The Neisseria Transcriptome in Septic Shock in Infants, a Force in Precision Cellular Dysfunction Detection?

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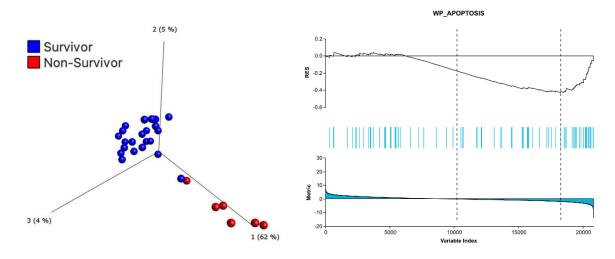
Aims and objectives

Tracking changes in transcriptomes in pediatric septic shock and relating it to clinical outcomes have not been studied extensively. We planned to study the temporal changes in the transcriptome and relate it with clinical outcomes in infants with meningococcal septic shock (MSS).

Materials and methods

Design – Retrospective descriptive analysis of microarray datasets

Setting – Children admitted in Pediatric intensive care with meningococcal septic shock
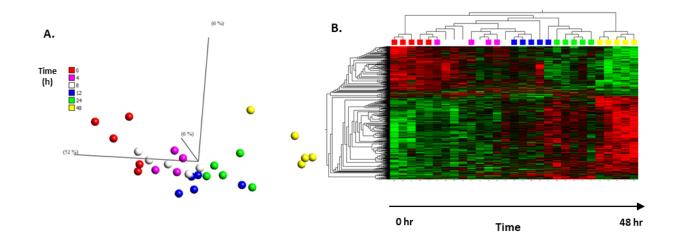
Methods - Gene-expression data was parsed through Qlucore Ohms explorer (QOE) software. Temporal changes in transcriptome were studied using Primary Component analysis (PCA) and Gene Set Expression Analysis (GSEA)

Results

Two paediatric datasets were included; Meningococcal Group B Sepsis study (MSS1) from the United Kingdom (29 samples) and, from Holland (41 samples) (MSS2). PCA plots were generated using qlucore bioinformatics Anova multi-group analysis.

GSEA showed significant upregulation of inflammation associated gene sets for both datasets as well as gene-sets related to electrolytes and clotting. For MSS1, GSEA comparison of the non-survivors and survivors showed differential gene down-regulation for apoptosis (normalised expression score -1.60, p = 0.02 and q = 0.15), for ICAM3, TNF and Cytokine gene expression.
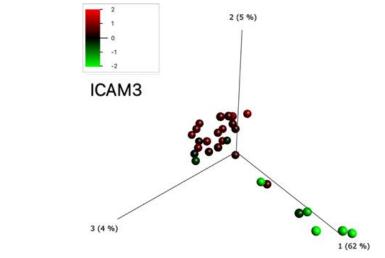

Box plots suggested similarities between MSS1 and MSS2 for MMP9, TIMP1, NFKB1 gene expression and allowed survival analysis suggesting down-regulation of ICAM3 gene-expression in non-survivors.

Discussion

- Our study illustrates temporal changes of the transcriptome over an acute period of Meningococcal septic shock in infants.
- Changes in ICAM-3 signaling suggests apoptotic effects and demonstrates the potential for the transcriptome to be used for survival analysis.
- The exploitability of the transcriptome for theranostics requires further investigation.