Deciphering the efficacy of emerging therapeutic agents against multi-drug resistant ESKAPE pathogens through molecular characterisation, systems and structural biology approaches

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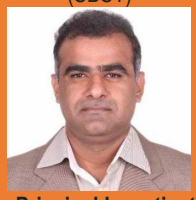

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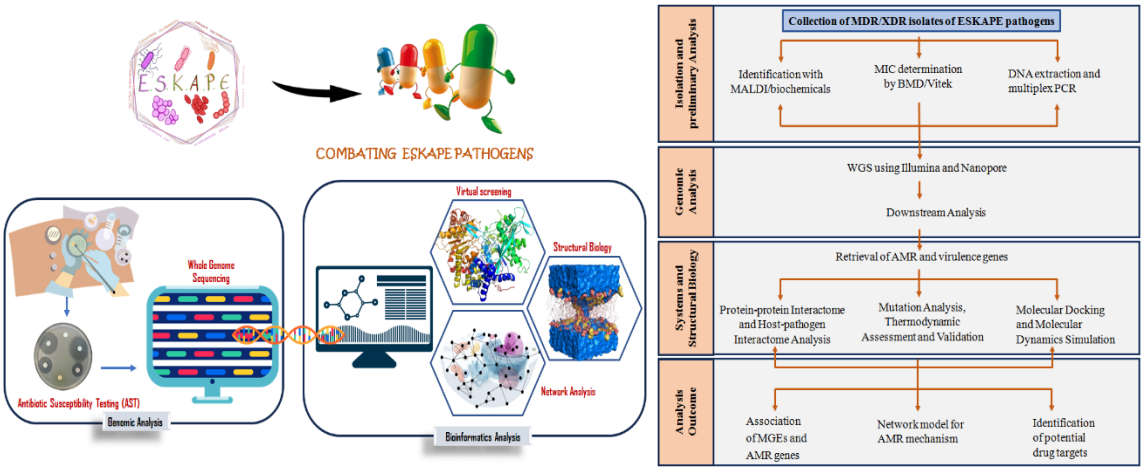
Name of the Funding Agency
Indian Council of Medical Research (ICMR)

Name of the Scheme
Extramural Research Programme

Sanctioned Amount (in Rupees)
Rs. 60,39,362

Duration of the Project (years)
3

Graphical Abstract

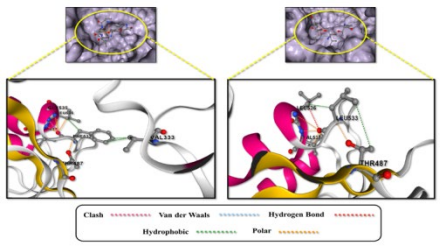


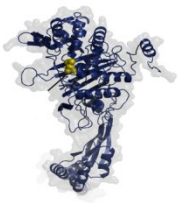
Project Description

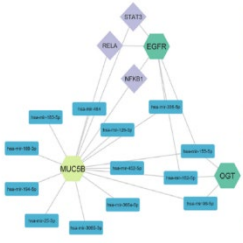
Irrational antimicrobial usage in recent years has increased the propensity for antimicrobial resistance (AMR) and associated adverse reactions. The emergence of multi-drug resistant (MDR) and extensively-drug resistant (XDR) strains has posed severe challenges in their therapeutic interventions, especially among ESKAPE pathogens (*Enterococcus faecium*, *Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa*, and *Enterobacter* species). Several non-synonymous single nucleotide polymorphisms (nsSNPs) have been detected, which cause drug-target alterations and reduce antimicrobial efficacy. To avoid such adversities, an *in-silico* approach may prove crucial for screening and designing potential therapeutic agents.

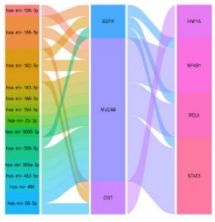
The objective of the project is to find novel drug combinations against mutated targets through systems biology, intermolecular interaction analysis, structural biology, and molecular dynamics, further complementing the *in-vitro* findings. These techniques help in identifying therapeutic biomarkers and exploring potential leads to combat resistance. The project aims to counter AMR in emerging MDR/XDR nosocomial strains in ESKAPE pathogens.

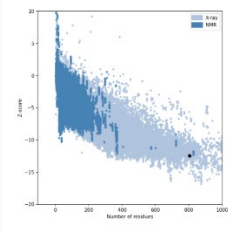
Products/ Instruments/ Results/ Outreach Activities

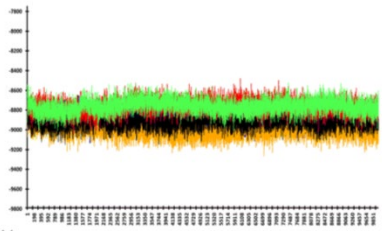












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