Mammalian Target of Rapamycin Signaling in Cardiac Physiology and Disease

Sebastiano Sciarretta, Massimo Volpe, Junichi Sadoshima

Abstract: The protein kinase mammalian or mechanistic target of rapamycin (mTOR) is an atypical serine/threonine kinase that exerts its main cellular functions by interacting with specific adaptor proteins to form 2 different multiprotein complexes, mTOR complex 1 (mTORC1) and mTOR complex 2 (mTORC2). mTORC1 regulates protein synthesis, cell growth and proliferation, autophagy, cell metabolism, and stress responses, whereas mTORC2 seems to regulate cell survival and polarity. The mTOR pathway plays a key regulatory function in cardiovascular physiology and pathology. However, the majority of information available about mTOR function in the cardiovascular system is related to the role of mTORC1 in the unstressed and stressed heart. mTORC1 is required for embryonic cardiovascular development and for postnatal maintenance of cardiac structure and function. In addition, mTORC1 is necessary for cardiac adaptation to pressure overload and development of compensatory hypertrophy. However, partial and selective pharmacological and genetic inhibition of mTORC1 was shown to extend life span in mammals, reduce pathological hypertrophy and heart failure caused by increased load or genetic cardiomyopathies, reduce myocardial damage after acute and chronic myocardial infarction, and reduce cardiac derangements caused by metabolic disorders. The optimal therapeutic strategy to target mTORC1 and increase cardioprotection is under intense investigation. This article reviews the information available regarding the effects exerted by mTOR signaling in cardiovascular physiology and pathological states. (Circ Res. 2014;114:549-564.)

Key Words: autophagy ■ heart ■ hypertrophy ■ ischemia ■ metabolism ■ mechanistic target of rapamycin complex 1 ■ sirolimus

The protein kinase mammalian target of rapamycin (mTOR) was purified and characterized for the first time in mammalian cells in the independent works conducted by Brown et al., Sabatini et al., and Sabers et al. in 1994 and 1995. mTOR is an atypical serine/threonine kinase that exerts its main cellular functions by interacting with specific adaptor proteins to form 2 distinct multiprotein complexes, mTOR complex 1 (mTORC1) and mTOR complex 2 (mTORC2). mTOR signaling plays a key role in the regulation of cell homeostasis and stress responses. mTORC1 is a master regulator of protein synthesis, cell growth and proliferation, ribosomal and mitochondrial biogenesis, autophagy, and metabolism. In addition, mTORC1 inhibition during stress is an adaptive response that promotes the upregulation of stress responsive mechanisms. Whereas, mTORC2 seems to regulate cell survival and polarity (Figure 1).

Studies of animal models with loss of function of the components of mTOR complexes have indicated that mTOR is involved in the regulation of embryonic cardiovascular development and in the control of vital cellular processes necessary for normal postnatal growth and maintenance of cardiac function. Cardiac deletion of mTOR is associated with a high rate of embryonic lethality, and cardiac disruption of the components of mTORC1 is associated with cardiac dilation, dysfunction, apoptosis, mitochondrial and metabolic derangements, heart failure, and, ultimately, mortality in the postnatal stage. In addition, complete genetic disruption of mTORC1 impairs the ability of the heart to respond to pressure overload and to undergo compensatory hypertrophy, resulting in the development of dilated cardiomyopathy. However, the available evidence suggests that partial and selective inhibition of mTORC1 is cardioprotective during aging and cardiac stress. mTORC1 inhibition extends the life span of mice. It also reduces cardiac hypertrophy and improves cardiac function in the presence of pressure overload and genetic cardiomyopathies and reduces ischemic injury after acute and chronic myocardial infarction. Finally, the inhibition of mTORC1 reactivates cardiac autophagy, which is impaired in the presence of obesity and metabolic syndrome. These results are likely dependent on the fact that partial inhibition of mTORC1 eliminates the detrimental effects of the maladaptive functions of mTORC1 during cardiac stress, while maintaining its physiological functions. In this regard, it is known that rapalogs do not inhibit all the functions of mTORC1.

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The degree of mTORC1 inhibition and the mTORC1 physiological functions needed to be preserved to convert mTORC1 inhibition from detrimental into beneficial during cardiac stress are unclear. In contrast, information about the pathophysiological functions of mTORC2 in the heart is still scarce.

This article reviews and interprets the evidence currently available regarding the role of mTOR signaling pathway in cardiovascular physiology and disease (Table).

Biology of the mTOR Pathway

The mTOR kinase is an atypical serine/threonine kinase of 289 kDa and belongs to the family of phosphoinositide 3-kinase. It is encoded by a single gene in mammals, but it exerts its main cellular functions by forming mTORC1 and mTORC2 through assembly with specific adaptor proteins.3–8 mTORC1 and mTORC2 signaling pathways are evolutionarily conserved, and these represent the functional homologs of yeast TOR1 and TOR2. However, TOR1 and TOR2 are encoded by distinct genes in yeast, as first identified in Michael Hall’s laboratory in 1991.25 mTOR was isolated and cloned as a physical target of rapamycin through a cellular screening aimed at identifying the binding proteins of FK506-binding protein of 12 kDa–rapamycin complex.1–3 Rapamycin and its analogs bind to the cytosolic FK506-binding protein of 12 kDa, thereby forming a protein complex that only targets a specific domain of the mTOR protein when it is part of mTORC1. As a consequence of rapamycin–FK506-binding protein of 12 kDa binding, mTORC1 activity is strongly inhibited.4–8 Conversely, mTORC2 is relatively insensitive to rapamycin, although it has been demonstrated that prolonged treatment with rapamycin can also reduce the activity of mTORC2 by disrupting the complex.5,25 To date, proteins that are known to bind to mTOR in mTORC1 include regulatory-associated protein of mTOR (Rictor),35 stress-activated map kinase-interacting protein (S6K),36 protein observed with rictor,37 mammalian lethal with sec-13 protein (S6K),38 proline-rich Akt substrate 40 (PRAS40),39 and mammalian lethal with sec-13 protein 8 (S6K-1).40 However, based on available evidence, it is difficult to distinguish the function of 1 complex completely from the other. It has been shown that the 2 complexes are functionally interconnected, and most of the studies that investigated the role of mTORC1 in the regulation of cellular homeostasis did not precisely rule out the involvement of mTORC2 in these mechanisms. In general, much more is known about the biology of mTORC1 than that of mTORC2 (Figure 2). mTORC1 plays a crucial role in the regulation of cellular homeostasis, growth, and response to stress. The main functions of mTORC1 are promotion of protein synthesis and, subsequently, cellular growth. The most studied substrates of mTORC1 are S6 kinase-1 (S6K1) and eukaryotic translation initiation factor 4E (eIF4E)-binding protein-1 (4E-BP1). mTORC1 phosphorylates and activates S6K1, which in turn promotes mRNA biogenesis and activates the protein translation process. In contrast, mTORC1 inhibits 4E-BP1 and allows the formation of the eIF4E complex that triggers cap-dependent translation.4–8 Additionally, mTORC1 promotes protein synthesis through the translation of 5’ terminal oligopyrimidine tract mRNAs and the promotion of ribosomal biogenesis.4–8 This mechanism explains why mTORC1 activity is often found to be increased in cancer cells.4–8

**Figure 1. General cellular functions of mammalian target of rapamycin complex 1 (mTORC1) and mTORC2.** The figure summarizes the most well-characterized functions of mTORC1 and mTORC2. mTORC1 regulates protein synthesis and autophagy in response to growth factors and stress. mTORC2 is known to regulate cell growth, survival, and polarity. Akt indicates protein kinase B; and AMPK, adenosine monophosphate-activated protein kinase.

<table>
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<th>Nonstandard Abbreviations and Acronyms</th>
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<td>4E-BP1</td>
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(Continued)
mTORC1 also promotes cell proliferation by promoting the de novo synthesis of cellular membrane lipids through the sterol regulatory element-binding protein 1/2–dependent expression of lipogenic genes.338 However, mTORC1 not only activates anabolic processes but also inhibits catabolic processes. mTORC1 strongly inhibits autophagy, an evolutionarily conserved intracellular bulk degradation process responsible for cellular degradation of proteins and organelles.6,7,39,40 mTORC1 seems to regulate autophagy both at post-translational and transcriptional levels. It phosphorylates the autophagic protein unc-51-like kinase (ULK) 1/2, thereby inhibiting the macrocomplex ULK1/autophagy-related gene (Atg) 13/focal adhesion kinase family interacting protein-200 which promotes autophagosome formation.41 Additionally, mTORC1 activation inhibits the expression of autophagic proteins, particularly Atg7,23 which is crucial for the initiation of the autophagic process.39 It has been shown that mTOR significantly inhibits the p73 factor and the transcription factor EB that can induce autophagy through the upregulation of autophagic proteins, particularly Atg7,23 which is crucial for the initiation of the autophagic process.39 It has been shown that mTOR significantly inhibits the p73 factor and the transcription factor EB that can induce autophagy through the upregulation of autophagic proteins such as Atg7,23 which is crucial for the initiation of the autophagic process.41 Additionally, mTORC1 inhibition activates mTOR or inhibits PRAS40, an endogenous mTORC1 factor, Akt is activated and, in turn, phosphorylates and activates mTOR or inhibits PRAS40, an endogenous mTORC1 inhibitor.4,46,32,41,42 Whereas, AMPK, which is inactive in the presence of nutrients and high ATP levels, is strongly activated during energy deprivation and other types of cellular stress. AMPK activates the tuberous sclerosis protein (TSC) 1/TSC2 complex,45 which displays a strong GTPase activity and inhibits the small GTP-binding protein Ras homolog enriched in brain (Rheb), a direct mTORC1 activator.46 Glycogen synthase kinase (GSK) 3β can also activate the TSC1/TSC2 complex and inhibit mTORC1 during energy stress.45 Alternatively, regulated in development and DNA damage response 1, which is upregulated during hypoxia, activates TSC2 independently of AMPK and GSK-3β.55 Rheb can also be inhibited by p38-regulated/activated kinase during energy deprivation, independently of TSC2.52 Conversely, the Akt, extracellular signal regulated kinase (ERK) 1/2, and inhibitor of NF-κB kinase-β pathways inhibit the TSC1/TSC2 complex in response to growth factors and cytokines.53,55 Recently, a new mechanism promoting the activation of mTORC1 has been elucidated. In the presence of amino acids, Rag GTPases are activated and mediate mTORC1 translocation to lysosome membranes, where mTORC1 is activated by Rheb.56,57

Table. Continued

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<thead>
<tr>
<th>Cardiac Condition</th>
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<th>Type of mTOR Modulation and Animal Model</th>
<th>Effect on the Heart</th>
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<td>Metabolic disorders</td>
<td>Wang et al124</td>
<td>Rapamycin treatment during high-fat diet–induced obesity</td>
<td>Akt and mTOR are activated in the vasculature of obese animals; rapamycin inhibits endothelial senescence and the susceptibility to peripheral ischemia in obese animals</td>
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<td>Sciarretta et al23</td>
<td>Rapamycin treatment and partial inducible mTOR genetic disruption in mice with high-fat diet–induced obesity and metabolic syndrome subjected to prolonged ischemia</td>
<td>Ischemia-induced autophagy activation is inhibited in the hearts of obese animals through deregulated activation of Rheb and mTORC1; infarct size after ischemia is larger in obese animals; pharmacological and partial genetic inhibition of mTOR rescue autophagy and reduce ischemic injury in obese mice</td>
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<td></td>
<td>Li et al126</td>
<td>Swine model of metabolic syndrome</td>
<td>Increased cardiac mTOR level and reduction of cardiac autophagy that is proportional to the degree of derangements of cardiac structure and function</td>
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<td>Guo et al27</td>
<td>Rapamycin in mice with high-fat diet–induced obesity</td>
<td>Increased mTOR activity and reduced autophagosome formation in the hearts of obese mice, associated with a reduction of cardiac function; cardiac function is rescued by rapamycin and deteriorated by genetic adiponectin disruption</td>
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<td>Xu et al128</td>
<td>Mice with systemic Akt2 knockout subjected to high-fat diet</td>
<td>mTOR activation and disruption of autophagic flux in the hearts of obese mice; Akt2 deletion rescues autophagic flux and cardiac dysfunction in obese animals</td>
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<td>Xu et al129</td>
<td>Streptozotocin-induced diabetes mellitus</td>
<td>Cardiac autophagosome formation and flux are impaired in diabetic mice; these effects are associated with increased mTOR activity</td>
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AAV9 indicates adeno-associated virus 9; Akt, protein kinase B; GSK-3β, glycogen synthase kinase-3β; i/R, ischemia/reperfusion; LEOPARD, Lentigines, ECG conduction abnormalities, Ocular hypertelorism, Pulmonic stenosis, Abnormal genitalia, Retardation of growth and sensorineural Deafness; mTOR, mammalian target of rapamycin; mTORC1, mTOR complex 1; NF-κB, nuclear factor-κB; PRAS40, proline-rich Akt substrate 40; Rheb, Ras homolog enriched in brain; Rictor, rapamycin-sensitive companion of mTOR; S6K, S6 kinase; and TAC, transverse aortic constriction.
This process seems to be negatively regulated by microtubule-associated protein/microtubule affinity-regulating kinase 4, independently of Rheb activity.\(^5^8\)

mTORC2 can be activated by insulin and growth factors, whereas it is relatively insensitive to nutrient deprivation.\(^5^,^6^\)

The phosphoinositide 3 kinase (PI3K) pathway was shown to activate mTORC2,\(^5^9\) and it seems that the TSC1/2 complex does as well.\(^6^0\) mTORC1 seems to inhibit mTORC2 through phosphorylation of Rictor,\(^6^1\) suggesting that mTORC1 and mTORC2 are functionally interconnected. This hypothesis is also strongly supported by the fact that the best known substrate of mTORC2 is Akt, which is phosphorylated at serine 473, particularly in response to insulin.\(^6^2,^6^3\)

The biological importance of mTORC2-dependent phosphorylation of Akt is not yet understood, because it has been shown that mTORC2 is dispensable for Akt phosphorylation in certain cell types and conditions.\(^6^4\) Both protein kinase C-\(\alpha\)\(^6^5\) and serum- and glucocorticoid-induced protein kinase-1 (SGK-1)\(^6^6\) have been shown to be substrates of mTORC2, despite mTORC1 also being shown to regulate SGK-1.\(^6^7\) Whether SGK-1 exerts different functions in cardiomyocytes when it is activated by mTORC1 or mTORC2 is unclear. The most studied function of mTORC2 is the regulation of survival and growth, likely through the regulation of Akt and SGK-1. SGK-1 has been shown to promote cardiomyocyte survival while inhibiting hypertrophy,\(^6^8\) whereas SGK-1 chronic activation during heart failure is detrimental.\(^6^9\)

mTORC2 also regulates cell polarity and cytoskeletal organization through the regulation of protein kinase C-\(\alpha\) and Ras homolog gene family member A.\(^7^0\)

Protein kinase C-\(\alpha\) has also been shown to negatively regulate cardiac contractility.\(^7^1\)

### Role of mTOR Signaling in the Regulation of Cardiac Homeostasis and Physiological Growth

Given its myriad cellular functions, it is not surprising that mTOR kinase is necessary for normal regulation of cardiomyocyte homeostasis and growth during both development and postnatal period (Figure 3). Systemic mTOR- and Raptor-knockout embryos die early during development, right after implantation.\(^8^0\) However, embryos with constitutive \(\alpha\)-MHC-Cre-mediated mTOR deletion also display a dramatic mortality starting around E13.5, with only 8% of embryos surviving the developmental stage. Cardiac-specific mTOR-knockout embryos present a significant reduction in cardiomyocyte...
proliferation and an increase in apoptosis, with a 34% reduction in cardiomyocyte number. As a result, cardiac-specific mTOR-knockout embryos present cardiac dilation and dysfunction, with signs of terminal cardiac failure. Consistent with these results, systemic deletion of the *rheb1* gene that extensively reduces mTORC1 activity is embryonically lethal, most likely because of cardiac defects such as ventricular wall thinning and cardiomyocyte apoptosis. Global *rictor* gene deletion that selectively disrupts mTORC2 is also lethal in the developmental stage, and embryos with *rictor* deletion display significant cardiovascular abnormalities. Thus, both mTORC1 and mTORC2 are highly important for cardiac development and embryo survival.

The mTOR pathway also seems vital for the maintenance of cardiac structure and function in the postnatal period and adulthood. Mice with *α*-MHC-Cre–mediated cardiac mTOR disruption that are born alive die within a few weeks after birth from massive cardiac dilation, dysfunction, and heart failure. mTOR-knockout mice present with derangements in fatty acid metabolism in the heart. Inducible cardiac-specific mTOR deletion in adulthood also leads to cardiac dysfunction and heart failure, with chamber dilation and wall thinning. mTOR-knockout mice display massive apoptosis, fibrosis, autophagy, mitochondrial abnormalities and dysfunction, sarcomere disarray, and ultimately death <8 weeks after tamoxifen-induced gene deletion. There is a reduction in S6K activity in the hearts of these mice, a surprising overactivation of Akt phosphorylation at serine 473, despite the inactivation of mTORC2, and a marked and progressive accumulation of 4E-BP1. Concomitant ablation of the *Eif4ebp1* gene partially rescues the detrimental effects of mTOR ablation in knockout mice. These data suggest that the main detrimental effect of mTOR deletion in cardiomyocytes is the inhibition of cap-dependent protein translation. Mice with inducible cardiac-specific *raptor* deletion also progressively develop cardiac dilation and dysfunction associated with apoptosis, autophagy, and mitochondrial abnormalities. Raptor-knockout mice die a few weeks after cardiac-specific tamoxifen-induced gene deletion. A switch from fatty acid to glucose oxidation is observed in Raptor-knockout mice. Mice with constitutive *α*-MHC-Cre–mediated cardiac *rheb1* deletion display a dramatic inhibition of the cardiac mTORC1 pathway 5 days after birth, but mTORC1 activity is maintained until ≤3 days after birth. This suggests that Rheb regulates mTORC1 in the heart only in the postnatal period. Rho-knockout mice also rapidly develop cardiac dilation and dysfunction and die ≤10 days after birth. This dramatic phenotype is accompanied by a defect in cardiomyocyte growth and sarcomere disarray. Rheb-knockout mice do not show increased cardiomyocyte apoptosis and may not die during gestation, differing somewhat from the constitutive cardiac-specific mTOR-knockout phenotype. Again, genetic deletion of the *Eif4ebp1* gene partially rescues the phenotype of Rheb-knockout mice. Conversely, genetic disruption of *atg5* does not rescue the cardiac phenotype of Rheb-knockout mice, thus ruling out the involvement of autophagy in these mechanisms. Of note, a significant increase in the LC3II/I ratio was observed in the hearts of Rheb-knockout mice, which suggests an increase in autophagy. However, the absolute LC3II level was not found to be increased in these mice, in which Rheb deletion is constitutive (chronic). The apparent discrepancy between these mice and those with inducible (acute) mTOR or raptor gene deletion, in which the cardiac LC3II level is significantly increased, may be explained by the fact that LC3 is rapidly degraded when autophagic flux is chronically activated, making it more difficult to observe.

**Figure 3.** Role of mammalian target of rapamycin (mTOR) in the regulation of cardiac homeostasis. mTOR is required for cardiomyocyte growth and for the preservation of cardiac structure and function in unstressed conditions. However, partial inhibition of mTOR seems to be beneficial during the aging process. The pharmacological modulators of mTOR and the animal models with genetic modifications of the components of mTOR signaling pathway that have been used in the studies focused on the role of mTOR in cardiac physiology are displayed. KO indicates knockout; mTORC1, mTOR complex 1; Raptor, regulatory-associated protein of mTOR; Rheb1, Ras homolog enriched in brain 1; and ROS, reactive oxygen species.
any significant LC3II accumulation. 72 Collectively, these data indicate that mTORC1 is required for the maintenance of cardiac structure and function and regulation of cellular metabolism in the postnatal period. No evidence is available thus far regarding the specific role of mTORC2 in the heart in unstressed conditions.

However, although complete deletion of the mTOR pathway in the heart is not compatible with life, both pharmacological and partial genetic disruption of mTORC1 exert beneficial effects during the aging process and seem to increase cardiomyocyte resistance to aging stress. mTORC1 inhibition extends life span in lower organisms, 4–8 and pharmacological and partial genetic inhibition of mTOR extends life span in mammals. 13–15 Rapamycin treatment significantly extended life span in mice, regardless of whether it was started early or late in life. 13 Mice with hypomorphic mTOR alleles also live longer, with a significant reduction in the age-dependent functional decline of some organs. 15 S6K1 genetic disruption increases life span in female, though not in male, mice. 73 These beneficial effects may be because of a reduction in energy expenditure over time, inhibition of protein synthesis with reduced cellular senescence and misfolded protein accumulation, renewal of the endogenous stem cell pool, improvement of mitochondrial function, and reduction of reactive oxygen species and activation of autophagy. 5,7,64 mTOR inhibition might also be beneficial during aging, particularly in the presence of obesity, through an increase in skeletal muscle insulin sensitivity due to an interruption of the negative feedback on insulin receptor substrate-1 by mTORC1. 74,75 However, it has been demonstrated that chronic rapamycin treatment causes a diabetes mellitus–like syndrome because of a loss of pancreatic β-cells. 75,76 Pharmacological mTOR inhibition has been shown to reduce age-related cardiac abnormalities, such as cardiac hypertrophy and systolic dysfunction. Rapamycin treatment reduced age-induced cardiac inflammation and fibrosis and upregulated genes involved in metabolic function and energy metabolism, 74–76 in line with the rapamycin-induced increase in mitochondrial function. 4,44 Accordingly, caloric restriction, which also increases life span in lower organisms and mammals, was shown to improve diastolic function and reduce cellular senescence in aged hearts, and these effects were associated with a reduction in mTORC1/S6K pathway signaling. 5,8,77

Chronic mTOR activation seems to accelerate the cardiac aging process. Obesity and metabolic syndrome, which are associated with chronic cardiac activation of mTOR, accelerate cardiac aging. 23,78,79 Mice with systemic GSK-3α deletion present with cardiac hypertrophy, dysfunction, and sarcomere abnormalities during aging because of deregulated activation of mTORC1 and inhibition of autophagy. 90 This indicates that GSK-3α is an important negative regulator of mTORC1 function during aging. Chronic Akt1 activation, which activates mTORC1, was shown to worsen aging-induced cardiac hypertrophy and myocardial contractile dysfunction through inhibition of autophagy. 91 This further suggests a potential role of autophagy in the beneficial effects of mTORC1 inhibition during aging. A recent study confirmed that rapamycin extends life span but failed to demonstrate that it prevents senescence in the cardiovascular system. 82 Therefore, additional studies are needed to elucidate the actual impact of mTORC1 inhibition on age-related cardiac abnormalities.

Role of mTOR Signaling in the Regulation of Cardiac Hypertrophy

The mTOR pathway seems to play a key role in the development of cardiac hypertrophy (Figure 4). This is not particularly surprising if we consider that cardiac hypertrophy is a process that requires a marked increase in the synthesis of sarcomeric proteins and that the mTOR pathway is a master promoter of protein synthesis. mTORC1 activity is increased during the cardiomyocyte hypertrophic response to β-adrenergic stimulation. 83 Angiotensin-II, 44 and insulin growth factor-1, 85 and inhibition of mTORC1 inhibits hypertrophy development. mTORC1 is activated during physiological hypertrophy induced by physical exercise and during pathological hypertrophy induced by transverse aortic constriction (TAC) and spontaneous hypertension. However, there is evidence that mTORC1 is later inactivated when cardiac function deteriorates and heart failure develops. 10,11,86 The PI3K/Akt pathway contributes significantly to the activation of mTORC1 during the development of cardiac hypertrophy, particularly in response to physical exercise. 18,87,88 However, β-adrenergic signaling, the ERK pathway, and nitric oxide signaling are also involved in the activation of mTORC1 during the development of cardiac hypertrophy. 83,89,90 Furthermore, biomechanical activation of transient receptor potential channels and focal adhesion kinase promote mTORC1 activation during pressure overload. 91,92 and glucose-6-phosphate accumulation contributes to mTORC1 activation in the overloaded heart as well. 81 Thus, a complex network of mechanical, biochemical, and metabolic signals is sensed by mTORC1 signaling during cardiac pressure overload.

mTOR inhibition significantly reduces cardiac hypertrophy. Mice with inducible cardiac-specific mTOR or raptor deletion do not develop compensatory hypertrophy in response to pressure overload and rapidly develop ventricular dilation and cardiac dysfunction associated with apoptosis, autophagy, and mitochondrial derangements. 10,11 Protein synthesis in these animals is significantly reduced. These observations indicate that mTOR is necessary for the development of compensatory cardiomyocyte growth and for cardiac adaptation to pressure overload. Total disruption of mTOR signaling not only abrogates hypertrophy but also impairs the capacity of the heart to adapt to stress.

In contrast, partial genetic and pharmacological inhibition of mTORC1 seems to inhibit pathological cardiac hypertrophy while still maintaining the ability of the heart to adapt to increased load (Figure 4). Rapamycin pretreatment blunts cardiac hypertrophy development in response to pressure overload. 16 Rapamycin administration also regresses both established compensated and decompensated cardiac hypertrophy induced by TAC and improves cardiac function in mice with decompensated hypertrophy. 97 Rapamycin activates Akt, promotes protein ubiquitination, and inhibits apoptosis in the pressure-overloaded rat myocardium, 94 and it reduces cardiac hypertrophy and fibrosis in spontaneously hypertensive rats. 95 Mice with heterozygous cardiac-specific rheb1 deletion show reduced activation of mTORC1 during pressure overload and improved cardiac function during pathological hypertrophy.
overload and reduced cardiac hypertrophy and fibrosis.19 The mTORC1 inhibitor astragaloside IV also reduces hypertrophy and fibrosis during pressure overload.19 An interesting study recently showed that mTORC1 is activated during pressure overload through Akt-dependent inactivation of PRAS40. Cardiac overexpression of PRAS40 inhibited mTORC1 signaling, prevented cardiac hypertrophy development during TAC, and even reduced established TAC-induced hypertrophy. Importantly, PRAS40 overexpression preserved cardiac function during long-term pressure overload and reduced fibrosis.18 A constitutively active form of PRAS40 was also able to reduce the development of physiological hypertrophy in response to physical exercise.18 This is consistent with the evidence that PI3K inhibition and Akt1 disruption blunt the establishment of physiological hypertrophy in response to exercise.87,88 However, whether this effect is dependent on mTORC1 activation still needs to be addressed. In fact, it has been shown that cardiomyocyte-restricted overexpression of a dominant negative form of mTOR that efficiently inhibits mTORC1 signaling does not affect the development of either exercise-induced or isoproterenol-induced hypertrophy.97 Additional studies of the mTORC1 components using loss-of-function animal models would be useful to further investigate this issue. Furthermore, it will be important to elucidate the downstream signals that mediate the prohypertrophic effects of mTORC1. Of note, existing evidence indicates that S6Ks are not involved in the regulation of either physiological or pathological hypertrophy,98 whereas it is likely that 4E-BPs play a role.10

Although a considerable amount of evidence indicates that mTORC1 activation is absolutely required for the development of pathological cardiac hypertrophy, it seems that mTORC1 activation alone is not sufficient to induce cardiac hypertrophy. In fact, neither constitutively active nor wild-type mTOR overexpression can reverse the development of pathological hypertrophy induced by pressure overload in the mouse heart. The most reasonable explanation for the lack of induction of hypertrophy by mTOR overexpression is the existence of multiple signaling pathways that are modulated and contribute in an integrated manner to the synthesis of sarcomeric myofibrils and increase cardiomyocyte volume during the establishment of pathological hypertrophy. Each of these pathways is strictly required for inducing hypertrophy, but if they are activated individually, particularly in the absence of a mechanical load, they cannot induce hypertrophy. Of note, Song et al99 showed that cardiac overexpression of wild-type mTOR preserves cardiac function during pressure overload through the inhibition of nuclear factor-κB (NF-κB) signaling and myocardial inflammation, in apparent disagreement with the beneficial effects of mTORC1 inhibition discussed above. mTOR overexpression did not significantly increase mTORC1 signaling during TAC in this study; instead, it actually decreased phosphorylation of S6K. Therefore, it is possible that, in the specific transgenic mouse model described in this article, overexpressed mTOR preferentially modulates signaling pathways that are cardioprotective without activating maladaptive signals. The activation of mTORC2 by mTOR overexpression may also contribute to the preservation of cardiac function during TAC. Unfortunately, information on the specific role of mTORC2 in the regulation of cardiomyocyte growth and cardiac adaptation to pressure overload is scarce, and no studies on cardiac-specific mTORC2 using loss-of-function animal models have been published.

Therefore, mTORC1 seems to be a potentially highly therapeutic target for treating human diseases associated with pathological cardiac hypertrophy and cardiomyopathy. In mouse models of LEOPARD (Lentigines, ECG conduction abnormalities, Ocular hypertelorism, Pulmonic stenosis, Abnormal genitalia, Retardation of growth and sensorineural Deafness) disease, which is caused by a mutation of the PTPN11 gene that abolishes the catalytic activity of the SH2 domain–containing protein tyrosine phosphatase-2 protein, cardiac ERK/mitogen-activated protein kinase signaling is inactivated and mTOR activity is increased in a deregulated manner. LEOPARD disease is characterized by the presence of...
of hypertrophic cardiomyopathy, myocardial disarray, fibrosis, conduction defects, and cardiac dysfunction. mTORC1 inhibition by rapamycin completely rescues the cardiac phenotype of these animals. In a model of hypertrophic cardiomyopathy caused by a mutation of the TRIM63 gene encoding for the muscle RING-finger protein-1, cardiac mTOR was also found to be activated. Cardiac mTOR activation and autophagy inhibition were observed even in mouse models of cardiomyopathy caused by Lamin A/C gene mutation, through ERK1/2-dependent activation of dual specificity protein phosphatase 4. Pharmacological mTORC1 inhibition reactivated autophagy and significantly improved cardiac function, muscle dystrophy, and survival of these animals. These effects were associated with a reduction of abnormal desmin accumulation. Overall, these results indicate that deregulated cardiac mTORC1 activation is the pathophysiological mediator of cardiac hypertrophy and dysfunction in different types of cardiomyopathy. The exception to this general observation is represented by doxorubicin-induced cardiomyopathy, in which mTOR signaling inhibition seems to contribute to a reduction of cardiac mass and development of cardiac dysfunction independently of cardiomyocyte apoptosis. Thus, it seems that, in this condition, the combination of doxorubicin toxicity and mTOR inhibition affects cardiomyocytes detrimentally by promoting cardiac atrophy. Whether an exaggerated activation of autophagy plays a role in the detrimental effects induced by doxorubicin is unclear.

Role of mTOR Signaling in Ischemic Injury

Accumulating lines of evidence indicate that mTOR regulates cardiomyocyte response to energy deprivation and ischemia (Figure 5). In lower organisms and mammalian cell lines, mTORC1 is inhibited during energy deprivation. mTORC1 inhibition preserves the energy status through the reduction of cellular energy expenditure and activation of autophagy and, thus, promotes survival. Through these effects, mTORC1 inhibition is required for postnatal survival before lactation begins and preserves skeletal muscle integrity and function. Similarly, rapamycin promotes the survival of nutrient-deprived cardiomyocytes through autophagy activation. We recently demonstrated that mTORC1 is inhibited during cardiomyocyte energy deprivation and ischemia through the inhibition of Rheb. Forced reactivation of Rheb/mTORC1 signaling inhibited autophagy activation in energy-deprived cardiomyocytes through Atg7 inhibition and promoted cardiomyocyte death both in vitro and in vivo. This effect was associated with the depletion of ATP levels and misfolded protein accumulation. Whereas, the inhibition of Rheb/mTORC1 signaling pathway limited cardiomyocyte death during energy stress. These results indicate that Rheb is a main regulator of mTORC1 during cardiomyocyte energy stress and that Rheb/mTORC1 inhibition is an adaptive cellular response that promotes survival through activation of autophagy. In fact, when autophagy was restored in Rheb-overexpressing cardiomyocytes, cell survival was rescued during energy stress. Autophagy is also regulated during energy deprivation through mTORC1-independent mechanisms, such as AMPK-dependent ULK1 phosphorylation, phosphorylation/activation of TIP60 by GSK-3β, which in turn activates ULK1, and production of reactive oxygen species by Nox4 in the endoplasmic reticulum. However, Rheb/mTORC1 inhibition is a required signaling event to promote autophagy activation in energy-deprived cardiomyocytes in tight coordination with other pathways regulating the autophagic machinery. Of note, we previously observed that, during prolonged myocardial ischemia without reperfusion, the inhibition of GSK-3β activation was associated with autophagy inhibition and increased ischemic injury through mTORC1 reactivation, which was rescued by rapamycin treatment. The inhibition of AMPK activation in the ischemic heart also led to decreased autophagy and increased ischemic injury. Therefore, based on our findings, we propose that Rheb integrates the signals from AMPK and GSK-3β in ischemic cardiomyocytes, thereby mediating mTORC1 inhibition and autophagy activation.

mTORC1 inhibition also seems to be beneficial during chronic ischemic injury (Figure 5). mTORC1 is activated in the remote myocardium during chronic myocardial infarction as a consequence of increased load and contributes to ventricular remodeling. Pharmacological mTORC1 inhibition with everolimus reduces cardiac dilation and infarct size and improves cardiac function during chronic myocardial infarction. These effects are associated with the activation of autophagy and inhibition of proteosome activity. Mice with partial cardiac Rheb deletion display better cardiac function after experimental myocardial infarction and a reduction of infarct size and cardiac dilation as compared with control mice, thus corroborating our evidence of a beneficial effect of Rheb inhibition during acute ischemia. Rapamycin and S6K inhibitors reduce cardiac ischemic remodeling and cardiomyocyte apoptosis through phosphoinositide-dependent kinase-1–dependent activation of the Akt pathway. Volkers et al provided compelling evidence that the balance between mTORC1 and mTORC2 activity is important for the regulation of ischemic damage and cardiac remodeling after myocardial infarction. They demonstrated that cardiac overexpression of PRAS40 inhibits mTORC1; reduces ischemic injury, apoptosis, and cardiac remodeling; and improves cardiac function through the preservation of sarco/endoplasmic reticulum Ca2+-ATPase 2a function during chronic myocardial infarction. The protective effects of PRAS40 were mediated by mTORC2 and by activation of the Akt pathway. Conversely, mTORC2 inhibition by in vivo adenovirus 9–mediated cardiac Rictor knockdown caused deterioration of cardiac function and remodeling after myocardial infarction. Therefore, although this study confirms the beneficial effects of mTORC1 inhibition during ischemic injury, it also demonstrates that mTORC2 promotes survival under ischemic conditions and highlights the importance of developing new selective mTORC1 inhibitors that do not affect or possibly even increase mTORC2 activity. PRAS40 or Rheb inhibitors could be suitable drugs for this purpose. Additional studies should be conducted to elucidate the substrates that mediate the protective effects of mTORC2 in the ischemic heart. Akt1 is certainly one of these. Previous studies demonstrated that, in some cases, genetic inhibition of PI3K or Akt1 can confer beneficial effects to the ischemic heart. Therefore, it is likely that mTORC2 also protects the ischemic heart through other Akt1-independent mechanisms.
In this regard, in a recent elegant work, mTOR overexpression was found to reduce cardiomyocyte death partially during hypoxia in vitro through mTOR-dependent direct activation of NF-κB and inhibition of BCL2/adenovirus E1B 19 kDa protein–interacting protein 3 expression. It will be interesting to evaluate the relative contribution of mTORC2 activation by mTOR overexpression with respect to mTORC1 in regulating these mechanisms. This intriguing hypothesis would also be consistent with the evidence that mTORC2 activates Akt1 and that Akt1 is a positive regulator of NF-κB.

The role of mTOR signaling in reperfusion injury is still controversial (Figure 5). mTORC1 is rapidly activated in the heart during reperfusion. Rapamycin reduces infarct size in ex vivo and in vivo ischemia/reperfusion models through the activation of the Janus kinase 2/signal transducer and activator of transcription 3 signaling pathway when administered before ischemia. Simvastatin reduces ischemia/reperfusion injury through the inhibition of mTOR and activation of mitophagy. Whereas, rapamycin was not cardioprotective during ischemia/reperfusion when administered before the reperfusion phase. We previously observed that the inhibition of GSK-3β in transgenic mice with cardiac-specific overexpression of dominant negative GSK-3β reduces reperfusion injury through mTORC1 hyperactivation. These results suggest that mTORC1 may exert some protective effects during the reperfusion phase. We found that mTORC1 activation by GSK-3β inhibition reduces reperfusion injury by limiting exaggerated activation of autophagy, which is maladaptive. Alternatively, mTORC1 may regulate mitochondrial permeability transition pore opening; promotes mitochondrial biogenesis, which may favor cardiac recovery after ischemia; and may promote the upregulation of antioxidant genes through the activation of PGC-1α.

Consistent with the idea that mTORC1 exerts a protective role in ischemia/reperfusion, mTORC1 inhibition is protective during ischemia through the upregulation of adaptive mechanisms. Whereas, mTOR is reactivated during reperfusion and takes part in the regulation of physiological processes. The pharmacological modulators of mTOR and the animal models with genetic modifications of the components of mTOR signaling pathway that have been used in the studies focused on the role of mTOR in ischemia/reperfusion are displayed. AMPK indicates adenosine monophosphate-activated protein kinase; ER, endoplasmic reticulum; GSK-3β, glycogen synthase kinase-3β; HET, heterozygous; KO, knockout; mPTP, mitochondrial permeability transition pore; PRAS40, proline-rich Akt substrate 40; Rheb, Ras homolog enriched in brain; ROS, reactive oxygen species; and S6K, S6 kinase.
effect during reperfusion damage, a recent study found that cardiac-specific mTOR overexpression reduces chronic cardiac remodeling after in vivo ischemia/reperfusion. Although the effects of mTOR overexpression on acute ischemic injury after ischemia/reperfusion were not evaluated in vivo, mTOR overexpression was found to reduce necrosis, as evaluated by Evans blue dye perfusion, and myocardial inflammation in an ex vivo model of ischemia/reperfusion.\(^\text{11}\) It is also possible that, in this study, the protective effects mediated by mTOR overexpression are dependent on mTORC2 activation, which is required for cardiomyocyte survival during ischemia and limitation of chronic ischemic remodeling.\(^\text{26}\) Collectively, these data indicate that mTORC1 inhibition is protective during ischemia through the activation of autophagy, reduction of protein synthesis, and subsequent activation of mTORC2. Whereas, mTORC1 seems to potentiate physiological mechanisms during reperfusion. Ideally, mTORC1 should be inhibited before an ischemic episode and reactivated at the time of reperfusion in patients with an acute myocardial infarction. However, in the clinical setting, patients with acute myocardial infarction usually experience prolonged periods of ischemia before coronary perfusion can be reestablished. Furthermore, in certain cases, coronary flow is not restored or coronary reperfusion is not indicated. Ischemia is a major determinant of myocardial damage in patients with acute coronary syndrome.\(^\text{120}\) Therefore, it is likely that, in patients with acute myocardial ischemia, the beneficial effects of mTORC1 inhibition largely overcome the potential harmful effects during reperfusion. Additional studies are needed to better understand this issue.

**Role of mTOR in the Regulation of Cardiac Metabolism**

mTOR signaling seems to be deeply involved in the regulation of cardiac metabolism. In mice with cardiac mTOR disruption induced in adulthood, fatty acid oxidation was significantly decreased, whereas glucose oxidation was increased.\(^\text{121}\) The expression of fatty acid metabolism genes, such as fatty acid-binding protein 3, medium-chain acyl-CoA dehydrogenase, and hydroxacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein)-α and -β, was reduced, and carnitine palmitoyl transferase-1 and -2 enzymatic activities were also decreased. These metabolic abnormalities were not associated with a reduction in the abundance of PGC-1α, a master regulator of fatty acid oxidation genes.\(^\text{121}\) In contrast, in cardiac-specific Raptor-knockout mice, significant downregulation of ERRα, PGC-1α, and peroxisome proliferator-activated receptor-α was observed.\(^\text{11}\) Again, fatty acid oxidation was reduced and glucose utilization was increased in the hearts of Raptor-knockout mice. This was accompanied by a reduction in carnitine palmitoyl transferase-1β and malonyl-CoA decarboxylase-1 expression levels. Importantly, all these changes were observed in mTOR- and Raptor-knockout mice while cardiac function was still preserved. In Raptor-knockout mice, a reduction of mitochondrial content was also seen after TAC, which is consistent with a reduction of PGC-1α, because PGC-1α promotes mitochondrial biogenesis and function.\(^\text{11}\) Of note, recent evidence suggests that mTOR can also promote cardiomyocyte mitochondrial function in response to insulin through the regulation of NF-κB.\(^\text{122}\)

However, mTOR not only regulates metabolism but is also affected by metabolic alterations. It is now well established that tissue mTORC1 activity is increased in the presence of nutritional excess, obesity, and metabolic syndrome (Figure 6).\(^\text{4,7,25}\) Deregulated mTORC1 activation further deteriorates the cellular metabolic status, promotes cellular senescence, and ultimately leads to organ dysfunction.\(^\text{4,6,7,25,123}\) AMPK is usually inhibited under these conditions, suggesting that it is involved in a main intracellular mechanism leading to mTORC1 activation. It is possible that Rag GTPases also contribute to organ mTORC1 activation in obesity and metabolic syndrome. In the presence of metabolic alterations, it is known that increased energy status, high cardiac and circulating levels of lipids and amino acids, hyperinsulinemia, and increased serum levels of cytokines and adipokines would all likely lead to the activation of mTORC1 signaling.\(^\text{5,4,7,25,123}\)

In dietary and genetic models of obesity and metabolic syndrome, basal mTORC1 activity was found to be increased in the liver, where it promotes insulin resistance, contributes to dyslipidemia, and may predispose to cancer development, in adipose tissue, where it promotes fat deposition, in the kidney where it causes autophagy inhibition and podocyte loss, in skeletal muscle where it promotes insulin resistance and fat deposition, and, ultimately, in the vasculature and the heart.\(^\text{4,6,7,25,123}\) High-fat diet–induced obesity leads to an increased activation of the Akt/mTOR pathway in the vascu- lature, which causes endothelial senescence and increases the susceptibility to peripheral ischemia. These effects are rescued by rapamycin.\(^\text{124}\) We recently found that, in a model of dietary obesity and metabolic syndrome, autophagy is suppressed in the heart through deregulated activation of Rheb and mTORC1 activity. This suggests that Rheb/mTORC1 activation contributes to pathological cardiac growth in obesity and metabolic disorders.\(^\text{125}\) We found that the activity of Rheb and mTORC1 remains higher during ischemia, which, in contrast, is associated with Rheb/mTORC1 inhibition in the hearts of lean animals.\(^\text{23}\) Accordingly, autophagy was significantly inhibited in the hearts of obese mice, and this was associated with increased susceptibility to ischemic injury. Rapamycin administration or partial mTOR deletion significantly reduced infarct size after ischemia through the restoration of autophagy.\(^\text{23}\) Therefore, our results provide a mechanistic explanation for the reduction in ischemic tolerance associated with metabolic abnormalities and suggest that mTORC1 inhibition is a valid therapeutic option to reduce ischemic injury in subjects with acute coronary syndromes, particularly those with metabolic syndrome. Subsequent studies have confirmed that either autophagosome formation or autophagic flux is impaired in the hearts of obese and diabetic animals, and these effects were found to be associated with increased mTORC1 activity and development of cardiac abnormalities. In a swine model of metabolic syndrome, a reduction in autophagosome formation was associated with mTOR activation, increased apoptosis, reduced mitochondrial function, and derangements of cardiac structure and function.\(^\text{126}\) In a model of high-fat diet–induced obesity, cardiac autophagosome formation was reduced, mTOR activity was increased, and cardiac function
was decreased. These effects were rescued by rapamycin and worsened by genetic adiponectin disruption. Interestingly, obesity and metabolic syndrome affect not only autophagosome formation but also autophagic flux. Deregulated activation of cardiac Akt2 is involved in the activation of the mTOR pathway and in the disruption of autophagic flux in the hearts of obese mice. These abnormalities are rescued by Akt2 genetic disruption. In a model of streptozotocin-induced diabetes mellitus, autophagosome formation and flux were impaired in the heart, and these effects were associated with increased mTOR activity. However, whether autophagy inhibition in the diabetic heart is maladaptive or adaptive at baseline is still unclear. Obesity was also found to be associated with the inhibition of autophagosome formation in the kidney through mTORC1 activation and in the liver in mice. This suggests that mTORC1 inhibition in subjects with obesity could be beneficial not only to the heart but also to other organs, specifically through autophagy reactivation. Additional studies to investigate this issue are encouraged.

Perspectives

Many aspects of the pathophysiology of mTOR signaling still remain unclear. First of all, it will be important to study the specific function of mTORC2 at baseline and during stress. This can be achieved through the characterization of cardiac-specific Rictor-knockout mice. Much effort still needs to be made to discover the substrates of mTORC1 and mTORC2 that mediate their specific effects and the mechanisms that regulate them in response to growth factors, nutrients, and stress. Not much is known about the crosstalk between mTORC1 and mTORC2, but it is likely that the complexes tightly regulate one another in specific contexts and share some functions. In addition, the specific functions of different adaptor proteins of mTORC1 and mTORC2 in different cardiomyocyte cellular processes need to be addressed. Finally, the subcellular localization of mTORC1 and mTORC2 in cardiomyocytes at baseline and during stress should be investigated.

mTORC1 activation is maladaptive during aging, cardiac hypertrophy development, myocardial ischemia, and in the presence of obesity and metabolic syndrome. Therefore, it is important to find the optimal mTORC1 inhibitor that would be most beneficial under these conditions. Ideally, this inhibitor should selectively inhibit the maladaptive functions of mTORC1 without affecting its physiological effects. It is known, for example, that prolonged treatment with rapamycin disrupts mTORC2 and can cause insulin resistance. It will be important to study the direct regulators of mTORC1 involved in its maladaptive functions, such as Rheb, PRAS40, or astrin, and its direct substrates in these mechanisms. Additional studies of different components of mTOR signaling with heterozygous loss-of-function models are also encouraged. It will also be interesting to investigate whether there is a structural advantage to having the mTORC1 protein present, even if it is inhibited. Of note, previous studies indicated a beneficial effect of mTORC1 inhibition in preserving the stem cell pool, reducing stem cell exhaustion, and increasing stem cell function. Cardiac stem cells have been shown to be involved in the regulation of cardiomyocyte turnover, but the cardiac stem cell pool decreases during aging and disease. It would be interesting to evaluate whether mTORC1 inhibition can preserve the cardiac stem cell pool during stress and, if so, whether this effect contributes to the protective effects of mTORC1 inhibition in cardiac diseases.

Finally, information about the physiological role of mTOR signaling in the vasculature is scarce. There is some evidence indicating that prolonged rapamycin treatment reduces endothelial cell viability and function and promotes monocyte recruitment, vascular inflammation, and susceptibility to thrombosis. Conversely, S6K inhibition reduces tissue factor release and vascular inflammation. mTORC2 was found to promote survival and proliferation of pulmonary artery vascular smooth muscle cell during pulmonary hypertension. Studies of mTOR components via vascular-specific loss-of-function models are required to understand the involvement of mTOR signaling in vascular cellular processes.

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Disclosures

None.

References


mTOR Signaling in Cardiovascular System


