on the surface of infected red blood cells and may have a role in severe malaria, but they remain sparsely studied in natural infections. We measured the RNA expression of these antigens in Malian children with severe or mild malaria illness. METHODS/STUDY POPULATION: We collected blood samples from Malian children aged six months to five years, including 14 with cerebral malaria, 10 with severe malarial anemia, and demographic-matched controls with mild, uncomplicated malaria. We extracted total RNA from each patient and used a custom capture array to selectively enrich Plasmodium falciparum parasite RNA. We then performed Illumina next-generation RNA sequencing and reconstructed parasite transcriptomes using reference-free de novo assembly. We identified RNA encoding RIFINs and STEVORs using an in-house classifier, then measured the diversity and abundance of gene expression for each infection. Expression diversity was defined as the number of unique variants transcribed. Expression abundance was calculated as transcripts per million (TPM). RESULTS/ANTICIPATED RESULTS: Cerebral malaria cases, but not severe malarial anemia cases, had higher diversity and abundance of RIFIN expression compared to mild infections. Type A RIFINs predominated over Type B RIFINs, and the same two RIFINs were predominantly expressed in all disease phenotypes. We anticipate that predominantly expressed RIFINs share high sequence homology with variants previously shown to bind blood antigens or immune inhibitory receptors. STEVOR expression was also higher in cerebral malaria compared to mild malaria, but STEVOR transcripts were sparse overall. DISCUSSION/SIGNIFICANCE: Elevated RIFIN expression in cerebral malaria over mild malaria supports a role for these antigens in pathogenesis. Severe malarial anemia may progress through a different pathogenic mechanism. Predominantly expressed RIFIN variants may be promising targets for vaccines and therapeutics to protect children against cerebral malaria.

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Dystonia is associated with macro and microstructural abnormalities of the cerebellum: A nested case-control study.

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OBJECTIVES/GOALS: Dystonia is a brain disorder which causes excessive muscle activation, manifesting as abnormal movements. Neuroimaging studies of dystonia have revealed changes in a network involving the cerebellum. We sought out to determine whether subjects with dystonia in the UK Biobank exhibit MRI-based cerebellar pathology. METHODS/STUDY POPULATION: This nested case-control study drew from the UK Biobank, a cohort of >500,000 subjects in the United Kingdom, aged 40-69, enrolled 2006-2010. Eligible subjects must have undergone diffusion-weighted brain MRI. Dystonia cases were ascertained using ICD10 codes. We selected controls without neurologic diagnoses, matched (1:3) on age, sex, imaging site, and medical comorbidities. Mean diffusivity, fractional anisotropy, intracellular and isotropic volume fractions, and orientation dispersion were extracted from four white-matter tracts (inferior, middle, superior cerebellar peduncles; superior thalamic radiations) along with cerebellum, basal ganglia, and whole-brain grey and white-matter volumes. Means were compared using two-tailed t-tests and the Benjamini-Hochberg procedure (FDR = 0.05). RESULTS/ANTICIPATED RESULTS: 23 cases of dystonia and 69 control subjects were selected and ascertained. After correcting for multiple-comparisons (40 volumetric and 35 diffusion-related), intracellular-volume-fraction (ICVF) of the middle- and superior-cerebellar peduncles was significantly lower in subjects with dystonia, suggesting reduced axon density. Volumetric analysis showed significantly reduced volumes of the motor cerebellum (lobules VI and VIII). There were no differences in basal ganglia, cortical, or whole-brain volumes. DISCUSSION/SIGNIFICANCE: These findings support the hypothesis that abnormalities of cerebellar networks contribute to dystonia. In future we will use similar techniques to assess these tracts in subjects with dystonia who are undergoing Deep Brain Stimulation, with the goal of guiding stimulation targeting, and predicting therapeutic outcomes.

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Early life antibiotic exposure and genetic risk in neurodevelopmental disorders: effects on neurogenesis, the gut microbiome, and behavior

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OBJECTIVES/GOALS: Our long-term goal is to understand how both genetic and environmental (GxE) factors contribute to neurodevelopmental disorders (NDDs) so that we may potentially intervene in disease pathogenesis and design therapies to address functional deficiencies. METHODS/STUDY POPULATION: Our studies use a novel GxE model to determine how cephalosporin antibiotic exposure alters the gut microbiome, hippocampal neurogenesis, and behavior in the genetically vulnerable 16p11.2 microdeletion (16pDel) mouse. This mouse models one of the most frequently observed genetic risk variants implicated in NDDs, including ~1% of autism diagnoses. Wildtype and 16pDel littermates were exposed to saline or the cephalosporin, cefdinir, from postnatal days 5-9. We quantified changes in gut microbiota composition using 16S rRNA gene sequencing and utilized immunoblotting, immunohistochemistry, and bulk RNA gene sequencing to assess changes in hippocampal neurogenesis. An additional cohort of saline or cefdinir-exposed mice were subjected to a behavioral battery to assess changes in sociability and anxiety. RESULTS/ANTICIPATED RESULTS: We leveraged the next-generation microbiome bioinformatics platform, Quantitative Insights Into Microbial Ecology 2 (QIIME2) to analyze 16S rRNA gene sequencing datasets of P13 cecal samples from saline- and cefdinir-exposed mice. We found successful perturbations to the gut microbiome following early life cefdinir exposure. Further, we found a robust 50% reduction in hippocampal cyclin E protein in cefdinir-exposed 16pDel male mice, which was replicated in a second independent experiment. This reduction extended to the S-phase cell entry and general stem cell population, quantified by EdU+ and Ki67+ cell numbers, respectively. Lastly, in our first cohort of mice for behavioral studies, we found reduced sociability and increased anxiety-like behaviors in cefdinir-exposed mice. DISCUSSION/SIGNIFICANCE: The findings from this GxE model will provide mechanistic insights into the causes of NDDs; they may inform practice guidelines so as to reduce this environmental exposure; and may suggest interventions like probiotics for those at risk in order to overcome altered gut microbiome composition and restore hippocampal neurogenesis defects.

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