

Temporal Profile Of Serum Mitochondrial DNA (MTDNA) In Patients With Aneurysmal Subarachnoid Hemorrhage (ASAH)

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Purpose:

Subarachnoid hemorrhage is a highly complex disease with majority of survivors confronting post-SAH complications. Tissue damage during early brain injury lead to release damage associated molecular pattern molecules (DAMP) that may initiate and sustain inflammation during the course of SAH via pattern recognition receptors. Mitochondrial DNA due to unmethylated CpG motifs acts as DAMP via binding to toll-like receptor-9. The aim of this study was to investigate the cell free circulating mtDNA in SAH patients and its association with post-SAH complications and clinical outcome.

Materials and Methods:

The DNA was extracted from the serum of 80 SAH patients at days 1, 3, 5, 7, 9, 11, 13 and from 18 healthy controls. Three representative mitochondrial gene fragments including Cytochrome B (CytB), D-Loop and Cytochrome c oxidase subunit-1 (COX-1) were quantified using a Taqman-probes based qPCR. Clinical outcome was assessed by Glasgow outcome scale (GOS) and modified Rankin scale (mRS).

Results :

Serum D-Loop and COX-1 were significantly elevated early after aSAH and remained high over first 2 weeks. CytB levels were however, elevated later at day 7. Cumulative levels over two weeks showed significant correlations with post-SAH complications including a negative correlation of D-Loop with pneumonia, hydrocephalus and epilepsy, a positive correlation of Cyt B with occurrence of CVS and a negative correlation of COX-1 with systemic infections and seizures. Cumulative D-Loop values negatively correlated with clinical outcome.

Conclusion:

Our data suggest that mtDNA may directly or indirectly influence post-SAH complications and clinical outcome