Official Journal of TESMA
Regenerative Research
www.regres.tesma.org.my
E-ISSN 2232-0822
Tissue Engineering and Regenerative Medicine Society of Malaysia

Regenerative Research 7(1) 2018 139

IDENTIFICATION OF FACTORS SECRETED BY NASAL FIBROBLAST CONDITIONED MEDIUM IN PROMOTING *IN VITRO* WOUND HEALING OF RESPIRATORY EPITHELIAL CELLS

Rohaina C Man[1], Yogeswaran Lokanathan[1], Wan Izlina W Ibrahim[2], Aminuddin B Saim[3], Ruszymah Bt Hj Idrus[4]*

[1]Tissue Engineering Centre, Faculty of Medicine, Universiti Kebangsaan Malaysia Medical Centre, Clinical Block, Jalan Yaacob Latif, 56000, Cheras, Kuala Lumpur, Malaysia
[2]Medical Biotechnology Laboratory, Faculty of Medicine, University of Malaya, 50603 Kuala Lumpur, Malaysia
[3]Ear, Nose & Throat Consultant Clinic, Ampang Puteri Specialist Hospital, 1, Jalan Mamanda 9, Taman Dato Ahmad Razali, 68000, Ampang, Selangor, Malaysia
[4]Department of Physiology, Faculty of Medicine, Universiti Kebangsaan Malaysia Medical Centre, Pre-Clinical Block, Jalan Yaacob Latif, 56000, Cheras, Kuala Lumpur, Malaysia

ARTICLE INFO

Published: 26th August 2018
*Corresponding author: Ruszymah Bt. Hj Idrus
Email: ruszyidrus@gmail.com

KEYWORDS

Respiratory epithelial cells;
Nasal fibroblast;
Conditioned medium;
Wound healing

SUMMARY

Secretory proteins are known to play a crucial role in many physiological processes including cell attachment, proliferation and cell migration that eventually leads to wound healing. The objective of this study was to identify the factors secreted by nasal fibroblast conditioned medium and the protein interactions in promoting *in vitro* wound healing of respiratory epithelial cells (RECs). Nasal turbinates were collected from consenting patients underwent turbinectomy. RECs and fibroblasts were co-cultured in Defined Keratinocytes Serum Free Medium (DKSFM), F-12 and Dulbecco's Modified Eagle's Medium (DMEM) supplemented with bovine serum. Fibroblasts were differentially trypsinized and cultured either in DKSFM or serum free F12: DMEM to acquire the conditioned media, which served as NFCM_DKSFM and NFCM_FD. Nano LC-MS/MS analysis was conducted to evaluate the differential expressed proteins, followed by quantitation of false discovery rate (FDR) by STRING10 software, which represented the value of pathways involved in four functional enrichments. The analysis showed that the total secreted proteins in NFCM_FD and NFCM_DKSFM were 104 and 83, respectively. In biological processes category, the extra cellular matrix (ECM) organization pathway showed the lowest FDR values in NFCM_FD (2.27×10^{-37}) and NFCM_DKSFM (6.76×10^{-37}) while for molecular function, ECM structural constituents showed FDR values of 4.30×10^{-16} in NFCM_FD and 8.13×10^{-14} in NFCM_DKSFM. Cellular components category illustrated low FDR values for extracellular space in NFCM_FD (6.06×10^{-70}) and NFCM_DKSFM (1.21×10^{-61}) while for Kyoto Encyclopaedia of Genes and Genomes (KEGG) enrichment, ECM-receptor interactions demonstrated FDR values of 3.53×10^{-24} in NFCM_FD and 7.49×10^{-17} in NFCM_DKSFM. The finding suggested that many protein interactions were identified according to several clusters of proteins. Hence, all the secreted proteins were actively interacted, either directly or indirectly, in conjunction with each other rather than alone to promote the wound healing process.

Acknowledgement: This study was made possible by a UKM research grant from the Ministry of Education Malaysia (DPP-204-121 and AP-2013-015).