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Adaptation of Diarrheal Pathogens During Human Infection

Bacterial intestinal infections are an unparalleled burden on humanity. Billions of days of human productivity are lost annually due to symptomatic intestinal disease. The most prominent symptom of bacterial intestinal infections is diarrhea, and profuse diarrhea can lead to dehy-



dration and death, particularly in children of low resource areas. This work focuses on two major global intestinal pathogens, *Campylobacter jejuni* and Enterotoxigenic *Escherichia coli* (ETEC), which were first identified as causes of infectious diarrhea in the early 1970s. Using two separate controlled human infection models, we investigated how these two diarrheal pathogens adapt during infections. High-resolution genomic sequencing and transcriptome analysis was used to track pathogen adaptation from inoculum through acute and persistent disease. This work provided insight into the scope of conserved pathogen adaptations during human infection and revealed new targets for therapy design.