

## **O 01 • A 19-MIRNA SIGNATURE PREDICTS RELAPSE IN AVERAGE RISK PRE-B ACUTE LYMPHOBLASTIC LEUKEMIA**

**Lammens, TL**, Ghent University • **Ghazavi, Farzaneh**, Ghent University • **Suciu, SS**, EORTC Headquarters, Brussels, Belgium • **Bakkus, MB**, VUB, Brussels, Belgium • **Ferster, AF**, Hôpital Universitaire Des Enfants Reine Fabiola, Brussels • **Uyttebroeck, AU**, University of Leuven • **Lutz, PL**, University Hospital, Strasbourg, France • **Cave, HC**, Hôpital Robert Debré AP-HP, Paris, France • **Plat, GP**, CHU Toulouse, Hopital Des Enfants, France • **Dresse, MFD**, CHU Ulg - CHR Citadelle, Liège •

**INTRODUCTION** Risk stratification has led to a tremendous improvement of the 5-year overall survival rates in childhood acute lymphoblastic leukemia (ALL). The average risk group (AR) where nor favorable nor unfavorable factors are found is the largest patient group, accounting for more than 85% of patients. Despite the good overall survival rate the total number of relapses observed in this AR group is considerable.

**AIM** In this study, we aimed at identifying a marker able to predict relapse at the stage of diagnosis. We focused our study on the recently discovered microRNAs (miRNAs) of which their expression has been reported to hold prognostic power in other cancer types.

**METHOD** A total of 693 miRNAs were profiled using automated high-throughput quantitative stem-loop RT-PCR in a cohort of diagnostic bone marrow samples from AR pediatric precursor B-cell ALL patients in remission or experiencing relapse. All patients were treated according to the EORTC-CLG protocol 58951. The ethical committee approved the study and informed consent was obtained from the patients and/or their parents. Statistics were performed using SPSS17 and R (bioconductor).

**RESULTS** Genome-wide microRNA (miRNA) profiling allowed us to identify a 19-microRNA prognostic signature, predictive for relapse within the AR group. The signature holds an accuracy, sensitivity and specificity of respectively 77 %, 69 % and 84 %. Currently, the signature is evaluated in an independent validation cohort. Notably, many of the miRNAs present in this signature are known oncogenes or tumor suppressor genes.

**CONCLUSION** We identified a 19 miRNA signature, allowing us to accurately predict relapse in AR childhood ALL patients. Absence of any other prognostic parameter within this patient group makes the identified signature a unique and powerful tool for further risk-stratification. The method and signature are suitable for laboratory routine testing, and, will be further evaluated in a prospective study.