Identification of Genetic Networks during Mesenchymal Stem Cell Transformation into Neurons

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摘要

Abstract

The aim of this experiment is to identify related genes for human umbilical mesenchymal stem cells transformation into nervous cells. After the human umbilical mesenchymal stem cells were treated with neuronal conditioned medium (NCM) for 9 days, the gene expression groups are compared to those only treated with DMEM. The related genes for cell cycles, the human umbilical mesenchymal stem cells treated with DMEM increases the amount of cells that remain in the G2/M phase and S phase, including CAV1, EBF, NRG1, CDH13, MLH1. After treatment, the human umbilical cord mesenchymal stem cells with NCM for 9 days, gene expression related to the G0/G1 phase are also increased, including MYC, CSF3, PETN. Gene expressions related to neural regeneration and neural stem cells also increase significantly, such as CXCL1, BMP2, NRCAM, FGF2, SPG7. This study thereby provides a foundation for a more detailed understanding of HUMSCs neuronal differentiation.