Antibiotic resistance gene burden and diversity vary in the general population according to demographics, diet, health and geography

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4g. Microbiome studies (incl. clinical and diagnostic studies, One Health aspects)
Likely attendance
Onsite
Oral presentation

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Background

The antibiotic resistance crisis is a significant threat to human welfare comparable to climate change. According to estimates by the World Health Organization, in 2050, antimicrobial resistance will be the leading cause of death.
Despite the remarkable efforts to map the overall composition and health associations of the human gut microbiome over the last decade, targeted population-level metagenome analyses of antibiotic resistance remain scarce.

Methods

Gut metagenome samples from > 7000 Finns were sequences using shallow shotgun metagenomics. The microbiome's taxonomic composition was analyzed using MetaPhlan3, and the antibiotic resistance genes (ARGs) were mapped with Bowtie2 against the ResFinder database. The cohort participants were collected during the FINRISK project, with extensive health, diet, lifestyle, and medication use data and links to the Finnish national registers. We, for example, used drug reimbursement data to obtain information for past medication.
We investigated the associations of the resistance load in the cohort participants using boosted generalized linear modeling and linked the vast participant metadata of geography, demography, lifestyle, and health to the antibiotic resistance gene load, diversity, and composition.

Results

Antibiotic use was linked to higher ARG loads, as expected, but also other drug classes, such as psycholeptics, were positively correlated with ARG loads. We also observed that the consumption frequency of raw vegetables and poultry (both foods containing high abundances of resistant bacteria) was positively associated with higher ARG loads and diversity.

We observed that the ARG loads, composition, and diversity were structured according to geography and demography. People living in Western Finland had more ARGs and morediverse resistomes than those living in the East, and population density was

positivelyassociated with ARG load and diversity.Interestingly, ARG loads had clear variation according to demographics, with women andparticipants of the high-income classes having

more resistance genes.

Conclusions

Antibiotic resistance is structured according to geography, demographics, and diet. This has possible implications for the antibiotic resistance crisis as more and more people live in densely populated areas and cities and have access to more expensive types of foods, such as meat, and fresh produce, and medication, with the global average income on the rise.
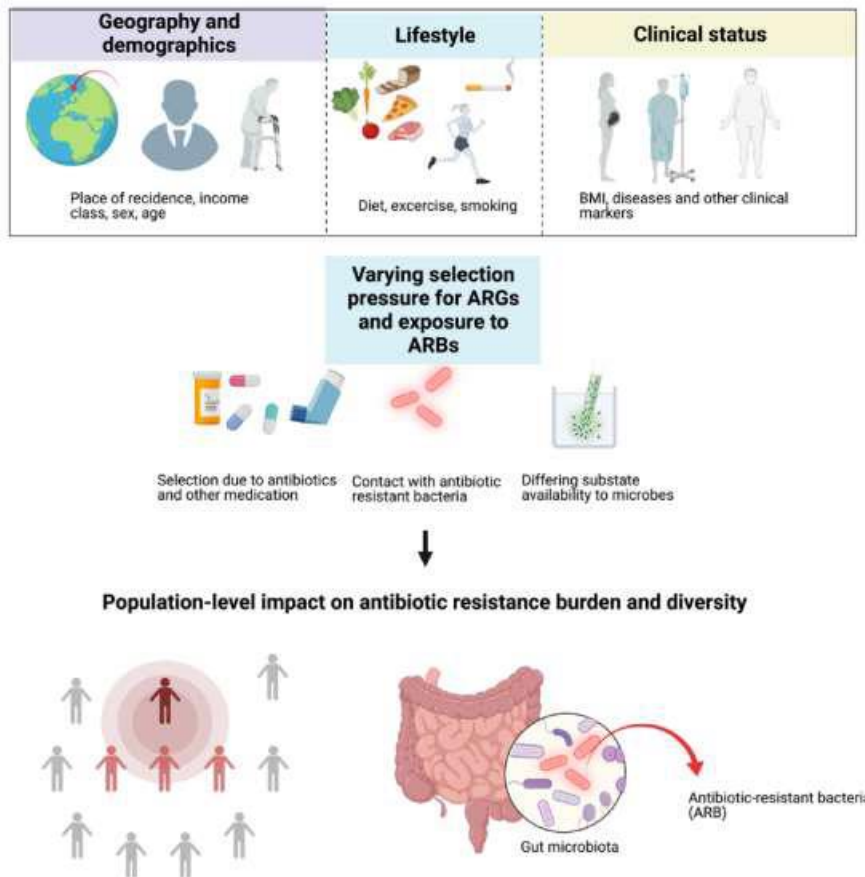
Keyword 1
Antimicrobial resistance (AMR)
Keyword 2
Genomics and metagenomics
Keyword 3
Population studies