



Bioinformatic analysis of endothelial progenitor cells exposed to folic acid in type 1 diabetes mellitus

D.N. Fang¹, X.D. He², X.H. Li¹, H. Jia³, P.Y. Li⁴, Q. Lu⁵, Z. Quan⁶ and Q.L. Wang⁷

¹Department of Gastroenterology, Shanghai Eighth People's Hospital, Shanghai, China

²Department of Endocrinology the First Affiliated Hospital of Xinjiang Medical University, Xinjiang, China

³Department of Emergency Medicine, The Fourth Affiliated Hospital of China Medical University, Shenyang, China

⁴Department of Anatomy and Embryology, Shanghai Medical College of Fudan University, Shanghai, China

⁵Department of Obstetrics and Gynecology, Central Hospital, Fengxian District, Shanghai, China

⁶Department of Neurosurgery, Central Hospital, Fengxian District, Shanghai, China

⁷Department of Histology and Embryology, School of Basic Medical, Shanghai University of Traditional Chinese Medicine, Shanghai, China

Corresponding authors: Z. Quan / Q.L. Wang

E-mail: zhequanzq@hotmail.com / wlei810@gmail.com

Genet. Mol. Res. 13 (1): 1-10 (2014)

Received April 31, 2013

Accepted October 4, 2013

Published January 3, 2014

DOI <http://dx.doi.org/10.4238/2014.January.3.1>

ABSTRACT. We investigated the effects of type 1 diabetes mellitus (T1DM) on endothelial progenitor cells (EPCs) at the molecular level and assessed the therapeutic potential of folic acid (FA) in DM. We downloaded the gene expression profile of the EPCs from T1DM patients before and after treatment with FA and from healthy controls. We identified the

differentially expressed genes (DEGs) in the EPCs from T1DM patients before and after a four-week period of FA treatment and compared them with those obtained from the healthy subjects by using limma package in R language. Then, functional annotation of the DEGs was performed using the online tool Database for Annotation, Visualization and Integrated Discovery (DAVID) based on the Kyoto Encyclopedia of Genes and Genomes database. The expression of 696 genes was altered in the EPCs from T1DM patients compared to those from the healthy controls. These genes were mainly involved in the pathways associated with immune response. FA can normalize majority of the altered gene expression profiles of EPCs from T1DM patients to resemble those of healthy subjects, albeit with some side effects. FA can be a potential therapeutic agent for the treatment of T1DM. However, focused efforts are required to ensure that the dose of FA falls within the permissible pharmacological range.

Key words: Type 1 diabetes mellitus; Folic acid; Immune response; Endothelial progenitor cells; Differentially expressed genes