

ADRENAL GLAND TLR EXPRESSION IN ApoE DEFICIENT HOMOZYGOUS (ApoE KO^{-/-}) MICE WITH IMPAIRED THYROID FUNCTION

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Abstract

The main aim of our study was to investigate the expression of TLR receptors in the adrenal gland of ApoE knockout mice in context of ApoE deficiency as well as impaired thyroid function (hypo- and hyperthyroidism). The study was conducted on two following experimental animal groups: hypothyroid homozygous mice (*ApoE KO^{-/-}*) treated with PTU; hyperthyroid homozygous mice (*ApoE KO^{-/-}*) treated with L-thyroxine (T₄) and two control groups: euthyroid homozygous mice (*ApoE KO^{-/-}*) and euthyroid wild-type C57BL/6 mice (Bb). Determination of TLR gene expression in the adrenal gland was performed by RT-PCR reaction with semi-quantitative detection of populations of mRNA molecules transcribed from the TLR2, TLR4 and TLR9 genes in the adrenal gland in the treated experimental groups and the two untreated control groups. The results of our study are in support of the hypothesis that both conditions of impaired thyroid function produce TLR agonists that increase the expression of TLR in the adrenal gland (p<0,05). Also, in the untreated/control group of mice (*ApoE KO^{-/-}*), an increased expression of TLR was found compared to the wild strain C57BL/6 mice (Bb) as a control group (p<0.001).

Keywords: TLR receptors, adrenal gland, ApoE deficiency, Hypothyroid, Hyperthyroid

Introduction

Tool-like receptors (TLRs) belong to the family of transmembrane receptors with a crucial role in the activation of the immune system during various types of inflammation (sterile or non-sterile nature), playing the role of signaling receptor molecules that regulate the production of various chemokines and cytokines [1].

Ligands that activate TLR can be of endogenous or exogenous origin.

The known exogenous ligands which tend to activate TLRs are mainly LPS derived from bacterial cell wall, bacterial DNA fragment with cytosine-phosphate-guanine (CpG) motif, and viral RNA fragments. Endogenous ligands for TLR activation are the endogenous LPS, fibrinogen, mm-LDL and oxy-LDL, heat-shock proteins (HSPs), oxygen radicals as well as other products of oxidative stress.

Although TLRs are mainly involved in the inflammations of an infectious origin, they are also increasingly attributed to the recognition of endogenous ligands, the products of tissue damage of various origins [2]. It has also been shown that the major atherogenic process of lipid accumulation in the vascular wall occurs through TLR activation by various endogenous and exogenous ligands. Increased expression of TLR-1, TLR-2, and TLR-3 has been found in atherosclerotic plaques [1].

In addition to previously mentioned local effects in atherosclerotic lesions, some studies suggest systemic effects of TLR, primarily through their activation and enhanced expression in the adrenal gland that correlate with increased levels of inflammatory cytokines (TNF- α , IL-1 β , IL-6, IL-10 and IL-12), both in vitro and in vivo [3].

Conditions of impaired thyroid function (hypo- and hyperthyroidism) are characterized by complex symptomatology as a consequence of the endocrine and metabolic disorders. Both of them, mainly

hypothyroidism, increase the risk of developing atherosclerosis. Some of the products of these disorders are endogenous TLR agonists and ligands, which can lead to increased expression of TLR genes [4-6].

The main goal of this study was to investigate the influence of apolipoprotein E deficiency, as well as thyroid status on TLR gene expression in adrenal glands in ApoE deficient homozygous (ApoE KO^{-/-}) mice as animal models.

Material and Methods

Animal models

Our study was performed on 16 week old male homozygous ApoE^{-/-} mice with C57BL/6 genetic basis and wild type (WT) - C57BL/6 male mice as a control group [7].

For the purposes of our study, the following experimental groups were established:

- Hypothyroid ApoE KO^{-/-} mice (n = 30) where hypothyroidism was induced by propylthiouracil (PTU) 1mg/ml dissolved in drinking water. [8, 9].
- Hyperthyroid ApoE KO^{-/-} mice (n = 30) where hyperthyroidism was induced by L-thyroxine 2g/ml dissolved in drinking water [8, 10].
- Euthyroid ApoE KO^{-/-} mice (n = 30) as a control group.
- Euthyroid isogenic ApoE KO^{-/-} with C57BL/6 genetic basis (n = 30) as a control group.

Each of the experimental groups consisted of 5 male individuals in a cage. The treatment of the animals lasted 12 weeks, during which the animals were acclimated to room temperature (18-23°C), with light regime of 12 hours light and 12 hours dark. The daily dose of PTU and L-thyroxine was determined based on the daily drinking water of each group, divided by the number of animals in each cage.

After overnight 12-hours fasting, the animals were sacrificed by exsanguination under ketamine/xylazine anesthesia (90 mg/kg i.p. and 10 mg/kg, i.p. respectively).

Formalin-fixed and paraffin embedded thyroid glands, and immediately frozen, measured and stored at -80°C adrenal glands were used for histomorphometric analysis and TLR gene expression, respectively.

The thyroid status of the experimental groups was determined by morphometric histological analysis of experimental animals' thyroid glands with hematoxylin/eosin (H&E) technique, while morphometric features were analyzed by light microscope connected to a video camera (Nikon-Eclipse E600, Program Lucia 4.21).

The measurements were made in thirty follicles, at five random different points at microscope field of view. Follicular epithelium height and follicular diameter from the peripheral and central parts of the thyroid lobes were measured. Ocular for morphometric analysis and the Weibel's multipurpose test system M₄₂ (Wild, Switzerland) with 100 x and 40 x magnification for epithelium height and follicular diameter were used respectively [11].

Determination of TLR gene expression in the adrenal gland by RT-PCR analysis

The RT-PCR reaction in this study was used for semi-quantitative detection of populations of mRNA molecules transcribed from the TLR2, TLR4 and TLR9 genes in the adrenal gland of the treated experimental groups, untreated ApoE KO^{-/-} control group, as well as wild-type (Bb) control group.

The cellular RNA was isolated from each sample by the guanidine-phenol-chloroform extraction method [12]. Each isolate was treated with 20 units of *RNasin* ribonuclease inhibitor (Sigma-Aldrich) and stored at -75 to -80° C.

RT-PCR analysis was performed with the *Enhanced Avian HS RT-PCR* (Sigma-Aldrich) reverse transcription system. Briefly, the following reaction mixture was assembled for first-strand cDNA synthesis:

about 0.5 µg RNA isolate, 3.5 M oligotimidylate primer (oligo-dT), 1 unit of *Enhanced AMV* reverse transcriptase, 1 unit of RN-ase inhibitor, 3 mM magnesium chloride and 10 mM of each dNTP.

The tubes were incubated at 25°C for 15 minutes and then at 42°C for 50 minutes.,

Region-specific PCR amplification of the corresponding genes was performed from the synthesized cDNA. 2µL of the synthesized cDNA, 1U/reaction of thermostable polymerase (JumpStart AccuTaq, Sigma-Aldrich), 200 mM of each dNTP, 3 mM of magnesium chloride and 0.4 mM of the following oligonucleotide were applied to the reaction mixture:

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mB-actinF 5'- G T G G G G C G C C C C A G G C A C C A -3'
mB-actin R 5'- C T C C T T A A T G T C A C G C A C G A T -3'
TLR2 F 5'- A G C T C T T T G G C T C T T C T G -3'
TLR2 R 5'- A G A A C T G G G G A T A T G C -3';
TLR4 F 5'- G C A T G G C T T A C A C C A C C T C T -3'
TLR4 R 5'- G T G C T G A A A A T C C A G G T G C T -3';
TLR9 F 5'- T C C C T G T A T A G A A T G T G -3'
TLR9 R 5'- T G G A G G C G T G A G A G -3';
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PCR amplifications were performed with the following program: initial denaturation at 94°C for 3 minutes and followed by 33 cycles, each consisting of 3 steps, denaturation at 94°C for 1 minute, annealing at 60°C for 1 minute and extension at 68°C for 1 minute and 45 seconds. The terminal extension is performed at 68°C for 10 minutes [13].

PCR products were separated by gel electrophoresis in 2% agarose.

The gels were stained with ethidium bromide, visualized on a UV transluminator and digitally photographed (Canon PowerShot A70).

The fluorescence intensities of the gene-specific electrophoretic strip and the control of β-actin from each sample were digitally quantified by the gel analysis function of ImageJ software, version 1.33u [Rasband, W.S., ImageJ, National Institutes of Health, Bethesda, Maryland, USA, <http://rsb.info.nih.gov/ij/>, 1997-2004].,

The fluorescence intensities of the gene transcript bands were compared with the corresponding internal gene transcript bands of the β-actin gene in semi-quantitative measurements.

Results

Morphometric analysis of the thyroid gland confirmed the corresponding thyroid status of the respective experimental groups, as shown in Figure 1, and Tables 1 and 2 respectively.

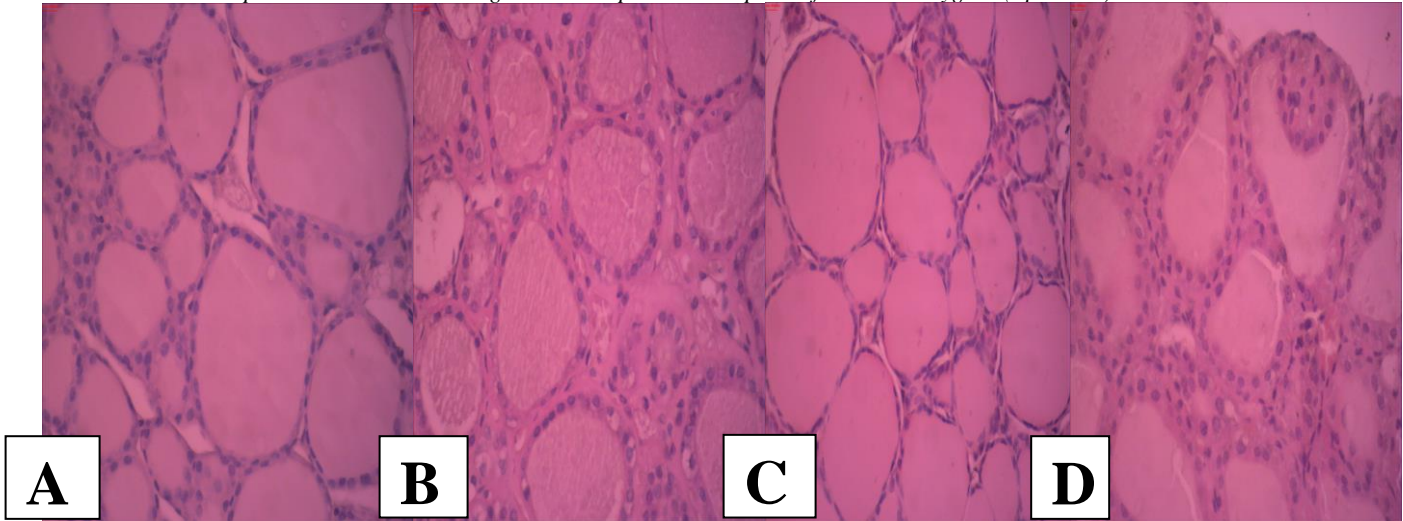


Figure 1. Micrographs of the thyroid gland (H&E staining, X 40). (A) Wild strain-Bb; (B) ApoE^{-/-} control; (C) ApoE^{-/-} T₄; (D) ApoE^{-/-} PTU;

Table 1. The average diameter of the thyroid follicles and the height of the follicular epithelium in the treated experimental groups compared with ApoE^{-/-} control group.

There are significant differences between treated experimental groups and the ApoE^{-/-} control group:

* p < 0.05; ** p < 0.01; *** p < 0.001. Values are represented as mean ± SD.

	Bb control	ApoE^{-/-} control	
peripheral follicles (µm)	110,30±27,3	108,95±20,5	
	ApoE^{-/-} control	ApoE^{-/-} T₄	ApoE^{-/-} PTU
peripheral follicles (µm)	108,95 ± 20,5	124,05 ± 44,5**	150,30 ± 21,9***
peripheral follicular epithelium (µm)	9,90 ± 2,1	4,95 ± 1,1***	13,40 ± 1,75***
central follicles (µm)	68,45 ± 17,5	52,20 ± 8,8**	80,90 ± 17,3*
central follicular epithelium (µm)	10,30 ± 1,90	4,10 ± 1,30***	11,50 ± 1,50**
peripheral follicular epithelium (µm)	6,50±1,9	9,90±2,1***	
central follicles (µm)	64,70±16,0	68,45±17,5	
central follicular epithelium (µm)	6,85±1,30	10,30±1,90***	

There are significant differences between ApoE^{-/-} and Bb control groups: *** p < 0.001.

Bb = wild-type mice (Bb) with C57BL/6 genetic basis

Our study determined the adrenal expression of TLR2, TLR4, and TLR9 in the two treated experimental groups, untreated ApoE^{-/-} control group, as well as in the wild-type Bb control group. The results of the statistical analysis showed significantly higher expression of the three TLRs in the two treated experimental groups than in the ApoE^{-/-} control group, and in the ApoE^{-/-} control group compared to the Bb control group. These results are shown in Tables 3 and 4.

Table 2. The average diameter of the thyroid follicles and the height of the follicular epithelium in the control groups.

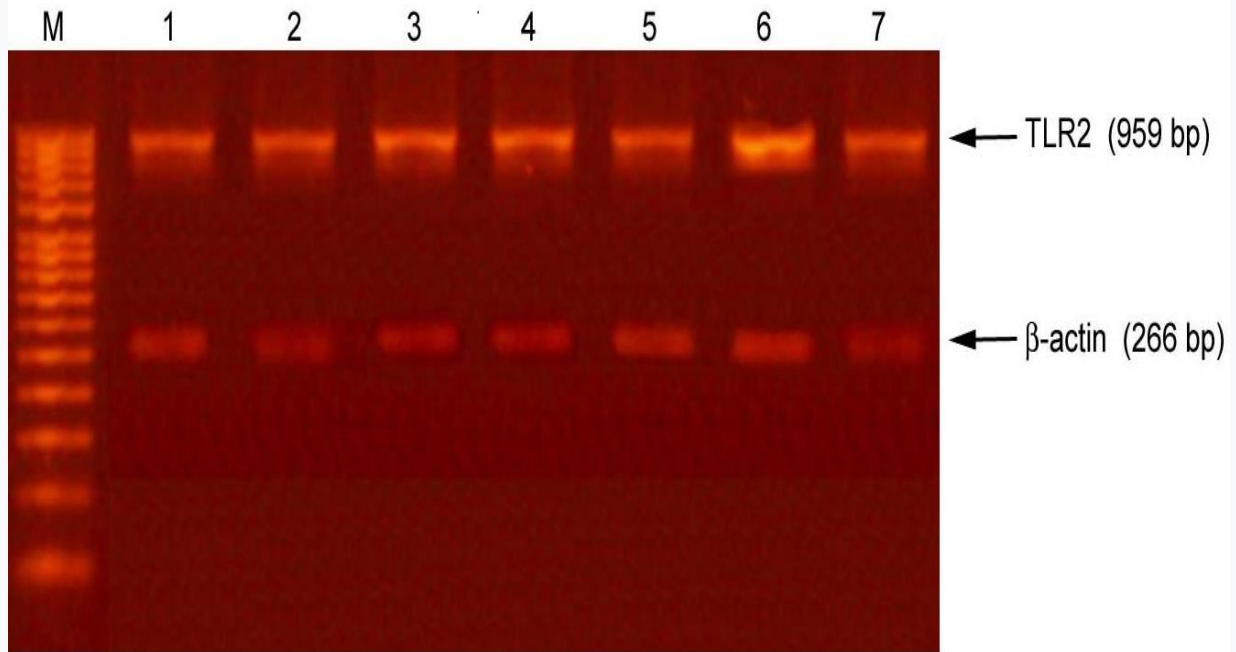


Figure 2. Representative image from TLR2 RT-PCR.

Table 3. Adrenal TLR expression in the treated experimental groups compared with the ApoE^{-/-} control group.

	ApoE ^{-/-} control	ApoE ^{-/-} T4	ApoE ^{-/-} PTU
TLR 2	3,65±1,72	5,59±1,57*	6,01±2,05*
TLR 4	5,77±2,97	8,58±2,38*	9,85±3,38*
TLR 9	5,74±1,90	9,99±4,23*	10,23±4,71*

There are significant differences between the treated experimental groups and the ApoE^{-/-} control group: * p <0.05.

Table 4. Adrenal TLR expression in ApoE^{-/-} and Bb control groups

	Bb control	ApoE ^{-/-} control
TLR 2	2,25±0,50	3,65±1,72***
TLR 4	3,09±1,13	5,77±2,97***
TLR 9	3,28±1,32	5,74±1,90***

There are significant differences between ApoE^{-/-} and Bb control groups: *** p <0.001.

Discussion

Although the main role of TLR is to activate the immune response under the influence of ligands of microbial origin, many studies have shown that they can also be activated by endogenous ligands from a variety of cellular damage processes, such as those caused by oxidative stress [6,14-17].

According to this, as well as the wide tissue distribution of TLRs, their mediating role in the development of sterile inflammation in various tissues and organs (including atherogenesis) is emphasized [1,18-19].

In addition to participating in the local occurrence and development of atherosclerotic plaques [4], some authors believe that TLRs also have a systemic proatherogenic effect by stimulating the adrenal gland [20, 21]. The main motive in our study was to examine the expression of some TLR genes in the conditions of impaired thyroid function and concomitant ApoE lipoprotein deficiency.

The results obtained from this segment of the study showed increased expression of the examined TLR genes in all treated experimental groups, however, the data for constitutively increased expression in the untreated control ApoE^{-/-} group was also interesting.

The major atheroprotective function of ApoE lipoprotein is its participation in plasma clearance of atherogenic lipoproteins. Numerous studies indicate its other properties that prevent the initiation and development of atherosclerosis, regardless of its involvement in lipoprotein metabolism.

This refers to the ability of ApoE lipoprotein to inhibit lipid oxidation and thus prevent oxidative cell damage [22], a role in preventing the expression of adhesive molecules on the surface of vascular endothelium [23], as well as inhibition of vascular smooth muscle activation [24,25].

Additional confirmation to the multifunctional character of ApoE lipoprotein is the possession of anti-inflammatory properties. Studies have shown that the ApoE lipoprotein, whether synthesized locally or from the circulation, inhibits macrophage secretion of proinflammatory cytokines, thus suppressing the inflammatory response of tissues induced by various agents [26].

A possible mechanism for the anti-inflammatory effect of ApoE lipoprotein is the perturbation of the membrane microenvironment that occurs during cholesterol efflux from the cells, which interrupts the signal for the production of cytokines mediated by the activation of TLR, and thus consequent secretion of IL-6, IL-1 β and TNF- α [26,27].

These findings may be an addition to explaining the results of our study of the constitutive activity of the examined TLR genes in the untreated control ApoE^{-/-} group.

The hyperthyroid condition is characterized not only by increased oxidative stress but also by increased lipolysis and consequent increase in free fatty acids [28].

Based on previous research, it has been established that oxidative stress products and free fatty acids such as endogenous TLR ligands play a role in the activation of proinflammatory signaling pathways and the pathogenesis of many diseases, such as peripheral insulin resistance [29,30,15,16,17].

This would be particularly important for the development of insulin resistance and the consequent complications of hyperthyroidism [31].

Based on the above, we hypothesized that the increased expression of TLR genes in the thyroxine-treated experimental group could be caused precisely by the endogenous oxidative products and free fatty acids generated during the hyperthyroid state.

Among the endogenous ligands that activate TLR are the oxidized forms of LDL (ox-LDL and mm-LDL), which have been shown to occur in significant quantities during the pathological conditions accompanied by oxidative stress and hyperlipidemia, such as hypothyroidism [32,33].

This finding was a starting point for explaining the results of our study regarding the greater expression of TLR in the hypothyroid group.

Oxidatively modified forms of LDL cholesterol, that play a central role in the formation of atherosclerotic plaques by activating TLR (primarily TLR2 and TLR4), affect local inflammatory processes in atherosclerosis.

The minimally modified form of LDL (mm-LDL) via TLR stimulates vascular endothelial and smooth muscle cells towards synthesis of proinflammatory cytokines, chemokines, and adhesive molecules. In this way, monocytes are attracted and retained, migrating to the subendothelial space, where under the influence of proinflammatory cytokines and growth factors they differentiate into macrophages [5].

Conditions characterized by chronic hyperlipidaemia and consequent oxidative modification of cholesterol inevitably lead to their excessive intracellular accumulation and foam cell formation.

The epilogue of such events is often cell apoptosis and the release of proinflammatory oxidized lipid derivatives into plaque, leading to exacerbation of local inflammation. One of the consequences of oxidative stress in the process of atherogenesis is the damage to mitochondria, which usually results in their autophagy, as an evolutionarily conserved process in lysosomal recycling of cytoplasmic material [34].

Mitochondrial DNA (mtDNA), which avoids this process of autophagy and is released into the extracellular space, activates TLR9 and thus elicits an appropriate inflammatory response [35-36].

Namely, similar to bacterial DNA, mtDNA also contains an inflammatory non-methylated CpG motif, unlike nuclear DNA which is modified with additional methyl groups in some sequences, known as CpG motifs, which distinguishes the immune system from microbial DNA [37].

In addition to the aforementioned local effects, the widespread distribution of TLR, especially in endocrine cells (thyrocytes, adipocytes, Langerhans islets, adrenal glands), imposes the concept of their systemic effects on the etiopathogenesis of multiple diseases.

Our assumptions about the indirect effects of hypo- and hyperthyroidism on atherogenesis, through the activation of TLR in the adrenal gland and the subsequent increased production of glucocorticoids, as well as the activation of the renin-angiotensin-aldosterone system are made in this context.

The conditions of hypo- and hyperthyroidism that were subject of our study are characterized by a disturbed hypothalamic-pituitary regulatory axis [38-39].

The results of our study are in support of the hypothesis that both conditions of impaired thyroid function produce TLR agonists that increase the expression of TLR in the adrenal gland. We based our assumptions on the results of studies showing that direct activation of TLR in the adrenal gland induces increased production of corticosteroids [20,21].

On the other hand, TLR deficiency or their dysfunction is accompanied by a reduction in the steroid adrenal response in experimentally induced endotoxemia [40].

Similar to local TLR activation [4], mineralocorticoids and glucocorticoids stimulate the formation of cholesterol esters as well as the expression of adipocyte fatty acid binding protein2 (aP2) in macrophages [41-43].

The aP2 protein is a member of the family of cytoplasmic fatty acid binding proteins (FABPs), which participates in the intracellular distribution of fatty acids across cell compartments, modulates intracellular lipid metabolism, and participates in the regulation of gene expression [44,45].

Its increased expression in macrophages enhances intracellular fatty acid deposition, thereby stimulating foam cell formation and development of atherosclerosis [4,46].

In addition to these local effects, glucocorticoids have systemic hemodynamic effects that indirectly increase the predisposition to initiate and develop atherosclerosis. The influence of sodium retention on the increase of plasma volume is minor, while the greatest effect is accomplished through the increased peripheral vascular resistance caused by the suppressive action of glucocorticoids on the kallikrein-kinin system, prostaglandins and nitric oxide and activation of the renin-angiotensin system, as well as stimulation of α 1-adrenergic receptors and angiotensin type II receptors [47,48].

Conclusion

Under the experimental conditions of our study, an increased expression of the TLR genes was observed in all treated experimental groups, as well as a constitutively increased expression in the untreated control ApoE^{-/-} group compared to the control Bb group.

These findings suggest that the two states of impaired thyroid function (hypo- and hyperthyroidism) through the altered metabolism and consequent metabolic products lead to increased expression of TLR in the adrenal gland in both treated experimental groups.

Also, the deficiency of ApoE lipoprotein itself leads to increased expression of TLR genes, through altered liver function and subsequently altered peripheral metabolism of thyroid hormones in

ApoE^{-/-} mice, which can be a consequence of ApoE deficiency and consequently impaired cellular internalization of thyroid hormones.

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