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# De novo assembly of MAGs revealed prevalent anti-microbial resistant microbial strains among human community and their impact in individual microbiome

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Antibiotic abuse in modern society has led to the occurrence of antimicrobial resistance (AMR) bacteria, which has become a most urgent medical problem. However, many studies were limited in either exploring the whole resistome or specific clinically relevant pathobionts. In this study, we reanalyze longitudinal metagenome data from 12 healthy adults after antibiotic cocktail treatment. Through constructing Metagenome-Assembled Genome (MAG), we observe AMR dynamics and distribution within bacterial communities in specie level. We find personal differences in resistance to antibiotic-induced AMR enrichment, and enriched AMR genes are accumulated in few bacteria species. Next, we make a comprehensive comparison in resistome, taxonomy, and functional ability between Extremely Accumulated Resistant Bacteria (EARB; AMR gene possess ≥ 17), Sporadically Accumulated Resistant Bacteria (SARB; AMR gene possess < 17), and None Accumulated Resistant Bacteria (NARB; AMR gene possess = 0). We find that EARB possess multiple drug class resistance without specific enrichment of treated drug class, whereas SARB possess mostly tetracyclin and fluoroquinolone resistant genes. Surprisingly, EARB show the highest functional importance in community power analysis which suggests EARB might have the potential to shape antibiotic-treated environment in a different direction than commensal bacteria. Next, through SNP analysis of EARB E. coli strains, we discover multiple EARB E. coli strains are endogenous in the healthy human gut, and occurs through strain-sweeping. Finally, we confirm the existence of EARB and its high metabolic potential using other cohort data (recurrent urinary tract infection, liver cirrhosis, preterm infant), in which patients are frequently exposed to antibiotic treatment. Our findings will deepen the knowledge of the distribution, enrichment of AMR gene within bacterial strains, and the metabolic importance of multi-resistant bacteria in the antibiotic-treated gut community.