Online journal ISSN - 1676-5680
GMR Genetics and Molecular Research
EVOLUTION AND TECHNOLOGY

Expression of Rap1GAP in human myeloid disease following microarray selection

X. Qi, Z. Chen, J. Qian, J. Cen and M. Gu

Leukemia Research Division, Jiangsu Institute of Hematology,
Key Laboratory of Thrombosis and Hemostasis, Ministry of Health,
First Affiliated Hospital, Soochow University, Suzhou, China

Corresponding author: Z. Chen
E-mail: szchenzx@263.net

Genet. Mol. Res. 7 (2): 379-387 (2008)
Received November 25, 2007
Accepted February 15, 2008
Published April 29, 2008

ABSTRACT. To find the underlying causes of primary myelodysplastic syndrome (MDS), the gene expression profiling of both $CD34^+$ cells and bone marrow mononuclear cells from MDS patients was performed using oligonucleotide microarray and cDNA microarrays, respectively. Several candidate genes which were differentially expressed in MDS patients versus normal controls were selected and confirmed in expanding samples by quantitative real-time reverse transcription-polymerase chain reaction after clustering and bioinformatics analysis. One of these genes, RAP1GAP, was found to be expressed at a significantly higher level in patients with MDS in comparison with those suffering from other hematopoietic diseases including leukemia ($P < 0.01$). We propose that over-expression of RAP1GAP gene may play a role in the pathogenesis of MDS.

Key words: Myelodysplastic syndrome; RAP1GAP; Real-time PCR

