

The Evolutionary Logic of Antimicrobial Resistance

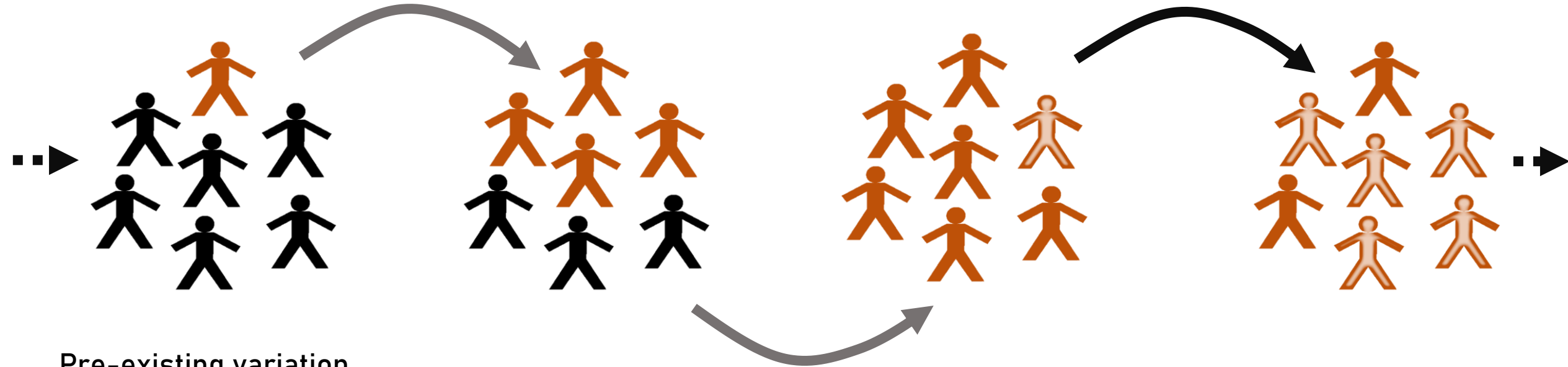
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Mutation, mechanism, selection and evolution

Natural selection 101

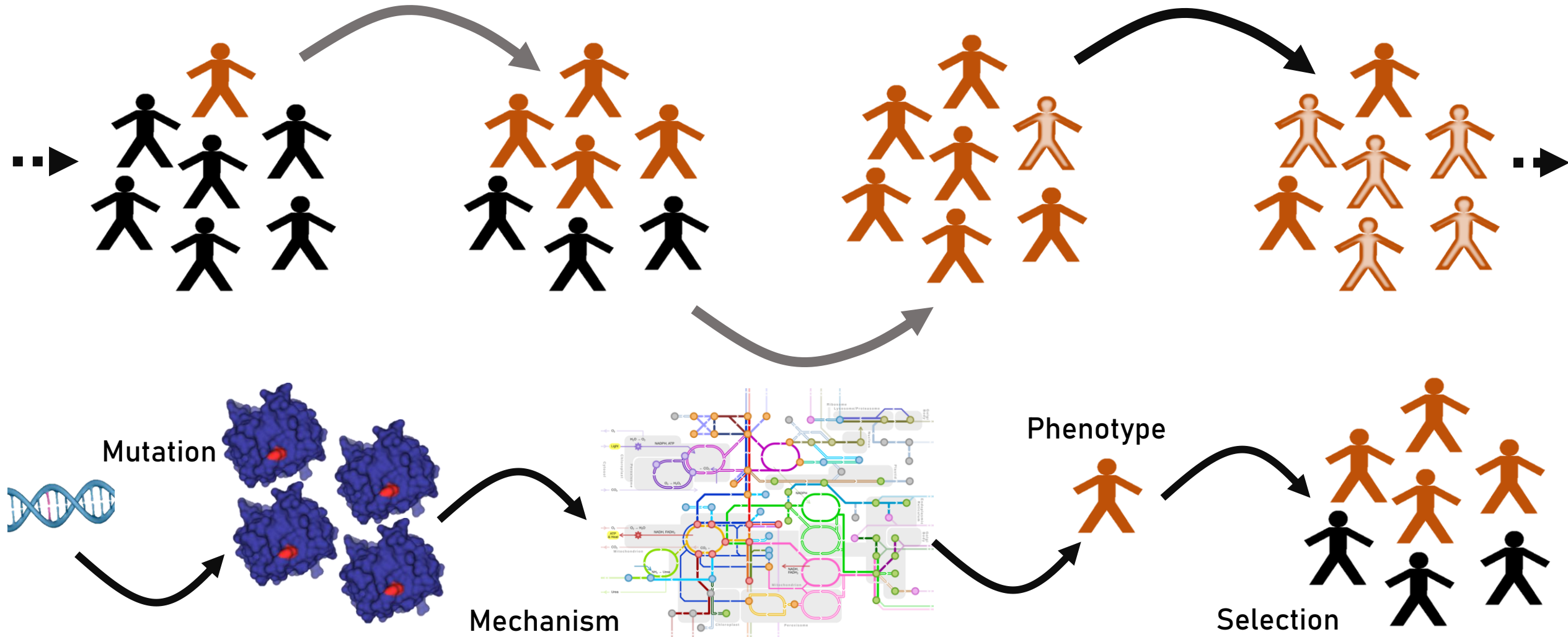


Pre-existing variation

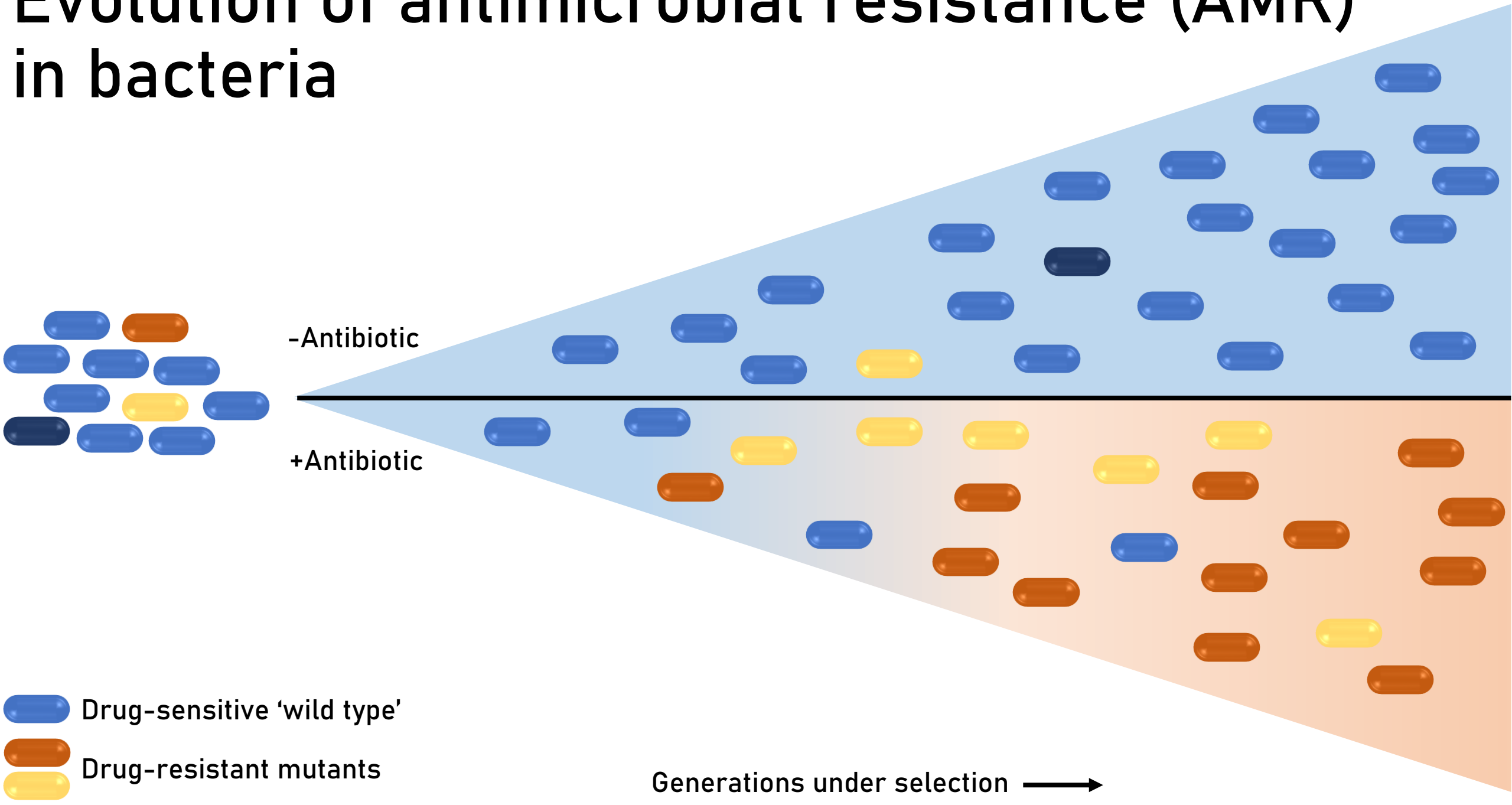
Differential
reproductive success

Phenotypes differences
are heritable

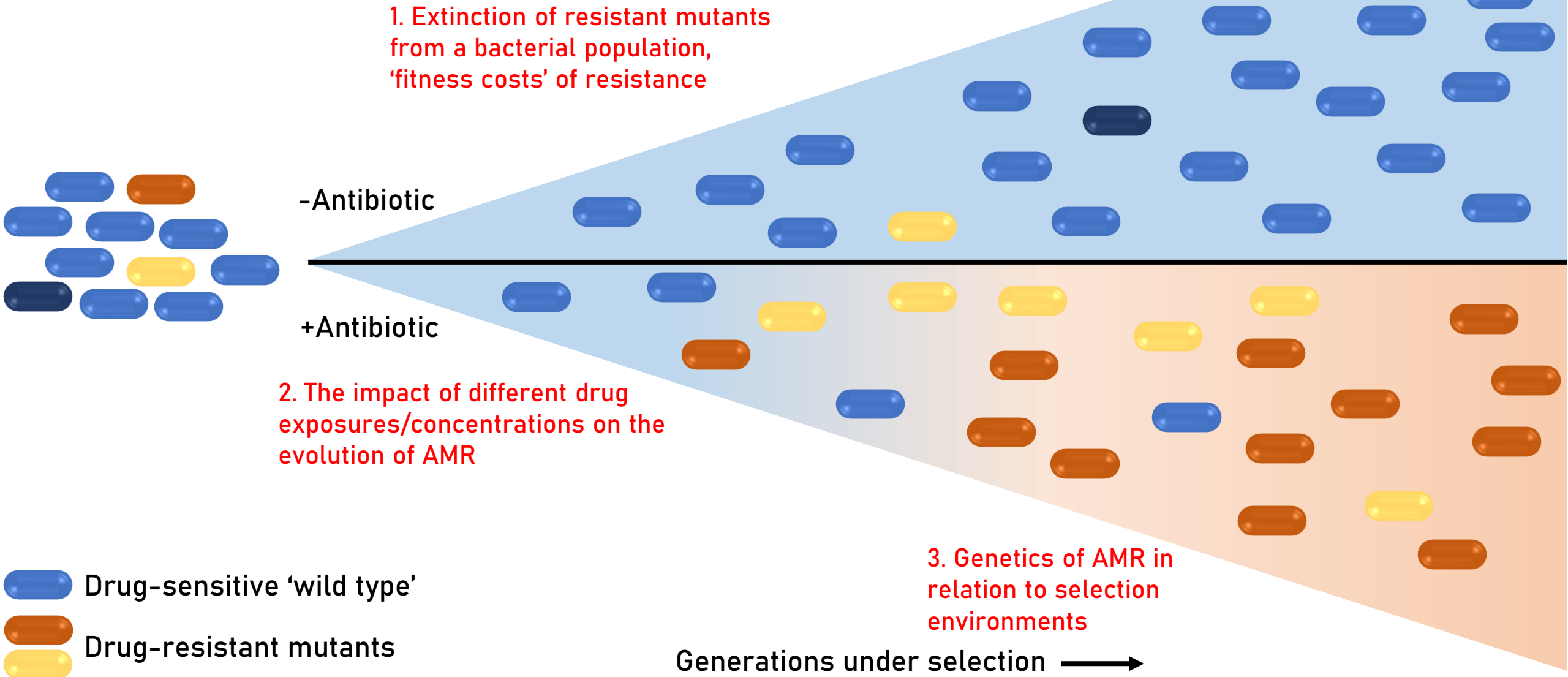
Mutation, mechanism, selection and evolution



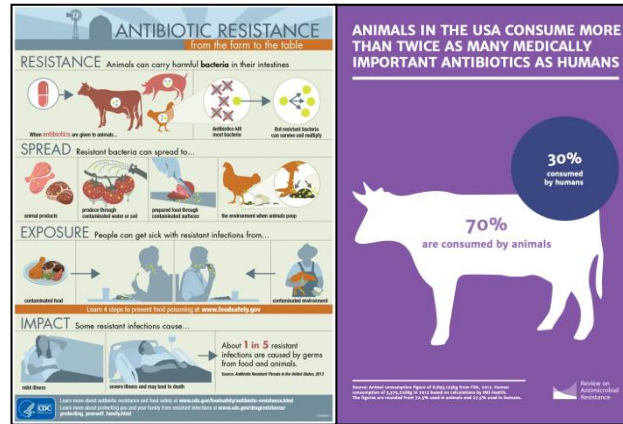
Evolution of antimicrobial resistance (AMR) in bacteria



Evolution of antimicrobial resistance (AMR) in bacteria



Sub-lethal drug environments: Facilitators of AMR evolution



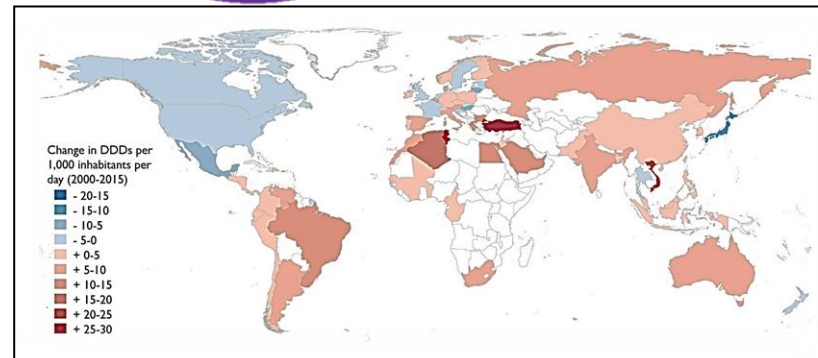
GROUND ZERO | COMMENT
The superbugs of Hyderabad

Source: Trafalgar Scientific



Journal of Clinical Periodontology
EFP

Subantimicrobial dose doxycycline as an adjunct to scaling and root planing: post-treatment effects



Kleina et al. PNAS 2018

Evolutionary trajectories to resistance differ at low and high drug pressures



ARTICLE

DOI: 10.1038/s41467-018-04059-1

OPEN

Evolution of high-level resistance during low-level antibiotic exposure

Erik Wistrand-Yuen¹, Michael Knopp¹, Karin Hjort¹, Sanna Koskiniemi², Otto G. Berg² & Dan I. Andersson¹

Drug Resistance Updates

journal homepage: www.elsevier.com/locate/drug

Evolution of antibiotic resistance at non-lethal drug concentrations

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Department of Medical Biochemistry and Microbiology, Box 582, SE-75123 Uppsala, Sweden

MBE

Strength of Selection Pressure Is an Important Parameter Contributing to the Complexity of Antibiotic Resistance Evolution

Tugce Oz,^{†,1} Aysegul Guvenek,^{†,1} Sadik Yildiz,^{†,1} Enes Karaboga,¹ Yusuf Talha Tamer,¹ Nirva Mumcuyan,¹ Vedat Burak Ozan,¹ Gizem Hazal Senturk,¹ Murat Cokol,¹ Pamela Yeh,² and Erdal Toprak^{*,†,1}

GENETICS | INVESTIGATION

Adaptation Through Lifestyle Switching Sculpts the Fitness Landscape of Evolving Populations: Implications for the Selection of Drug-Resistant Bacteria at Low Drug Pressures

Nishad Matange,¹ Sushmitha Hegde, and Swapnil Bodkhe

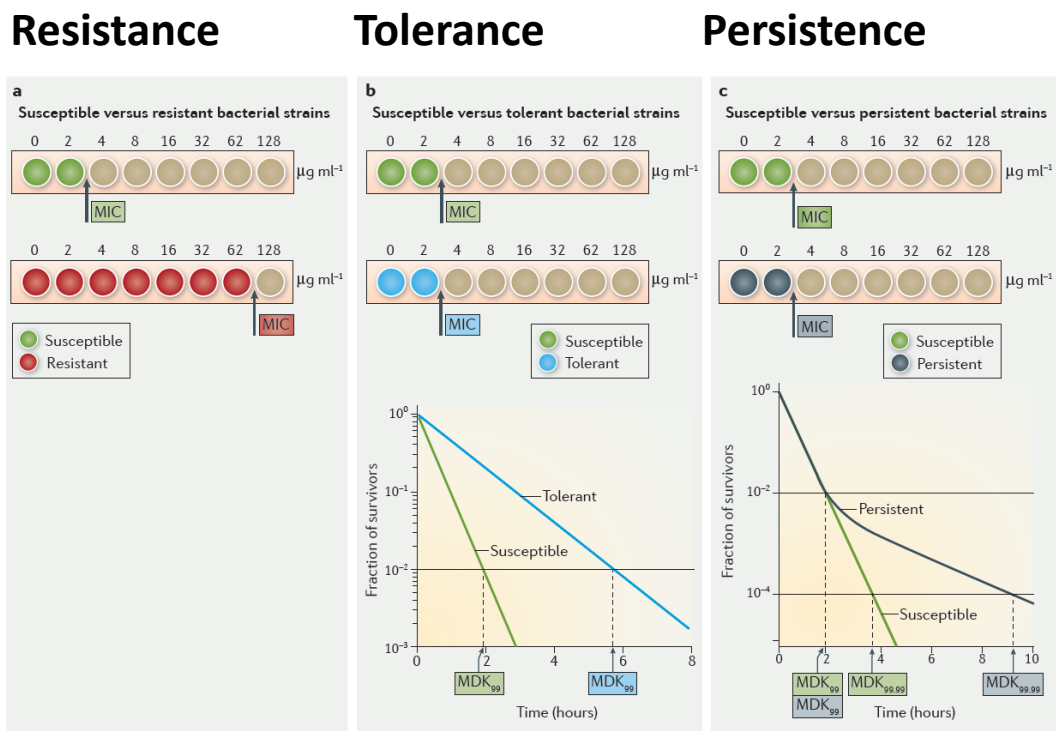
Department of Biology, Indian Institute of Science Education and Research, Pune, India

The Journal of Infectious Diseases

Selection of Antibiotic-Resistant Bacterial Mutants: Allelic Diversity among Fluoroquinolone-Resistant Mutations

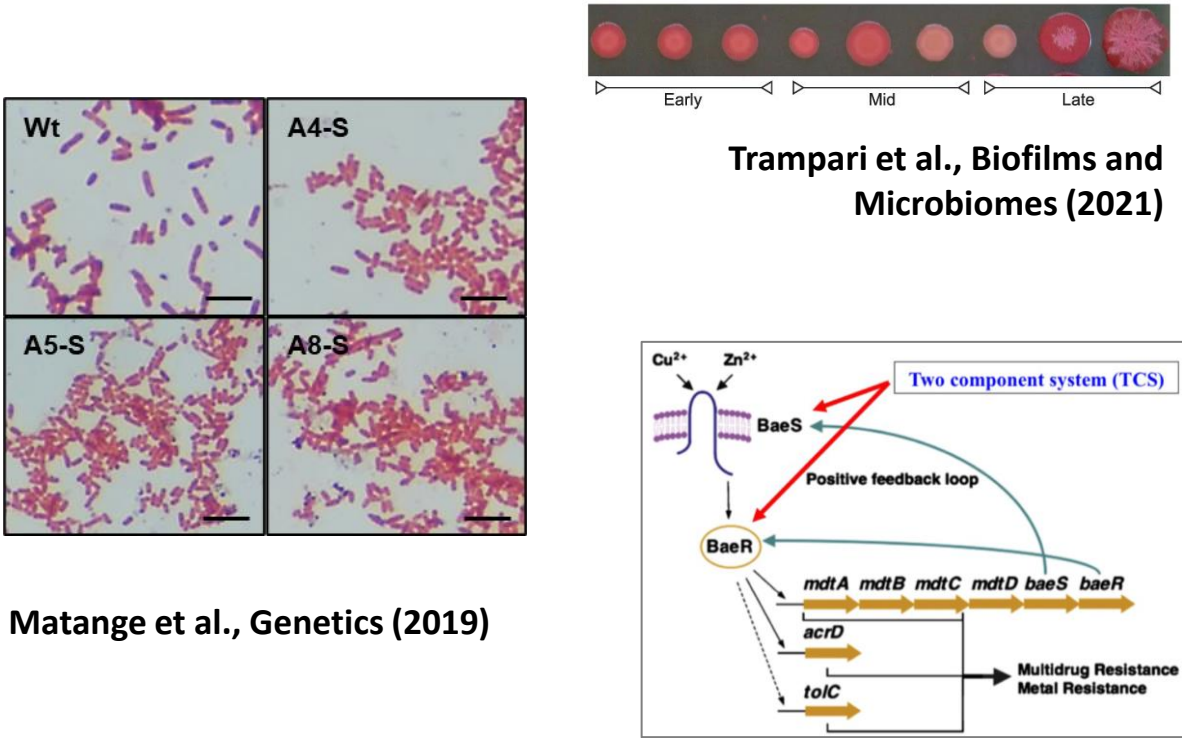
Jianfeng Zhou,¹ Yuzhi Dong,¹ Xilin Zhao,¹
Sungwoo Lee,^{1,a} Amol Amin,² Srinivas Ramaswamy,^{2,3}
John Domagala,⁴ James M. Musser,^{2,3} and Karl Drlica¹

Many flavours of adaptation to antibiotics



Brauner et al., Nat. Rev. Microbiol. (2016)

Antibiotic-induced phenotypic changes

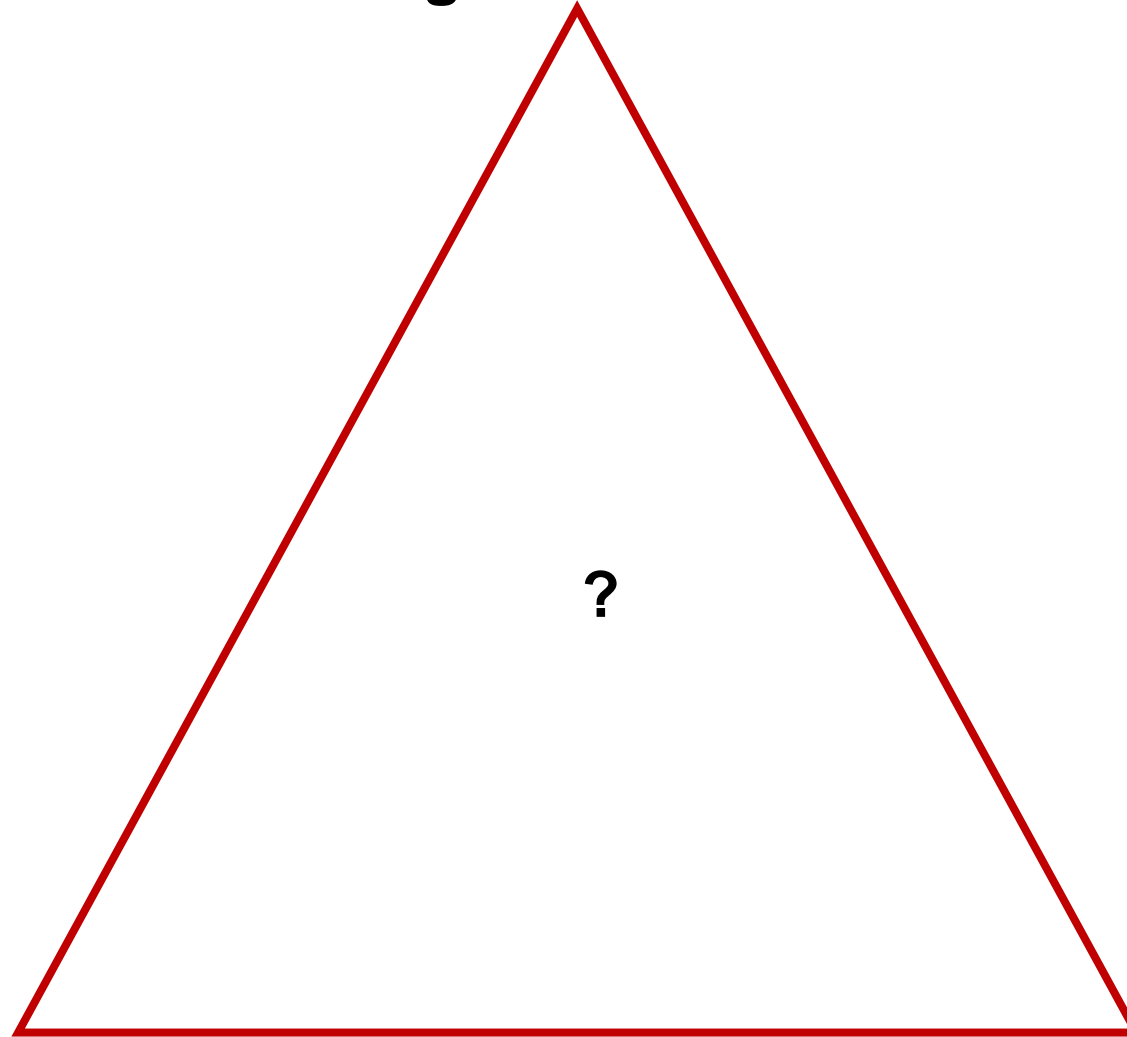


Strength of selection

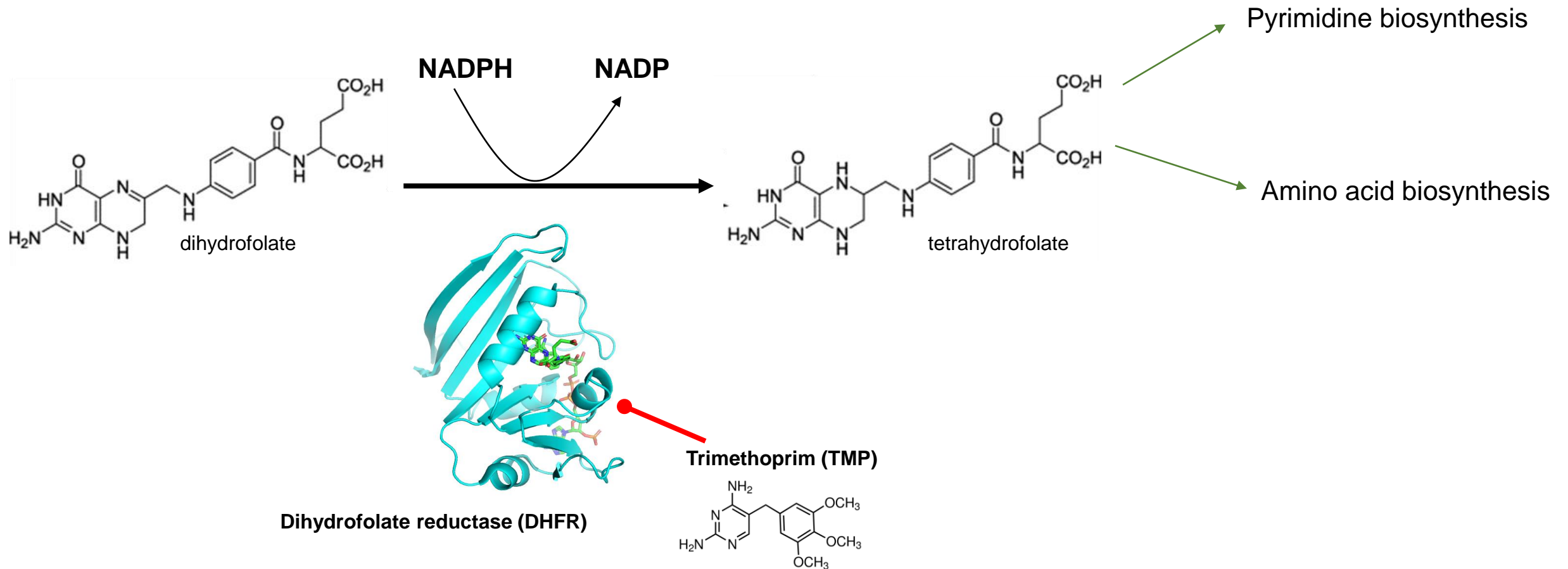
?

Molecular mechanisms

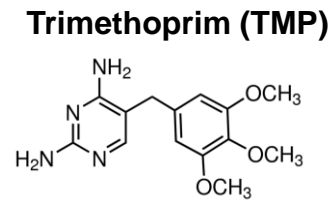
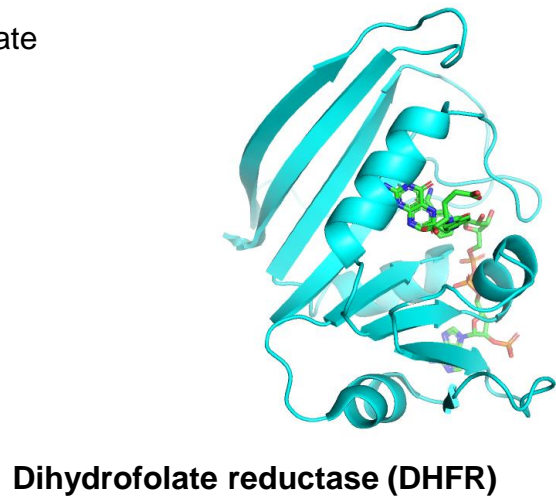
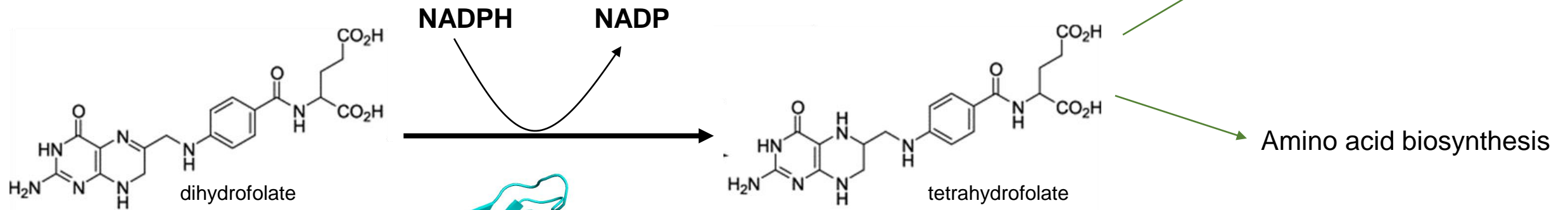
Modes of adaptation



Our model: Trimethoprim resistance in *Escherichia coli*



Our model: Trimethoprim resistance in *Escherichia coli*

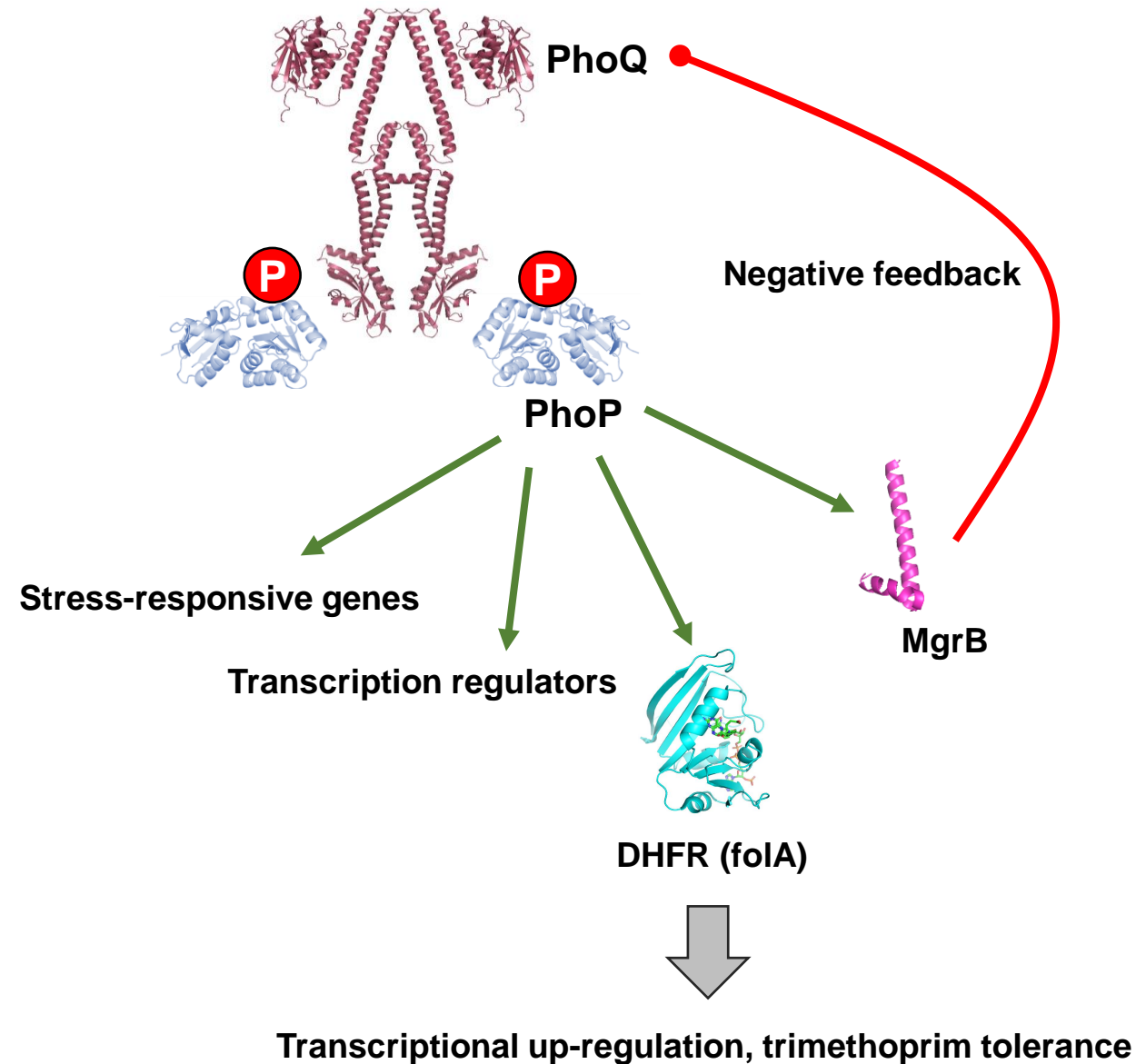
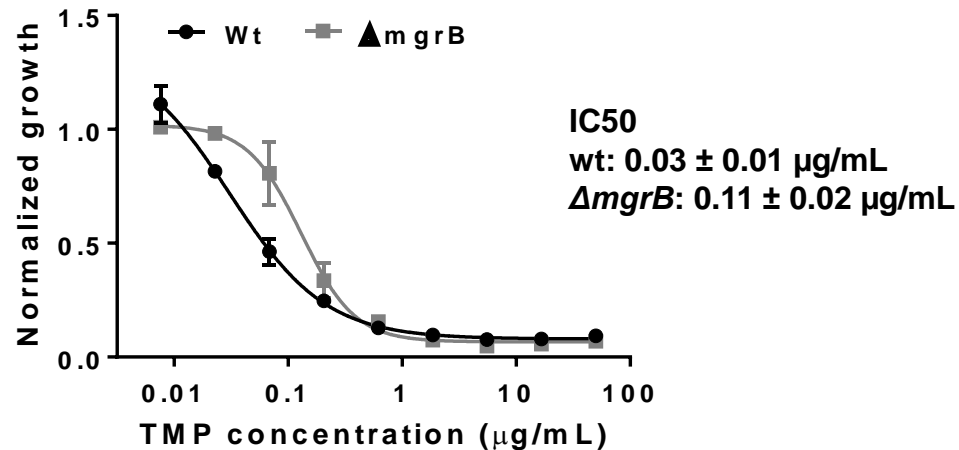
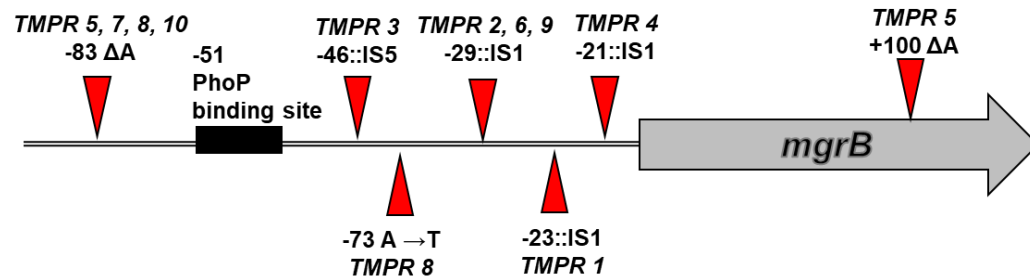


Horizontally-acquired TMP-resistant DHFRs

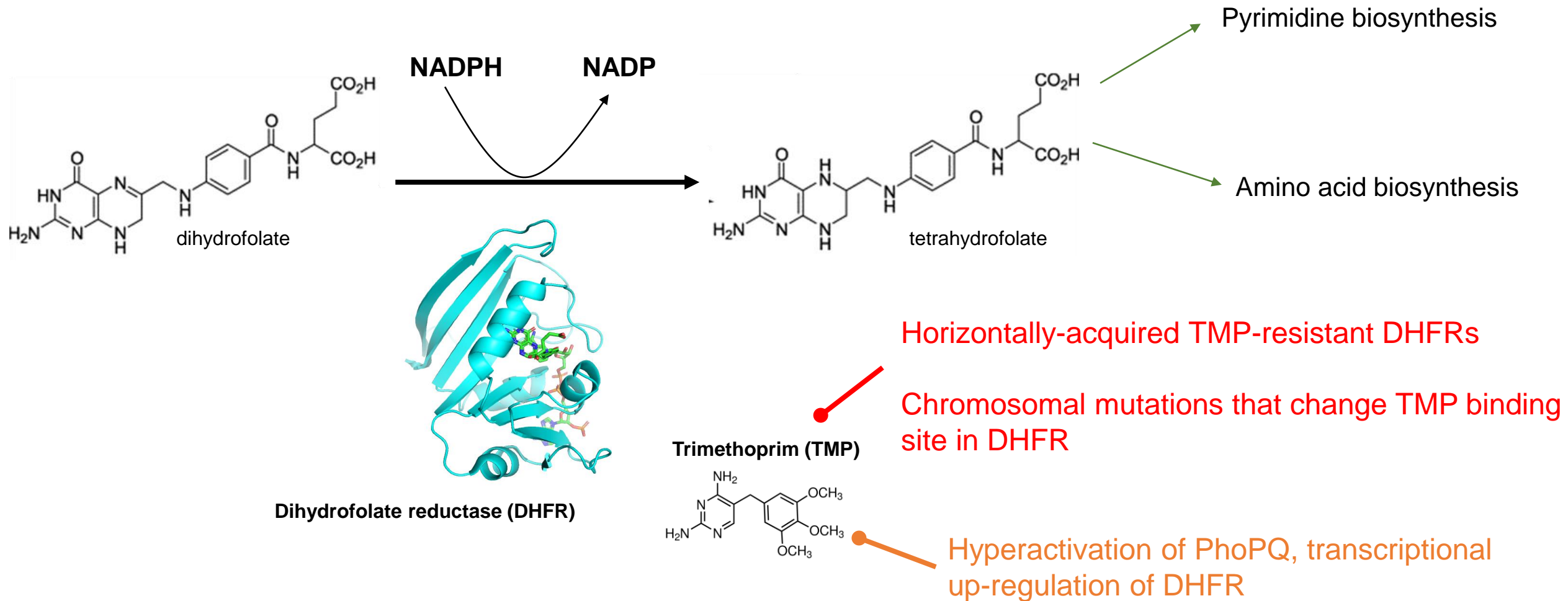
Chromosomal mutations that change TMP binding site in DHFR

Trimethoprim-resistance in *E. coli* is preceded by trimethoprim tolerance

Loss-of-function mutations in the 'mgrB' gene or its promoter confer trimethoprim tolerance to *E. coli*

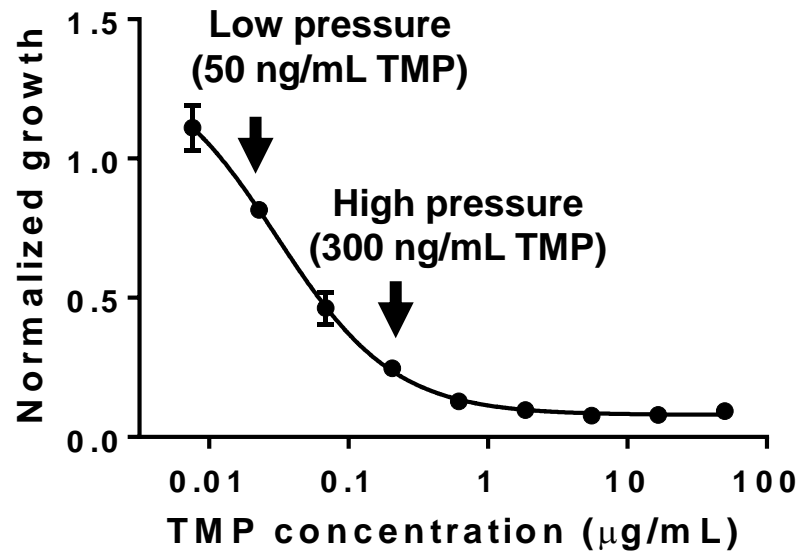


Our model: Trimethoprim resistance in *Escherichia coli*



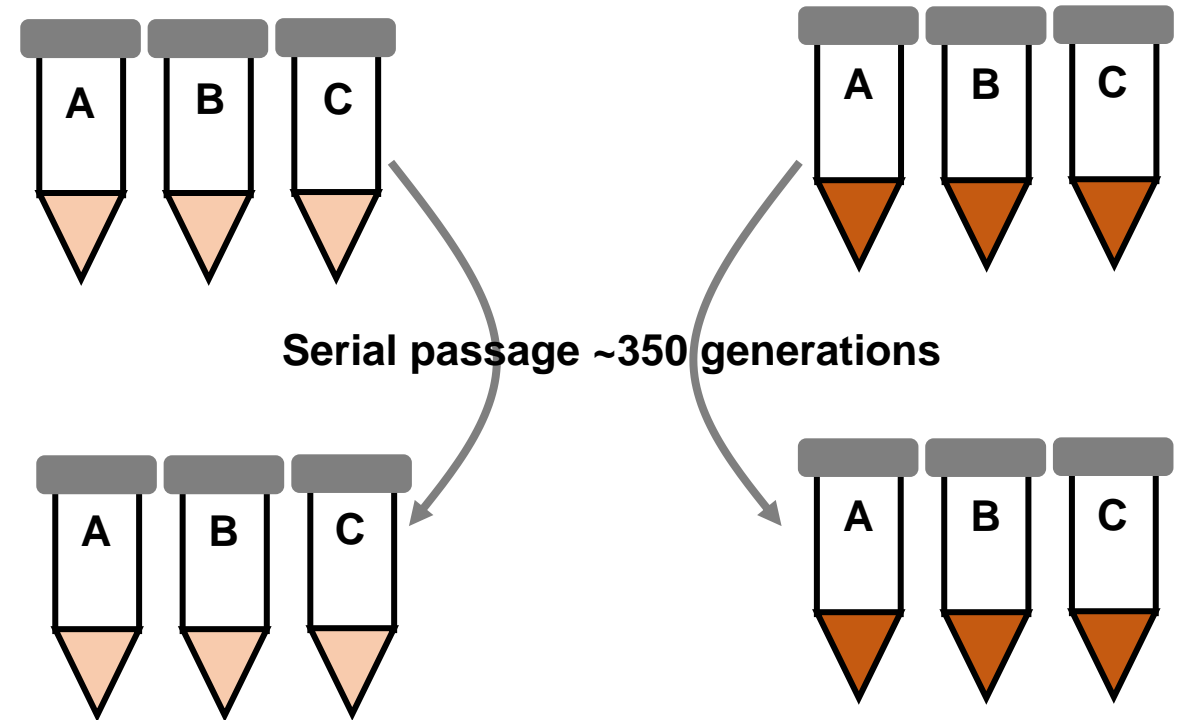
Do selection dynamics of resistant bacteria vary at different selection pressures?

Antibiotic dose vs growth for wild type *E. coli*

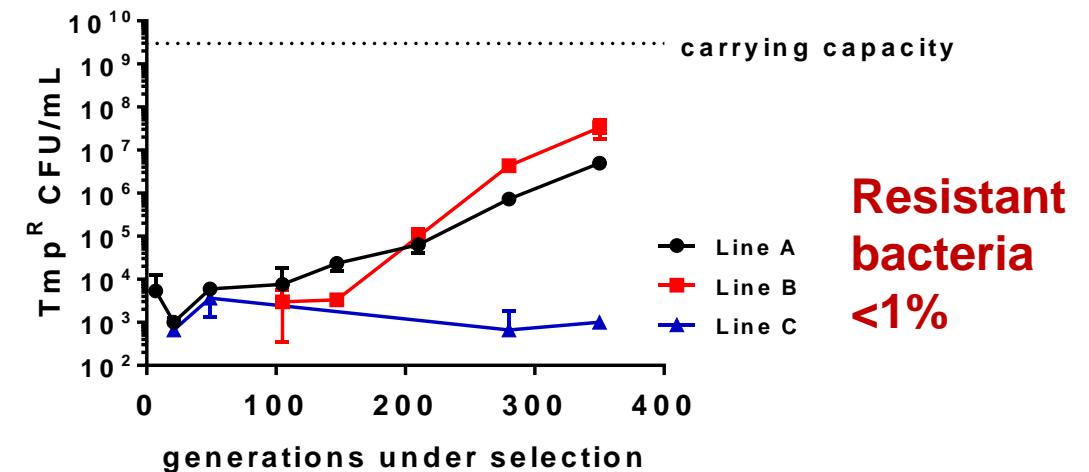
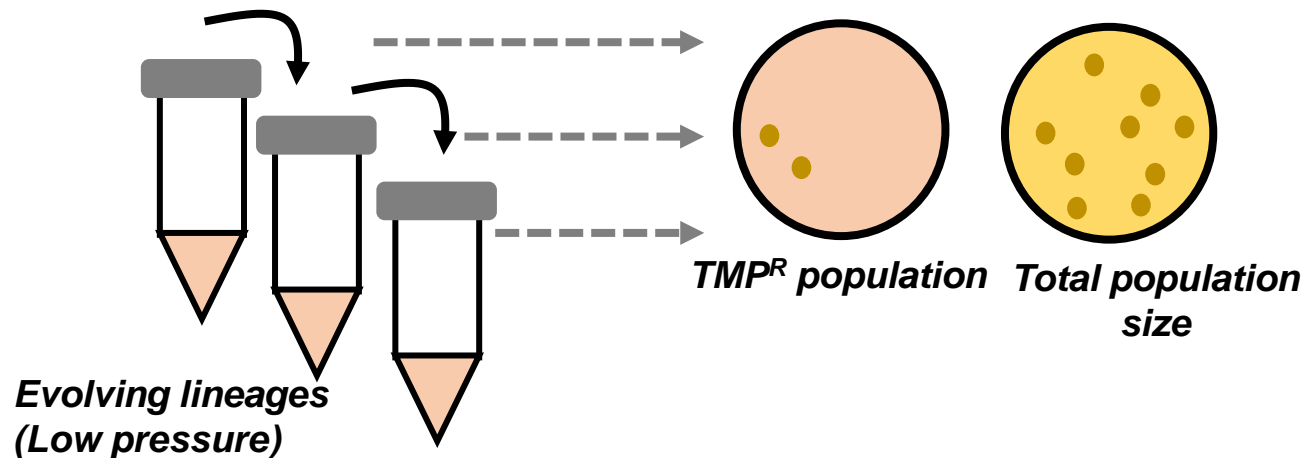
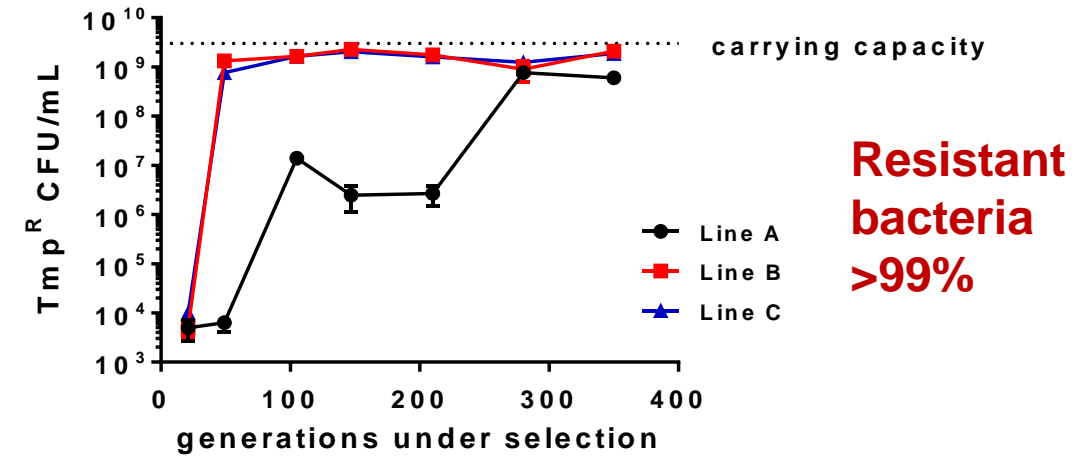
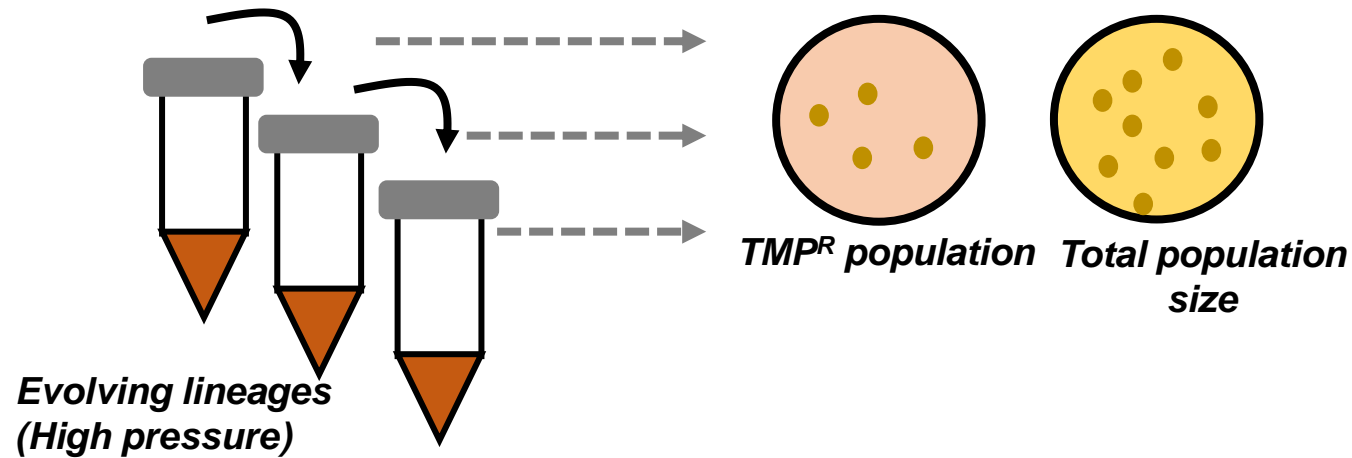


Low TMP exposure lines

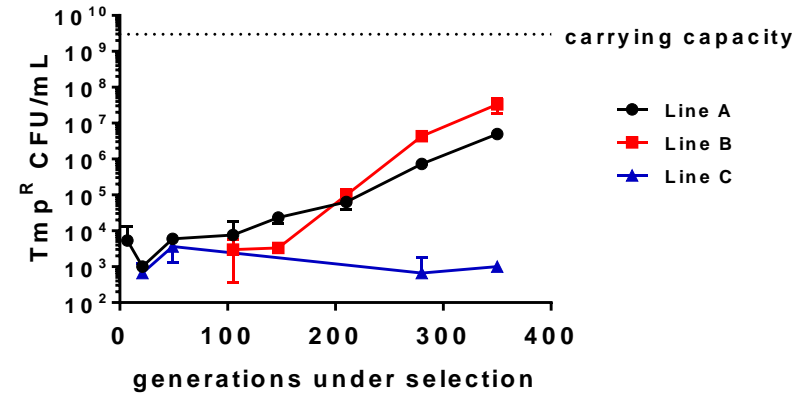
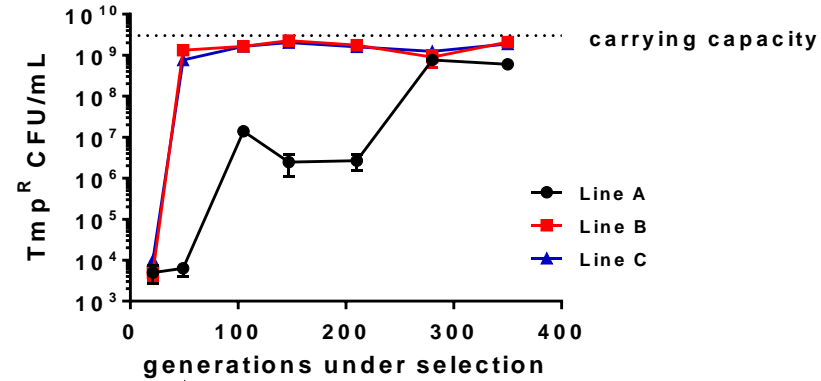
High TMP exposure lines



Do selection dynamics of resistant bacteria vary at different selection pressures?



Drug-tolerant bacteria are fixed early in high and low pressure lineages



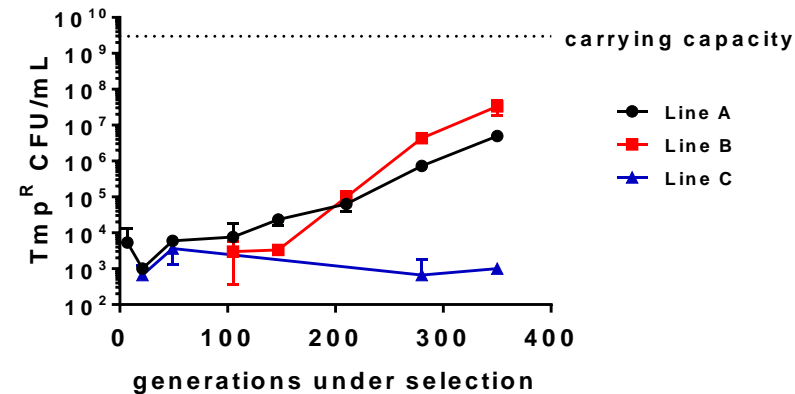
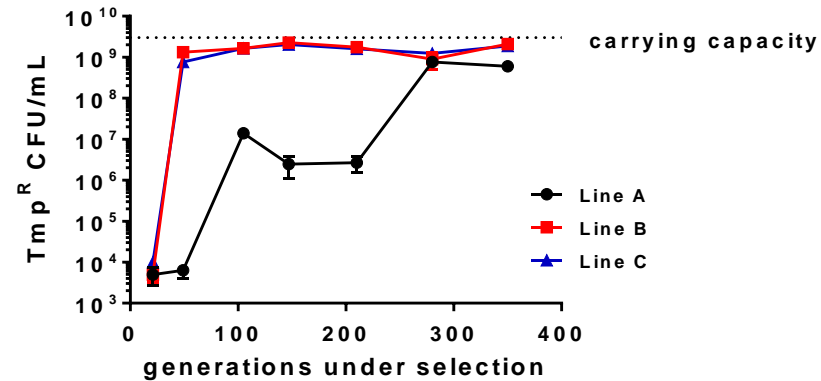
Genome sequence populations
from ~20 generations of selection

No mutations in DHFR detected

Loss of mgrB ~70-80% of populations

**Tolerance precedes resistance at both
selection pressures**

Drug-resistant bacteria are derived from drug-tolerant bacteria in high and low pressure lineages



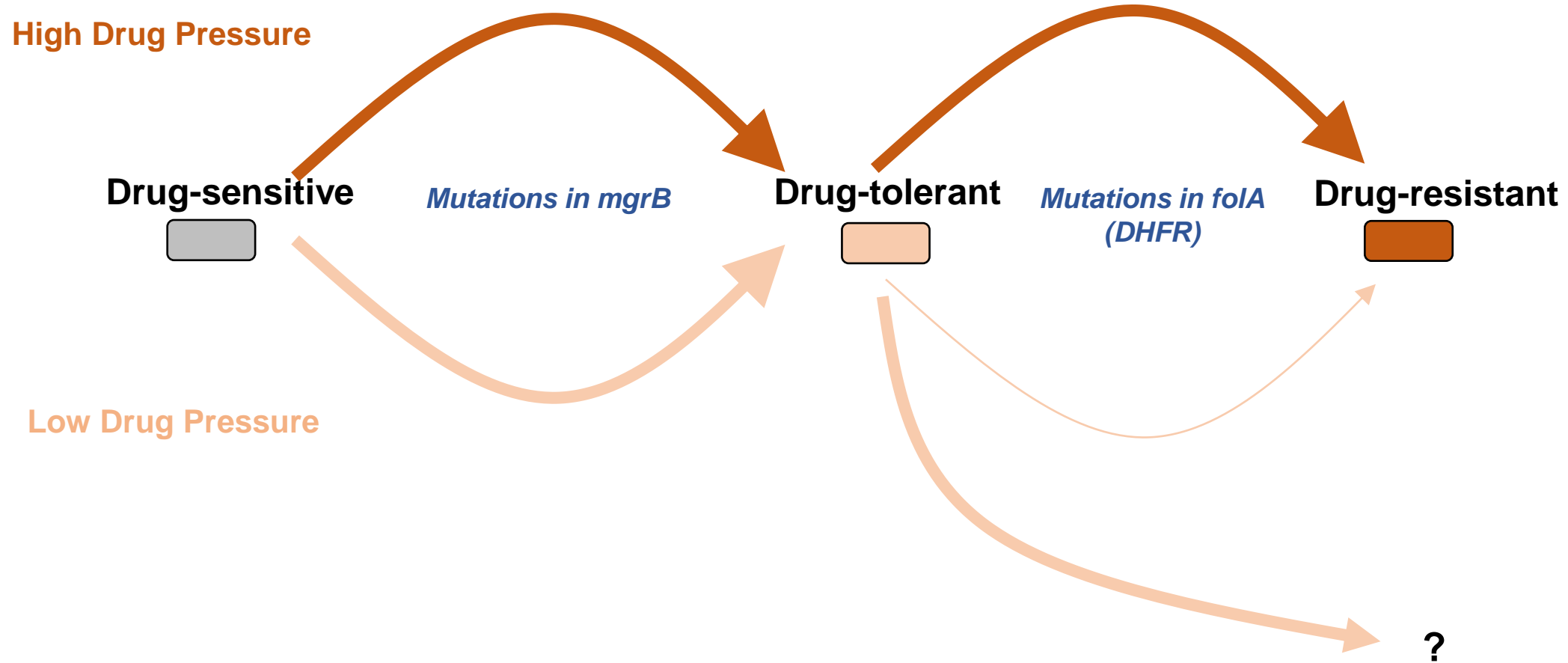
Genome sequence resistant
isolates from ~150 generations of
selection

Resistant bacteria harbour
mutations in DHFR in addition to
loss-of-function mutations in mgrB

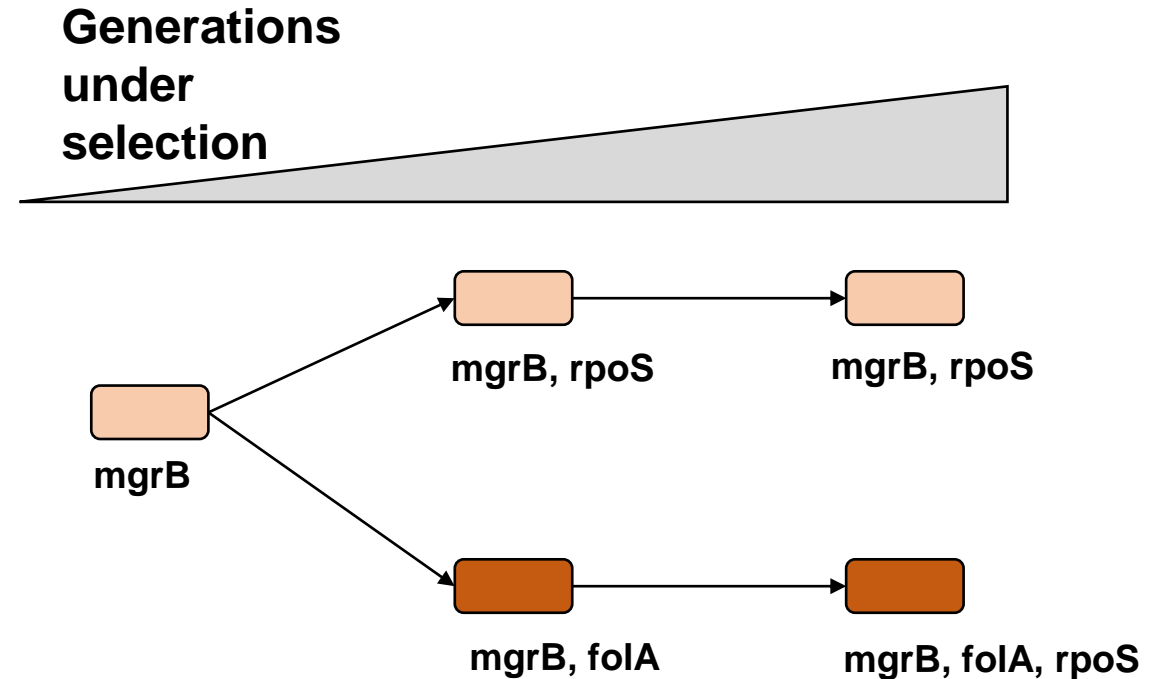
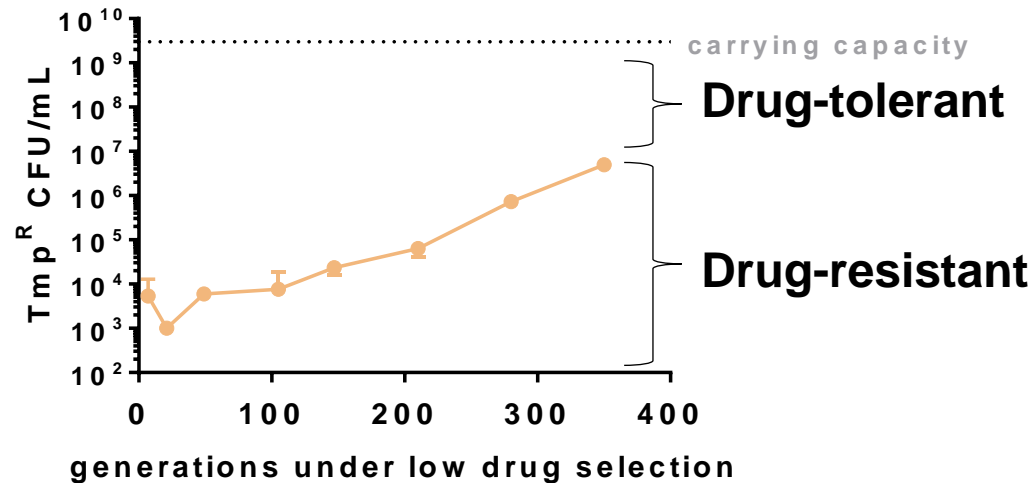
Few additional mutations in high
selection lineages

Resistant bacteria are derived from
tolerant bacteria in high and low
pressure lineages

Phenotypic transitions during selection of resistance: Dependency on selection pressure



Low pressure lineages show two different genetic trajectories of adaptation

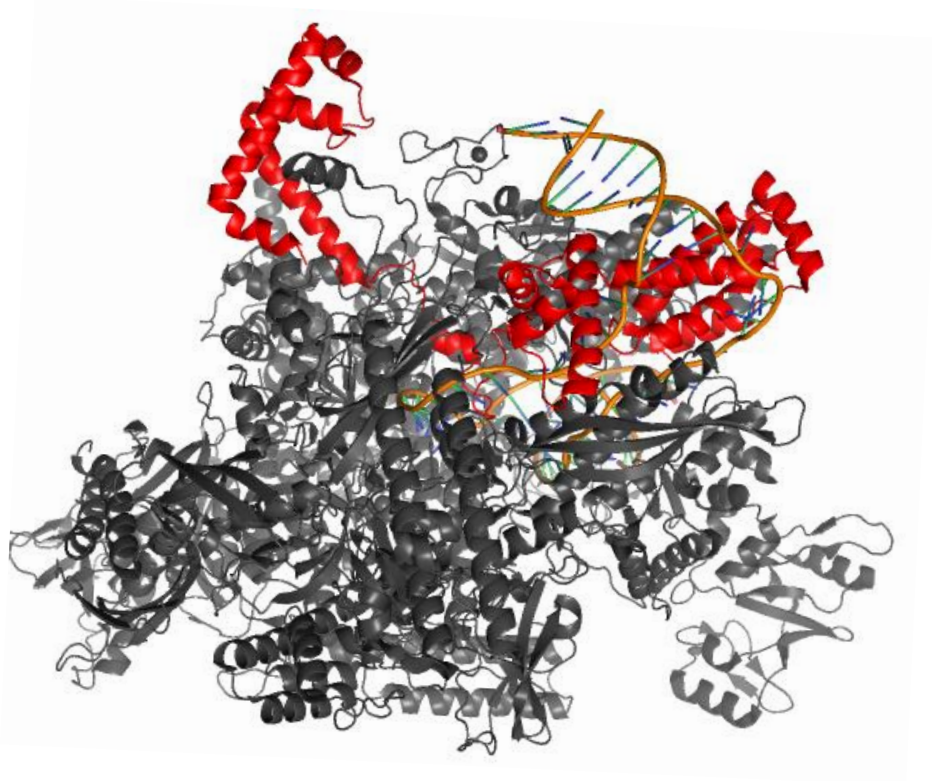


Loss of function mutations in RpoS

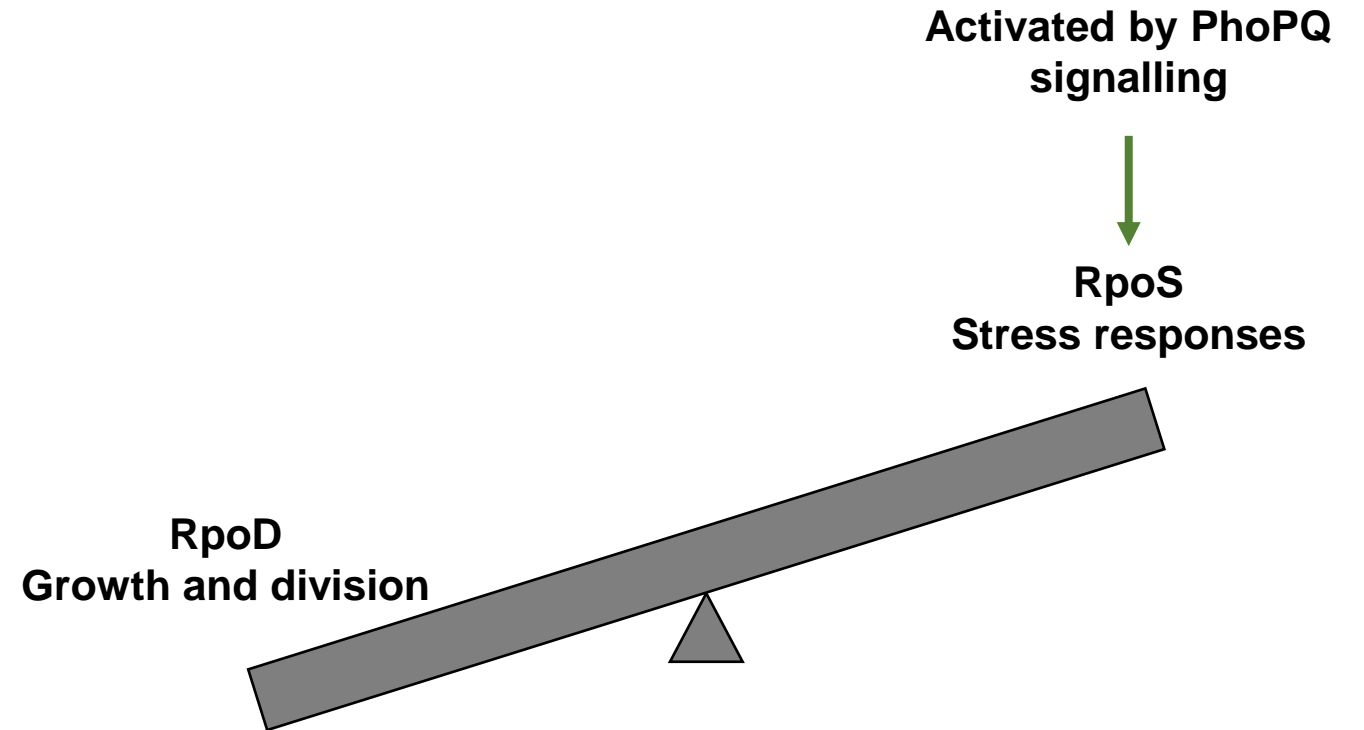
RpoS-deficiency does not enhance trimethoprim resistance

What drives the fixation of mutations in RpoS?

RpoS is an activator of bacterial stress responses and a target of PhoPQ signalling

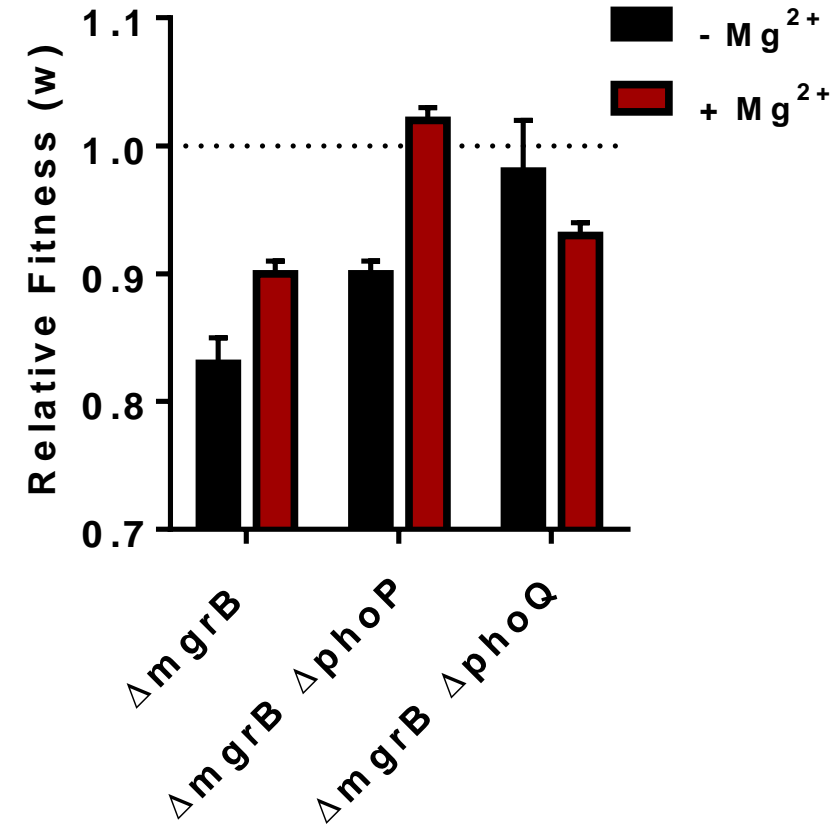
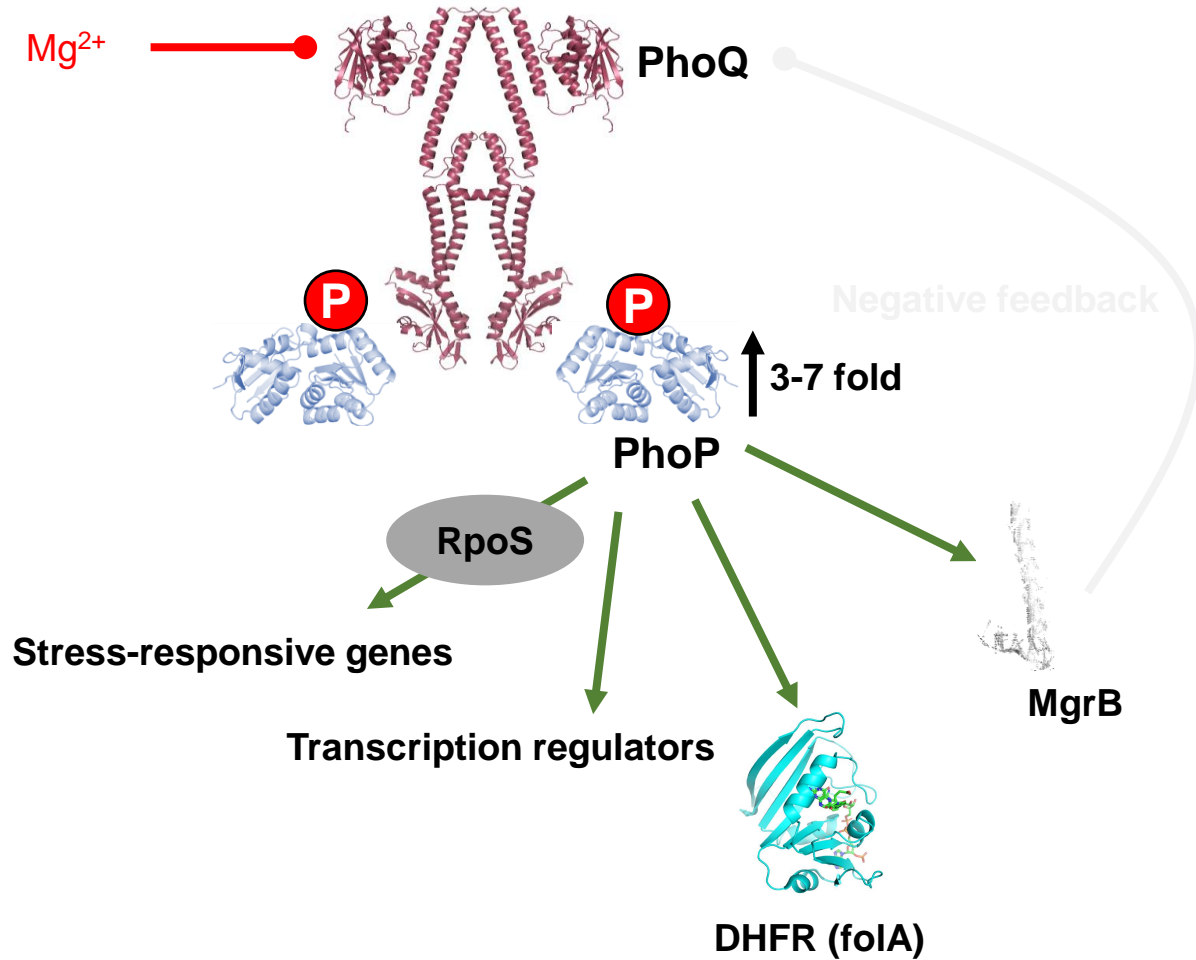


RpoS (red) bound to DNA, part of RNA polymerase holoenzyme (PDB: 5IPL)

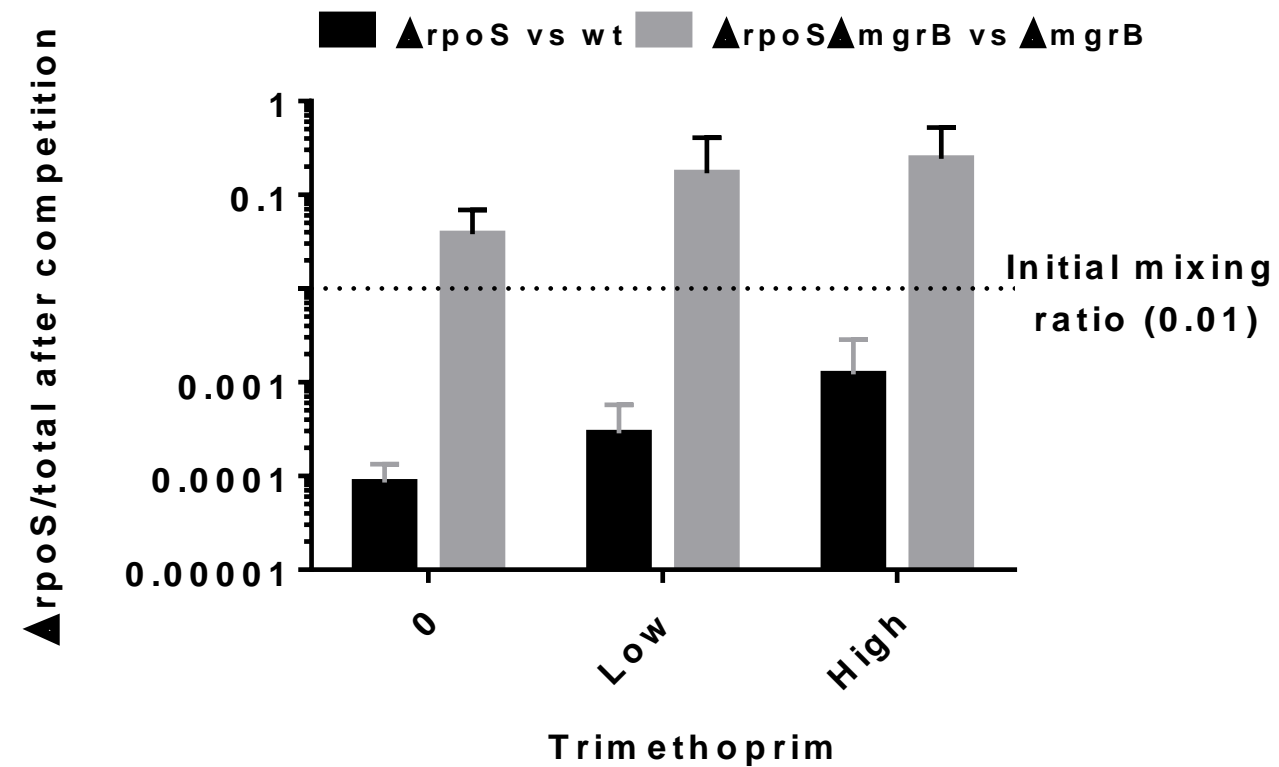
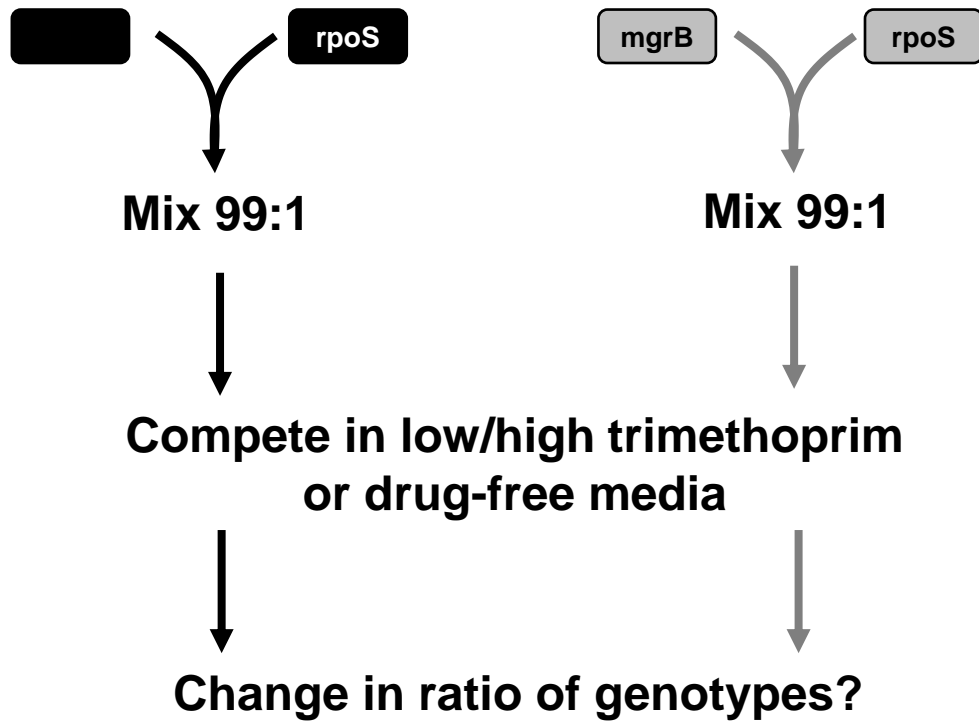


Could loss of RpoS alleviate the detrimental effects of hyperactive PhoPQ signalling in drug-tolerant bacteria?

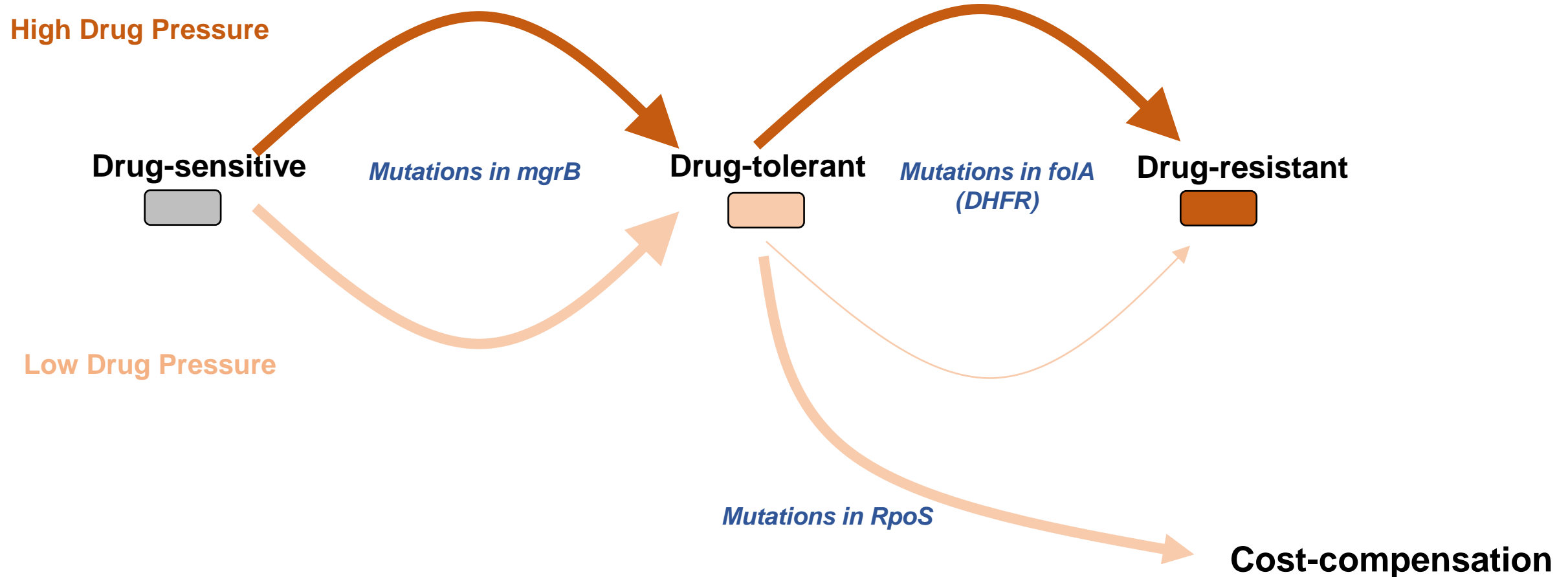
Loss of mgrB, unwanted gene expression and fitness costs



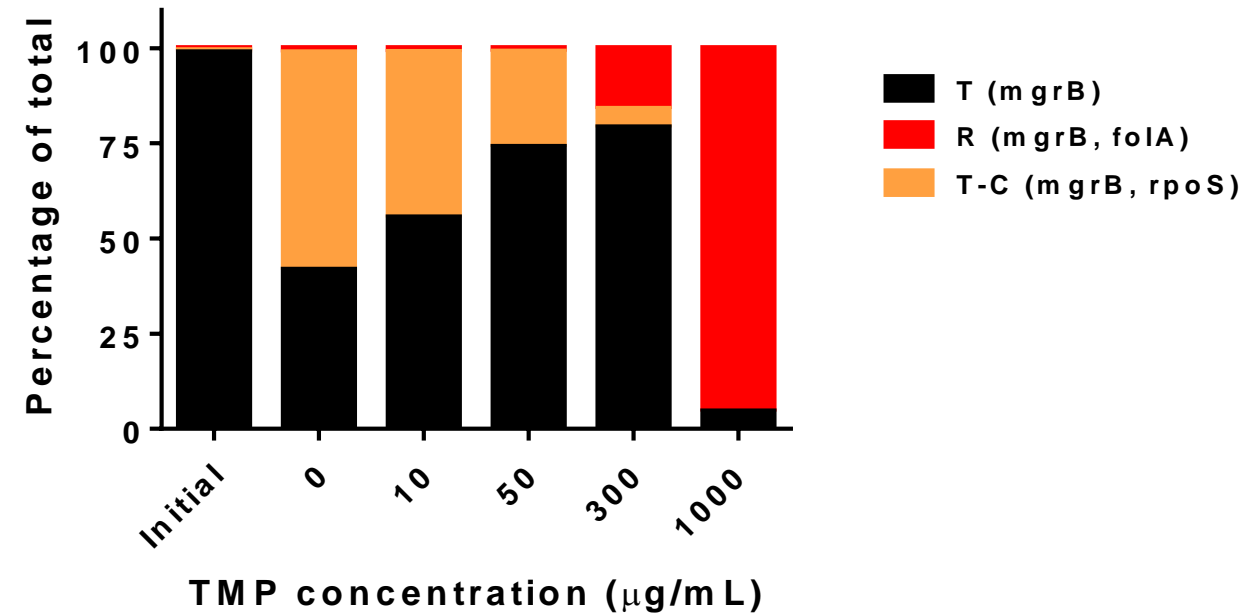
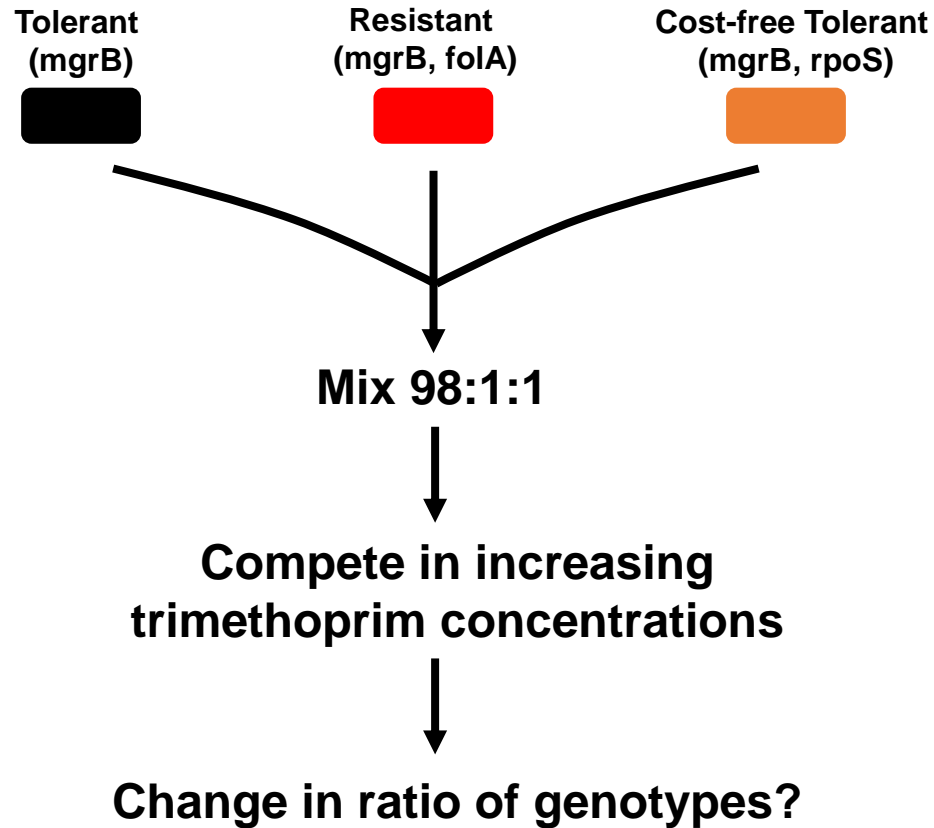
Inactivation of RpoS is beneficial in mgrB-deficient *E. coli* regardless of antibiotic



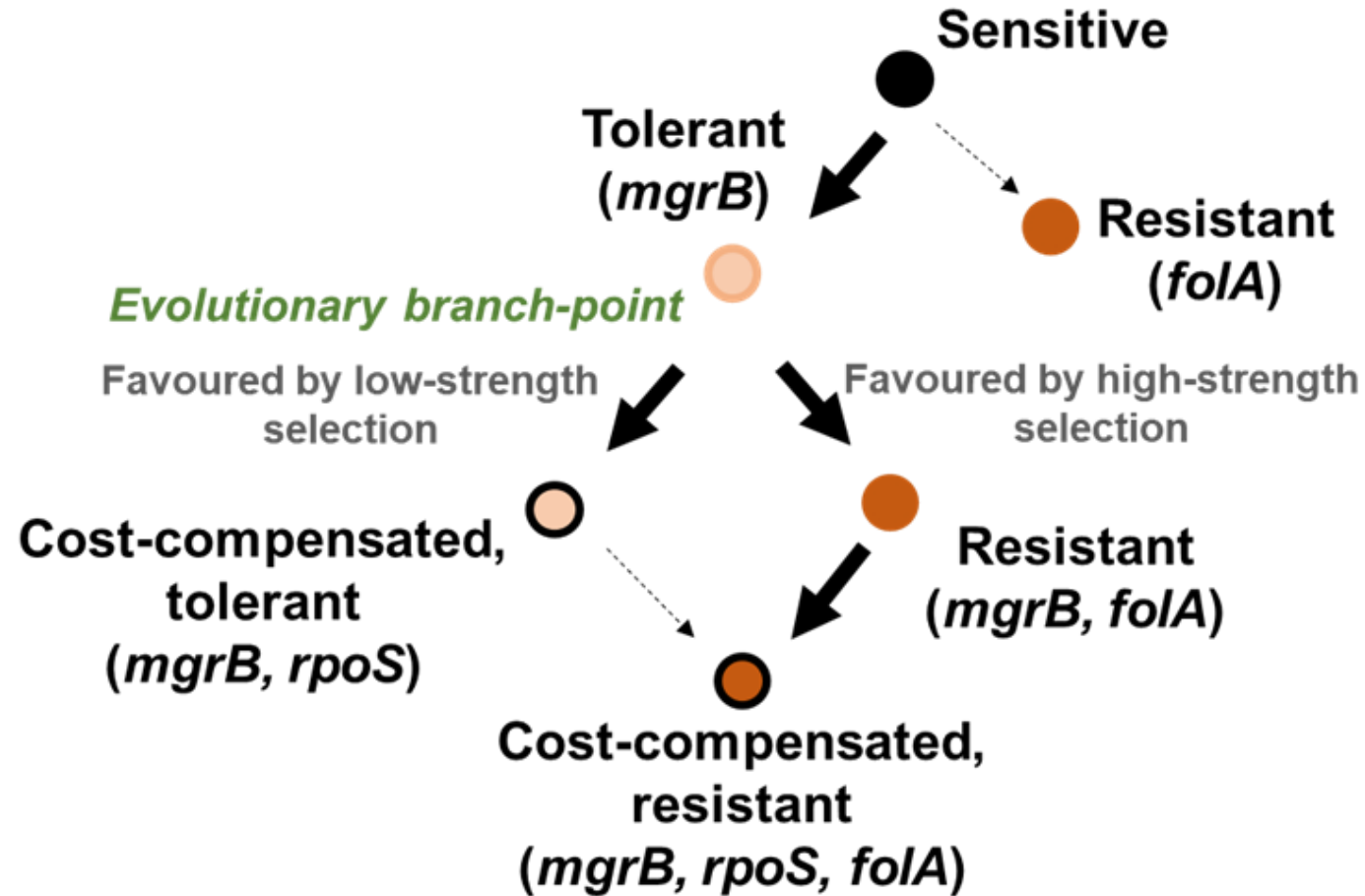
Phenotypic transitions during selection of resistance: Dependency on selection pressure



Strength of antibiotic pressure determines the most successful adaptive strategy



Phenotypic transitions during selection of resistance: Dependency on selection pressure



Take home!

- **There are many ways to improve fitness in an environment**
- **Strength of selection determines which route will be preferred**
- **Adaptive strategies are not insulated from one another**
- **Genetic structures of adapting populations can be mechanistically explained**