

LXRs: key regulators of intermediary metabolism in metabolic syndrome

Abstract

The prevalence of the metabolic syndrome (MetS) and its various manifestations as a significant health epidemic is currently affecting populations of developed and developing countries worldwide. It is characterized by a group of metabolic abnormalities including central adiposity, insulin resistance, high blood pressure, glucose intolerance and dyslipidemia. Individuals with MetS have the greater risk of developing major complications include fatty liver, type 2 diabetes mellitus and cardiovascular diseases. Nuclear receptors are master regulators of gene transcription, often regulating several different metabolic pathways. Among them LXR α/β play a key role in regulation of lipogenesis, cholesterol/glucose homeostasis and inflammatory pathways, via the induction/repression of target genes. However, along with their established role in metabolic homeostasis and disease, lipogenesis and hypertriglyceridemia should be considered as the most important negative features of LXR activation. Given the importance of lipid and carbohydrate metabolism and inflammation in the development of metabolic disorders, this review focuses on the impact of the LXRs signaling on the risk of MetS and its related phenotypes with an emphasis on their potential therapeutic applications in treatment of MetS. Taken together, a growing body of evidences supports the notion that LXRs may represent potential drug targets for the treatment of MetS

Keywords: liver X receptor; metabolic syndrome; metabolic disorder

Background

Metabolic syndrome (MetS), also known as syndrome X or insulin resistance syndrome, refers to a group of metabolic abnormalities, including central obesity, dyslipidemia, insulin resistance, hyperglycemia and raised blood pressure (1). People who develop the MetS have a higher risk of developing diabetes and cardiovascular disease compared with people without MetS (2). The prevalence of the MetS is increasing throughout the world; however, its patterns vary among geographical regions and ethnicities and there has been an alarming increase in Asia (3). It is widely recognized, however, that developing strategies for decreasing the MetS incidence require careful examination of genetic and environmental contributions to the MetS and better understanding of its development and pathophysiology. The exact cause of MetS is not known but like many other multifactorial diseases the full expression of the syndrome depends on a complex interaction between genetic susceptibility and environmental factors related mainly to sedentary lifestyles and high-energy diets (4). Several large population-based studies have shown that the mutations and polymorphisms in the genes associated with insulin resistance, obesity favor dyslipidemia, hypertension, chronic inflammation, and autonomic imbalance may contribute in a polygenic manner in predisposing to components of the MetS (5-10). Identification of genes underlying susceptibility to the MetS is important in order to elucidate better the mechanisms of pathways leading to MetS and to identify new molecular based strategies for the treatment of the metabolic derived disorders. Some epidemiological and animal studies investigating LXR genes regarding to the risk of MetS and related parameters have indicated a potentially important regulatory role of LXRs in several metabolic signaling pathways involved in MetS and supported this hypothesis that drugs, which target LXRs, may offer benefits in the treatment of metabolic disorders (11-16).

Liver X receptors (LXR α and LXR β)

Liver X receptors commonly known as LXR α and LXR β (encoded by NR1H3 and NR1H2 genes respectively) are ligand-dependent transcription factors belonging to the family of nuclear receptors activated by oxysterols (17). Being as “cholesterol sensors”, they sense elevated cellular cholesterol and work in a manner to decrease cholesterol level via the increased expression of target genes associated with reverse cholesterol transport, intestinal cholesterol absorption and cholesterol conversion to bile acid. LXR α encoded by NR1H3 gene located on chromosome 11p11.2, is expressed in tissues involved in lipid metabolism, including the liver, spleen, kidney, small intestine, adipose tissue, and macrophages, whereas LXR β encoded by NR1H2 gene located on 19q13.33–q13.43 is expressed throughout the body (18).

Upon activation with endogenous LXR ligands, named the cholesterol-derived oxysterols, particularly 22(R)-hydroxycholesterol, 24(S),25-epoxycholesterol, 24(S)-hydroxycholesterol and 27-hydroxycholesterol (19) or by glucose (20), LXR-mediated gene regulation occurs through two mechanisms. One is a DNA-dependent pathway in which liganded LXR after the formation of heterodimer with retinoid X receptor and recruitment additional proteins, known as co-factors in the nucleus, is bounded to LXR response element of target genes involved essentially in lipid metabolism, lipogenesis and cholesterol/glucose homeostasis (21, 22). The other is an LXR response element-independent pathway that involves interference with other transcription factor pathways (23). Several co-regulators linked to metabolic processes, including PGC-1b, RIP140, GPS2, and ACS-2, have been shown to interact with LXRs and influence their transcriptional activity (24-26).

LXRs target genes involved in metabolic syndrome

LXR signaling depending on the nutritional state of the cell induces the expression of a variety of target genes involved in lipid and glucose metabolism. LXR has been shown to activate genes such as Sterol Regulatory Element-Binding Protein 1c (SREBP-1c) (27) (which serves as a trigger for down-stream transcriptional events), fatty acid synthase (FAS) (28), phosphoenolpyruvate carboxykinase (PEPCK) (29, 30) acetyl-CoA carboxylase (ACC) (which are involved in lipogenesis) and the ATP binding cassette transporters A (ABCA) (31) that are involved in cholesterol transport. Moreover, LXRs have been shown to mediate repression of inflammatory pathways through mechanisms collectively known as trans-repression. Then, it is reasonable to conclude that dysregulation of LXRs signaling may contribute in increased risk of the MetS.

Role of LXRs in regulation of metabolic functions

During the last decade, the physiological role of LXRs as key regulators of many target genes involved in cholesterol/glucose homeostasis, inflammation, lipid uptake and efflux and lipoprotein metabolism in different tissues has been demonstrated.

In general, LXRs activators promote (i) the lipogenesis via the regulation of hepatic fatty acid biosynthesis in both an SREBP-1c-dependent, as well as an SREBP-1c-independent manner (32) and the cellular transmembrane transport of endogenous lipid substrates via the induction of ABCA1, ABCG1, ABCG5, ABCG4, and ABCG8, in human macrophages and intestine (33-35); (ii) the cholesterol homeostasis via inducing the transcription of genes that protect cells from cholesterol overload and also inducing the cholesterol trafficking from the endosome/lysosome to the plasma membrane through the activation of Niemann-Pick C (NPC) 1 and NPC2 expression in human macrophages (36). The activation of LXR results in bile acid synthesis and

metabolism/excretion, reverse cholesterol transport (RCT) and cholesterol absorption/excretion in the intestine; (iii) The inducing expression of the cholesterol transporters ABCA1 and ABCG1 and the regulation of acceptors in cholesterol efflux such as ApoE, ApoCI, ApoCII and ApoCIV expression in adipocytes and macrophages (37); (iv) The remodeling of lipoproteins through the control of modifying enzymes such as lipoprotein lipase (LPL) and phospholipid transfer protein (PLTP) in liver and macrophages (38); (v) The hepatic conversion of excess carbohydrate to lipids via regulation of carbohydrate response element-binding protein (ChREBP) as a glucose-sensitive transcription factor; (vi) The increasing insulin-mediated glucose uptake into adipose tissue and muscle via upregulation of the glucose transporter GLUT4 (39); and (vii) The regulation of inflammation and immunity via induction of classical inflammatory genes and various chemokines in response to bacterial, LPS, TNF- α , or IL-1 β stimuli and inducing the expression of anti-inflammatory genes (39).

To support all these physiological roles of LXRs, analyzing gene expression in LXR α and LXR β deficient mice and also LXRS agonists has confirmed the results (40-42). Therefore, LXRs play a central role in many pathways involved in the onset of the MetS, especially in HDL-cholesterol metabolism, fatty acid and carbohydrate metabolism in the liver, macrophages and intestine.

LXRs as potential drug targets for the metabolic syndrome

Owing to the fact that LXRs play a central role in cholesterol metabolism and are key regulators of lipogenesis and have an impact on systemic glucose homeostasis, understanding the mechanisms by which LXR signaling regulates diverse aspects of metabolism homeostasis has emerged new insights with respect to pharmacological manipulation of the LXR pathway for therapeutic intervention in human metabolism (43). The ability of LXRs to integrate metabolic

and inflammatory signaling has made them to appear attractive targets for drugs development. In addition to known endogenous oxysterols (oxidized derivatives of cholesterol) ligands for LXR activation which have similar affinities for both LXR isoforms, considerable efforts have been made to develop synthetic agonists' ligands to modulate activity of LXR-signaling pathways.

A number of synthetic LXR ligands have been developed that promote cholesterol efflux and inhibit inflammation *in vivo* and inhibit the development of atherosclerosis, metabolic disorders as well as inflammatory conditions in animal models, which suggests a broad spectrum of potential clinical applications (44). The nonsteroidal compounds T0901317 and GW3965 are two examples of such LXR activator that their beneficial outcome on cholesterol homeostasis has been proved in cell-based or *in vivo* in mice (45, 46). However, data from other *in vivo* studies revealed that the deleterious lipogenic effects of these first-generation synthetic ligands of LXR should be taken into account (27, 45, 46).

The lipogenic effects of LXRs has presented a major problem in strategies for development of LXR agonists and recent efforts have benefited from isoform-specific LXR ligands which is considered to be one of the most important options to develop LXR ligands with partial agonists property, exhibiting a LXR subtype-specificity which activate or block the receptor in a tissue specific manner (47). In other words, selective pharmacological activation of LXR β may induce cholesterol-related effects of LXR but circumvent the lipogenic effects that are attributed to LXR α (48, 49). Recently, two synthetic LXR agonists, ATI-829, and DMHCA have been developed that selectively activate LXR target genes expression in certain tissues but have no impact on genes involved in liver lipogenesis (50). These data suggests that developing LXR modulators with no effect on hepatic lipogenic genes would lead to better therapeutic strategies.

Although a large body of studies have investigated to develop LXR agonists, the concept of undesirable lipogenic effect of LXR has prompted the development of LXR antagonists as an alternative approach for pharmacologically inhibition of LXR-driven lipogenesis and reduction in hepatic complications. Evidences from global loss of LXR activity studies suggests that LXR antagonist by improving insulin sensitivity in a tissue specific manner might have therapeutic utility for metabolic syndrome (51). Further studies will be necessary to find a suitable balance between desirable and adverse effects of both LXR agonists and antagonists on various aspects of metabolic syndrome and other metabolic related disease, before they could be considered as an ideal candidate for therapeutic purpose.

Conclusion

Given that the prevalence of MetS and its various manifestations is increasing globally and the consequences of this syndrome can include such outcomes as type 2 diabetes and cardiovascular diseases, the roles of LXRs as key regulators of intermediary metabolism have evoked interest in these receptors as targets for development of new ligands for the treatment of MetS. A number of synthetic LXR ligands have been designed that have beneficial outcome on cholesterol homeostasis with some undesirable lipogenic effects. With respect to this, further efforts are in progress to define possible approaches to avoid from such serious adverse effects, most importantly increasing plasma levels of triglyceride. One alternative approach is selective pharmacological activation of LXR subtype through the development of LXR ligands with partial agonist property or applying LXR antagonists repressing lipogenic gene expression in tissue specific manner. Finally, it must be noted that, most investigations revealing the beneficial outcome of LXR activation have been performed in animal model and have not been tested in humans. Thus, with considering the interspecies metabolic differences and genetic evolution, those

findings could be translated into human or further studies should be performed in human-based to verify such animal-based findings.

Declarations:

Ethics (and consent to participate): Not applicable

Consent to publish: Not applicable

Competing interests: The authors declare that there are no conflicts of interest.

Funding: No funding was received

Authors' contributions: Conceived, designed and wrote the paper: HMM. Participated in revising and editing the manuscripts: JA & YR

Availability of data and materials: Not applicable

List of abbreviations used: MetS; Metabolic syndrome, LXRs; liver X receptors, NR1H3; nuclear receptor subfamily 1 group H member 3, NR1H2; nuclear receptor subfamily 1 group H member 2, DNA; deoxyribonucleic acid, PGC-1b; Peroxisome proliferator-activated receptor gamma coactivator 1beta, RIP140; receptor-interacting protein 140, GPS2; G Protein Pathway Suppressor 2, ACS-2; Acetyl-coenzyme A synthetase 2, SREBP-1c; Sterol Regulatory Element-Binding Protein 1c, FAS; fatty acid synthase, PEPCCK; phosphoenolpyruvate carboxykinase, ACC; acetyl-CoA carboxylase, ABCA; ATP binding cassette transporters A, NPC; Niemann-Pick C, RCT; reverse cholesterol transport, LPL; lipoprotein lipase, PLTP; phospholipid transfer protein, ChREBP, carbohydrate response element-binding protein, ATI-829; [3a,6a,24-trihydroxy-24, 24-di(trifluoromethyl)-5b-cholane], DMHCA; [N,N-dimethyl-3b-hydroxy-cholenamide],

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