GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Abnormal gene expression profile reveals the common key signatures associated with clear cell renal cell carcinoma: a meta-analysis

H.J. Zhang, Z.Q. Sun, W.Q. Qian and L. Sheng

Department of Urology, Huadong Hospital, Fudan University, Shanghai, China

Corresponding author: L. Sheng
E-mail: shengludoctor@126.com

Genet. Mol. Res. 14 (1): 2216-2224 (2015)
Received January 21, 2014
Accepted October 21, 2014
Published March 27, 2015
DOI http://dx.doi.org/10.4238/2015.March.27.7

ABSTRACT. The aims of this study were to identify the common gene signatures of clear cell renal cell carcinoma (CCRCC), and to expand the respective protein-protein interaction networks associated with CCRCC regulation. For the latter, we utilized multiple gene expression data sets from the National Center for Biotechnology Information (NCBI) Gene Expression Omnibus (GEO), with which we could analyze the aberrant gene expression patterns at the transcriptome level that distinguish cancer from normal samples. We obtained the GSE781 and GSE6344 clear cell renal cell carcinoma gene expression datasets from GEO, which contained a total of 37 cancer and 37 normal samples. Subsequent R language analysis allowed identification of the differentially expressed genes. The genes that exhibited significant up or downregulation in cancers were entered into the Database for Annotation, Visualization, and Integrated Discovery to perform analysis of gene functional annotations, resulting in the generation of two protein-protein interaction networks that included the most significantly up or downregulated genes in CCRCC. These allowed us to identify the key factor genes, which could potentially be utilized

to separate cancer versus normal samples. The differentially regulated genes are also highly likely to be functionally important regulatory factors in renal cell carcinoma: cell functions showing enrichment of these genes include amine biosynthetic and vitamin metabolic processes, ion binding, extracellular transport function, and regulation of biosynthesis. Together, the results from our study offer further reason to pursue diagnosis and therapy of CCRCC at the molecular level.

Key words: Gene expression; Microarray; Protein-protein interaction; Network; Renal cell carcinoma