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عنوان مقاله:

Identification of Cranial Mesenchymal Stem Cells Soluble Factors Regulating Retinal Pigmented Epithelium Cells Development

محل انتشار:

هشتمین همایش تحقیقات چشم پزشکی و علوم بینایی ایران (سال: 1397)

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خلاصه مقاله:

Sharif University of Technology, Royan Institute for Stem Cell Biology and Technology, Iran University of Science and Technology Purpose: Replacing defective retinal pigment epithelial (RPE) cells with those derived from human embryonic stem cells (hESCs) is a potential strategy for treating retinal degenerative diseases and several clinical trials are underway. Although several protocols describing differentiation of RPE from hESCs have been described, there has been considerable interest in developing protocols to generate RPE cells with high efficiency and purity, yet. In the present study, co-culture of mesenchymal stem cells from different parts of the body during differentiation of hESC-RPE cells results in distinct differentiation efficiencies. More specifically, co-culture of mesenchymal stem cells from the head has a significantly higher efficiency enhancement than body-origin. This experimental observation suggests that mesenchymal from head and trunk may have secreted factors that play a direct role in the induction of RPE cells.Methods: Therefore, using a bioinformatics approach, we compared expression profiles of mesenchymal stem cells originating from human head and body, in order to find effective factors in RPE induction. All samples were obtained from the NCBI GEO database, and we included only healthy and untreated adult donor samples. To counterbalance tissue-specific effects, we integrated mesenchymal cells from variant tissues in the body. Using R/Bioconductor, we performed batch effect removal, quality control, dimension reduction and visualization of the data.Results: From 16393 genes present in all samples, we identified 76 genes that were significantly upregulated in head-derived mesenchymal cells. Then, we focused on the genes with extra-cellular functions. This narrowed down our candidates to 22 genes. By scrutinizing pathways and biological functions of these candidates, we selected WNT5B, FBN2, and FBLN1 as the final candidates, to be experimentally validated.Conclusion: Altogether, these data indicate the promising role of bioinformatics analysis in enhancing experimental procedures of cellular differentiation, for regenerative medicine applications.

کلمات کلیدی:

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