Jinqing Li et al., J Tissue Sci Eng 2013, 4:2
http://dx.doi.org/10.4172/2157-7552.S1.012

OMICS Group Conferences
Accelerating Scientific Discovery

2nd International Conference on
Tissue Science & Regenerative Medicine
August 26-28, 2013 DoubleTree by Hilton, Raleigh, NC, USA

Where vascular tissue engineering meets integrated omics: Discovering markers in pericytes and circulatory progenitor cells mimetic

Jinqing Li[1,2], Harsha P. Gunawardena[1], Hong Tan[3], Lisa Samuelson[1], Xueyong Li[2], Caibin Cui[1] and David Gerber[1]
[1]University of North Carolina at Chapel Hill, USA
[2]Tangdu Hospital, China
[3]University of Colorado, USA

The vascularization of tissues with functional capillary vessels remains a key challenge in tissue engineering. Progresses have been made in the engineering of small blood vessels, but barely any progresses have been seen in realm of functional capillary vessels. The lack of stem cells that can mimic pericytes that makes up the basement membrane of the vascular endothelium has been the main impediment in engineering functional capillary vessels. The pericyte mimetic should be easily isolated and purified, and have the physiological functions of pericytes that includes inhibition of angiogenesis *in vivo*, inhibition of vascular endothelial cells (VECs) proliferation and tube formation *in vitro*, and production of basal membrane components.

We have identified the circulating progenitor cells (CPCs) which is circulating in peripheral blood, inhibiting both the proliferation and the apoptosis of VECs, and inhibiting angiogenesis in both the wound healing model and the matrigel model. In addition, CPCs can control the tube formation under the stimulation of growth factors and prevent the regression of VECs tube upon growth factor retraction. Furthermore, when co-cultured with VECs in 3D collagen gel, the CPCs migrated to the surface of the VECs tubes, formed the basal membrane, and connected with VECs with gap junctions.

In order to understand the underlying biochemistry of the CPCs in the context of VECs requires profiling of functional pathways in both pericytes and CPCs. We are using a systems biology approach to systematically perturb the relevant pathway and then examine global changes at the genetic and proteomic level. Using gene expression chip assay, we found that the CPCs cultured alone has only about 1507 differentially expressed genes compared with that of pericytes, and the number further decreased to 202 after the circulating progenitor cells co-cultured with VECs. The gene expression data can be co-analyzed with proteomic data for further elucidating the similarities and differences between pericytes and CPCs. Currently we are using a multiplex quantitative proteomic method that uses tandem mass tags (TMT) to simultaneously measure protein expression levels in these two cells types by independently co-culturing pericytes and CPCs with VECs under various stimulatory conditions. The proteomic data will provide an extra dimension to understanding the regulatory networks present in the CPCs. We will present the results from our multi-omics approach to elicit differences and similarities between CPCs and pericytes in the context of VECs. The biochemical data in support of CPCs differentiation into pericytes under the induction of VECs will guide the selection and refinement of other cellular mimetic for functional capillary vessel engineering.

Biography

Jinqing Li completed his M.D. at the age of 29 from Fourth Military Medical University in China and went to University of South Carolina School of Medicine for postdoctoral training. Now he is a visiting research scientist in University of North Carolina School of Medicine. He is the Associate Professor of Fourth Military Medical University and Vice Director of Department of Plastic and Burn Surgery. He has published more than 16 papers in reputed journals and serving as a committee member of China Association of Plastic Surgery.

jinqingl@email.unc.edu