



Antimicrobial resistance genes

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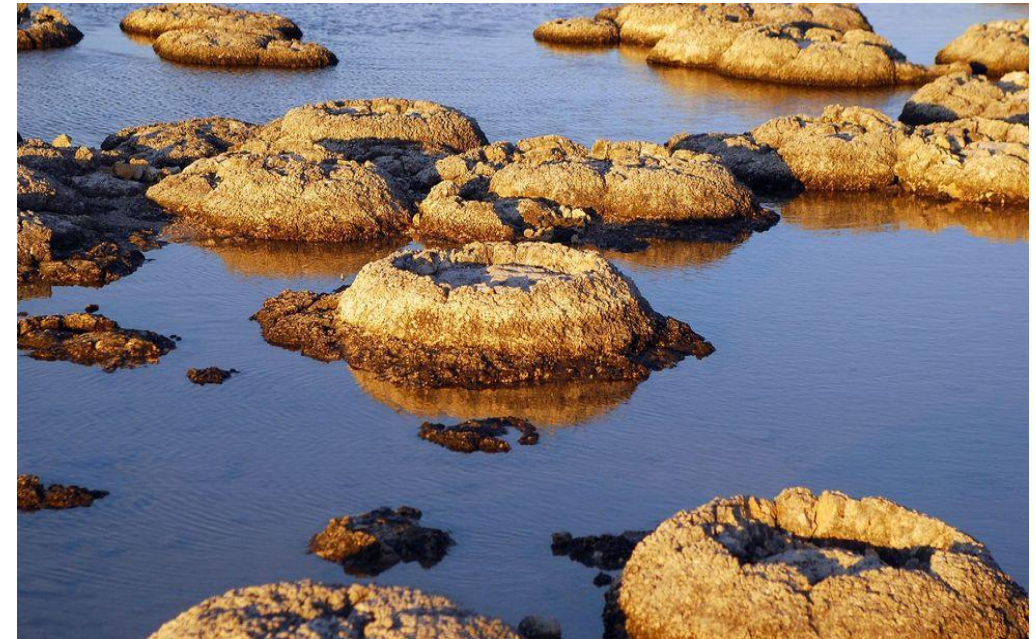
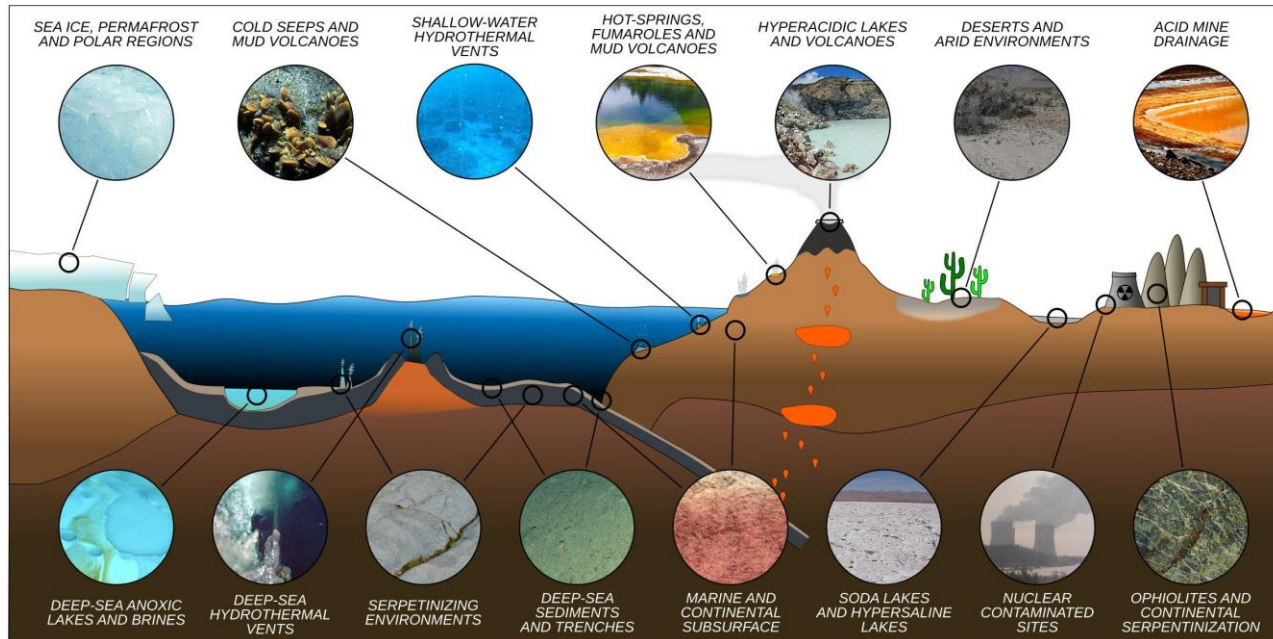
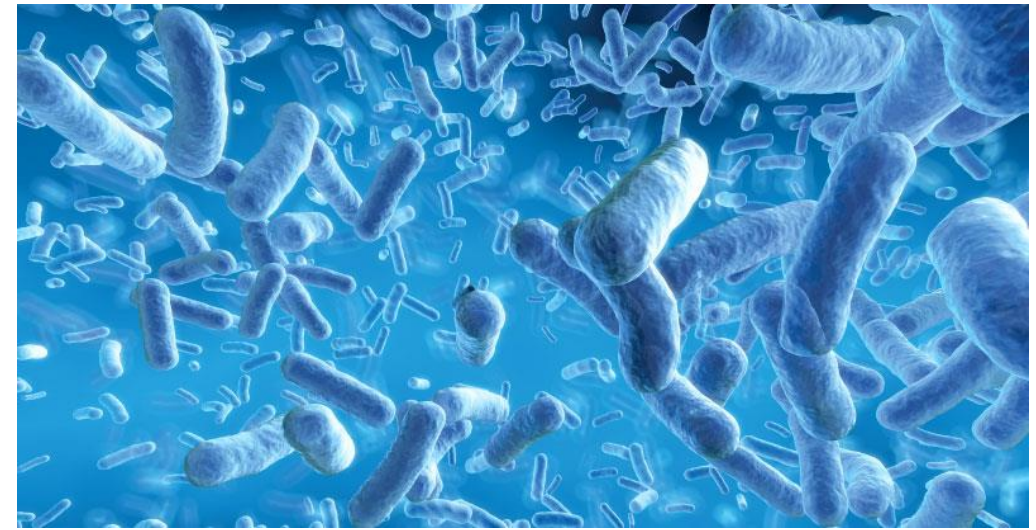
Molecular Biology and Genetics

- Microbiology
- Live vaccines
- Antibiotic resistance
- eDNA
- Population genetics



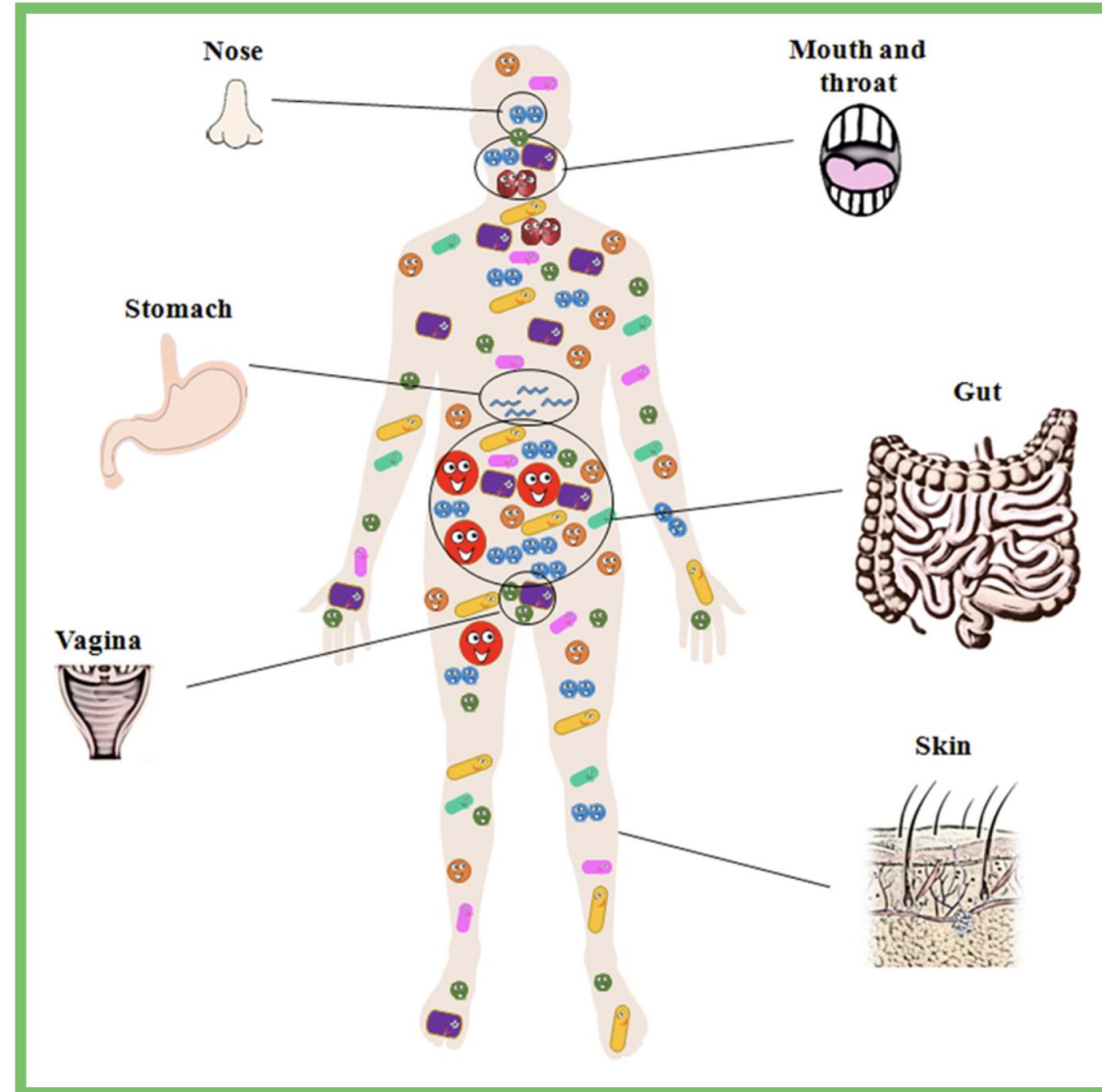
Bacteria

- The most diverse and abundant life form
- Adapted to use any nutritional source
- Ecosystem services



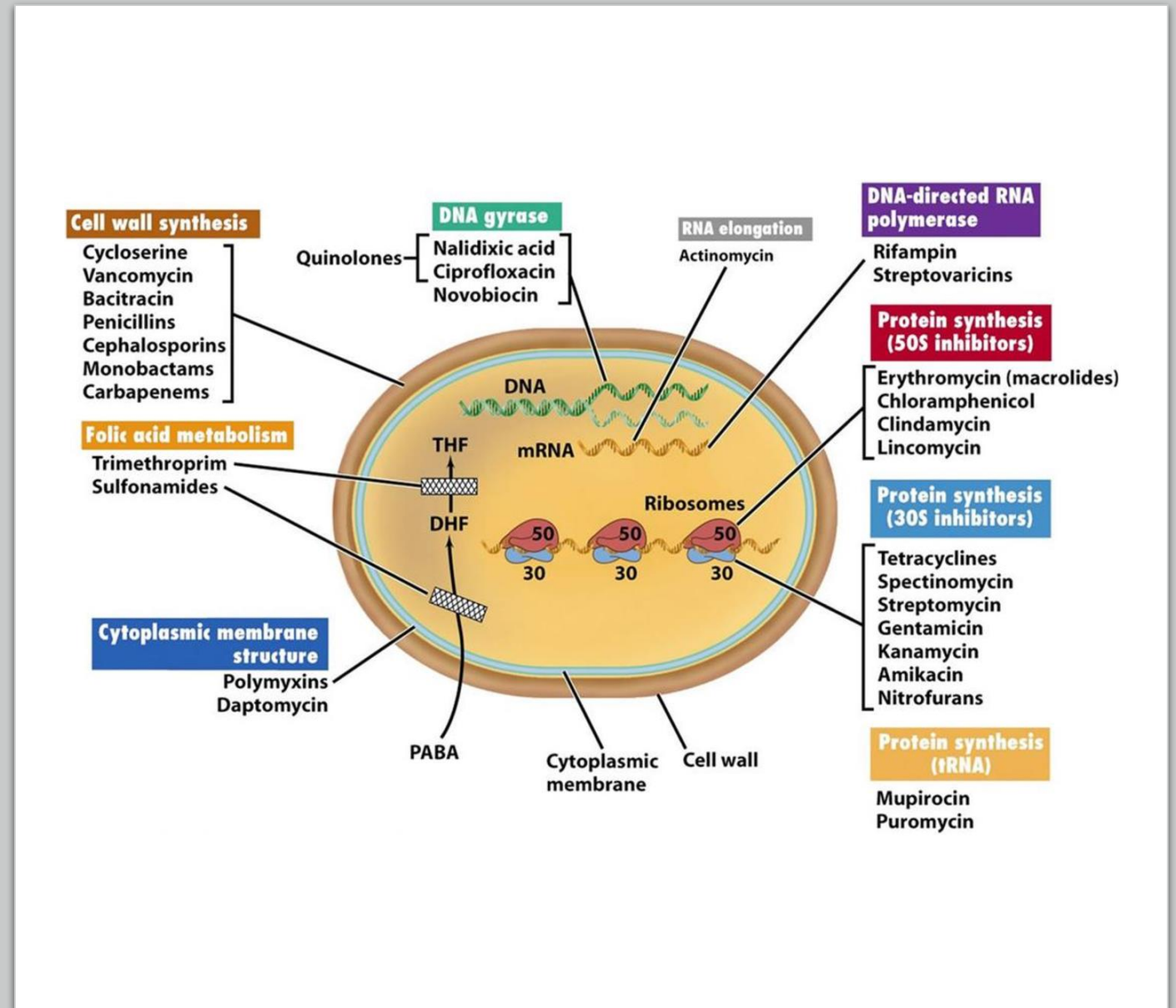
Microbiota

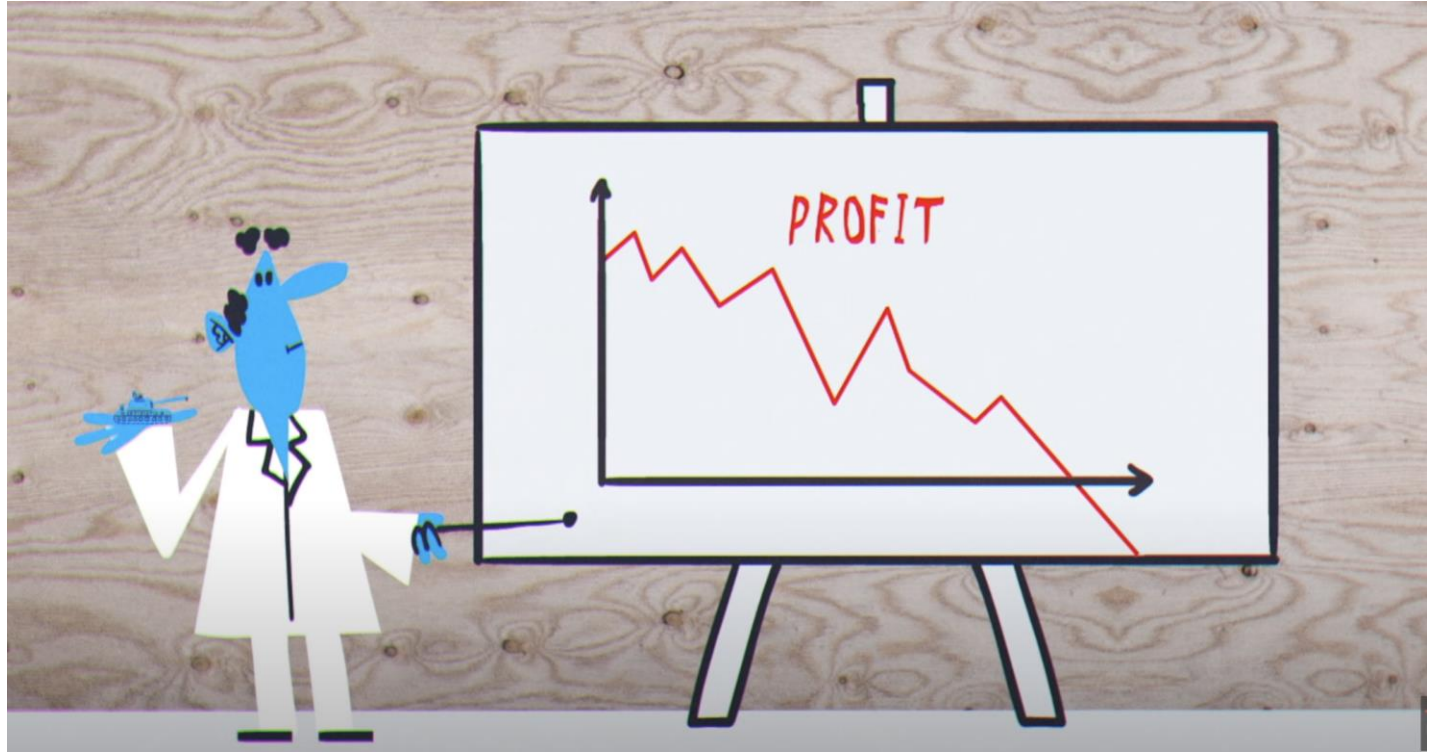
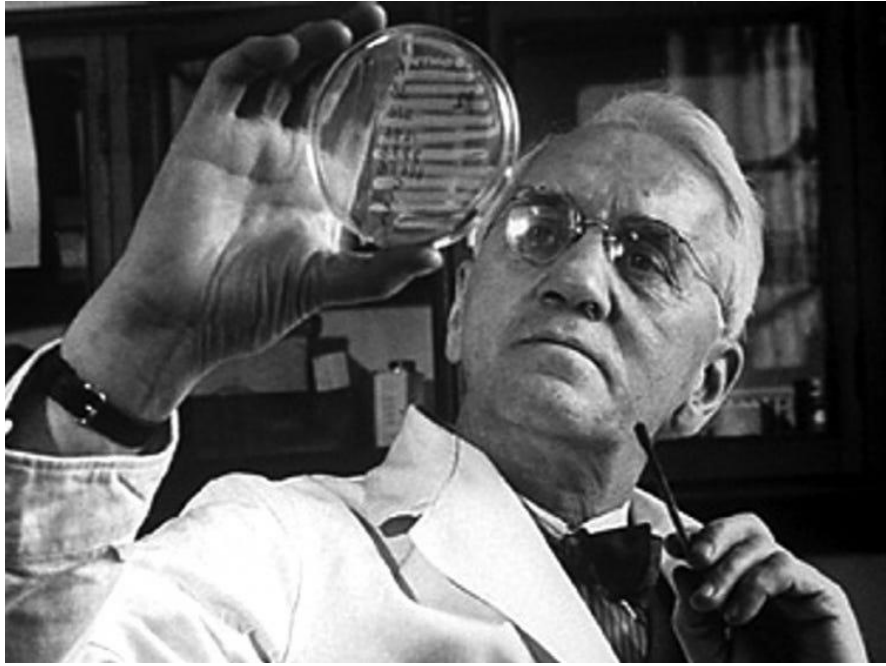
- Bacteria outnumber human cells by 10 to 1
- 5% is considered pathogens

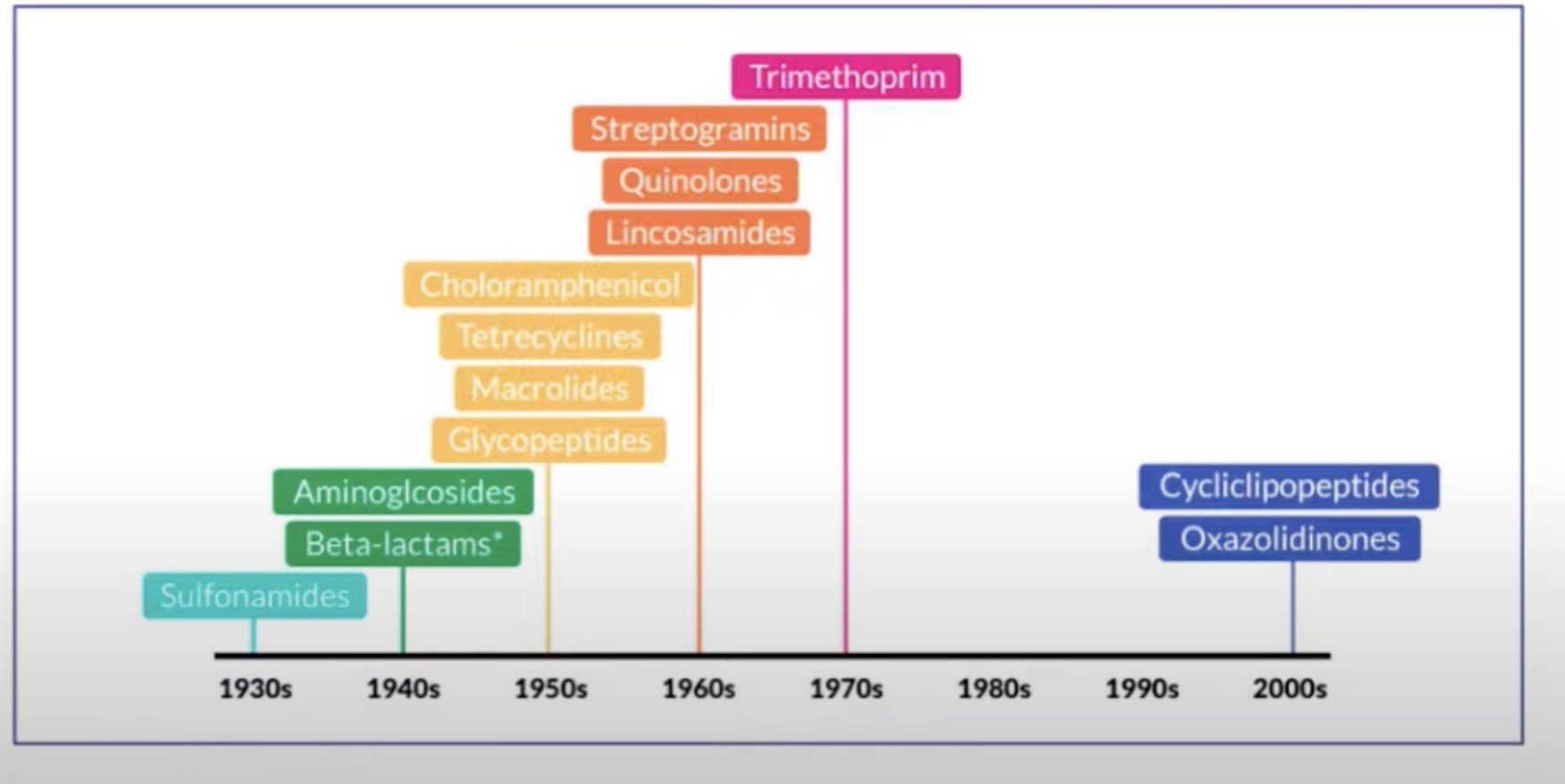


Antibiotics Mechanism of Action

- Inhibition of Cell wall Synthesis
- Inhibition of Protein Synthesis
- Alteration of Cell Membranes
- Inhibition of Nucleic Acid Synthesis



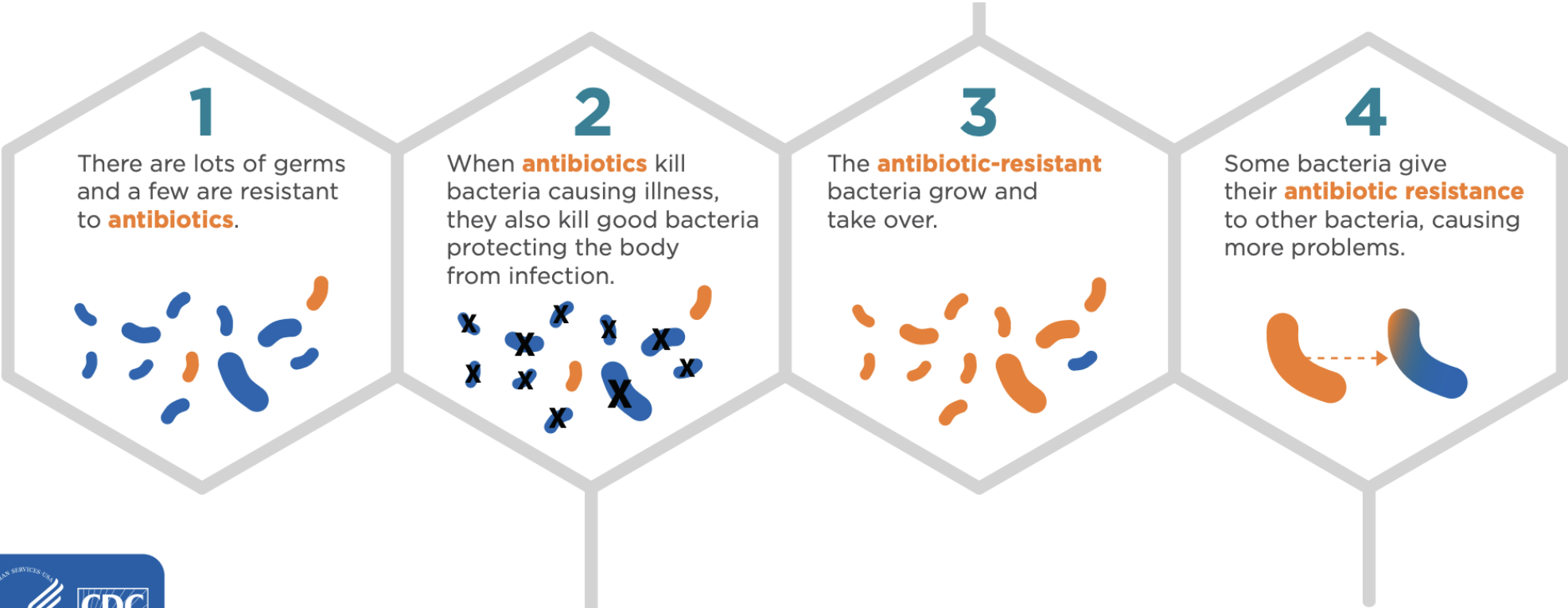


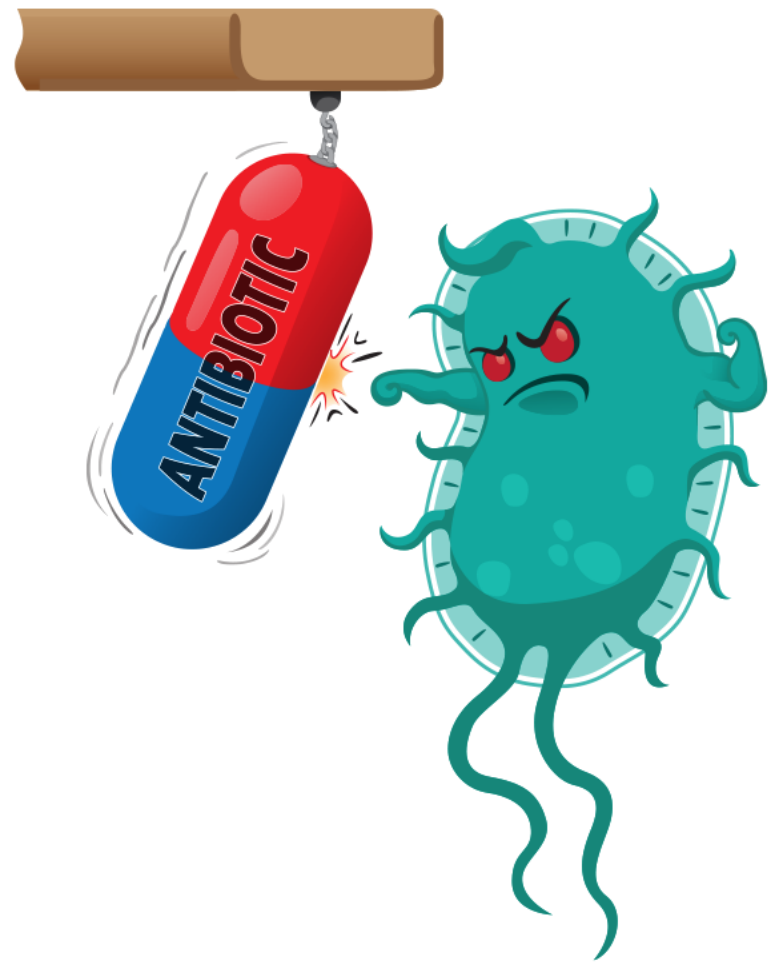


“If we use antibiotics when not needed,
we may not have them when they are
most needed”

Dr. Tom Frieden, Former Director U.S. CDC

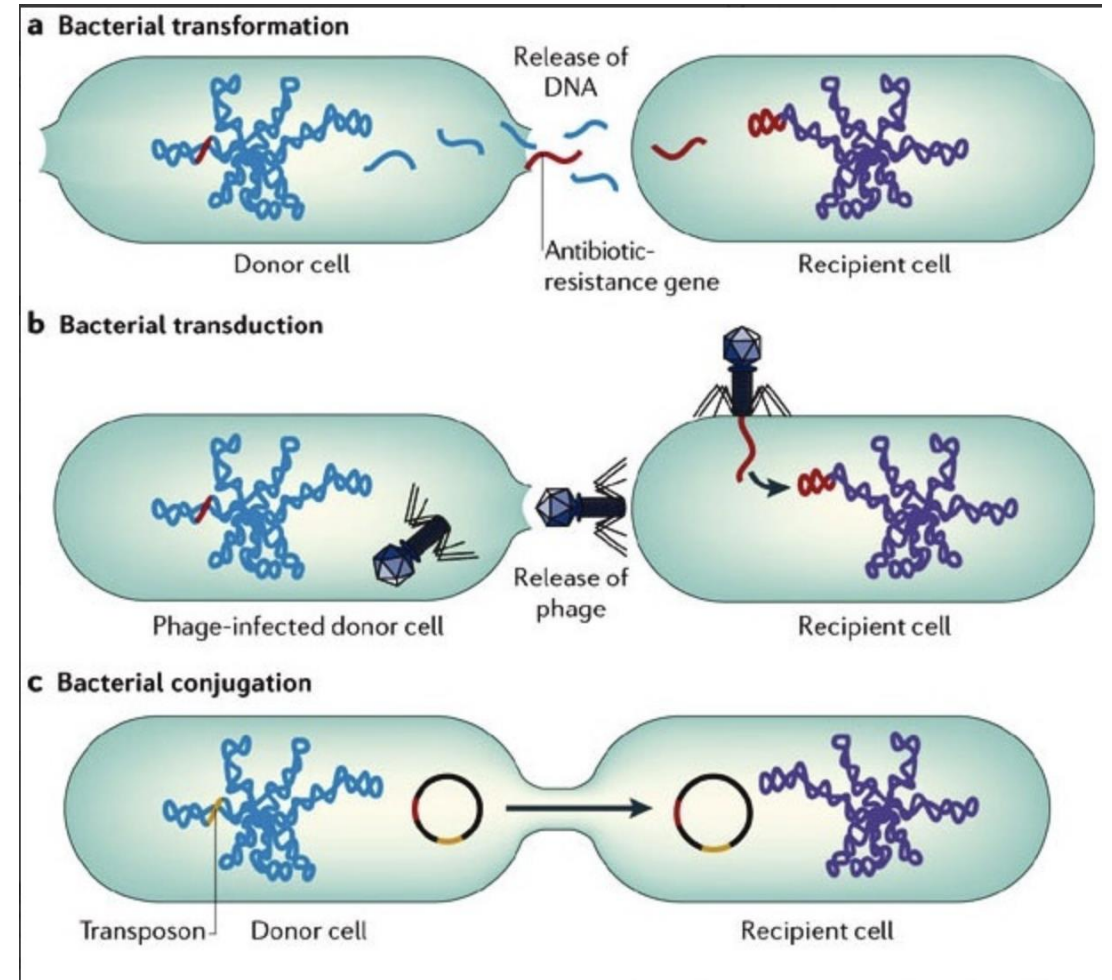
How Antibiotic Resistance Happens



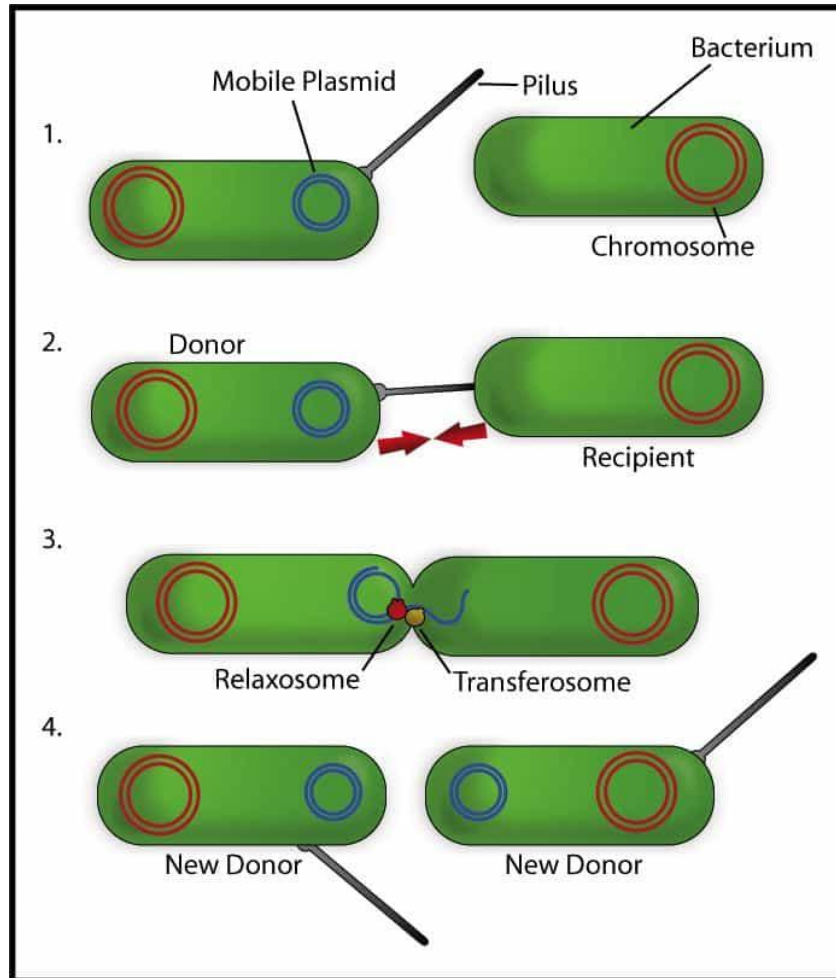


Horizontal Gene Transfer

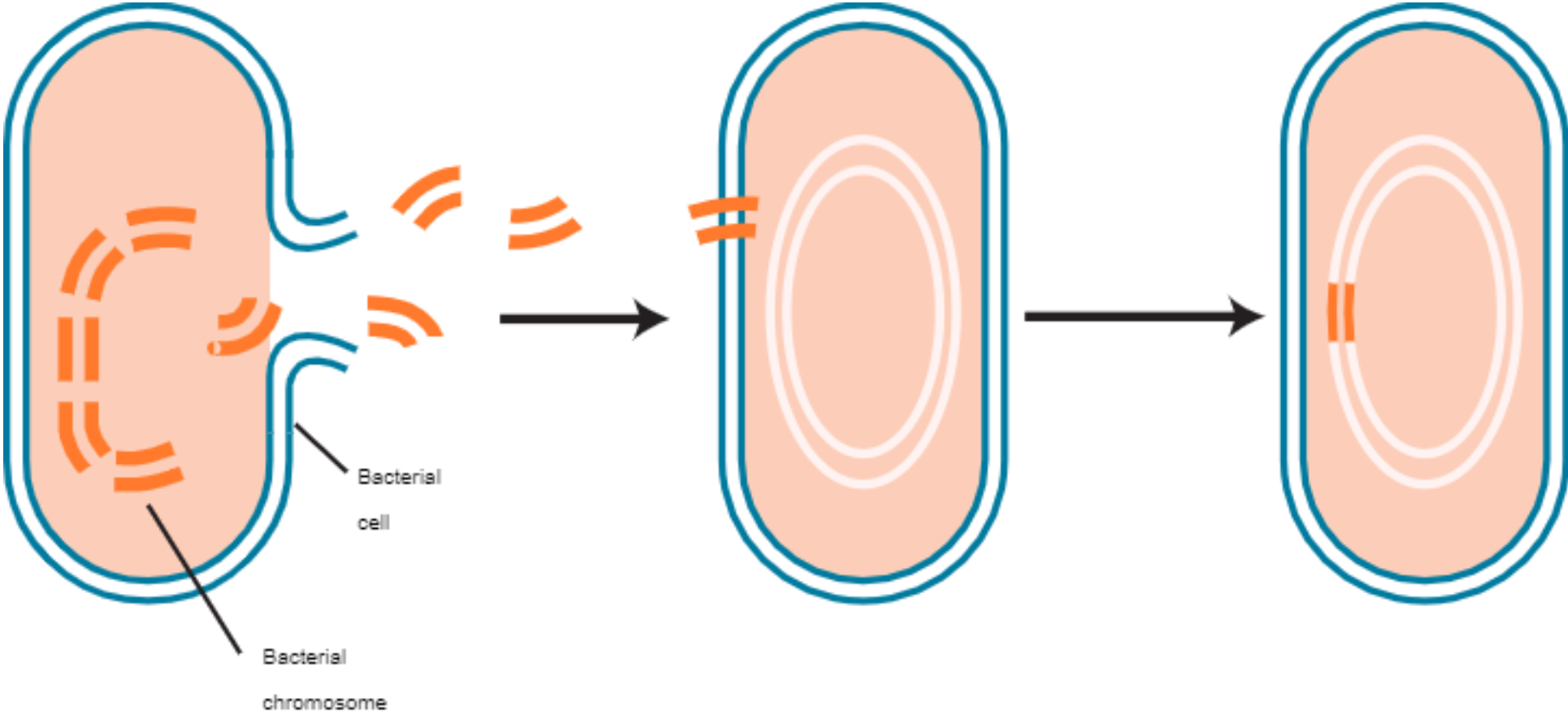
- Conjugation
- Transformation
- Transduction
- Gene transfer agents

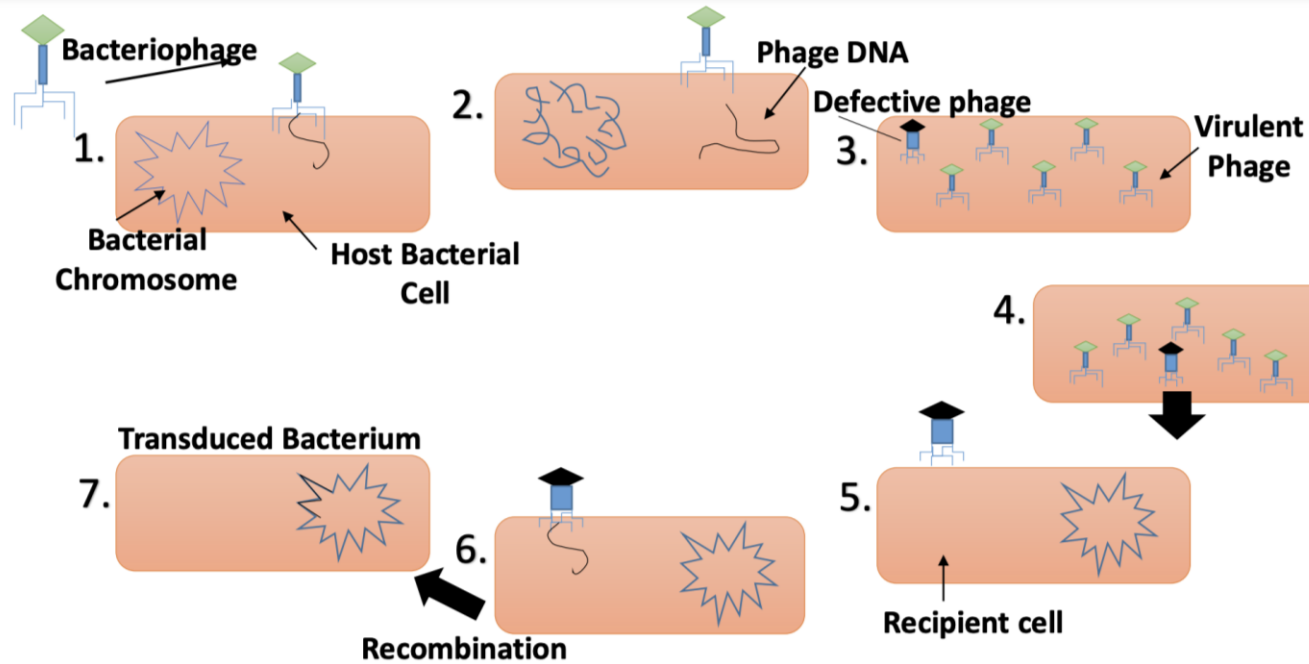


Conjugation



Transformation





1. Phage injects DNA
2. Phage enzyme breaks down host DNA
- 3-4. Cell creates new phages, including phage and host DNA
- 5-6. Transducing phage inserts donor DNA
7. Donor DNA included in recipient's chromosome due to recombination

Transduction

Transfer of portion of DNA from one bacteria to another by Bacteriophages

Assesing Presence of ARGs-Sanger

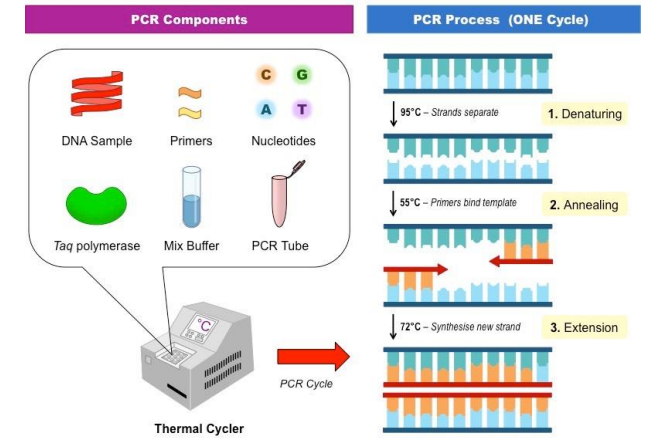
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2



3



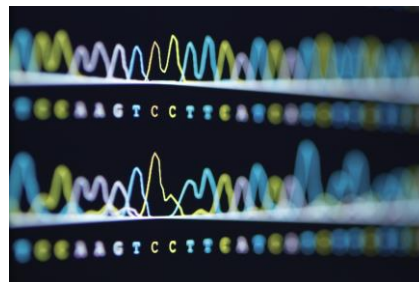
6

Escherichia coli strain 2011C-3911, complete genome
Sequence ID: [CP015240.1](#) Length: 4863599 Number of Matches: 4

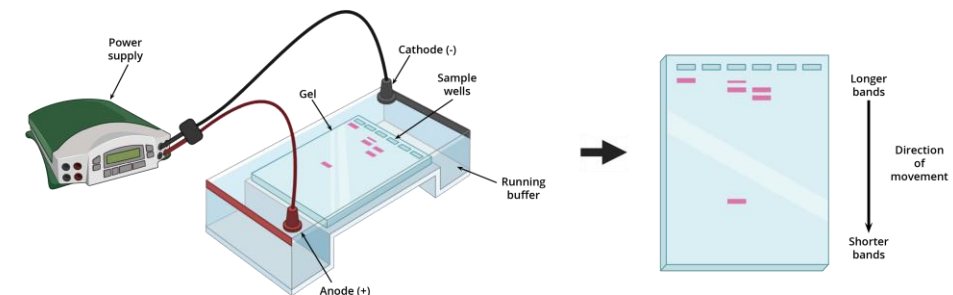
Range 1: 4671753 to 4701689 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand			
55042 bits(29806)	0.0	29896/29940(99%)	3/29940(0%)	Plus/Plus			
Query 1	CCTCCCAAAC	TGGCGATATC	CAGTCTGGTAAAC	AGCCTCAAAGCGTAT	CGGGTAGGTTA	60	
Sbjct	4671753	CCTCCCAAAC	TGGCGATATC	CAGTCTGGTAAAC	AGCCTCAAAGCGTAT	CGGGTAGGTTA	4671812
Query 61	CTGCGACGAGAT	CGACAGATATTG	CAGTCAGGTATTACT	ACAAAGCGTTTTG	TGGAGT	120	
Sbjct	4671813	CTGCGACGAGAT	CGACAGATATTG	CAGTCAGGTATTACT	ACAAAGCGTTTTG	TGGAGT	4671872
Query 121	CCTGGCTATTTT	GCCAGTAGCTG	CGGAGGTGCGCCAAT	ATCCGTCATCCG	CAATACATT	180	
Sbjct	4671873	CCTGGCTATTTT	GCCAGTAGCTG	CGGAGGTGCGCCAAT	ATCCGTCATCCG	CAATACATT	4671932

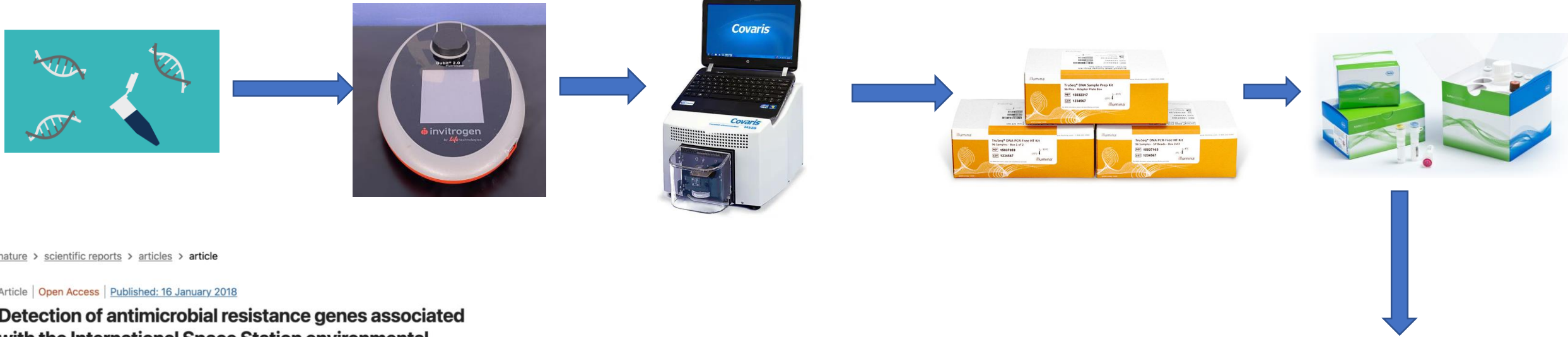
5



4



Assesing Presence of ARGs-NGS



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Article | [Open Access](#) | [Published: 16 January 2018](#)

Detection of antimicrobial resistance genes associated with the International Space Station environmental surfaces

C. Urbaniak, A. Checinska Sielaff, K. G. Frey, J. E. Allen, N. Singh, C. Jaing, K. Wheeler & K. Venkateswaran [✉](#)

[Scientific Reports](#) 8, Article number: 814 (2018) | [Cite this article](#)

15k Accesses | 49 Citations | 195 Altmetric | [Metrics](#)

Abstract

Antimicrobial resistance (AMR) is a global health issue. In an effort to minimize this threat to astronauts, who may be immunocompromised and thus at a greater risk of infection from antimicrobial resistant pathogens, a comprehensive study of the ISS 'resistome' was conducted. Using whole genome sequencing (WGS) and disc diffusion antibiotic resistance assays, 9 biosafety level 2 organisms isolated from the ISS were assessed for their antibiotic resistance. Molecular analysis of AMR genes from 24 surface samples collected from the ISS



Lactococcosis

- *Lactococcus garvieae*
- Gram positive
- 20 archival strains from each partner

JOURNAL OF FISH DISEASES

RESEARCH ARTICLE

NGS analysis revealed that *Lactococcus garvieae* Lg-Per was *Lactococcus petauri* in Türkiye

Ilhan Altinok, Rafet Cagri Ozturk, Mustafa Ture

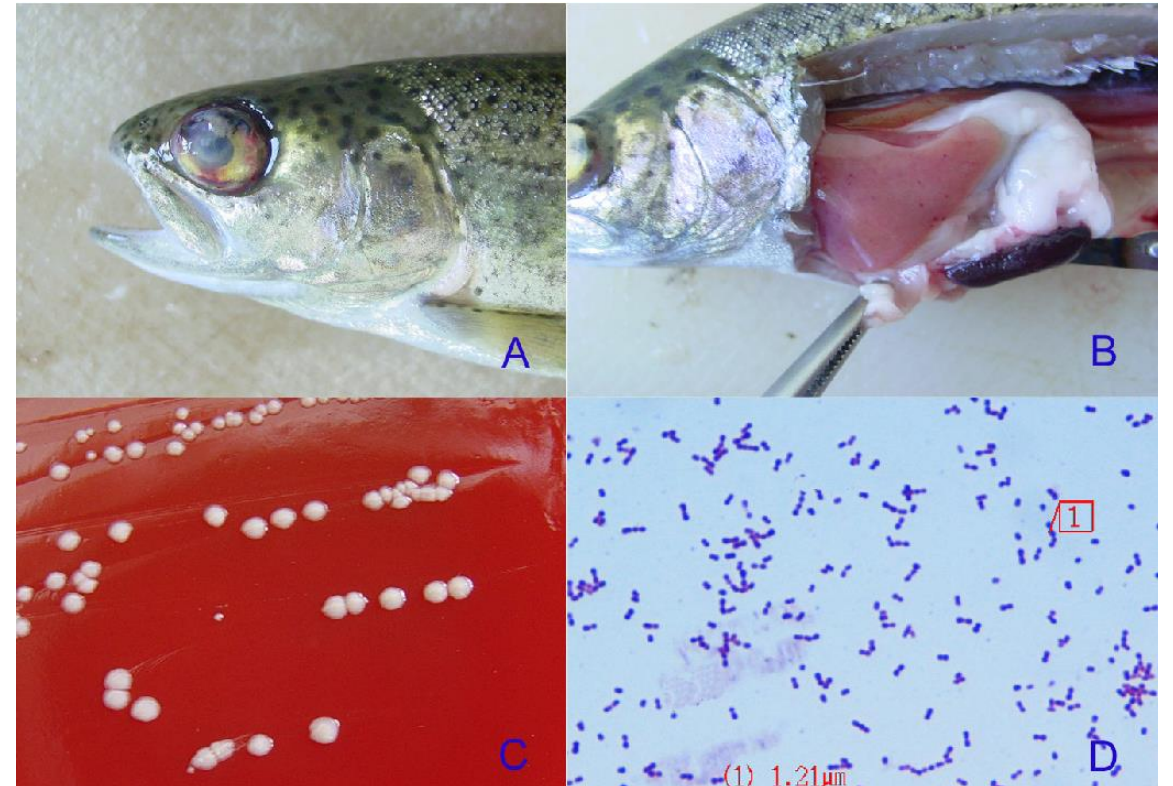
First published: 13 August 2022 | <https://doi.org/10.1111/jfd.13708>

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Abstract

Lactococcus garvieae Lg-per was originally isolated from rainbow trout cultured in cages located on the Turkish coast of the Black Sea in 2011. A whole genome sequence of Lg-per was performed in the present study. The complete genome of Lg-per mapped to the reference genomes of *L. garvieae* (GCF_000269925.1) and *Lactococcus petauri* (GCF_014830225.1) had a total of 1,694,407 and 1,945,297 base pairs, respectively. Lg-per had 1955 protein-coding genes and 4 rRNA, 46 tRNA and 1 tmRNA operons. The orthoANI value was 98.30% between Lg-per and *L. petauri* (GCF_014830225.1) and 93.1% between Lg-per and *L. garvieae* (GCF_000269925.1). A phylogenetic tree generated from the whole genome sequences (WGS) of several *Lactococcus* species found that *L. petauri* (GCA_002154895) was closely related to the Lg-per strain with 98% similarity. Although *L. garvieae* Lg-per was confirmed as *L. garvieae* based on phenotypical, biochemical and 16S rRNA sequence, WGS of the Lg-per strain revealed that Lg-per was *L. petauri*. Using a





Antibiotics	Gene	Tm	Primers	Fragment size	References
Florfenicol	floR	55	F: 5'-TTATCTCCCTGTCGTTCCAGCG-3' R: 5'-CCTATGAGCACACGGGGAGC-3'	526	Iwanaga et al. (2004)
Tetracycline	tetA	56	F: 5'-GGTTCACTCGAACGACGTC-3' R: 5'-CTGTCCGACAAGTTGCATGA-3'	577	Randall et al. (2004)
	tetB	56	F: 5'-CCTCAGCTTCTCAACGCGTG-3' R: 5'-GCACCTTGCTGATGACTCTT-3'	634	
	tetC	62	F: 5'-GCGGGATATCGTCCATTCCG-3' R: 5'-GCGTAGAGGATCCACAGGACG-3'	207	Lucarelli et al. (2010)
	tetG	56	F: 5'-CCGGTCTTATGGGTGCTCTA-3' R: 5'-CCAGAAGAACGAAGCCAGTC-3'	603	
Macrolides	ErmA	54	F: 5'-GCGGTAAACCCCTCTGAG-3' R: 5'-GCCTGTCGGAATTGG-3'	434	Werckenthin and Schwarz (2000)
	ErmB	55	F: 5'-CATTTAACGACGAAACTGGC-3' R: 5'-GGAACATCTGTGGTATGGCG-3'	425	Jensen et al. (1999)
	ErmC	54	F: 5'-ATCTTTGAAATCGGCTCAGG-3' R: 5'-CAAACCCGTATTCCACGATT-3'	295	
Streptomycin	strB	54	F: 5'-GGCACCCATAAGCGTACGCC-3' R: 5'-TGCCGAGCACGGCGACTACC-3'	470	Dalsgaard et al. (1999)
β-lactamase ampicillin	blaSH V	56	F: 5'-TTATCTCCCTGTTAGCCACC-3' R: 5'-GATTTGCTGATTTGCTCGG-3'	796	Prabu and Menon (2013)
	blaO XA	55	F: 5'-ACCAGATTCAACTTTCAA-3' R: 5'-TCTTGGCTTTTATGCTTG-3'	589	
	blaTE M	56	F: 5'-ATA AAA TTC TTG AAG AC R: 5'-TTA CCA ATG CTT AAT CA-3'	1073	
Quinolones oxalinic acid	qnrA	54	F: 5'-GGGTATGGATATTATTGATAAAG-3' R: 5'-CTAATCCGGCAGCACTATTTA-3'	670	Mammeri et al. (2005)
Quinolones flumequine	gyrA	54	F: 5'-TGTCGAGATGGCCTGAAGC-3' R: 5'-TACCGTCATAGTTATCCACG-3'	347	Griggs et al. (1996)
Capsule genes	6329 F- 7175 R		F: 5'-AAAAACGGAGGGCAACAAGC 3' R: 5'-CACTTGTACAGGCCACTGGT 3'	785	Ture and Altinok (2016)
	5358 F 6007 R		F: 5'-TGGAGGGTATTGCCTACCGA 3' R: 5'-CCACAGCAGCTTCTTACCT 3'	650	Ture and Altinok (2016)

Presence of antibiotic resistance genes (%) in *L. garvieae* strains

Strains	tetA	tetB	tetC	tetG	ermA	ermB	ermC	floR	strB	blaSHV	blaOXA	blaTEM	qnrA	gyrA
Italian	0	21.25	13.75	23.75	0	1.25	22.5	0	1.25	0	1.25	2.5	1.25	12.5
Turkish	0	0	0	1.25	0	3.75	0	1.25	18.75	6.25	0	1.25	3.75	1.25
Spanish	2.5	0	18.75	0	2.5	0	1.25	0	3.75	0	3.75	0	5	0
Greek	1.25	0	25	8.75	0	2.5	0	1.25	1.25	0	3.75	3.75	3.75	1.25
Total	3.75	21.25	57.5	33.75	2.5	7.5	23.75	2.5	25	6.25	8.75	7.5	12.5	15

MAR Index

- $MAR = a/b$
- $MAR > 0.2$ high risk of contamination

