Medical Xpress

Major genetic study reveals how antibiotic resistance varies according to where you live, demographics and diet

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A genetic study analyzing the microbiome (bacteria in the gut) of a large nationally representative sample of the Finnish population finds that geographic, demographic, diet, and lifestyle factors are driving the

spread of antibiotic resistance in the general population.

The most comprehensive study of its kind by Dr. Katariina Pärnänen from the University of Turku in Finland and colleagues, being presented at this year's European Congress of Clinical Microbiology & Infectious Diseases (ECCMID) in Copenhagen, Denmark (15-18 April), highlights the urgent need for targeted interventions to reduce antibiotic resistance tailored to different demographics and lifestyles.

Antibiotic-resistant bacteria can spread through healthy adult populations and go largely unnoticed. Antimicrobial resistance poses a significant threat to humanity, and has become a leading cause of death worldwide, involved in an estimated 5 million deaths in 2019 and estimated to be the direct cause of 1.27 million deaths. Estimates suggest that antimicrobial resistance will overtake cancer as the leading cause of death worldwide by 2050.

Despite the remarkable efforts to map the overall composition and health associations of the gut microbiome over the last decade, a deeper understanding of the factors driving the distribution of antimicrobial resistance within the general population is urgently needed.

To find out more, researchers investigated the extent to which demographic, dietary, health and geographic factors influence the abundance of antibiotic resistance genes (ARGs) in gut metagenome fecal samples from 7,098 symptomless adults taking part in the national FINKRISK study—a large representative Finnish population survey carried out every 5 years since 1972.

The FINRISK project collects extensive health and lifestyle data, including major diagnoses, blood measurements, habitual diet, and prescription drug use, that are proxies for the three ecological mechanisms that influence ARG abundance—acquisition of external

ARGs from food; host health status (endemic resistance); and drug-mediated selection of resistant bacteria.

Researchers used shotgun metagenomes (untargeted genetic sequencing of all bacteria living in the gut) to examine the associations between participants' antibiotic resistance gene load, diversity, and composition and geography, demography, lifestyle, and health factors.

As expected, the analyses found that antibiotic use was linked to higher ARG loads, but other drug classes, such as psycholeptic drugs (e.g., opioids and barbiturates), were also associated with higher abundance of ARGs.

The analyses also found that more frequent raw vegetable and poultry consumption (both foods containing high quantities of resistant bacteria) was associated with higher ARG loads and diversity.

What's more, ARG loads, composition, and diversity were also associated with geography. For example, people living in western Finland had a higher abundance and more diverse ARGs than those living in the east. And higher population density was also associated with higher ARG load and diversity.

Interestingly, ARG loads had clear variation according to demographics, with women and participants on higher incomes having more resistance genes.

"Our findings clearly show that geography, demographics, and diet play an underappreciated role in antibiotic resistance," says Dr. Pärnänen.

"This has important implications for the antibiotic resistance crisis as more and more people are living in densely populated areas and cities and are able to buy more expensive types of foods, such as meat, and

fresh produce, and also medication. Reducing or preventing the spread of antimicrobial resistance will require action plans at national levels that go beyond regulating the misuse of antibiotic prescriptions."

More information: Conference: www.eccmid.org/

Provided by European Society of Clinical Microbiology and Infectious Diseases