

Reversing antibiotic resistance among probiotics and other enteric bacteria found in gut

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On one hand development of new antibiotics require enormous capital and time, and on other side resistant strains keep emerging at huge pace. Dr. Bhabatosh Das's team at Translational Health Science and Technology Institute (THSTI), Faridabad has taken a different approach and attempted to reverse the antibiotic resistance in bacteria by inducing genome instability and loss of antibiotic resistance genes (ARGs). This approach may eventually help in rejuvenating old antibiotics that are no longer in use due to the problem of resistance.

Team is trying to identify two categories of genetic factors in the bacterial genome, one being responsible for function of mobile genetic elements (MGE) and the other category capable of stabilizing genetic elements present in addition to the chromosomes.

They have developed a bacterial reporter strain that may be used in the screening assays to find out the hits and improving the lead molecules which potentiates the loss of MGE's carrying resistance factors. The proposed strategy may help in identifying the compound that can help in re-sensitizing the gut microbiota (both pathogens and commensals) before onset of antibiotic treatment for their effective action.

Antimicrobial Resistance (AMR) is one of the most pressing problems worldwide. If not tackled now, AMR may cause one death in every three seconds by 2050. AMR is the ability of microbes to resist the action of the antimicrobials used against them. Although emergence of antibiotic resistance is a natural evolutionary process wherein few bacterial strains mutate, grow in the presence of the antibiotic, and outcompete the sensitive ones as well as spread across different biospheres. However, unchecked and intensive antibiotics use has enriched antimicrobial-resistant genes (ARGs) present in the genome of pathogens as well as symbiotic gut flora. Various MGEs, the genomic segments that facilitate the movement of genetic material between chromosomes, between bacteria of same and different species, were found to be linked with the

ARGs. MGEs are responsible for imparting AMR traits, and targeting their stability could thus be a potential strategy to combat AMR.

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