COBBLL1 Gene Expression as a Predictor of Treatment Response in Patients With Newly Diagnosed, Low-Risk Chronic Lymphocytic Leukemia

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Introduction

New approaches to treatment and risk stratification of chronic lymphocytic leukemia (CLL) depend on the study of several genes implicated in its evolution, such as TP53, IGHV, the BCL-2 family, LPL, COBBLL1, and some CDs, such as ZAP 70. Treatment options depend on these findings.

Aim

To evaluate the impact of genetic findings on response rates in newly diagnosed, fit patients with CLL treated with obinutuzumab and venetoclax.

Objectives

Impact of gene profile on treatment decision in low risk newly diagnosed CLL patients

Methods

We prospectively studied 26 newly diagnosed patients with CLL, all of whom were fit for treatment. They had non-mutated TP53 and mutated IGHV. LPL was weakly expressed in seven patients, ZAP 70 was weakly expressed in 10 patients and COBBLL1 was highly expressed in 10 patients. Five patients had 13q14.3 deletion.

Results

Response rate, defined as normalization of white blood cell count, varied among patients. Patients with high COBBLL1 expression showed a slow and unremarkable response during the first 2 months of treatment (P=0.04), whereas those with low LPL and ZAP70 expression responded more rapidly (P=0.03). There was no correlation between 13q14.3 deletion and response to treatment (P=0.06). Similarly, the toxicity profile was not correlated with any genetic or chromosomal defect (P=0.05).

Summary

Secondary players such as LPL and COBBLL1 might play a role in response prediction of CLL patients

Discussion

COBBLL1 gene expression can be used with other data to predict response to treatment in patients newly diagnosed with TP53 non-mutated and IGVH-mutated CLL.

References

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