Analyzing the differences in antibiotic resistance between the gut and mouth microbiome

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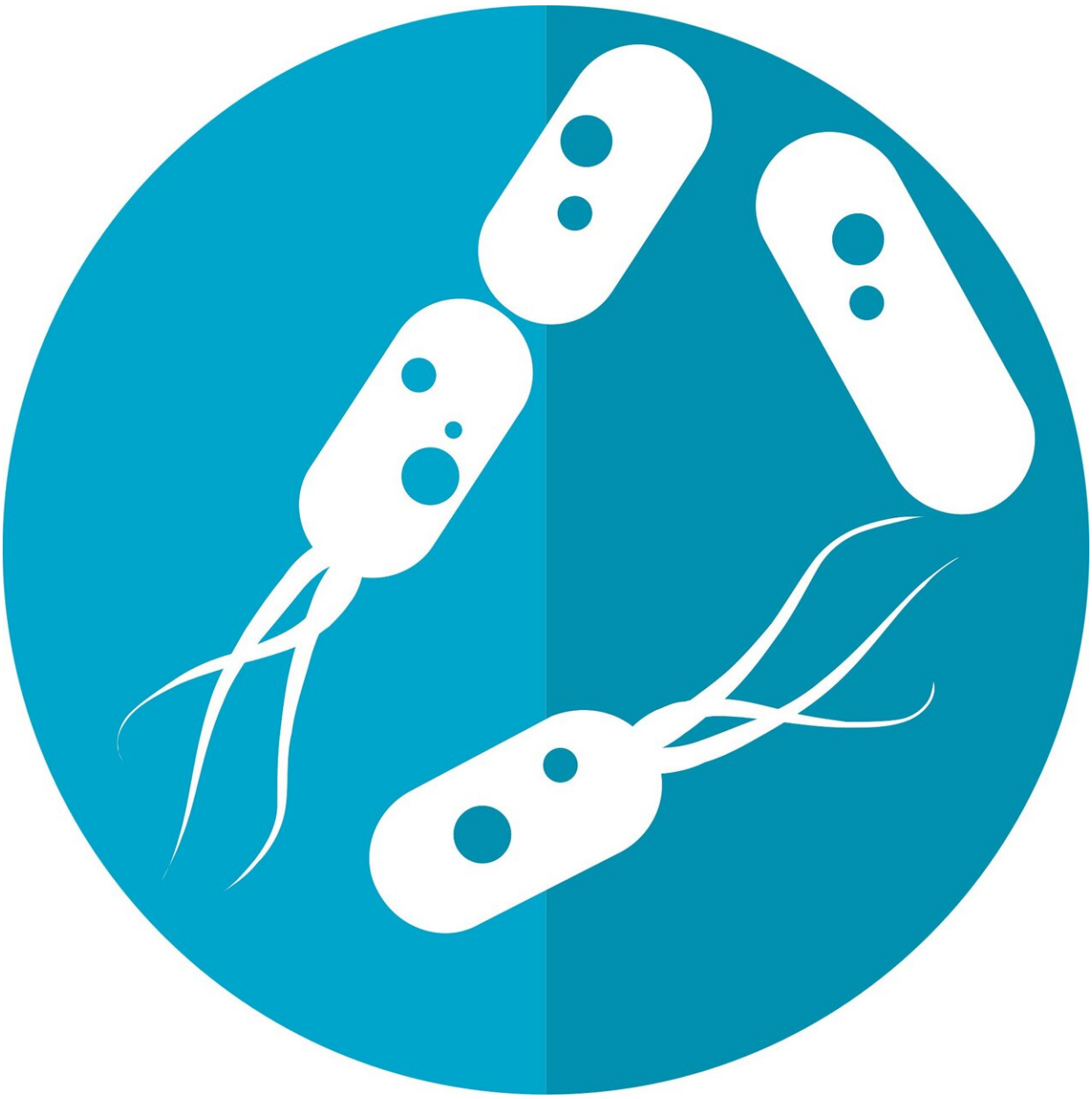

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The threat of antimicrobial resistance to medication is a global health issue. Recent years have seen a surge in our awareness of resistance genes; and as a result of the prevalence of these genes, antibiotics are becoming less effective at treating microbial infections, such as TB and gonorrhoea.

Although much work has been done analysing the human gut microbiome and its associated genes, little is currently known about these genes in the mouth.

In a paper published today in *Nature Communications*, academics from King's College London have taken the first step to examine the antimicrobial resistance potential of the mouth—the oral resistome. As the mouth is the first point of entry for food and many medications, it has the potential to influence the spread of antimicrobial resistance in the human microbiome. Antimicrobial resistance arises when the microbe acquires genes that attempt to avoid or destroy the drugs.

"Given what we are beginning to discover about the sheer variety of microbial species in the human microbiome, if we are to stand any hope of getting to grips with the spread and persistence of antimicrobial resistance, we need to expand human resistome studies to sample other body areas," explains Dr. David Moyes, Lecturer in Host-Microbiome Interactions at King's College London.

The research group accessed saliva, dental plaque and other oral data and analysed them using the Comprehensive Antibiotic Resistance Database

(CARD). They included data from several different regions within the study, including Asia, Pacific, European and American locations.

They found that there were unique resistome profiles in the mouth compared to the gut. Further, whilst there was less diversity of antimicrobial resistance genes in the mouth, those genes present were more pervasive across the populations studied.

Dr. Moyes asks: "If body sites have different resistomes, can a gut resistome represent the entirety of the human resistome? We must continue analysis of the microbiomes at other body sites to realise the huge potential for unlocking insights from open-source datasets of previously sampled cohorts. If we look hard enough, the answers could be right under our noses."

Provided by King's College London

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