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RESEARCH ARTICLE

Certain Blood Lipid Profile and Immunological Alterations Accompanied Vascular Inflammation in Hypertensive Patients

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Abstract

The current study was conducted to examine certain blood biochemical and immunological changes associated with high blood pressure in hypertensive patients. Hundred blood samples were collected from normal and hypertensive people, at Al-Hussein teaching Hospital, for assessment of Fatty lipids such as total cholesterol, triglyceride, low-density lipoprotein, and high-density lipoprotein as well as the study of IL-1ß and TNF-α genes expression levels. The results of hypertensive patients showed significant increase of T. Cholesterol , TG and LDL and significant decrease of HDL, whereas the molecular analysis revealed significant increase in the expression ranks of both IL-1ß and TNF-α genes in comparison with normal people. In conclusion, hypertension could be accompanied by lipidemia and decreased immunity.

Keywords: *Hypertension, Lipid profile, Immunity IL-1β, TNF-α.*

Introduction

Inflammation theatres a key character in the commencement, development, and development of various circulatory illnesses such as hypertension, arteriosclerosis, nephropathy, myocardial infarction, and narrowing of constriction after balloon angioplasty [1].Atherosclerosis is a prime example of how inflammation develops in cardiovascular disease by activating endothelial cells through inflammatory cytokines. Functional dysfunction is associated with the lining of the membrane due to inflammation of the cardiovascular system, including high blood pressure or diabetes or obesity [2].

The tumor necrosis factor (TNF) is a major proinflammatory cytokine that regulates the expression of many inflammatory genes, oxidative stress, and anti-apical signaling pathways, in almost all cell types, where abnormal TNFα signals lead to the development of pathological conditions including cardiovascular disease, While the therapeutic prohibition of TNFα signaling was proposed to treat many inflammatory diseases, especially rheumatoid arthritis and bowel disease [3]. NF-κB, an influential agent of inflammation in TNFα, plays a central role in Regulation of the expression of vascular provocative intermediaries such as interleukin-1 beta (IL-1ß), interleukin-6 (IL-6), TNFα, and MCP-1 in endothelial cells and other cell types [4]. NF-inB activation stimulates the multiplying of vascular smooth muscle cells and mediates neointima hypertrophy after vascular injury [5]. The current study aims to assess changes in blood lipid levels and levels of expression of IL-1ß and TNFα accompanied by high blood pressure.

Materials and Methods

Samples Collection

One hundred blood samples were collected from both men with hypertension and normal age between 50 and 65 years at the Al-Hussein teaching hospital, Thi-Qar, Iraq. The blood samples were divided into two parts, one for the purpose of analyzing the gene expression and the other for the separation of the serum for the purpose of biochemical analysis.

Laboratory Assessments

Blood samples were obtained after fasting for at least 10 hours. Blood serum was obtained and analyzed for lipid profiles, including T. Cholesterol, TG, LDL and HDL, using Siemens RXL (Diamond Diagnostics, Holliston, MA).

Molecular Analysis

Total RNA was isolated from blood samples rendering to the procedure labelled by the TRIzol® detector constructer (Promega Co. USA). After isolation, the amount (ng / µl) and total RNA quality were determined using the Nanodrop / VIS UV spectrometer (OPTIZEN POP. MECASYS, Korea). RNA purity was also determined by reading spectral absorption at 260 and 280 nm, where the RNA integration amount was better than 7.0 in qRT-PCR analysis. Then, isolated DNA testers were preserved with DNase I to eliminate drop quantities of DNA from the entire RNA applied according to the method described by Promega co., United States of America.

DNA samples (DNase-I) were used in a cDNA synthesis step using the AccuPower® RocktScript RT PreMix range supplied by Pioneer, Korea and implemented in accordance with the company's instructions. CDNA mono-cue was converted to a next part cDNA that was charity as a pattern for transcription interaction. QRTPCR was implemented using AccuPower® Greenstar ™ qPCR PreMix (Bioneer, Korea) and Exicycler ™ 96 (real-time thermal planetary) instruments (Bioneer, Korea). As well as to estimate the PCR amplification numbers compared to the relative numbers of the DNA DNA qRT-PCR curve. To determine the amount of gene expression in the study group samples in a duplicate version, the inner control inner control gene (GAPDH) was used to standardize the levels of gene expression. After the interaction was completed, a data analysis was performed. The housework gene (GapdH) was represented as normal genes that could be used to calculate the qualified gene expression or change the fold of the target gene (IL-1ß and TNF-a gene).

Statistical Analysis

The results were expressed as mean standard deviation. A comparison was made between groups using a t-test for students. The differences were considered significant at P <0.05. Statistical analysis was performed using the Graph Pad publication (SAS Institute, Inc., USA).

Results

Serum Lipid Profile

As shown in Table (1), an important rise (P <0.05) of T. Cholesterol, TG and LDL serum and significant decrease (P <0.05) of serum HDL concentration were observed in patients with high Blood pressure in comparison with ordinary people.

Quantitative Cytotoxicity IL-1β and TNF-a Expression

In the current study, a important rise (P <0.05) of IL-1ß blood (Fig. 1) and TNF-a (Fig. 2) Patients with hypertension compared to ordinary people.

Table 1: Serum lipid profile in normal and patients

Parameters	Control	Patients
T. Cholesterol (mmol/L)	4.77±0.02	6.012±0.03 *
TG	1.33±0.081	2.238±0.05 *
HDL	1.391±0.074 *	0.921±0.017
LDL	2.66±0.027	2.978±0.034 *

The values are expressed as M±SD
The stars signify important change (p<0.05) between studied groups

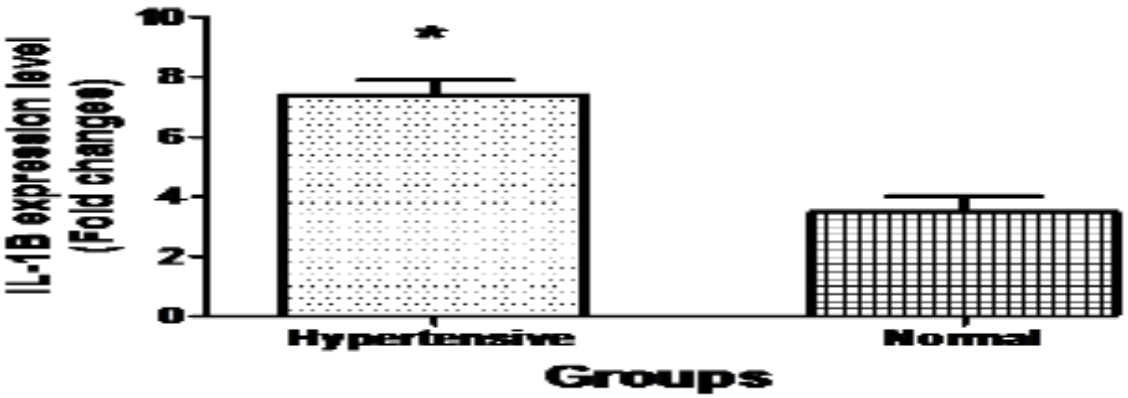

Figure 1: Gene expression levels (fold changes) of blood *IL-1β* gene in normal and hypertensive people
The values are expressed as M±SD
The stars signify important change (p<0.05) between studied groups

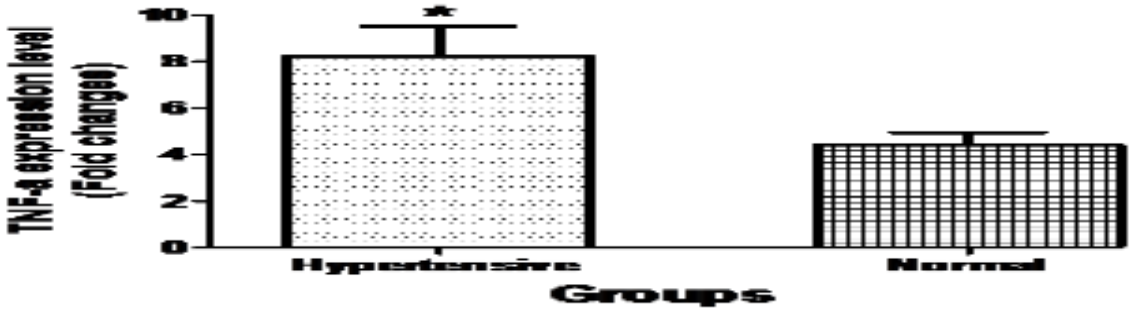

Figure 2: Gene expression levels (fold changes) of Blood *TNF-a* gene in normal and Patients peoples
The values are expressed as M±SD
The stars signify important change (p<0.05) between studied groups

Discussion

Hypertension is a common disease worldwide, as it kills humans and causes many deaths. Our current study concluded that high blood pressure is associated with the rise and fall of several criteria, be it immune or fatty, according to our current study design. In this reading, we explored the connection amid the fatty profile of the serum and high blood pressure. The results of this reading showed that the cruel ethics of TC, TG and serum LDL were meaningfully advanced and statistically important among hypertensive illess than standard. The cruel HDL level was lower in hypertension compared with the norm and was statistically important. Global hypertension is documented as a main danger factor for cardiovascular disease, hit, and diabetes and kidney illess [6].

About 80% of people with high blood pressure suffer from concomitant diseases such as Obesity, glucose intolerance, and irregularities in fat absorption. Among other things, comparing the status of fat in hypertension, 16 patients compared with normotensive controls recorded TC high TC, TG, and LDL, which are consistent with our study [7]. Our discoveries from improved TC levels in hypertensive illess are alike to those in some other studies.

However, few studies have documented a robust connotation of hypertension and dyslipidemia, and there was important variability of serum TC, TG, HDL, and LDL in hypertensive patients. Therefore, the results of investigations into these standards may enhance routine control of hypertensive patients in daily clinical practice to prevent cardiovascular disease and other adverse effects of hypertension [8].A great-ruler study conducted in Mexico create that the most common anomalies in urban adults in Mexico aged 20-69 were HDL cholesterol in the blood less than 0.9 mmol / l (46.2% for men and 28.7% for women) . Elevated blood lipid (2.26 mmol / L) was the second most common anomaly (24.3%). LDL (24.21 mmol / L) was detected in 11.2% of the sample. Half of people with hyperlipidemia had mixed blood lipid or low HDL cholesterol. More than 50% of cases with low HDL are not associated with increased blood lipids [9]. The tumor necrosis factor alpha (TNFα) is a key cytokine-prophylactic regulating the expression of many inflammatory genes, oxidative stress, and pathway signaling. In fact, in all cell types, distant TNFα signals lead to pathological progression. This is a CVD, therapeutic blockage of TNFα signaling for the treatment of many inflammatory diseases, especially rheumatoid arthritis and bowel disease [3].

TNFα dilates vessels by endothelial cells in the coronary arteries or carotid artery via superoxide superoxide production [10]. Patients with high levels of TNFα have a greater risk of cardiovascular disease [11]. In endothelial cells, TNFα stimulates the expression of interleukin-6 (IL6), a single-cell molecule (MCP-1), and cellular adhesion molecules (CAM) [12]. Transcription of TNFα in rats prevents intraocular influx after carotid artery injury [13], whereas increased TNFα expression exacerbates pulmonary hypertension in mice [14].

TNFα-mediated inflammation theaters an imperative role in the re-realization of blood vessels. Smooth human carotid artery cells respond to TNFα with increased cell proliferation, while diffuse TNFα inhibition inhibits the reconstitution of carotid leukemia and forms neointima in mice [15].TNF to inhibit TNF has been exposed to improve endothelial function by stimulating

endothelial cell regeneration [16]. NF-κB, an influential agent of irritation in TNFα, plays a central role in regulating the expression of vascular inflammatory intermediaries such as interalukin-1 beta (IL-1ß) and interleukin-6 (IL-6) and TNFα and MCP-1 in endothelial cells.NF-inB activation stimulates the explosion of vascular smooth muscle cells and mediates neointima hypertrophy after vascular injury [17].

Conclusion

It can be concluded that high blood pressure can be associated with important variations in the image of lipid, cell and / or brachial immunity.

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