup>. Previous report showed that high concentrations of the methanolic extract have been reported to be more effective in quenching free radicals in the system<sup>46</sup>. The free radical; 1,1-diphenyl-2-picrylhydrazyl (DPPH) is a stable free radical that has been used extensively to determine the free radical scavenging ability of various compounds, as a measure of their antioxidant potential<sup>47</sup>. The present study suggested that *J. curcas* extracts possessed a quantitative examination and showed that there was a general trend of significantly higher antioxidant activity. It has been well established that plant extracts and their active compounds enhances DNA repair mechanism and inhibits DNA strand breaks in radiation exposed cells<sup>48</sup>. Antioxidant potential of *J. curcas* has been proposed for its

anti-genotoxic potential. Because DNA damage induced by benzene is mainly mediated by ROS, compound with antioxidant potential has capable to intercept the ROS before it attack DNA. Several investigators have demonstrated that natural antioxidants scavenge ROS and protect cellular DNA against agents-induced oxidative damage<sup>49</sup>. Hence, it can be postulated that *J. curcas*, by virtue of its free radical scavenging capacity and DNA repairing capacity restore DNA damage induced by STZ. The DNA damage induced by STZ is reduced by *J. curcas*, extracts as measured by the decrease DNA fragmentation and gene expression alterations. The antioxidant activity of the *J. curcas* extracts is attributed to the hydrogen donating ability of phenolic compounds present in the extracts<sup>50</sup>. The present study declared that, treatment of diabetic rats with several extracts of *Jatropha curcas* especially PE and EA extracts decreased the alteration in the expression of diabetic related genes (IGF1R, IGFBP2, IGFBP3, GRIN2C and VEGFA) induced by STZ in diabetic-rats. Up to date, there are no data concerning the effect of *Jatropha curcas* on diabetic related genes. Diabetic rats revealed decrease in the expression of IGF1R, IGFBP2, IGFBP3 and VEGFA genes as well as increase in the expression of GRIN2C gene which agreed with our results<sup>51</sup>. Medicinal plant extracts contain valuable anti-diabetic agents and may involve one or more active components responsible for blood glucose reduction<sup>52</sup>. Thus, the hypoglycemic effect of *J. curcas* in this study may be linked to the presence of flavonoids and terpenes in the extracts regulate the expression of diabetic related genes. These compounds have been implicated in the antidiabetic activities of many plants<sup>53</sup>. In this study, the hypoglycemic action of *J. curcas* different extracts may be by potentiating the insulin effect, either by increasing the pancreatic secretion of insulin from the cells of langerhans islets or its release from bound insulin in which these biological actions are regulated by the expression of several genes responsible on the diabetes pathways<sup>54</sup>.

## CONCLUSION

The application of *J. curcas* extracts reduced the high levels of adhesion molecules. The administration of *J. curcas* extracts exhibited relatively rats of DNA damage similar to these of control group. Beside ,*J. curcas* extracts altered the expression of diabetes related genes and appeared similar to these of the

control group. It could be concluded that *J. curcas* extracts might be a promising regulator supplements for hyperglycemia and the expression of genes related DM.

## CONFLICT OF INTEREST

Conflict of interest declared none.

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