



AB026. Gene expression for disease stratification and prognostication in neonatal encephalopathy

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Abstract: Neonatal encephalopathy is a leading cause of neonatal death and lifelong disability accounting for 1 million deaths every year with 99% of the disease burden in developing countries. Most putative neuroprotectants, including cooling therapy, are effective only when initiated within few hours of birth, hence early identification of ‘at risk’ encephalopathic infants is vital. Magnetic resonance imaging and spectroscopy are considered gold standard for predicting long-term adverse outcomes after neonatal

encephalopathy. However, they are limited by the inability to perform a scan as soon as possible after birth. Inevitably, clinicians have to make treatment decisions before this information is available. Therefore, it is vitally important to identify babies at risk of long-term neurodisability as early as possible after birth, to initiate preventative therapy. In the past decade, genomic and transcriptomic signatures have revolutionized personalised chemotherapy, particularly in breast cancer. Our group and others have effectively exploited host transcriptomic profiling for the rapid diagnosis of bacterial infection and Kawasaki disease, and for disease stratification in tuberculosis. We have recently shown that babies with neonatal encephalopathy have a different gene expression profile, when compared with age matched healthy newborn babies and that transcriptomic signatures at birth can identify the babies who develop adverse outcomes with high accuracy. These findings highlight that gene expression hold great potential as prognostic and treatment decision biomarker.

Keywords: Gene expression; neonatal encephalopathy; stratification; prognostication

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