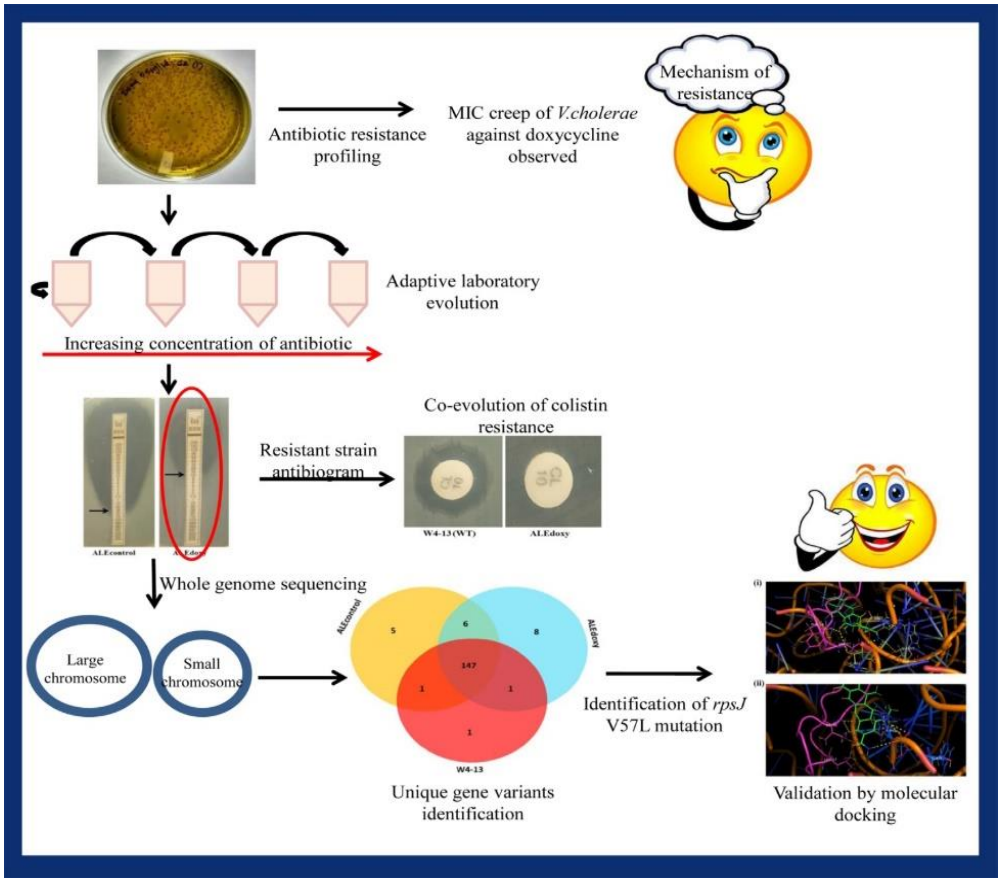
DBT-RGCB team elucidated the mechanism of doxycycline resistance in *Vibrio cholerae*

Dr. Sabu Thomas and his team at DBT's Rajiv Gandhi Center for Biotechnology (DBT-RGCB), Thiruvananthapuram hypothesized that the antibiotic doxycycline residues could cause selective pressure on microbes to evolve in environment. To prove this, Dr. Sabu's team did whole genome sequencing of adaptive laboratory evolved doxycycline resistant *Vibrio cholera*e. On screening the acquired single nucleotide polymorphisms, missense mutation (a point mutation that leads to an amino acid change) in *rpsJ* (V57L) gene was identified to be responsible for doxycycline resistance (graphical representation figure). The mutation was identified to alter the ribosome structure near doxycycline binding site and cause resistance.

The doxycycline selected resistant strain also acquired co-resistance to colistin, a last resort drug to treat extensively drug resistant bacteria and collateral sensitivity towards azithromycin and kanamycin antibiotics. The present study for the first time illustrated a possible mechanism of doxycycline resistance. The study warrants strict restrictions on the indiscriminate use of antibiotics and recommends the 'One Health' platform, as has been envisaged in the AMR action plan.



Emergence of antibiotic resistant bacteria is a serious threat to health care. *V. cholera*e that causes cholera has been endemic to India. Antibiotic resistance profiling of the strains circulating in south India over a decade revealed a minimum inhibitory concentration (MIC) 'creep' against doxycycline. Doxycycline is used as the first line drug of choice to treat cholera in India and to treat many bacterial and parasitic infections in humans and also used in veterinary medicine.

Link: https://www.sciencedirect.com/science/article/abs/pii/S0924857920302788

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