

STRONG CHILDREN'S RESEARCH CENTER

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Name: Janine Corley

School: University of North Carolina at Chapel Hill

Mentor: George J. Schwartz, MD and Jeffrey M. Purkerson, PhD

ABSTRACT

Title: Metabolic acidosis impairs clearance of UPEC-UTI

Background: Acute pyelonephritis (AN), commonly caused by vesicoureteral reflux (VUR), is a serious kidney infection in children and is often associated with metabolic acidosis. Previous studies from the laboratory have shown that metabolic acidosis induced by NH_4Cl supplementation in food impairs clearance of uropathogenic *E. coli* (UPEC-UTI) in a refluxing mouse model. NH_4Cl supplementation in H_2O has been associated with dehydration and increased aquaporin-2 (*Aqp2*) expression, which is upregulated in response to arginine vasopressin (AVP).^{1,2} AVP signaling via V2R attenuates Toll-like receptor 4 (TLR4)-dependent inflammatory responses and thereby impairs UPEC clearance.³

Objective: To determine whether NH_4Cl supplementation in food upregulates *Aqp2* gene expression in the collecting duct (CD), as an indicator of dehydration in the mouse model.

Methods: C57Bl/6 mice (8-10 wks.) were split into three different conditions: 2% NH_4Cl supplemented food; 2% NH_4Cl supplemented food in conjunction with continuous acetazolamide (ACZ) dosage of 50 mg/kg/day via Alzet osmotic pump; and normal diet. Kidneys were harvested at 3 days, and total RNA was isolated from collecting duct segments enriched by DBA-lectin mediated magnetic sorting. Since *Cxcl12* (SDF-1) gene expression is upregulated in mice experiencing metabolic acidosis through HIF1 α -dependent regulation, we examined expression of HIF1 α target genes *Defb2* (β -defensin 2) and *Camp*.^{4,5} Relative abundance of *Aqp2*, *Cxcl12*, *Cxcr4*, *Lcn2*, and antimicrobial peptides *Defb1*, *Defb2*, and *Camp* mRNA was quantified by qRT-PCR, with *Gapdh*, *Actb* (β -Actin), and *Cdh1* (E-Cadherin) as references.

Results: The $\text{s}[\text{HCO}_3^-]$, urine pH, and UPEC burden/norm for normal mice were 22.2 ± 0.7 , 6.8 ± 0.0 , and 1; for NH_4Cl -fed mice were 15.5 ± 0.3 , 5.8 ± 0.02 , and 10^3 - 10^5 ; and for NH_4Cl -fed mice in conjunction with ACZ were 14.4 ± 0.4 , 6.8 , and 10^3 , respectively. In acidotic mice, *Cxcl12* mRNA abundance was induced 4.3 ± 0.4 fold, and *Aqp2* mRNA abundance was decreased 0.5 ± 0.1 fold. Expression of the *Defb2* and *Camp* mRNA in mouse CD was 5.5×10^3 - 7.3×10^4 fold less than *Defb1*, which is known to be expressed in the CD, and was not induced by acidosis.⁶

Conclusion: Decreased *Aqp2* gene expression in acidotic mice eliminates modulation to TLR4 signaling by AVP upregulation as a possible cause of the persistent infection. Normalization of urine pH in acidotic mice with ACZ treatment did not change UPEC burden. Thus, impaired clearance of UPEC-UTI cannot be explained by an effect of urine acidification on urothelial barrier function. Since metabolic stress-associated acidosis impairs UPEC clearance, correction of acidosis may limit renal injury-associated pyelonephritis.

References:

1. Andriole V. T. (1970). Water, acidosis, and experimental pyelonephritis. *The Journal of clinical investigation*, 49(1), 21–30. doi:10.1172/JCI106218
2. Regulation of aquaporin-2 by metabolic acidosis: Letters to the editor. (2004). *American Journal of Physiology - Cell Physiology*, 287, C814-C815.
3. Chassin, C., Hornef, M. W., Bens, M., Lotz, M., Goujon, J. M., Vimont, S., ... Vandewalle, A. (2007). Hormonal control of the renal immune response and antibacterial host defense by arginine vasopressin. *The Journal of experimental medicine*, 204(12), 2837–2852. doi:10.1084/jem.20071032
4. Schwartz, G. J., Gao, X., Tsuruoka, S., Purkerson, J. M., Peng, H., D'Agati, V., . . . Al-Awqati, Q. (2015). SDF1 induction by acidosis from principal cells regulates intercalated cell subtype distribution. *Journal of Clinical Investigation*, 125(12), 4365-4374. doi:10.1172/jci80225
5. Zarembek, K. A. (2005). HIF-1alpha: A master regulator of innate host defenses? *Journal of Clinical Investigation*, 115(7), 1702-1704. doi:10.1172/jci25740
6. Lee, J. W., Chou, C. L., & Knepper, M. A. (2015). Deep Sequencing in Microdissected Renal Tubules Identifies Nephron Segment-Specific Transcriptomes. *Journal of the American Society of Nephrology*, 26(11), 2669-2677. doi:10.1681/asn.2014111067