

The Roll of Nfkb in Aneurysms-A Mini Review

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Introduction

The transcription factor nuclear factor-kappa B (NF-κB) regulates cell growth and maturation on the one hand, and NF-κB is a component of signaling pathways of immune defense and inflammation on the other. After its activation, it migrates from the cytoplasm of the cell to the nucleus. Activated via a variety of stimuli such as viruses, bacteria, cytokines, free radicals, carcinogens, tumor promoters, and endotoxins, NF-κB regulates the expression of nearly 400 different genes, including enzymes (COX-2 and iNOS), cytokines (TNF, IL-1, IL-6, IL-8, and chemokines), which influence the production of adhesion molecules, cell cycle regulatory molecules, viral proteins, and angiogenic factors. The reciprocal influence of NF-κB and the genes activated by NF-κB is highly complex. For example, TNF-α activates NF-κB, which itself transcriptionally induces TNF-α. A similarly complex induction pathway exists between NF-κB and COX-2 prostaglandin E2-EP2-NF-κB pathway. COX-2 induced by hemodynamic stress induces and produces prostaglandin E2, which further induces NF-κB. Constitutive NFκB activation is involved in the pathogenesis of cancer, diabetes, allergy, rheumatoid arthritis, Crohn's disease, cardiovascular disease, atherosclerosis, and other diseases. Among others, its role in various aneurysms has been highlighted. The present work provides some complex interactions of NF-κB in the context of various aneurysms.

General inflammatory response

In the pathogenesis of aneurysms, vascular inflammation starting from activated stromal cells represents a major pathomechanism [1]. In this process, the cytokines IL-6, IL-1β, and the MCP-1 chemokine receptor CCR2 appear to play a central role [2-4]. In contrast, deficiency of AT1aR (Ang-II type 1a receptor), pattern recognition receptor TLR4 (Toll-like receptor 4), and adaptor protein MyD8836 exerts a protective effect, suggesting the key role of proinflammatory transcription factor NF-κB/RelA [5,6]. In the Ang II model of AAA, an interaction between proliferating resident adventitial fibroblasts with infiltrating monocytes has been shown several times. This activates an ECM destruction-promoting cytokine amplification loop. Therefore, loss of vascular integrity and aortic dilatation is preceded by adventitial inflammation [7]. A subpopulation of fibroblasts, namely the specialized myofibroblasts and Col1A-expressing synthetic VSMCs, plays an important role in fibrosis and

formation/remodeling of the aortic ECM [8,9]. Ang II leads to RelA activation and IL-6 production in both the adventitial and medial layers of the abdominal aorta [10].

Endothelial NF- κ B signaling

Endothelial NF- κ B signaling not only promotes leukocyte-endothelium interaction in the vasa vasorum, a necessary step toward Ang II-induced aneurysms [11]. A significant association of the common 1166C variant of the angiotensin II type 1a receptor gene with AAA was demonstrated in 3 independent, geographically distinct but ethnically similar case-control cohorts [12]. The AGTR1 1166C risk association is not with peripheral or coronary artery disease. Although AAA and atherosclerotic occlusive pAVD represent distinct pathophysiological entities, a large association of MMP9 C-1562T SNP and AGTR1 1166C genotypes was found between AAA and patients with peripheral arterial disease [13].

NF- κ B and the perivascular adipose tissue (PVAT)

A growing interest in large artery disease is the transcriptome of Perivascular Adipose Tissue (PVAT), as this plays a basic role in the regulation of vascular physiology and its dysfunction influences the development of dilated and atherosclerotic aortic disease [14-19]. Only by focusing research not only on the aortic wall but also on the perivascular adipose tissue has it been possible to gain insight into the complicated pathomechanism of AAA development. In this regard, an altered immune response in the perivascular adipose tissue represents a crucial pathogenetic element for the development of AAA [20-22]. Reconstruction of regulatory networks shows that the combination of multiple pathobiological factors (disease genes, hubs) in complex relationships with each other lead to the development of AAA [23]. Thus, in addition to SPIB and TBP (i.e., "hub" TFs), NFKB1 has been identified as the major regulator of the resulting gene regulatory network because it exhibits the greatest connectivity with co-expressed genes associated with diseased PVAT [22]. Most importantly, on the one hand, the NFKB1 transcriptional cluster leads to positive regulation of lymphocyte proliferation and, together with TBP, to the expression of genes involved in the innate immune response, i.e., Toll-Like Receptor (TLR) signaling [22,24,25].

In addition, NFKB1, REL, and RELA may affect T-cell proliferation, macrophage infiltration, and osteoclastogenic dehydration in different ways. At the end of this activation chain is the inflammatory response in vascular smooth muscle cells and mesenchymal cells [26-30]. In addition, the protein kinases MAPK1 and GSK3B and the nuclear receptor RXRA (a type of retinoid X receptor) play critical roles in the pathogenesis of AAA. Directly, MAPKs and GSK3s are mainly involved in innate immunity including TLR-related signaling, including TLR-related signaling that modulates the activity of matrix metalloproteinases during AAA formation [31,32]. Regulation of the ERK1 and ERK2 cascade in the perivascular adipose tissue transcriptome via the NFKB1, SPIB, and TBP transcriptional clusters highlights the role of NFKB1 and protein kinases in aneurysm formation [33,34]. Although inhibition of angiotensin type 1 receptor in vascular smooth muscle cells by activation of retinoid X receptors (RXR

activation) may influence AAA development, this mechanism is not considered to be important [35-37]. Other protein kinases, albeit with less importance in the regulatory network, such as histone deacetylase 1 (HDCA1), may also directly interact with NFKB1 and with TBP to influence AAA development [38,39]. In close interaction, perivascular adipocytes secrete soluble factors e.g., adipokines, chemokines, or proinflammatory, which may lead to NF- κ B activation [40,41].

NF- κ B and hub genes

Molecular Complex Detection (MCODE) identified a total of 55 hub genes, of which the genes for positive regulation of cytosolic calcium ion concentration, lymphocyte activation, and regulation of cytosolic calcium ion concentration were found to be the most important for the development of AAA [42]. The hub genes in MCODE 6, hsa04064, R-HSA-5668541, and R-HSA-5676594 can activate the NF-kappa B pathway via tumor necrosis factor (TNF) [42,43]. The other three genes lymphotoxin- α and - β (LTA=TNF- β and LTB) and TNF receptor-associated factor 3 (TRAF3) can lead to NF-kappa B activation [44-46]. Angiotensin II (Ang II) is able to increase the expression of phospho-p65 P65 subunit of NF- κ B, which itself has been shown to induce a pro-inflammatory state leading to the increased expression of MMP9, MCP1, VCAM1, ICAM1, and IL1beta [47-49]. Direct interaction of FKBP11 with the NF- κ B p65 subunit promotes endothelial inflammation through secretion of pro-inflammatory cytokines [49].

NF- κ B and ALOX5

The reciprocal action of ALOX5 and Nfkb contributes significantly to the formation of AAA. ALOX5 encodes the enzyme arachidonate-5-lipoxygenase in the eicosanoid synthesis pathway, which, in conjunction with the ALOX5AP protein [24], catalyzes the conversion of 5-HPETE to leukotriene A4 (LTA4) [50]. This in turn promotes proinflammatory leukotriene biosynthesis [51]. Increasing leukotriene B4 signaling increases immune cell infiltration [52]. Cathepsin K (CTSK) is also modulated by ALOX5, which directly affects AAA development through collagen turnover, T-cell proliferation, and apoptosis [53-55]. Down-regulation of miRNA-125b-5p and miR-193a-3p in AAA tissues leads to up-regulation of the ALOX5 gene, which initiates primary aortic wall inflammation in AAA development via leukotriene production [56,57]. As a general inflammatory response, increased expression of 5-LOX, NF- κ B, and iNOS has already been found in ischemic cerebral ischemia [58-60]. Inhibition of NF- κ B luciferase activity in vitro and translocation of p65 to the nucleus by the 5-LOX inhibitor BW-B 70C reinforces the hypothesis that 5-LOX/NF- κ B signaling results from its direct interaction with the p65 subunit of NF- κ B [57,61,62]. Decreased iNOS expression by BW-B 70C argues for primary activation of 5-LOX upon inflammation, which then initiates NF- κ B and iNOS expression [57].

NF- κ B and cyclooxygenase 2 (COX-2)

Cyclooxygenase 2 (COX-2), known as prostaglandin synthase-2, catalyzes the isomerization of the COX product prostaglandin H2 to prostaglandin E2, which itself initiates nuclear factor- κ B expression

via activation from the endothelial prostaglandin receptor [61-67]. On the one hand, COX-2 expression is initiated by the involvement of protein kinase C (PKC), Ras, and Wnt signaling pathways through the activation of mitogen-activated protein kinase (MAPK), kinase family proteins such as extracellular-signal-regulated kinase (ERK), C-Jun N-terminal kinase (JNK), and p38 [68-72]. On the other hand, DNA binding sites for transcription factors NF- κ B, AP1, cAMP response element-binding protein (CREB C/EBP), NF-IL6, MEF2, and transcription factor 4/LEF1 in the COX-2 promoter indicate their functional regulation of COX-2 transcription [73,74]. Nuclear factor- κ B (NF- κ B) plays a key role in both the initiation and progression of intracerebral aneurysms, in which macrophage recruitment via activation of inflammatory genes [75], vascular cell adhesion protein (VCAM)-1 and monocyte chemoattractant protein (MCP)-1 trigger endothelial dysfunction and initiate endothelial cell membrane (ECM) degradation through interleukin [IL]-1 β -mediated downregulation of procollagen genes [76-80]. Besides, tumor necrosis factor- α , mitogen-activated protein kinases, ANRIL, also called CDKN2B-AS, CDKN2A/B, Krüppel-like factor 2, caspase recruitment domain family, member 8, etc., contribute a major part in the development of cerebral aneurysms [81-99].

NF- κ B polymorphisms

Several NFKB polymorphisms can lead to the initiation of cardiovascular disease. One of the best known and regulating NF- κ B expression and activity polymorphisms within the promoter of the NFKB1 gene is -94 ins/del ATTG rs28362491 [100], which show increased susceptibility to atherosclerosis. The (rs696) polymorphism in the 3'UTR region of the NFKBIA gene leads to an alteration in the expression of I κ B α protein, an inhibitory version of NF- κ B protein, which is also encoded by NFKB1A [101]. In apolipoprotein E (ApoE)-deficient mice, expression of the NF- κ B inhibitor I κ B α -superrepressor (DN I κ B α) resulted in inhibition of atheromatous plaque development [102].

NF- κ B and microRNAs

The role of microRNAs (mi RNAs) in the regulation of gene expression involved in inflammation is moving to the center of the etiology of cardiovascular disease [103,104]. In particular, mi-146a, an NF- κ B target gene, is thought to play an essential role in inflammatory cardiovascular disease [105]. Single nucleotide polymorphisms (SNPs) of pre-miR-146a, for example, can modify the expression level of mature miRNA-146a and influence the progression of cardiovascular disease [106-108]. Based on this assumption, downregulation of miR-146a expression via interleukin-1 receptor-associated kinase 1 (IRAK-1), TNF receptor-associated factor 6 (TRAF6), and toll-like receptor -4 (TLR-4) by angiotensin receptor blockers and statins has been suggested [109,110]. A similar effect with delay of miR-146a expression has been attributed to estrogens and progesterone [111,112]. This may provide an explanation for the gender difference in the occurrence of aneurysms. Drugs in the statin group may have led to suppression of both miR-126-3p and miR-146a expression levels, thereby preventing aortic disease [113].

Other miRs have also been implicated in the very complex AAA development. Whereas miR-146a-5p is overexpressed in AAA tissue samples, miR 146a regulates inflammation in the AAA via CARD10 [114]. MiR-144-3p regulates ABCA1 in macrophages and influences the production of proinflammatory cytokines and thus plaque morphology through inhibition from reverse cholesterol transport [115-119]. In this context, the expressions of individual miR in AAA tissues and plasma of patients with AAA are controversial and also different. In this regard, some research groups found downregulation of miR-133b, miR-29b-3p, and miR-27b-3p in AAA tissues [120-124], whereas other authors found upregulation of the same [113,125]. Different plasma and AAA tissue levels of miR were pointed out several times for miR-221-3p and miR-27b-3p, among others [112,113,126-129]. However, miR-195 and miR-29b can also suppress AAA development via the TNF- α /NF- κ B and VEGF/PI3K/Akt signaling pathways [130-132]. Surprisingly, the missing -94Ins/DelATTG promoter polymorphism in the transcription factor NF- κ B in patients with popliteal aneurysm has been recently reported, opening new molecular biological aspects in the development of aneurysms [133].

Conclusion

Nfkb as one of the main factors is involved in AAA development in many mutual complex processes, based on which new therapy approaches are being tested.

Conflict of Interest

I hereby declare that there were no financial or other interests in the execution and evaluation of this work.

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