In conclusion, rhEPO following allo-HCT did not have an impact on survival in long-term analyses.

**O.7 NOTCH1 c.7544-7545 delCt mutation identifies a subgroup of lymphocytic leukemia patients with poor outcome**

S. Franke1, C. Herens2, M. Jamar3, N. Mongiovì3, B. De Prijck1, F. Lambert2

1CHU Liège, Liège, Belgium, 2CHU Liège - Human Genetics, Liège, Belgium, 3CHU Liège Hematology, Liège, Belgium

NOTCH1 has been found recurrently mutated in a subset of patients with chronic lymphocytic leukemia (CLL). Recent studies showed that activating mutations of NOTCH1 proto-oncogene occur in about 10% of CLL at diagnosis and are associated with an unfavorable clinical outcome (Rossi et al., 2012).

We have investigated 105 samples (collected between 2008-2013) of CLL patients for the NOTCH1 mutation: c.7544-7545 delCt. The NOTCH1 mutation was investigated by amplification refractory mutation system (ARMS) PCR of the CLL patients at diagnosis, with a median age of 65 years (range 40-87), 60 males and 45 females. Additionally, other prognostic markers in CLL have been investigated. FISH analysis was performed for the detection of trisomy 12, deletion 11q, deletion 13q and deletion 17p. TheIGH gene mutational status was performed by DNA sequencing.

We found NOTCH1 c.7544-7545 delCt mutations in 16.2% of the cases. The results of the NOTCH1 mutation analysis were compared with the results of the other prognostic factors as trisomy 12, deletion 11q, deletion 13q, deletion 17p and IGHV gene mutation status. All patients harboring a NOTCH1 mutation and consequently had a poor prognosis did not show a deletion 13q as the sole aberration which is connected with a good prognosis. Trisomy 12, deletion 11q, deletion 17p have been found in NOTCH1 mutated as well as in NOTCH1 wild type cases. Half of all cases show an unmaturated IGHV gene and/or c.7544-7545 delCt mutation which predicts a poor outcome.

NOTCH1 seems to be an independent predictive marker for poor outcome in CLL patients. Because of the importance as diagnostic marker in CLL the NOTCH1 c.7544-7545 delCt analyses is included in our spectrum of tests for CLL patients. In the future the follow-up of the patients will give us more information of the clinical impact of the NOTCH1 mutation.

**O.8 JAK2 V617F-Negative AND MPL W515K/L-Negative Essential Thrombocythemia: a High Resolution SNP Array Study**

C. Al Assaf1, E. Lierman1, T. Devo1, C. Graux1, J. Billiet1, J. Finael Ferreiro1, P. Vandenberghe1

1KU Leuven, Leuven, Belgium, 2UZ Leuven, Leuven, Belgium, 3Mont-Godinne University Hospital, Yvoir, Belgium, 4AZ Sint-Jan, Bruges, Belgium

**Background**

JAK2 V617F and MPL W515K/L are the most common mutations in essential thrombocythemia (ET), occurring in approximately 60% of cases. The molecular cause of the remaining ET cases is still largely unknown.

**Aims**

We sought to investigate JAK2 V617F-negative and MPL W515K/L-negative ET for regions of copy number variations (CNV) and loss of heterozygosity (LOH).

**Methods**

We studied blood or bone marrow samples from a series of 64 JAK2 V617F-negative and MPL W515K/L-negative ET cases. They