Multiple etiologies of liver injury are associated with fibrosis in which the key event is the activation of hepatic stellate cells (HSCs). Although microRNAs (miRNAs) are reportedly involved in fibrogenesis, the complete array of miRNA signatures associated with the disease has yet to be elucidated. Here, deep sequencing analysis revealed that compared to controls, 80 miRNAs were upregulated and 21 miRNAs were downregulated significantly in the thioacetamide (TAA)-induced mouse fibrotic liver. Interestingly, 58 of the upregulated miRNAs were localized to an oncogenic miRNA megacluster upregulated in liver cancer. Differential expression of some of the TAA-responsive miRNAs was confirmed, and their human orthologs were similarly deregulated in TGF-β1-activated HSCs. Moreover, a functional analysis of the experimentally validated high-confidence miRNA targets revealed significant enrichment for the GO terms and KEGG pathways involved in HSC activation and liver fibrogenesis. This is the first comprehensive report of miRNAs profiles during TAA-induced mouse liver fibrosis.

We identified 80 upregulated miRNAs and 21 downregulated miRNAs associated with TAA-induced liver fibrosis in mice.