Harnessing functional omics to decipher how probiotics reduce antibiotic resistance gene carriage in infants' gut

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The human microbiome plays a crucial role in infection prevention, as the resident microorganisms can shield their host from harmful pathogens. The rise in antibiotic-resistant opportunistic pathogens is a major global challenge. This issue is particularly pressing for infants, who are vulnerable due to their developing immune systems. Our research explores the potential of probiotic bacteria of the Bifidobacterium species in reducing the colonization with antibiotic-resistant bacteria in the gut, specifically extended-spectrum betalactamase-producing Enterobacteriales (ESBL-E). The infant's gut exhibits a relatively higher carriage of antibiotic resistance genes (ARGs) than that of adults, even for infants never exposed to antibiotics. As a first step, we characterized the factors that influence the ARG carriage by analyzing metagenomic data from 14 cohorts, covering 3,981 stool samples of 1,270 infants. We identified factors that significantly influenced the gut resistome, including birth mode, gestational age, antibiotic exposure, and geographical location. A gradual decrease of Escherichia coli was a key factor contributing to the reduction in ARGs as the infants matured. Next, we examined metagenomic data from 800 Kenyan newborns who participated in a clinical trial investigating the potential of probiotic use for infection prevention (ProRIDE). Our initial results indicate that bifidobacteria-based probiotics reduce colonization by ESBL-E without raising any safety concerns. This work aims to clarify whether the observed decrease of drug-resistant bacteria is linked to altered fecal metabolome. The results support the use of probiotics as part of strategies to combat antimicrobial resistance and related infections in infants.