World Academy of Science, Engineering and Technology
International Journal of Bioengineering and Life Sciences
Vol:9, No:09, 2015

# Monoallelic and Biallelic Deletions of 13q14 in a Group of 36 CLL Patients Investigated by CGH Haematological Cancer and SNP Array (8x60K)

**Authors :** B. Grygalewicz, R. Woroniecka, J. Rygier, K. Borkowska, A. Labak, B. Nowakowska, B. Pienkowska-Grela

**Abstract :** Introduction: Chronic lymphocytic leukemia (CLL) is the most common form of adult leukemia in the Western world. Hemizygous and or homozygous loss at 13q14 occur in more than half of cases and constitute the most frequent chromosomal abnormality in CLL. It is believed that deletions 13q14 play a role in CLL pathogenesis. Two microRNA genes miR-15a and miR- 16-1 are targets of 13q14 deletions and plays a tumor suppressor role by targeting antiapoptotic BCL2 gene. Deletion size, as a single change detected in FISH analysis, has haprognostic significance. Patients with small deletions, without RB1 gene involvement, have the best prognosis and the longest overall survival time (OS 133 months). In patients with bigger deletion region, containing RB1 gene, prognosis drops to intermediate, like in patients with normal karyotype and without changes in FISH with overall survival 111 months. Aim: Precise delineation of 13q14 deletions regions in two groups of CLL patients, with mono- and biallelic deletions and qualifications of their prognostic significance. Methods: Detection of 13q14 deletions was performed by FISH analysis with CLL probe panel (D13S319, LAMP1, TP53, ATM, CEP-12). Accurate deletion size detection was performed by CGH Haematological Cancer and SNP array (8x60K). Results: Our investigated group of CLL patients with the 13q14 deletion, detected by FISH analysis, comprised two groups: 18 patients with monoallelic deletions and 18 patients with biallelic deletions. In FISH analysis, in the monoallelic group the range of cells with deletion, was 43% to 97%, while in biallelic group deletion was detected in 11% to 94% of cells. Microarray analysis revealed precise deletion regions. In the monoallelic group, the range of size was 348,12 Kb to 34,82 Mb, with median deletion size 7,93 Mb. In biallelic group discrepancy of total deletions, size was 135,27 Kb to 33,33 Mb, with median deletion size 2,52 Mb. The median size of smaller deletion regions on one copy chromosome 13 was 1,08 Mb while the average region of bigger deletion on the second chromosome 13 was 4,04 Mb. In the monoallelic group, in 8/18 deletion region covered RB1 gene. In the biallelic group, in 4/18 cases, revealed deletion on one copy of biallelic deletion and in 2/18 showed deletion of RB1 gene on both deleted 13q14 regions. All minimal deleted regions included miR-15a and miR-16-1 genes. Genetic results will be correlated with clinical data. Conclusions: Application of CGH microarrays technique in CLL allows accurately delineate the size of 13q14 deletion regions, what have a prognostic value. All deleted regions included miR15a and miR-16-1, what confirms the essential role of these genes in CLL pathogenesis. In our investigated groups of CLL patients with mono- and biallelic 13q14 deletions, patients with biallelic deletion presented smaller deletion sizes (2,52 Mb vs 7,93 Mb), what is connected with better prognosis.

**Keywords :** CLL, deletion 13q14, CGH microarrays, SNP array
**Conference Title :** ICHG 2015 : International Conference on Human Genetics
**Conference Location :** London, United Kingdom
**Conference Dates :** September 25-26, 2015