

## microRNA deregulation in keloids: an opportunity for clinical intervention?

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### Abstract

Keloids are defined as benign dermal scars invading adjacent healthy tissue, characterized by aberrant fibroblast dynamics and overproduction of extracellular matrix. However, the aetiology and molecular mechanism of keloid production remain poorly understood. Recent discoveries have shed new light on the involvement of a class of non-coding RNAs known as microRNAs (miRNA), in keloid formation. A number of miRNAs have differential expression in keloid tissues and keloid-derived fibroblasts. These miRNAs have been characterized as novel regulators of cellular processes pertinent to wound healing, including extracellular matrix deposition and fibroblast proliferation. Delineating the functional significance of miRNA deregulation may help us better understand pathogenesis of keloids, and promote development of miRNA-directed therapeutics against this condition.

### Introduction

Keloids are clinically defined as being benign dermal scars invading adjacent healthy tissue, due to abnormal wound healing (1–3). Other clinical manifestations of keloids include itching, aching and cosmetic disfigurement. Overproduction of extracellular matrix (ECM), such as collagen, fibronectin and elastin, occurs in keloid fibrosis (4,5). Disruption of cellular dynamics characterized by increased fibroblast proliferation and

reduced fibroblast apoptosis has also been implicated in their formation (6,7). However, aetiology and molecular mechanisms of keloid deposition remain poorly understood. In addition, their management is a major clinical challenge for dermatologists and plastic surgeons (8–10). Although many conservative treatments have been adopted, their therapeutic efficacies are often inconsistent (11–13). Thus, alternative treatment methods are needed, and these require better understanding of pathophysiological processes of keloid formation (14,15).

microRNAs (miRNAs) are a group of short non-coding RNAs involved in post-transcriptional regulation of gene expression (16–20). They play important roles in many biological and pathological processes, including ECM production and aberrant cell proliferation (18,21–27). Importantly, accumulating evidence shows that miRNAs are deregulated in many inflammatory and malignant skin diseases (28–30). Recent studies also have reported abnormal miRNA expression in keloids (31–33), and these studies indicate that miRNAs may play significant roles in their development (31–33). Investigating keloid miRNA deregulation and functions may thus help in understanding their molecular mechanisms. In this review, we summarize current evidence concerning deregulation and functional roles of miRNAs in keloid formation and also discuss the implications of miRNAs as potential therapeutic tools for their clinical management.

### Altered miRNA expression profiles

Genome-wide expression analysis has been widely used for evaluation of differential gene and miRNA expression between diseased tissues and normal controls (34–36). In miRNA research, microarray profiling followed by validation with quantitative reverse transcription-PCR (qRT-PCR) is a common approach for identifying deregulated miRNAs in clinical specimens (37–39). Accumu-

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lating studies show that many miRNAs are deregulated in keloids, using this miRNA profiling approach (40). Here, we summarize data on miRNA expression profiling in keloids.

Liu *et al.* profiled miRNA expression in 12 pairs of keloid tissue and corresponding normal skin using miRNA microarrays and qRT-PCR (31), in which a total of 32 differentially expressed miRNAs were identified. Of these, 23 miRNAs (e.g. miR-21, miR-4269, miR-382) were up-regulated while nine miRNAs (e.g. miR-203, miR-205, miR-200b/c) were down-regulated compared to normal skin tissues. Furthermore, bioinformatic analysis predicted that these differentially expressed miRNAs might participate in signalling pathways related to wound healing, such as mitogen-activated protein kinase (MAPK), focal adhesion and biosynthesis of collagen protein. MAPK and focal adhesion have been shown to be involved in collagen synthesis and fibroblast mechanotransduction during scar formation (41,42), suggesting that deregulated miRNAs might contribute to pathogenesis of keloids.

In a further study, Li *et al.* compared miRNA expression in fibroblasts isolated from keloid and normal dermis using miRNA microarrays (33). They demonstrated that miRNA expression profiles in keloid fibroblasts were different from those derived from normal skin, with six miRNAs (miR-152, miR-23b-3p, miR-31-5p, miR-320c, miR-30a-5p, hsv1-miR-H7) up-regulated and three (miR-4328, miR-145-5p, miR-143-3p) down-regulated. Furthermore, these differentially expressed miRNAs were predicted to participate in signalling pathways relevant to scar formation. These data suggest that altered miRNA expression may contribute to keloid development by deregulating fibroblast functions.

### Specific deregulated miRNAs with functional implications

#### *miR-7*

Expression of miR-7 is low in keloid tissues compared to normal skin, as revealed by PCR array analysis. Interestingly, inhibiting miR-7 in normal dermal fibroblasts increased expression of type I  $\alpha 2$  collagen *in vitro*, suggesting reduced miR-7 expression might contribute to pathogenesis of keloids by collagen overproduction (43). It is noteworthy that miR-7 has been reported to function as a tumour suppressor in breast cancer (44) but exerts oncogenic effects in lung cancer, hepatocellular carcinoma (HCC) and gastric cancer (45–48), indicating that this miRNA might function in an organ- or tissue-specific manner.

#### *miR-21*

miR-21 is up-regulated and acts oncogenically in many types of cancer (49–52), and it has been documented as targeting many cancer-related genes, such as *PTEN*, *TPM1* and *PDCD* (50,53). In the skin, miR-21 is up-regulated after injury and is closely related to major events during wound healing; it also plays a significant role in wound contraction (54). There is also evidence that miR-21 promotes keratinocyte migration and re-epithelialization during wound healing by targeting *TIMP3* and *TIAM1* (55). miR-21 expression is high in keloid tissues in comparison to adjacent normal skin tissues; in addition, protein expression of *PTEN* is inversely correlated to miR-21 and is also high during fibroblast proliferation in normal skin. Thus, miR-21 may assume a significant role in regulation of keloid fibroblast proliferation (56).

#### *miR-196a*

miRNA-196a has been reported to be down-regulated in sera and involved skin, of patients with localized scleroderma (57). Kashiya *et al.* compared miRNA expression between keloid-derived fibroblasts and normal fibroblasts using miRNA expression microarrays (32). They demonstrated that 27 miRNAs were differentially expressed in keloid-derived fibroblasts compared to their normal counterparts. Of these differentially expressed miRNAs, miR-196a exhibited highest fold-change down-regulation in keloid-derived fibroblasts. Furthermore, miR-196a inhibits expression of secreted type I/III collagens. Importantly, direct binding of miR-196a to *COL1A1* and *COL3A1* has been demonstrated in reporter assays (32). These data suggest that down-regulation of miR-196a may underlie increased collagen deposition in keloids.

#### *miR-199a-5p*

miR-199a-5p is deregulated in various diseases, including organ fibrosis and malignancies (58–62). For example, Shen *et al.* found that expression of miR-199a-5p was low in HCC where its down-regulation promoted metastasis by inhibiting *DDR1* (63). In addition, miR-199a-5p inhibited proliferation, migration and invasion of testicular cancer cells (64). Nevertheless, miR-199a is up-regulated in gastric cancers compared to normal gastric tissues (65). Using miRNA microarrays, 17 miRNAs were found to be differentially expressed in keloid tissues compared to normal skin (40). Of these, miR-199a-5p down-regulation in keloids was confirmed by qRT-PCR and its restored expression inhibited fibroblast proliferation with length-

ened S and G<sub>2</sub>/M phases (40), suggesting its down-regulation in keloids might promote abnormal fibroblast proliferation by influencing the cell cycle.

### miR-200b

miR-200b belongs to the miR-200 family, which is deregulated in many types of cancer (66–69). miR-200b has been associated with aberrant proliferation of fibroblasts (67,70) and deregulated in various fibrogenic diseases, including biliary atresia and liver fibrotic progression (71,72). Previous data have reported that up-regulation of miR-200b repressed proliferation and induced apoptosis of hypertrophic scar fibroblasts, whereas its down-regulation had the opposite effect (70). miR-200b is down-regulated in hypertrophic scar tissues and human hypertrophic scar fibroblasts, suggesting a correlation between miR-200b expression and hypertrophic scarring. In addition, miR-200b represses hypertrophic scarring by targeting type I/III collagen I, fibronectin, transforming growth factor- $\beta$ 1 and  $\alpha$  smooth muscle actin (70). Thus, miR-200b may be a potential therapeutic miRNA for management of hypertrophic scarring.

### Conclusion

miRNAs play significant roles in formation and progression of keloids by regulating many processes, including transforming growth factor- $\beta$  signalling, ECM deposition and fibroblast proliferation. As few treatment options are effective against keloids, miRNA modulation might be a novel therapeutic approach. Some down-regulated miRNAs in keloids may play significant anti-fibrotic roles and thus could potentially be used as therapeutic agents. In contrast, miRNA inhibitors could target up-regulated miRNAs. Nevertheless, further translational studies are needed for establishing therapeutic values of these miRNA-based agents.

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