vesicle (EV)-based vaccine generated using lab-strain Salmonella against wastewater-derived Salmonella. METHODS/STUDY POPULATION: We isolated Non-Typhoidal Salmonella (NTS) from raw influent wastewater samples collected from two wastewater reclamation facilities (WRF) in Gainesville, FL. Whole genome sequencing was performed on each isolate and compared to sequences of clinically-derived isolates in FL during our study period to identify a clinical and subclinical isolate for assessing EV based vaccine protection. Mouse serum and stool samples were collected from a cohort of EV-vaccinated mice. Surrogates of protection against Salmonella used anti-Salmonella IgA in the feces of these mice, and anti-Salmonella IgG in serum of the mice, by using ELISAs coated with whole cell lysate collected from the two wastewater-derived isolates. RESULTS/ANTICIPATED RESULTS: We have previously shown that an EV vaccine provides protection against Salmonella enterica Serovar Typhimurium, the serovar used in the generation of the EV vaccine. We anticipate that the EV vaccine generates additional protection against the community-acquired strains, which will be characterized by increases in fecal IgA and serum IgG against two community Salmonella isolates that is similar to responses against the serovar used to generate the EV vaccine (Typhimurium). DISCUSSION/SIGNIFICANCE: This study will improve the translation of our vaccine studies by demonstrating the efficacy of our novel EV vaccine against circulating Salmonella isolates.

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A CTS Team Approach to Fetal Hyperinsulinemia in Diabetic Pregnancy and its Effects on Vasculature and Early Life Metabolism

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OBJECTIVES/GOALS: Fetal glucose dynamics mediate many of the adverse outcomes seen in infants of diabetic mothers (IDM). The goals of this study are to identify: (1) rates of blood glucose change in normoglycemic and hypoglycemic IDM; (2) their relation to in-utero insulin exposure; and (3) their transcriptional impacts on placental and umbilical vasculature. METHODS/STUDY POPULATION: Using a longitudinal prospective study design, placental/umbilical cord tissue and maternal hemoglobin A1c (HbA1c) are being collected from mothers diagnosed with Type 1, Type 2, or gestational diabetes mellitus. Blood glucose levels are also collected from their infants at birth, and every 3-4 hours for up to 9 hours to determine the rate of change. Linear regression modeling will be used to determine associations between placental and umbilical endothelial RNA expression, umbilical cord insulin levels, and maternal HbA1c within each diabetic sub-type. Gene expression from endothelial specimens will be compared between diabetic subtypes and between normoglycemic and hypoglycemic infants via paired t-tests using Benjamini-Hochberg procedure for false discovery rate correction. RESULTS/ANTICIPATED RESULTS: We hypothesize the following; (1) glucose levels will have a steeper rate of change in hypoglycemic infants; (2) maternal HbA1c and in-utero insulin levels will correlate with the level of transcriptional change identified in placental and umbilical endothelial samples; (3) a negative association will exist between cord insulin levels and the rate of change in infant glucose levels; and (4) a positive association will exist between cord insulin level and transcriptional change on the placental and umbilical endothelium. DISCUSSION/SIGNIFICANCE: Identifying gene expression changes in diabetic placental/umbilical endothelium, and the role of insulin/glucose in these changes, is key to managing diabetic vasculopathy and its adverse outcomes. Understanding infant insulin response may also guide management of hypoglycemia and decrease the risk for neonatal intensive care unit admission.

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A CTS team approach to identifying thematic constructs related to kratom use during pregnancy and breastfeeding: A qualitative analysis of social media posts

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OBJECTIVES/GOALS: Research on the safety of perinatal kratom use - an herb that acts on opioid receptors - is scarce. Our transdisciplinary clinical and translational science (CTS) team is conducting parallel qualitative analyses of subreddit posts related to kratom use during (1) pregnancy and (2) breastfeeding. METHODS/STUDY POPULATION: Pregnancy- and breastfeeding-related keywords are being used to extract posts and selected metadata from the following subreddit communities: r/kratom, r/quittingkratom, r/pregnant, and/or r/breastfeeding. After the removal of duplicate posts, posts written in a non-English language and those that state in the post text and/or title that they were published by minors (RESULTS/ANTICIPATED RESULTS: Among the eligible posts, the number of unique usernames of the sources publishing the posts; the range of publication dates; and the mean, median, & range of the number of comments per post will be presented. Inter-rater concordance in thematic coding will be computed. A word cloud will be created with the most used nouns from the eligible posts. Verbatim quotes will be shown to illustrate themes depicted in the sample. The quantitative and qualitative analyses will be conducted separately for the posts related to kratom use during pregnancy and breastfeeding. DISCUSSION/SIGNIFICANCE: These findings could assist clinicians in identifying questions that obstetric patients may have regarding the perinatal use of this emerging substance of concern. Further research is needed to validate these findings using other social media data, such as Twitter.

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A novel mouse model of COVID-19

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OBJECTIVES/GOALS: Rodents are the most widely used experimental animals to study disease mechanisms due to their availability and cost-effectiveness. An international drive to investigate the pathophysiology of COVID-19 is inhibited by the resistance of rats and mice to SARS-CoV-2 infection. Our goal was to establish an appropriate small animal model. METHODS/STUDY POPULATION: To recreate the cytokine storm that is associated with COVID-19, we injected angiotensin converting enzyme 2 knockout (ACE2KO) mice (C57BI/6 strain) with lipopolysaccharide (LPS) intraperitoneally and measured the expression of multiple cytokines as a function of time

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