



IX INTERNATIONAL
CONFERENCE
ON MALIGNANT
LYMPHOMA

Lugano, Switzerland
June 8-11, 2005

ANNALS OF ONCOLOGY
Volume 16, 2005
Supplement 5

ABSTRACT # 148

CHROMOSOME 11Q21 -> TER GENE EXPRESSION IN DIFFUSE LARGE B CELL LYMPHOMAS (DLBCL)

A. Rinaldi¹, A. M. Chiaravalli², I. Kwee¹, E. Zucca¹, M. G. Tibiletti², C. Catapano¹, C. Capella², F. Bertoni¹

¹Experimental Oncology, Oncology Institute of Southern Switzerland, Bellinzona, Switzerland; ²Ospedale di Circolo, Università della Insubria, Varese, Italy

Introduction: Chromosome 11q22-23 is frequently deleted especially in chronic lymphocytic leukemia (CLL) and mantle cell lymphoma (MCL).

Partially supported by S. Salvatore Foundation, Swiss Bridge Foundation and Oncosuisse.

11q21-24 is amplified in a subset of DLBCL. The aim of this study is to identify genes mapped at 11q21->ter and deregulated in DLBCL.

Methods: Raw Affymetrix MAS5 expression data were obtained from published lymphoma series (Shipp 2002; Klein, 2001-2003; Küppers, 2003; Savage, 2004) and individually imported in GeneSpring. Chromosome 11q21->ter cytogenetic band-specific probe lists were created. Genes were filtered for signal intensity and for up- or down-regulation among samples. Genes were ranked according to the number of conditions in which their expression level was differentially expressed, using a t-test based deviation from one with 0.2 -value cut-off. RNA was extracted from lymphoma samples and cell lines, and from normal naïve, centrocytes, centroblasts, and memory B cells obtained from 3 donors by cell sorting. Real-time PCR was performed on an ABI-7000.

Results: Genes were shown to be differentially expressed in datasets: MMP12, MMP1, MMP7 at 11q22; HTR3A and SORL1 at 11q23; FEZ1 at 11q24. Genes were validated on 10 DLBCL, 8 follicular lymphomas, 7 CLL, 2 MCL, and 14 cell lines, as well on normal B cells.

Metalloproteases were likely to be expressed by infiltrating non-lymphoma cells, while characteristic patterns of expression were observed for HTR3A and FEZ1. RNA and protein data will be presented.

Conclusions: The combination of expression and mapping allowed the identification of candidate genes for B cell development and lymphoma pathogenesis. We report the first evidence of two 11q genes active also in normal and neoplastic B cells.