A MicroRNA Circuitry Links Macrophage Polarization to Metabolic Homeostasis

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Macrophages play an important role in tissue repair and remodeling and innate immune response. Tissue macrophages are highly heterogeneous and can undergo 2 distinct programs of functional specification termed classical (M1) and alternative (M2) activation. In response to signals elicited by bacterial infections, such as lipopolysaccharide (LPS) and interferon-γ, macrophages adopt a proinflammatory phenotype and contribute to defense against invading pathogens through phagocytosis, bactericidal activity, and the secretion of proinflammatory cytokines and chemokines. In contrast, interleukin-4 (IL-4) and IL-13 promote alternative activation of macrophages that favors tissue remodeling and repair, parasite elimination, and tumor progression. At the molecular level, M1 and M2 macrophages express unique cell surface markers and secrete distinct sets of effector molecules. Classically activated macrophages secrete proinflammatory cytokines and chemokines. Classically activated macrophages secrete proinflammatory cytokines and chemokines. Alternative activation of macrophages that favors tissue remodeling and repair, parasite elimination, and tumor progression is termed classical inflammation.

In obesity, macrophages adopt an alternatively activated phenotype. Signal transducer and activator of transcription 6 is a transcription factor downstream of IL-4 and IL-13 which promotes M2 macrophage polarization through a dual mechanism: activation of M2 genetic program cooperatively with signal transducer and activator of transcription 6 and active repression of M1 macrophage gene expression.

The relationship between macrophage polarization and insulin sensitivity extends beyond simple correlation. In fact, mouse models with defective proinflammatory cytokine signaling tend to have improved glucose homeostasis and insulin sensitivity after diet-induced obesity. On the contrary, genetic and pharmacological manipulations that impair macrophage alternative activation exacerbate obesity-induced insulin resistance and associated metabolic disorders, such as hepatic steatosis. Anti-inflammation therapies have demonstrated promising effects in lowering blood glucose in recent clinical studies.

How is macrophage polarization fine-tuned in metabolic tissues? One of the most striking aspects of nutrient excess-induced inflammation is that certain nutrients are capable of directly engaging inflammatory signaling pathways. Saturated fatty acids bind to toll-like receptor (TLR) and activate proinflammatory response whereas polyunsaturated fatty acids elicit beneficial metabolic effects in part through repressing inflammatory signaling. Chronic nutrient excess also promotes endoplasmic reticulum stress and stimulates c-Jun N-terminal kinase/IκB kinase signaling, leading to nuclear factor κB activation and the induction of proinflammatory gene expression. Recent studies have identified several transcription factors and coactivators that regulate macrophage alternative activation. Signal transducer and activator of transcription 6 is an important regulator of metabolic homeostasis (Figure). MicroRNAs (miRNAs) are short non-coding RNAs that are approximately 22 nucleotide in length and modulate gene expression through binding to target mRNAs. The pairing of miRNA to its target mRNAs...
typically results in their degradation and/or repression of translation. Accumulating evidence has demonstrated that miRNAs represent an important layer of gene regulation in the context of metabolic homeostasis. For example, miR-33a and miR-33b, whose host genes are SREBF2 and SREBF1, respectively, are critical regulators of cholesterol metabolism, whereas miR-103 and miR-107 regulate insulin sensitivity and glucose homeostasis by modulating caveolin-1 in adipocytes. Previous studies have implicated different miRNA members in the regulation of innate and adaptive immune responses as well as immune cell differentiation. However, a role for miRNA in macrophage polarization has not been explored.

MiR-223 is highly enriched in bone marrow and macrophages isolated from adipose tissue, whereas its expression in adipocytes is relatively low. In cultured bone marrow–derived macrophages, miR-223 expression was dramatically induced in response to IL-4 but significantly repressed by LPS treatments, suggesting that miR-223 may regulate certain aspects of macrophage activation. In support of this, miR-223–deficient macrophages elicited a heightened response to LPS in the induction of tumor necrosis factor α gene expression. In contrast, the expression of Arginase 1, a marker for M2 macrophages, was blunted in the absence of miR-223. Consistently, the expression of proinflammatory cytokines, such as tumor necrosis factor α, IL-6, and IL-1β, in miR-223–null adipose tissue was also elevated. These studies demonstrate that miR-223 likely exerts cell-autonomous effects on macrophage polarization. In vivo metabolic analyses revealed that miR-223–deficient mice developed more severe insulin resistance after high-fat feeding that was accompanied with adipose tissue inflammation. Compared with control, adipose tissue macrophages from miR-223–null mice adopted a more proinflammatory profile. Given that miR-223 is highly enriched in myeloid cells, the authors transplanted syngeneic wild-type mice with bone marrow cells isolated from miR-223–deficient mice. Myeloid-specific miR-223 deficiency recapitulated insulin resistance and glucose intolerance observed in miR-223–null mice, suggesting that the metabolic actions of miR-223 are largely attributed to its function in the hematopoietic lineages.

As miR-223 expression is highly responsive to IL-4 and LPS, it could be predicted that its abundance in adipose tissues is likely regulated by diet-induced obesity, which causes a switch from M2 to M1 polarization. Paradoxically, Zhuang et al found that the expression of miR-223 in adipose tissue remains similar between lean and obese groups. Previous studies have demonstrated that miR-223 is also expressed in other cell types, such as granulocytes. As such, it cannot be ruled out that changes in the abundance of other immune cells within adipose tissue may mask the regulation of miR-223 in adipose tissue macrophages in obesity. At the molecular level, a major target of miR-223 in macrophages is Pknox1, which itself favors the classical activation pathway. In fact, RNAi knockdown of Pknox1 blunted the induction of proinflammatory cytokine IL-1β expression by LPS while augmenting Arginase 1 expression in macrophages. Ectopic overexpression of Pknox1 promotes polarization toward proinflammatory phenotype. An important question that remains unanswered is how the miR-223/Pknox1 pathway interacts with known regulatory pathways that control macrophage activation. In the context of granulocyte differentiation, the expression of miR-223 is controlled by antagonistic action of two transcriptional factors, nuclear factor I A and CCAAT/enhancer-binding protein alpha. Interestingly, the expression of nuclear factor I A is negatively regulated by miR-223, illustrating the ability of miR-223 to form regulatory circuitry with other transcription factors. Elucidating the exact mechanisms of the crosstalk between miR-223 and peroxisome proliferator-activated receptors, peroxisome proliferator-activated receptor gamma coactivator-1β, and Kruppel-like factor 4 may shed new light on the control of macrophage polarization and its role in metabolic homeostasis.

Of note, recent studies found that certain miRNAs can be secreted into circulation in the form of microvesicles or lipoprotein particles or in complex with Argonaute proteins. In fact, several disease conditions, including cancer, type 2 diabetes, and cardiovascular diseases, are associated with unique expression signatures of plasma miRNAs, suggesting that circulating miRNAs could serve as novel diagnostic biomarkers. In addition, the presence of relatively
stable miRNAs in circulation supports an emerging role of miRNAs as potential signaling molecules.17

Interestingly, recent work has shown that plasma levels of 5 miRNAs, including miR-223, were significantly decreased in patients with type 2 diabetes.25 In the current study, the authors showed that insulin-stimulated AKT phosphorylation in adipocytes is attenuated in the presence of miR-223–null bone marrow–derived macrophage coculture. Although increased expression of proinflammatory cytokines in miR-223 deficiency provides a plausible explanation, an alternative interpretation of these findings is that miR-223 secreted from the bone marrow–derived macrophages may directly target adipocytes and modulate their insulin sensitivity. To extend this scenario in vivo, it is possible that miR-223 secreted by macrophages may target distal metabolic tissues and exert its effects on energy metabolism in a non–cell autonomous manner. As such, decreased plasma levels of miR-223 in type 2 diabetes mellitus and in miR-223–deficient mice may not only affect macrophage polarization but also regulate metabolic signaling in other tissues. Future experiments are needed to elucidate these intriguing possibilities.

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None.

References


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