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## Application of metabolomics to neonatal meningitis

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The risk of infant meningitis has been dramatically reduced by successful vaccination programs over the last several decades(1). A study of 931 infants 28 days old (nearly all 36 weeks or greater at birth) with a history of fever presenting for evaluation to the emergency room between 2006 and 2017 found just 5 cases (0.54% of febrile infants) of bacterial meningitis(2). Compared to the risk in term infants, bacterial meningitis is only slightly more common among preterm infants cared for in the neonatal intensive care unit (NICU). Over a 7-year period among 28144 neonates <33 weeks completed gestation cared for in Canadian Neonatal Network NICUs, there were 215 cases (0.76% of all infants) of meningitis (all pathogen causes)(3). This result is similar to work published nearly two decades ago among 11028 very low birth weight infants (<1500 grams) cared for in the *Eunice Kennedy Shriver* National Institute of Child Health and Development Neonatal Research Network over a 3-year period (1998-2001). They found bacterial meningitis in 1.1% of all infants and in 4% of infants evaluated with a CSF culture after day 3 (excluded 187 infants with shunts)(4). Bacterial meningitis is strongly associated with mortality, as well as with poor mental and neurodevelopmental outcome among preterm survivors(4-7). Preterm infants with post-hemorrhagic hydrocephalus may require placement of a shunt that significantly increases the risk of bacterial meningitis. A study of 1036 children with CSF shunts placed, for which 22% were preterm infants with post-hemorrhagic hydrocephalus as the indication, revealed bacterial infection occurred in 11%(8). Taken together, bacterial meningitis remains a severe but infrequent diagnosis among neonates that is much more likely in the setting of a shunt.

*Gordon and Colleagues* performed a nested cohort analysis on prospectively enrolled infants aged 0–12 months cared for in the Neonatal Intensive Care Units (NICUs) at Children’s Hospital of Philadelphia who underwent LP or withdrawal of CSF from indwelling neurosurgical hardware (ventriculo-peritoneal [VP] shunt or *Ommaya* reservoir) for

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evaluation of possible meningitis(9). Patients for whom the CSF culture result was positive for a bacterial pathogen and that received prolonged antibacterial treatment were considered to have bacterial meningitis (n=19). An uninfected group (n=19) of matched patients (by gestational age, postnatal age, sex, and race) was selected for comparison with both negative CSF culture results as well as no laboratory evidence of meningitis in samples obtained *prior to* the initiation of antibacterial treatment. The CSF metabolome was determined via mass spectroscopy on all samples. Using a machine learning approach, a metabolomic signature of bacterial meningitis was developed on a small number of patients in the cohort and validated on the remaining patients. The number of metabolites in the model were then systematically reduced with the aim to reach the smallest number of predictive analytes with the greatest accuracy for the diagnosis of bacterial meningitis. The derived metabolic signature predicted bacterial meningitis equally well in preterm and term infants of varying post-natal ages. Importantly, the authors found no metabolites significantly differed between infants with shunt- or reservoir-associated bacterial meningitis and infants with bacterial meningitis without indwelling neurosurgical hardware. This finding is particularly important because CNS hardware was present in nine infants with bacterial meningitis versus only one infant among the uninfected group. Pathways that were over-represented in CSF from patients with bacterial meningitis included alanine, aspartate, and glutamate metabolism. Taken together, these data strongly suggest glutamate dysregulation may play a key role in diagnosis and pathophysiology of BM in infants. Use of the top 6 metabolites found altered in the training set of patients, resulted in an AUC for bacterial meningitis of 0.97.

The potential ability to identify the metabolic milieu consistent with meningitis in neonates brings with it the exciting possibility of precision medicine-based interventions in this population. The diagnosis of bacterial meningitis requires the isolation of a bacterial pathogen from cerebral spinal fluid (CSF); most often performed using classic culture methods. A lumbar puncture (LP) performed is not universally performed at the time of a sepsis evaluation and in some cases may only be performed after a diagnosis of bacteremia has been made(4). A delay in the timing of LP relative to when a blood culture and initiation of antibacterial treatment are performed, decreases the likelihood of isolating a pathogen in CSF, and increases the dependence upon CSF studies (chemistry, cell count) to make the diagnosis of meningitis. The interpretation of CSF culture results, chemistry, and cell counts is often challenging due to a high frequency of contaminating blood. Patients with equivocal CSF studies may receive prolonged, and perhaps unnecessary, antibacterial treatment. These important clinical conundrums and diagnostic test limitations might be successfully mitigated by the presence or absence of a CSF metabolic signature that has strong diagnostic utility.

A diagnosis of meningitis remains only a simple yes/no decision followed by prolonged treatment with anti-bacterials and supportive care because at present we lack the understanding and sophistication to modify the pathologic process based on *when* the infant is in the disease process. The potential to address this critical deficiency is particularly fascinating when one considers the pathogen-specific responses that the authors touched on by presenting the signature associated with Group B *Streptococcus*. By determining and incorporating the overlap between mechanistic preclinical animal modeling and human 'omic' observational results such as these, we begin to construct a detailed molecular

landscape of the dynamic process for which we now have only a mere snapshot. The work from *Gordon and Colleagues* takes us one step closer to a time when the question “*Will this test change my management?*” actually could prompt an affirmative response.

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