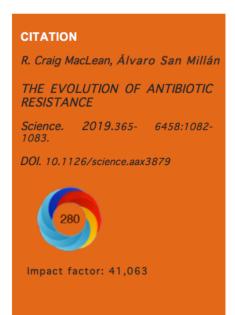
IRYCIS OUTSTANDING PUBLICATION

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become increasingly clear that there are substantial gaps between these two approaches. Experimenta studies have not placed enough emphasis on understanding the evolution of success oil strains that have driven the rise of re sistance in the clinic. To bridge these gaps and identify strategies to counternext ABR experimental studies should shift focus to ward investigating clinically relevant resis

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Published by AAA

Mobile genetic elements promote the evolution of antibiotic resistance

THE EVOLUTION OF ANTIBIOTIC RESISTANCE

For most of human history, bacterial pathogens have been a major cause of disease and mortality. The development of antibiotics provided a simple and effective treatment for bacterial infections, and antibiotics have since had huge effects on human health and longevity. These are threatened with the rise of antibiotic resistance (ABR): Many pathogenic bacteria have evolved resistance to the main classes of antibiotics, and multidrug-resistant bacteria have caused untreatable infections. ABR already imposes substantial health and economic burdens, and the global annual cost of ABR could increase to 10 million deaths and US\$100 trillion by 2050 (1). Understanding how ABR evolves and spreads is therefore key to improving antibiotic treatment strategies.

Why do you highligth this publication?

This perspective paper underlines the need for bringing together the fields of evolutionary biology and clinical microbiology in order to the counteract the evolution of antibiotic resistance. Understanding the evolutionary drivers of antibiotic resistance could make a substantial contribution to preserving the efficacy of next-generation antimicrobials, but realizing this potential will require a fundamental shift in how evolutionary biologists think about, and study, antibiotic resistance.

"Clinically relevant evolution studies are needed to help fight the spread of antibiotic resistance". – Alvaro San Millán

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