Acute metabolic decompensation due to influenza

in a mouse model of ornithine transcarbamylase deficiency

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SUMMARY

The urea cycle functions to incorporate ammonia, generated by normal metabolism, into urea. Urea cycle disorders (UCD) are caused by loss of function in any of the enzymes responsible for ureagenesis, and are characterized by life-threatening episodes of acute metabolic decompensation with hyperammonemia (HA). A prospective analysis of interim HA events in a cohort of patients with ornithine transcarbamylase (OTC) deficiency, the most common UCD, revealed that intercurrent infection was the most common precipitant of acute HA and was associated with markers of increased morbidity when compared to other precipitants. To further understand these clinical observations, we developed a model system of metabolic decompensation with HA triggered by viral infection (PR8 influenza) using spf-ash mice, a model of OTC deficiency. Both WT and spf-ash displayed similar cytokine profiles and lung viral titers in response to PR8 influenza infection. During infection, spf-ash displayed an increase in liver transaminases suggesting a hepatic sensitivity to the inflammatory response and an altered hepatic immune response. Despite having no visible pathologic changes by histology, WT and spf-ash had reduced CPS1 and OTC enzyme activities, and unlike WT, spf-ash failed to increase ureagenesis. Depression of urea cycle function was seen in liver amino acid analysis with reductions seen in aspartate, ornithine and arginine during infection. In conclusion, we developed a model system of acute metabolic decompensation due to infection in a mouse model of a urea cycle disorder. In addition, we have identified metabolic perturbations during infection in the spf-ash mice, including a reduction of urea cycle intermediates. This model of acute metabolic decompensation with HA due to infection in UCD serves as a platform for exploring biochemical perturbations and the efficacy of treatments, and may be adapted to explore acute decompensation in other types of inborn errors of metabolism.
INTRODUCTION

The urea cycle (UC, Supplemental Figure 1) is present only in the liver and serves two purposes: (1) the *de novo* biosynthesis and degradation of arginine, and (2) the incorporation of excess nitrogen into urea. Urea cycle disorders (UCD) are caused by loss of function in any of the enzymes responsible for ureagenesis, and are characterized by life-threatening episodes of acute metabolic decompensation with hyperammonemia (HA). The incidence of these disorders has been estimated at 1 in 30,000 live births (1). UCD can be considered in two groups. In proximal (mitochondrial) UCD (N-acetylglutamate synthetase [NAGS], carbamoyl phosphate synthase [CPS1], and ornithine transcarbamylase [OTC] deficiencies), ammonia disposal is severely compromised. In distal (cytosolic) UCD (arginosuccinate synthetase [ASS], arginosuccinate lyase [ASL]), and arginase [ARG1] deficiencies), ammonia disposal is not as severely impaired and characteristic amino acid metabolites accumulate.

Acute metabolic decompensation with HA in UCD is precipitated by dietary non-adherence, enhanced protein catabolism due to protein/caloric over-restriction or intercurrent infection (2). Intercurrent infection, particularly with respiratory viruses, is the most common trigger of HA, accounting for >34% of episodes in a cohort of UCD subjects (2, 3). Although it has not been systematically examined, intercurrent infection is suspected to result in greater morbidity versus other precipitants based on anecdotal clinical experience (4). For UCD, morbidity may manifest as elevated plasma ammonia of greater duration that results in prolonged hospital stays and increased utilization of medical resources. The current paradigm for acute HA treatment centers on addressing the increased whole body protein catabolism brought on by protein/caloric insufficiency that can occur in dietary over-restriction or intercurrent infection. Reversing catabolism by drastically increasing parenteral caloric intake, regardless of the precipitant, has been the mainstay of acute HA crisis treatment (4). However, the pathophysiologic processes behind different HA precipitants may be distinct, raising the possibility of targeted therapies that may alter the hospital course of UCD patients.
Given the well-recognized propensity of patients with UCD to experience severe and at times fatal HA, a translational approach was undertaken to develop a model of acute HA due to infection in UCD and describe the mechanisms of acute metabolic decompensation. To explore the etiology, clinical characteristics and morbidity associated with HA events, the longitudinal database of the Urea Cycle Disorders Consortium was queried to assess the severity of HA experienced by patients with the most common UCD, ornithine transcarbamylase (OTC) deficiency. Infection was noted to be the most common precipitant of acute HA, with indicators of increased morbidity present compared to other precipitants. To recapitulate a robust inflammatory response and to explore further perturbations in UC function as experienced by OTC patients during infection, an experimental model of infection associated acute HA was created by inoculating spf-ash mice, a model of OTC-deficiency, with the influenza A/Puerto Rico/8/34 (PR8) virus. Both WT and spf-ash displayed perturbations in UC enzyme activity and intermediates suggesting that influenza infection may suppress a subset of hepatic functions, including enzymes that are already compromised in patients with UCD.
RESULTS

Infection is associated with indicators of increased morbidity in patients with OTC

The longitudinal database of the Urea Cycle Disorders Consortium (UCDC) of the Rare Disease Clinical Research Network gathers prospective data on the clinical characteristics of this unique patient population, which can help provide insight into common HA triggers associated with these disorders. Given the anecdotal clinical evidence that patients with UCD experience more severe HA in the setting of intercurrent illness (4), the longitudinal database of the UCDC was queried for interim events in hospitalized OTC patients between March 1, 2005 and August 7, 2012. Infectious etiologies of HA were scored when there was clinical and laboratory evidence of viral and bacterial infections. Dietary etiologies included non-adherence and changes in protein and calories. Overall, 57 OTC patients had a reported 148 hyperammonemic (HA) events. Confirmed infectious etiologies accounted for 39/148 (26%) of HA events, while dietary perturbations accounted for 28/148 (19%) of HA events (Figure 1A). The remaining etiologies (55%) occurred in lower frequencies individually and were varied: stress, medication changes, menses, and unknown causes. Since patients with UCD may have elevated plasma ammonia at baseline, we determined changes in plasma ammonia from baseline during infectious and dietary precipitants. Baseline ammonias were calculated as an average of three previous plasma ammonia levels from well clinic visits. Changes in plasma ammonia from baseline were not significantly different between infectious and dietary precipitants (172 ± 100 versus 147 ± 88 μM, P=0.34, Figure 1B). A single individual with elevated baseline ammonia experienced a decrease from baseline during a dietary precipitant. To examine whether increased morbidity was associated with infection, we next examined hospitalization rate, length of hospital stay (LOS) and IV ammonia scavenger use in a dichotomous fashion for infectious versus non-infectious etiologies. For OTC patients, the hospitalization rate (Figure 1C) for infection was 22% higher (P = 0.04). The average LOS was increased by 1.7 days (Figure 1D), although, this finding was not significant (P = 0.20). With symptomatic HA, OTC patients typically require the administration of IV
ammonia scavengers. When IV ammonia scavengers were used as a surrogate for morbidity during hospitalization (Figure 1E), the rate of inpatient utilization during acute HA due to infectious (31/39 events; 79%) versus non-infectious precipitants (56/102; 55%) was significantly increased (P<0.0001). Overall, these data indicate that infectious precipitants of acute HA in UCD have unique clinical parameters, raising the possibility of distinct pathophysiologic mechanisms of ammonia metabolism during infection.

Development of a model of acute HA due to viral illness

Because of the distinct epidemiologic parameters of infection in UCD (Figure 1), we next sought to develop an in vivo model of acute HA due to infection. Two well-characterized experimental systems—the spf-ash mouse, and the mouse-adapted PR8 influenza virus—were combined to create a murine model of viral infection in the setting of a UCD. Spf-ash and WT mice were infected on Day 0 using an infection aerosolization apparatus and euthanized on Day 5 (Supplemental Figures 2A and 2B). Spf-ash and WT challenged with PR8 were observed to have ruffled fur and decreased social and grooming behaviors beginning at Day 2-3 of the infection protocol (Supplemental Figure 2A, gray shading). Protein intake, assessed by weighing the food daily, was recorded during the course of infection and expressed on a g/kg/day basis (Figure 2A). Spf-ash mice had a lower body weight and protein intake (Day 1, 45.2 g/kg/day) compared to WT (136.6 g/kg/day) and had much lower body weights at baseline, typically weighing 20% less than sex and age matched littermates. Both groups decreased their protein intake over the course of the infection with WT demonstrating a greater decrease (81.6%) versus spf-ash (72.8%) by Day 5. WT animals also lost a greater percentage of body weight at Day 5 likely reflecting greater body stores at baseline (Figure 2A); controls were 97.4% of starting body weight while spf-ash were 101.3% of starting body weight (P=0.01). From Day 2-5, with onset of sickness behaviors, both WT and spf-ash lost weight at similar rates.

Spf-ash and WT mice have similar lung infectious parameters
Although *spf-ash* and WT animals both displayed physiologic and behavioral characteristics suggestive of viral infection, we assessed viral titers and cytokine profiles in the lungs to confirm that infectious parameters were similar between the strains. Viral titers (Figure 2B) were measured on Day 5 for lung homogenates using serial dilutions and measuring infectivity in Madin-Darby Canine Kidney epithelial cells (MDCK) cells. Whole lungs from infected WT and *spf-ash* mice displayed no differences in viral titers on Day 5 of infection (P = 0.77). Lung cytokine profiles were determined using a fluorescent bead-based multiplex assay (Table 1). Both WT and *spf-ash* showed a robust response to viral infection with significant increases in a number of colony stimulating, chemotactic, and inflammatory cytokines (Infection (Inf), P < 0.05;). No significant genotype differences were seen (Genotype (Gen), P > 0.05). With the exception of lower GM-CSF concentrations at Day 5 in *spf-ash* (Inf X Gen, P < 0.031), all remaining infection X genotype interactions were not statistically significant (Inf X Gen, P > 0.05). Thus, WT and *spf-ash* displayed similar infectious and inflammatory parameters during PR8 influenza infection.

**Hepatic response during PR8 infection**

It is well documented that humans and certain mouse strains may develop elevated serum AST and ALT during respiratory viral infection (5). However, whether these signs of hepatic insult translate into alterations in UC function has not been studied. Given the similar parameters of PR8 infection in both WT and *spf-ash*, we performed further biochemical studies to evaluate hepatic metabolic function (Figure 3). *Spf-ash* mice displayed greater hepatocyte sensitivity to infection with increases in serum AST 3x over control animals (Figure 3A, P = 0.007). Serum ALT was on average 2x higher than controls, although this finding was not significant (Figure 3A, P = 0.25). Furthermore, the mean AST/ALT ratio in the infected *spf-ash* was 5.4 (Figure 3A, P = 0.01), suggesting an exogenous insult as the cause of the hepatitis. Acute metabolic decompensation due to intercurrent illness in patients with UCD is characterized by HA. Consistent with the previous studies in these mice, plasma ammonia was 3-4x greater at baseline in *spf-ash* mice compared to WT. However, during
PR8 infection, plasma ammonia increased over 100 μg/dL in some animals (P = 0.04), while WT remained unchanged from baseline (Figure 3B). With significant elevations of markers of hepatic damage, liver histology was investigated in infected spf-ash and controls. Significant inflammation, necrosis, and apoptosis were absent in all the liver samples (Supplemental Figure 3). Although the increase in liver transaminases and ammonia seen in the plasma were suggestive of Reye syndrome in the spf-ash mice, macrovesicular (H/E stain, Supplemental Figure 3A) and microvesicular (oil red O stain with baking, Supplemental Figure 3C) steatosis were absent.

For qRT-PCR (data not shown) and titer in the liver (Figure 3C), no PR8 virus was detected. Despite a lack of virus detection in unperfused livers, spf-ash livers showed signs of hepatic sensitivity and damage (Figure 3A). Profiling of the hepatic response to lung PR8 infection in WT B6 mice using mRNA expression arrays showed significant increases in the acute phase response and anti-viral response pathways (unpublished data). To examine the hepatic response to PR8 infection, we profiled a select panel of expressed acute phase response and anti-viral response genes in WT and spf-ash mice during infection (Figure 3D). Both WT and spf-ash showed a robust increase in serum amyloid A1 (SAA1) and lipocalin 2 (LCN2), markers of the acute phase response (P <0.05 for both). However, when profiling the hepatic anti-viral immune response, some discrepancies emerged. Spf-ash showed elevations in TLR3, TLR7, MDA5 and RIG-I at baseline and unlike WT failed to show a clear differentiation in levels of expression with infection. Overall, these data suggest that spf-ash have an abnormal hepatic immune response to infection, and in some instances, increased activation of anti-viral pathways at baseline.

**CPS1 and OTC enzyme activities are reduced in WT and spf-ash during infection**

In the setting of biochemical abnormalities indicating hepatitis with increased hyperammonemia, we hypothesized that perturbations in hepatic nitrogen metabolism might be exacerbated during infection.
Previous studies have indicated altered mitochondrial UC enzyme function in the setting of influenza infection (6) but did not account for protein intake, which we find varies between WT and spf-ash animals. Since the expression of UC enzymes are responsive to dietary signals (7), all animals were housed individually and matched for protein intake on a g/kg/day basis during the 5 days of infection to correct for protein intake differences (Figure 2A). Protein matching resulted in a factorial design (Supplemental Figures 4A, B). Under this caloric restriction regimen, weight loss in all experimental groups was similar on Day 5 (Supplemental Figure 4C). To assess the depression of mitochondrial UC function, CPS1 and OTC activities were measured in liver homogenates (Figure 4A). During infection, CPS1 activity decreased by 40% (P = 0.001) in WT and 28% (P = 0.018) in spf-ash while OTC activity decreased by 7% (P = 0.005) in WT and 21% (P = 0.015) in spf-ash (Figure 4A). These results suggest that reduction of CPS1 and OTC enzyme activities are part of the normal hepatic physiology of PR8 infection, which may not be tolerated by a compromised UC in spf-ash.

To further characterize the mechanism of decreased enzyme activity, CPS1 and OTC were quantified for protein expression differences (Figure 4B). Surprisingly, CPS1 protein levels were 3-fold higher in spf-ash compared to WT, and infection had no significant effect on CPS1 protein levels in either the WT (P = 0.787) or spf-ash (P = 0.804) animals. The amount of OTC tended (P = 0.086) to be reduced in WT littermates during infection whereas OTC protein levels remained unchanged in the spf-ash.

Given the increased immunoreactive CPS1 in the spf-ash liver extracts, we hypothesized that the hepatocytes had an increase in either protein content or number as a compensation for OTC deficiency. To determine whether there was an increase in mitochondrial number, we examined livers from WT and spf-ash by electron microscopy on Day 5 of infection (Figure 3C). WT and spf-ash displayed occasional mitophagy, and on average, similar numbers of mitochondria of normal morphology.
Altered nitrogen disposal in spf-ash during infection

Given the demonstration of mitochondrial UC dysfunction by enzymology, stable isotopic tracing was employed to assess alterations in ureagenesis. Using a standard published protocol, enrichment of plasma $^{15}N$-urea was determined following an intraperitoneal injection of a single dose of $^{15}N$-ammonium chloride (4 mmol/kg, $^{15}$NH$_4$Cl) on Day 5 (Figure 4D). The end product of ammonia disposal, plasma $[^{15}N]_\text{urea}$, was enriched in WT mice on Day 5 of infection ($P = 0.03$). Conversely, plasma $[^{15}N]_\text{urea}$ enrichment was not only lower in spf-ash mice during the uninfected state but there was also a failure to increase incorporation of $^{15}$NH$_3$ into urea during the infected state ($P < 0.01$).

Given this failure to increase ureagenesis, we next examined free amino acids in liver homogenates to evaluate UC intermediates (Table 2). Spf-ash had elevated ornithine (Gen, $P = 0.01$), aspartate (Gen, $P = 0.024$), and arginine (Gen, $P < 0.01$) in the absence of infection. However, a depression of these levels was observed during infection, suggesting a strong genotype x infection interaction (ornithine Gen X Inf, $P = 0.018$, aspartate Gen X Inf, $P = 0.015$, and arginine Gen X Inf, $P < 0.01$). Thus, during infection, perturbations in UCD function can be seen in spf-ash at the enzyme and metabolite levels.
DISCUSSION

Life-threatening, acute HA is a significant source of morbidity and mortality for patients with UCD who may experience up to 2.2 – 2.8 episodes per year depending upon the underlying enzymatic defect (2). Prospective analyses of the OTC cohort presented here revealed that infectious precipitants led to increased hospitalization rates (Figure 1C) and hospital stays (Figure 1D). Consistent with our findings, a recent paper found that inborn errors of metabolism in general are an independent risk factor for hospitalization due to respiratory illnesses such as Respiratory Syncytial Virus (RSV) infection (8). In addition to increased hospitalization rates and length of stay, infection-associated HA was also accompanied by increased utilization of IV ammonia scavengers (Figure 1E). Since IV ammonia scavengers are usually reserved for patients with hyperammonemic encephalopathy, this surrogate marker of severity suggests increased morbidity when this patient population is exposed to infectious precipitants. In light of these parameters suggestive of increased morbidity, we aimed to investigate the pathophysiology underlying acute hyperammonemia induced by infection.

We hypothesized that infection would lead to activation of the immune system with concomitant perturbations in UC function. The factorial design (Supplemental Figure 4A) adopted in the present study allowed the effects of infection to be assessed in isolation of those related to dietary insufficiency, another common precipitant of HA. In this respect, while dietary insufficiency is present in both conditions, our results clearly indicate that there are distinct metabolic sequelae due to infection.

While spf-ash and WT mice displayed similar markers of lung inflammation (Table 1), the hepatic immune response in spf-ash showed some key differences (Figure 3D). Although virus was not detected in WT livers (Figure 2B), mRNA elevations in TLR3, TLR7, MDA5, RIG-I and IRF7, were seen in response to infection.
Activators of these pathways include the pathogen associated molecular patterns (PAMPs) dsRNA and ssRNA, which can be seen during viral infection (9). In addition to PAMPs, these pathways may be activated in response to dying host cells by damage associated molecular patterns (DAMPs, e.g. dsRNA, ssRNA, mtDNA). Our findings in WT lead us to suggest that the liver is either reacting to undetectable levels of PR8 virus in the blood and/or liver sinusoidal spaces, or tissue damage from the lung. Interestingly, spf-ash display elevations in AST and ALT and markers of innate immune activation in the uninfected state (Figure 3D). These data suggest that spf-ash may be experiencing baseline liver damage with innate immune activation via DAMPs. The baseline immune activation may also account for the hepatic sensitivity seen with infection (AST and ALT, Figure 3A) and remains to be explored.

A previous study examining the effect of influenza infection on CPS1 and OTC activities in WT B6 mice showed appreciable reductions in CPS1 (12%) and OTC (17%) enzyme activities (6). In the present study, we observed a greater reduction in CPS1 activity likely due to the intake matching strategy applied (Figure 4). These findings imply that a reduction in CPS1 and OTC activities is part of the normal physiologic response to PR8 infection and may compound the pre-existing OTC deficiency in spf-ash. Interestingly, despite lower enzyme activity, immunoreactive CPS1 was actually increased in spf-ash mice with normal mitochondrial number and morphology (Figures 4B and 4C). Indeed, spf-ash liver contains 33% more mitochondrial protein per gram of liver when compared to WT (10). Nonetheless, despite greater CPS1 protein, spf-ash CPS1 enzyme activity was 15% lower in spf-ash mice. Our results suggest that even in the uninfected state, a proportion of the CPS1 pool is inactive or subactive in spf-ash mice. This in vitro reduction in CPS1 activity may be related to altered post-translational modifications such as lysine acylation or acetylation (11, 12), which further suggests an avenue of investigation.
In our model, spf-ash mice appear to have lower ureagenesis during dietary restriction (Figure 4D), however, these findings were not significant. More importantly, unlike WT, spf-ash failed to increase ureagenesis during infection (Figure 4D) and experienced hyperammonemia (Figure 3B). This failure of increased ureagenesis was due to a depression in the pool of UC intermediates during infection (Table 2). While these data reflect a metabolic snapshot of a dynamic process, they are consistent with our additional findings. Overall, the depressions seen in UC intermediates may be due to the observed depression of UC activity (Figures 4A and 4D), their incorporation into protein synthesis (Arg and Asp), or activation of other pathways such as polyamine synthesis (Arg and Orn). Spf-ash mice are able to maintain ureagenesis when given a balanced nitrogen challenge (14, 15). When challenged with an unbalanced nitrogen load, profound hyperammonemia and decreased ureagenesis follows. These results suggest that the prevision of UC intermediates in the balanced nitrogen load can sustain ureagenesis in the setting of a hypomorphic OTC enzyme. As further evidence, supplementation with UC intermediates may also prevent ammonia toxicity after a lethal dose of ammonia (16, 17) or an unbalanced nitrogen load (15). Of particular interest is ornithine. In B6 mice, an I.P. challenge with ammonium chloride results in elevations in hepatic ornithine within 5 minutes of injection, suggesting its importance in the incorporation of ammonia (18). In spf-ash primary hepatocytes, ornithine increased ureagenesis and reduced orotic acid production (19). In the spf-ash mouse, ornithine supplementation restored ureagenesis and mitigated hyperammonemia during parenteral nitrogen loading (14). Inhibition of ornithine aminotransferase, may also be effective (20). This efficacy of ornithine seems to be related to an increase in OTC and CPS1 activities, and a decrease in carbamoyl phosphate degradation (9, 13, 16, 21).

In conclusion, we have developed a model of acute metabolic decompensation due to infection in the spf-ash mouse. From a therapeutic standpoint, given the depletion of hepatic arginine and ornithine in our model, formal studies on hyperammonemia and ureagenesis during infection while supplementing these amino acids
will provide insight into their efficacy. Overall, this model may serve as a platform for describing biochemical perturbations and the efficacy of treatments during acute metabolic decompensation in UCD due to a common precipitant. In addition, this model system may be adapted to explore acute decompensation due to infection in other types of inborn errors of metabolism such as organic acidemias and fatty acid oxidation defects.
MATERIALS AND METHODS

Infection with A/PR/8/34 (PR8)

The experiments outlined were performed on B6 x B6EiC3Sn\textit{a/Otc}\textsuperscript{spf-ash}/J (spf-ash) and littermate controls (The Jackson Laboratory, Bar Harbor, ME). Mice were housed in a pathogen-free facility, caged individually, had access to a 24% protein mush-based feed, Nutragel (Bio-Serv, Frenchtown, NJ), and autoclaved reverse osmosis water. Mice were kept in a temperature (22 \pm 2\textdegree C) and humidity (30-70\%) controlled environment with a 12-hour light cycle. Mouse adapted human influenza virus A/PR/8/34 (PR8) for infection was produced as described previously (22). Four-to 6-week-old spf-ash and littermate control mice were exposed to an infective dose of PR8 of 500 TCID\textsubscript{50} in an aerosolization chamber (Glas-Col, Terre Haute, IN) (23). Mice were sacrificed on Day 0 and Day 5 of infection by 5\% Isoflurane inhalation with cervical dislocation. Plasma, serum and tissues were separated from whole blood and stored at -80\degree C until use. All animal care and procedures were carried out according to the criteria outlined in the "Guide for the Care and Use of Laboratory Animals" prepared by the National Academy of Sciences and published by the National Institutes of Health (NIH publication 86-23 revised 1985) and were authorized by the Animal Care and Use Committees of the National Human Genome Research Institute and the Institutional Animal Care and Use Committee of the Mount Sinai School of Medicine.

Viral lung titer

Viral titers were determined using published assay based on the infection of MDCK cells (24). The inverse of the dilution at which 50\% of the wells showed CPE was recorded as the 50\% tissue culture infectious dose (TCID\textsubscript{50}).
**Lung cytokines**

On Day 5 of infection, lungs were removed and immediately homogenized with a TissueRuptor (Qiagen, Valencia, CA) handheld rotor-stator homogenizer in PBS. Cytokine detection in clarified tissue lysates was performed using a mouse cytokine panel (Millipore, Billerica, MA) with detection using a multiplex platform (Luminex, Austin, TX). Cytokine amounts were normalized to lung weight in grams.

**Histology**

Hematoxylin and eosin staining was performed on sectioned paraffin-embedded lung and liver tissue by the Department of Pathology, Mount Sinai Medical Center. Detection of apoptotic cells was performed using the ApopTag Plus Peroxidase In Situ Apoptosis Detection Kit (Millipore, Billerica, MA).

**Biochemical studies**

Plasma ammonia was determined using a glutamate dehydrogenase-based assay according to manufacturer instructions (Sigma-Aldrich). Serum aspartate aminotransferase, alanine aminotransferase, and urea determination were performed in the Center for Comparative Medicine and Surgery, Mount Sinai School of Medicine. Liver amino acids were quantified by ion-exchange chromatography using a Biochrom 30 Amino Acid Analyzer (Biochrom, Cambridge, UK). Amino acid concentrations were calculated as μmol / 100 gram of tissue and expressed as ratios relative to controls.

**Measurement of ureagenesis**

Mice were administered a dose of nitrogen as (15N)-labeled ammonium chloride according to experiments described previously (25, 26). After a 3-hour fast, mice received 4 mmol/kg of 15NH4Cl (Cambridge Isotope Laboratories, Andover, MA) by i.p. injection. Heparinized blood was collected by retro orbital bleeding 20
minutes after injection, and the plasma analyzed for the % of $^{15}$N isotope enrichment of urea by gas chromatography/mass spectrometry (27).

**Ornithine transcarbamylase and carbamoyl phosphate synthetase 1 enzyme assays**

Ornithine transcarbamylase enzyme activity was measured using a published colorimetric assay that detects the formation of L-citrulline (28). Carbamoyl phosphate synthetase I enzymatic activity was performed using lysates prepared as in the OTC assay according to a published assay (29).

**qRT-PCR**

Liver tissue was thawed and homogenized in RIPA buffer on ice. DNA and RNA was extracted from homogenized liver tissue or cell pellets using a kit (Qiagen). For RNA, 1 µg was reverse transcribed to cDNA using a modified MMLV-reverse transcriptase (iScript, Bio-Rad, Hercules, CA). Real-time quantitative PCR reactions were carried out in 50µL using iQ SYBR Green Supermix (Bio Rad, Hercules, CA) or TaqMan systems (Applied Biosciences, Carlsbad, CA). Reactions were cycled and quantitated with an ABI 7500 Fast Real Time PCR System (Applied Bio systems, Foster City, CA).

**Western blot analysis**

For western blot analysis, 30 µg of protein was loaded on 4-20% Tris-glycine polyacrylamide gels. The gels were transferred to polyvinylidene difluoride membrane using the iBlot Dry Blotting System (Life Technologies, Grand Island, NY). The membranes were blocked and probed with primary antibodies according to the manufacturers suggested dilutions: CPS1 (Abcam, Cambridge, MA), OTC (Novus Biologicals, Littleton, CO) and β-actin (Sigma-Aldrich, St. Louis, MO). Incubation was done with appropriate secondary antibodies. Image analyses were performed using an Odyssey Imager (LiCor, Lincoln, NE).
Electron Microscopy

Mouse livers (1 mm$^3$) were fixed overnight at 4$^\circ$C in 2% glutaraldehyde in 0.1M cacodylate buffer (pH 7.4) and washed with cacodylate buffer three times. The tissues were fixed with 2% OsO$_4$ for two hours, washed again with 0.1M cacodylate buffer three times, washed with water and placed in 1% uranyl acetate for one hour. The tissues were subsequently serially dehydrated in ethanol and propylene oxide and embedded in EMBed 812 resin (Electron Microscopy Sciences, Hatfield, PA, USA). Thin sections, approx. 80 nm, were obtained by utilizing the Leica ultracut-UCT ultramicrotome (Leica, Deerfield, IL, USA) and placed onto 300 mesh copper grids and stained with saturated uranyl acetate in 50% methanol and then with lead citrate. The grids were viewed in the JEM-1200EXII electron microscope (JEOL Ltd, Tokyo, Japan) at 80kV and images were recorded on the XR611M, mid mounted, 10.5Mpixel, CCD camera (Advanced Microscopy Techniques Corp, Danvers, MA, USA).

Statistical analyses

For the Rare Disease Clinical Research Network-sponsored Urea Cycle Disorders Consortium (RDCRN UCDC) longitudinal study, OTC patients who were hospitalized due to HA events during the course of the study were examined. Since each participant can experience more than one HA event, the generalized estimating equation (GEE) adjusted for age at the HA event was used. Observed frequency (%) for categorized variables and the mean (standard deviation) for continuous variables were reported. $P$-values less than 0.05 were used to indicate statistical significance.
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COMPETING INTERESTS STATEMENT

The authors declare that they do not have any competing or financial interests.

AUTHOR CONTRIBUTIONS

P.J.M. and G.A.D. conceived and designed the experiments. T.N.T., T.W., E.L., P.Z., B.J.B. performed the experiments. P.J.M. and H.S.L. analysed the data. T.M. contributed reagents and materials. P.J.M. wrote the paper.

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REFERENCES


FIGURE LEGENDS

Figure 1
Clinical findings due to infectious and dietary precipitants. Data from a prospective cohort of OTC patients was characterized for interim HA events. (A) Proportion of interim HA events (plasma ammonia > 100 μmol/L) due to infectious and dietary precipitants. (B) Change from baseline ammonia (C) Hospitalization rate due to non-infectious and infectious precipitants. (D) Length of stay (LOS) for non-infectious and infectious precipitants. (E) Use of IV ammonia scavengers for hospitalized non-infectious and infectious precipitants. Hatched bars indicate p < 0.05.

Figure 2
Infectious parameters in WT and spf-ash mice. Mice infected with PR8 influenza were euthanized at Day 5 and lungs were harvested. (A) Food intake and weight loss (N = 5 / group). Shaded areas indicate appearance of sickness behaviors. (B) Viral titers in homogenized lungs on Day 5 (N = 5-6 / group). For food intake and weight * = < 0.05.

Figure 3
Hepatic immune response to infection. Mice infected with PR8 influenza (N = 5 - 8 / group) were euthanized at Day 5 and tissues were collected by cardiac puncture. (A) Liver transaminases AST and ALT and AST/ALT ratio. (B) Plasma ammonia concentration. (C) Liver viral titer. Control – infected mouse lung tissue. (D) qRT-PCR for liver immune response. SAA1 – serum amyloid A1, LCN2 – lipocalin 2, TLR3 – toll like receptor 3, TLR7 – toll like receptor 7, IRF7 – interferon regulatory factor, MDA5 - melanoma differentiation-associated gene 5, RIG-I - retinoic acid-inducible gene 1, TRIF - TIR-domain-containing adapter-inducing interferon-β. For clinical chemistry floating bar graphs, top = highest value, bottom = lowest value, line = mean. For qRT-PCR, box plots were used. For all, hatched line indicates p < 0.05. Each experiment was repeated 3 times.

Figure 4

Hepatic metabolic response during infection. Mice (N = 4 / group) matched for intake +/- infection with PR8 influenza were euthanized at Day 5 and livers were harvested. (A) CPS1 enzyme activity and OTC enzyme activity. (B) Immunoblot of CPS1 and OTC protein. (C) Electron microscopy of livers on Day 5 of infection and (D) Ureagenesis during infection. For ureagenesis, mice were injected with 4mmol/kg of $^{15}$NH$_4$Cl and sacrificed 20 minutes after injection (N=4 / group) (26). $^{15}$N-urea enrichment was determined by GC-MS. For all, hatched line indicates p < 0.05.
TABLES

Table 1

Lung cytokines produced during acute infection with PR8. WT and spf-ash mice were infected with PR8 influenza by aerosolization and sacrificed on Day 5 (N = 4 / group). Cytokine determinations were made in lung homogenates using a multiplex assay. Inf = infection, Gen = Genotype. Univariate analysis with P < 0.05.

Table 2

Liver amino acids during acute infection. For liver amino acids, livers were homogenized in sulfosalicylic acid and were determined by an amino acid analyzer (N = 4 / group). Inf = infection, Gen = Genotype. Univariate analysis with P < 0.05.
TRANSLATIONAL IMPACT

Clinical issue
The urea cycle functions to incorporate ammonia, generated by normal metabolism, into urea. Urea cycle disorders (UCD) are caused by loss of function in any of the enzymes responsible for ureagenesis, and are characterized by potentially life-threatening episodes of acute metabolic decompensation with hyperammonemia (HA). Acute HA in UCD may be precipitated by any factor that affects metabolic balance such as: dietary indiscretion, enhanced protein catabolism due to dietary over-restriction, or infection. Intercurrent infection is the most common precipitant of acute HA with respiratory viruses being a leading cause.

Results
The aim of this study was to explore perturbations in UC function as experienced by UCD patients during infection. In a prospective analysis of a cohort of patients with ornithine transcarbamylase deficiency (OTCD), the most common urea cycle disorder, the authors found that infection was the most common identifiable cause of acute decompensation with HA and was associated with markers of increased morbidity. To further understand these clinical observations, the authors developed a model system of metabolic decompensation with HA triggered by viral infection (influenza A/Puerto Rico/8/34 (PR8) virus) using spf-ash mice, a model of OTCD. During infection with PR8, spf-ash displayed an altered hepatic immune response to infection. Unlike wild-type (WT), spf-ash also displayed elevated liver transaminases suggesting a hepatic sensitivity to infection. Despite having no visible pathologic changes by histology, WT and spf-ash had reduced enzyme activities in the first two enzymes of the urea cycle: carbamoyl phosphate synthetase I and ornithine transcarbamylase. Along with these enzyme perturbations, spf-ash had increasing hyperammonia and unlike WT, failed to
increase ureagenesis during infection. Liver amino acid analysis revealed further perturbations in UC function with reductions seen in the intermediates aspartate, ornithine and arginine during infection.

**Implications and future directions**

The clinical significance and translational importance of these findings are highlighted in the current management of acute HA in UCD. Regardless of the acute HA precipitant, the medical management strategy is the same: cut protein intake and supplement with high caloric intake. These measures are not always successful. The findings outlined here provide novel insight into the metabolic pathophysiology behind acute infection and a platform for evaluating the efficacy of urea cycle intermediates alone or in combination or immune modifiers. This model may also be adapted to explore acute decompensation and the efficacy of treatments in other types of inborn errors of metabolism.
<table>
<thead>
<tr>
<th>Cytokine pg/g tissue, Mean (SD)</th>
<th>WT Control</th>
<th>WT Infected</th>
<th>spf-ash Control</th>
<th>spf-ash Infected</th>
<th>P values</th>
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<tbody>
<tr>
<td>TNFα</td>
<td>76.2 (16.3)</td>
<td>308.1 (33.2)</td>
<td>73.9 (8.5)</td>
<td>294.6 (91.1)</td>
<td>&lt;0.0001</td>
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<tr>
<td>IFNγ</td>
<td>96.5 (29.1)</td>
<td>1713.0 (1294.4)</td>
<td>68.7 (6.9)</td>
<td>1520.3 (1865.4)</td>
<td>0.029</td>
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<tr>
<td>IL-6</td>
<td>1284.9 (321.1)</td>
<td>(4586.1)</td>
<td>552.6 (453.2)</td>
<td>7269.5 (5056.9)</td>
<td>&lt;0.0001</td>
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<td>IL-10</td>
<td>275.6 (99.8)</td>
<td>190.8 (53.8)</td>
<td>208.1 (68.7)</td>
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<td>IL-12p40</td>
<td>265.0 (66.7)</td>
<td>288.0 (88.9)</td>
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<td>IL-17</td>
<td>179.6 (87.1)</td>
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<td>MIP-1α</td>
<td>481.7 (55.1)</td>
<td>4848.8 (727.1)</td>
<td>411.8 (108.1)</td>
<td>4593.9 (1772.5)</td>
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<td>RANTES</td>
<td>1058.8 (448.9)</td>
<td>9175.1 (5408.0)</td>
<td>891.0 (267.7)</td>
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<td>KC</td>
<td>845.2 (434.7)</td>
<td>(6871.1)</td>
<td>661.8 (156.2)</td>
<td>13785.9 (6007.1)</td>
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<td>MCP-1</td>
<td>530.9 (388.6)</td>
<td>(4222.9)</td>
<td>419.4 (96.0)</td>
<td>18670.0 (5359.4)</td>
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<tr>
<td>G-CSF</td>
<td>315.5 (97.1)</td>
<td>22859.6</td>
<td>255.0 (28.8)</td>
<td>15528.5 (8787.0)</td>
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<td>GM-CSF</td>
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<td>M-CSF</td>
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P values: Inf (Infected), Gen (Genotype), Gen x Inf (Interaction between Genotype and Infected).
<table>
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<tr>
<th>Amino acid*</th>
<th>WT Mean (SD)</th>
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<th>spf-ash Mean (SD)</th>
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<th>P values</th>
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<td>Control</td>
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<td>Control</td>
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<td>Gen</td>
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<td>Gen x Inf</td>
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<td>Glu</td>
<td>291.4 (47.3)</td>
<td>419.7 (6.4)</td>
<td>297.5 (22.4)</td>
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<td>Gly</td>
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<td>269.7 (35.0)</td>
<td>262.8 (9.2)</td>
<td>255.1 (8.9)</td>
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<td>Glu</td>
<td>123.4 (12.5)</td>
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<td>Orn</td>
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<td>55.5 (5.1)</td>
<td>327.0 (152.0)</td>
<td>73.9 (14.5)</td>
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<td>Cit</td>
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<td>4.1 (0.5)</td>
<td>24.9 (27.3)</td>
<td>5.7 (0.9)</td>
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<td>Asp</td>
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<td>288.5 (32.2)</td>
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<td>Arg</td>
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<td>1.1 (0.2)</td>
<td>4.1 (0.3)</td>
<td>1.2 (0.2)</td>
<td>Gen &lt; 0.01</td>
</tr>
</tbody>
</table>

*μmol/100g wet weight
Supplemental Figure 1

A depiction of the urea cycle indicating the source of nitrogen groups for ureagenesis (Blue - ammonia; Red – aspartate).
Supplemental Figure 2

Protocol and methods used in PR8 infection. (A) Study design employed for defining infectious parameters.

Sac – sacrificed. (B) Inhalation apparatus used for PR8 virus delivery.
Supplemental Figure 3

Representative histologic evaluation of the liver on Day 5. (A) Representative H/E stain (N = 5). (B) Representative TUNEL stain (N = 5). (C) Oil Red O stain with baking (N = 5). For TUNEL stain, positive control is normal female rodent mammary gland included in the kit used. For Oil Red O stain, control liver tissue is from a mouse model of alcohol induced liver disease.
Supplemental Figure 4

Methods and feeding parameters for matched intake study design. (A) Study design for matched protein/caloric intake in infected and uninfected animals. Infected spf-ash decrease food intake over the 5 days of infection. To match food intake, the average amount eaten by spf-ash was determined previously, and intake for all other animals was subsequently matched on a g/kg/day basis. Sac – sacrificed. (B) Protein intake applied to individually housed animals. (C) Weight loss due to different conditions (N = 6-8 / group).