MicroRNA regulation pathway study in the case of cardiomyocyte differentiation of murine ESCs

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Abstract

Differentiation of embryonic stem cells (ESCs) is a comprehensive biological process controlled by many regulators. A better understanding of differentiation process is an essential base for development research, tissue engineering and pharmaceutical oriented ESC research. Recent studies demonstrated that microRNAs (miRNA) play a central role in the regulation of ESC differentiation. In the present study, a transgenic murine ESC line was applied as a model for miRNA regulation study in cardiomyocyte specific differentiation. miRNA expression was profiled using high throughput microarray platforms for samples obtained at undifferentiated stage (day0) and different time points during cardiomyocyte specific differentiation and maturation (day12, day19 and day26). 50 miRNAs were identified as plausibly different expressed during the process from ESCs to mature cardiomyocytes and therefore recognized as candidate regulator miRNAs involved in cardiomyocyte specific differentiation procedure. Parallel to miRNA profiling, a genome wide transcriptome analysis was performed for the same samples. This analysis discovered regulation effects between undifferentiated ESCs and cardiomyocytes on transcriptional level. Functional analysis of regulated genes and miRNA target genes reveals possible regulatory pathway of candidate miRNAs. Although it is widely believed that miRNA regulators act on both transcriptional and translational levels, this study concentrated on finding correlation between miRNA regulator and target gene transcript. Regulated miRNA target genes showed enrichment in important pathways involved in cardiomyocyte specific differentiation process.

Further studies can surely complete the scenario of cardiomyocyte specific ESC differentiation.