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Data Article

Dynamics of hepatic gene expression and serum cytokine profiles in single and double-hit burn and sepsis animal models

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ABSTRACT

We simulate the pathophysiology of severe burn trauma and burn-induced sepsis, using rat models of experimental burn injury and cecal ligation and puncture (CLP) either individually (singe-hit model) or in combination (double-hit model). The experimental burn injury simulates a systemic but sterile pro-inflammatory response, while the CLP simulates the effect of polymicrobial sepsis. Given the liver's central role in mediating the host immune response and onset of hypermetabolism after burn injury, elucidating the alterations in hepatic gene expression in response to injury can lead to a better understanding of the regulation of the inflammatory response, whereas circulating cytokine protein expression, reflects key systemic inflammatory mediators. In this article, we present both the hepatic gene expression and circulating cytokine/chemokine protein expression data for the above-mentioned experimental model to gain insights into the temporal dynamics of the inflammatory and hypermetabolic response following burn and septic injury. This data article supports results discussed in research articles (Yang et al., 2012 [1,4]; Mattick et al. 2012, 2013 [2,3]; Nguyen et al., 2014 [5]; Orman et al., 2011, 2012 [6–8]).

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Specifications table

Subject area	Biology
More specific subject area	Inflammation, sepsis, burns, bioinformatics
Type of data	Gene expression data (.CEL files) and serum cytokine profiles (Excel tables)
How data was acquired	mRNA expression using Affymetrix Rat Genome 230 2.0 Array Microarrays, Cytokine expression using MILLIPLEX Rat Cytokine/Chemokine Panel
Data format	Raw (.CEL files) gene expression data. Analyzed data for serum cytokine profiles
Experimental factors	Collected liver samples were flash frozen for off-line microarray analysis
Experimental features	Combination of non-lethal rat models of burn injury and cecal ligation and puncture
Data source location	599 Taylor Road, Piscataway, New Jersey,08854, U.S.A.
Data accessibility	Data is presented along with this article

Value of the data

- We present a uniquely comprehensive dataset describing the short-term (up to 24 h) and long-term (up to 10 days) responses of hepatic gene expression and circulating cytokine dynamics in a combination of single- and double-hit animal models of experimental burn and sepsis (CLP). By obtaining short-term and long-term data both the immediate onset as well as the evolution of the inflammatory response to injury can be studied.
- Temporal expression profiles of rat hepatic mRNA are obtained for the various injury models by microarray analysis using a Rat Genome 230 2.0 Array (GeneChip, Affymetrix, Santa Clara, CA, USA) that consists of 31099 probe sets analyzing over 28,000 genes. Further information regarding the array is available at the manufacturer's website (http://www.affymetrix.com) [1–5].
- Temporal variation in serum concentrations of a panel of 23 serum cytokines and chemokines is analyzed at the protein (peptide) level [6–8]. The selected panel includes both pro-inflammatory and anti-inflammatory cytokines and chemokines whose expression is commonly altered after burn injury and sepsis.
- The short-term hepatic gene expression response in single-hit experimental burn and sepsis animal models is characterized [1,4].
- The long-term gene expression dynamics in the single-hit animal model of sepsis is determined [2].
- The effect of burn priming on metabolic and immune gene expression in the rat liver is determined in the animal model of sepsis [3].
- The dynamics of the early and long-term response in serum cytokine profiles is determined in the single-hit burn model and the single-hit sepsis model as well as in the double-hit burn and sepsis model [7,6,8].
- The data can be used to identify patterns of circadian gene expression in the homeostatic rat liver [5].

1. Methods

6–7 week old male Sprague–Dawley rats weighing between 150 and 200 g were used for this study. Animals were housed in a temperature-controlled environment (maintained at 25 °C) with a 12-h light–dark cycle and provided water and standard chow ad libitum. All experimental procedures were in accordance with the National Research Council guidelines and approved by the Rutgers University Animal Care and Facilities Committee.