RESEARCH AREA I
HIGHLIGHT

01
TITLE OF THE WORK

Antibiotic combination efficacy (ACE) networks for a *Pseudomonas aeruginosa* model.

02
SOME BACKGROUND

Evolution is central to the current antibiotic crisis, because it is the pathogen's ability to adapt that has caused the dramatic spread of multidrug resistance. Surprisingly, however, the evolutionary potential of pathogens is usually ignored during the design of novel therapy.

03
WHAT DID SCIENTISTS DISCOVER?

Using evolution experiments, antibiotic combinations were identified that ensure two key aims of therapy: bacterial clearance and reduced adaptation rates. Treatment optimality was achieved by using drug pairs, which enhance each other's effects (i.e., synergistic combinations) or evolve collateral sensitivity to each other (i.e., evolution of resistance against one drug automatically increases sensitivity to the second drug).

04
WHY IS IT IMPORTANT?

We are in dire need of new treatment designs to counter the threat of spreading multidrug resistance. Two key factors have now been identified that can help to use the available antibiotics in a more refined and rational way to achieve both pathogen elimination and reduced resistance evolution.

05
WHO DID THE RESEARCH?

Camilo Barbosa [a]
Robert Beardmore [b]
Hinrich Schulenburg [a,c*]
Gunther Jansena [a*]

[a] — Evolutionary Ecology and Genetics, University of Kiel, Germany

[b] — Biosciences, University of Exeter, United Kingdom

[c] — Antibiotic resistance evolution group, Max Planck Institute for Evolutionary Biology, Plön, Germany

[*] — Equal contribution as senior authors

06
WHY DID THEY CHOOSE THE DESCRIBED METHODS?

Evolution experiments are performed under controlled laboratory conditions, thereby allowing tests of causality. This experimental approach could be used to test and pinpoint different factors as causes for enhanced resistance evolution or increased bacterial clearance.

07
DETAILS FOR SCIENTISTS – PUBLICATION

Barbosa C, Beardmore R, Schulenburg H*, Jansen G* (2018) Antibiotic combination efficacy (ACE) networks for a *Pseudomonas aeruginosa* model. PLoS Biol 16(4): e2004356.

ACE network on extinction numbers

Number of extinctions (out of 8 replicates) 0 1 2 3 4 5 6 7 8