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Mohammadjavad Sotoudeheian*, SeyedAhmad Hoseini, Seyed-Mohamad-Sadegh Mirahmadi

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Review

Therapeutic Properties of Polyphenols Affect AMPK Molecular Pathway in Hyperlipidemia

Mohammadjavad Sotoudeheian 1,*, SeyedAhmad Hoseini 1 and Seyed-Mohamad-Sadegh Mirahmadi 2

- ¹ Faculty of Medicine, Iran University of Medical Sciences, Tehran, Iran; dsahan74@gmail.com
- ² Department of General Medicine, School of Medicine, Iran University of Medical Sciences, Tehran, Iran; rgs.of.2013@gmail.com
- * Correspondence: javadsotoud@gmail.com

Abstract: Hyperlipidemia is the fat particles excess in the serum. Hyperlipidemia increases the mortality rate that occurs with other metabolic disorders. Hyperlipidemia is classified into familial and acquired subgroups. Moreover, Hyperlipidemia etiology is based on environmental or genetic factors. For instance, abnormal HMG-CoA regulation down-regulates ubiquitin ligase and targets variable oxidative stress-related condition proteins. There has been proven reactive oxygen species (ROS) overshoot happens during hyperlipidemia occurrence. OS, directly and indirectly, regulates molecular cascades within the cell and leads to gene expression alteration. At this molecular juncture, AMPK is affected by ROS. AMPK is a serine-threonine kinase and a critical energy balance. Low energy conditions result in AMPK activation due to the down-regulation of protein and lipid synthesis. Furthermore, ER stress and activated unfolded protein proteasomal response and autophagy are AMPK mediated. Polyphenols are widespread dietary plant-based compounds that regulate gene expression and signal conduction. Through the hyperlipidemic state, FFAs releasing indirectly connect to AMPK/NF-κB pathway then polyphenols target them. AMPK, during this FFA exposure, down-regulates de novo lipid molecules generation. Likewise, if AMPK/mTOR pathway failure is prolonged, the hyperlipidemic state may be explicit, activated by natural herbal mediators, e.g., polyphenols. Polyphenols activate the AMPK signaling pathway and influence lipid metabolism. Polyphenol-mediated AMPK activation results in lipogenesis inhibition and lipophagy. Cholesterol efflux mediated polyphenols lipid-lowering effects, accessing LXR pathway. All these clues persist on direct or indirect AMPK-related polyphenolic anti-hyperlipidemic effects.

Keywords: AMPK; polyphenols; dyslipidemia; Nrf2

Introduction

Hyperlipidemia, also called hyperlipoproteinemia, is the excess fat particles in the serum [1–5]. This prevalent disorder is the leading cause of atherosclerosis [5–7] and metabolic syndrome [8,9]. Lipids, derived from exogenous resources or hepato-intestinal synthesized, are transported in the blood via many kinds of lipoproteins, including chylomicrons, low-density lipoproteins (LDL), and high-density lipoproteins (HDL) [2,9–11]. Lipid concentration overshoot, hyperlipidemia, raises the mortality rate when accompanied by other metabolic diseases [8,9]. It is also the most prevalent risk factor for atherosclerotic-based cardiovascular diseases [12–19]. Although many hyperlipidemia therapeutic compounds have been enhanced in past decades, it is still a significant health complication [20].

Since hyperlipidemia is associated with high morbidity and mortality, its control has become an essential scientific issue. In this article, according to past studies, we intend to review the role of a group of natural substances with medicinal properties in treating hyperlipidemia. In this article, we try to review the information available in the literature about a practical molecular pathway in the pathogenesis of dyslipidemia.

Molecular Pathogenesis of Hyperlipidemia

Hyperlipidemia is asserted in two significant types: familial or primary and acquired or secondary [1], based on environmental or genetic factors [21]. The most important clinical feature of hyperlipidemia is LDL level elevation [21–23] and apolipoprotein B (ApoB) [24,25]. So, LDL reduction is a common approach in hyperlipidemia which mainly occur by hepatic 3-hydroxy-3-methyl glutaryl coenzyme A (HMG-CoA) reductase inhibitors [26–30], which reduce the hepatic endogenous synthesis of cholesterol and decrease the LDL receptors expression [4,31–34] and increases baroreflex sensitivity [35]. It was also demonstrated that HMG-CoA reductase inhibitors have anti-oxidative effects [36] and anti-platelet aggregation effects [37].

HMG-CoA reductase, in combination with lecithin-cholesterol acyl transferase (LCAT), cholesterol 7α -hydroxylase (CYP7A1), and acyl CoA: cholesterol acetyltransferase (ACAT) plays a crucial role in lipids metabolisms [28,38–41]. Although HMG-CoA in hyperlipidemia incidence enrolls as the core enzyme, two other hepatic enzymes, alanine aminotransferase (ALT) and aspartate aminotransferase (AST), also gather with this disorder [42–44].

Abnormal HMG-CoA regulation down-regulates a ubiquitin ligase called neural precursor cell expressed down-regulated 4 (NEDD4) and other less critical ubiquitin proteasome cascade proteins, including BIRC3, USP6, and UBE2D1 [45,46] developmentally. These pathway targets are variable, but oxidative stress (OS) -related condition proteins are mainly targeted by this cascade [47,48].

OS is a well-known mechanism of cellular change. Research indicates that an essential molecular system, reactive oxygen species (ROS), overshoots during hyperlipidemia [49–54]. The head enzymes of ROS-induced OS are NADPH oxidase, xanthine oxidase, superoxidase dismutase (SOD), and glutathione peroxidase (GSH-Px), which lead to more lipid peroxidation [49,55–60].

Some theoretical relation between ROS-induced mitochondrial dysfunction and mechanistic target of rapamycin complex 1 (mTORC1) pathway-related hyperlipidemic states had been determined [61–63], in which lipid homeostasis deregulated [64]. Also, an immune biomarker for hyperlipidemia, neopterin, is recognized as an OS-mediated molecule [65].

In addition to this mechanism, endoplasmic reticulum (ER) stress is another cellular stress condition combined with ubiquitin-proteasome-based lipid dysfunction disorders [66,67]. ER stress induces NEDD4 expression via E3 ubiquitin ligase [49,68], tightly in combination with HRD1 or SYVN1 [69]. Furthermore, NADPH oxidase, OS-related enzyme, Mdm2-p53 pathway, and glutamate receptor subunit 1 (GluA1) are related to ER stress-induced NEDD4 expression [70–75] and HMG-CoA reductase down-regulation [68]. NEDD4 indirectly down-regulates phosphatidyl inositol 3-kinase (PI3K) [76] but especially targets phosphatase and tensin homologue (PTEN) [45] and is activated via LDL receptors [77].

PTEN, a phosphatase, down-regulates the PI3K/AKT-mTORC1 pathway [78,79]. This pathway plays a role in cell proliferation, metabolism, and migration [80,81]. PI3K/AKT-mTOR pathway, which regulates apoproteins secretion [82], is also directly induced through the Mdm2-p53 pathway [70,71,75]. PI3K, as the AKT activator, in combination with mTORC1, is engaged with a Cullin-RING finger E3 ligases, CRC7 [76], which on by own regulated through neddylation, NEDD8 attachment [83]. However, neddylation is a critical mechanism in PI3K/AKT-mTOR direct regulation, and it may down-regulate this pathway indirectly via glycogen synthase kinase 3 (GSK3) [84–86]. The activation of GSK-3 also may lead to more nuclear factor kappa B (NF-κB) phosphorylation [87,88] involving PI3K/AKT signaling pathway [89–91].

Many studies firmly confirmed the NF-κB pathway role in obesity and OS-mediated disorders such as hyperlipidemia [92–94], in which Maf A [95] and apoprotein synthesis regulate [82].

This cascade prescribed not only the role of NF- κ B induced cellular stress but also the combination of the Nrf2 signaling pathway with this disorder [93,96,97]. Phosphorylation, as the main component of this pathway [98], affects 26S proteasomal degeneration and NF- κ B translocation [99]. NF- κ B then binds to a specific genome region which promotes OS head enzymes via an anti-oxidant response element (ARE) [100,101]. Signal transducer and activator of transcription (STAT) can inactivate NF- κ B [102] and enhance Nrf2-ARE mediated phase II detoxifying enzymes [103], e.g., heme oxygenase 1 (HO-1) [104].

Nrf2 ubiquitination and degeneration based on cullin3/Rbx 1 complex link this molecule to Kelch-like ECH-associated protein 1 (Kap1) [90,105]; then, sirt1/Nrf2 pathway inhibition, activates P38/mitogen-activated protein kinase (MAPK) pathway accelerates the hepatic changes in hyperlipidemia [106].

Thus, the P38/MAPK signaling pathway is composed via the microRNA1- myosin light chain kinase (MLCK) pathway and LDL oxidation [107]. In addition, some other microRNAs, including microRNA144, emerged during hyperlipidemic states through the liver x receptor (LXR) signaling pathway [108].

LXR signaling cascade is also combined with peroxisome proliferation-activated receptors (PPARs) [109], which are responsible for lipid metabolism regulation [51,110]. Although PPARs overshooting may lead to liver damage [111], proper regulation has anti-inflammatory and lipid regulatory effects [112]. Also, the LXR/PPARs pathway is directly controlled by a cluster of differentiation 36 (CD36) [113].

CD36 expression on monocytes and platelet surface increased during free fatty acid (FFA) elevation [110,114,115]. CD36/CD36 receptor interaction up-regulates platelet activity during hyperlipidemia [115]. In monocyte differentiation, when CD36 appears on the cell surface, the NF- κ B transcription factor activates. This pathway is inhibited when sirt1 is expressed in the cell [116]. CD36/sirt1 pathway affects fatty acid metabolism [117]. Moreover, sirt1 indirectly phosphorylates AMP-activated protein kinase (AMPK) [118]. This promotion of AMPK then leads to PPAR γ coactivator 1α deacetylation, which up-regulates PPAR α expression in the nucleus and interacts with CD36.

Further, AMPK activation conducts mTOR inhibition [119], which regulates Nrf2 [106]. Decreased AMPK levels and increased SREBP1 induce hyperlipidemic conditions [120,121]. Moreover, AMPK activation inhibits de novo lipogenesis [122], which increases the 5-lipoxygenase substrate [123].

So, AMPK phosphorylation increases the fluidity of the FFA oxidation pathway [124].

AMPK

AMPK, a serine-threonine kinase and a vital energy balance regulator in mammalian eukaryotic cell roles first identified in 1973 [125–128]. AMPK is rule outs as a heterodimeric substance with α catalytic, γ regulatory, and β scaffolding subunits [125,129,130].

Low energy conditions induced, with a high AMP/ATP ratio, AMPK activation increases adenosine triphosphate (ATP) de novo production [131–133] due to protein and lipid synthesis down-regulation [134]. It was also identified in such metabolic stresses that protein kinase A activation overshoots [135]. So, AMPK phosphorylation on threonine 172 regulates fatty acid oxidative pathways [136]; through acetyl CoA carboxylase [137], glycolysis [138], and ER stress [139]. The protease phosphate pathway also induces ROS, where AMPK inhibits and, as a result, ACC-related lipogenesis may be affected [140]. Threonine 172 phosphorylation linkage with liver kinase B1 (LKB1), also named serine/threonine kinase II (STK II), is well-identified; however, this effect exegesis is still unclear [125,141–143].

In 2003, LKB1 was recognized as the significant AMPK activator kinase [144,145], which phosphorylates downstream molecules by itself [146,147], mentioned further. It is also a target of metformin, an anti-diabetic drug [148]. LKB1 regulates AMPK activation in almost all tissues [149,150], such as the atrium [151] and in the liver, which leads to hepatic fibrosis [150]. In addition, two other AMPK upstream kinases were recognized; calmodulin-dependent protein kinase β (Cankk β), which is based on Ca²⁺ homeostasis, and TGF β activated kinase 1 (TAK1) (Figure 1) [143,152–154].

Figure 1. LKB1 regulates AMPK activation in almost all tissues, such as the atrium and liver, leading to hepatic fibrosis. In addition, calmodulin-dependent protein kinase β (Cankk β), which is based on Ca2+ homeostasis, modulates AMPK phosphorylation.

An extracellular signal-regulated kinase (ERK) leads to LKB1 phosphorylation on serine 248, which interrupts the AMPK/LKB1 cascade [155] and p53/AMPK pathway [152]. Moreover, the adiponectin-mediated apoptotic cascade is AMPK/ERK pathway-dependent [156], and ERK inhibits via AMPK-derived ATP binding cassette transporter A1 (ABCA1) overexpression [157]. Furthermore, the LKB1/AMPK pathway affected during metabolic stress can regulate autophagy and apoptosis [158] and enhance adipogenesis [159] at the lysosome surface [160]. Also, LKB1 promoters E-box may affect by DEC1, and LKB1 activity level is reduced, which is related to circadian rhythm. This occurrence leads to AMPK activity depression [142]. Notch1 also results in specific tissues, such as the heart [161], or specific cell lines, e.g., T cells [162,163].

AMPK-induced lipid metabolism regulation is also supervised by PPARs and SREBP, which are impressed in adipogenesis in adipocytes [164,165]. SREBP1 is associated with triglyceride production, whereas SREBP2 is linked to cholesterol synthesis [166], which regulates LDL receptor genes [167]. PPAR γ activation caused weight gain and some other side effects [168]. PPAR reduction, at the gene level, is associated with advanced glycosylation end products (AGEs) [169] and plays a critical role in hepatic stellate cell inactivation, which is combined with hepatic fibrosis [170].

The β oxidation and cholesterol synthesis primary regulator genes, PPAR [171,172], indirectly, through AMPK, is combined with mitochondrial biogenesis [173]. PPAR γ co-activator 1α (PGC1 α) during the mitochondrial biogenesis up-regulates the expression of nuclear respiratory factor (NRF), a transcription factor [174], resulting in energy imbalance and thereby AMPK pathway activation [175,176], related to NF- κ B [177]. In addition to all these pathways, AMPK suppresses PPAR γ to inhibit the differentiation of pre-adipocytes [178]; and the PGC1 α level rising is assumed to promote hypo-methylation [179]. Adaption to mitochondrial dysfunction is not related to PGC1 α and sirt1;

however, it is AMPK phosphorylation-related [175]. PGC1 α phosphorylation and PGC1 α and PGC1 α deacetylation through sirt1 regulate mitochondrial biogenetic activity [180–182] and anti-inflammatory features [183].

Novel researches indicate sirt1 mitochondrial anti-oxidant features [184,185]; however, it may reduce the up-regulation of SREBP1 if over-expressed [186]. SREBP1 regulates PCSK9, LDL receptor, and angiopoietin-like 4, controlling cholesterolemia [187–191]. This NAD+-dependent relation with the sirt1/AMPK pathway regulates the lipid metabolism network [192,193].

Although NFR and PPARs induced sirt1 activation firmly depend on some promoting proteins, for instance, MFN1/2 [194]; moreover, the α subunit of AMPK activity is sirt3 mediated [195], and PGC1 α mediated Pdk4 up-regulation in lipid metabolism involves AMPK/sirt1/PGC1 α pathway in combination with forkhead box O3 (FoxO3) (Figure 2) [196].

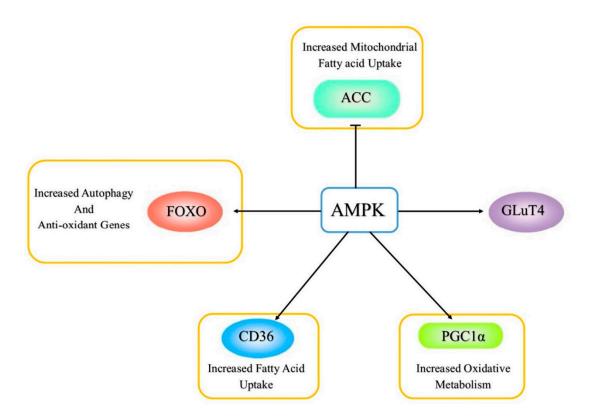


Figure 2. Activated AMPK upgrade glucose uptake via glucose transporter 4 (GLuT4) during mTOR-related PI3K/AKT pathway activating. In addition to all these pathways, AMPK suppresses PPAR γ to inhibit the differentiation of pre-adipocytes; and the PGC1 α level rising is assumed to promote hypo-methylation. PGC1 α phosphorylation and PGC1 α and PGC1 α deacetylation through sirt1 regulate mitochondrial biogenetic activity and anti-inflammatory features. PGC1 α mediated Pdk4 up-regulation in lipid metabolism involves AMPK/sirt1/PGC1 α pathway in combination with forkhead box O3 (FoxO3). Moreover, CD36/CD36 receptor interaction up-regulates platelet activity during hyperlipidemia. CD36/sirt1 pathway affects fatty acid metabolism. However, sirt1 indirectly phosphorylates AMPK. This promotion of AMPK then leads to PPAR γ co-activator 1 α deacetylation, which up-regulates PPAR α expression in the nucleus and interacts with CD36. Also, the protease phosphate pathway induces ROS, where AMPK inhibits, and ACC-related lipogenesis may be affected. Besides, AMPK induced ACC activation contact with the NF- κ B pathway. However, NF- κ B inhibition enhances monocyte cholesterol efflux.

Sirt1 level reduction indicates increased energy prevention related tightly to the mTOR pathway [197,198] and AMPK/glucagon-like peptide 1 (GLP1) [199,200]. This sirt1 level reduction down-regulates the NF- κ B p65 subunit acetylation and phosphorylation, thereby, nuclear translocation [201,202]. So, sirt1 and NF- κ B pathways show antagonistic features [203]. NF- κ B activated when I κ B- α degradation and ubiquitination occur, which is a result of I κ B- α phosphorylation. Then NF- κ B acts as an intra-nuclear transcription factor [204], which increases Bcl-2 after AMPK activation [205]. Besides, AMPK induced ACC activation contact with the NF- κ B pathway [206]. However, NF- κ B inhibition enhances monocyte cholesterol efflux [207].

Multiple cytokines, such as IL1 β , TNF α also regulates NF- κ B activation directly [208,209] and indirectly lead to pro-inflammatory molecules activation, e.g., COX2 [210]. AMPK activation is also related to TNF α -regulated NF- κ B nuclear translocation [211]. Likewise, AMPK activation inhibits the mTOR signaling pathway [210], which leads to UNC51-like kinase 1 (ULK1) activation via dephosphorylation at serine 757; however, AMPK directly enhances ULK1 activation [211–213].

AMPK activation leads to tuberous sclerosis complex 2 (TSC2) threonine 1227 and serine 1345 phosphorylation [159,160] and then mTORC1 inactivation and lipogenesis suppression, an antagonistic effect [212,214–217]. In addition, rapamycin, the mTOR inhibitor, down-regulates mTORC2, and PPARγ, leading to the inhibition of adipocyte differentiation [218]. All this pathway may be a result of ROS [219]. The mTORC2 subunits, which regulate glucocorticoid inducible kinase1/2, SAPK-interacting protein (SIN1), and rapamycin-insensitive companion of mTOR (RAPTOR), and its substrates, such as AKT and autophagy-related proteins, are also undergrowth factors regulation [220–222]. However, protein phosphatase 3A activation and AMPK inhibition affect this regulatory pathway [223].

Nevertheless, mTORC1 regulates via amino acids linked to the lysosome and is needed for AMPK activation [224]. Activated AMPK upgrade glucose uptake via glucose transporter 4 (GLuT4) during mTOR-related PI3K/AKT pathway activating [225–228], which persists on OS [129] and regulates by IGF-1 [221], and down-regulates glycolysis (Warburg effect) [229]. If this activation becomes chronic, PGC1 α -dependent angiotensin II reduction decreases endothelial dysfunction [230,231]; and lipid homeostatic unremarkable un-enrollment [232]. However, mitochondrial AMPK activation and mTOR/AKT inhibition may not remain long, especially in hepatocytes [233–235]. This AMPK activation and mTOR inhibition indirectly link Nrf2 to this pathway as an upstream regulatory molecule [236].

Moreover, PI3K inhibits VLDL production, based on insulin effects [234], and augments apoprotein A1 in adipocytes [237]. So, AMPK related PI3K/mTOR/ULK1signaling pathway causes insulin resistance [238], which targets vascular sorting protein 34 (Vps34) and Vps15/PI3K/ULK1 pathway too [239], by which mitochondrial endothelial NO synthase (eNOS) is regulated (240–244], broadcasts cytotoxicity effects [245] and as a small GTPases family member stimulates angiogenesis on partnership with MAPK/ERK pathway [246]. With all this, hepatocyte activation could be inhibited explicitly via an AMPK-specific inhibitor; however, PI3K/AKT inhibitors do not act like that [247–249]. However, AKT and AMPK are tightly linked [250,251], and sticking out on microRNA 41 inhibition in FFA-related inflammatory states [252], regularize Ca²⁺ homeostasis [253], microtubule transportation system organizing [252], amplifying insulin sensitivity through protein kinase B in some unique cell lines [254,255], and rolling as anti-oxidative conditions in cooperation with Nrf2 [256,257], and NF-κB [258].

The AKT/PI3K pathway activation by PDGF up-regulates S phase kinase-associated protein 2 (SKP2) [259], and leads to LKB1/AMPK activation [260], which by its own regulates PTEN, inhibits mTOR/S6 kinase 1 [261,262] and enhance ULK1 phosphorylated form [263], which is associated predominantly with autophagy cascade, and may directly activate by AMPK [264], within hepatocytes in addition to mTORC1 induction [265]. ULK1, which is needed for the autophagosome constitution, has two closely near phosphorylation sites modified by AMPK and mTOR, which interact with the lysosomal autophagic regulator, transcription factor EB (TFEB) [266].

Moreover, ER stress and activated unfolded protein proteasomal response and autophagy are AMPK mediated [267–269]. ER stress is the initial OS condition key [270–272]. Some studies

importune on ER stress-dependent JNK-mediated hyperglycemic induced apoptosis, which is related to AMPK also [272]. Moreover, apoptosis is induced via activated AMPK/JNK stimulation in some types of cells [273]. JNK and NF- κ B are two necessary inflammatory molecular signals [274]. It should be noticed here that although JNK/NF- κ B molecular cascade provides the initial part of autophagy, AMPK phosphorylates TSC2 and inhibit mTORC1 and perform an impressive impact on autophagy [261]. Figure 3 shows a brief review of AMPK cascades.

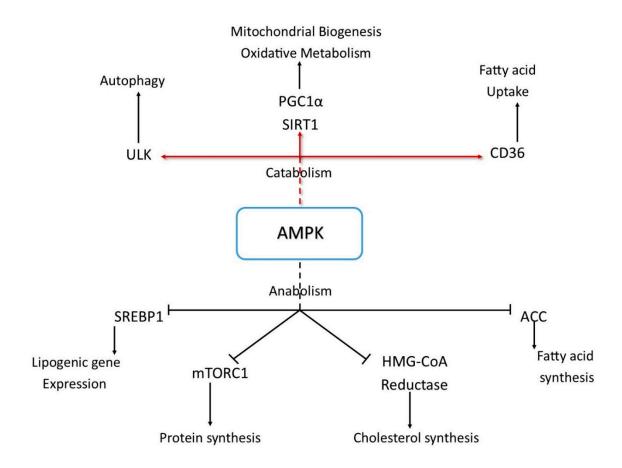


Figure 3. a brief review of AMPK cascades and effects.

Role of AMPK in Hyperlipidemia

AMPK, as the primary molecule in energy versus nutrient supply homeostasis, acts incorrectly during chronic disorders occurrence [275,276], such as obesity [277], and regulates some cellular conditions, e.g., oxidative stress [278].

Activated AMPK inhibited fatty acid synthesis via HMG-CoA reductase inactivation [279] and up-regulated PI3K pathway, leading to glucose over-uptake through insulin stimulation [280].

AMPK activation by intracellular Ca²⁺ level changes [281] and ER stress inhibits NADPH oxidase-induced OS and approves PPARs expression regulation [120,282], and governs GSK 3β [283]. However, fatty acid changes may reduce PPAR and improve SREBP1 in hepatocytes [124] during lipogenesis [284]. AMPK directly acts as the SREBP2 phosphorylase and, via this mechanism, blocks HMG-CoA reductase expression and activity [285,286] and up-regulates GLuT4 transcription [277]. In this protein synthesis, the mTOR system is the crucial point under the AMPK regulatory mechanism [287]. Otherwise, SREBP inhibits through activated AMPK. SREBP is a significant factor in fatty acid synthesis [288]. Also, de novo cholesterol production is controlled by AMPK/SREBP pathway [289].

PI3K/AMPK pathway uses ARE-mediated gene regulation and cooperates with the Nrf2 molecular system [278]. Here it should be noticed that PI3K/AKT-mTORC2/S6K is negatively

regulated by PTEN [80,81], which is induced via Mdm2 [70,75]. However, Nrf2/ARE regulation of the PI3K/AKT pathway is more prior [93]. PI3K pathway affects eNOS, which is indirectly enhanced through AMPK. AMPK also down-regulates lipogenesis and cholesterol synthesis [229,240]; Through PPAR [51] and HMG-CoA reductase [285], expressed previously.

Although AMPK phosphorylation through AKT is essential, diacylglycerol, induced during hyperlipidemia, blocks AMPK activity via protein kinase C [276]. Moreover, AMPK promotes GLuT4 activity on the adipocyte cell membrane, reducing lipid agglomeration [277].

Alongside all these pathways, AMPK inhibits adipogenesis through growth factor independence 1 (Gif1)/Runt-related transcription factor 2 (Runx2)/PPAR γ related pathway. In this case, AMPK up-regulates osteopontin (OPN) when adipogenesis tees off and decreases PPAR; however, Gif1 pickle on OPN promoter reduces AMPK effects [290]. Nonetheless, PPAR regulation via AMPK plays a pivotal role in lipid metabolism in which SREBP1 enlisted a therapeutic target for the lipid-based disorder [291].

AMPK and Polyphenols

Polyphenols are formed a widespread phytochemical unnecessary dietary nucleophilic group of plant-based compounds [292–294]. Too many polyphenols are classified into sub-classes such as phenolic acids, flavonoids, and tannins [294,295]. Nowadays, 8000 backbone molecules and 25000 polyphenols are determined [295,296]. Polyphenols' pharmacological activities, including gene regulation and signal conduction, have been widely explained during past decades [292,293].

As a diet-based gathering, polyphenols, health-beneficial nutrients [297], have medicinal and therapeutic effects in some diseases [298,299], as they relieve non-desired cellular conditions, including OS [300], in cooperation with Nrf2/, ARE signaling pathway [297]. While it involves PGC1 α [301], it is followed by high glucose disclosing [302] in the presence of Quercetin, a polyphenol that up-regulates Nrf2 [303]. It also had been investigated that, Nrf2 indirectly related to sirt1 through FoxO3 [304]. On the other hand, Nrf2-linked pathways break out via polyphenol-induced situations, such as PI3K/AKT pathway [305].

The current pathway is occupied in insulin signaling [306] and GSK3 β inhibition [307] and is affected during some polyphenols impression cascades, such as curcumin anti-apoptotic effect [308] and mitogenic stress concerning JNK signals inhibition [305,309]. The PI3K/AKT pathway inactivates YSC1, which is inhibited by AMPK/LKB1 on the other side [310]. Also, TSC1 indirectly regulates the mTORC1 pathway (Figure 4) [311]. mTOR suppresses the FoxO pathway, which may also be inactivated during ROS-induced PTEN and sirt1 inhibition [312,313]. Not only ROS medicated indirect mTOR effect, but also energy stress leads to mTOR activation; with the co-molecule diversity, the AMPK [314,315], which together are polyphenols proven targets in some disorders [316,317], such as breast cancer [318], and IBD [319].

AMPK/mTOR pathway affects Ca²⁺ concentration, whether it affects PI3K/AKT pathway [320], linked to NF- κ B and MAPK/P38 pathway [321], and TGF β activated kinase 1 [322], changing autophagic states [323,324], OS [325], and mitochondrial dysfunction [326,327]. Likewise, mTOR natural polyphenol-induced inhibition may start an autophagic cascade. Some polyphenols such as resveratrol blurt this non-ideal result [328], despite the fact they relieve inflammatory conditions influencing AMPK/sirt1/Nrf2 pathway [329,330], PGC1 α molecular signals [331], and TSC2 [332], protecting cells during UV exposure [332], and induce AMPK within the heart [334].

Other polyphenols, e.g., Epigallocatechin 3 Gallate (EGCG), Glabridin, and Quercetin, impress the AMPK/Ca²⁺ pathway, so decrease hepatic gluconeogenesis [335–337]. It also may impel cells to express GLuT4 [338–340]. Furthermore, naringenin, another polyphenol, enhance muscular and neuronal glucose uptake through PI3K/AMPK/Ca²⁺ pathway [341–343].

In addition, Quercetin improves eNOS synthesis through the AMPK-mediated pathway [344,345]. As well as, both resveratrol and EGCG activate PGC1 α /sirt1/AMPK pathway to ameliorate severe mitochondrial disturbances [346], and AMPK-related berberine, polyphenolic compound effects reduce mitochondrial OS upheaval so that lipid-based disorders may be adjusted through that [347].

Figure 4. The AKT/PI3K pathway activation by PDGF up-regulates S phase kinase-associated protein 2 (SKP2) and leads to TSC activation. LKB1/AMPK also activates TSC. AMPK phosphorylates TSC2 and inhibits mTORC1, and performs an impressive impact on autophagy.

Targeting AMPK by Polyphenols: A Novel Therapeutic Strategy for Hyperlipidemia

Nowadays, routine statins are already used to reduce hyperlipidemic states [348], including LDL overshot level [21,22], as the primary approach in hyperlipidemia progression [23].

As we discussed previously, HMG-CoA may be a target for therapeutic agents during hyperlipidemia management [36,45], which is tightly linked to NEDD4, PTEN, and PI3K/AKT pathway [45,79]. Moreover, PI3K is related to mTOR and AMPK [78,82].

AMPK, a cellular energy balance modifier [125], regulates some cellular conditions as a checkpoint, including AMP/ATP ratio imbalance [349]. During hyperlipidemic situations, FFAs released into the circulation, PPARs act here, and adipocyte inferred peroxisome, indirectly connecting to AMPK/NF-κB pathway [350,351], and polyphenols target them [352]. AMPK, during this FFA exposure, down-regulates novel lipid molecules generation [122,353] and interlocks mTOR, Nrf2, GLuT4, and PI3K to this mechanism [209,228,252,354,355], and GSK3β to mitochondrial dysfunction [356], a momentous event when hyperlipidemia engender [61,63]. Moreover, if the AMPK/mTOR pathway malfunction is prolonged, the hyperlipidemic conditions may be explicit [313], which are activated by natural herbal mediators, polyphenols [357,358], and dietary antioxidant [359].

Polyphenols target AMPK, activate the AMPK signaling pathway, and influence lipid metabolism [360] and ROS-mediated energy stress [361,362]. Indeed, polyphenolic AMPK activation results in lipogenesis inhibition and lipophagy [363] through SREBP1/PPAR/AMPK pathway [364], JAK2 [365,366], sirt1 [367]. In addition, polyphenols in mid-white adipose tissue prevent lipotoxicity [368]. In addition, cholesterol efflux mediated polyphenols lipid-lowering effects, consulting LXR pathway [369]. LXR cumulates hepatic lipids and reacts to cholesterol at the extreme upper level through SREBP1 [370].

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All these pathways accede to AMPK eventually [186], which may directly or indirectly inhibit via polyphenolic compounds [371]. AMPK also inhibits SREBP1, which reduces hepatic lipogenesis [372], and triglyceride [332], regulating PI3K/AKT pathway [373], induces sirt1, which progresses PGC1 α deacetylation and regulates mitochondrial biogenesis [374]. All these clues persist on direct or indirect AMPK-mediated polyphenolic anti-hyperlipidemic effects [375], resulting in a new hyperlipidemia therapeutic approach.

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