

Genomic Analysis of Pediatric Systemic Inflammatory Response Syndrome (SIR)

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Synopsis:

This study seeks to utilize the novel genetics, microarray chip technology to determine pattern of expression of > 10,000 human genes in peripheral whole blood and to determine the correlation between alterations in gene expression patterns and the subsequent development of organ dysfunction and mortality in the systemic inflammatory response syndrome (SIRS) in children. The goal of the project is to generate a substantial database of gene expression patterns in SIRS/sepsis in children in order to both identify the crucial molecular markers that predispose to the development of SIRS/sepsis and predict progression towards multiple organ dysfunction and/or mortality. The aims of the project are:

1. Development of a web-enabled, secure, national-level, ethnically diverse, genomic database of children with SIRS, septic shock, and/or MODS.
2. Perform microarray analysis for >10,000 known genes in selected patients derived from the database established in Specific Aim I.
3. Confirm microarray results with protein expression profiles.