ID: 00951
Type: Oral Comunication
Topic: Tumor biology

LONG NON CODING RNA EXPRESSION IN ETV6-RUNX1 PAEDRIATIC ACUTE LYMPHOBLASTIC LEUKEMIA

Marta Cuadros[1] , Carlos Baliñas[2] , Isabel F. Coira[2] , Álvaro Andrades[2] , Mª Isabel Rodríguez[2] , Juan Carlos Álvarez[2] , Antonio Jiménez-Velasco[3] , Pilar Jiménez[4] , Mireia Camós[5] , Pedro P Medina[2]

1) Department of Biochemistry and Molecular Biology III e Immunology, University of Granada and GENYO, Centre for Genomics and Oncological Research, Granada, Spain 2) Department of Biochemistry and Molecular Biology I, University of Granada and GENYO, Centre for Genomics and Oncological Research, Granada, Spain 3) Department of Hematology, Hospital Regional de Málaga, Málaga, Spain 4) Departemnet of Clinical Analysis Laboratory and Immunology, Hospital Universitario Virgen de las Nieves, Granada, Spain 5) Department of Paediatric Haematology and Oncology, Hospital San Juan de Dios, Barcelona, Spain

Long non-coding RNA (lncRNA) play important roles in numerous diseases and represent an emerging layer of cancer biology. However, the role that lncRNAs play in the pathogenesis of pediatric B-cell leukemia (B-ALL) with t(12;21)[ETV6-RUNX1] translocation is unknown. In this study, the lncRNA expression profiles of 42 pediatric B-ALL (24 with and 18 without the t(12;21)) and 4 bone marrows from healthy patients were assessed using the Arraystar Human LncRNA Array. Using microarray data, we identified 117 lncRNA that were differentially expressed (fold change> 1.5 and FDR > 0.05) between the B-ALL subgroups (ETV6-RUNX1-positive and ETV6-RUNX1-negative). The most upregulated lncRNA in ETV6-RUNX1 positive B-ALL were TCL6, RP4-697K14.3, LOC100292680, RP11-345I18.1, LINC00599 and TRAF3IP2-AS1, while the most downregulated were RP11-135F9.1, RP11-561B11.1, AK095221, RP11-463H12.1, AC007283.4 and CCDC26. Coding-non-coding gene co-expression networks were constructed to identify lncRNAs with potential functions in ETV6-RUNX1 translocation. Levels of representative lncRNA-mRNAs pairs were further detected by qRT-PCR in patients with pediatric B-ALL. Thus, these findings provide the first detailed description of lncRNA expression profiles related to t(12;21) translocation in pediatric B-ALL, such lncRNA profiles may play important roles in driving normal cells to leukemic cells. These lncRNAs may provide novel molecular biomarkers and offer new basis for combating pediatric B-ALL.

[files191=2;500;500][fileShow][/files]