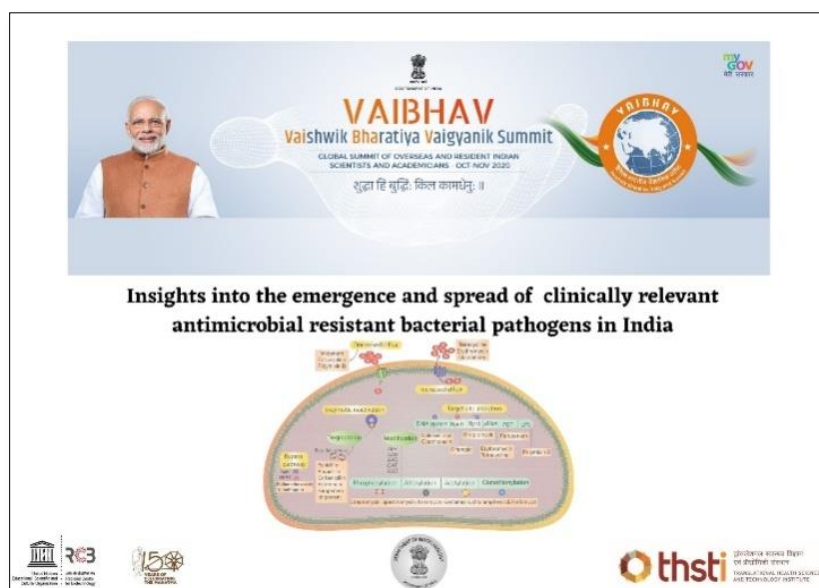


## DBT's THSTI and RCB jointly hosted a session on antimicrobial resistance for VaiBhaV Summit 2020

Faridabad-based DBT's autonomous institutes DBT-Translational Health Science and Technology Institute (THSTI) and Regional Centre for Biotechnology (RCB) co-organized a session of the VaiBhaV Summit 2020 of the Government of India, themed antimicrobial resistance on 17<sup>th</sup> October with experts from India and overseas. The session was titled “*Insights into the emergence and spread of clinically relevant antimicrobial resistant bacterial pathogens in India.*” The experts discussed prevalence of AMR pathogens, their evolution, mode of dissemination and potential strategy to overcome the crisis.



Antibiotics have always been considered one of the most crucial drugs in the history of medicine. Antibiotics have saved countless lives and played a critical role in ensuring the average life expectancy in the world that has increased from 47 years in 1950 to 73 years in 2020. However, since its discovery, it was observed that antibiotics have two contrary properties: First, inhibiting the multiplication of microbes by impeding essential microbial cellular functions and the second, fostering the emergence and spread of antibiotic resistant bacterial species by providing a less competitive growth environment through elimination of sensitive variants.

Antimicrobial resistance (AMR) in pathogenic bacteria poses a major public health problem across the globe. Indiscriminate use of antibiotics in health, agriculture sectors, animal farming, and live stock has led to the appearance of multidrug resistant (MDR) and extensively drug

resistant (XDR) bacterial strains that can survive in the presence of most, if not all, known antibiotics. In India, antibiotics are easily accessible and there is an increasing incidence of multidrug resistance among common infectious bacteria such as *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and *Mycobacterium tuberculosis*.

Advancement of next generation DNA sequencing and availability of genome sequences of thousands clinical and environmental isolates clearly demonstrated that although chromosomal mutations can contribute to AMR, the frequent acquisition of extrachromosomal mobile genetic elements (MGEs) are the major players in the emergence of drug resistant bacterial pathogens. A number of processes that mediate the horizontal gene transfer (HGT) like transformation, conjugation and transduction foster the rapid emergence and spread of AMR pathogens. Different AMR genes identified in MDR and XDR strains can contribute in AMR by (i) reducing the cellular permeability or increasing efflux of the antibiotics, (ii) modification of the antibiotic targets by introducing new chemical moiety, and (iii) hydrolysis or chemical modification of antibiotics.

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