Aiding Antibiotic Development with Deep Analysis of Resistance Evolution

Rendicontazione

Informazioni relative al progetto

Aware

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Progetto chiuso

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Sintesi del contesto e degli obiettivi generali del progetto

Multi-drug resistant bacterial infections have been recognized as a major public health concern, and are responsible for a significant proportion of deaths worldwide. Alarmingly, the World Health Organization estimates that the mortality of drug-resistant bacterial infections might exceed that of malignant tumours by 2050, unless the current trends are reversed. Paradoxically, however, many pharmaceutical companies have discontinued their antibiotic research programs. This is principally due to the rapid spread of multi-drug resistant bacteria, which makes the commercial success of new antimicrobial drugs unpredictable.

At an early phase of drug discovery, researchers typically identify numerous molecules with antibacterial activities. It is imperative to estimate the rate of resistance evolution at this early stage of antibacterial drug discovery. However, identification of antibiotics with limited resistance is a complex problem, and can only be handled by more advanced methodologies. Standard microbial protocols are slow, have low coverage, and frequently fail to predict the frequency and molecular mechanisms of antibiotic resistance Therefore, it is common that companies waste considerable resources on less promising drug candidates that are prone to resistance formation during clinical trials. To overcome these limitations, Csaba Pal and his team have recently developed a unique proprietary targeted mutagenesis technology, termed DIvERGE. DIvERGE finds resistance mutations in antibiotic resistance genes at an unprecedentedly comprehensive manner, and thereby it offers a unique opportunity for pharmaceutical companies to identify antimicrobial agents with potentially longer clinical efficacy at an early stage of drug development.

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