Review Article

Mechanism of Immune Response Through mRNA/miRNA Effect in Vascular Dysfunctions

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Abstract

With the aim of understanding the socioeconomic burden of autoimmune diseases, attenuating ACS introduce the phenomenon of the immunological regulation system provoking all stages of predisposing lesions criticizing the arousal of prognostic metabolic role at cellular biogenesis. The basic methodologies of repairs focus on the significance of mRNA/miRNA triggering the kinetics of pharmacodynamics obstacles at CVD mortality, identify the systematic therapeutics of exertions in the miRNAs of 21, 29, 23, 27, 24, 126, 143 and 145 insights the signaling of platelet aggregation associates the gene expressions in the form of supportive biomarker targets.

1. Introduction

Over 1500 miRNAs the estimation of 60% human genome at worldwide ranges the reparative strategies for cardiovascular disorders in the endogenous discovery of non-coding mRNAs binding process risk factor the adaptive responses. At the prevalence of vascular disease, the stress conditions novel the catalyzes of genetic modification that primarily engages in the complexity of cellular short single- stranded phenotype. The diverse critical form of ischemia process the diagnostic progression of initiative oxidation stress, angiogenesis and plaque formation constituting the immunological metabolic differences in detectable extracellular prognosis. And also the real quantitative time of miRNA reveal the physiological responses at expressed profiles of pathologies signal the cascade of transduction via the unclear modulators interdependence of complications networking accompanying the analysis of miRNA-epigenetics. At the residual consideration of VSMCs facilitating the macrophages predict the degradation at translational miRNAs of several pathways prognosis the novel of the biomarker at CAD [1]. Thus the emergence of size units and number of particles evident the cell origin in the functional contribution of exosomes cooperative to the protective and regenerative outcome.

The inhibitory effects of neuro-cellular diseases in an association of CVD on the basis of the oncological aspect establish the genetic mutations of contributing differentiation, proliferation, hypertension, erythropoiesis switching the bicistronic upregulating myocardial infarction in the correlations of replacing preventive adhesiveness [2]. As published in 2006, the expressed miRNA for heart disease follow-up the alterations of tissue role in fibrosis, angiogenesis, heart failure, cardiac hypertrophy, and stenosis [3, 4] for a fundamental action of targeting drug therapy conventional at systemic impact. In result, the perspective of disease context at *in vivo* leads the requisite of molecular intervention in approving the clinical concept of better efficacy and reversal path physiological functioning apart from structure issue.

This review outline, the critical role of immune staging diagnostic for potentially differing CAD events by its fate of regulating smooth muscle cells in brief as a primer with the number of miRNAs.

2. Mechanism

The maturation in miRNA begin by the process of transcription binding the genes at cytoplasm inducing the multiprotein complexes converting the inotropic non-coding miRNA from RNA polymerase (RISC) II into III with the clustered primary RNA pri(RNA) as a genomic of multiple polycistronic bases prolong the characteristic of biogenesis in the megakaryocytes of impairing platelets. The principles of biotechnology in the theoretical studies of expected the pairing of miRNA-mRNA substantially relate the protein adjustments [5] with the delicates of gene expression in the responses of microenvironmental protein production moving to the translation process upregulate the IL β interactions to the bacterium of obtaining the dramatic filter staging. The proposal of hyperactivity in the self-regulation of receptor expressions of P2Y12 presents only 30% of transcriptome at the levels of proteome explaining the communications of speculations in intracellular and extracellular plasma membrane originating the transfer of lumen inwards of cytic vesicles utilize the capability of endosomal intra-lumen vesicles [6,7]. The vascular nature of interacting the selective proteins of different cell types derives the glycolipids, cermide, and sphingomyelin in the exposure of transduction signaling the transmembraneous action heterogeneously [8] via lumen in the miRNA composition of segregating the hematologies disorders by the existence of surface cell antigen enables the maturity in miRNAs in the presence of megakaryocytic include the vera of polycythemia and thrombocytopenia disorders at the higher pro-platelets processes of granules, nucleolus containing TRBP, Dicer-exosome and Ago2 [9].

At *in vivo*, the monocyte cells transcript the platelet-derived endothelium familiar of miRNA stimulate its own RNAs by focusing the recognition of sequence targets. The role of simultaneous platelets in ST- elevation opposes the analysis of microparticles activation behaving time dependant avenue of diagnostic disease allowance specifically vasculatures correlating the advantageous RNA presence. The cues of reactivity based on platelet profiles lunk the miRNA/ mRNA paramount the unknown RNA affects elucidate the CVD events at high BMI impact the homeostatic maintenance personalizing the combined 3 studies together strongly novel the vessels influences [10, 11].

The precursors of sequential primary RNA yield the cofactor of 70 nucleotides interacting the multiprotein at the

junctions of exon and coding miRNA regions contributing the results of degrading the translational regression process. The endogenous RNA competing for the gene regulations mediating the act of sponges at biology effect entitle the analog of miRNA compensating the re-arrangements of protein balance in the altered network of homologous diminishes. However, the sensitivity in the exacerbations of resistance and injury impinges the pathways of at responding the diagnostic of CVD [12, 13]. And therefore, the under stress dependence trigger the effect of downstreaming existence implying the inactive differential mechanistic behavior of performances.

At the different plasma levels of overexpressed miRNA at the pathology of circulation levels into tissue independently create the scenario of endothelial dysfunctions, calculating the stages of injuries in measuring the arterial tissues of the carotid [14], controlling the distinct lesions [15] and cholesterol linking of increasing hydrolysis. The illustration of direct genes targets at larger clinical studies report the formation of neointimal lesions deposits the amorphous collagen I and macrophages causing the hyperplasia at the genetic dysfunctions in the establishment of miRNAs deletions. The highlighted adenovirus-mediated genes explain the pathogenesis of ROS in atherosclerosis expressing the hydrogen peroxide, restenosis development after angioplasty, reversal cell apoptosis, down regulations and depletions [16] targeting the molecular adhesions, leukocyte consequences and environmental interactions along with the risk factors of hypertension and hypercholesterolemia generally hyper aggregate the acute thrombosis event lacking the significance of nuclear DNA promoting the end products in vascular endothelial cells. The exertion of insulin growth factor releasing the scavenging microvesicles and lipoproteins argonaute the complexes of recipient cells by micro screening the co-expression of stimulating differentiating miRNA series i.e. miR223, 21, 24, 197 subjecting pro-thrombin, acute MI and atherogenesis [17].

Based on the cellular alteration levels of cholesterol homeostasis carrying the lipoproteins in the association of metabolic disease exerts the pleiotropic communications incorporated ceramide-dependent pathway oxidizing the involvement of LDL, HDL transport miRNA for expanding the circuits of plasma levels by delivering the macrophages to surface receptors. The implicated enrichment of miRNA production at multi organs experiment the synthesis of fatty acids, lipoproteins, and cholesterol [18] broadly repress the genes up-taking cholesterol (HMGSI, SC4MOL, SRBI) and lipids (PPARG, GPAM, ANGPTL3 and NDSTI) remodeling the potent networking of apoB-containing lipoprotein. However, epidemiologically the critical efflux of excessive cholesterol removal pathways directing atherosclerotic plaques understands the hepatic biogenesis from peripheral cells. The opposing transcriptional process of fatty acid oxidation 80% of macrophages enhance the transportation to plasma retaining anti- inflammation, excreting bile and endothelial cells protection from induced cytokines [19]. Subsequently, the characteristic foster of T cells activity in the paradox aerobic glycolysis and mitochondrial oxidative phoshorylation at the reports of atheroprotective plasma accumulation is the suggestive of antagonism [20] beyond the beneficial effect of genetic deletion in the terms of hepatosteatosis and triglycerides conflicting the warrants of species of utility inhibiting dyslipidemia treatment [21]. The studies of accumulation in inflammatory responses signal the NF-KB cytoplasmic-nuclear translocation targets the sustained predisposing lesion formation in the biomechanical stimuli undergo the process of time durational changes promoting the adherence of leukocyte recruitment sprouting protein I to the vessels

wall virtue to the selective unknown miRNAs activation cause vascular integrated fibroblast. Hence the distinctive pro-inflammatory factor of thrombosis components of NF-KB independently suppress the atherosclerotic prone ApoE consistency to the transgenic negative effect 50% reduction at vascular endothelium subjecting the myeloid cells diverse to sepsis opportunistic of replacement therapy.

In vitro, the encode of MAFB derive the cell lineage in the repression of myeloid cells overlapping the GP IIb genes [20, 21] and GP IIIa adhere the binding of fibrinogens with miR 130a at the mutations of 3UTR MAFB to control platelet counts. According to the oncology exposure of MPLr mature the functioning of platelet cyclase site the injury recruits selectively to agonist potent to P2Y12 receptor co-expressed in miR223 luciferase gene assays.

The circadian rhythm of cryptochrome genes at the miR107 complex the phosphorylation of VWF locomotor output cycles at platelet membranes for the previously prothrombic state attached surface membrane infusion release. And at the subunits of PKA inactive enzyme catalysis the release of granules expressed by second messenger (CAMP) for demonstrating the dose of epinephrine suppress hypoactive state at miR200b direct unnecessary activation of megakaryocytes [22].

The replenishment of disease blockade the complimentary synthesizes relying on the accuracy of single biomarker opportunistic to stimuli, indicative phenotype, gene polymorphism, disease risk factor and uniquely diagnostic signature of antisense therapy in the conjugation of cholesterol. Moreover, the positive effects in the use of amplified miRNA at the notion of disease in the potential form capture the cross-reactivity of passengers in the resistance of abolished cancerous cells undesirable to side effects with the evolutionary to pathology disrupt the anti-miRNA therapy susceptible to inter-individual functional management [23]. The distinguishable developmental progression enhance the targets of identifying ‘seed region’ firmly documenting the pharmacokinetics and pharmacodynamics resistance to the habour of phosphorothioate modifications facilitating the conjugation of tissue type lacking the nucleic acid i.e 2’-O-methoxyethyl MoE and 2’-fluoro possessing the high affinity of atherosclerosis risk factor, hepatic physiology, specificity analysis, toxicity and therapeutic clotting factor to the intrinsic factor.

The studies of sugar absorption accumulate at renal and hepatic site differentiating diagnosis the properties of relatively in the mechanism of action, storage system, half-life chemistries, stability, inhibition modes, and the independent pathways of degradation leading the mature miRNA [24-27). The resolved questionnaire of excessive antimiR copies, long-lasting effects, active miRNA, and release into cellular depots of storage kinetics remained current issues of needing an indication of reversibility [26, 27]. And further at safety carrier, the displaying chemical histology of tissue distribution involves the molecular solubility of masses detecting the trapped persistence of extracellular spaces by administrating pharmaco drugs uptaking the gradual release within few weeks [28] that greatly accomplish oligonucleotide antimiR systems.

3. Risk factors

1. Cholesterol and lipoprotein homeostasis

   The impeding early stage of atherosclerosis pertubate the initiation of bounded regulation of (SREBPs) transcription gene in the metabolism of high cholesterol [29] target the liver organ directly in controlling β oxidation at miR-370 modulating the HMGCS1, HMGCR and SQLE synthesis with the unknown environmental factors of lipid metabolism at miR-122 levels. The efflux of lipoprotein uptake reverse the cholesterol transport matures the HDL in the biogenesis of deficiencies that cause CVD risk factors [30]. The imbalances of lipoprotein levels enrich the physiological circulation of LDL and HDL metabolite the hepatic functioning of hepatocyte genes in the responses of cholesterol MTTP (Microsomal triglyceride transfer protein) carrying the lipogenesis of (LPGATL) 17 lysophosphatidyl glycerol acyltransferase 1 mitigate the desire of athero-progression at MTP inhibitions.

2. Inflammation and plaque formation

   The characteristic of lipid cone at VSMC evolve the calcification of osteoblast surrounding the foam cells at monocytes of miR-155, miR125a-5p with scavenging receptors of macrophages promoting the instability of fatty streaks at the evolution of neointima targets miR-26a [31]. The pro-oxidants and proteolytic factors in the regards of elastin, COI3A1, Fibrillin in the conditions of intra-plaque hemorrhages stimulate H_2O_2 apoptosis that destabilizes the mononuclear or cells expressed manifestation of rupture at an aortic aneurysm in the cause of cell death. The genomic miRNA of lineage functioning of endogenous cyclin E protein in the influences of interleukin IL-17 production at hematopoietic platelet abundance shed the assessment of clopidogrel in NSTEMI of ACS [32]. And also the significance of transfection at glycation exert the heterotypic regulation overexpress the primary carcinomas and metastatic gastric cancer with poor survival rates [33].

3. Vascular dysfunctions-remodeling

   At *in vivo*, the participation of cellular communication within the tissue paradigm of tunneling nanotubes (TNF) [34] support the passage of VSMC-EC passage in the overloads of trans-aortic pressure at the active TGF-β arteries constriction confer the miRNAs 143/145 for the vascular protection. And the derived apoptotic bodies based in animal studies of a miR126 duplex to the exposure at KlF2-dependent maintain the contractile of VSMC [35] conditional to fibrous plaques at all different phases challenge the cytoskeletal conditions of actin fibers and dynamics impairment by the effect of ACEs analog ELK-1 and KLFs on the exhibition of baseline BP reduction. Therefore, at invivo the bicistronic gene cluster risk factor of adenovirus and lentivirus of KLF4 provoking the injuries can be neutralized by miR21 anti-genetic of the post-transcriptional process in maintaining the smed proteins of DROSHA-maturation for cardiac remodeling.

4. Atherosclerosis

At the beneficial of systemic multi-organ targets of miR29a and miR29b correlate the increase of extracellular matrix-related genes in the responses of fibrosis, aortic dilation in the aneurysms of collagen expression and MI enhancing the efficacy of miR29 dramatically explain the elastin insufficiencies stimulating liver and kidneys at animal model trials. The vascular pathologies composed of miR23,miR27,miR24 and miR21 hallmark -the disrupted integrity of neoangiogenesis in the silences of post-injury mediate the origin of LDL infiltrations oxidizing the adherence of (ICAM-1, VCAM-1) stimulations. Whereas, the endothelial dysfunctions lie in the hypercholesterolemia grip the leukocyte factor of intima thickness consequences flowing the pathways of KLF-2 or KLF-4 [36]. The antagomir based infarction trace the GATA2 and p21-activated kinase 4 (PAK 4) measure the relevance of cardiomyocytes reacting with cell death in the impairment of the inner wall thickness of adventitia vasa overloaded with cholesterol productions oxygen diffusion macrophages synthase (eVOS) by STATA5A effect the angiogenesis at miR17 and miR92 making contradictory results [37, 38].

At the assumed immunological events of leukocyte recruitment and atherosclerosis activation in the differentiation of secretion, lipoprotein retention and the mediation of cytokines and chemokines summarize the efflux of cholesterol esterification ACAT 1, LDL-CD30, ABCA1 [39] conversely focus on gene therapy promote number of miR26, miR33, miR106, miR144, miR128-1, miR1306, miR148a, miR3016, miR302a, and miR758 emphasizing at higher degrees for safer evaluations at miR145. And indeed, the maintenance of 2 phenotypes M1and M2 of miR-let7a, miR199, 21, 27a, 33, 124, 125a, 155, 146a, 214, and 223 with immune cells of T cells and dendritic cells explore the functions milieu of triggering specific antigen antisense the oligonucleotides (ASOs) target the miR33and miR122 in the prospective of pharmacological compounds.

5. CAD and HTN

The roles of miR143/145 knock out the pathogenesis of ApoE spontaneously in circulating lipid retention and inflammations exhibit the normal serum levels of cholesterol quantifying the unstable angina risk factor of hypertension a predictable 24hrs DBP monitoring, vascular injury in the absence of diabetes and the hypothesis of CHD magnifying the assurance of peripheral blood levels in acute MI on the measurements of troponin T levels [40]. The animal studies demonstrate the aortic plaque sites circulating brachiocephalic arteries contractile the laminar blood flow in the transduction stress levels of JAM-A endothelial cells [41, 42].

At clinical studies, the proliferative state of chronic stress level at worsening of hypertension persist the extracellular signaling uniform at the junctional route of kinase regulation contribute the biomarkers of myocardin and KLR4 express the cause of myogenic responsive generation at RAAS system that mutant the BMPR2 type 2 receptor in the significant risk factor of hypoxia [43]. At *in vivo*, the cardiac growth factor at structural growth effect of fibroblast in the elevation of EGF and BCI-2 levels and invitro, the cardiomyocyte

hypertrophy induction asymmetry the oncogenic predominance of particular 6 sites (lungs, breast, colon, stomach, pancreas, and prostate) at the enzymatic activity of nitric oxide, programme the cell death (PDCD4) by miR21 observing the additional tumorigenic feature of cervical carcinoma and glioblastoma cells target pded4 leading CHD involve regeneration at defensive superoxide dismutase reduction [44].

6. Dyslipidemia and DM

   The leading potential of metabolic syndrome relative to lung cancer risk factor immortal to brachial epithelial cells, HBEC downregulate the pancreatic cancer cells cooperative to motility colon cancer cells suppress the mechanism of p120 catenin at suggestive of miR33a and miR336 target the transporters of ABCA1 and ABCG1 responding the protein genes SREBF2 and SREBF1 cassette [45]. The leading domain of embryogenesis containing EVH1 in the subunits of PIK3R2 block VCAM-1 feedback the early growth of atherosclerosis synthesis HDL by suppressing VLDL and triglyceride levels establish genetic difference of ablation in T2DM percutaneous administrative of aspirin [46].

7. Ischemia and AMI

   The stratified unstable angina elusive to troponin values compares the rigorous effect of chest pain distinctive to cardiac diseases at a higher incidence of ischemic necrosis with regards of different types of peripheral circulation favoring specificity and sensitivity. The measures of STEMI and NSTEMI with an n value of 32=36 risk ratio the correlated values of CK-MB and CTnT essential for controlling CHF in the generalized improvement of myocardial injury. The reperfusion injury in the myocyte necrosis activate the deposition of cardiac fibroblast at extracellular matrix (ECM) express the clusters of miR29a, miR29b1, miR2962 and miR29c concomitant towards the remodeling. And at the targets of miR29 mimics in fibrosis-related genes cause side effects at larger organs through its blood vessels at aorta structurally elevate many anti-apoptotic proteins overexpress the elevation of family members (miR15a, miR56, miR16-1, miR16-2, miR195 and miR497 leading heart failure crucial for the pathogenic heart disease. At the suppression of family member in the biological diverse of multiplicity of sequence can be prevented by a single antisense 8-meroligonucleotide inhibitor at conducting the pharmacological experiments on ischemia-reperfusion of infarction restoring cardiac functions upregulating miR214 interchanging Na/Ca regulation for decreasing the NC×I failing heart events by restorations of AAV9, SERCA2A gene therapy at miR-1 expression [47, 48].

4. Conclusion

The evidence of vascular injury in the responses of VSMCs of plasma miR143 and 145 links the risk factors with the warrants of effectiveness in the modifications of exchangeable cellular communication strengthening the defensive conditions at clotting factor. The RNA profiles of platelet in calculating the total number of proteins target the profounded effect in the least pathways of 50% chances of side effects validating the complex role of cells assuming diseases precisely. The fascinating functions of miRNAs in the regulation of transcription classify mRNA/miRNAs in

the action of issues at the preclinical use express the limitations of therapeutic studies for a long-term enthusiasm in the attested phases. At invivo and invitro the antisense oligo (ASOs) in the association of HDL familial hypercholesterolemia beyond the multi-strategy silence the functions of tissue bonding the affinity of cholesterol beneficial mimicking the malignancies at hematologies consider the CAD residual burden at delivering networking of blood vessels.

Conflicts of interest

The authors indicated no potential conflicts of interest.

References

1. Creemers EE, Tijsen AJ, Pinto YM. Circulating microRNAs: novel biomarkers and extracellular communicators in cardiovascular disease? Circ Res 110 (2012): 483-495.
2. M. V. Iorio and C. M. Croce. "MicroRNA dysregulation in cancer: Diagnostics, monitoring and therapeutics. A comprehensive review. EMBO Molecular Medicine 4 (2012): 143-159.
3. Thum T, *et al.* MicroRNAs in the human heart: a clue to fetal gene reprogramming in heart failure. Circulation 116 (2007): 258–267.
4. Thum, T. *et al.* MicroRNA-21 contributes to myocardial disease by stimulating MAP kinase signalling . Nature 456 (2008): 980–984.
5. Lee CT, Risom T, Strauss WM. Evolutionary conservation of microRNA regulatory circuits: An examination of microRNA gene complexity and conserved microRNA-target interactions through metazoan phylogeny. DNA Cell Biol 26 (2007): 209–218.
6. McRedmond JP, Park SD, Reilly DF, Coppinger JA, Maguire PB, Shields DC, Fitzgerald DJ. Integration of proteomics and genomics in platelets: a profile of platelet proteins and plateletspecificgenes. Mol Cell Proteomics 3 (2004): 133–144.
7. Londin ER, Hatzimichael E, Loher P, Edelstein L, Shaw C, Delgrosso K, Fortina P, Bray PF, McKenzie SE, Rigoutsos I. The human platelet: strong transcriptome correlations among individuals associate weakly with the platelet proteome. Biol Direct 9 (2014): 3.
8. Zakharova L, SvetlovaM, Fomina AF. T cell exosomes induce cholesterol accumulation in human monocytes via phosphatidylserine receptor. J Cell Physiol 212 (2007): 174–181.
9. Hussein K, Theophile K, Dralle W, Wiese B, Kreipe H, Bock O. MicroRNA expression profiling of megakaryocytes in primary myelofibrosis and essential thrombocythemia. Platelets 20 (2009): 391–400.
10. Freedman JE, Larson MG, Tanriverdi K, O'Donnell CJ, Morin K, Hakanson AS, Vasan RS, Johnson AD, Iafrati MD, Benjamin EJ. Relation of platelet and leukocyte inflammatory transcripts to body mass index in the Framingham heart study. Circulation 122 (2010): 119–29.
11. Healy AM, Pickard MD, Pradhan AD, Wang Y, Chen Z, Croce K, Sakuma M, Shi C, Zago AC, Garasic J, Damokosh AI, Dowie TL, Poisson L, Lillie J, Libby P, Ridker PM, Simon DI. Platelet expression profiling

and clinical validation of myeloidrelated protein-14 as a novel determinant of cardiovascular events. Circulation 113 (2006): 2278–2284.

12. Boon RA, Iekushi K, Lechner S, Seeger T, Fischer A, et al. MicroRNA-34a regulates cardiac ageing and function. Nature 495 (2013): 107–110.
13. Montgomery RL, Hullinger TG, SemusHM, Dickinson BA, Seto AG, et al. Therapeutic inhibition of miR-208a improves cardiac function and survival during heart failure. Circulation 124 (2011): 1537–1547.
14. Liu X, Cheng Y, Zhang S, Lin Y, Yang J, Zhang C. A necessary role of miR-221 and miR-222 in vascular smooth muscle cell proliferation and neointimal hyperplasia. Circulation Research 104 (2009): 476–487.
15. Cordes KR, Sheehy NT, White MP, Berry EC, Morton SU, Muth AN, et al. miR-145 and miR-143 regulate smooth muscle cell fate and plasticity. Nature 460 (2009): 705–710.
16. Ji R, Cheng Y, Yue J, Yang J, Liu X, Chen H, et al. MicroRNA expression signature and antisense-mediated depletion reveal an essential role of MicroRNA in vascular neointimal lesion formation. Circulation Research 100 (2007): 1579–1588.
17. P. Willeit, A. Zampetaki, K. Dudek, et al., Circulating microRNAs as novel biomarkers for platelet activation, Circ. Res. 112 (2013): 595–600.
18. Elmen J, Lindow M, Schutz S, Lawrence M, Petri A, Obad S, Lindholm M, Hedtjarn M, Hansen HF, Berger U, Gullans S, Kearney P, Sarnow P, Straarup EM, Kauppinen S. LNA-mediated microRNA silencing in non-human primates. Nature 452 (2008): 896–899.
19. Rayner KJ, Sheedy FJ, Esau CC, Hussain FN, Temel RE, Parathath S, van Gils JM, Rayner AJ, Chang AN, Suarez Y, Fernandez-Hernando C, Fisher EA, Moore KJ. Antagonism of miR-33 in mice promotes reverse cholesterol transport and regression of atherosclerosis. The Journal of clinical investigation 121 (2011): 2921–31.
20. Ouimet M, Ediriweera HN, Gundra UM, Sheedy FJ, Ramkhelawon B, et al. MicroRNA-33-dependent regulation of macrophage metabolism directs immune cell polarization in atherosclerosis. The Journal of clinical investigation 2015.
21. Horie T, Nishino T, Baba O, Kuwabara Y, Nakao T, et al. MicroRNA-33 regulates sterol regulatory element-binding protein 1 expression in mice. Nature communications 4 (2013): 2883.
22. Nagalla S, Shaw C, Kong X, Kondkar AA, Edelstein LC, et al. Platelet microRNA-mRNA coexpression profiles correlate with platelet reactivity. Blood 117 (2011): 5189–5197.
23. Ambros V. The functions of animal microRNAs. Nature 431 (2004): 350–355.
24. Filipowicz W. RNAi: The nuts and bolts of the RISC machine. Cell 122 (2005): 17–20.
25. Zamore PD, Haley B. Ribo-gnome: The big world of small RNAs. Science 309 (2005): 1519–1524.
26. Girardot M, Pecquet C, Boukour S, Knoops L, Ferrant A, et al. miR-28 is a thrombopoietin receptor targeting microRNA detected in a fraction of myeloproliferative neoplasm patient platelets. Blood 116 (2010): 437–445.
27. Jin J, Kunapuli SP. Coactivation of two different G proteincoupled receptors is essential for ADP induced platelet aggregation. Proc Natl Acad Sci 95 (1998): 8070–8074.

28. Bruchova H, Merkerova M, Prchal JT. Aberrant expression of microRNA in polycythemia vera. Haematologica 93 (2008): 1009–1016.
29. Marquart TJ, Allen RM, Ory DS, Baldan A. miR-33 links SREBP-2 induction to repression of sterol transporters. Proc Natl Acad Sci 107 (2010): 12228–12232.
30. Brown MS, Goldstein JL. Familial hypercholesterolemia: A genetic defect in the low-density lipoprotein receptor. The New England journal of medicine 294 (1976): 1386–1390.
31. Leeper NJ, Raiesdana A, Kojima Y, et al. MicroRNA-26a is a novel regulator of vascular smooth muscle cell function. J Cell Physiol 226 (2011): 1035–1043.
32. R. Shi, L. Ge, X. Zhou, et al., Decreased platelet miR-223 expression is associated with high on-clopidogrel platelet reactivity. Thromb Res 131 (2013): 508–513.
33. X. Li, Y. Zhang, H. Zhang, et al., miRNA-223 promotes gastric cancer invasion and metastasis by targeting tumor suppressor EPB41L3, Molecular Cancer Research: MCR 9 (2011): 824–833.
34. Climent M, Quintavalle M, Miragoli M, Chen J, Condorelli G, Elia L. TGFbeta Triggers miR-143/145 Transfer From Smooth Muscle Cells to Endothelial Cells, Thereby Modulating Vessel Stabilization. Circulation research 116 (2015): 1753–1764.
35. Zhou J, Li YS, Nguyen P, Wang KC, Weiss A, et al. Regulation of vascular smooth muscle cell turnover by endothelial cell-secreted microRNA-126: role of shear stress. Circulation research 113 (2013): 40–51.
36. Wu W, Xiao H, Laguna-Fernandez A, et al. Flow-Dependent Regulation of Kruppel-Like Factor 2 Is Mediated by MicroRNA-92a. Circulation 124 (2011): 633–641.
37. Suarez Y. Microregulation of plaque neovascularization. Arterioscler Thromb Vasc Biol 30 (2010): 1500–1501.
38. Sun HX, Zeng DY, Li RT, et al. Essential role of microRNA-155 in regulating endotheliumdependent vasorelaxation by targeting endothelial nitric oxide synthase. Hypertension 60 (2012): 1407–1414.
39. Zhang M, Wu JF, Chen WJ, Tang SL, Mo ZC, et al. MicroRNA-27a/b regulates cellular cholesterol efflux, influx and esterification/hydrolysis in THP-1 macrophages. Atherosclerosis 234 (2014): 54–64.
40. S. Fichtlscherer, S. De Rosa, H. Fox et al. Circulating microRNAs in patients with coronary artery disease. Circulation Research 107 (2010): 677–684.
41. E. Hergenreider, S. Heydt, K. Tr´eguer et al. Atheroprotective communication between endothelial cells and smooth muscle cells through miRNAs. Nature Cell Biology 14 (2012): 249–256.
42. M. M. N. Schmitt, R. T. A. Megens, A. Zernecke et al. Endothelial junctional adhesion molecule-a guides monocytes into flow-dependent predilection sites of atherosclerosis. Circulation 129 (2014): 66–76.
43. P. Caruso, Y Dempsie, H. C. Stevens et al. Arole for miR-145 in pulmonary arterial hypertension: evidence frommouse models and patient samples. Circulation Research 111 (2012): 290–300.
44. M.E. Hatley, D.M. Patrick, M.R. Garcia, et al. Modulation of K-Ras-dependent lung tumorigenesis by MicroRNA-21. Cancer Cell 18 (2010): 282–293.
45. D.B. Stairs, L.J. Bayne, B. Rhoades, et al. Deletion of p120-catenin results in a tumor microenvironment with inflammation and cancer that establishes it as a tumor suppressor gene. Cancer Cell 19 (2011): 470–483.

46. Zampetaki P, Willeit L. Tilling, et al. Prospective study on circulating MicroRNAs and risk of myocardial infarction. J Am Coll Cardiol 60 (2012): 290–299.
47. Soh J, Iqbal J, Queiroz J, Fernandez-Hernando C, Hussain MM. MicroRNA-30c reduces hyperlipidemia and atherosclerosis in mice by decreasing lipid synthesis and lipoprotein secretion. Nature medicine 19 (2013): 892–900.
48. Rayner KJ, Suarez Y, Davalos A, Parathath S, Fitzgerald ML, Tamehiro N, Fisher EA, Moore KJ, Fernandez-Hernando C. MiR-33 contributes to the regulation of cholesterol homeostasis. Science 328 (2010): 1570–1573.

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