Title:

The Interaction between the Intestinal Microbiome and the Enteric Pathogen Cryptosporidium parvum

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Abstract:

Cryptosporidiosis can be severe in immune compromised persons and is highly prevalent in infants in developing countries. The lack of effective anti-cryptosporidial drugs motivated us to explore the interaction between Cryptosporidium parvum and the host intestinal microbiome. Our aim is to understand to what extent the enteric protozoan parasite C. parvum impacts the intestinal microbiome and to assess whether parasite development can be modulated by the intestinal microbiome. Experiments were performed with laboratory-propagated C. parvum isolates of animal and human origin. Immune suppressed mice were populated with human fecal bacteria. Mice were infected with C. parvum oocysts and fecal samples were collected from infected and uninfected mice. We extracted fecal DNA and deep-sequenced 16S amplicons using an Illumina sequencer operated by the Tufts Genomics core facility. Observed changes in the composition of the bacterial microbiome revealed that the microbiome was impacted by infection with C. parvum. In some experiments changes in the fecal bacterial population became apparent 2-3 days post-infection and persisted until the infection was cleared. The taxonomic composition of the microbiome is being analyzed to identify bacterial taxa affected by the infection. To assess the impact of the intestinal microbiome on the pathogen, the microbiome was perturbed with different antibiotics. We found that oral administration of bacitracin to C. parvum infected mice mitigates the infection. Since this antibiotic does not inhibit C. parvum in culture, we hypothesize that perturbation of the bacterial microbiome in the gut is the cause of reduced parasite development. The possibility that C. parvum and the intestinal microbiome mutually influence each other opens new possibilities for understanding the importance of intestinal microorganisms in modulating the virulence of enteric infections and to find better strategies for managing cryptosporidiosis in humans and livestock.