

Leukemia

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Abstract

In the context of a heterogeneous malignant disease, such as CLL-B, this simple and inexpensive ELISA method, such as employed in this study, proves useful for identifying patients to be considered as candidates for personalized therapeutic strategies, based on the mutation of the TP- 53 gene and the presence of p-53 isoform protein. The presented research has an impact on the clinical management of patients and requires adequate therapeutic adaptation in a personalized medicine.

Background

CLL is a neoplasm of mature B cells that is typically manifested within the peripheral blood.

The risk of progression to overt CLL for low-count MBL, however, is unknown until this data. It was discovered in the last few years that the production of some percentage of mutant p-53 proteins, with the increased stability in type B lymphocytes, leads to the carcinogenesis process, [1].

This discovery led to the identification and quantification of the p-53 protein by different methods such as immunohistochemistry (IHC), polymerase chain reaction (PCR), single-stranded peptide microarray, (SSPM-a), next-generation sequencing (NGS), and the sandwich enzyme-linked immunosorbent assay (sandwich ELISA).

Objective

The monoclonal antibody PAb 240 recognizes an epitope that is structurally hidden in the wild-type conformation of p-53 and becomes exposed by denaturing the p-53 protein or the mutant conformations of p-53, where point mutations in the P-53 gene alter the terminal structure of the p-53 protein.

Note remarks: Recently been suggested that the edited LLC cell lines, CRISPR / Cas9, could be useful models for estimating the response to treatment in CLL with del (11q), mutant P-53, trisomy 12, high-risk, providing a preclinical tool for exploring new therapeutic strategies, such as tyrosine kinase inhibitors or anti-BCL-2 protein, in combination with ibrutinib or immune control point inhibitors, PD-1 / PD-L1 inhibitor, or CAR-T therapy, (Innovative Leukemia Treatment), in this subset of LLC cases, [2]. Personalized treatments will be applied by combining diagnostic tools, immunohistochemistry (IHC), polymerase chain reaction (PCR), single-chain peptide microarray (SSPMa), next-generation sequencing (NGS), knowledge databases and therapeutic drugs.

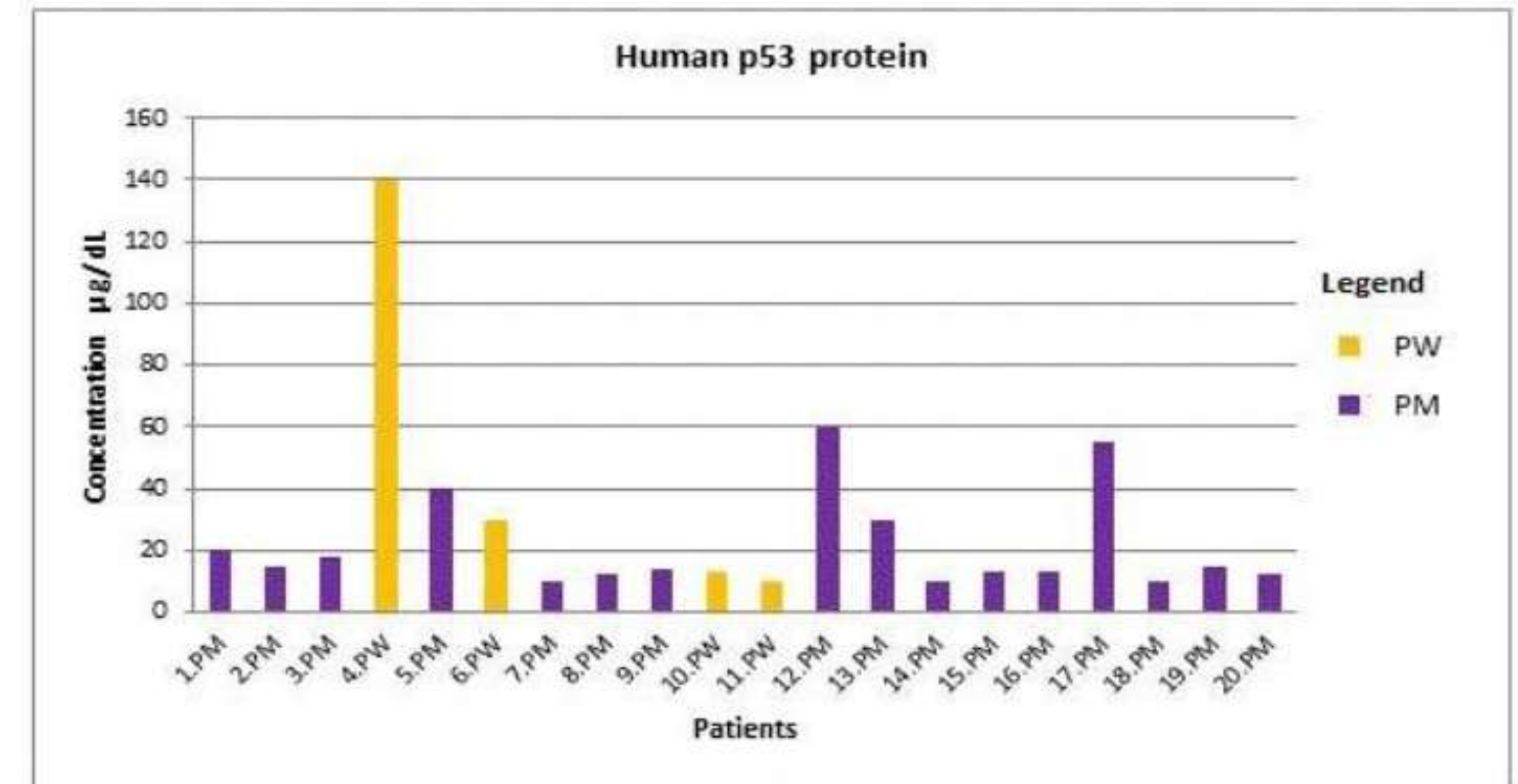
Materials & Methods

Flow cytometry of the first sample screened for CLL was done at using antibodies anti-CD5, CD19, CD20, CD23, CD38. Expression of CD38 was also evaluated to help further classify the clonal B-cell process. CD20 expression is bright in MCL but dim in CLL.

Altogether, CRISPR/Cas9-edited CLL cell lines could be useful models to further predict treatment response of high risk del(11q) TP-53 mut CLL cells, providing a pre-clinical tool to explore novel therapeutic strategies such as ATR inhibitors in this subset of CLL cases, but at this moment is an expensive method, [2].

ELISA kit is recommended for use in serum, plasma or tissue homogenates. The sample collection protocols below were adapted from the references. In the context of a heterogeneous malignant disease, such as CLL-B, this simple and inexpensive ELISA method, such as employed in this study, proves useful for identifying patients to be considered as candidates for personalized therapeutic strategies, based on the mutation of the TP- 53 gene and the presence of p-53. isoform protein.

Summary



Discussion

Investigations have also identified a number of high-risk genetic features and markers, including the most commonly mutated gene detected at diagnosis in patients, CLL with NOTCH1 gene, a well characterized oncogene in T cell acute lymphoblastic leukemia (T-ALL)59, with a prevalence of ~4–20%.

Reference

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