Interleukin-1 (IL-1) is thought to have a significant role in the pathophysiology of heat stroke (HS), although little is known regarding the actions or expression patterns of the IL-1 family. This study tested the hypotheses that following HS IL-1 family gene expression is dynamic, while loss of IL-1 signaling enhances recovery. IL-1 family expression was determined in plasma, spleen, and liver from C57BL/6J mice (n = 24 control, n = 20 HS) at maximum core temperature (Tc,Max), hypothermia, and 24 h post-HS (24 h). Soluble IL-1 receptor subtype I (sIL-1RI) protein expression peaked at 24 h (14,659.01 + 2,016.28 pg/ml, P < 0.05), while sIL-1RII peaked at hypothermia (19,099.30 + 1,177.07 pg/ml). IL-1α gene expression in the spleen (ninefold) and liver (fourfold) along with IL-1RI (threefold spleen and fivefold liver) were maximal at hypothermia. Spleen IL-1β gene expression peaked at Tc,Max (fourfold) but at hypothermia (fourfold) in liver. Gene expression of the IL-1 family member IL-18 peaked (2.5-fold) at Tc,Max but was similar at all other time points. Subsequent studies revealed that despite accruing a greater heating area (298 + 16 vs. 247 + 12°Cmin, P < 0.05) IL-1RI knockout (KO) mice (n = 14) showed an attenuated hypothermia depth (28.5 ± 0.2 vs. 27.3 ±...
Tissue and circulating expression of IL-1 family members following heat stroke

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Helwig BG, Leon LR. Tissue and circulating expression of IL-1 family members following heat stroke. Physiol Genomics 43: 1096–1104, 2011. First published August 9, 2011; doi:10.1152/physiolgenomics.00076.2011.—Interleukin-1 (IL-1) is thought to have a significant role in the pathophysiology of heat stroke (HS), although little is known regarding the actions or expression patterns of the IL-1 family. This study tested the hypotheses that following HS IL-1 family gene expression is dynamic, while loss of IL-1 signaling enhances recovery. IL-1 family expression was determined in plasma, spleen, and liver from C57BL/6J mice (n = 24 control, n = 20 HS) at maximum core temperature (Tc,Max), hypothermia, and 24 h post-HS (24 h). Soluble IL-1 receptor subtype I (sIL-1RI) protein expression peaked at 24 h (14,659.01 ± 2,016.28 pg/ml, P < 0.05), while sIL-1RII peaked at hypothermia (19,099.30 ± 1,177.07 pg/ml). IL-1α gene expression in the spleen (ninefold) and liver (fourfold) along with IL-1RII (threefold spleen and fivefold liver) were maximal at hypothermia. Spleen IL-1β gene expression peaked at Tc,Max (fourfold) but at hypothermia (fourfold) in liver. Gene expression of the IL-1 family member IL-18 peaked (2.5-fold) at Tc,Max but was similar at all other time points. Subsequent studies revealed that despite accruing a greater heating area (298 ± 16 vs. 247 ± 13°C-min, P < 0.05), IL-1RI knockout (KO) mice (n = 14) showed an attenuated hypothermia depth (28.5 ± 0.2 vs. 27.3 ± 0.5°C, P < 0.05) and duration (675 ± 82 vs. 1,283 ± 390 min, P < 0.05) with a higher 24 h Tc (36.9 vs. 34.1°C, P < 0.05) compared with C57BL/6J mice (n = 8). The current results demonstrate that following HS IL-1 family gene expression is altered and IL-1RII KO mice display Tc responses consistent with a more rapid recovery.

HEAT STROKE (HS) induced multiorgan failure (MOF) is thought to be due to the systemic inflammatory response syndrome (SIRS) that ensues following endotoxin leakage from ischemic gut barrier membranes (23, 24). Endotoxin is believed to stimulate proinflammatory cytokine release, which contributes to core temperature (Tc) and inflammatory disturbances resulting in MOF and death. The mediators of HS morbidity/mortality have not been specifically identified, but results of correlation studies have implicated cytokines, including interleukin-1 (IL-1), as having important actions in the pathophysiology of HS.

Knowledge regarding the role of the IL-1 family in mediating HS morbidity/mortality is based solely on results of circulating plasma levels as no study has reported organ-specific cytokine changes as a result of HS. For example, high circulating levels of IL-1α and IL-1β correlated with the severity of hyperthermia at the time of clinical admission in HS patients (8, 9, 21, 36). In animal models, high central nervous system and/or circulating IL-1β levels were associated with hyperthermia at the time of HS collapse (32–34). Previously we reported that mice develop hypothermia (Tc ~29°C) within ~2 h of HS recovery a Tc response that was correlated with high plasma IL-1β (but not IL-1α) levels (27).

The initial step in physiological responses directly mediated by IL-1α and IL-1β require that the cytokine bind the IL-1 subtype I receptor (IL-1RI), the interaction then allows for recruitment of the IL-1 receptor accessory protein (IL-1RACP) to the ligand/receptor complex resulting in formation of a functional signaling complex. IL-1 cytokines can also bind the IL-1 subtype II receptor (IL-1RII). However, the short intracellular tail of the IL-1RII prevents signal transduction following binding of the IL-1 ligand, thereby creating an antagonistic receptor that sequesters excess circulating IL-1. Tissue-bound receptors can also be truncated resulting in the formation of soluble forms of the receptors, sIL-RI and sIL-1RII. Similar to the tissue bound IL-1RII receptor both soluble receptors act as antagonists of IL-1 and can influence physiological actions of the cytokines. Although overlooked to date, understanding the actions of tissue and soluble receptors provides critical insight regarding the regulation of IL-1 in the HS syndrome.

Similar to IL-1α and IL-1β, IL-18, a recently identified member of the IL-1 family, is induced by lipopolysaccharide (LPS) injection (37) and has significant proinflammatory properties (14, 15). While injections of the cytokine do not directly induce a rise in Tc, administration of the cytokine attenuates IL-1β-induced elevations in Tc (17). These results suggest the cytokine may influence Tc responses following HS, although like IL-1 receptors, expression patterns of the cytokine in response to HS have yet to be determined.

Clearly, the time course of production, actions, and tissue-specific expression patterns of the IL-1 family members in the HS syndrome remain poorly understood. Insight regarding the expression patterns of IL-1 family members is especially important in organs such as the liver and spleen as both are major immune organs known to produce and respond to cytokines during inflammation. Furthermore, we have previously shown that the organs display a differential time course of injury in our mouse HS model (26, 27). Thus, understanding expression patterns of the IL-1 family members may provide important insight regarding the source and potential therapeutic benefit of targeted treatment strategies against select cytokines.

The purpose of this study was to examine IL-1 family expression at maximum Tc (Tc,Max) and during recovery from HS in plasma, liver, and spleen of C57BL/6J mice. We hypothesized that HS recovery would be characterized by significant alterations in IL-1 family gene and protein expression in

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plasma, spleen, and liver samples. The results of gene expression studies revealed that HS was accompanied by dynamic changes in IL-1 cytokine expression. To further understand the physiological impact of changes in IL-1 expression during HS and recovery, we performed a follow-up set of experiments in which we investigated the role of IL-1 using our previously established mouse model of HS (28).

Current knowledge regarding the actions of IL-1 during HS have been derived from animal studies administering the IL-1 receptor antagonist (IL-1ra), a ligand that competes for the IL-1 binding site, thereby blocking IL-1-mediated actions (10, 11, 32, 33). However, use of the IL-1ra has yielded inconclusive results regarding the actions of IL-1 during and in recovery from HS. Alternatively, the IL-1 receptor subtype I knockout (IL-1RI KO) mouse lacks the IL-1R1, the only known IL-1 receptor subtype that can directly propagate a signaling cascade. The use of a conscious IL-1RI KO mouse model of HS is favorable because of normal heat dissipation mechanisms while circumventing pharmacokinetic issues associated with injection of the receptor antagonist. Using the IL-1RI KO mouse a second goal of this study was to determine the effects of the loss of IL-1 signaling on Tc responses following HS in a conscious mouse model (28–30). We hypothesized that following HS IL-1RI KO mice would demonstrate Tc responses that are indicative of a more rapid recovery compared with C57BL/6J mice.

**MATERIALS AND METHODS**

*Animals.* Specific pathogen-free male C57BL/6J mice and IL-1RI KO mice (Jackson Laboratories, Bar Harbor, ME) were used. For the C57BL/6J gene expression and plasma protein studies the control (n = 24) and HS (n = 20) groups weighed 30.8 ± 0.4 g and 31.5 ± 0.5 g, respectively (27). For the C57BL/6J (n = 8) and IL-1RI KO (n = 14) HS studies animals weighed 29.1 ± 0.6 g (2–3 mo old) and 32.1 ± 0.6 g (2 mo old), respectively.

Mice were individually housed in Nalgene polycarbonate cages (11.5 × 7.5 × 5 in) fitted with HEPA-filter cage tops and wood chip bedding (Prion-Chip, PFI Industries). Rodent laboratory chow (LM-485; Harlan Teklad, Madison, WI) and water were provided ad libitum under standard laboratory conditions (25 ± 2°C, 12:12 h light-dark cycle, lights on at 0700). (27). In conducting research using animals, we adhered to the *Guide for the Care and Use of Laboratory Animals* (39) in an Association for Assessment and Accreditation of Laboratory Animal Care-approved facility. All procedures received Institutional Animal Care and Use Committee approval before experimentation.

**Blood and tissue harvesting.** Blood, liver, and spleen were collected from C57BL/6J mice as described in detail previously (27). In brief, C57BL/6J mice were heat stressed and randomly assigned to the following groups for blood and tissue collection: Baseline (Tc < 36.0°C), Tc_Max (42.7°C), hypothermia (lowest Tc value with cooling rate of 0.01°C/min during recovery), or 24 h following the start of heat exposure. Control groups were analyzed at each time point to account for any circadian influences on gene (tissue) and protein (plasma) expression. Sampling time of each control mouse was matched to that of a mouse in the corresponding HS group (27). C57BL/6J mice were rapidly anesthetized (<1 min) with isoflurane (5% in 100% O3, flow rate = 3.0 l/min) and exsanguinated following thoracotomy and intracardiac puncture (heparinized 1 ml syringe, 23 gauge needle); blood was transferred to 1.5 ml heparinized microcentrifuge tubes and immediately placed onto ice until plasma could be separated by centrifugation (4°C, 5 min, ~3,500 rpm). Plasma samples were aliquoted into ≤150 μl volumes and stored at −80°C until assayed. The spleen and liver were rapidly excised, frozen in liquid nitrogen, and stored at −80°C until analysis.

**Plasma cytokine measurements.** sIL-1RI and sIL-1RII concentrations were determined on duplicate plasma samples with kits specific for mouse soluble cytokine receptors (sensitivity 2 pg/ml) (27). Plasma samples were analyzed using the FlowMetrix System (Lumix, Austin, TX), which is a “Multiplexed Fluorescent Bead-Based Immunoassay.” Control groups at each time point revealed virtually identical sIL-1RI and sIL-1RII levels thus control groups were combined for ease of presentation. The immunoassay procedure used in this protocol detects the soluble receptor regardless of whether or not it is bound to an IL-1 ligand. Thus the results presented represent total binding and are not segregated into bound and unbound fractions.

**RNA extraction.** Frozen liver and spleen samples were placed in TRI Reagent, homogenized, and RNA isolated using the RiboPure Kit (Ambion, Austin, TX). RNA concentration and quality were determined using a Nanodrop 8000 spectrophotometer (Nanodrop Products, Wilmington, DE). RNA concentration was calculated from the 260 nm reading. RNA purity for all samples used in real-time PCR analysis was ≥1.8 and ≥1.95 for the 260/230 and 260/280 nm ratios, respectively.

**Reverse transcription and real-time PCR.** RNA samples were reverse transcribed into cDNA using the High Capacity Reverse Transcription Kit (Applied Biosystems, Foster City, CA). Samples were reverse transcribed at 37°C for 2 h, and the resultant cDNA was used in real-time PCR experiments.

**TaqMan Expression Assays** containing 0.9 μM of each primer and 0.25 μM of a TaqMan MGB probe, comprising an FAM reporter dye at the 5′-end and a nonfluorescent quencher at the 3′-end, were combined with 50 ng cDNA and water in a final reaction volume of 20 μl. Primers and probe sets for murine IL-1α, IL-1β, IL-1RI, IL-1RII, IL-1RαP, IL-18, β-actin (Actb), β-glucuronidase (Gusb), phosphoglycerate kinase-1 (PGK-1), and 18s RNA were obtained from Applied Biosystems. Efficiency for the primer/probe sets was >90% for all genes. To further ensure specificity of primer combinations PCR products from randomly chosen reactions were separated on a 1% agarose gel revealing the presence of a single band for each PCR product. Amplification of PCR products was performed under the following conditions: 10 min at 95°C followed by 40 cycles consisting of 95°C for 15 s and 1 min at 60°C.

The threshold cycle (Ct) for each gene sample defined as the PCR cycle at which the emitted fluorescence signal was greater than the background level of fluorescence (18). Changes in target gene expression within spleen or liver were calculated as fold change relative to the controls at the same time point (Tc,Max, hypothermia, 24 h) using the 2−ΔΔCt method (35). Data were normalized, denoted as the ΔCt, by determining differences in Ct values between the target gene of interest and average of the internal control genes (ΔCt = Ct of target gene − Ct average of internal control genes). Mean normalized Ct values at baseline (control n = 6), Tc_Max (control n = 7, heat n = 7), hypothermia (control n = 5, heat n = 7), and 24 h (control n = 6, heat n = 6) were compared, and fold change was calculated if statistically significant changes in ΔCt existed. Fold change was calculated as 2ΔΔCt = 2ΔCtMax − 2ΔCtwere, where ΔCtMax − ΔCt was the difference between the sample (heated ΔCt) and control (nonheated ΔCt) at a specific time point.

A panel of genes were screened using the 2−ΔΔCt method where −ΔΔCt = Ctbaseline − CtTime Point to identify appropriate internal control genes that did not change in response to heating (44). Target ΔCt values in liver samples were normalized to the expression levels of the internal control genes Gusb, PKG-1, and 18s, which were unaffected by the heating protocol. Within spleen tissue Actb was the only gene not significantly affected by the heating protocol and was used to normalize target gene ΔCt values in this tissue. Results of PCR data are presented as bar graphs of the mean fold change without error bars. This is necessary as cycle threshold is exponentially related to copy number, which is converted to fold change to derive linear comparisons. Thus 2−ΔΔCt estimates the error using ΔΔCt plus and ΔΔCt minus the SD (35).
**RESULTS**

**Plasma sIL-1RI and sIL-1RII levels.** sIL-1RI and sIL-1RII showed a differential time course of expression in C57BL/6J mice during 24 h of HS recovery. Plasma levels of sIL-1RI were not different from controls (2.890.6 ± 101.7 pg/ml) at T<sub>c</sub><sub>Max</sub> (2.727.6 ± 500.1 pg/ml) or hypothermia (4.621.2 ± 707.8 pg/ml, Fig. 1A). At 24 h post-HS sIL-1RI levels (14.659.0 ± 2.016.3) were significantly elevated compared with all other time points (ANOVA, P < 0.001; Fig. 1A). Conversely, plasma sIL-1RII levels were significantly higher at hypothermia (19,099.3 ± 1,177.1 pg/ml) compared with all other time points (−15,520 pg/ml; ANOVA, P = 0.015; Fig. 1B). Interestingly, plasma sIL-1RII levels were about four- to sixfold higher than plasma sIL-1RI levels at all time points except 24 h of recovery when they were similar (Fig. 1, A and B).

**Spleen and liver gene expression in C57BL/6J animals following HS.** Control mice showed no difference in gene expression profiles at any time points and were combined into a single group for presentation purposes and arbitrarily assigned a value of 1 (dashed line, Fig. 2, A–H). Compared with controls, spleen gene expression of IL-1α continued to significantly increase from T<sub>c</sub>max through hypothermia (3.4- and 9.2-fold increase, respectively; ANOVA, P < 0.001) and returned to baseline levels by 24 h (Fig. 2A). Liver IL-1α gene expression levels showed a significant increase at hypothermia (4.3-fold increase) compared with controls and heated animals at T<sub>c</sub>max and 24 h (ANOVA, P < 0.001; Fig. 2B). By 24 h, IL-1α returned to baseline levels in the liver (Fig. 2B).

**Spleen IL-1β gene expression peaked at T<sub>c</sub>max (4.4-fold increase) and continued to be expressed at significantly higher levels than controls throughout hypothermia (3.5-fold higher; ANOVA, P < 0.001; Fig. 2C) but returned to baseline levels by 24 h. In comparison, liver IL-1β gene expression showed a progressive increase above control levels from T<sub>c</sub>max to hypothermia (1.4- and 3.9-fold, respectively; ANOVA, P < 0.001), before returning to control levels by 24 h (Fig. 2D).

**IL-18 gene expression in the spleen showed a 2.5-fold increase above controls at T<sub>c</sub>max and remained significantly elevated at hypothermia (1.7-fold increase; ANOVA, P < 0.001; Fig. 2E).** Spleen IL-18 levels were not significantly higher than controls at any time point.
**IL-1 AND HEAT STROKE RECOVERY**

**DISCUSSION**

The initial goal of this study was to determine plasma, liver, and spleen IL-1 family expression patterns in C57BL/6J mice, in which HS-induced tissue damage had been previously determined (27). The major findings of this study are threefold. First, plasma levels of sIL-1RI and sIL-1RII were elevated at 24 h and hypothermia, respectively. Second, spleen and liver IL-1 family gene expression was altered throughout 24 h of recovery following HS. Third, loss of IL-1 signaling increased cytokines and HS have focused largely on the relationship between circulating levels of IL-1 and/or IL-1ra at the time of collapse and during recovery and their relation to mortality rates (6, 8, 9, 21, 36). A critical, but often overlooked aspect of IL-1-
Fig. 2. Changes in spleen (left) and liver (right) gene expression of IL-1α (A, B), IL-1β (C, D), IL-18 (E, F), IL-1RI (G, H) in C57BL/6J mice following HS. Gene expression was measured by real-time PCR in controls (n = 24), at Tc,Max (n = 7), hypothermia (n = 7), and 24 h (n = 6). Values are mean fold change calculated from threshold cycle (Ct) values, with the range of fold change provided below each bar as described in MATERIALS AND METHODS. Control gene expression was similar among groups, assigned a value of 1, and combined for presentation purposes. *P < 0.05 vs. controls; †P < 0.05 vs. 24 h; §P < 0.05 vs. Tc,Max.
mediated physiological responses is the relationship of the endogenous cytokine to tissue and soluble forms of the receptor. Cleavage products of the transmembrane type I and II receptors result in the formation of sIL-1RI and sIL-RII, which act as natural antagonists of IL-1 (2, 43). The presence of increased levels of circulating soluble receptors following HS expands previous studies using the same C57BL/6J mice population in which IL-1β/H9252, the high-affinity ligand for sIL-1RII, was elevated at hypothermia (27). Taken together, the results of current and previous studies suggest that elevations in sIL-1RII at hypothermia may be an endogenous mechanism that works to enhance recovery from HS in wild-type (i.e., C57BL/6J) mice by sequestering excess circulating IL-1β. Interestingly, increased sIL-1RII levels are also found in septic patients (19), further supporting that HS is accompanied by a septic-like response in recovery. In comparison the sIL-1RI has the greatest affinity for the IL-1Ra followed by IL-1β/H9251 (13, 41). Although in the current study, at 24 h the sIL-1RI was significantly increased, circulating IL-1β was not found to be elevated in the same animals (27). Unfortunately the limited

Table 1. Core temperature responses of heat-stressed IL-1RI KO and C57BL/6J mice

<table>
<thead>
<tr>
<th>Tc Response</th>
<th>IL-1RI KO Heat</th>
<th>Range</th>
<th>C57BL/6J Heat</th>
<th>Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Time to Tc,max, min</td>
<td>320.4 ± 14.0*</td>
<td>(222-404)</td>
<td>254.6 ± 8.5</td>
<td>(223-297)</td>
</tr>
<tr>
<td>Time to Tc,min, min</td>
<td>208.5 ± 16.6*</td>
<td>(127-335)</td>
<td>315.8 ± 58.1</td>
<td>(164-653)</td>
</tr>
<tr>
<td>Hypothermia, °C</td>
<td>28.5 ± 0.2*</td>
<td>(28-30)</td>
<td>27.2 ± 0.5</td>
<td>(24-28)</td>
</tr>
<tr>
<td>Heating area, C·min</td>
<td>298.5 ± 15.7*</td>
<td>(194-392)</td>
<td>246.8 ± 13.4</td>
<td>(207-295)</td>
</tr>
<tr>
<td>Hypothermia duration, min</td>
<td>675.8 ± 82.1*</td>
<td>(333-1,307)</td>
<td>1283.4 ± 390.5</td>
<td>(565-2,657)</td>
</tr>
<tr>
<td>Rewarming time, min</td>
<td>476.6 ± 54.7*</td>
<td>(251-775)</td>
<td>782.2 ± 166.4</td>
<td>(433-801)</td>
</tr>
<tr>
<td>24 h Tc, °C</td>
<td>36.9 ± 0.5*</td>
<td>(32-38)</td>
<td>34.1 ± 1.3</td>
<td>(29-37)</td>
</tr>
</tbody>
</table>

Core temperature (Tc) responses were calculated for heating curves shown in Fig. 3 as described previously (20). Values are means ± SE with range of values shown in parentheses. *P < 0.05 vs. C57BL/6J mice. KO, knockout; Tc,max, maximum core temperature; Tc,min, lowest Tc during recovery.
plasma volume in the mouse prevented measurements of IL-1Ra, and thus its relation to IL-1RI expression could not be determined in the current study.

The current study is unique in that it investigated the pathophysiology of HS at the tissue level following HS. Specifically, IL-1 family of cytokines and receptors was examined in the liver and spleen as the organs have significant roles in the innate immune response (16, 46) and are thought to have critical clearance roles with respect to the HS-induced endotoxin release (24). Furthermore, the organs show a different time course of injury with cytokotoxic damage to the spleen present at Tc,Max (27). Consistent with the onset of damage, spleen IL-1β and IL-18 gene expression also peaked at Tc,Max, suggesting increased expression of these cytokines may be associated with HS morbidity in this organ. In contrast to spleen damage, the appearance of liver damage in our HS model was delayed (26), and the liver gene expression of IL-1α, IL-1β, and IL1R1, along with IL-1α and IL1R1 in the spleen, was maximal at hypothermia in the current study. Thus the elevated levels of IL-1 family gene expression at hypothermia may act internally to contribute to the delayed liver damage previously seen in C57BL/6J mice (26).

Although the organ-derived sources of circulating IL-1 and IL-1 receptors was not a focus of the current study, the increased gene expression in the liver and spleen suggests that the issues may contribute to circulating IL-1 family protein levels following HS. This may be particularly true of the spleen, an organ made up of red and white pulp with the latter comprising B and T lymphocytes and having a significant role in the immune response. However, in the absence of translational studies that include tagging proteins, the association of spleen and liver IL-1 and circulating levels is unclear. Instead the purpose of identifying IL-1 family gene expression was to determine if spleen and liver damage was associated with altered levels of IL-1 gene expression, an association that has been implicated in HS morbidity and mortality, albeit never investigated.

Surprisingly, we detected only very low levels of IL-1RII and were unable to detect IL-1RαCp gene expression in the spleen and liver. This finding may be related to a lack of expression in these tissues, the timing of transcription and translation, or methodological limitations. However, the latter seems unlikely as multiple primer sets were utilized in an effort to detect the accessory portion of the receptor complex. Gene expression of IL-18, a recently discovered IL-1 family member that possesses potent proinflammatory properties, was examined for the first time in the context of HS and was shown to be increased in the spleen at Tc,Max and hypothermia but decreased in the liver at all time points. IL-18 interacts with IL-12 to induce cell-mediated immunity in response to endotoxin (e.g., LPS; Refs. 3, 14). Previously we observed elevated plasma IL-12 levels at Tc,Max, and it is intriguing to speculate that IL-18/IL-12 interactions are occurring in our HS model (27). However, we were unable to examine plasma IL-18 levels in the current study due to a lack of mouse reagents for this cytokine, and we did not measure IL-12 in our spleen samples as that was beyond the scope of this study.

In a comparison of the α- and β-isofoms of IL-1 gene expression, the contributions and role of IL-1α are not well known, although release of the cytokine has been shown to occur in response to endotoxin injection (4) and severe inflamma-
nonheated controls. Compared with IL-1RI KO mice, the delayed and variable transition from hypothermia toward a fever-like state in C57BL/6J mice is consistent with our previous findings in this strain (28). Determination of the physiological mechanisms contributing to the leftward shift in the recovery profile of IL-1RI KO mice was not a goal of this study. However, IL-1β is known to contribute to fever development following LPS injection (5) and has been shown to induce fever when injected into the intracerebroventricular space (40). Furthermore, systemic administration of LPS increases IL-1β mRNA expression in the rat anterior hypothalamus (38), while thermosensitive neurons in the same region are influenced by the cytokine (47). Specifically, the presence of IL-1β reduces the sensitivity of temperature-sensitive neurons in the anterior hypothalamus and decreases their firing frequency (45), an effect that is attenuated when the IL-1ra is given (47). Collectively these studies combined with our earlier work showing that following HS mice experience fever (29) suggest that IL-1 may modulate thermoregulatory effector responses during heat exposure and provide an immune (i.e., IL-1) link to central responses associated with HS.

A caveat in the current study regarding experimental design should be noted. The Tc patterns of HS mice were followed for 48 h to compare differences in HS recovery between knockout (IL-1RI KO) and wild-type (C57BL/6J) mice. In contrast the C57BL/6J mouse tissues for which gene expression data are presented were harvested as part of a previous protocol in which animals were tracked for 24 h post-HS (27). Studying recovery in IL-1RI KO compared with C57BL/6J animals was a goal of this study, hence we tracked animals over a 48 h time period, a time that allowed recovery of Tc to baseline values in both strains. Contrasting this, instead of determining gene expression patterns in IL-1RI KO mice, we sought to track gene expression changes at predefined Tc biomarkers in those animals (i.e., C57BL/6J) in which tissue damage had already been determined (26, 27).

While the current study provides evidence suggesting the IL-1 family of cytokines plays a significant role in the morbidity and recovery associated with HS, future studies that investigate changes in the cytokine milieu are needed to better understand additive, synergistic, or competing actions of these proteins in understanding the pathophysiology and SIRS-like responses associated with HS. In addition, future studies designed to measure tissue protein levels would provide more direct evidence in support of a role for IL-1 in support of morbidity associated with HS. It would also be beneficial to examine other organs known to be involved in the SIRS (e.g., brain, kidney).

Perspectives

Collectively, these studies provide insight into a molecular mechanism that may serve as a future therapeutic target for HS patients. Although the role of cytokines in HS recovery is not well understood, the use of knockout models provides unique insight into the pathophysiology of HS and the role cytokines play during recovery. Furthermore, the use of knockout animals avoids the pharmacological challenges encountered when using antibodies and peptides to block the actions of cytokines allowing for a more in-depth study of the actions of a single cytokine. However, because cytokines have redundant action and rarely act in isolation, studies in wild-type animals will continue to be critical in understanding the contributions of the cytokine milieu to HS recovery.

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DISCLOSURES

No conflicts of interest (financial or otherwise) are declared by the author(s).

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