MicroRNAs in Metabolic Disease

Carlos Fernández-Hernando, Cristina M. Ramírez, Leigh Goedeke, Yajaira Suárez

Abstract—Alterations in the metabolic control of lipid and glucose homeostasis predispose an individual to develop cardiometabolic diseases, such as type 2-diabetes mellitus and atherosclerosis. Work over the last years has suggested that microRNAs (miRNAs) play an important role in regulating these physiological processes. The contribution of miRNAs in regulating metabolism is exemplified by miR-33, an intronic miRNA encoded in the Srebp genes. miR-33 controls cellular cholesterol export and fatty acid degradation, whereas its host genes stimulate cholesterol and fatty acid synthesis. Other miRNAs, such as miR-122, also play a critical role in regulating lipid homeostasis by controlling cholesterol synthesis and lipoprotein secretion in the liver. This review article summarizes the recent findings in the field, highlighting the contribution of miRNAs in regulating lipid and glucose metabolism. We will also discuss how the modulation of specific miRNAs may be a promising strategy to treat metabolic diseases. (Arterioscler Thromb Vasc Biol. 2013;33:178-185.)

Key Words: miRNAs ▪ metabolic disease ▪ lipoprotein metabolism

MicroRNAs (miRNAs) are small (18–25 nucleotides in length), evolutionarily conserved, noncoding RNAs that have an important function in gene regulation, acting predominantly at the posttranscriptional level. Mature miRNA products are generated from a longer primary miRNA transcript through sequential processing by the ribonucleases DROSHA and DICER. miRNAs typically control the expression of their target genes by imperfect base pairing to the 3′-untranslated regions of mRNAs, thereby inducing repression of their target mRNAs. This inhibitory effect can occur by either transcript destabilization, translational inhibition, or both (more detailed information about miRNA biogenesis, function, and targeting activity can be found in recent reviews covering these topics). Importantly, a single miRNA can regulate the expression of hundreds of genes, and the expression of a single gene can be regulated by multiple miRNAs. The effect of a particular miRNA on gene expression is likely to be dictated by the relative expression of the miRNA and its target genes, which can compete for the binding in their 3′-untranslated regions. Of note, 1 miRNA often regulates multiple genes that are involved in a specific signaling cascade or cellular mechanism, thus making miRNAs potent biological regulators. Since miRNAs have been described in the early 1990s as regulators of developmental timing in Caenorhabditis elegans, they have been shown to participate in almost every cellular process investigated, including metabolic homeostasis.

Growing evidence suggests that faulty regulation of lipid metabolism promotes metabolic diseases. In addition to the classical transcriptional regulators, sterol regulatory element-binding proteins (SREBPs) and liver X receptors (LXRs), several miRNAs have been shown to posttranscriptionally regulate the expression of key genes involved in lipid homeostasis, including miR-122, miR-33, miR-106, miR-758, miR-26, miR-370, miR-378/378*, let-7, miR-27, miR-143, miR34a, and miR-335. In the present review, we will focus our attention on the liver-specific miR-122 and the well-characterized intronic miR-33.

miR-122

miR-122 is the most abundant miRNA in the liver, with approximately up to 135 000 copies per human hepatocyte, accounting for ≈75% of total miRNA expression in this organ. miR-122 plays important roles in a wide variety of liver functions, ranging from cholesterol metabolism, liver cancer, stress responses, and viral infection to circadian regulation of hepatic genes. Two pioneering studies have shown that antisense targeting of miR-122 results in a significant reduction of plasma cholesterol levels. The first study shows that the effect on plasma cholesterol results most likely from decreased expression of many cholesterol biosynthetic genes, including 3-hydroxy-3-methylglutaryl-coenzyme A reductase (Hmgcr), the rate-limiting enzyme in the cholesterol biosynthesis pathway. Despite this, the effects of miR-122 on cholesterol biosynthesis are indirect

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and it is unclear which direct targets of miR-122 mediate them. Interestingly, this study underlines that a miRNA loss-of-function phenotype may be caused by genes that are not directly targeted by the miRNA. The second study implements a similar antisense technology (2′-O-methoxyethyl phosphorothioate antisense oligonucleotides) against miR-122 in mice and not only confirms the effect on plasma cholesterol, but also reports a significant decrease in plasma triglycerides (TGs), as well as decreased hepatic steatosis, in high-fat diet-fed mice.7 Furthermore, hepatocytes isolated from ASO-miR-122–treated mice display decreased hepatic fatty acid and sterol synthesis and increased fatty acid oxidation, likely attributable to the observed increased levels of AMP-activated kinase.7 Subsequent studies using locked nucleic acid chemistry in mice and nonhuman primates corroborate the reduced plasma cholesterol levels without any apparent liver toxicity.25 Recently, miR-122 liver-specific knockout and miR-122 germline knockout mice have been shown to have a significant reduction (∼30%) in total serum cholesterol and TG levels and, therefore, recapitulate the effects observed with antisense inhibitors of miR-122.21,25 Interestingly, the study of Tsai et al25 also found a significant downregulation of the microsomal TG transfer protein, which is essential for the assembly of lipoproteins. Intriguingly, Mttp is not a direct target of miR-122, and the mechanism by which miR-122 regulates its expression is still unknown. Altogether, these results demonstrate that miR-122 plays an important role in regulating serum cholesterol and TG levels by controlling cholesterol biosynthesis and very-low-density lipoprotein secretion in the liver.

In addition, a recent report has also shown that the knockdown of miR-122 results in the regulation of hundreds of mRNAs, of which a disproportionately high fraction accumulates in a circadian fashion.26 The transcripts associated with these pathways indeed show the strongest time point–specific changes on miR-122 depletion. The identification of peroxisome proliferator-activated receptor α, β, and γ and the peroxisome proliferator-activated receptor α coactivator, SmaRdc1/Baf60a, as novel targets of miR-122 suggest an involvement of the circadian metabolic regulators of the Ppar family in miR-122–mediated metabolic control.26 Taken together these results suggest that inhibition of miR-122 might be a feasible therapeutic approach. In another study, 46 miRNAs were differentially

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**Figure.** microRNA (miRNA) regulation of lipid metabolism, insulin signaling, and glucose homeostasis. Schematic overview of miRNAs involved in the regulation of glucose and lipid metabolism. Red boxes highlight genes involved in lipid metabolism, and blue boxes highlight those genes related to insulin signaling and glucose homeostasis. Unknown direct target genes or molecular mechanisms that regulate the highlighted genes are marked with a question mark. Note that the target genes showed in the figure are those validated experimentally, but these genes can be also modulated by other miRNAs, and the miRNAs highlighted can regulate other genes that do not appear in the figure. IRS indicates insulin receptor substrate 2; SIRT 6, sirtuin 6; AMPK, AMP-activated kinase; ABC, ATP binding cassette; NPC1, Niemann-Pick C1; CROT, carnitine O-octanyl transferase; CPT, carnitine palmitoyltransferase; HMGCR, 3-hydroxy-3-methylglutaryl-coenzyme A reductase; MTPP, microsomal TG transfer protein; CAV1, caveolin-1; PPAR, peroxisome proliferator-activated receptor; MCT 1, monocarboxylate transporter 1; and MTPN, miR-375 targets myotrophin.
expressed in humans with nonalcoholic fatty liver disease (NAFLD). miR-122 was downregulated in NAFLD, and this was correlated with increased expression of lipogenic genes in human livers. Knockdown of miR-122 in HepG2 cells recapitulated the lipogenic gene expression profile observed in individuals with NAFLD. In this case, it seems likely that miR-122 downregulation is a compensatory mechanism that counters increasing hepatic lipid levels, rather than a causative agent in the development of NAFLD. Future studies should clarify this apparent discrepancy. In line with these observations, some of the above-mentioned reports have also shown that antagonism of miR-122, in both mice and nonhuman primates, not only lowers low-density lipoproteins levels but the levels of high-density lipoproteins (HDL) as well. These a priori adverse effects, together with the recently reported increased risk of developing hepatocellular carcinoma, challenge the therapeutic approach of miR-122 inhibition for the treatment of metabolic lipid diseases.

### miR-33

miR-33 consists of 2 intronic miRNAs, miR-33a and miR-33b, which are encoded within the introns of the Srebpb2 and Srebpl1 genes, respectively. Although miR-33a and miR-33b share their target activity, they differ in their pattern of evolutionary conservation. miR-33a is encoded within intron 16 of the human Srebpb2 gene and is conserved in many animal species. However, the conservation of miR-33b, which is found within intron 17 of the human Srebpl1 gene, is lost in many species, including rodents and rabbits. miR-33a and miR-33b are cotranscribed with their respective host genes, thereby participating in the regulation of physiological processes related to Srebpb2 and Srebpl1. Indeed, we and others have found that miR-33a and miR-33b regulate intracellular cholesterol and fatty acid homeostasis in concert with their host genes. Specifically, miR-33a has been shown to target genes involved in cholesterol export, such as the ATP binding cassette (ABC) transporters Abca1 and Abcg1, and the endolysosomal transport protein Niemann-Pick C1 (Npc1). In agreement with the regulation

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of ABCA1 by miR-33, modulation of miR-33a levels results in encompassing effects in cholesterol efflux in macrophages, thus suggesting that miR-33 may participate in the regulation of HDL levels in vivo. Indeed, 3 independent studies have demonstrated that endogenous inhibition of miR-33 using different strategies leads to a significant increase in hepatic ABCA1 expression and plasma HDL levels.\textsuperscript{15,16,17} findings that were later confirmed in the miR-33 knockout mice.\textsuperscript{30} Most importantly, anti–miR-33 therapy also results in increased plasma HDL levels in non-human primates.\textsuperscript{31} Interestingly, in the well-characterized model for hypercholesterolemia, LDLr knockout mice, anti–miR-33 therapy promotes reverse cholesterol transport and atherosclerosis regression.\textsuperscript{32} Despite this, the effect of anti–miR-33 therapy on reverse cholesterol transport might not be solely attributable to ABCA1 upregulation, because it has been recently reported that miR-33 also targets 2 canalicular transporters, Abcb11 and Atp8b1, which regulate bile secretion.\textsuperscript{33}

In addition to the important role of miR-33a and its host gene, Srebp2, in regulating cholesterol metabolism, the genomic localization of miR-33b in an intron of the Srebp1 gene led several groups to study the contribution of miR-33 in controlling additional metabolic pathways, such as fatty acid metabolism.\textsuperscript{6,10} Importantly, miR-33a and miR-33b contribute to the regulation of fatty acid metabolism by controlling the expression of carnitine O-acetyl transferase (Crot), carnitine palmityltransferase 1A (Cpt1a), and hydroxyacyl-coenzyme A dehydrogenase-3-ketoacyl-coenzyme A thiolase-enzyme coenzyme A hydratase (trifunctional protein) β-subunit (Hadhb).\textsuperscript{6,10} O-acetyl transferase and carnitine palmityltransferase 1A regulate the transport of fatty acids to the mitochondria for their degradation, and HADHB is directly involved in mitochondrial fatty acid β-oxidation. Interestingly, endogenous inhibition of miR-33 in human hepatic cells increases the degradation rate of fatty acids, suggesting that anti–miR-33 therapy may be useful for treating hepatic steatosis by increasing the degradation rate of fatty acids in the liver.\textsuperscript{6,10} In this regard, non-human primates treated with anti–miR-33 oligonucleotides show a significant reduction of plasma very-low-density lipoprotein.\textsuperscript{31} These results could be explained by a reduced lipidation and secretion of apolipoprotein B–containing lipoproteins attributable to the increased fatty acid oxidation that might be occurring in the liver of non-human primates treated with anti-miR-33 oligonucleotides. However, this remains to be addressed.

In addition to the regulation of fatty acid oxidation, miR-33a and miR-33b have also been shown to control the expression of AMP-activated kinase (AMPKα1) and sirtuin 6 (Sirt6), which are involved in the regulation of lipid and glucose metabolism.\textsuperscript{6} The latter will be discussed in the following section. AMPKα1 regulates key lipogenic enzymes, including HMGR and acetyl-CoA carboxilase (ACC). Thus, inhibition of AMPKα1 by miR-33 may increase HMGR and ACC activity to boost intracellular levels of cholesterol and fatty acids. Altogether, these results suggest a paradigm in which miR-33a and miR-33b act in concert with their host genes, Srebp2 and Srebp1, to increase intracellular cholesterol and fatty acid levels by balancing transcriptional induction and posttranscriptional repression of lipid metabolism genes. Finally, insulin receptor substrate 2 (Irs2), an adaptor protein that controls insulin signaling in the liver, has also been shown to be a miR-33 target, thereby affecting the signaling of a complex downstream network of proteins, including protein kinase B (also known as AKT) phosphorylation and forhead box O1 cytoplasmic localization.\textsuperscript{6} Collectively, these data indicate that both isoforms of miR-33 participate in the regulation of relevant pathways that impact 3 of the primary risk factors of metabolic syndrome, namely insulin resistance, low HDL, and high very-low-density lipoprotein, and suggest that anti–miR-33 therapies may be an attractive approach for treating metabolic diseases.

In contrast to miR-122, miR-33 is less expressed in the liver compared with other tissues, such as the brain.\textsuperscript{16,21} However, the presence of multiple binding sites in the 3′-untranslated regions of some of the key target genes, including Abca1 and Crot, explain why anti–miR-33 therapy is able to increase their expression in the liver.\textsuperscript{6,10} The role of miR-33 in the brain is under intensive investigation because ABCA1 also plays an important role in regulating Apβ clearance and its expression has been associated with neurological disorders, including Alzheimer disease.\textsuperscript{34,35} Altogether, these findings show that miR-33 is playing key roles in controlling many physiological processes, and much work is necessary to understand the impact of anti–miR-33 therapy in human physiology to rule out possible adverse effects of the chronic treatment with anti–miR-33 oligonucleotides.

### Other miRNAs That Regulate Lipid Metabolism

Additional miRNAs (miR-106, miR-758, miR-26, miR-370, miR-378/378*, let-7, miR-27, miR34a, and miR-335) have been described to participate in the regulation of lipid metabolism. Among them, miR-758, miR-26, and miR-106b have been shown to regulate cellular cholesterol efflux by targeting ABCA1 in macrophages, hepatocytes, and neuronal cell lines, therefore indicating that the posttranscriptional regulation of ABCA1 expression is mediated by multiple miRNAs.\textsuperscript{12,18,36} miR-370 has been shown to reduce fatty acid β-oxidation via its targeting activity toward Cpt1a.\textsuperscript{11} In addition, miR-370 appears to participate in the regulation of miR-122 by increasing the expression of lipogenic genes, including Srebp1 and Dgat2.\textsuperscript{11} miR-34a targets hepatic sirtuin 1 (Sirt1) and interestingly, the expression of miR-34a was inversely correlated with levels of sirtuin 1 in fatty livers of diet-induced obese mice.\textsuperscript{37} Both strands of miR-378 have been shown to regulate TG synthesis in 3T3-L1 adipocytes, thereby cooperating in the regulation of lipid accumulation during adipogenesis.\textsuperscript{9} Interestingly, overexpression of miR378/378* in ST2 cells increases the expression of fatty acid binding protein 4 (FABP4), FASN, SCD1, Kruppel-like factor 15 (KLF15), and resistin.\textsuperscript{9} Finally, let-7, miR-143, miR-335, miR-27, and miR-103/107 were also reported to control adipocyte differentiation (Table).\textsuperscript{8,13,14,17,20,21}
miRNAs as Regulators of Glucose Metabolism and Insulin Signaling

Diabetes mellitus is the most common metabolic disorder worldwide and is a major risk factor for cardiovascular disease. Diabetes mellitus is characterized by elevated blood glucose levels attributable to a lack of insulin-producing pancreatic β-cells (type 1 diabetes mellitus) or insulin resistance in peripheral tissues (type 2 diabetes mellitus). Plasma glucose levels are tightly controlled by insulin and glucagon. Changes in circulating glucose modulate insulin production by the pancreatic β-cells, leading to an increase in glucose uptake in peripheral tissues, including the muscle and adipose tissue. Moreover, insulin inhibits glucose synthesis and glycogen degradation and stimulates lipid synthesis in the liver.

Insulin binds to its receptor and stimulates an intracellular signaling pathway involving insulin receptor substrate 1 and 2, phosphatidylinositol 3-kinase, and AKT. AKT phosphorylates and inactivates forkhead box O1, a key transcription factor that regulates glucose 6-phosphatase (G6pc) and phosphoenolpyruvate carboxykinase (Pck1) expression, leading to a significant reduction of glucose production in the liver. Insulin also stimulates the translocation of glucose transporters, such as GLUT-4 in the muscle and adipose tissues, thus promoting glucose clearance. In addition to hormones, miRNAs have emerged as critical regulators of glucose metabolism by regulating insulin production and secretion, as well as insulin sensitivity. The global impact of miRNAs in glucose production and pancreatic β-cell functions was defined with the generation of pancreas-specific dicer knockout mice. These mice survive until birth but fail to grow and die by postnatal day 3. The absence of miRNAs during pancreatic β-cell development causes defective Notch signaling, leading to an increase in cell death and several defects in all pancreatic cell lineages. To solve this problem, Melkman-Zehavi et al developed pancreatic dicer-conditional knockout mice inducible on treatment with tamoxifen. Inactivation of pancreatic dicer expression in adult mice results in enhanced blood glucose and reduced plasma insulin levels. Dicer-deficient β-cells show a significant decrease in insulin synthesis and secretion, which is associated with the upregulation of basic helix-loop-helix family member e22 (Bhlhe22) and Sox6, 2 transcriptional repressors of the insulin gene. Interestingly, 4 miRNAs, including miR-24, miR-26, miR-182, and miR-148, regulate Bhlhe22 and Sox6 expression at the posttranscriptional level and are significantly downregulated in dicer-deficient pancreatic β-cells.

Besides the studies in dicer null mice, several reports have recently shown the critical role of specific miRNAs in regulating insulin production and sensitivity. The importance of some of them will be discussed in the following sections of this review article.

miR-375

miR-375 is one of the most abundant miRNAs in the pancreas and regulates insulin secretion independently of changes in plasma glucose levels. miR-375 null mice are normoinsulinemic but hyperglycemic and glucose intolerant. These mice also have an increase in the number of pancreatic α-cells and fasting and fed plasma glucagon levels. The increase in plasma glucagon levels results in a significant increase in glucose 6-phosphatase and phosphoenolpyruvate carboxykinase expression and glucose production in the liver. miR-375 also regulates the expression of a cluster of genes controlling cellular growth and proliferation, including caveolin-1 (Cav-1), inhibitor of DNA binding 3 (Id3), Ras-dexometastase-induced-1 (Rasdl1), and the human antigen D/embryonic lethal abnormal vision-like 4 (Hud/Elavl4). Human antigen D/embryonic lethal abnormal vision-like 4 is an RNA-binding protein that regulates preproinsulin (Ins2) translation and insulin production. This finding suggests that the reduced insulin secretion observed in the pancreatic β-cells from the miR-375 null mice may be attributable to increased human antigen D expression in pancreatic β-cells. Moreover, miR-375 targets myotrophin (Mtpn), a gene involved in actin depolymerization and vesicular trafficking, thereby reducing insulin exocytosis.
Regulation of Insulin Signaling by miRNAs

Other miRNAs regulate insulin sensitivity in the liver and peripheral tissues by controlling the expression of many components of the insulin signaling pathway, including insulin-like growth factor receptor 1, insulin receptor, insulin receptor substrate 2, phosphatidylinositol 3-kinase regulatory subunit-α (PIK3IP1), AKT2, tuberous sclerosis protein 1, caveolin-1, and rapamycin-insensitive companion of mTOR (RICTOR).

Two independent groups have recently shown that the Let-7 family of miRNAs regulates glucose homeostasis and insulin sensitivity.54,55 Global and pancreas-specific overexpression of Let-7 in mice results in impaired glucose tolerance and reduced glucose-induced pancreatic insulin secretion.54,55 Specific knockdown of Let-7 in Let-7 transgenic mice reverses the phenotype by improving insulin sensitivity in the muscle and adipose tissues. Let-7 directly targets many components of the insulin-signaling pathway, such as Igf1r, Insr, Irs2, Pik3ip1, Akt2, Tsc1, and Rictor, thereby reducing insulin sensitivity.54,55 LIN28 tightly controls the expression of Let-7. This RNA-binding protein represses the biogenesis of Let-7 miRNAs and is highly expressed during normal embryogenesis and is upregulated in some cancers.56,57 Interestingly, Lin28 transgenic mice reduce the expression of Let-7 and improve glucose clearance and insulin sensitivity.55 By contrast, skeletal muscle-specific Lin28 knockout mice show impaired glucose tolerance.55 Altogether these studies strongly suggest that the Lin28/Let-7 axis regulates glucose metabolism.54,55

In addition to Let-7, other miRNAs, including miR-33, miR-103, miR-107, and miR-29a/b, also regulate the insulin-signaling pathway.6,52-58,59 As described before, miR-33 targets Irs2 and regulates insulin sensitivity in human hepatic cell lines. Moreover, miR-33 also regulates the expression of Ampkα and Sirt6, which are involved in regulating lipid and glucose metabolism.6,53 miR-103 and miR-107 were recently shown to be upregulated in obese mice.59 Moreover, the expression of both miRNAs is increased in subjects with NAFLD, a condition often associated with diabetes mellitus.60 miR-103 and miR-107 have similar mature sequences and are thought to target similar genes. Overexpression of miR-107 results in an increase in fasting glucose and insulin levels.59 Conversely, silencing of miR-103/miR-107 enhances insulin sensitivity in the liver and in the adipose tissue. Mechanistically, miR-103/107 inhibition increases the expression of caveolin-1, a scaffold protein required for caveolae formation, and enhances insulin signaling by increasing insulin receptor stability in the cell membrane.59 Indeed, miR-103/107 antagonors are not able to enhance insulin sensitivity in Cav-1 null mice. miR-29a and miR-29b are also upregulated in white adipose tissue and in the liver of diabetic rats. In addition, to targeting Cav-2, another caveolae structural component,52,58 the miR-29 family members also regulate phosphatidylinositol 3-kinase regulatory subunit α (PIK3R1), which regulates insulin signaling.

Other miRNAs That Regulate Glucose Homeostasis

The complexity of miRNAs in regulating physiological processes is exemplified by miR-208a, a heart-specific miRNA that also regulates glucose metabolism and energy homeostasis.60 miR-208 regulates the expression of the mediator complex 13, which controls the transcription of the thyroid hormone and other nuclear hormone receptors. Thyroid hormone enhances energy expenditure and regulates body weight. Interestingly, mice administrated with anti–miR-208 oligonucleotides are resistant to obesity and glucose intolerant.60 In contrast, Med13 cardiac-specific transgenic mice are resistant to diet-induced obesity with improved glucose tolerance.60 This remarkable finding demonstrates how a cardiac-specific miRNA is able to regulate systemic energy homeostasis.

Besides the role of miR-208 in the heart, another interesting possibility that could be explored is that this miRNA maybe secreted in microvesicles by the heart and regulate insulin signaling and glucose metabolism in other peripheral tissues. However, several studies have not be able detect miR-208 in the plasma of subjects with type 2 diabetes mellitus or dyslipidemia.61

In summary, multiple miRNAs are able to control glucose metabolism by regulating a network of genes in the liver and peripheral tissues. The contribution of specific miRNAs will be determined by the tissue and metabolic state.

Circulating miRNAs

Recently, several studies have highlighted the presence of miRNAs in the plasma. Plasma miRNAs are packaged in microvesicles (including exosomes) that protect them from degradation.62 Moreover, recent reports have also identified these small RNAs associated with proteins, including the RNA-binding protein Argonaute 2.63 The role of circulating miRNAs is under intense investigation, and some studies suggest that they might play important roles in regulating atherogenesis and endothelial cell functions. Some miRNAs are enriched in the plasma under pathological conditions, including myocardial infarction (miR-208, miR-1, miR-133a, and miR-21),64 hepatic steatosis and hepatic injury (miR-122),65 and hypertension (Let-7e)66 or reduced, such as miR-126 in type 2 diabetes mellitus;64 therefore they can be used as disease biomarkers. Finally, Vickers et al67 have also recently found miRNAs associated with lipoproteins. Interestingly, the HDL-miRNA profile of normal subjects is significantly different from that of familial hypercholesterolemia subjects.68 HDL-miRNAs can be delivered to hepatic cells via the scavenger receptor class B type I, however the physiological relevance of this process in regulating gene expression in the liver and peripheral tissues, including atherosclerotic plaque macrophages, remains unknown and warrants further investigation.

Concluding Remarks

miRNAs have emerged as key regulators of many physiological processes, including lipid and glucose metabolism. Several preclinical studies have pointed out that targeting specific miRNAs, such as miR-33, miR-122, miR-103/107, and let-7, may be a promising strategy.
to ameliorate cardiometabolic disorders. However, the complexity of gene networks that a single miRNA may control and the potential adverse effects of the total inhibition of a specific miRNA remain to be deeply explored. For example, a global deficiency of miR-122 results in reduced plasma cholesterol levels but increased hepatic steatosis and hepatic cancer.\textsuperscript{23,25} Contrastingly, miR-122 pharmacological inhibition for few a months leads to a significant reduction of plasma lipid levels and reverses hepatic steatosis in mice. These paradoxical results strongly suggest that much work is necessary to fully understand the role of a single miRNA in regulating animal physiology. New approaches that integrate RNA-sequencing, proteomics, and systems biology methodologies will help us to elucidate how the modulation of gene networks by miRNAs contribute to the regulation of metabolic processes.

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