Reciprocal Regulation of MicroRNA-1 and Insulin-Like Growth Factor-1 Signal Transduction Cascade in Cardiac and Skeletal Muscle in Physiological and Pathological Conditions

Leonardo Elia, PhD; Riccardo Contu, BSc; Manuela Quintavalle, PhD; Francesca Varrone, PhD; Cristina Chimenti, MD, PhD; Matteo Antonio Russo, MD; Vincenzo Cimino, MD; Laura De Marinis, MD; Andrea Frustaci, MD; Daniele Catalucci, PhD; Gianluigi Condorelli, MD, PhD

**Background**—MicroRNAs (miRNAs/miRs) are small conserved RNA molecules of 22 nucleotides that negatively modulate gene expression primarily through base paring to the 3′ untranslated region of target messenger RNAs. The muscle-specific miR-1 has been implicated in cardiac hypertrophy, heart development, cardiac stem cell differentiation, and arrhythmias through targeting of regulatory proteins. In this study, we investigated the molecular mechanisms through which miR-1 intervenes in regulation of muscle cell growth and differentiation.

**Methods and Results**—On the basis of bioinformatics tools, biochemical assays, and in vivo models, we demonstrate that (1) insulin-like growth factor-1 (IGF-1) and IGF-1 receptor are targets of miR-1; (2) miR-1 and IGF-1 protein levels are correlated inversely in models of cardiac hypertrophy and failure as well as in the C2C12 skeletal muscle cell model of differentiation; (3) the activation state of the IGF-1 signal transduction cascade reciprocally regulates miR-1 expression through the Foxo3a transcription factor; and (4) miR-1 expression correlates inversely with cardiac mass and thickness in myocardial biopsies of acromegalic patients, in which IGF-1 is overproduced after aberrant synthesis of growth hormone.

**Conclusions**—Our results reveal a critical role of miR-1 in mediating the effects of the IGF-1 pathway and demonstrate a feedback loop between miR-1 expression and the IGF-1 signal transduction cascade. (Circulation. 2009;120:2377-2385.)

**Key Words:** heart failure ■ hypertrophy ■ IGF-1 ■ microRNA ■ signal transduction

MicroRNAs (miRNAs/miRs) are small conserved RNA molecules of ~22 nucleotides that negatively modulate gene expression in eukaryotic organisms. The base pairing of a specific miR to the 3′ untranslated region (UTR) of its messenger RNA (mRNA) targets leads to mRNA cleavage and/or translation repression.1 Bioinformatic analysis predicts that each miR may regulate hundreds of targets, indicating their important role in most biological processes such as cell proliferation, apoptosis, and stress responses.2–5 Recently, these small RNA molecules have also been demonstrated to be involved in myocardial and cardiac stem cell development,6 cardiac hypertrophy and remodeling, and arrhythmias,7–11 as is the case of miR-1.12–14 The expression of which inversely correlates with cardiac hypertrophy.11,15 Notably, mice harboring deletion of miR-1 showed cardiac defects, including misregulation of cardiac morphogenesis, electric conduction, and cell proliferation.10,13 Among putative miR-1 targets, proteins such as growth factors (Toll-like), transcription factors, and signal transduction kinases have been validated as true targets.12,13

**Clinical Perspective on p 2385**

Insulin-like growth factor-1 (IGF-1) is a key regulator of growth, survival, and differentiation in most cell types,16 and its importance is demonstrated by the conservation throughout the evolutionary scale.16 In myocardial biology, IGF-1 and its signal transduction cascade are involved in the control of virtually every critical biological process, including development, cardiomyocyte size and survival, action potential, and excitation-contraction coupling.17,18 In this report, we...
demonstrate not only that IGF-1 is a target of miR-1 but, remarkably, that miR-1 expression per se depends on the activation state of the IGF-1 signal transduction cascade. Indeed, IGF-1 upregulation correlates with miR-1 depression and vice versa. Together, these findings unravel a unique reciprocal molecular circuit between miR-1 and IGF-1.

Methods

Animals
All procedures involving animals were performed in accordance with institutional guidelines for the care and use of laboratory animals. Transverse aortic constriction (TAC) experiments were performed on male C57/Bl6 mice ranging in age from 10 to 12 weeks, with 6 animals per group. AKT transgenic mice with cardiac-specific overexpression of constitutively active AKT were male mice aged 10 to 12 weeks.

Cell Cultures and Adenoviral Infection
Mouse neonatal cardiomyocytes were prepared as described previously.11 Mouse C2C12 and 293T cells were obtained from ATCC (Manassas, Va) and maintained in Dulbecco’s modified Eagle’s medium (Invitrogen, Carlsbad, Calif) supplemented with 4.5 g/L glucose, 4 mmol/L l-glutamine, 10% fetal bovine serum, and penicillin/streptomycin at 37°C in a 5% CO2 atmosphere. C2C12 cells were differentiated in Dulbecco’s modified Eagle’s medium supplemented with 4% horse serum. MiR-1 and miR-133 adenoviral vectors (Ad-miR-1 and Ad-miR-133, respectively) as well as the Ad-Empty control have been described previously.11

Bioinformatics
MiR-1 target prediction was performed with the use of the following algorithms: miRanda (http://microrna.sanger.ac.uk), TargetScan (http://www.targetscan.org), and PicTar (http://pic-tar.bio.nyu.edu). The 3’ UTR ΔG was calculated with the use of the software mFOLD (http://frontend.bioinfo.rpi.edu/applications/mfold/). MiR-1 promoter analysis was performed with the use of the software MatInspector (http://www.genomatix.de/products/MatInspector).
Reporter Assays

The miR-1 promoter, which contains 2 potential binding sites for Foxo3a, was amplified from mouse chromosome 2 with the use of KOD Taq polymerase (Novagen, San Diego, Calif) and the following primers: forward, 5'-CTCTCATCTCTCTCTCTC-3'; and reverse, 5'-GAGGACCTCCTGCGCCGGC-3'. The promoter was cloned into the reporter plasmid, pGL3.basic (Promega, Madison, Wis). For the promoter experiment, 293T cells were seeded in 24-well plates (Nunc, Rochester, NY) and infected with adenoviruses (Ad) carrying a dominant negative (DN) or dominant active (DA) form of AKT20,21 or Foxo3a22 (kindly provided by Dr. Domenico Accili, Columbia University) and subsequently cotransfected with the miR-1 promoter-luciferase reporter (100 ng) construct and the Renilla luciferase plasmid (10 ng) with the use of Lipofectamine 2000 (Invitrogen). For IGF-1 and IGF-1 receptor (IGF-1R) 3'UTR reporter assays, experiments were performed on human 293T and murine C2C12 cell lines. The 3'UTR segments of IGF-1 and IGF-1R 3'UTR mRNAs were subcloned by standard procedures into psiCHECK-2 (Promega) immediately downstream of the stop codon of the luciferase gene. MiR-1 seed mutagenesis was performed as described by the manufacturer (Stratagene, La Jolla, Calif). Neonatal cardiomyocytes, C2C12, and 293T cells were collected at different time points (24, 48 hours) and lysated with the use of RIPA buffer. The following antibodies were used: IGF-1 (Laboratory Vision Corporation, Fremont, Calif), β-myosin heavy chain (Abcam, Cambridge, Mass), troponin T (Thermo Scientific, Waltham, Calif), GAPDH (mouse anti-rabbit GAPDH, Cell Signaling, Danvers, Mass), total AKT (Cell Signaling), Ser473 P-AKT (Cell Signaling), total Foxo3a (Cell Signaling), and Tyr32 P-Foxo3a (Cell Signaling). Densitometry analyses were performed with the use of ImageJ (National Institute of Health).

RNA Quantification

For IGF-1 RNA quantification, total RNA was extracted with the use of TRIzol reagent (Invitrogen) according to the manufacturer’s protocol. Sybr green quantitative polymerase chain reaction was performed with the use of the following primers: IGF-1-5' (5-CACCTCAGACAGGCATTGTG-3'); IGF-1-3' (5-TCTGA- GTCTTGGGCGATGTA-3); GAPDH-5' (5-GACGGCCGCATCGGATTA-3'), GAPDH-3' (5-CACACCAGCTCACCATT-3). For miRNA quantitative reverse transcription–polymerase chain reaction, total RNA was extracted with the use of TRizol; primers and probes specific for human/mouse miR-1 and the internal controls Sno202 RNA and U6 were purchased from Applied Biosystems. Amplification and detection were performed with the use of the 7300 Sequence Detection System (ABI), with 40 cycles of denaturation at 55°C, annealing at 58°C, and extension at 72°C.

Western Blot Analyses

Neonatal cardiomyocytes, C2C12, and 293T cells were collected at different time points (24, 48 hours) and lysated with the use of RIPA buffer. The following antibodies were used: IGF-1 (Laboratory Vision Corporation, Fremont, Calif), β-myosin heavy chain (Abcam, Cambridge, Mass), troponin T (Thermo Scientific, Waltham, Calif), GAPDH (mouse anti-rabbit GAPDH, Cell Signaling, Danvers, Mass), total AKT (Cell Signaling), Ser473 P-AKT (Cell Signaling), total Foxo3a (Cell Signaling), and Tyr32 P-Foxo3a (Cell Signaling). Densitometry analyses were performed with the use of ImageJ (National Institute of Health).
95°C (15 seconds) and annealing/extension at 60°C (60 seconds). For the miRNA quantification, this was preceded by reverse transcription at 42°C for 30 minutes and denaturation at 85°C for 5 minutes.

Northern blotting was performed to confirm the expression levels of miR-1. Probes and anti-sense oligonucleotides against mature miR-1 and U6 were locked nucleic acid based (Exiqon, Vedbaek, Denmark). Densitometry analyses were performed with the use of ImageJ (National Institutes of Health).

Immunofluorescence
C2C12 myoblasts were plated in Laboratory-Tek 2-well chamber slides (2.10^5 cells per well). IGF-1 staining was performed with the use of primary antibody (Laboratory Vision Corporation) together with Alexa Fluor 594 phalloidin (Molecular Probes, Carlsbad, Calif), use of primary antibody (Laboratory Vision Corporation) together with Alexa Fluor 594 phalloidin (Molecular Probes, Carlsbad, Calif), and secondary antibody conjugated to Alexa Fluor 488 (Molecular Probes) as secondary antibody.

Myocardial Biopsies
Eight patients (6 male, 2 female; mean age, 46.8±13.6 years) with acromegaly were evaluated with noninvasive (ECG, 2-dimensional echocardiography) and invasive cardiac studies (cardiac catheterization, coronary and left ventricular angiography, and left ventricular endomyocardial biopsy) before neurosurgery and/or somatostatin analogue therapy. All invasive studies were performed after informed consent was obtained and with the approval of the ethics committee of the Department of Cardiovascular and Respiratory Science, University La Sapienza, Rome, Italy. Endomyocardial biopsies were drawn, stored, and processed as described previously.24

Statistical Analysis
Statistical and frequency distribution analysis was performed by GraphPad Prism 4.0 (GraphPad Software, Inc, La Jolla, Calif). Data in Figure 1 were analyzed with the use of a 2-way ANOVA adjusted pairwise test. Data in Figures 2 and 3 were analyzed with 2-way ANOVA adjusted for multiple comparisons and 1-way ANOVA, respectively. Data in Figures 4 and 5 were analyzed with 2-way ANOVA adjusted for multiple comparisons. Data in Figure 6 and Figure 1 in the online-only Data Supplement were analyzed with 1-way ANOVA and 2-way ANOVA adjusted for multiple comparisons, respectively. The linear correlation on acromegaly patient parameters was calculated with the Pearson product moment correlation coefficient. A value of P<0.05 was considered to be statistically significant.

Results
Bioinformatics
The identification of true miR target genes is a great challenge, and computational algorithms have been the major driving force in predicting miR targets to date.25–27 In the present study, we used the following target prediction algorithms: miRanda (http://microrna.sanger.ac.uk),28 TargetScan (http://www.targetscan.org),29 and PicTar (http://pic-tar.bio.nyu.edu).5,30 These approaches are based on the identification of elements in the 3’ UTR of target genes complementary to the seed sequence of the miR of interest, calculation of thermodynamic properties of 3’ UTRs, and phylogenetic conservation of complementary sequences in the 3’ UTRs of orthologous genes. To reduce the number of false-positive targets, we also analyzed mRNA secondary structure flanking the seed sequence. In fact, several lines of evidence have shown that complex mRNA tertiary structures might prevent miR/miRNA interactions that limit the number of single-stranded regions accessible for binding to miRs.10,13 Using this approach, we identified several putative targets of cardiac relevance, including, as shown recently, IGF-1.19 Its 3’ UTR contains only 1 seed sequence, which has a ΔG energy value of −4.5 and −11.9 kcal/mol for mRNA sequences 5’ and 3’ of the seed sequence, respectively. Interestingly, this sequence is evolutionally conserved between species (Figure 1A). Another putative target included IGF-1R, which is involved in the IGF-1 pathway (Figure 1A in the online-only Data Supplement). IGF-1R belongs to the large class of tyrosine kinase transmembrane receptors and is directly activated by IGF-1 as well as the related growth factor IGF-2.31 The ΔG energy values of the 5’ and 3’ RNA sequences around their seed sequences are −18 and −14 kcal/mol for IGF-1R.
IGF-1 Is a Target of miR-1 in Cardiac Myocytes

In neonatal cardiomyocytes, overexpression of miR-1 but not its physiologically coexpressed miR-133 resulted in a significant decrease in IGF-1 protein levels (Figure 1B and 1C). This was accompanied by an increase in the IGF-1 protein level. In contrast, no effect was observed when an unrelated miR (miR-143) with no complementarity to any seed sequence in the 3′ UTR of IGF-1 was used (Figure 1E). Consistent with these data, cotransfection of miR-1 with constructs containing mutated 3′ UTR seed sequences did not result in any decrease in luciferase activity (Figure 1E).

Reciprocal Regulation of miR-1 and IGF-1 During C2C12 Skeletal Muscle Cell Differentiation

It is well established that IGF-1 regulates skeletal muscle cell differentiation and that the miR-1 level changes during development in skeletal muscle cells. In the present study, we used C2C12 cells as an in vitro cell model that recapitulates skeletal muscle differentiation. On serum withdrawal, C2C12 myoblasts stop proliferating, irreversibly exit from the cell cycle, differentiate, and fuse into multinucleated skeletal myotubes after the concomitant coexpression of muscle differentiation markers. Consistent with that, upregulation of cell differentiation markers 2 days after serum withdrawal confirmed C2C12 differentiation (Figure 2A). Precursor and mature miR-1 levels, although absent at the myoblast stage, were remarkably increased at day 2 of differentiation (Figure 2B), confirming previous observations. The expression of miR-1 increased significantly after the switch to differentiation conditions and remained at a high level up to day 10, when myotube formation was completed and contractile activity could be observed (data not shown).

To monitor changes in the miR-1 level on C2C12 differentiation, we performed a luciferase assay by transfecting the IGF-1 luciferase construct in proliferating and differentiating C2C12 cells. Results show a significant reduction (>35%) in luciferase expression in differentiated cells compared with mutant IGF-1 3′ UTR vector and with myoblast state (Figure 2C), indicating that inhibition of the reporter gene was a consequence of the increased endogenous level of miR-1. No changes were obtained when a luciferase reporter not carrying any 3′ UTR was transfected (data not shown). In addition, immunofluorescence staining of C2C12 cells kept in differentiation medium demonstrated a striking decrease in the IGF-1 protein level starting from day 2 of differentiation (Figure 2D). In contrast, the IGF-1 mRNA level was unaltered (Figure 2E).

Reciprocal Regulation of miR-1 and IGF-1 Expression in the TAC and AKT Overexpression Mouse Models of Cardiac Hypertrophy

We11 and others15 have previously shown an inverse correlation between miR-1 expression and cardiac hypertrophy. We thus hypothesized that repression of miR-1 in the TAC model (Table 1 in the online-only Data Supplement) would be accompanied by an increase in the IGF-1 protein level. In agreement with this, Western blot analysis demonstrated an increased IGF-1 protein level after TAC, together with a decreased miR-1 level (Figure 3A and 3B). Similarly, a reduction in miR-1 expression was found in another mouse model.
model of cardiac hypertrophy, in which the downstream target of IGF-1, AKT, is constitutively overexpressed. Consistent with our observations, decreased miR-1 expression was accompanied by an increased IGF-1 protein level (Figure 3C and 3D).

The IGF-1 Pathway Controls miR-1 Levels Through Foxo3a Transcriptional Regulation

Molecular circuits in which miRs control the level of a factor that in turn regulates the same miRs have been described. For instance, Fontana and al described a circuitry involving sequentially miR-17-5p-20a-106a and AML1, in which miR-17-5p-20a-106a functions as a master gene complex interlinked with AML1 in a mutual negative feedback loop. We hypothesized that a circuit between miR-1 and IGF-1 might exist in striated muscle. To test this assumption, we measured miR-1 levels in different in vitro cell models in which IGF-1 activity was either diminished or increased. In neonatal cardiomyocytes treated with IGF-1, miR-1 expression was significantly decreased starting from 3 hours after treatment and remained depressed until 6 hours after treatment (Figure 4A). Notably, in C2C12 differentiated cells in which miR-1 is highly expressed, treatment with increasing IGF-1 doses induced a concomitant decrease in miR-1 expression with a significant reduction at a dose of 100 nmol/L IGF-1 (Figure 4B). A similar downregulation in miR-1 levels was observed when neonatal cardiomyocytes were infected with an adenovirus carrying a dominant active (DA-foxo) or dominant negative form (DN-foxo) of Foxo3a. In DA-foxo, all 3 potential AKT phosphorylation sites have been replaced by nonphosphorylatable amino acids, preventing it from being excluded from the nucleus in response to insulin, making it constitutively active. In DN-foxo, the transactivation domain (Δ256), which is important for coactivator recruitment, has been deleted. Our results demonstrate that although DA-foxo could upregulate miR-1 levels, the DN-foxo mutant could not (Figure 4C). These data strongly suggest that Foxo3a is able to influence miR-1 expression levels. Moreover, to test whether Foxo3a can regulate miR-1 promoter activity, we cloned a fragment containing the 2 potential binding sites mapped on mouse chromosome 2 into the luciferase vector. As shown in Figure 5B, DA-foxo, but not DN-foxo, induced a marked elevation of miR-1 promoter activity.

miR-1 overexpression should induce a decrease in the phosphorylation state of AKT and Foxo3 because of the decreased levels of IGF-1 and IGF-1R and thus a generalized decrease of IGF-1 signal transduction pathway. We therefore determined phospho-Foxo3a and phospho-AKT in differentiated C2C12 and neonatal cardiomyocytes infected with Ad-miR-1; data show a significant downregulation of both phospho-Foxo3a and phospho-AKT (Figure 5D). Taken together, these data suggest that Foxo3a can transcriptionally regulate miR-1 expression.

Repression of miR-1 Levels and Correlation With Cardiac Hypertrophy in Acromegalic Patients

Acromegaly is a syndrome that results from overproduction of growth hormone, which in turn increases IGF-1 synthesis in peripheral tissues and leads to a significant elevation in the IGF-1 plasma level. Cardiac hypertrophy is a dangerous consequence of growth hormone overproduction, and echo-
cardiographic analysis of cardiac function in patients with acromegaly consistently showed significantly increased left ventricular mass as well as end-diastolic left ventricular wall and septum thickness (Table).36 Furthermore, histological examination of myocardial biopsies showed hypertrophied cardiomyocytes with interstitial, perivascular, and focal replacement fibrosis (Figure 6A). Because blood levels of IGF-1 are elevated in patients with acromegaly, we measured miR-1 levels in myocardial biopsies by quantitative reverse transcription–polymerase chain reaction (Figure 6B). Interestingly, all patients showed a significant reduction in cardiac miR-1 levels compared with healthy donors, and there was a linear inverse correlation between miR-1 levels and left ventricular mass and end-diastolic left ventricular wall thickness (Figure 6C).

**Discussion**

MiR-mediated posttranscriptional gene regulation is now considered a fundamental player of many genetic programs. However, despite our ability to identify miRs, few regulatory targets have been established for vertebrate miRs. In this study, we demonstrated the potential feedback loop in which miR-1 and its target IGF-1 are reciprocally regulated.

Binding of IGF-1 to its receptor activates its intrinsic receptor tyrosine kinase, which phosphorylates several intracellular substrates such as the insulin receptor substrate-1 and Shc, leading to the activation of signaling pathways, including phosphatidylinositol 3-kinase/AKT pathways.39 Active AKT in turn phosphorylates and inhibits the winged-helix family of transcription factors, Foxo3a. In the present study, we demonstrated not only through IGF-1 stimulation but also with transfection of AKT or its downstream transcription factor Foxo3a that the IGF-1 pathway controls miR-1 expression (Figure 7). In fact, overexpression of AKT in neonatal cardiomyocytes reduces miR-1 expression, whereas overexpression of Foxo3a increases the miR level. These data are further supported by the identification of IGF-1R31 as a miR-1 target.

Several miR-1 cardiac targets involved in the control of hypertrophy, cell cycle, excitation-contraction coupling, and membrane excitability have been identified, including HDAC4,12 Hand2,13 the K+ channel subunit, Kir2.1 (KCNJ2), connexin 43 (GJA1),14 Ras GTPase–activating protein (Ras-GAP), cyclin-dependent kinase 9 (Cdk9), fibronectin, Ras homolog enriched in brain (Rheb),15 and, as recently shown, IGF-1.19 This indicates that miR-1 is involved in many different biological processes.

The importance of the IGF-1 pathway in cardiac function is well established.40 Indeed, the effects of IGF-1 on adult muscle are pleiotropic, ranging from antiapoptotic,18,41–43 hypertrophic, and regenerative effects on cardiac muscle.31,44,45 Thus, both miR-1 and IGF-1 are involved in most biological processes controlling cardiac function. Notably, our results strongly indicate miR-1 as a modifier and a regulator of the multiple effects of IGF-1 in cardiac muscle. The possibility that IGF-1 is a target of miR-1 has been suggested previously.19,46 However, we show here the biological relevance of this functional interaction and demonstrate that it is part of the autoregulatory circuit in cardiac and skeletal muscle (Figure 7). Our results also indicate that miR-1 may simultaneously downregulate IGF-1R together with IGF-1 protein, leading to a significant downmodulation of the whole downstream signal transduction cascade. The importance of our observation is strengthened by data from human samples, which strongly indicate the involvement of the miR-1 and IGF-1 regulatory loop in controlling human

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**Table. Clinical and Echocardiographic Characteristics of Acromegalic Patients**

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LV indicates left ventricular.

*Normal range=80-330 ng/mL.

†LV mass index calculated according to Devereux and Reichek36; normal values=91±20 g/m².
cardiac hypertrophy. Indeed, the striking inverse correlation between miR-1 levels and the degree of cardiac hypertrophy indicates that miR-1 is a key player in this process in humans. The interplay between IGF-I, AKT, Foxo3a, and miR-1 may provide a new paradigm to understand the manner in which IGF-1 modulates cardiac and skeletal muscle structure and function.\textsuperscript{18,47}

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**Disclosures**

None.

**References**


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**CLINICAL PERSPECTIVE**

MicroRNAs (miRNAs/miRs) are small conserved RNA molecules of 22 nucleotides that negatively modulate gene expression primarily through base paring to the 3′ untranslated region of target messenger RNAs. The muscle-specific miR-1 has been implicated in cardiac hypertrophy, heart development, cardiac stem cell differentiation, and arrhythmias through targeting of regulatory proteins. In this study, we investigated the molecular mechanisms through which miR-1 intervenes in regulation of cardiac and skeletal muscle cell growth and differentiation. We demonstrate that miR-1 controls the expression of insulin-like growth factor-1 (IGF-1) and IGF-1 receptor protein levels by translation. The IGF-1 pathway is critically involved in many aspects of cardiac development and cardiac function. We found that in conditions in which miR-1 is decreased, such as cardiac hypertrophy, IGF-1 is increased; the regulation is reciprocal because IGF-1 stimulation leads to downregulation of miR-1 levels. This effect is dependent on IGF-1 inhibition of the Foxo3 transcription factor, which regulates miR-1 promoter activity. The clinical relevance of these observations is demonstrated by analyzing the expression of miR-1 in cardiac biopsies of patients with acromegaly, a condition in which growth hormone and IGF-1 are overproduced and cardiac myocyte size is dramatically increased; miR-1 levels inversely correlate with echocardiographic parameters of cardiac mass in these patients. Our results add information in regard to the manner in which the IGF-1 pathway regulates cardiac function, demonstrating the role of miR-1 in response to cardiac stress and hypertrophy.
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Reciprocal regulation of microRNA-1 and IGF-1 signal transduction cascade in cardiac and skeletal muscle in physiological and pathological conditions

Elia: miR-1 and IGF-1 circuitry in cardiac muscle

Leonardo Elia, Ph.D., Riccardo Contu, B.Sc., Manuela Quintavalle, Ph.D, Francesca Varrone, Ph.D., Cristina Chimenti, M.D., Ph.D., Matteo Antonio Russo, M.D., Vincenzo Cimino, M.D., Laura De Marinis, M.D., Andrea Frustaci, M.D., Daniele Catalucci, Ph.D., Gianluigi Condorelli, M.D., Ph.D.
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<td>IVSD (mm)</td>
<td>0,84±0,05</td>
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**Supplementary Table 1. Echocardiographic characteristics of TAC mice.**

HW, heart weight (mg); BW, body weight (g); LVM, left ventricular mass (mg); LVPWTD, diastolic left ventricular posterior wall thickness (mm); IVSD, diastolic interventricular septum thickness (mm). Sham vs TAC: * p<0.05, **p<0.01, *** p<0.001
Supplementary Figure 1. IGF-1R regulation by miR-1.

(A) IGF-1R mouse and human seed sequences, (B) Luciferase reporter assay (mean ± S.E., minimum of 3 experiments per group) on 293T cells, performed by cotransfection of miR-1 oligonucleotide (20nM) with a luciferase reporter gene linked to wt IGF-1R (□)
and mt IGF-1R ( ■) 3’UTRs. (C) IGF-1R Western blot analysis on C2C12 cells cultured in GM and DM (DM1 and 3: differentiation medium at day 1 and 3), on the bottom densitometry quantification.

*P<0.05, versus control (wt 3’UTR using miR-133). Data are expressed as the mean ± S.E. of 3 independent experiments.