

## Evaluating the Prognostic Significance of Circulating mRNAs in Children with Refractory or Relapsed Neuroblastoma (RR-NBL); a BEACON-Neuroblastoma Biomarker Study

Matt Bentham[1], Susan A. Burchill[1], Elizabeth Roundhill[1], Rebekah Weston[2], Jennifer Laidler[2], Keith Wheatley[2], Lucas Moreno[3]

1. Leeds Institute of Medical Research, University of Leeds, Leeds, United Kingdom;
2. Cancer Research UK Clinical Trials Unit, University of Birmingham, United Kingdom;
3. Vall d'Hebrón Research Institute, Barcelona, Spain.

Members of the SIOPEN Molecular Monitoring Group and National co-ordinators of the BEACON1 trial

**Introduction/Background:** Despite therapeutic advances, high-risk neuroblastoma remains clinically challenging, with a 5-year survival below 50%. For relapsed/refractory (RR) cases, overall survival (OS) drops to <20%. Previously, we showed that detecting the adrenergic (ADR) neuroblastoma mRNAs, PHOX2B (paired-like homeobox 2B) and TH (tyrosine hydroxylase), in blood predicts prognosis (1). Given that neuroblastoma comprises both ADR and more mesenchymal-like (MES) cells, which influence progression and relapse (2,3), we analysed the expression of ADR and a panel of MES mRNAs in RR-NBL patients from the BEACON-Neuroblastoma trial (NCT02308527).

**Aims:** Early risk identification could improve outcomes by guiding treatment modifications. Using ADR markers we predict outcomes in 80% of high-risk patients using simple blood samples. We hypothesise that by including MES-marker expression prognostic information for the remaining 20% of patients could be obtained.

**Methods:** RNA was extracted from 2ml blood samples collected in PAXgene™ tubes at trial entry (n=74) and at cycles 2 (n=42), 4 (n=31), 6 (n=24), and end of treatment (n=25) (4). Panels of ADR and MES mRNAs were quantified by RT-qPCR using TaqMan Low Density Arrays (TLDA). Euclidean clustering generated heat maps identifying ADR and MES gene signatures.

**Results:** Baseline detection of TH, PHOX2B, or both correlated with reduced progression-free survival (PFS) and OS, with combined detection showing stronger associations (PFS HR 2.68; OS HR 2.84). Their presence post-cycle 2 and 6 correlated with progression and poor OS. Clustering of the TLDA data revealed an ADR signature at baseline, which intensified at treatment end, supporting its role in relapse. MES mRNA profiling further stratified patients, offering potential new biomarkers of risk.

**Conclusion/Implications:** Blood-based detection of TH and PHOX2B at trial entry and treatment end identifies RR-NBL patients at highest risk. MES mRNAs could enhance risk stratification. This simple test could help prioritise children for alternative therapies.

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