RESEARCH ARTICLE

Are So-Called Cancer-Testis Genes Expressed Only in Testis?

Soudeh Ghafouri-Fard*, Fatemeh Rezazadeh, Davood Zare-Abdollahi, Mir Davood Omrani, Abolfazl Movafagh

Abstract

Cancer-testis (CT) antigens are a group of tumor-associated antigens with restricted expression in normal tissues except testis and expression in a wide variety of tumor tissues. This pattern of expression makes them suitable targets for immunotherapy as well as potential biomarkers for early detection of cancer. However, some genes attributed to this family are now known to be expressed in other normal tissues which put their potential applications in immunotherapy and cancer detection under question. Here we analyzed expression of two previously known CT antigens, RHOXF2 and PIWIL2, in AML patients versus normal donors and found no significant difference in the expression of these genes between the two groups. As these two genes showed expression in normal leukocytes, their expression pattern seems to be wider than to be attributed to the CT gene family. Future research should focus on the expression profiles of so called CT antigens to find those with more testis specific expression.

Keywords: Cancer-testis antigen - RHOXF2 - PIWIL2 - leukocytes - specificity of expression

Introduction

Cancer-testis (CT) antigens with a restricted expression pattern in normal tissues except testis and expression in a wide variety of tumor tissues are promising targets for immunotherapy as well as potential biomarkers for early detection of cancer. However, some genes attributed to this family are now known to be expressed in other normal tissues which put their potential applications in immunotherapy and cancer detection under question. Here we analyzed expression of two previously known CT antigens, RHOXF2 and PIWIL2, in AML patients versus normal donors and found no significant difference in the expression of these genes between the two groups. As these two genes showed expression in normal leukocytes, their expression pattern seems to be wider than to be attributed to the CT gene family. Future research should focus on the expression profiles of so called CT antigens to find those with more testis specific expression.

Materials and Methods

Blood and tissue samples

Blood samples were collected from 40 patients (18 female and 22 male patients) with confirmed primary AML diagnosis (subtypes: M1, M2, M3, M4, M5 and...
Soudeh Ghafouri-Fard et al

M7) and from 10 healthy people. Patients were classified according to the French-American-British (FAB) diagnostic criteria. Informed consent was taken from all patients and healthy donors before inclusion into the study. Standard cytogenetic analysis was performed on patients’ samples. The approval was obtained through the Investigation Review Board at Shahid Beheshti University of Medical Sciences. Normal testis sample was obtained from a prostate cancer patient following orchiectomy and was used as positive control for analysis of testis specific genes expression.

RNA extraction, cDNA synthesis, and quantitative real-time RT-PCR

Peripheral blood mononuclear cells were isolated from blood samples using Biosera Lymphosep, Lymphocyte separation media. Total RNA was isolated from leukocytes of patients using Tripure isolation reagent (Roche, Mannheim, Germany) according to the manufacturer’s instructions. RNA was analyzed by Biowave II spectrophotometer (Biochrom Cambridge, England) to verify purity and concentration. Then, 1 µg of RNA was used for cDNA synthesis by Fermentas RevertAidTM H Minus First Strand cDNA Synthesis Kit. Synthesized cDNA was analyzed spectrophotometrically to confirm concentration. Quantitative real time RT-PCR reaction was carried out on a rotor gene 6000 corbette detection system using AccuPower® 2X Greenstar qPCR Master Mix (BIONEER, USA). Thermal cycling conditions were: 5 min at 95°C, 40 cycles of a denaturation step for 10 s at 95°C and a combined annealing/extension step for 30 s at 59°C. Each run contained no template control (NTC) consisting of H2O for target and reference genes. Beta 2 microglobulin (B2M) gene was used as normalizer. Primer sequences can be provided via request. Melting curve analysis was done to validate specificity of PCR products. Real time RT-PCR products were also electrophoresed on 1.5% agarose gel to verify product sizes and specificity.

Statistical analysis

Fold changes in gene expression were determined by LinRegPCR(2) (Software for analysis of quantitative real-time PCR data) and Relative Expression Software Tool-RG©-version 3 (Calculation Software for the Relative Expression in real-time PCR using Pair Wise Fixed Reallocation Randomization Test©). The amounts of mRNA for each gene in the blood samples were standardized to the B2M mRNA as follows: ΔΔCT=[CT Gene of interest - CT B2M]. The level of probability was set at p<0.05 as statistically significant.

Results

Cytogenetic analysis

Different cytogenetic abnormalities were seen in AML patients including t(8,21), t(15,17), t(16,16), +8, -5, -7 with the first one being the most prevalent. About 60% of AML patients had normal karyotypes. No significant correlation was seen between cytogenetic abnormalities and gene expression.

Discussion

Cancer stem cells are a subset of cells present in tumor bulks capable of self-renewal and the exclusive ability to reproduce malignant tumors indefinitely (Tabarestani and Ghafouri-Fard, 2012). The first cancer stem cells have been identified in AML. The detection of these cells has significant clinical implications especially to improve treatment outcome and prevent relapse of the disease (Chan and Huntly, 2008). In this study, we have evaluated the expression of two previously known stem cell markers (RHOXF2 and PIWIL2) in AML patients and normal donors. Previous data have indicated that both PIWIL2 and RHOXF2 have testis specific expression pattern. PIWIL2 has been shown to be expressed in various stages of breast cancers and cervical neoplasia, so proposed as a novel biomarker for these cancers (He et al., 2010; Liu et al., 2010). However, here we have shown for the first time that both PIWIL2 and PEPP2 are expressed in normal leukocytes. Some other genes have been believed to have testis specific or testis restricted expression but shown to be expressed in a variety of normal tissues. For instance, acrosin binding protein (ACRBP, OY-TES-1) was supposed to be expressed only in testis among normal tissues, and in a range of cancers such as bladder, breast, lung, liver, and colon cancers (Ono et al., 2001). It was at the center of attention for a period of time as cancer biomarker and target for immunotherapy. It has been also

Figure 1. Genes Expression Results in Blood Samples:
Lane 1: DNA Size Marker, Lane 2: Testis, Lanes: 3-4: Normal Samples, Lanes 5-8: AML Samples, Lane 9: Negative Control

RHOXF2 and PIWIL2 expression in normal lymphocytes

All 10 normal samples showed PIWIL2 expression, whereas 3 normal samples showed RHOXF2 expression (Figure 1).

RHOXF2 and PIWIL2 expression in AML patients

RHOXF2 expression was seen in 8 AML patients with similar distribution in both sexes. PIWIL2 expression was detected in 19 AML patients including 14 male and 5 female patients. Among those expressed PIWIL2, 10 had normal karyotypes. Five patients expressed both genes (Figure 1).

RHOXF2 and PIWIL2 expression ratios in AML patients and normal donors

No significant difference was seen in the expression ratios of these 2 genes between AML patients and normal donors.
shown to be expressed in mesenchymal stem cells of bone marrow at both mRNA and protein levels (Cen et al., 2012). However, recent data indicate that it is expressed in a variety of normal tissues (CTDatabase: http://www.cta.lncc.br/index.php). The main advantage of using CT genes in immunotherapy resides in their restricted expression in normal tissues which diminishes treatment side effects. In addition, as testis is considered as an immune-privileged site, the absence of CT expression in normal tissues except for testis and strong expression in cancer tissues increase the probability of eliciting immune responses. The data presented here can put the significance of these 2 genes for cancer immunotherapy under question.

Acknowledgements

This study was supported by a grant from Shahid Beheshti University of Medical Sciences and done as a part of M.Sc. thesis.

References


