

IRYCIS OUTSTANDING PUBLICATION

May 18th, 2020

CITATION

R. Craig MacLean, Álvaro San Millán

THE EVOLUTION OF ANTIBIOTIC RESISTANCE

Science. 2019.365- 6458:1082-1083.

DOI. 10.1126/science.aax3879



Impact factor: 41,063

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 highlight this publication?

This perspective paper underlines the need for bringing together the fields of evolutionary biology and clinical microbiology in order to 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.

become increasingly clear that there are substantial gaps between these two approaches. Experimental studies have not placed enough emphasis on understanding the evolution of successful strains that have driven the rise of resistance in the clinic. To bridge these gaps and identify strategies to counteract ABR, experimental studies should shift focus toward investigating clinically relevant resist-

Department of Zoology, University of Oxford, Oxford, UK; Department of Microbiology, Hospital Universitario Ramón y Cajal, Instituto Ramón y Cajal de Investigación Biomédica (IRYCIS) and Centro de Investigación Biomédica en Red sobre Enfermedades Infecciosas (CIBERESP), Madrid, Spain. Email: craigm@zoo.ox.ac.uk

has become clear that these communities of commensal bacteria provide a rich source of dedicated ABR genes (3). Mobile genetic elements, such as plasmids and bacteriophages (bacterial viruses), transfer these ABR genes between bacterial populations through the process of horizontal gene transfer (HGT) (see the figure). Crucially, HGT allows pathogenic bacteria to evolve resistance by acquiring preexisting ABR genes from commensal bacteria. The basic mechanisms of HGT were discovered more than 50 years ago, and the current challenges are to better understand the rate at which pathogens

ri
m
th
st
be
el
se
in
ni
pi
an
ce
el
ve

1082 | 10 SEPTEMBER 2019 • VOL. 365 | ISSUE 6458

Published by AAAS

Mobile genetic elements promote the evolution of antibiotic resistance

“Clinically relevant evolution studies are needed to help fight the spread of antibiotic resistance”.

– Alvaro San Millán

Publication commented by:

Dr. San Millán Cruz
Microbiology Department
Hospital Universitario Ramón y Cajal
IRYCIS