

Mechanisms of Cell Envelope Defense Against Antibiotics in Gram-positive

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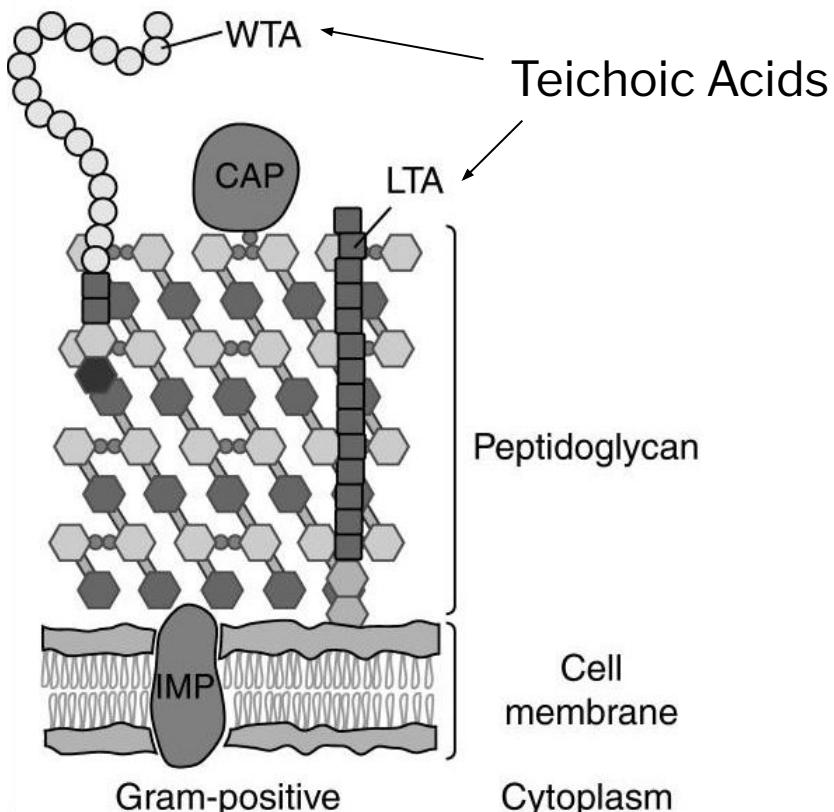
Disclosures

- Research support: Merck (ceftolozane-tazobactam), Entasis (sulbactam-durlobactam)
- Other: UpToDate (Enterococcal infections)

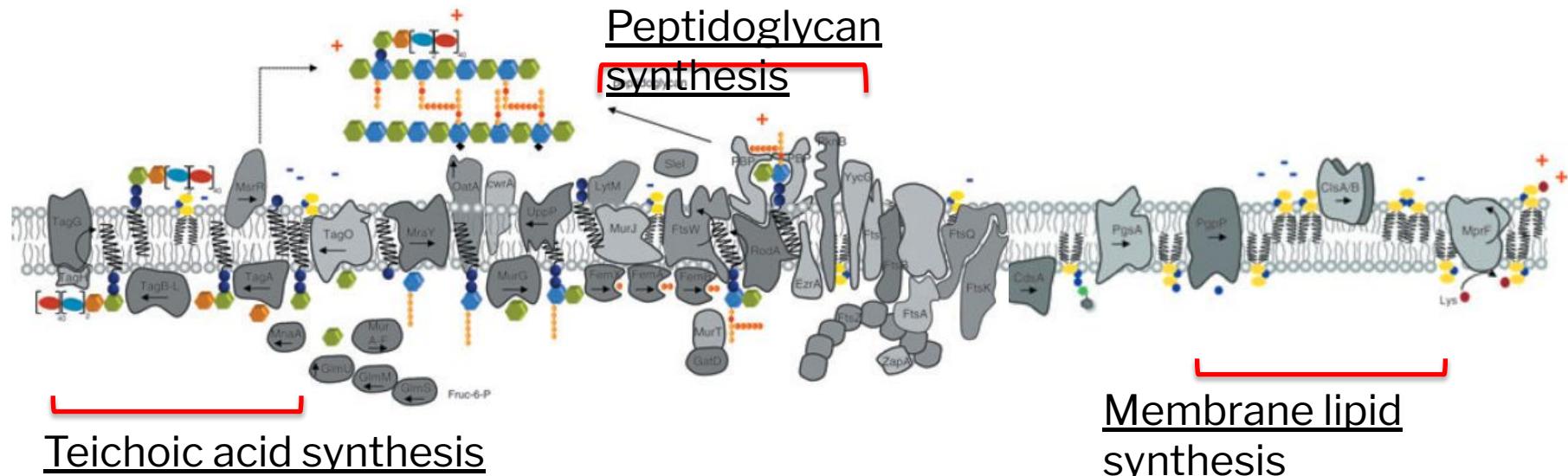
Overview

- Brief review of cell envelope synthesis
- Pathways of bacterial cell envelope defense in Gram-positive organisms
- Adaptation to cell envelope stress, a case study in *Enterococcus faecalis*

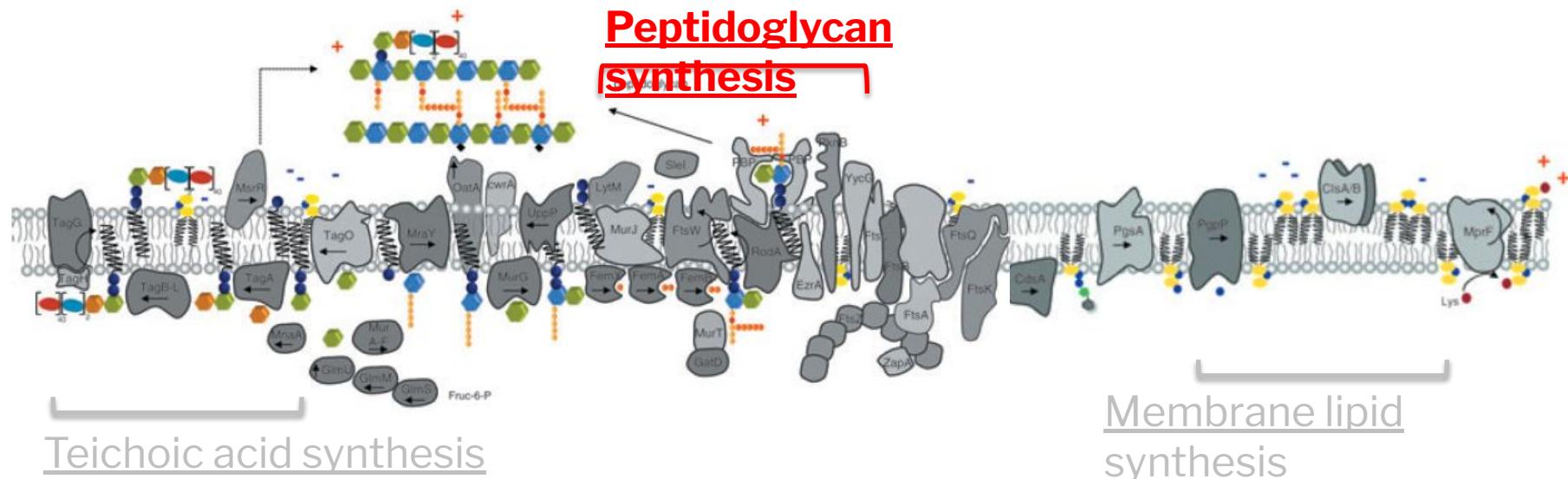
Gram-positive cell envelope



Cell envelope synthesis



Cell envelope synthesis

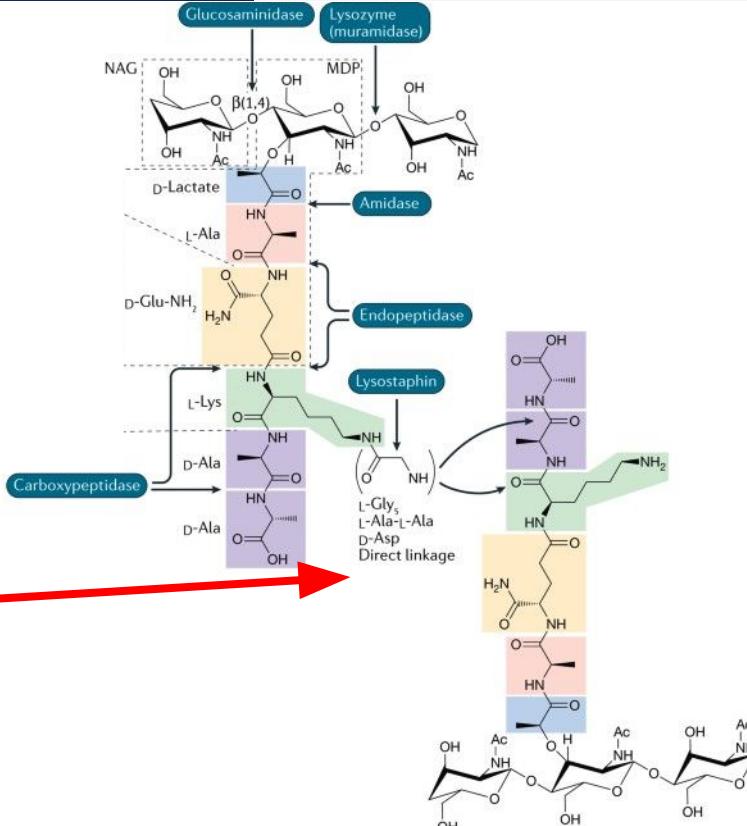


Peptidoglycan

- Polymer of N-acetylglucosamine (NAG) and N-acetylmuramic acid (NAM), with an oligopeptide chain attached to NAM
- Peptide chain serves as substrate for cross-linking

Crosslink:

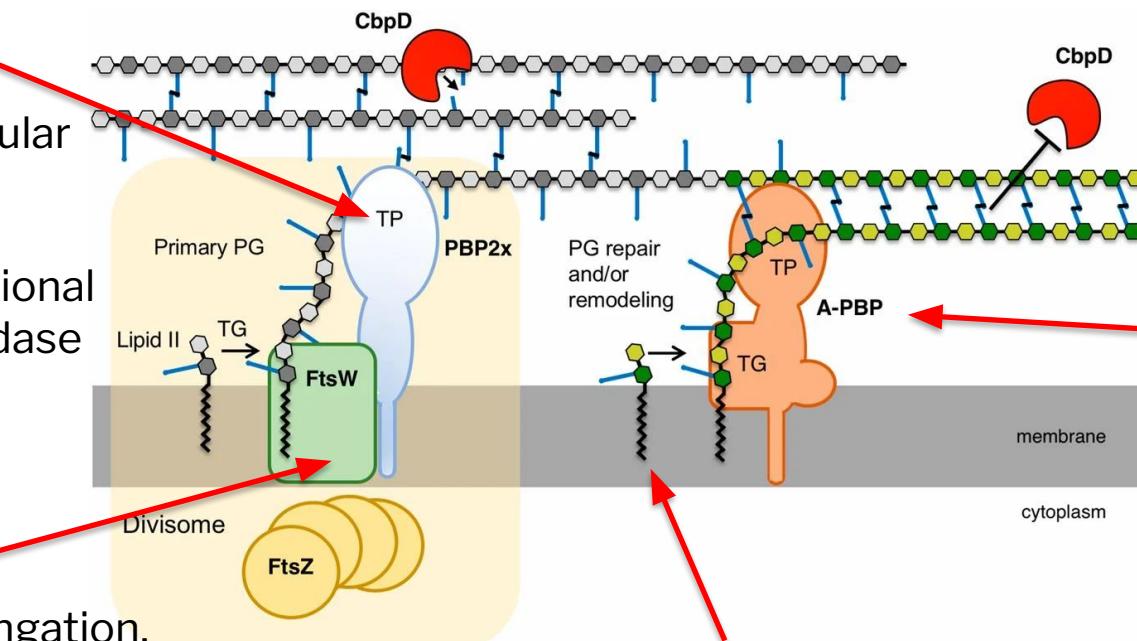
S. aureus – L-Gly₅
E. faecalis – L-Ala-L-Ala
E. faecium – D-Asp



Peptidoglycan synthesis

Class B PBP

- Low molecular weight
- Monofunctional transpeptidase activity



SEDS

- shape, elongation, division and sporulation
- Partner transglycosylase

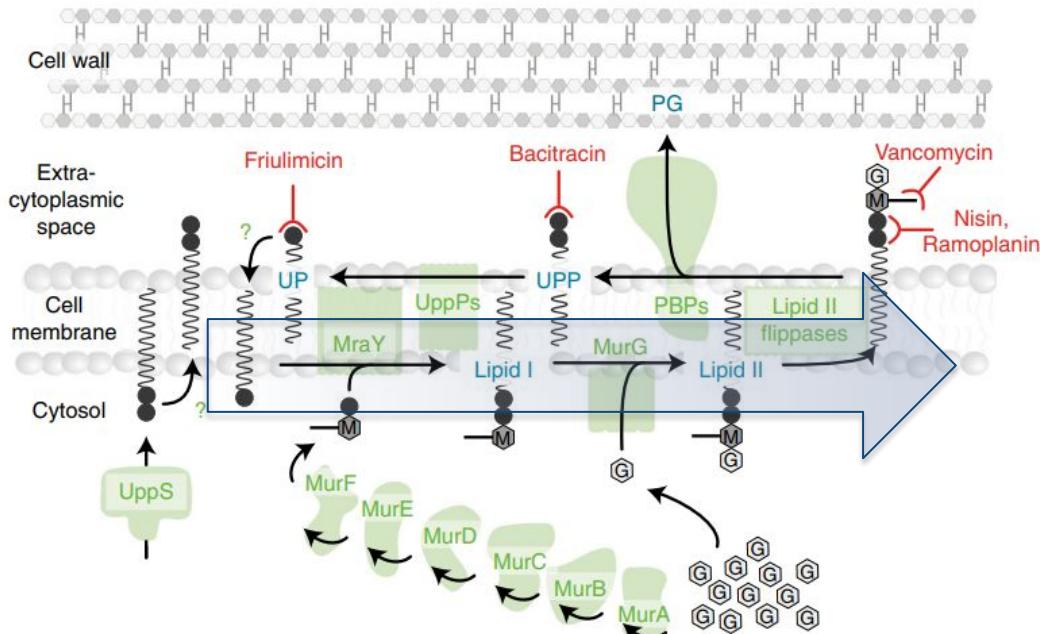
Nature. 2016 Sep 29; 537(7622): 634–638.
Proc Natl Acad Sci U S A. 2020 Mar
17; 117(11): 6162–6169.

Class A PBP

- High molecular weight
- Bifunctional enzyme – transglycosylase and transpeptidase activity

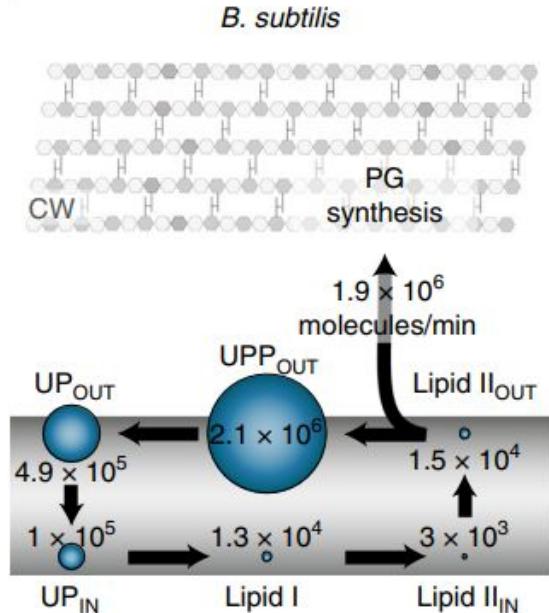
Lipid II (and its intermediates) are critical to cell wall synthesis

The cell wall supply chain



Passage of lipid intermediates is driven by a substrate affinity gradient

Nat Commun. 2019 Jun 21;10(1):2733.
Nat Commun. 2022 Apr 27;13(1):2278.

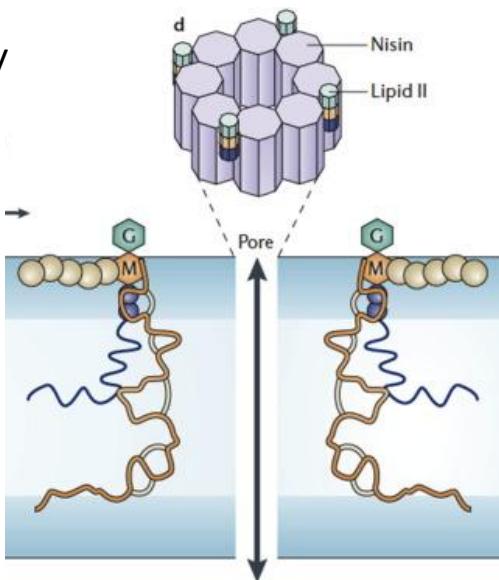


Antimicrobials targeting Lipid II flux

Nisin

Binding affinity
 $K_D - 0.015 \mu M$

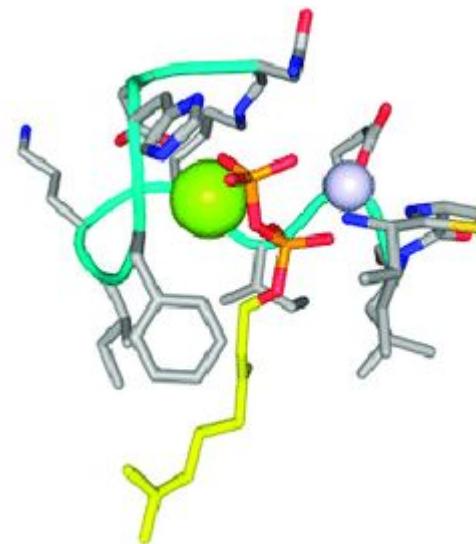
Effective concentration
 $\sim 1 \mu M$



Bacitracin

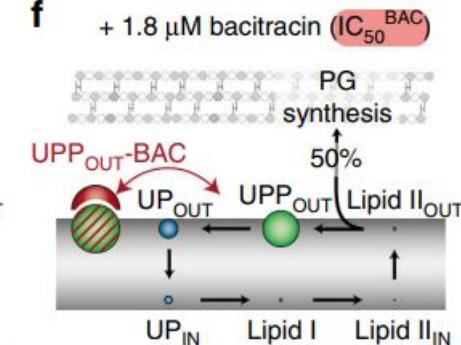
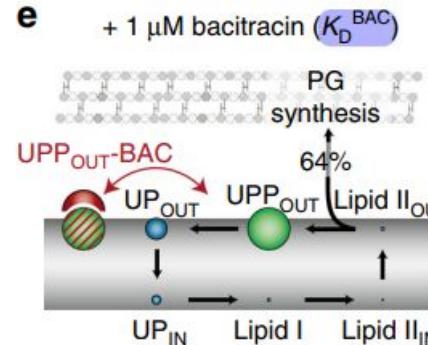
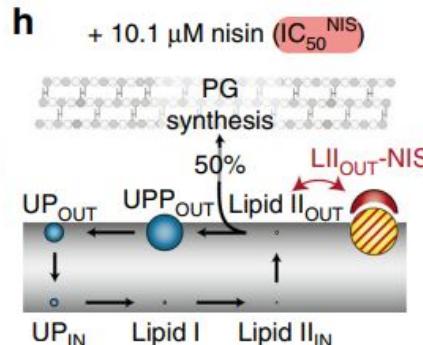
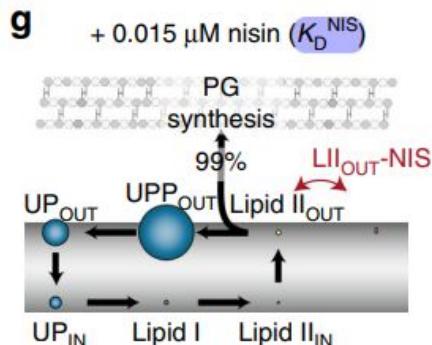
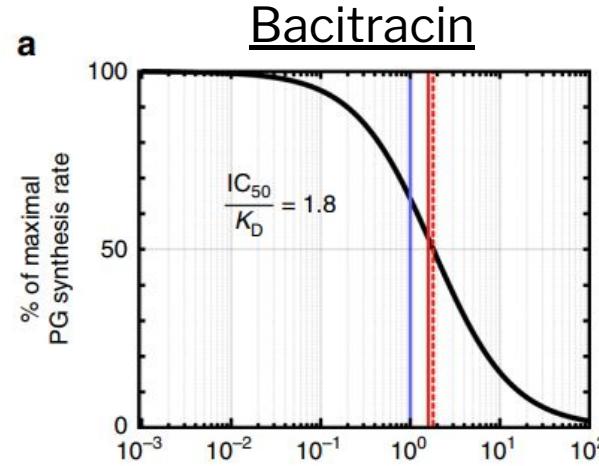
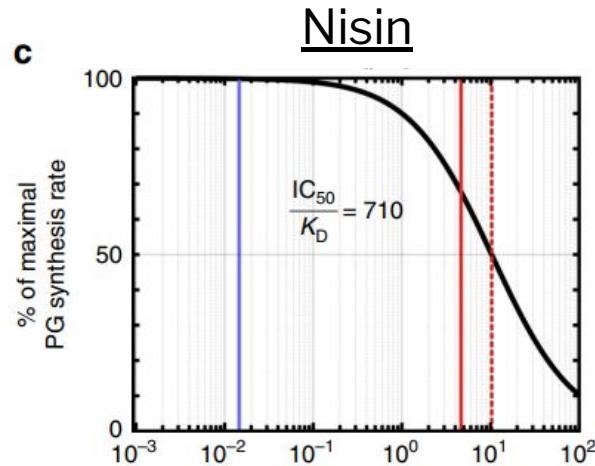
Binding affinity
 $K_D - 1 \mu M$

Effective concentration
 $\sim 1.8 \mu M$

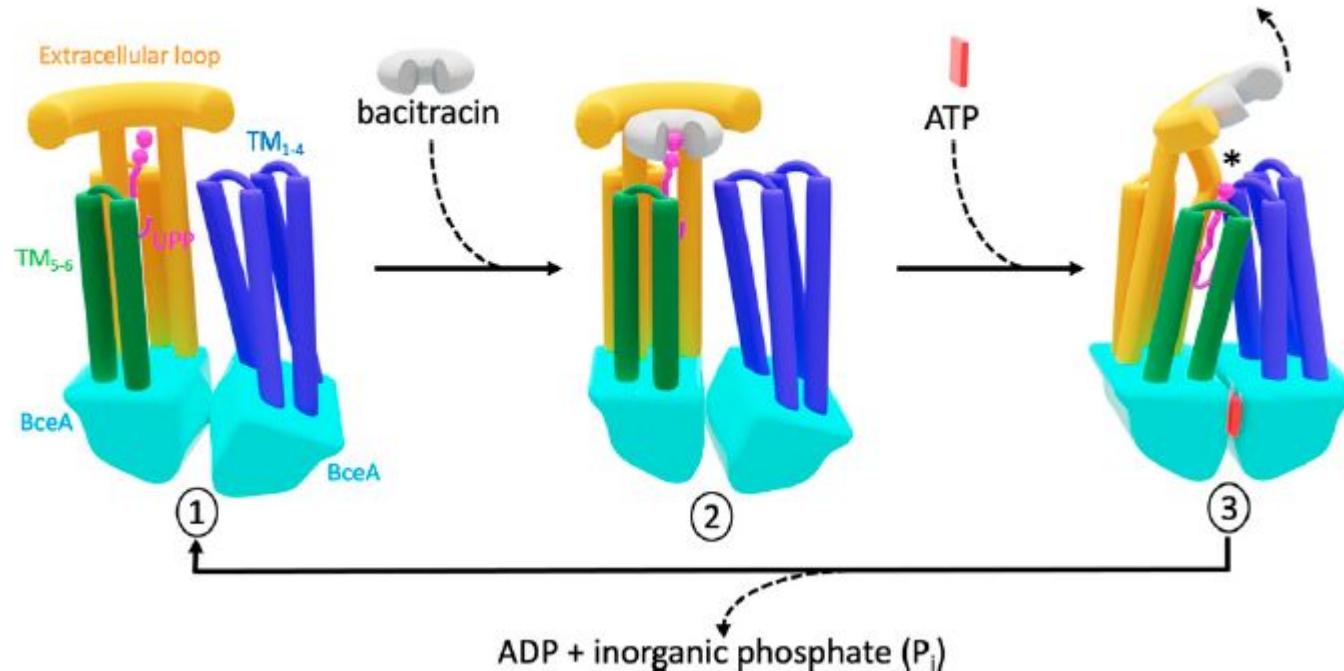


What accounts for the difference?

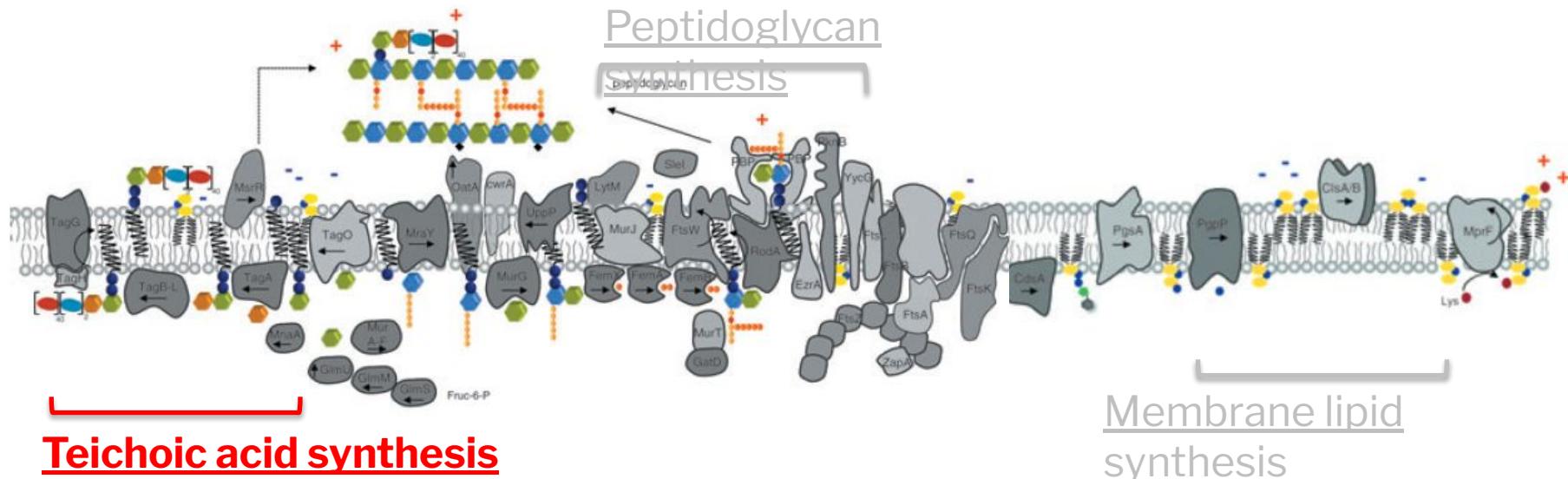
Lipid II cycling explains differential activity of antibiotics



Resistance to Bacitracin mediated by target protection



Cell envelope synthesis

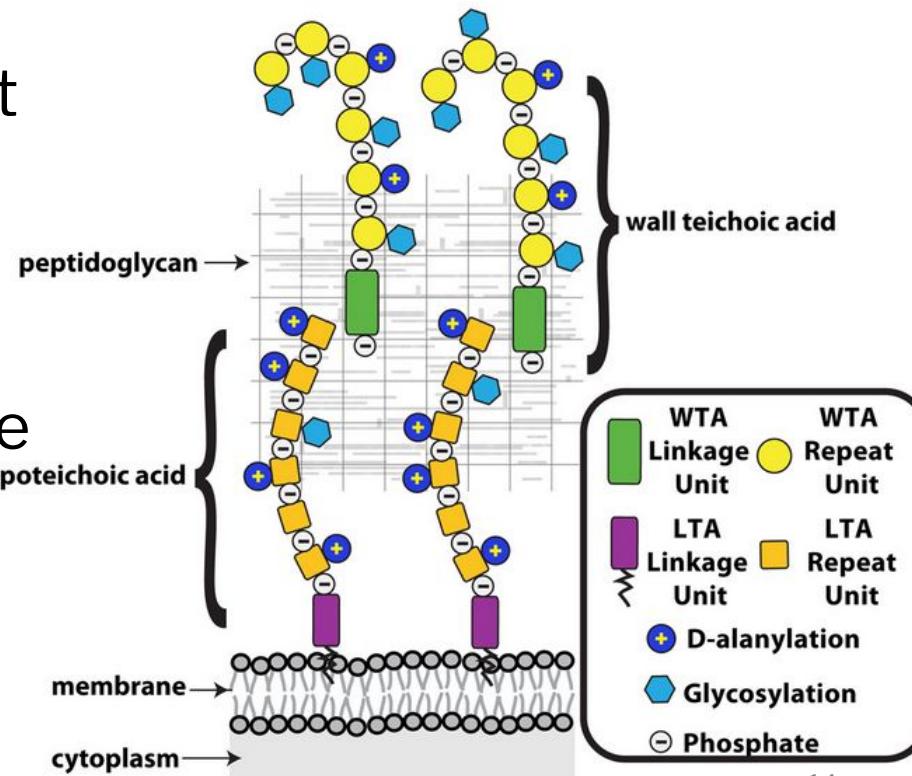


Teichoic Acids (TA)

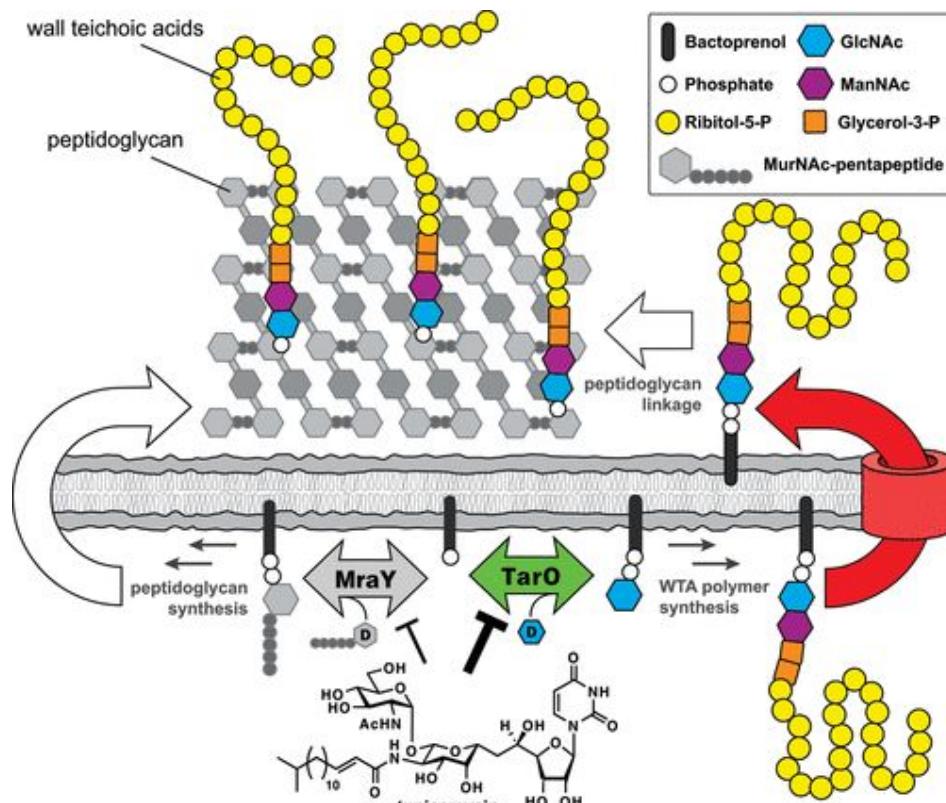
- Teichoic acids are glycopolymers present in most Gram-positive cell envelopes.

- Lipoteichoic acids (LTA) are anchored to the cell membrane

- Wall teichoic acids (WTA) are bound to the peptidoglycan matrix

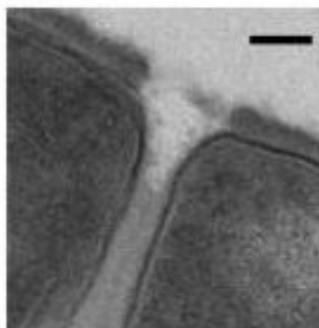
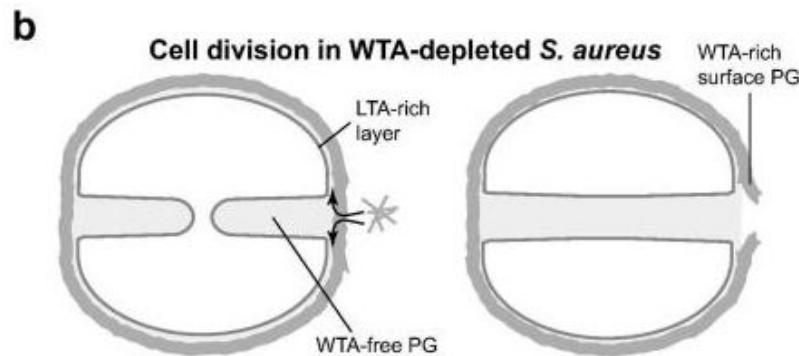
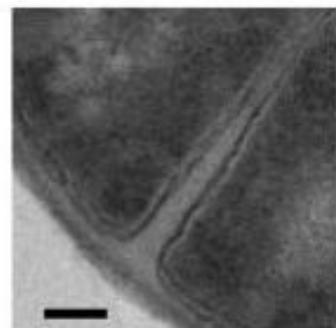
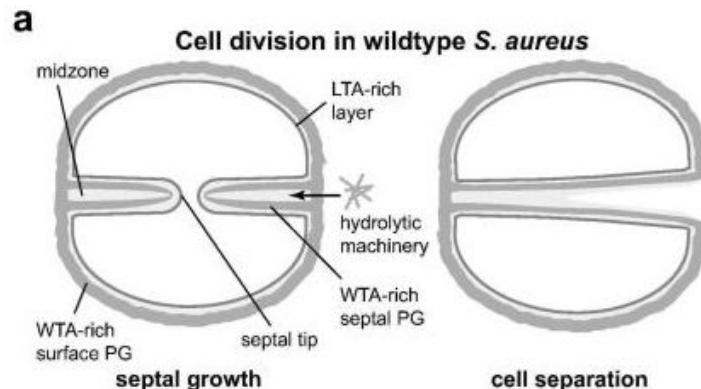


Wall teichoic acid synthesis

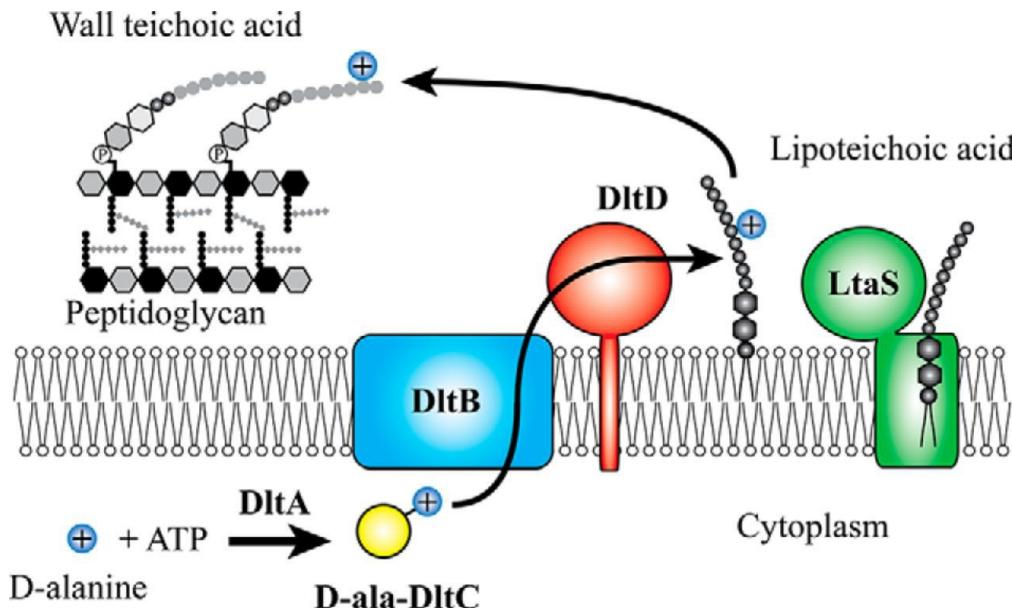


- TA synthesis shares the undecaprenyl pool with PG biosynthesis
- In *S. aureus*, WTA has been implicated in the cooperative action of PBP2 and PBP4
- Disrupting WTA synthesis leads to increased sensitivity to β -lactams which target PBP2

WTA regulate PG autolysis

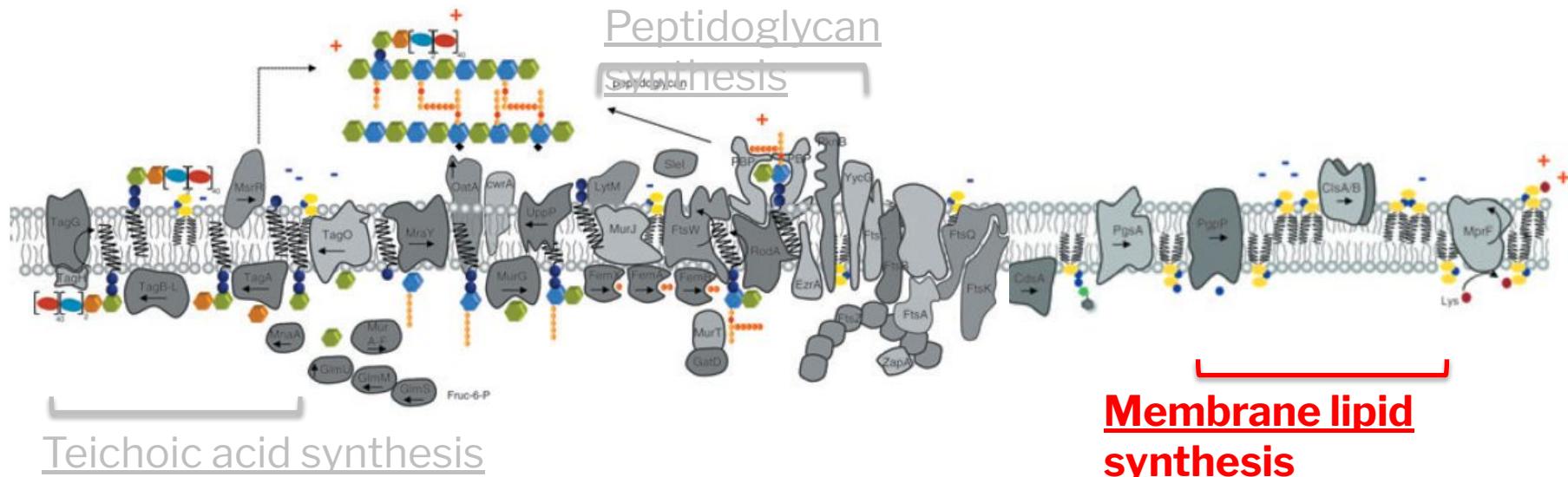


Teichoic Acids as reservoirs of positive charge

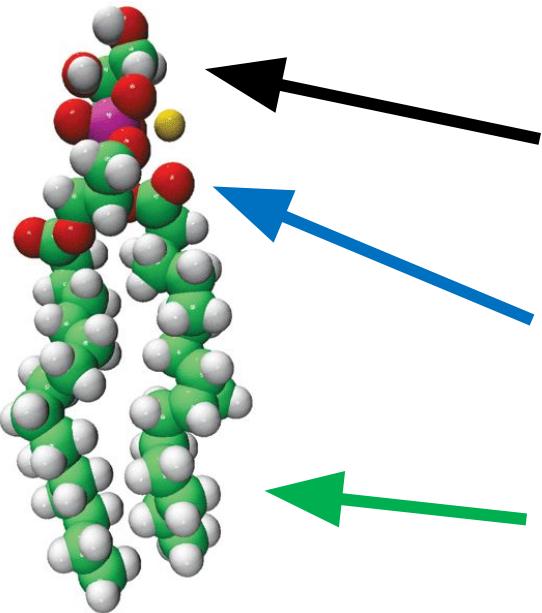


- D-alanylation of LTA occurs via pathway encoded by *dlt* operon
- This modulates the activity of PG hydrolases/amidases in the cell wall.
- WTA also functions in the pathway to resistance antimicrobial peptides and antibiotics active at the cell envelope.

Cell envelope synthesis



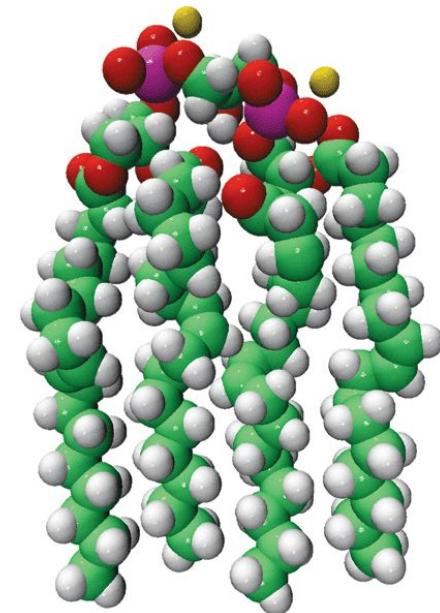
Membrane lipids



Phosphatidylglycerol
(PG)

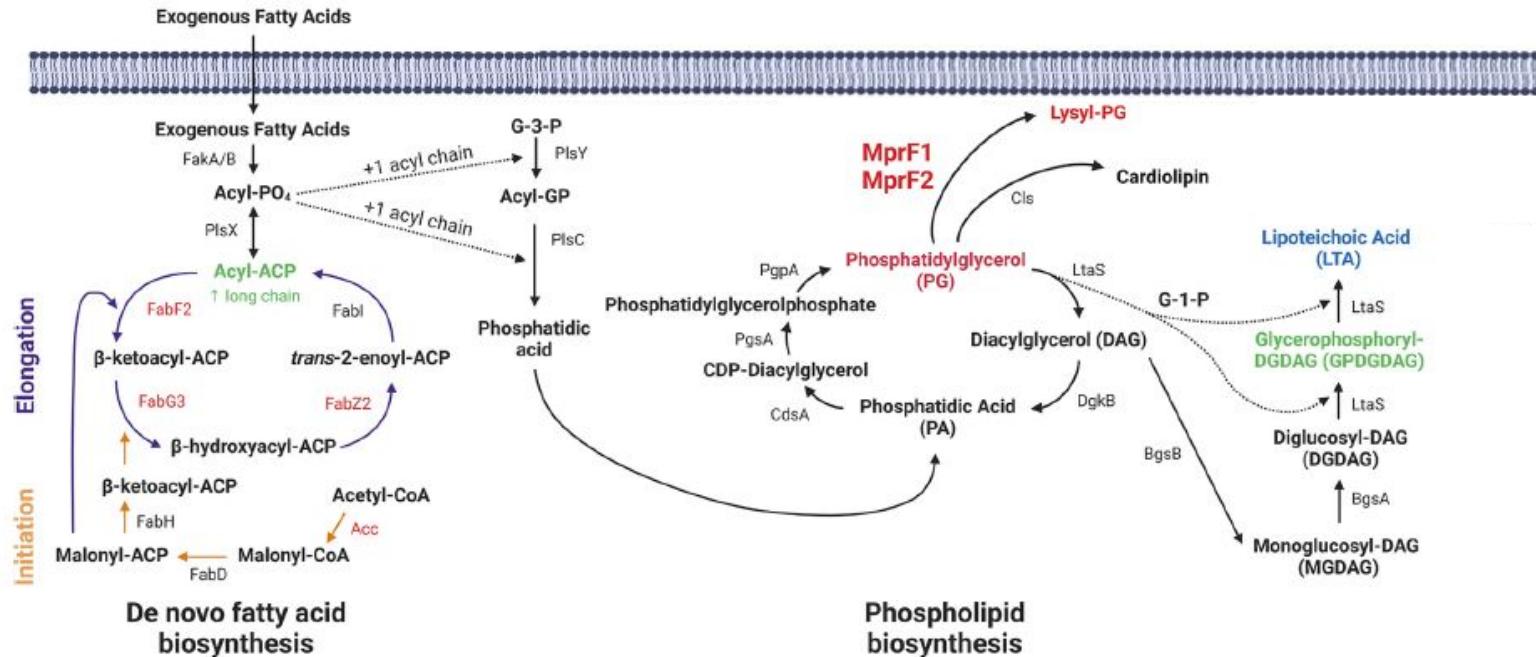
Polar head group
Glycerol

Fatty acid tail

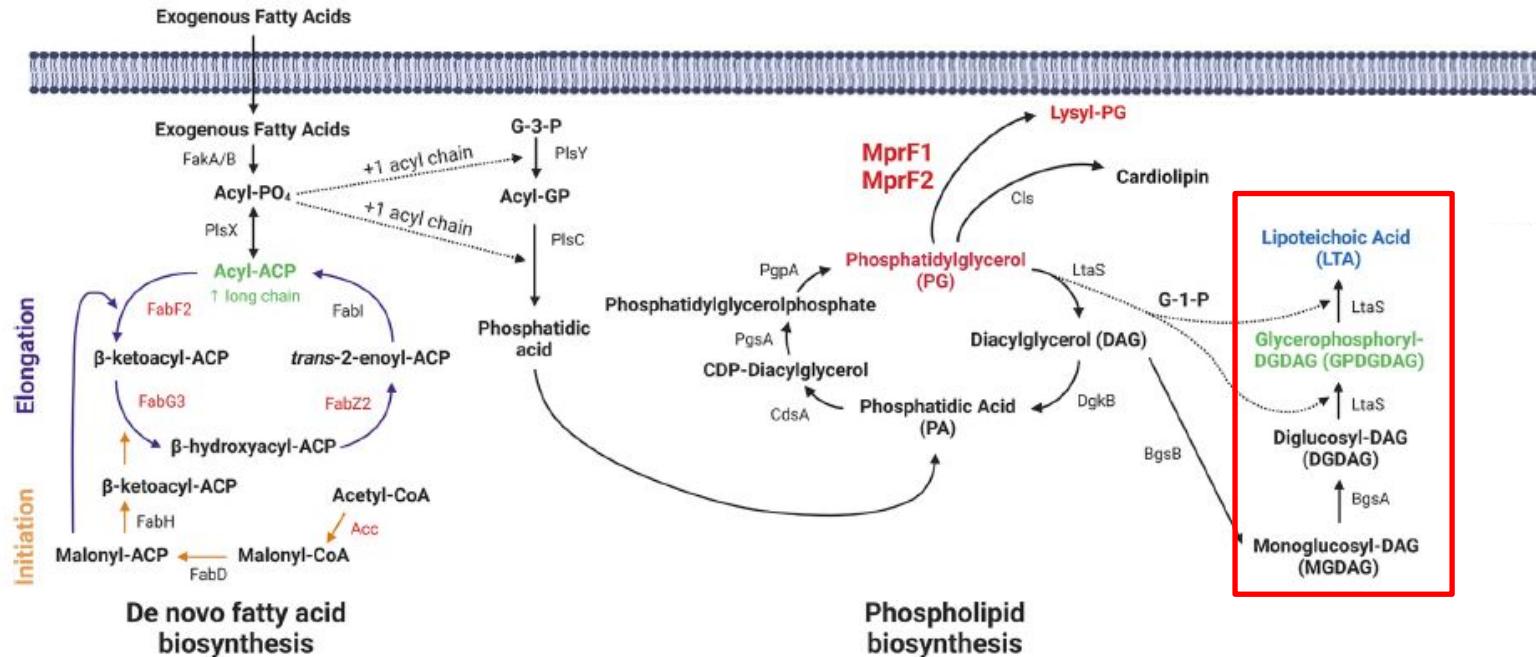


Cardiolipin
(CL)

Phospholipid synthesis

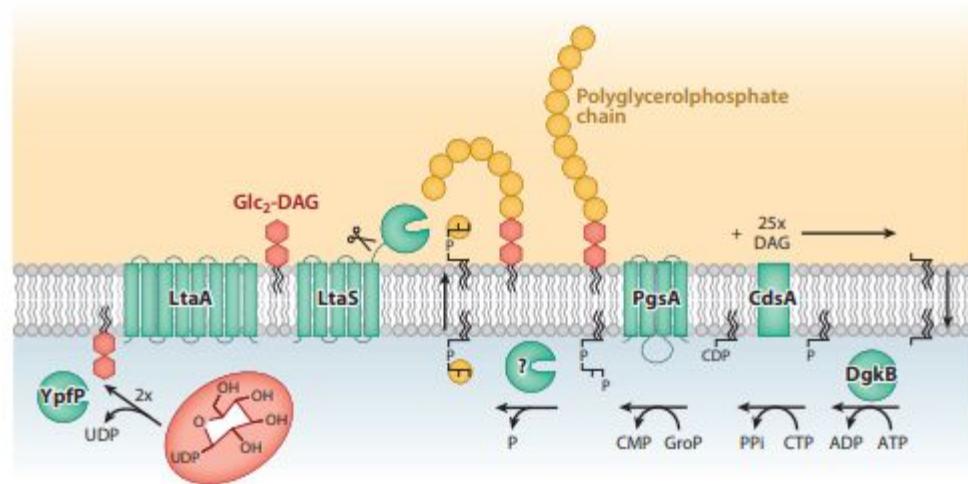


Phospholipid synthesis

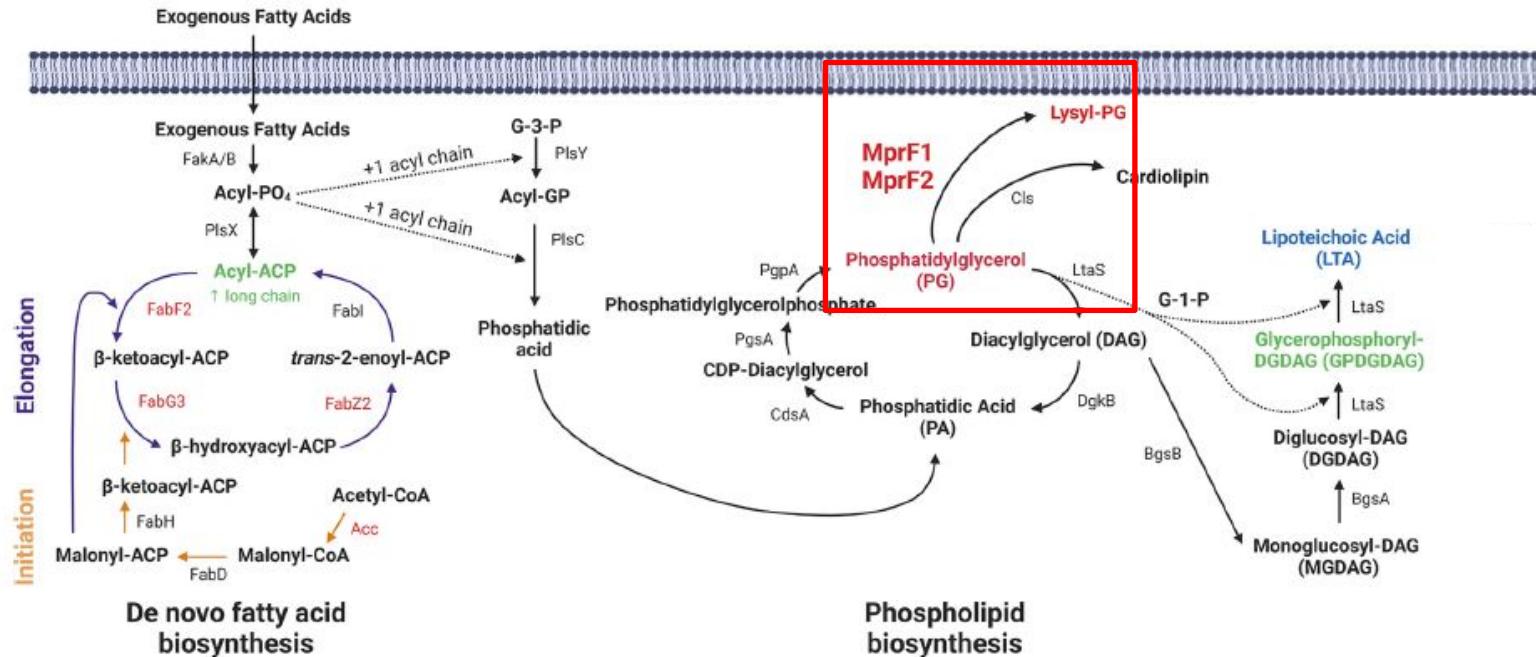


Lipoteichoic acid synthesis

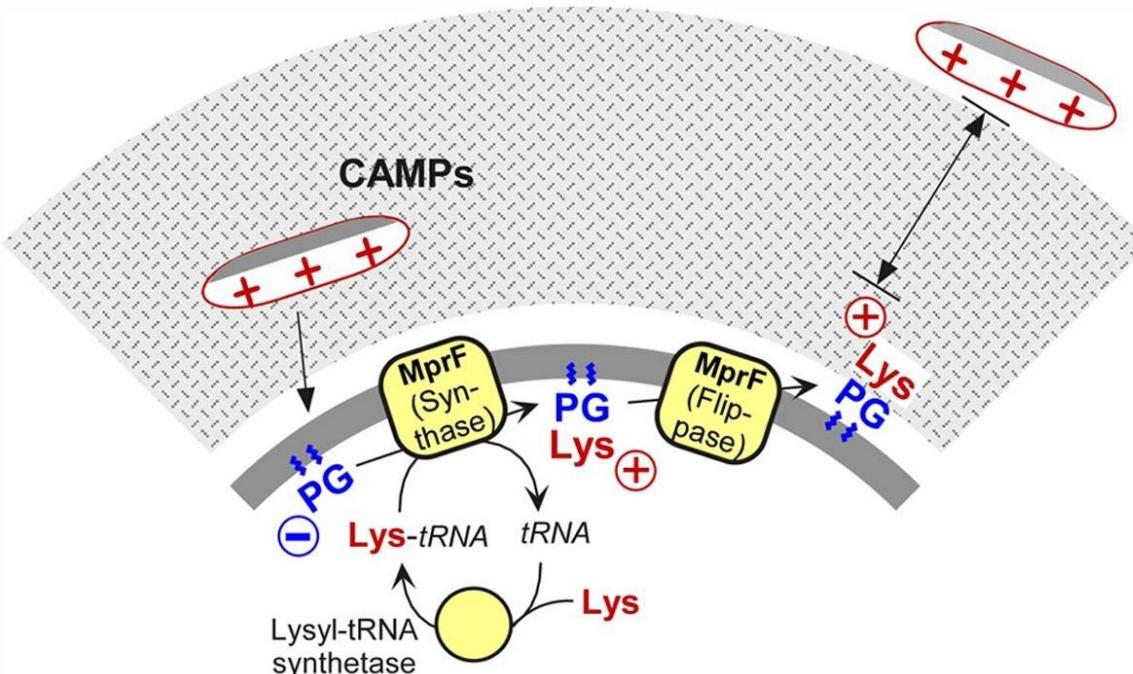
- Closely linked to lipid biosynthesis
- Each elongation with glycerolphosphate consumes one phosphatidylglycerol(PG) molecule
- Estimated that *S. aureus* will turn over the entire PG pool twice to support LTA synthesis each generation



Phospholipid synthesis

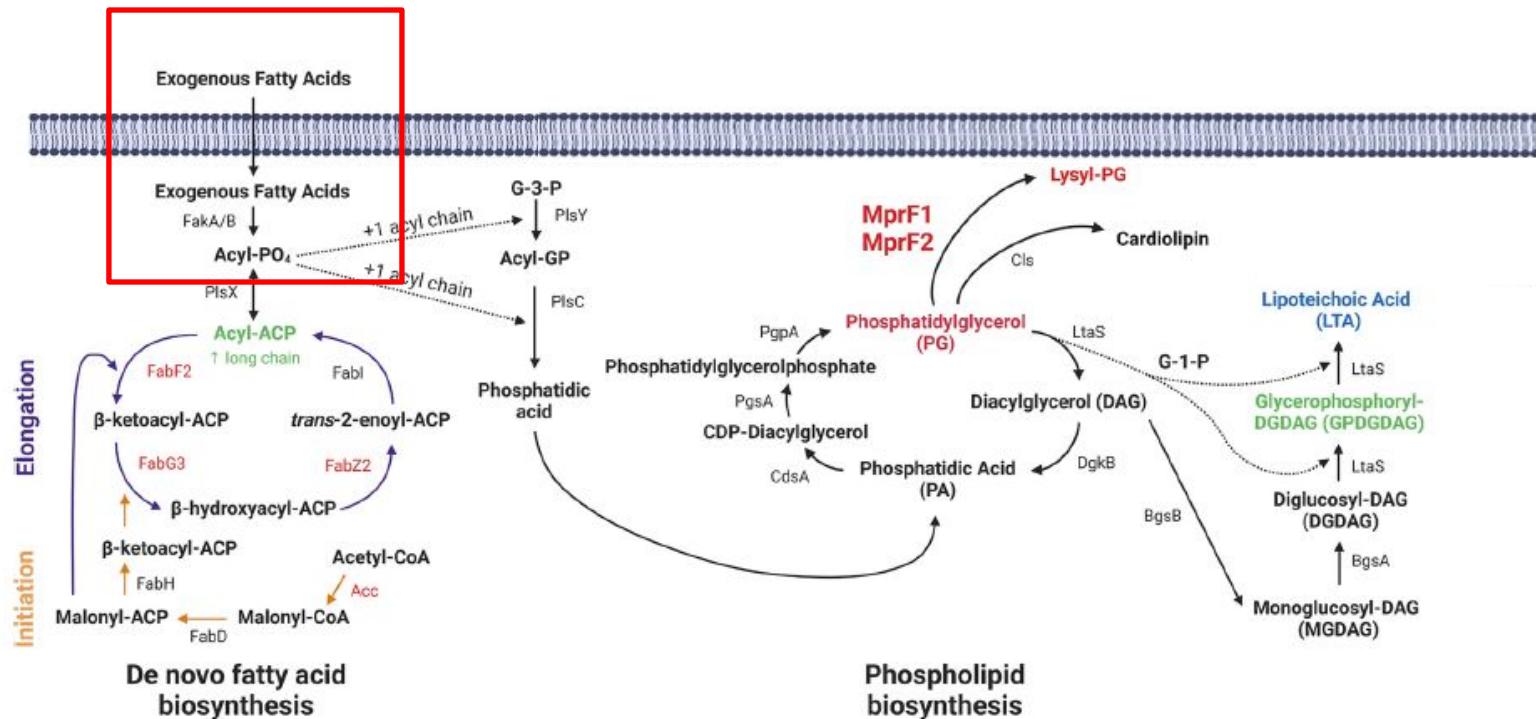


MprF and the repulsion hypothesis

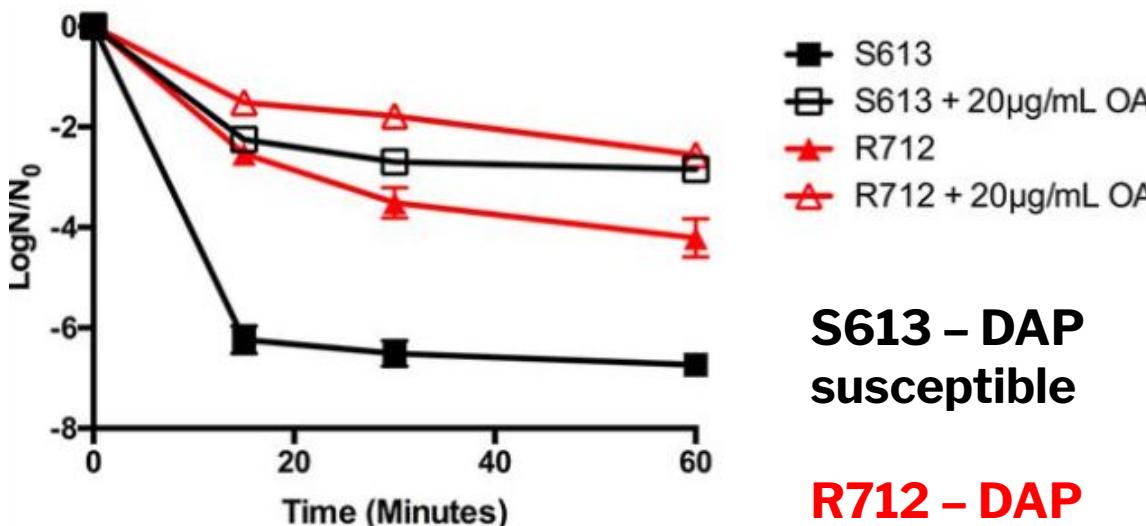


- MprF – Multiple peptide resistance factor
- Catalyzes transfer of lysine from Lys-tRNA to phosphatidylglycerol
- Alters cell surface charge and masks anionic phosphatidylglycerol
- Can change membrane composition and fluidity₄

Phospholipid synthesis



Exogenous fatty acids protect against membrane stress



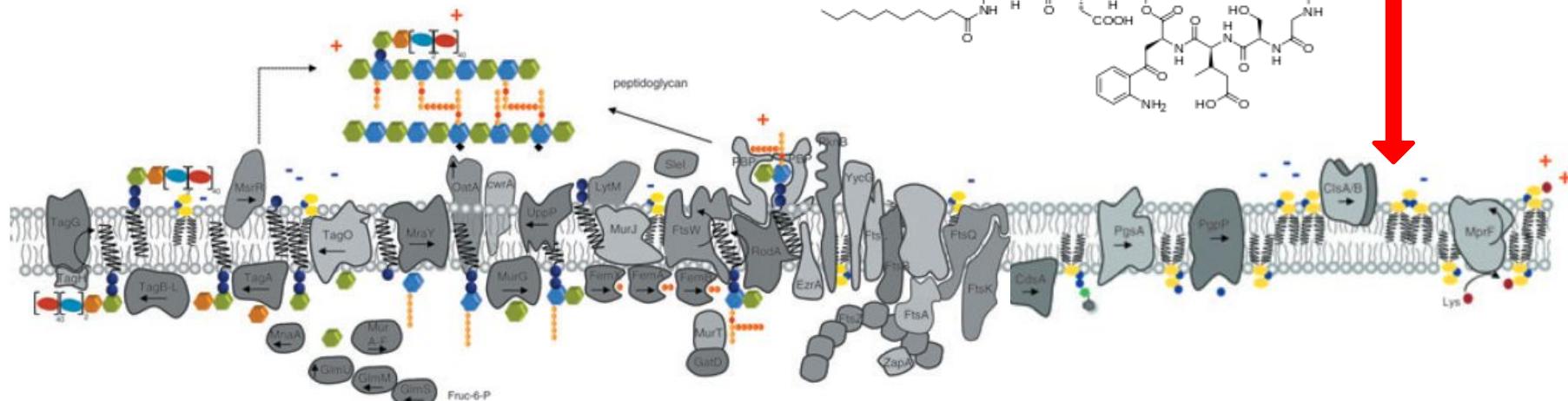
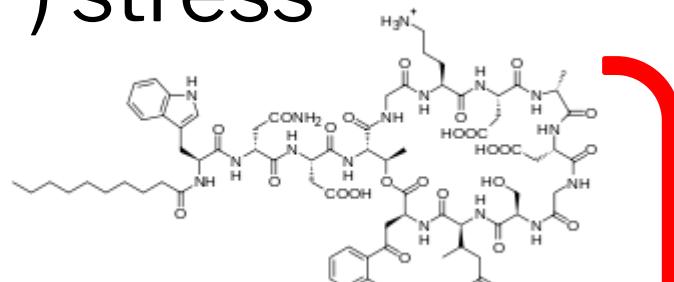
**S613 – DAP
susceptible**

**R712 – DAP
resistant**

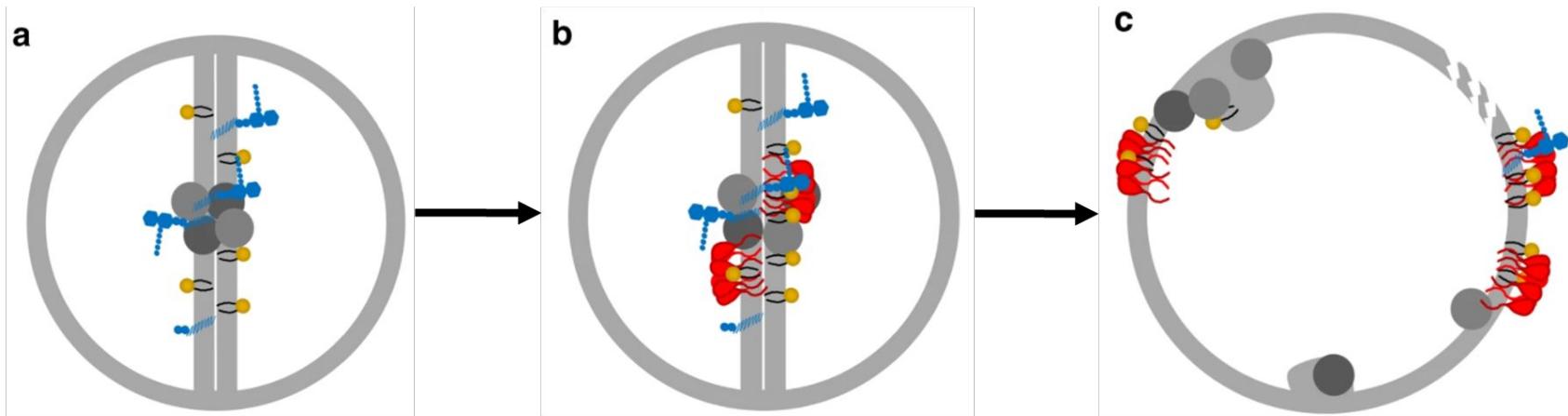
- Decreased killing with daptomycin seen with oleic acid ($C_{18:1\ cis-9}$) and linoleic acid ($C_{18:2\ cis-9,12}$)
- These lipids are derived from eukaryotic cells
- Supplementation with exogenous fatty acids altered membrane lipid acyl chains

Case Study

E. faecalis Cell envelope adaptation to daptomycin (DAP) stress



Daptomycin – mechanism of action



Septal synthesis



Bactoprenyl-coupled
lipid intermediates



PG



Ca²⁺ -DAP

**DAP binding at
septum**

**Enzyme delocalization
and loss of cell
envelope integrity**

Pathways linked to DAP-R in enterococci

Two Component Signaling Systems

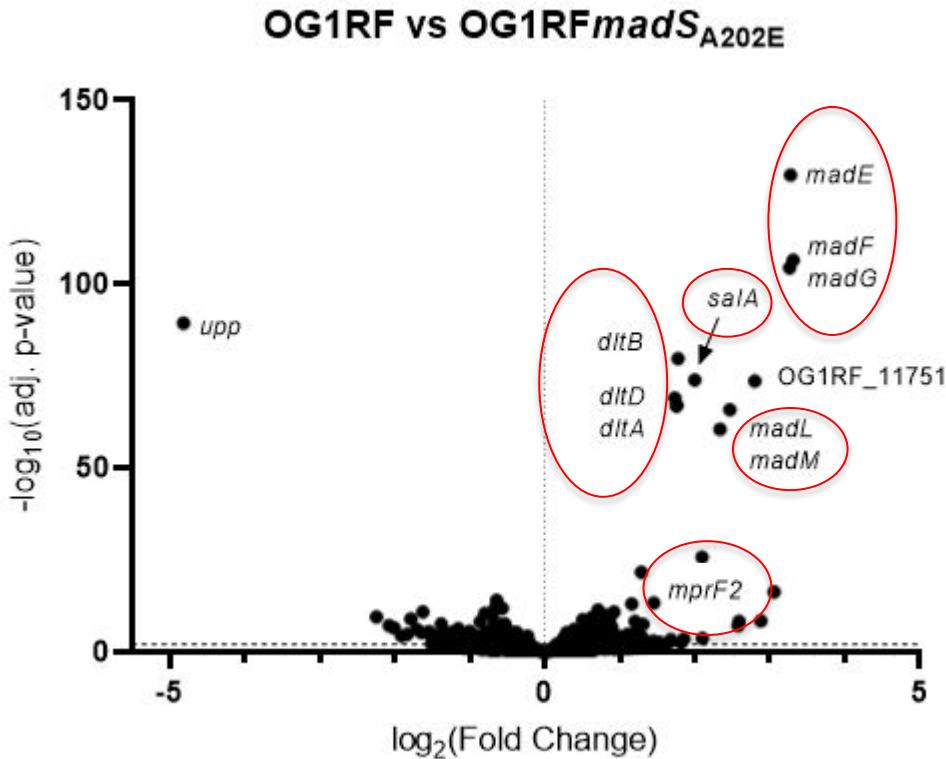
- LiaFSR
- YycFG (WalKR)

- YxdJK/YxdLM/YvcRS (MadRS)

Lipid metabolism

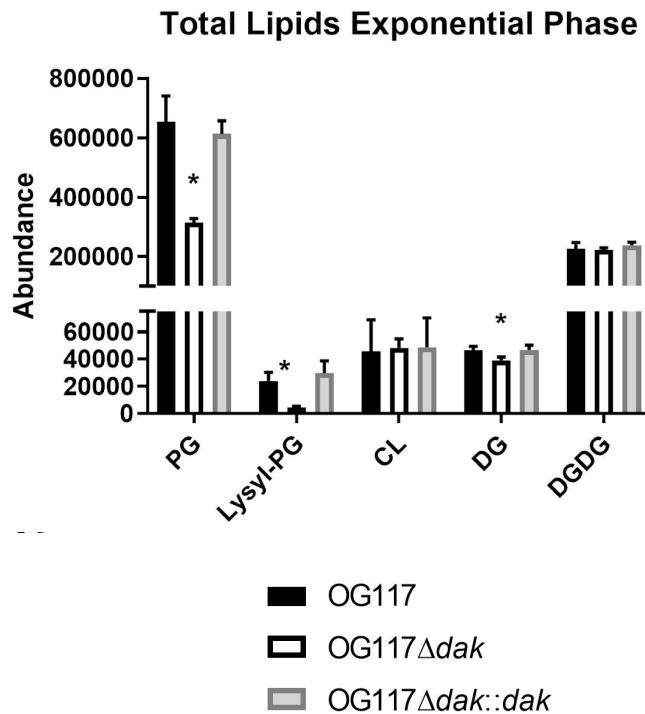
- Cardiolipin Synthase (ClS)
- GdpD (glycerophosphoryldiester phosphodiesterase)
- Cfa (cyclopropane fatty acid synthase)
- Dak (fatty acid kinase)

Activation of MadRS regulon



- Ala->Glu at position 202 leads to activation of MadS histidine kinase
- Upregulation of genes:
 - Target protection UPP
 - Target protection against antimicrobial peptides
 - D-ala of LTA
 - Lys-PG MprF
 - Peptidoglycan hydrolase

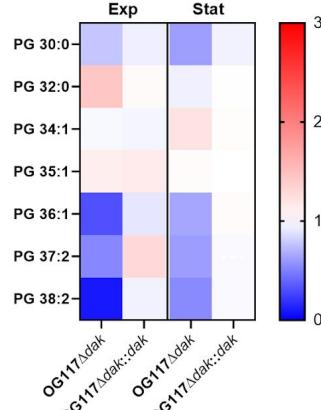
Loss of Dak is associated with alterations in membrane lipids



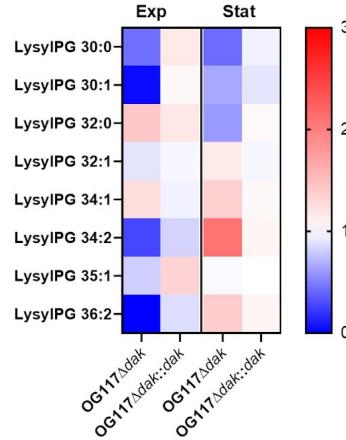
- Decreased levels of phosphatidylglycerol during exponential growth
- Decreased growth rate
- Increased membrane rigidity

Fatty acid profile in Dak mutant

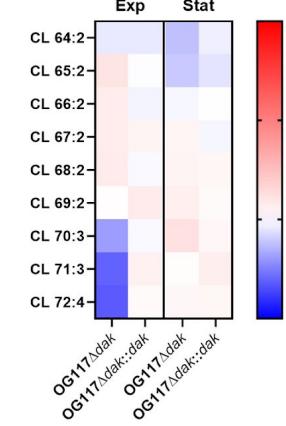
PG



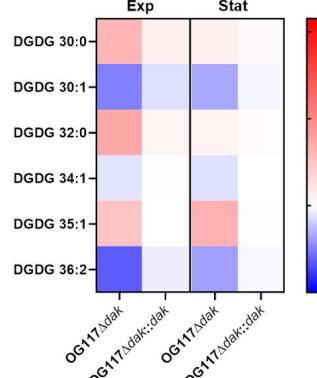
**LP
G**



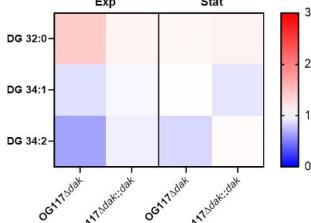
CL



**DGD
G**



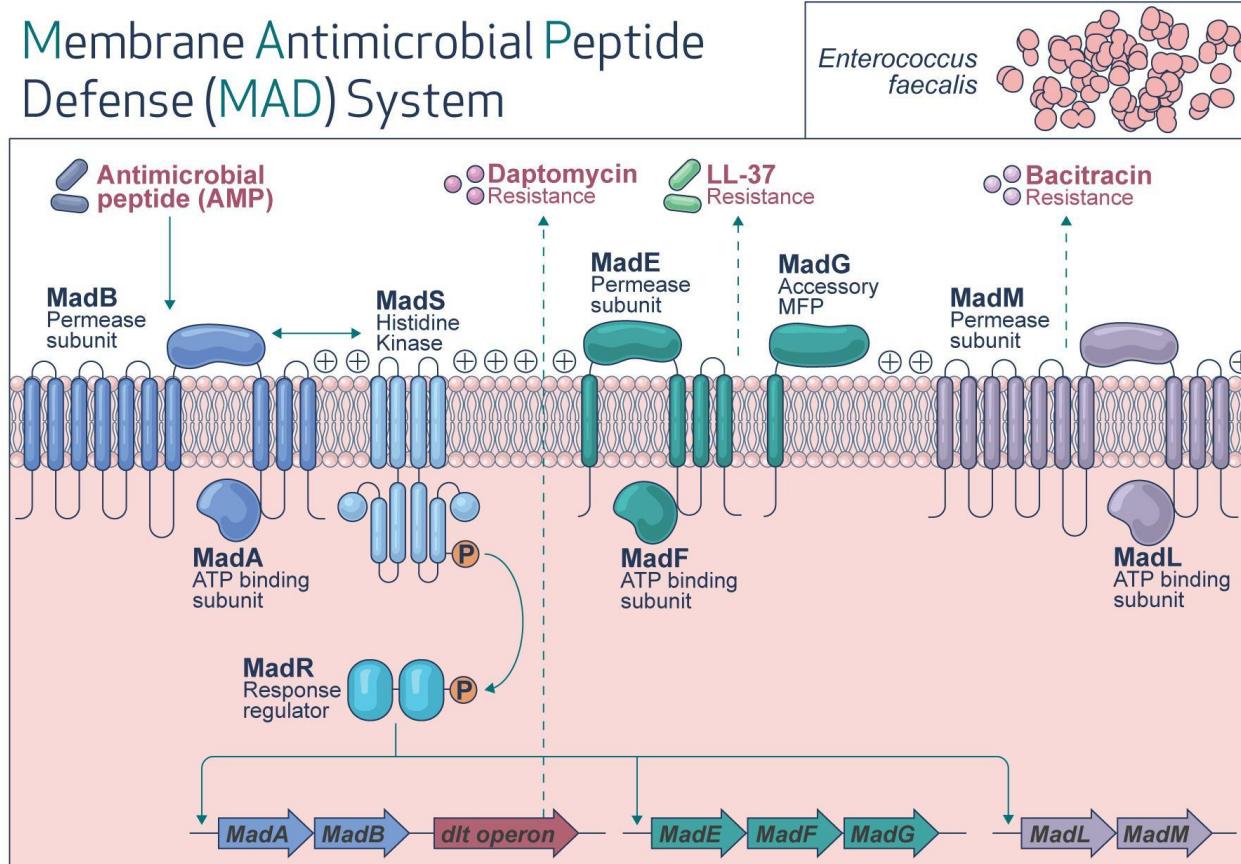
DG



Loss of *dak* is associated with decrease in unsaturated long chain fatty acids

MadRS System

Membrane Antimicrobial Peptide Defense (MAD) System



Summary

- The Gram-positive bacterial cell envelope is a complex, interwoven machine
- Bacteria possess a variety of stress response systems to respond to antibiotics and environmental stressors
- A potent resistance phenotype can emerge via activation of one or more of these pathways

Acknowledgements



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Questions?

