Background: Cancer subtype classification using microarray signatures has the potential to transform pathological diagnosis but measurement of Indicator genes in routine practice remains difficult. We have previously used real-time PCR measurement of Indicator genes for acute lymphoid leukaemia (ALL) and acute myeloid leukaemia (AML) as a method for application of microarray gene signatures. The specificity of these genes for this distinction was tested by their measurement in patients with, chronic myeloid leukaemia (CML) and normal bone marrow.

Methods: Mononuclear cells were sorted into unselected (total), CD34+ve and CD34-ve fractions, mRNA globally amplified using PolyA PCR and the expression of 17 Indicator genes measured by real-time PCR. Results: There was no statistically significant difference in expression for any gene between cases of CML. Cyclin D3 only (p≤0.04) was upregulated in CML in the CD34+ fraction, whilst HkrT-1 (p≤0.02) and fumarylacetoacetate (p≤0.03) were upregulated in AML. HOXA9 showed non-significant upregulation in AML, but in combination with proteoglycan 1 distinguished between AML and normal samples, in the CD34- fraction, in unsupervised clustering. Unsupervised clustering distinguished between AML and the other diagnostic groups.

Conclusion: These results show that the genes discriminatory between ALL and AML are uninformative in the context of CML and normal bone marrow, except for distinction with AML.

Microarray, PolyA PCR, RT-PCR, Gene Signature, Myeloid Leukaemia

Presentation: Poster