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# Interaction between SIRT1 and non-coding RNAs in different disorders

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SIRT1 is a member of the sirtuin family functioning in the process of removal of acetyl groups from different proteins. This protein has several biological functions and is involved in the pathogenesis of metabolic diseases, malignancy, aging, neurodegenerative disorders and inflammation. Several long non-coding RNAs (lncRNAs), microRNAs (miRNAs) and circular RNAs (circRNAs) have been found to interact with SIRT1. These interactions have been assessed in the contexts of sepsis, cardiomyopathy, heart failure, non-alcoholic fatty liver disease, chronic hepatitis, cardiac fibrosis, myocardial ischemia/reperfusion injury, diabetes, ischemic stroke, immune-related disorders and cancers. Notably, SIRT1 interacting non-coding RNAs have been found to interact with each other. Several circRNA/miRNA and lncRNA/miRNA pairs that interact with SIRT1 have been identified. These axes are potential targets for design of novel therapies for different disorders. In the current review, we summarize the interactions between three classes of non-coding RNAs and SIRT1.

KEYWORDS

SIRT1, lncRNA, miRNA, circRNA, biomar

### Introduction

As a member of the sirtuin family, Sirt1 has a function in removal of acetyl groups from different proteins. This nicotinamide adenosine dinucleotide (NAD)-dependent deacetylase has several biological functions and is involved in the pathogenesis of metabolic diseases, malignancy, aging, neurodegenerative disorders and inflammation (Rahman and Islam, 2011). SIRT1 has a lot of substrates including a number of transcription factors. These transcription factors include p53, FoxO family, HES1, HEY2, PPARγ, CTIP2, p300, PGC-1α, and NF-κB (Haigis and Guarente, 2006; Michan and Sinclair, 2007; Yamamoto et al., 2007; Pillarisetti, 2008). The enzymatic reaction catalyzed by SIRT1 leads to generation of nicotinamide and transfer of the acetyl group of the substrate to cleaved NAD, producing a distinctive metabolite, namely, O-acetyl-ADP ribose (Pillarisetti, 2008).

SIRT1 has an important role in the regulation of energy homeostasis in response to accessibility to nutrients. In the liver tissue, SIRT1 enhances expression of the nuclear

#### TABLE 1 SIRT1-interacting miRNAs.



#### TABLE 1 (Continued) SIRT1-interacting miRNAs.



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#### FIGURE 1

SIRT1 works with a lot of molecules, some of which are transcription factors. p53, the FoxO family, HES1, HEY2, PPAR, CTIP2, p300, PGC-1, and NF-B are all transcription factors. Dysregulation of SIRT1-targeting miRNAs plays a role in the pathogenesis of sepsis and its complications, chronic hepatitis, ischemia/reperfusion (I/R) injury to the liver and heart, cardiac fibrosis, myocardial infarction, osteoarthritis, diabetic nephropathy, and a number of malignant diseases like colorectal cancer.

receptor PPARα, thus regulating lipid homeostasis. Deletion of Sirt1 in this tissue has been shown to impair PPARα signaling and decrease ßoxidation of fatty acids, resulting in the development of hepatic steatosis, induction of inflammatory responses in liver, and endoplasmic reticulum stress (Purushotham et al., 2009).

In addition to the regulation of metabolic pathways, SIRT1 is involved in the carcinogenic processes. Its expression has been found to be increased in both hematological malignancies (Bradbury et al., 2005) and solid tumors (Huffman et al., 2007; Stünkel et al., 2007). Possibly acting as an oncogene, SIRT1 interacts with p53 and induces its deacetylation at its C-terminal Lys382 residue (Vaziri et al., 2001), thus inactivating this tumor suppressor.

In fact, SIRT1 is involved in a variety of human disorders including malignant and nonmalignant conditions. Recently, researchers have focused on identification of the interaction between noncoding RNAs and SIRT1 in these disorders. These investigations have led to identification of a number of long non-coding RNAs (lncRNAs), microRNAs (miRNAs) and circular RNAs (circRNAs) that regulate expression of SIRT1. In the current review, we provide an overview of these non-coding RNAs.

### SIRT1-interacting miRNAs

A class of non-coding RNAs known as miRNAs regulate gene expression by binding to specific target genes in distinct pathways, thereby modulating the expression of various genes (Ghafouri-Fard et al., 2021a; Hussen et al., 2021; Hussen et al., 2022a). Mature

#### TABLE 2 SIRT1-interacting circRNAs.



miRNAs are formed by further processing of pre-miRNAs, which are formed from the transcribed nucleic acids that make up primary miRNAs. Several miRNAs have been shown to target SIRT1, thus regulating its expression. Dysregulation of SIRT1-targeting miRNAs is involved in the pathogenesis of sepsis and its complications, nonalcoholic fatty liver disease (NAFLD), chronic hepatitis, hepatic and myocardial ischemia/reperfusion (I/R) injury, cardiac fibrosis, heart failure, myocardial infarction, osteoarthritis, kidney injury, diabetic nephropathy, cerebral I/R Injury, spinal cord injury, epilepsy and a number of malignant conditions (Table 1; Figure 1). In sepsis, upregulation of miR-181a (Wu Z. et al., 2021), miR-133a (Chen L. et al., 2020) and miR-195 (Yuan et al., 2020) has been shown to lead to downregulation of SIRT1 and aggravation of inflammatory responses. miR-29a, miR-34a and miR-182 are among SIRT1 interacting miRNAs being involved in the pathogenesis of hepatic disorders. For instance, miR-29a via modulating the GSK-3β/ SIRT1 could ameliorate mouse non-alcoholic steatohepatitis (Yang et al., 2020). Alterations in the miR-34a/SIRT1/FXR/ p53 axis have been found to induce NAFLD in rats (Alshehri et al., 2021). Moreover, miR-34a via mediating the SIRT1/ p53 axis could enhance liver fibrosis in patients with chronic hepatitis (Li X. et al., 2020).

miR-128 has been shown to be involved in the pathogenesis of chronic angiotensin II infusion-induced cardiac remodeling through modulation of SIRT1. Silencing this miRNA in the heart tissues of mice could ameliorate angiotensin II-induced cardiac dysfunction, hypertrophy, fibrosis and oxidative stress damage. Angiotensin II could induce upregulation of miR-128 in cell culture. Treatment of cells with miR-128 antagomir could attenuate angiotensin II -induced apoptosis and oxidative damage possibly through targeting the SIRT1/p53 pathway. Suppression of this miRNA could also activate PIK3R1/Akt/ mTOR pathway, restrain angiotensin II-induced autophagy in cardiomyocytes, and mitigate oxidative stress and apoptosis (Zhan et al., 2021).

SIRT1-interacting miRNAs are also involved in the pathogenic processes in the acute myocardial infarction. Suppression of miR-29a has been shown to protect against myocardial I/R injury through influencing expression of SIRT1 and subduing oxidative stress and NLRP3-associated pyroptosis (Ding et al., 2020). In addition, miR-200a-3p has been found to aggravate doxorubicin-induced cardiotoxic effects through targeting PEG3 via SIRT1/NF-κB signaling

pathway (Fu et al., 2021). miR-181a-5p is another miRNA which participates in the cardiomyocyte apoptosis induced by hypoxia–reoxygenation via regulation of SIRT1 (Qi et al., 2020). Moreover, an experiment in an animal model of acute myocardial infarction has shown that miR-124-3p targets SIRT1 to influence cell apoptosis, inflammatory responses, and oxidative stress through regulation of the FGF21/CREB/PGC1α axis (Wei et al., 2021). Besides, miRNAs that modulate expression of SIRT1 can affect pathogenesis of heart failure. For instance, downregulation of miR-22 by targeting SIRT1/PGC-1α could alleviate this disorder (Wang et al., 2021b). Finally, miR199/ SIRT1/P300 axis has apotential function in the patheticlogy of this disorder (Asensio-Lopez et al., 2021).

Lastly, three SIRT1-interacting miRNAs have been revealed to participate in the carcinogenesis. miR-373 is a tumor suppressor miRNA that inhibits proliferation of pancreatic cancer cells through influencing activity of SIRT1/PGC-1α/NRF2 axis (Yin et al., 2021). On the other hand, miR-34a acts as an immunosuppressive miRNA in colorectal cancer via regulation of SIRT1/NF-κB/B7-H3/TNF-α axis (Meng et al., 2021). Lastly, miR-199a-5p has a role in repression of stemness of squamous cell carcinoma cells through influencing activity of SIRT1 and CD44ICD cleavage signaling (Lu et al., 2020).



#### FIGURE 2

CircRNAs have been proven to serve as molecular sponges for miRNAs, thereby influencing the expression of miRNA targets. SIRT1 has been found to be the target of miRNA genes, which were already being sponged by different types of circRNAs that prevented or enhanced gene expression.

#### TABLE 3 SIRT1-interacting lncRNAs.





#### TABLE 3 (Continued) SIRT1-interacting lncRNAs.

# SIRT1-interacting circRNAs

Circular RNAs (CircRNAs) are common in all animals, from viruses to mammals. They are single-stranded, endogenous covalently closed RNA molecules with highly stability. The biosynthesis, regulation, localization, destruction, and modification of circRNAs have all seen great progress (Sayad et al., 2022). CircRNAs play a role in a wide range of human disorders, particularly malignancies (Ghafouri-Fard et al., 2021b; Ghafouri-Fard et al., 2022). The impact of SIRT1 interacting circRNAs in the regulation of SIRT1 has been assessed in diabetes and its complications, rheumatoid arthritis, chronic cerebral ischemia, osteoarthritis, intervertebral disc degeneration as well as malignant disorders, particularly glioma (Table 2). All of these circRNAs have been shown to act as molecular sponges for miRNAs to subsequently affect expression of miRNAs targets (Figure 2). For instance, hsa\_circ\_0115355 has been found to regulate activity of miR-145/SIRT1 axis, thus enhancing function of pancreatic  $\beta$ cells in patients with type 2 diabetes mellitus (Dai et al., 2022). CircHIPK3 is another circRNA which participates in the pathogenesis of diabetic complications. Expression of this circRNA has been significantly reduced in HK-2 cells following exposure with high glucose. Forced upregulation of circHIPK3 could reverse high glucose-induced pathologic events in HK-2 cells. SIRT1 has been found to be the target of miR-326 and miR-487a-3p, two downstream genes of circHIPK3. Silencing of these two miRNAs could induce proliferation and decrease apoptosis in high glucose-induced HK-2 cells. Taken together, upregulation of circHIPK3 can reduce the effects of high glucose in HK-2 cells via sponging miR-326 or miR-487a-3p and influencing expression of SIRT1 (Zhuang et al., 2021).

Hsa\_circ\_0044235 is another circRNA which has been shown to be downregulated in patients with rheumatoid arthritis (RA). Downregulation of this circRNA has been correlated with low levels of SIRT1 expression in these patients. Overexpression of hsa\_circ\_0044235 could attenuate joint inflammation, cell apoptosis, and joint injury, and reduce NLRP3-mediated pyroptosis but increasing SIRT1 expression. Upregulation of this circRNA could also inhibit caspase-1 content. Mechanistically, hsa\_circ\_0044235 increases expression of SIRT1 through sponging miR-135b-5p (Chen et al., 2021).

CircularNOP10 and circ0082374 are two putative oncogenic circRNAs that regulate expression of SIRT1. CircularNOP10 has a role in induction of progression of gastric cancer through



regulation of miR-204/SIRT1 pathway (Xu J. et al., 2021). In glioma cells, circ0082374 has a role in induction of cell viability, migration, invasion and glycolysis through regulation of miR-326/SIRT1 axis (Wang et al., 2020).

# SIRT1-interacting lncRNAs

Transcripts larger than 200 nt are known as long non-coding RNAs (lnRNAs), which cannot code for proteins and may possess small open reading frames (ORFs). Because they interact with various proteins, mRNAs and DNA sequences, lncRNAs play significant roles in a number of disorders (Sabaie et al., 2021; Hussen et al., 2022b). GAS5, LincRNA-p21, MCM3AP-AS1, TUG1, SNHG7, SNHG8, SNHG10, SNHG15, Oip5-as1, ILF3-AS1, ANRIL, UCA1 and KCNQ1OT1 are examples of lncRNAs that regulate expression of SIRT1 through sponging miRNAs. These lncRNAs can affect pathogenesis of RA, atherosclerosis, sepsis-associated renal injury (SARI), diabetic nephropathy, ischemic stroke and a number of malignant conditions (Table 3). For instance, GAS5 via regulating the miR-222-3p/Sirt1 axis could alleviate RA (Yang et al., 2021). Moreover, GAS5 via inhibiting the miR-579-3p and activating the SIRT1/PGC-1α/Nrf2 axis could reduce cell pyroptosis in SARI (Ling et al., 2021). In the context of osteoarthritis, MCM3AP-AS1 via modulating the miR-138-5p/SIRT1 axis could protect chondrocytes from IL-1β-induced inflammation (Shi et al., 2021).

SIRT1-interacting lncRNAs have also been shown to affect pathogenesis of malignant conditions. For instance, SNHG10 has been found to sponge miR-543 in non small cell lung cancer (Zhang Z. et al., 2020). Moreover, SNHG7 has been demonstrated to inhibit NLRP3-associated pyroptosis through regulating miR-34a/SIRT1 axis in liver cancer (Chen Z. et al., 2020). GAS5 can inhibit malignant progression of colorecatl cancer cells through regulating macroautophagy and forming a negative feedback loop with the miR-34a/mTOR/SIRT1 axis (Zhang HG. et al., 2021). On the other hand, UCA1 has a role in induction of cell proliferation and suppression of apoptosis through affecting expression of SIRT1 and miR-204 in pediatric AML (Liang et al., 2020). The known interactions that SIRT1 has with a variety of lnRNAs are illustrated in Figure 3.

A number of therapeutic agents such as anthocyanins, ginsenoside-R3, dexmedetomidine hydrochloride, berberine, sorafenib, 17β-Estradiol, phenylpyridinium, tetrahydroxy stilbene glycoside, cisplatin, resveratrol, sulforaphane and liraglutide have been found to affect expression of non-coding RNAs/SIRT1 axes (Table 4). For instance, experiments in animal model of asthma

#### TABLE 4 Effects of drugs on SIRT1-interacting ncRNAs.







have shown that anthocyanins suppresses inflammatory responses in airways through decreasing activity of NF-κB pathway via the miR-138-5p/SIRT1 axis (Liu Y. et al., 2022). Moreover, ginsenoside Rg3 can alleviate sepsis-related hepatic injury through modulation of TUG1/ miR-200c-3p/SIRT1 axis (Wu P. et al., 2021). TUG1/miR-194/ SIRT1 axis has been found to be targeted by dexmedetomidine hydrochloride to inhibit hepatocytes apoptosis and inflammatory responses (Gu et al., 2021). Additionally, the effects of berberine in amelioration of hepatic insulin resistance have been revealed to be mediated through regulation of miR-146b/SIRT1 axis (Sui et al., 2021).

### **Discussion**

SIRT1 has a role as a deacetylase and is able to deacetylate a range of substrates. Thus, it participates in the regulation of a wide array of physiological processes such as gene expression, metabolic pathways and aging (Haigis and Guarente, 2006; Michan and Sinclair, 2007). This protein has functional interactions with lncRNAs, miRNAs and circRNAs. In fact, a complicated network exists between these noncoding RNAs and SIRT1. Hsa\_circ\_0115355/miR-326, hsa\_circ\_ 0115355/miR-487a-3p, HIPK3/miR-145, hsa\_circ\_0044235/miR-135b-5p, circ\_0000296/miR-194-5p, circ\_0001103/miR-375, CIDN/ miR-34a-5p, NOP10/miR-204, circ-0082374/miR-324 are examples of circRNA/miRNA pairs that interact with SIRT1. Similarly, GAS5/ miR-222-3p, GAS5/miR-579-3p, GAS5/miR-34a, MCM3AP-AS1/ miR-138-5p, TUG1/miR-9-5p, TUG1/miR-29c-3p, TUG1/miR-204, SNHG8/miR-425-5p, SNHG7/miR-9, SNHG7/miR-34a, SNHG15/ miR-141, SNHG10/miR-543, Oip5-as1/miR-29a, ILF3-AS1/miR-212-3p, ANRIL/miR-7-5p, UCA1/miR-204 and KCNQ1OT1/miR-124 are lncRNA/miRNA pairs that regulate expression of SIRT1 in different contexts. These interactions are possibly involved in the pathoetiology of a number of human disorders such as sepsis, cardiomyopathy, heart failure, non-alcoholic fatty liver disease, chronic hepatitis, cardiac fibrosis, myocardial ischemia/reperfusion injury, diabetes, ischemic stroke, immune-related disorders and cancers. In cancers, SIRT1-interacting non-coding RNAs not only affect cell proliferation but also regulate stemness and immunosuppressive responses in the tumor niche.

SIRT1 is a potential target for design of novel therapies. Most importantly, a number of drugs used for treatment of diverse asthma, sepsis, liver injury, insulin resistance, postmenopausal osteoporosis, Parkinson's disease, diabetic nephropathy and cancers exert their effects through modulation of non-coding RNAs/SIRT1 axis. Thus, identification of the interactions between non-coding RNAs and SIRT1 has practical significance in design of novel therapeutic strategies for diverse disorders. Remarkably, non-coding RNAs that modulate expression of SIRT1 are putative modulators of the response of patients to different drugs.

## Author contributions

SG-F wrote the manuscript and revised it. MT and GS supervised and designed the study. HS, YP, and BH collected the data and designed the figures and tables. All authors read and approved the submitted version.

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# Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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# **Glossary**



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AML Pediatric acute myeloid leukemia

HCC Hepatocellular carcinoma NSCLC Non-small cell lung cancer I/R Ischemia-reperfusion