

Relation between ¹H and ³¹P MRS biomarkers and immunohistochemical markers of cell death and inflammation in a perinatal asphyxia piglet model

N. J. Robertson¹, M. Chandrasekaran¹, S. Faulkner¹, A. Bainbridge², D. Kelen¹, S. Thayyil¹, E. Cady¹, X. Golay³, and G. Raivich¹
¹Institute for Women's Health, University College London, London, United Kingdom, ²Medical Physics and Bioengineering, University College Hospitals, London, United Kingdom, ³UCL Institute of Neurology, United Kingdom

Background: Perinatal asphyxia affects 2-3/1000 term births in the developed world and is associated with high morbidity and mortality rates. A recent meta-analysis demonstrated that the cerebral ¹H-MRS lactate/N acetyl aspartate (NAA) peak area ratio acquired between 5-14 days after birth is the most sensitive and specific MR biomarker of long term neurodevelopmental outcome in infants following perinatal asphyxia¹; lactate/NAA is already used as a bridging biomarker in pre-clinical studies and as a surrogate endpoint in phase II neuroprotection trials in perinatal asphyxia. The reciprocal changes in lactate and NAA (increase and decrease respectively) following hypoxia-ischaemia enhance sensitivity to detect neural injury in the sub-acute phase after hypoxia-ischaemia.

Aim: To assess the relation between ¹H and ³¹P MRS biomarkers and immunohistochemical markers of cell death (quantified using TUNEL + nuclei) and neuroinflammation (microglial de-ramification reflecting phagocytosis of neural debris)² following global hypoxia-ischaemia.

Methods: Twenty-eight Large White male piglets (<24 h of age) underwent transient global hypoxia-ischaemia and serial ¹H (white matter (WM) and deep grey matter (DGM)) and ³¹P MRS (whole brain) data acquisitions up to 48h after injury. At 48h brains were perfusion fixed, post-fixed and paraffin embedded. Adjacent sections were stained for nuclear DNA fragmentation with TUNEL and IBA1 immunoreactivity. TUNEL+ nuclei were counted in 3 fields (at 40x magnification, area of 0.76mm²) and the average converted into counts per mm². IBA1+ microglial cell bodies and branch density were determined at 40x magnification using a 0.24x0.24mm square grid, placed in 3 fields for each brain region and counting the number of cell bodies inside the grid (CBD) and the average number of branches (B) crossing the 3 horizontal (top, middle and bottom) and the 3 vertical (left, middle, and right) 0.24mm long gridlines. This determined the microglial ramification index (B² / CBD). Correlation of metabolites detected by MRS biomarker AUCs (area under the curve, X-axis) with the average density of TUNEL+ cells (Y-axis) and microglial ramification across the forebrain were assessed.

Results: Of all MRS-based biomarkers, Lac/NAA showed a particularly strong positive correlation with TUNEL+ nuclei averaged across the forebrain 48h and NTP/EPP a strong correlation with microglial ramification (both p<0.01) after transient global hypoxia-ischaemia. The highest R² values were seen with WM Lac/NAA (R²=0.57) and Pi/EPP (R²= 0.52), decreasing gradually for Lac/Cr (R²=0.50), NAA/Cr (R²=0.49), NTP/EPP (R²=0.36) and PCr/EPP (0.32) with comparatively low levels for brain pHi (R² = 0.14). Cho/Cr AUCs showed no correlation. Microglial ramification was particularly correlated with NTP/EPP (R²=0.40) and less well correlated with Lac/NAA (R² = 0.24).

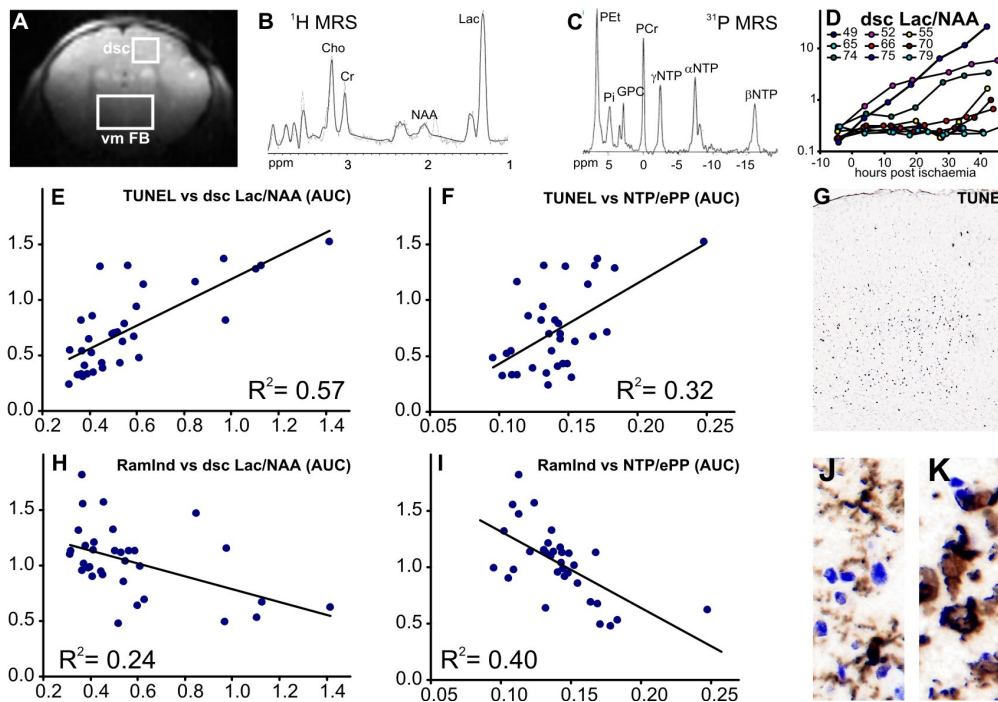


Fig. Scout MR image (A) showing voxel positions for the dsc (dorsal subcortical white matter) and vmFB (ventromedial forebrain) and representative (B) ¹H and (C) ³¹P MR spectra from an injured (B) and uninjured (C) animal. (D) Lac/NAA data plots following global hypoxia-ischaemia (HI) for untreated animals. Correlation of MRS biomarker AUCs (area under the curve, X-axis) for (E) Lac/NAA and (F) NTP/EPP in the 48h after global HI with average density of TUNEL+ cells (G) across the forebrain (Y-axis). Each data point represents a single animal. (I) Microglial ramification was most closely correlated with NTP/EPP and less with (H) Lac/NAA. Representative photomicrograph of IBA-1 staining of a naive brain with maximal microglial ramification (left) and almost total loss of microglial ramification with severe HI and no intervention (right).

Conclusion: Lac/NAA showed a particularly strong positive correlation with TUNEL+ nuclei averaged across the forebrain 48h after transient global hypoxia-ischaemia. This may reflect the gradual inability of neurons to metabolize lactate even before NAA and energy rich phosphates are depleted. Whole brain NTP/EPP showed a strong correlation with microglial ramification. Injury-associated activation and phagocytosis of neural debris (due to necrotic cell death) are associated with rapid microglial branch loss. Microglial de-ramification may thus reflect non-apoptotic forms of cell death.

References: 1. Thayyil et al., Pediatrics 2010;125:E 382-95

2. Bohatschek et al., J Neurosci Res 2001;5