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Monoamine oxidase A (MAO-A): a signature marker of alternatively activated monocytes/macrophages

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Abstract

Monocytes/macrophages are versatile cells centrally involved in host defense and immunity. Th1 cytokines induce a classical activation program in monocytes/macrophages leading to a proinflammatory M1 macrophage phenotype while Th2 cytokines IL-4 and IL-13 promote monocyte differentiation into an alternatively activated, anti-inflammatory M2 macrophage phenotype. Although monoamine oxidase A (MAO-A) is primarily known for its action in the nervous system, several recent studies have identified MAO-A as a signature marker of alternative activation of monocytes/macrophages. In this brief review we explore the signaling pathways/ molecules that regulate MAO-A expression in alternatively activated monocytes/macrophages. We further discuss the contribution of MAO-A to the resolution of inflammation and identify potential therapeutic targets for controlling inflammation. Altogether this review provides deeper insight into the role of MAO-A in alternative activation of monocytes/macrophages and their participation in the inflammatory response.

Introduction

Monocytes/macrophages are major mediators of inflammatory responses and play a key role in innate and adaptive immunity. Monocytes/macrophages can be broadly classified into two different categories based on their mode of activation. They are considered as (i) classically activated (M1 pro-inflammatory phenotype) when stimulated by LPS or IFN- $\gamma^{[1, 2]}$ and (ii) alternatively activated (M2 anti-inflammatory phenotype) when induced by Th2 cytokines like IL-4 and IL-13, IL-10, TGF-β etc.^[3–5]. The M2 subset of monocytes/macrophages can be further divided into three different subcategories namely M2a, M2b and M2c; that have specialized functions and express different M2 marker genes^[5]. IL-4 and IL-13 activate monocytes/macrophages toward the M2a phenotype leading to the upregulation of several gene products involved in inflammatory resolution. Among the most strongly upregulated genes in IL-4/IL-13-activated monocytes/macrophages with potential anti-inflammatory

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properties are 15-lipoxygenase (15-LO), monoamine oxidase A (MAO-A), scavenger receptor CD36, fibronectin and coagulation factor $XIII^{[6-14]}$.

MAO-A, a pro-oxidative enzyme encoded by the X chromosome, is located in the outer mitochondrial membrane and cytosol^[15]. This enzyme is a catalytically active flavoprotein that converts biogenic amines like serotonin, dopamine and norepinephrine into their corresponding aldehydes^[16, 17]. This enzyme reaction requires molecular dioxygen and generates stoichiometric amounts of hydrogen peroxide and ammonia^[18, 19]. MAO-A hyperactivity has been shown to be associated with depression and previous reports implicate MAO-A inhibitors as effective therapeutics against clinical depression and anxiety^[20, 21]. Previous studies also demonstrated the involvement of MAO-A in neurodegeneration including Parkinson's and Alzheimer's diseases by inducing oxidative stress-mediated apoptosis^[22, 23]. MAO-A deficiency and abnormal activity has been associated with impulsive aggressive behavior^[24], neuropsychiatric disorders^[25], pancreatic beta cell function^[26] and glucose metabolism^[27]. MAO-A has also been implicated as a vital regulator of embryonic brain development^[19]. In addition to neuroinflammatory syndromes, recent studies suggest that MAO-A is a useful prognostic marker in the management of cholangiocarcinoma^[28] and MAO-A has also been implicated in the pathogenesis of many cardiovascular disorders. The predominant role of MAO-A has been reported in myocardial injury^[29], heart failure^[30], cardiac cell apoptosis^[31] and vascular wall remodeling^[32] and MAO-A promoter methylation has been shown to be associated with atherosclerosis^[33].

In this brief review we focus on understanding the regulatory mechanisms controlling MAO-A gene expression in alternatively activated monocyte/macrophages and also the involvement of MAO-A in the inflammatory response.

Regulation of MAO-A expression during alternative activation of monocytes/macrophages

Alternatively activated monocytes/macrophages play a major role in the immune system by controlling inflammation^[3, 34]. IL-4/IL-13-mediated induction of MAO-A in monocytes/ macrophages suggests the involvement of this enzyme in the Th2 responses and switching naive monocytes/macrophages into a resolving phenotype. Although some recent studies focused on understanding the role of MAO-A during the alternative activation of monocytes/macrophages, much remains to be investigated about the regulation of MAO-A expression and the precise role of MAO-A during the resolution phase of inflammation.

During monocyte/macrophage activation both IL-4 and IL-13 interact with specific receptors that share a common IL-4R α chain^[3, 34, 35]. IL-4R α can signal either using the common gamma chain receptor component, IL-2Rγc (Type I IL-4R, generally used by IL-4 signaling) or it can partner with IL-13R α 1 (Type II IL-4R, receptor for IL-13)^[35–37]. The receptor-associated Jaks that are attached with the Type I and Type II IL-4R and activated by IL-4/IL-13 stimulation include Jak1, Jak2 and Tyk2^[14, 35]. Although Jak3 is known to be associated with IL-2R $\gamma c^{[38, 39]}$, it is not activated in response to IL-4 signaling^[14]. Jak kinase-mediated activation of Stat3 and Stat6 seems to be the common effect of IL-4 and

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IL-13 signaling pathways during alternative activation of monocytes/macrophages^[14, 40]. In contrast, Stat1 activity is an integral part of IL-13 signaling and contributes substantially to IL-13-driven gene expression^[14].

MAO-A is one of the signature genes that is modulated by both IL-4 and IL-13 in monocytes/macrophages^[34]. Recently we identified Hck, a non-receptor tyrosine kinase of the Src family, as an essential upstream regulator of a panel of genes including both 15-LO and MAO-A in alternatively activated monocytes/macrophages^[12]. Moreover, we presented evidence that Stat transcription factors, that control 15-LO gene expression^[14, 40, 41], are also involved in regulating MAO-A expression^[14] in response to IL-4/IL-13 stimulation. Altogether our data indicated the participation of several signaling pathways including IL-4Rα/Jak1/Stat3, IL-4Rα/Jak1/Stat6, IL-4Rα/Jak2/Stat3, IL-13Rα1/Tyk2/Stat1 and IL-13Rα1/Tyk2/Stat6 in the upregulation of both 15-LO and MAO-A during alternative monocyte/macrophage activation as illustrated in our proposed models^[12, 14, 40, 41].

In addition to requiring tyrosine phosphorylation for activation, Stat transcriptional activity is also enhanced by serine phosphorylation. In this regard, our group further demonstrated the involvement of several Ser/Thr kinases including p38MAPK, ERK1/2 and PKCδ in regulating Stat serine phosphorylation and Stat-dependent gene transcription leading to the expression of both 15-LO^[40–43] and MAO-A (A. Bhattacharjee and M.K. Cathcart, unpublished observations).

Two other critical regulators involved in the transcriptional control of 15-LO, CREB and EGR-1 $[43]$, were also found to act as essential regulators of MAO-A gene expression (A. Bhattacharjee and M.K. Cathcart, unpublished observations). The existence of Stat, EGR-1 and CREB transcription factor binding sequences in the promoter of 15-LO gene and our demonstration of their regulatory role in 15-LO gene transcription in alternatively activated monocytes/macrophages (A. Bhattacharjee and M.K. Cathcart, unpublished observations) $[41, 43]$ led us to speculate the presence of the cognate binding sequences for these transcription factors in the promoter of the MAO-A gene but this speculation needs further confirmation; however, our unpublished observations showed significant inhibition of MAO-A gene expression by transfecting 15-LO antisense oligonucleotides in IL-13 stimulated monocytes thus suggesting that MAO-A gene expression is directly dependent on 15-LO expression/activity in alternatively activated monocytes/macrophages (A. Bhattacharjee and M.K. Cathcart, unpublished observations).

Recent investigations introduce Kruppel-like factors (KLFs), members of the zinc finger family of transcriptional regulators, as major contributors to the regulation of M1/M2 polarization and specifically identify KLF4 and KLF6 as the critical regulators of this process^[44, 45]. Macrophage KLF4 expression is strongly induced in M2 macrophages and significantly downregulated in M1 macrophages^[44]. In contrast, KLF6 expression is robustly stimulated by M1 stimuli and substantially reduced by M2 stimuli^[45]. Mechanistically KLF4 cooperates with Stat6 and acts as a positive regulator of the M2 genetic program, whereas it inhibits M1 targets probably by competing with NFkB for the key coactivators required for its transcriptional activity^[44]. In contrast, KLF6 suppresses the M2 phenotype by negatively regulating PPARγ expression while promoting the M1

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phenotype through cooperation with NFkB^[45]. Therefore, a balance between KLF4 and KLF6 is required for optimal M2 gene expression in alternatively activated monocytes/ macrophages via modulation of Stat6. Furthermore, these findings also identify both KLF4 and KLF6 as probable transcriptional regulators of Stat6-mediated MAO-A gene expression which needs to be verified by further experimentation.

Integrins are adhesion receptor molecules that control monocyte migration and macrophage differentiation. During inflammation, integrin activation mediates adhesion of monocytes to endothelial cells and subsequent migration through the extracellular matrix (ECM) to sites of inflammation^[46]. The β_2 subfamily of integrins plays a significant role in monocyte migration and the immune-inflammatory response. Recently we investigated how β_2 integrins regulate monocyte activation in response to IL-13 stimulation. In this study we found that IL-13 induction of 15-LO expression is inhibited during $β_2$ integrin activation or clustering through a_M integrin^[13]. We also demonstrated that whereas IL-13 stimulation promotes the surface expression of scavenger receptor CD36, a key protein for the development of inflammation and atherosclerosis, activation of β_2 integrin substantially blocks this effect^[13]. We further focused on exploring the molecular mechanisms that inhibit CD36 expression and CD36-mediated foam cell formation in IL-13-stimulated monocytes/macrophages after $\alpha_M\beta_2$ integrin activation. Our data showed that, $\alpha_M\beta_2$ integrin activation controls CD36 expression and foam cell formation in alternatively activated monocyte/macrophages via a 15-LO-dependent pathway involving peroxisome proliferatoractivated receptor-γ (PPARγ) activation^[47]. As our unpublished observations support the fact that MAO-A expression is controlled by 15-LO in alternatively activated monocyte/ macrophages, we predict at this stage that $\alpha_M\beta_2$ integrin activation may inhibit MAO-A expression in these cells. Moreover, like 15-LO products (13-HPODE/13-HODE, 15- HPETE/15-HETE) which are PPAR γ ligands and regulate CD36 expression^[48], PPAR γ activation by the products of MAO-A (e.g., the serotonin metabolite 5-methoxy-indole acetate)^[49] may influence the expression of M2 markers including CD36 in alternatively activated monocytes/macrophages^[50, 51].

IL-13-activated pathways in human macrophages can additionally be modulated by microRNA-155^[52]. MicroRNA-155 (miR-155) has been extensively studied during inflammation and immune function^[53–55] and is known to be upregulated by several pro-Th1 factors during inflammation. MicroRNA-155 directly targets IL-13Rα1 3'-UTR to diminish IL-13Rα1 protein expression leading to the downregulation of Stat6 activation and Stat6-dependent gene expression^[52]. Hence miR-155 regulates Th1/Th2 equilibrium, facilitating the classical activation of macrophages to the M1 phenotype by reducing the expression of several IL-13-dependent M2 genes. As Stat6 is the major regulator of the signaling cascades triggered by $IL-13^{[14, 56, 57]}$ and controls $IL-13$ -driven MAO-A gene expression^[14], it is very likely that miR-155 will prove to be an essential regulator of MAO-A gene expression in alternatively activated macrophages.

MAO-A-mediated ROS generation in alternatively activated monocytes/ macrophages and its implication

Although MAO-A expression is strongly upregulated in alternatively activated monocytes/ macrophages^[9, 10, 12, 14, 58], the biological importance of MAO-A for monocyte physiology has not been determined. In peripheral tissues, MAO-A is involved in the oxidative catabolism of biogenic amines thereby preventing those amines from entering the circulation. Unfortunately, the metabolism of dietary amines in inflamed tissues during the acute inflammation has not been thoroughly studied. As biogenic amines such as histamines and serotonin are well-known inflammatory mediators^[59–61] and preferentially oxidized by MAO-A, removal of these pro-inflammatory mediators from the site of inflammation may switch naive monocytes from pro-to anti-inflammatory phenotypes and thereby reverse the inflammatory symptoms.

Recently we demonstrated for the first time that MAO-A is involved in generating ROS (H_2O_2) in alternatively activated monocytes/macrophages^[14]. Interesting studies have shown that MAO-generated H_2O_2 is an important inhibitor of inducible nitric oxide synthase $(NOS2)$ expression^[62]. Although NOS2 generation of NO is differently regulated in murine and human macrophages, we speculate that the expression of MAO-A in M2 macrophages may stabilize this anti-inflammatory phenotype in part by preventing the expression of NOS2 and generation of NO. In other studies, H_2O_2 was shown to inhibit macrophage IL-12 expression, an M1 macrophage marker, by inhibiting c-Rel translocation to the nucleus^[63] and mitochondria-derived H_2O_2 was shown to inhibit the transcription factors SP-1 and AP-1 in macrophages^[64]. Thus there are many potential avenues by which MAO-A and MAO-A-derived H_2O_2 may influence gene expression in M2 macrophages.

ROS generated during the oxidation of biogenic amines can trigger various signaling pathways that ultimately lead to oxidative stress. Although superoxide anion production and oxidative stress have been implicated in proinflammatory pathways, e.g. LDL oxidation and atherogenesis, the formation of ROS and their biologic effects are in delicate balance with their catabolism (via SOD/catalase) thus influencing physiologic effects.

Role in potential endogenous PPARγ **ligand production**

PPARγ, a lipid activated nuclear receptor, is a critical regulator of cellular lipid metabolism and shows anti-inflammatory activities^[65, 66]. Although alternative activation of monocytes/ macrophages by IL-4/IL-13 and PPARγ-mediated transcriptional regulation are interlinked, the underlying mechanisms that connect these two processes are not well understood. A recent study proposed the requirement of PPARγ activity for alternative activation of macrophages *in vivo*^[67]. It further showed that the IL-4-Stat6-PPARγ signaling axis in monocytes is crucial for their differentiation into alternatively activated macrophages and for innate immunity^[67]. Although a later study reported substantial enhancement of PPAR_Y signaling by IL-4 in human monocyte derived macrophages or mouse bone marrow derived macrophages, the direct involvement of PPARγ in IL-4-stimulated alternative activation could not be demonstrated since the markers of alternative activation were not changed in PPAR_Y-deficient cells^[68]. This study thus recognized PPAR_Y as a downstream target of

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IL-4 signaling rather than a direct regulator of alternatively activated monocytes/ macrophages^[68].

There are several possible mechanisms that could be responsible for the interaction between IL-4/IL-13 signaling and $PPAR\gamma$ transcriptional activities during alternative macrophage activation. PPARγ is a ligand activated transcription factor which can prime the native monocytes (in presence of an appropriate M2 stimulus such as IL-4 or IL-13) to an enhanced M2 phenotype. Therefore we speculate that IL-4/IL-13 stimulation not only leads to PPAR γ activation but also can induce mechanisms that are involved in the generation of PPARγ ligands. This type of mechanism has been described in alternatively activated monocytes/ macrophages where IL-4/IL-13 induces the expression of 15-lipoxygenase, which metabolizes arachidonic and linoleic acids to produce 15-HETE/13-HODE that serve as endogenous ligands of PPAR $\gamma^{[47,48,69]}$. As mentioned above, IL-4 and IL-13 also enhance MAO-A expression which may lead to an enhanced serotonin metabolism in alternatively activated macrophages. The serotonin metabolite 5-methoxy-indole acetate was shown to be a PPAR_Y activator^[49, 50]. Serotonin was also shown to induce PPAR_Y target gene expression like FABP4 in differentiating macrophages in the presence of IL-4^[50]. The ability of serotonin to induce *in vitro* PPARγ transcriptional activity is interesting and requires further studies involving pharmacological or genetic manipulations of the specific PPAR γ ligand producing enzymes.

Conclusion

IL-4/IL-13 stimulation leads to the induction of 15-LO and MAO-A genes whose protein products are already recognized as critical markers of alternatively activated monocytes/ macrophages. 15-LO and its products can directly control MAO-A gene expression in monocytes/macrophages during alternative activation. It is well known that 15-LO metabolites can act as endogenous ligands of PPARγ and control the expression and function of scavenger receptor CD36 in a PPARγ-dependent manner to affect inflammatory signaling pathways in pathophysiologic responses. As MAO-A-generated metabolites can also act as endogenous ligands of PPARγ and can regulate PPARγ-dependent gene expression, it is quite likely that MAO-A-generated metabolites also control CD36 expression level. Thus, the coordinated action of the 15-LO/MAO-A \rightarrow PPAR $\gamma \rightarrow$ CD36 axis may prove to be of central importance for monocyte/macrophage physiology and function during alternative activation and resolution of inflammation. The components of this pathway may prove to be important targets for controlling the pathogenesis of atherosclerosis and chronic inflammation.

Although MAO-A is associated with the resolution of inflammation in M2 macrophages, MAO-A-mediated ROS generation in alternatively activated monocytes/macrophages and subsequent oxidative stress could promote inflammation in cardiovascular diseases like atherosclerosis. Hence the participation of MAO-A in promoting or resolving inflammation appears to rely on the delicate balance of ROS formation and catabolism as well as the influence of MAO-A on regulating bioactive amine levels and generating PPARγ ligands. This balance is determined by the cellular and tissue microenvironment of MAO-A expression and is altered in different disease states. It is clear that M1 and M2 are the two

extreme cases of an entire spectrum of macrophage activation and function which needs further characterization of marker genes that can differentiate between the subtypes of activation states. In this context it is imperative to perform additional detailed investigations to fully understand the role of MAO-A during alternative activation of monocytes/ macrophages and its contribution to the resolution of inflammation.

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