

Emerging themes in bacterial cell-cell communication networks

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Recognition and Communication in the Unicellular Bacterial World

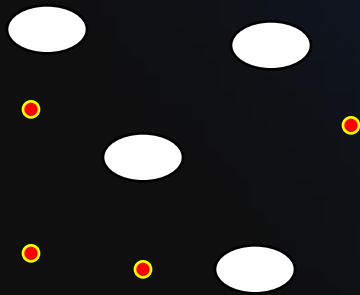
- **Sexual Exchange – Conjugation**
- **Protecting Your Niche**
- **Combating Host Defences**
- **Population Migration**



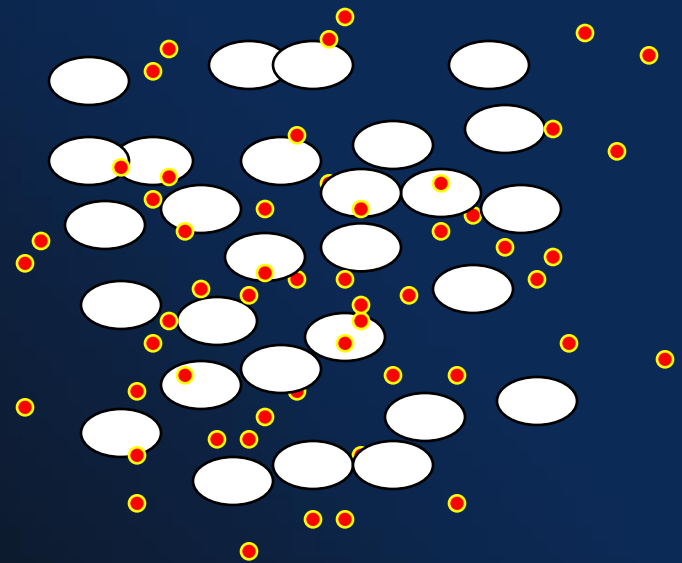
Bacteria Communication: Quorum Sensing

Cell-to-cell communication via
a diffusible signal molecule

Low Population Density



High Population Density

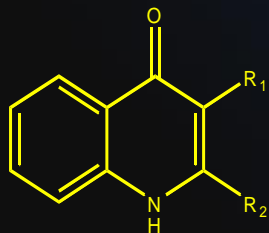
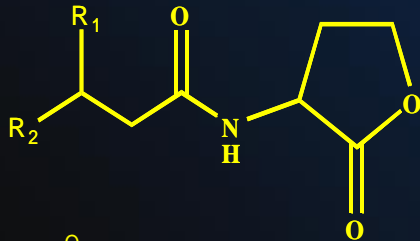


- phenotypic change



QS Signal Molecules are Chemically Diverse

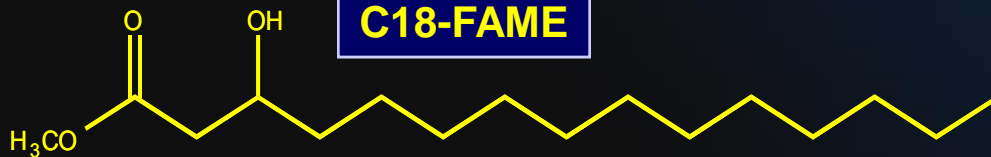
N-Acylhomoserine Lactones (AHLs)



2-Alkyl-4-Quinolones

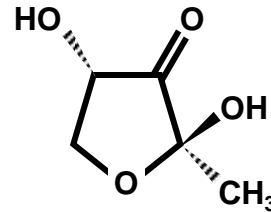


DSF

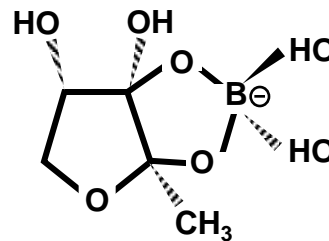


C18-FAME

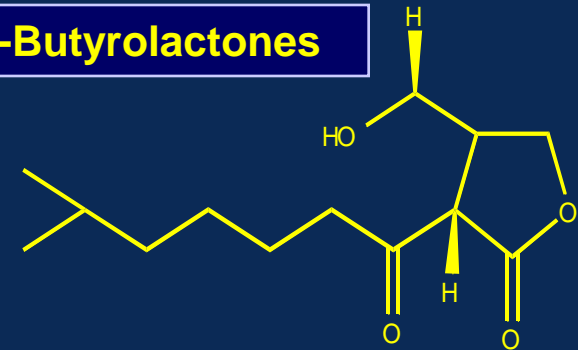
Gram-negative



AI-2?



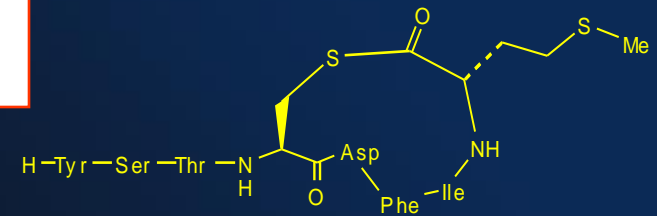
γ -Butyrolactones



Linear Peptides

$^2\text{HN-EMRLSKFFRDFILQRKK-COOH}$

CSP-1

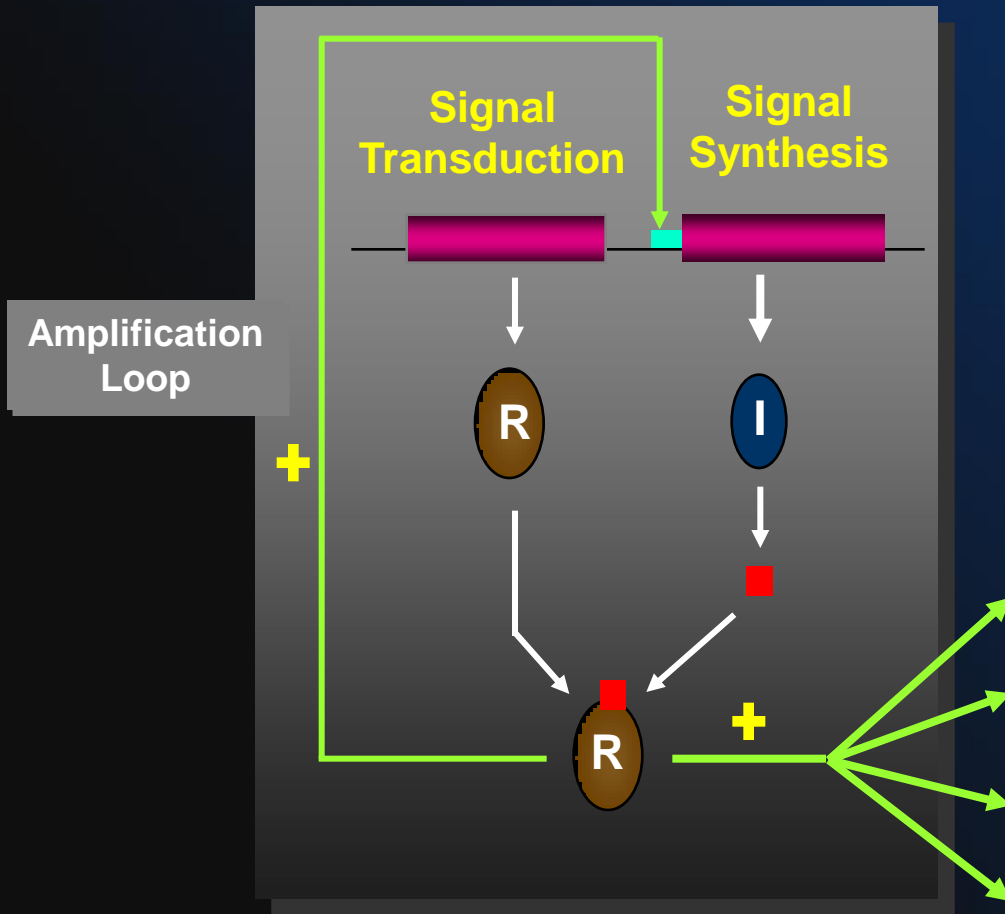


Cyclic Peptides

Gram-positive



Quorum Sensing Regulatory Circuits



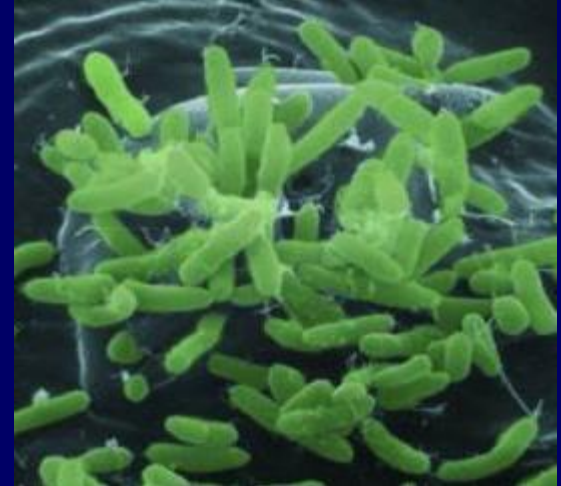
Multiple Gene Expression

- Virulence
- Secondary Metabolites
- Motility and Swarming
- Conjugation
- Biofilm Development
- Growth Inhibition

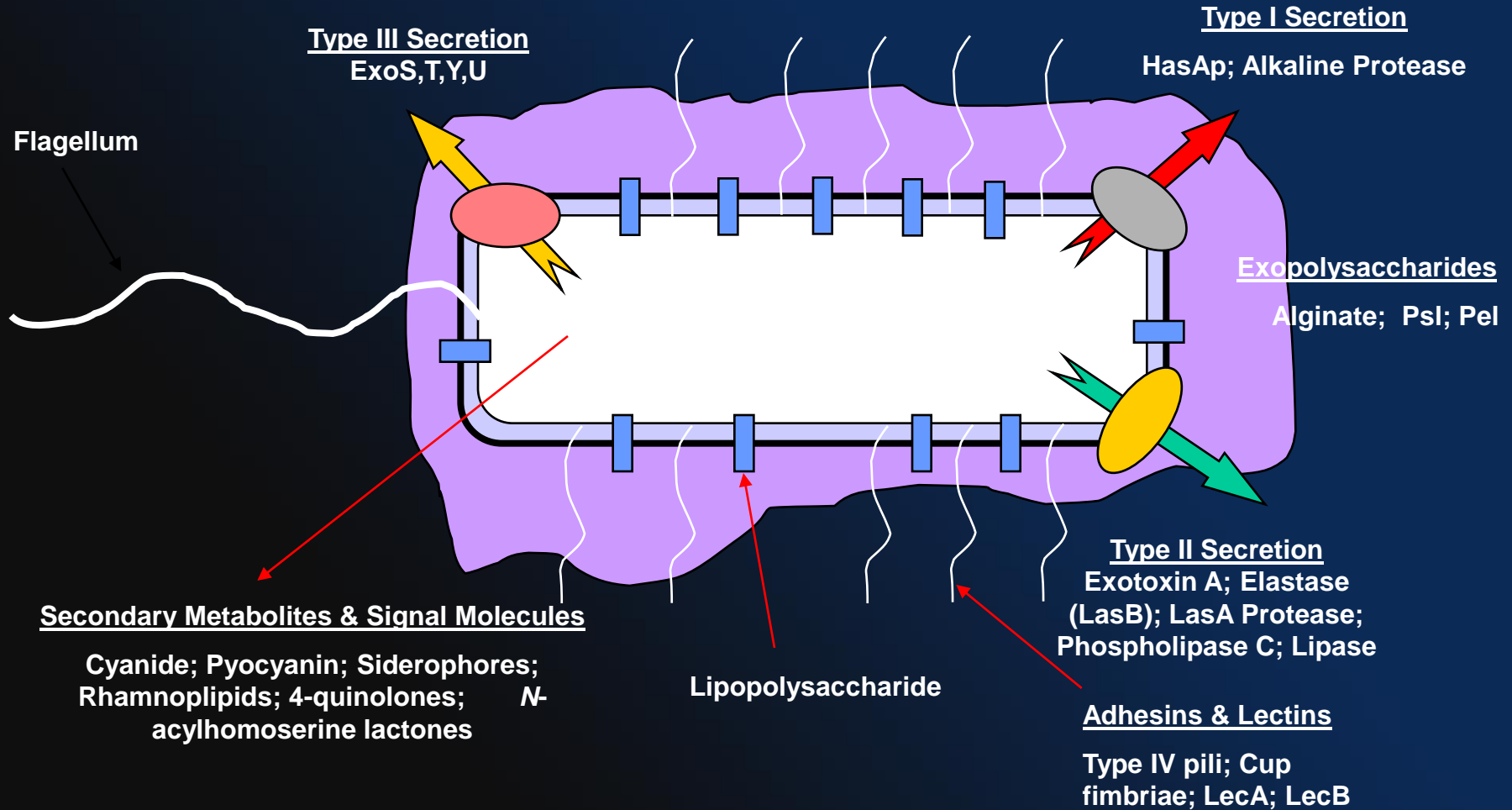


The Lifestyle of *Pseudomonas aeruginosa*

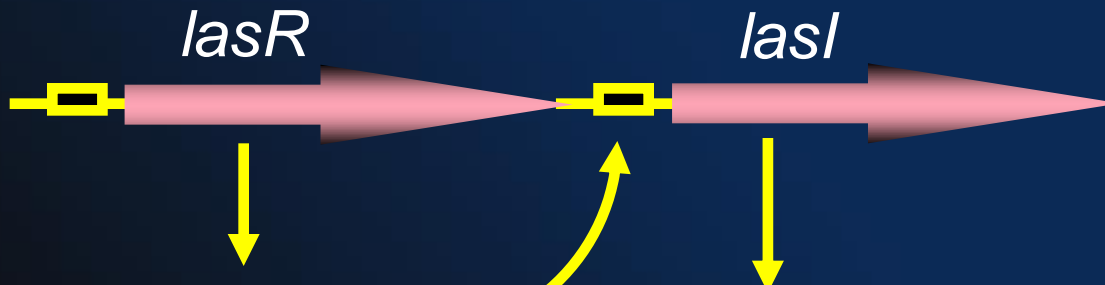
- Gram-negative - Ubiquitous in soil and water
- Environmentally highly adaptable
 - *6.3 MB genome*
 - *5,570 predicted ORFs*
 - *521 Putative Regulatory Genes*
- Opportunistic pathogen
 - *Wide spectrum of infections in humans*
 - *Cystic fibrosis*
- Intrinsically antibiotic resistant
- Multiple surface-associated and extracellular virulence determinants



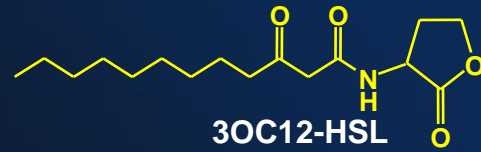
Virulence Determinants of *P. aeruginosa*



A Hierarchical Quorum Sensing Cascade in *P. aeruginosa*



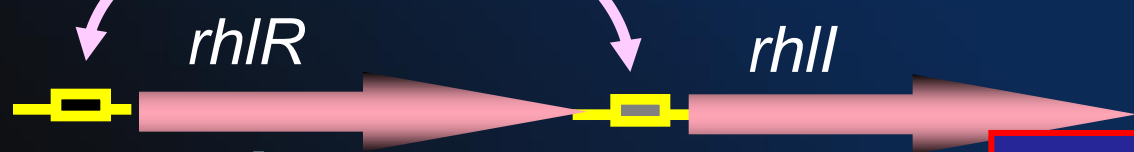
LasR



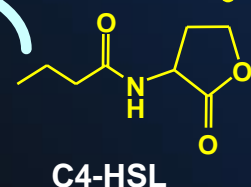
Immune modulation

Antibacterial

- Elastase
- Exotoxin A
- LasA Protease
- Alk. Protease
- Neuraminidase
- Biofilms
- Xcp Secretion
- Catalase
- SOD PrpL
- Aminopeptidase



RhIR

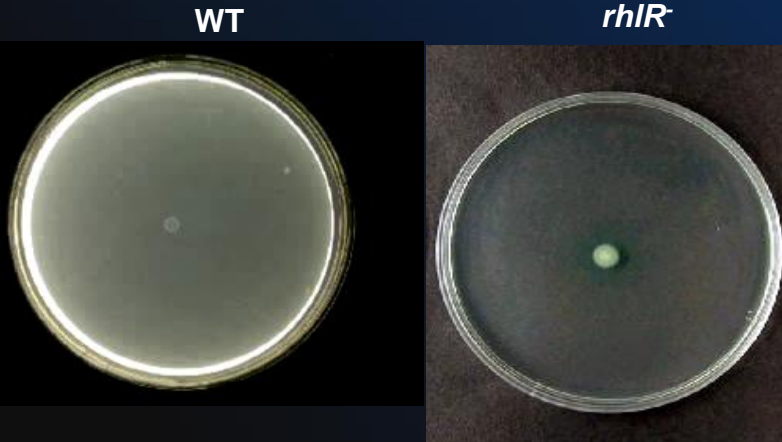


- Elastase, HCN, Lectins; Swarming
- Alk. Protease, Pyocyanin, Lipase, Chitinase, Chitin BP
- Rhamnolipids, Type II Secretion
- Type III Secretion, Pyoverdinin; Multi-Drug Efflux Pumps, Biofilms

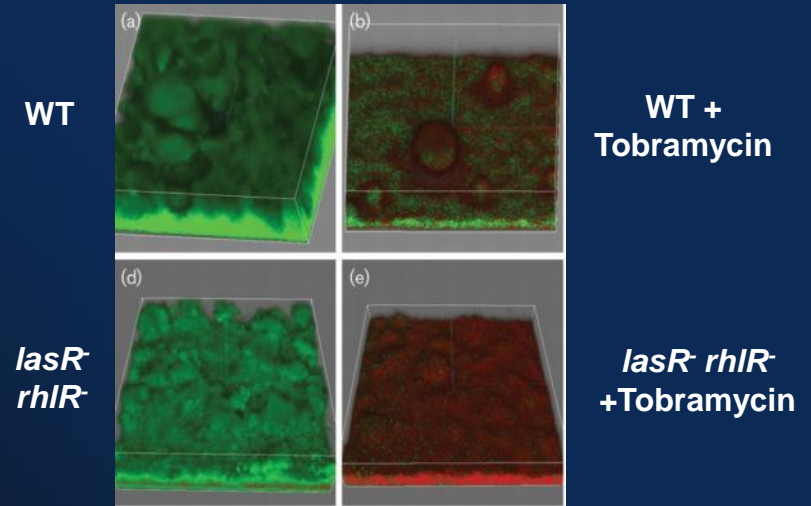
Microarray studies indicate QS regulon consists of ~10% of genome

QS controls community behaviour in *P. aeruginosa*

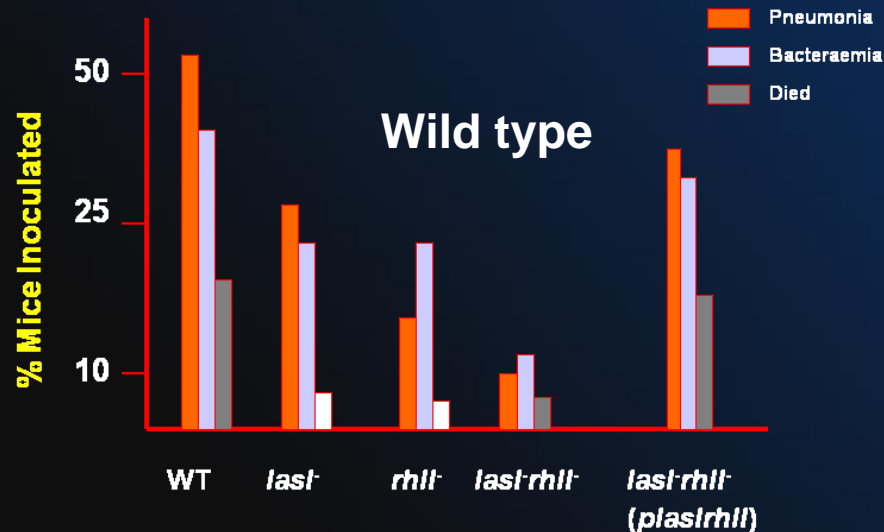
1. Swarming Motility



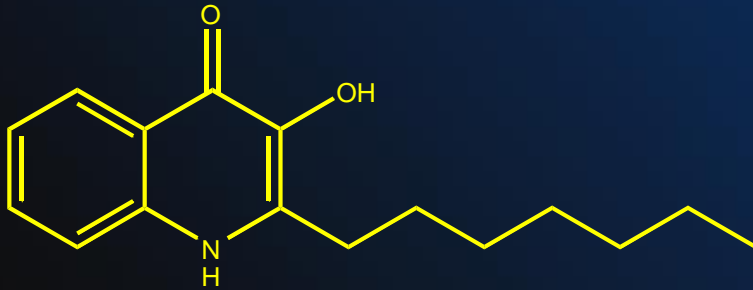
2. Biofilms Antibiotics



3. Virulence in mouse pneumonia model

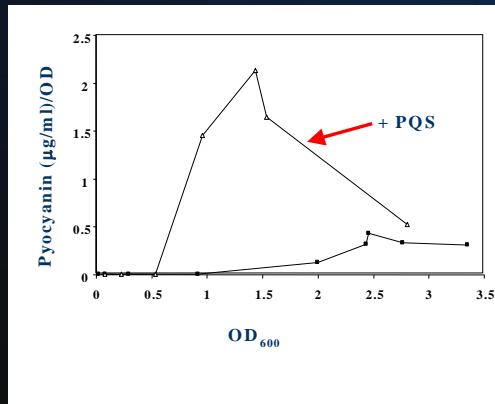


P. aeruginosa is bilingual

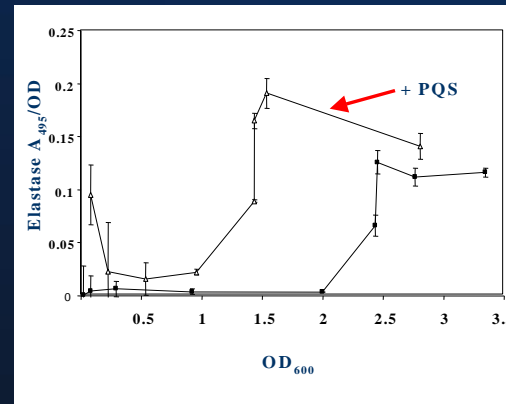


2-heptyl-3-hydroxy-4-quinolone (PQS)

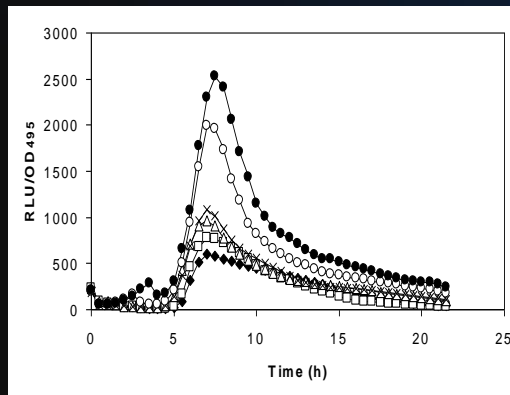
Pyocyanin



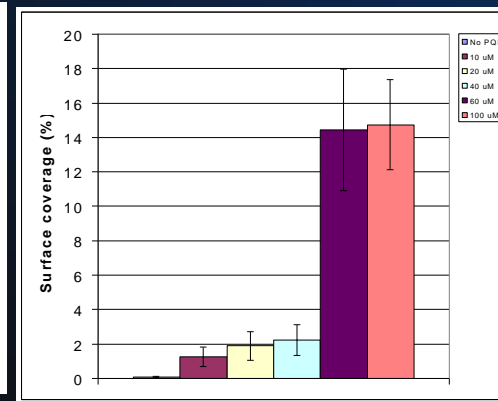
Elastase



lecA expression



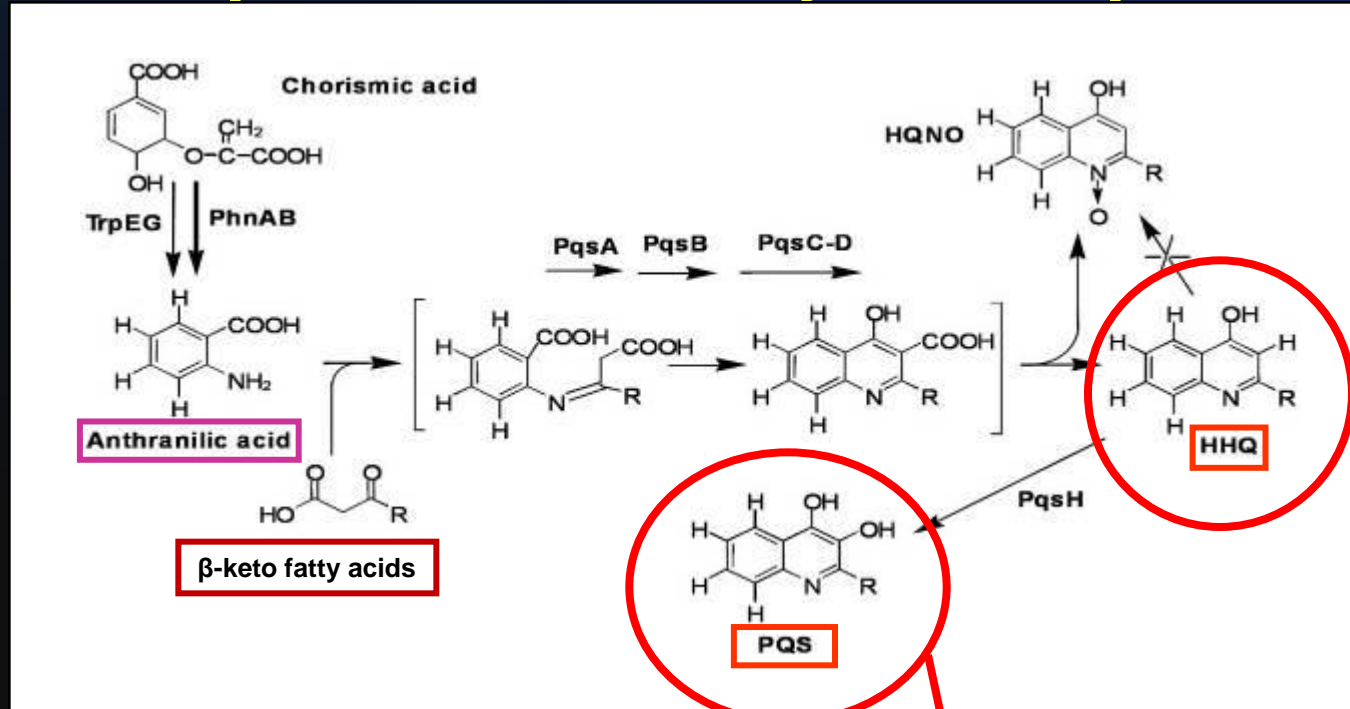
surface coverage



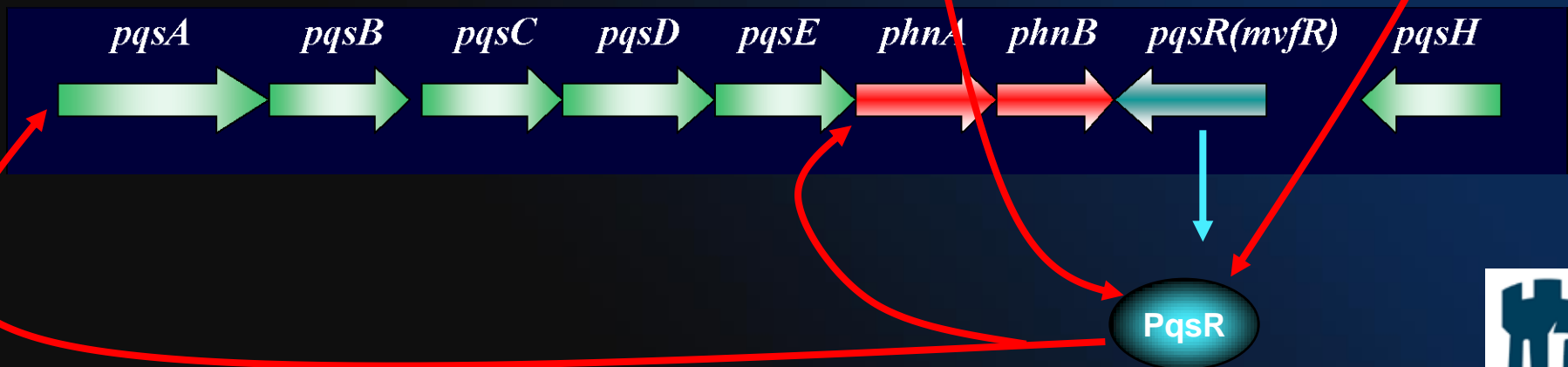
Biofilm



Proposed PQS biosynthetic pathway

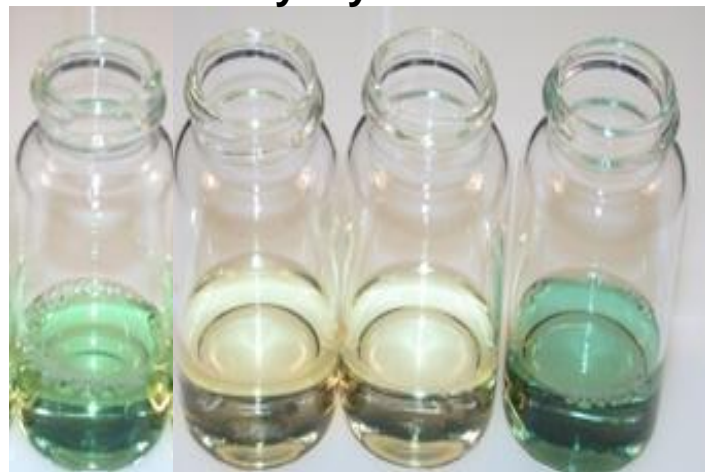


Déziel et al. (2004)
Proc. Natl. Acad. Sci.
USA 101, 1339-1344



PqsE restores virulence independent of PqsR and PQS

Pyocyanin

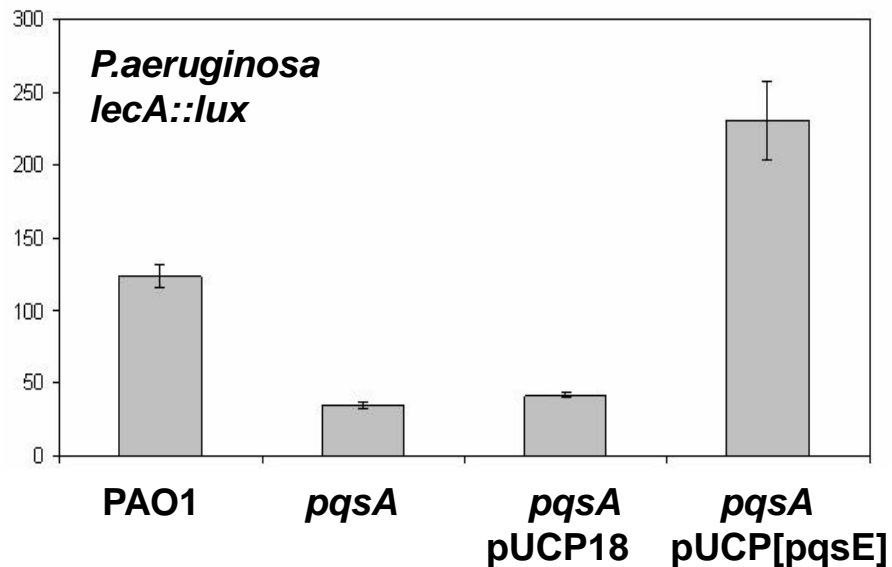


PAO1

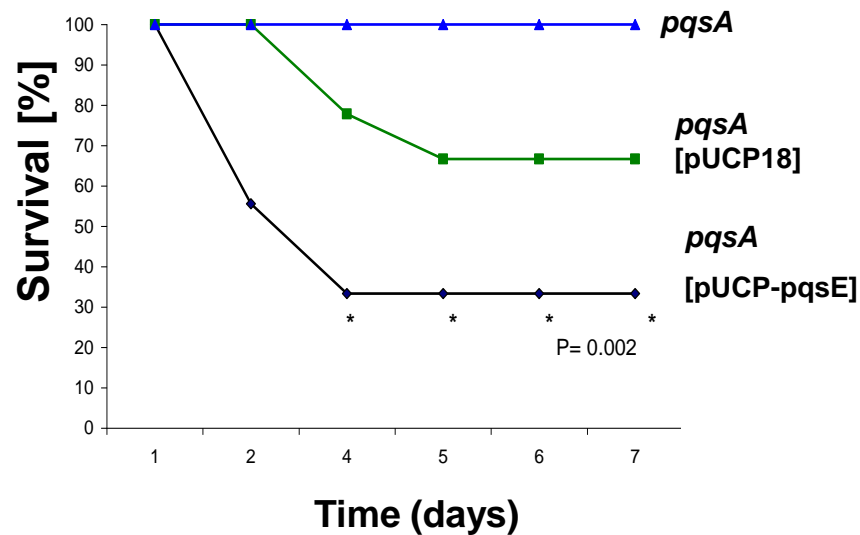
pqsR

pqsR
pUCP18

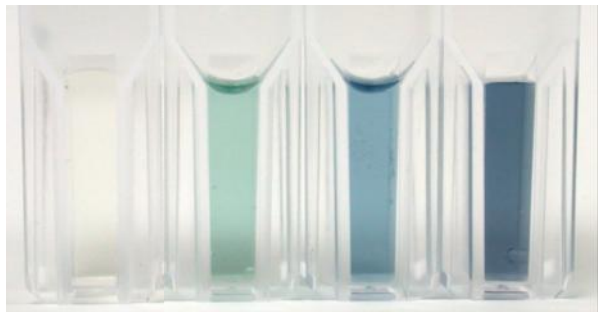
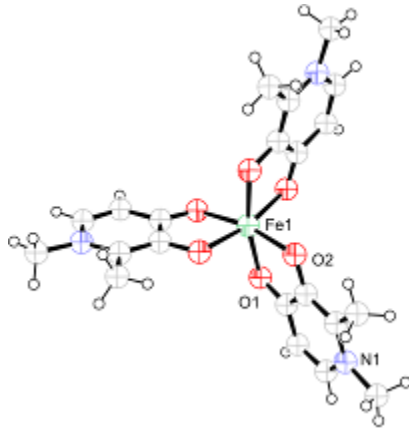
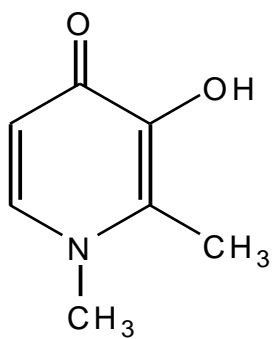
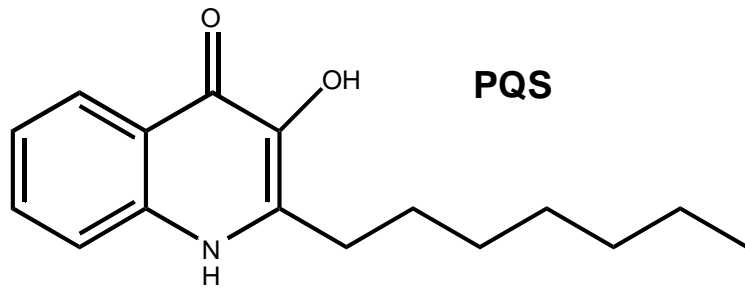
pqsR
pUCP[*pqsE*]



Mouse Wound Infection Model



P. aeruginosa PQS

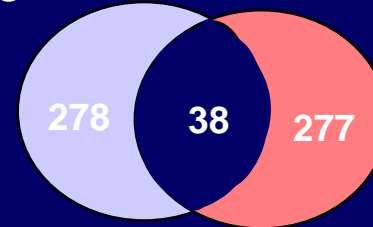


Fe^{3+}

$\text{Fe}^{3+} + \text{PQS}$

Genes upregulated upon addition of PQS (316)

Genes upregulated upon addition of 3O-C12-HSL/C4-HSL (315)

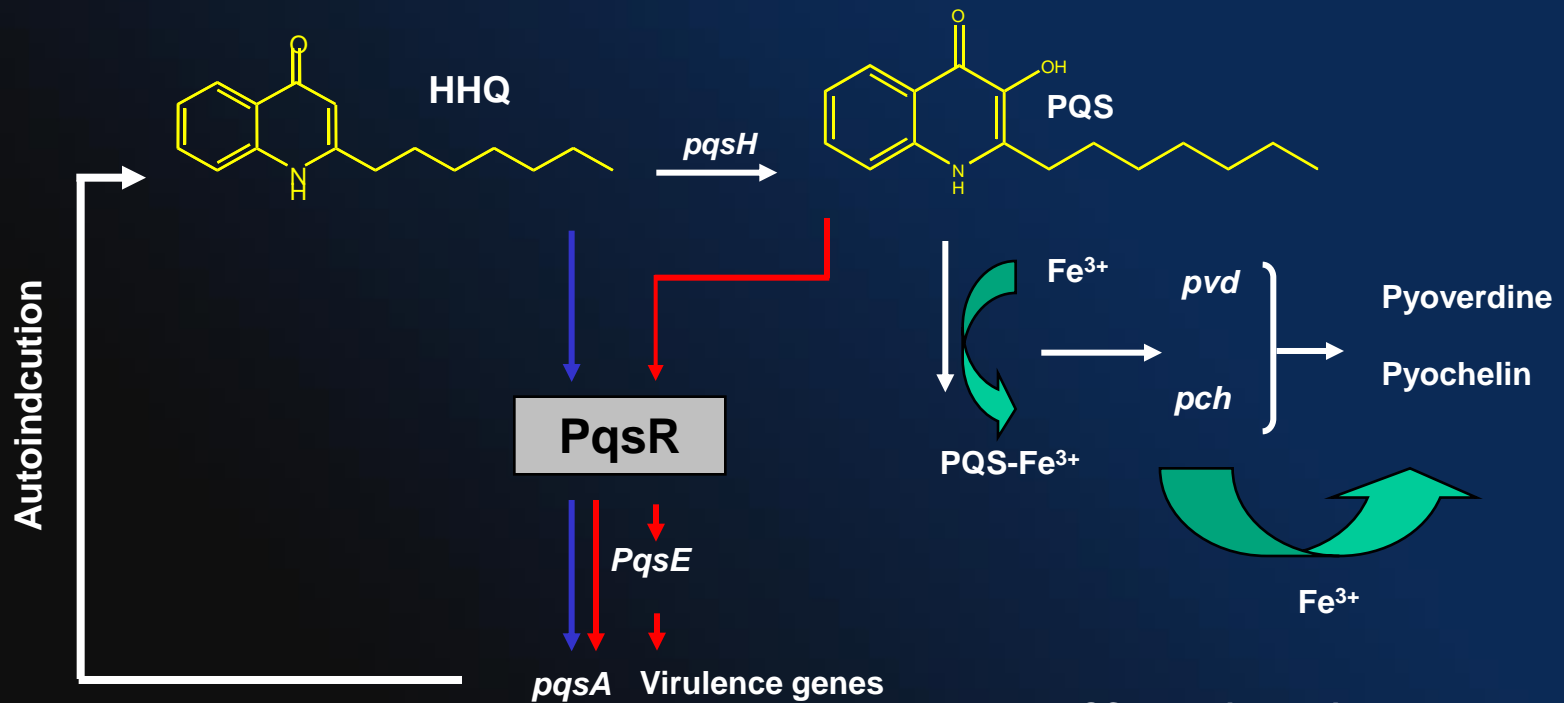


Transcriptome comparison

- Chelator properties
- Positive regulator of iron uptake mechanisms
- Autoinduction



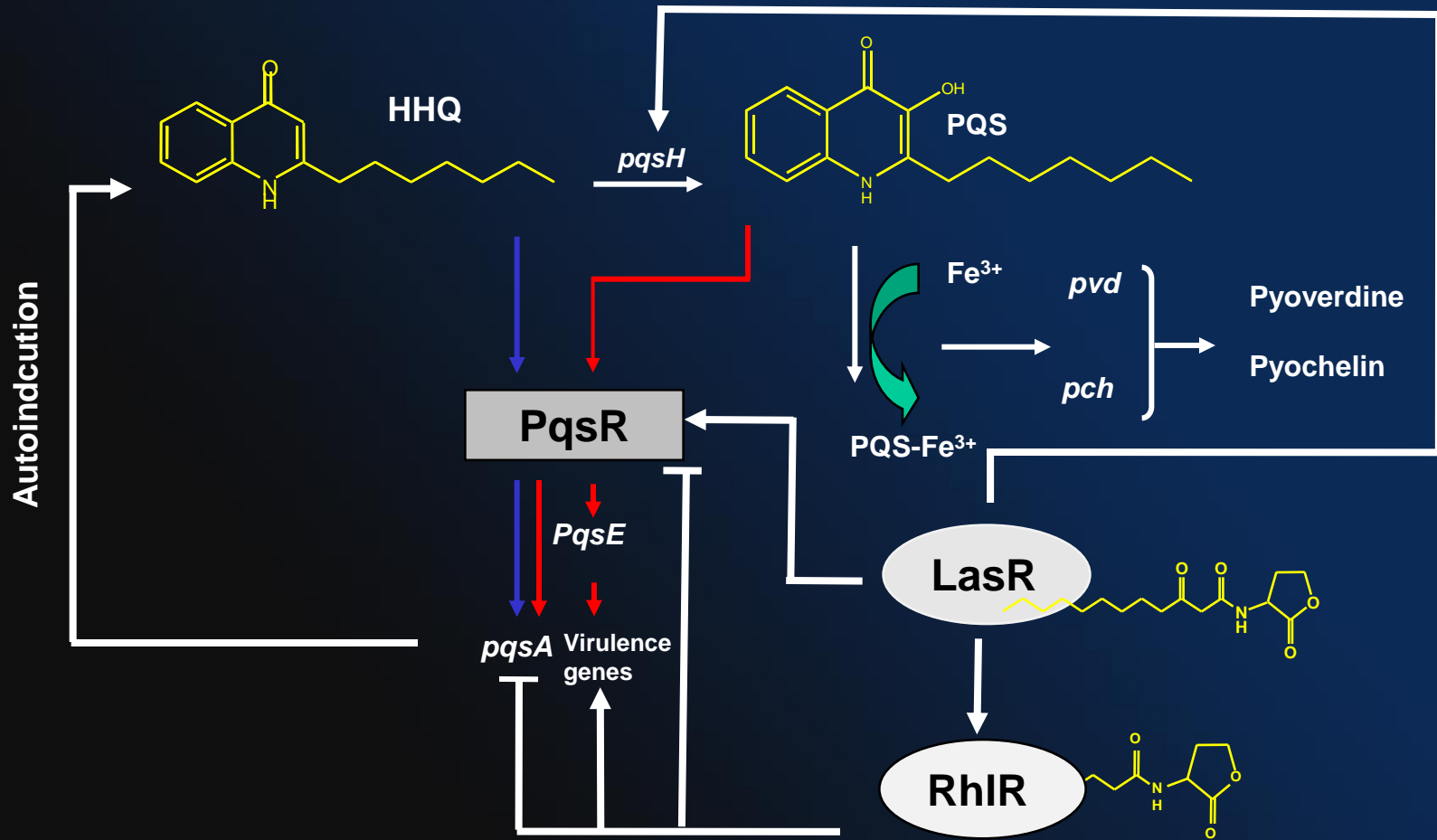
PQS and HHQ play multi-functional roles in signalling and iron entrapment



PQS associates with the cell envelope and appears to act as an iron trap delivering iron to receptor associated pyochelin and pyoverdin



An integrated quorum sensing transcriptional network in *P. aeruginosa*



Transcriptional

Vfr
VqsR
QscR
VqsM

MvfR
ANR
RpoS
AmpR



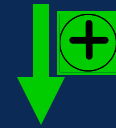
Two Component Systems

GacA/S

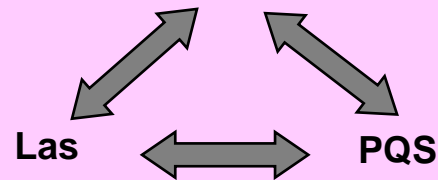


Post-Transcriptional

RsmZ
DksA



Rhl



Transcriptional

MvaT
RsaL
RpoS

RpoN
AmpR



Post-transcriptional

RsmA
RelA



Post-transcriptional regulation by RsmA

DNA




Transcription of
target gene



+1 RBS AUG CGU CAG ... mRNA



Post-transcriptional regulation by RsmA

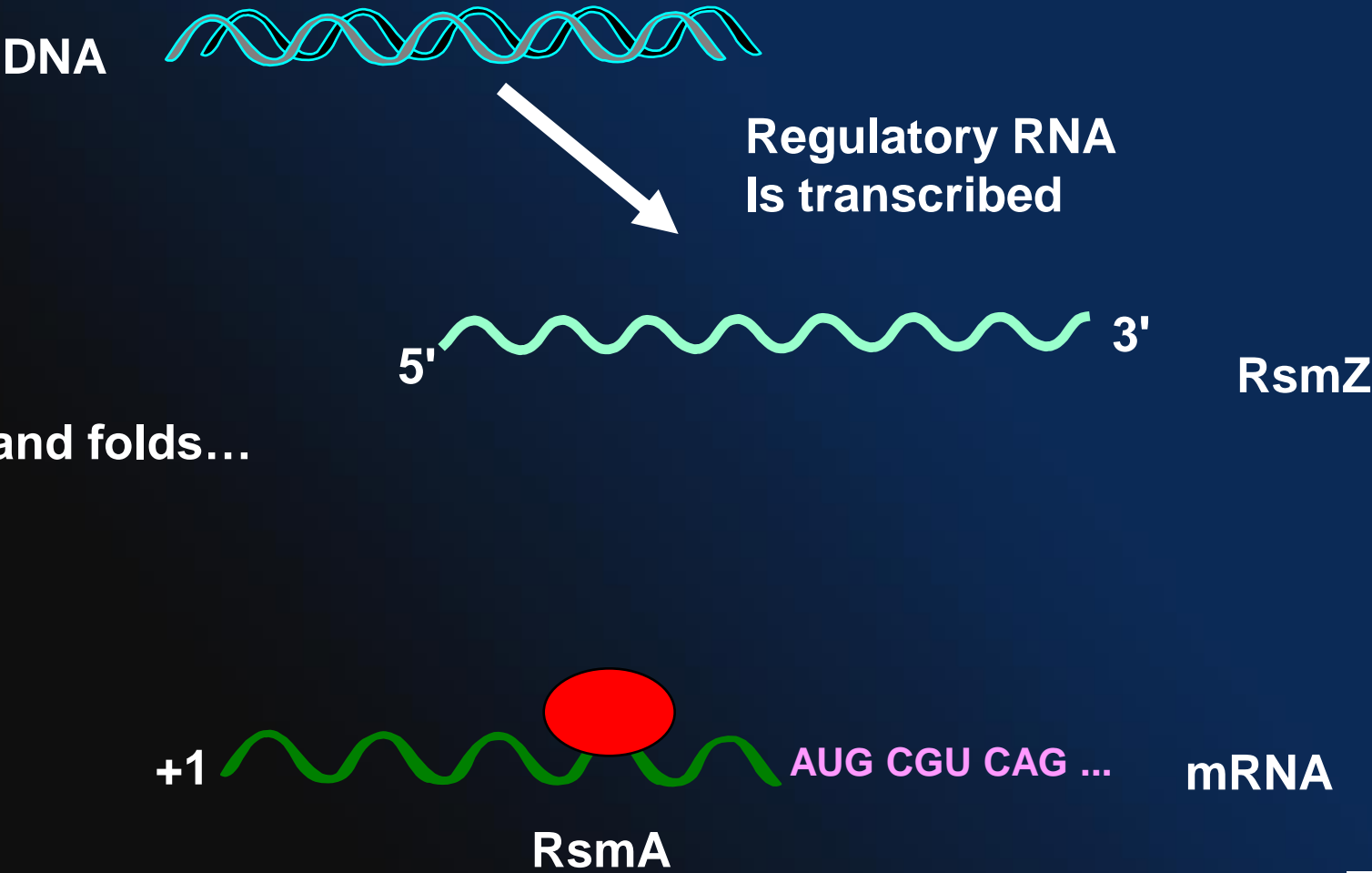
DNA 

RsmA binds near RBS
and prevents translation

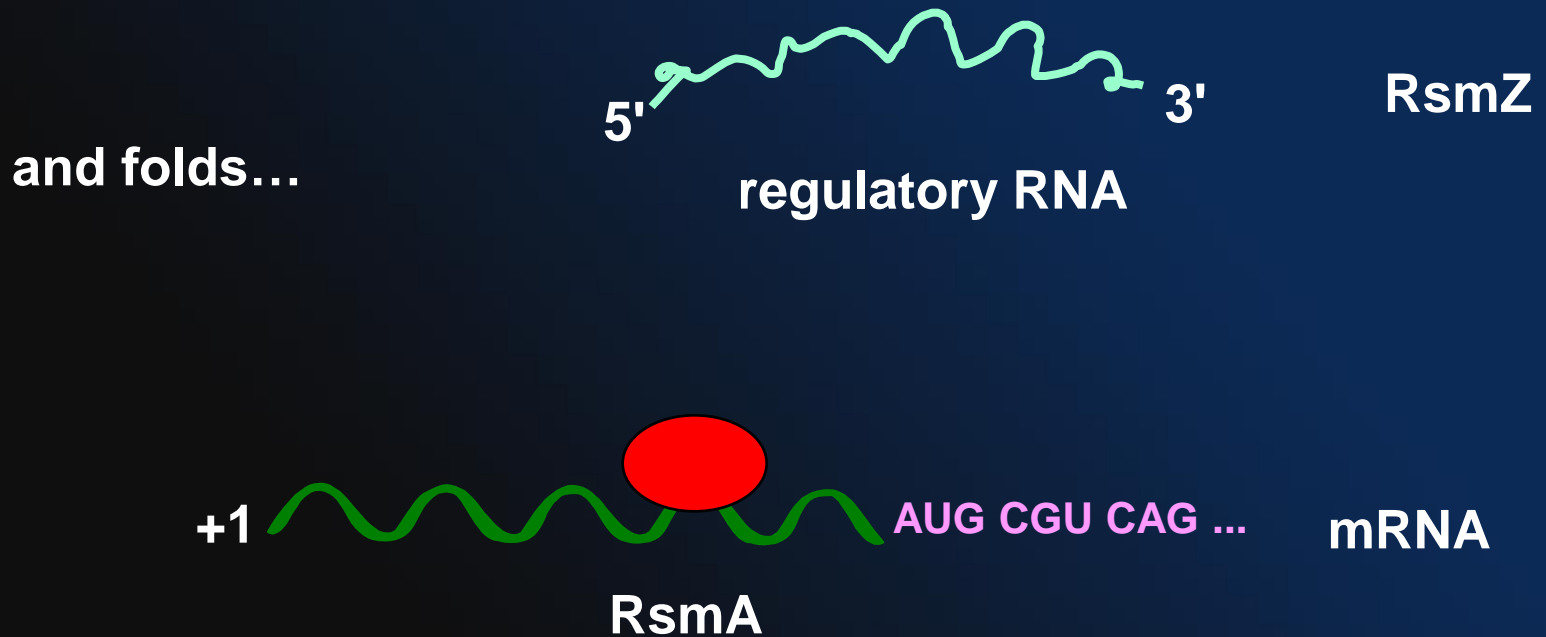
+1  AUG CGU CAG ... mRNA
RsmA



Post-transcriptional regulation by RsmA



Post-transcriptional regulation by RsmA



Post-transcriptional regulation by RsmA

and folds...



RsmZ



Post-transcriptional regulation by RsmA

and folds...



RsmZ



Post-transcriptional regulation by RsmA

and folds...



regulatory RNA

RsmZ



RsmA



Post-transcriptional regulation by RsmA



RsmZ

and folds...

regulatory RNA

to titrate RsmA
from the RBS...



Post-transcriptional regulation by RsmA



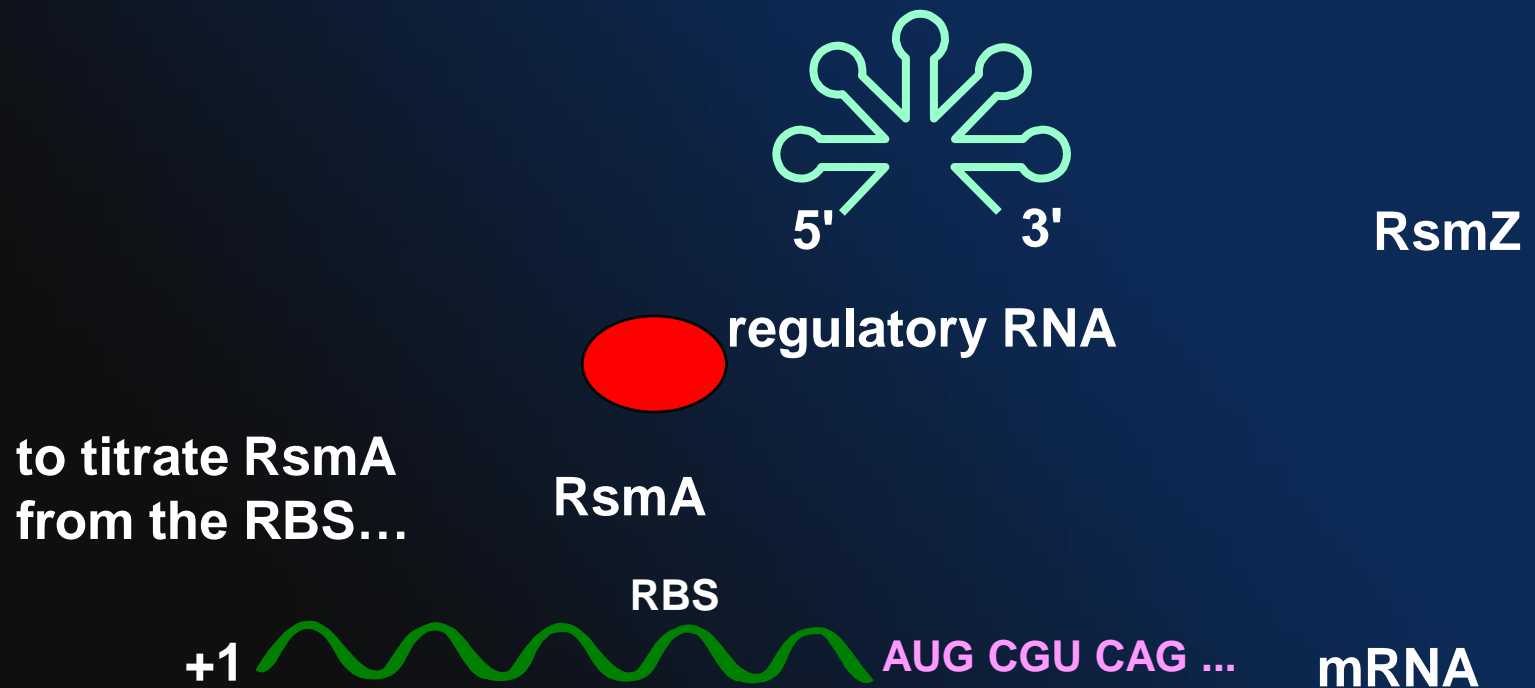
regulatory RNA

RsmZ

to titrate RsmA
from the RBS...



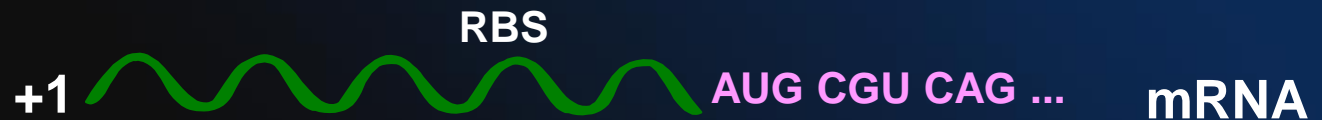
Post-transcriptional regulation by RsmA



Post-transcriptional regulation by RsmA



to titrate RsmA
from the RBS...



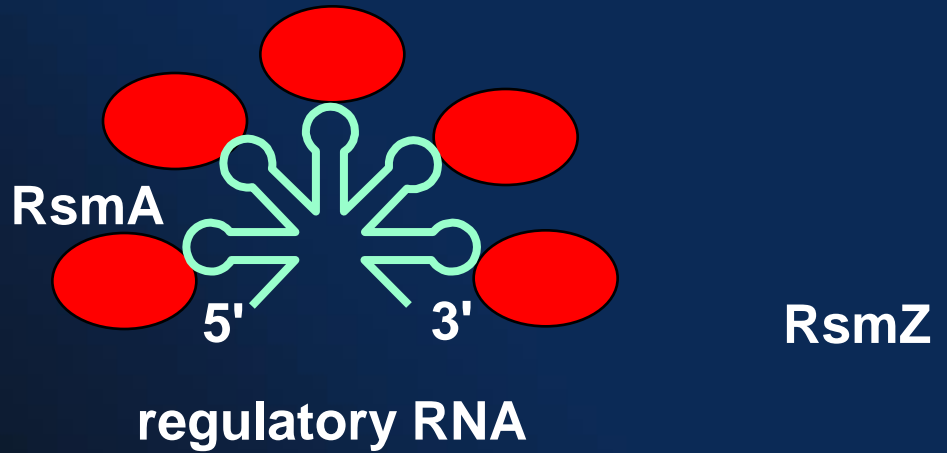
Post-transcriptional regulation by RsmA



to titrate RsmA
from the RBS...



Post-transcriptional regulation by RsmA



to titrate RsmA
from the RBS...



...allowing translation

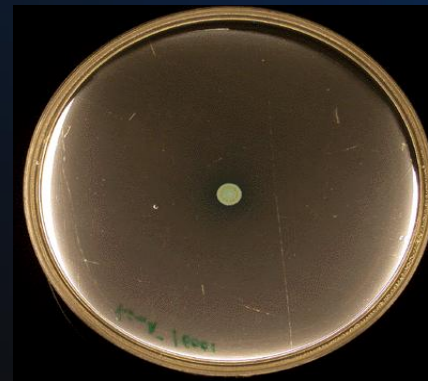
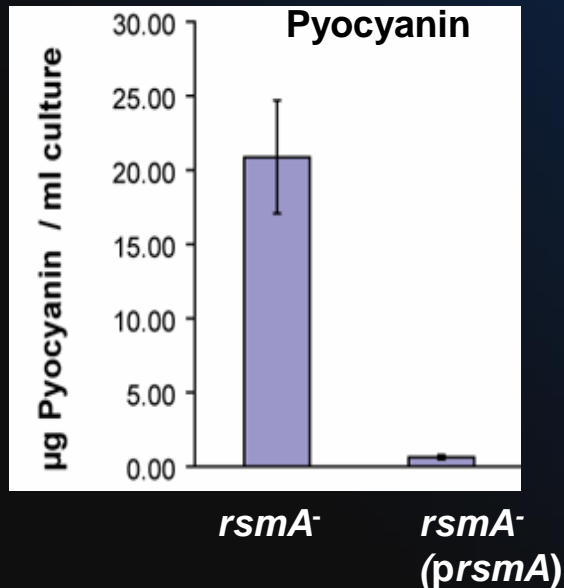


RsmA-regulated phenotypes in *P. aeruginosa*

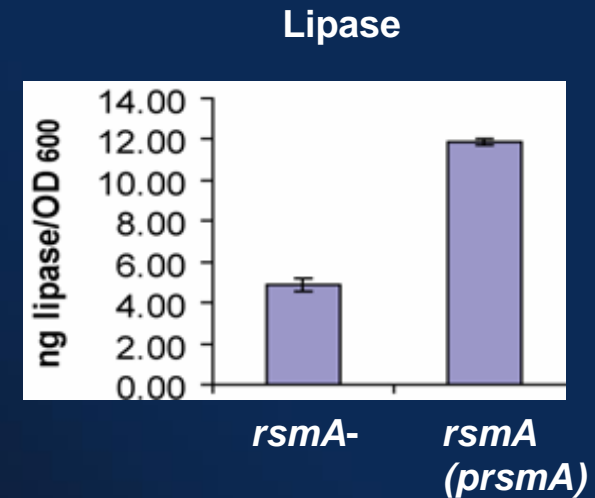
Negative: Exoprotease, elastase, cyanide, lectin, pyocyanin, staphylolytic activity

Positive: swarming motility, lipase

PAO1 (WT)



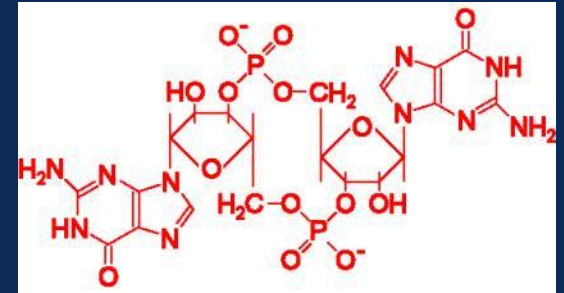
rsmA mutant



These are all QS AHL-regulated phenotypes



Cyclic-di-GMP signalling



- Universal bacterial secondary messenger – intracellular signalling
- Involved in reciprocal control of motile or sessile growth
 - ↓ c-di-GMP → motility
 - ↑ c-di-GMP → biofilm
- GGDEF (cyclase), EAL (phosphodiesterase) and HD-GYP (phosphodiesterase) domain proteins produce and turnover c-di-GMP
- PilZ and PeID domain proteins are c-di-GMP binding proteins
- *P.aeruginosa* has 33 GGDEF, 16 EAL, 3 HD-GYP and 9 c-di-GMP receptors

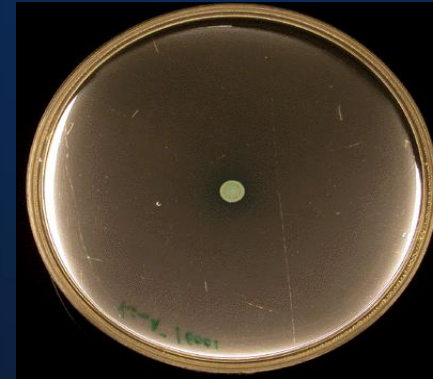
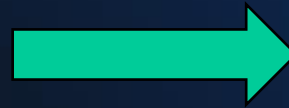


Restoration of swarming in an *RsmA* mutant

PAO1 (WT)

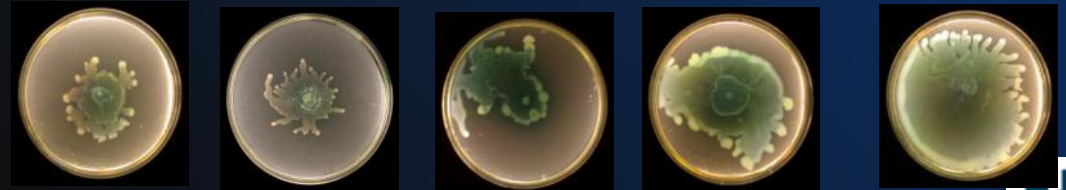


Gene library

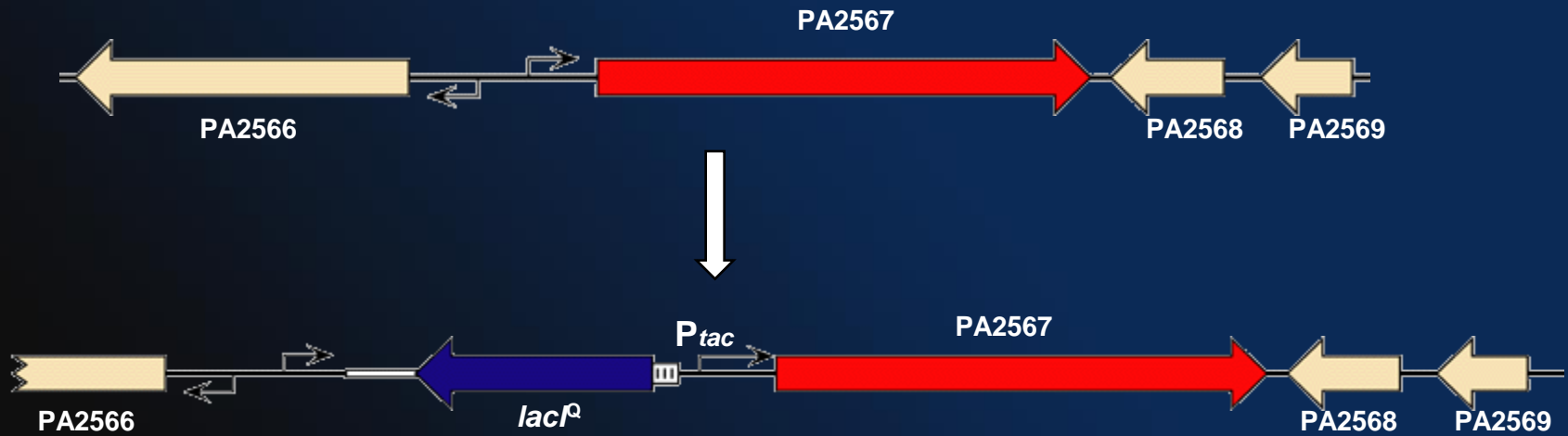


rsmA mutant

Screen for restoration of swarming



Inducible expression of PA2567



control plate



RsmA mutant

+ IPTG



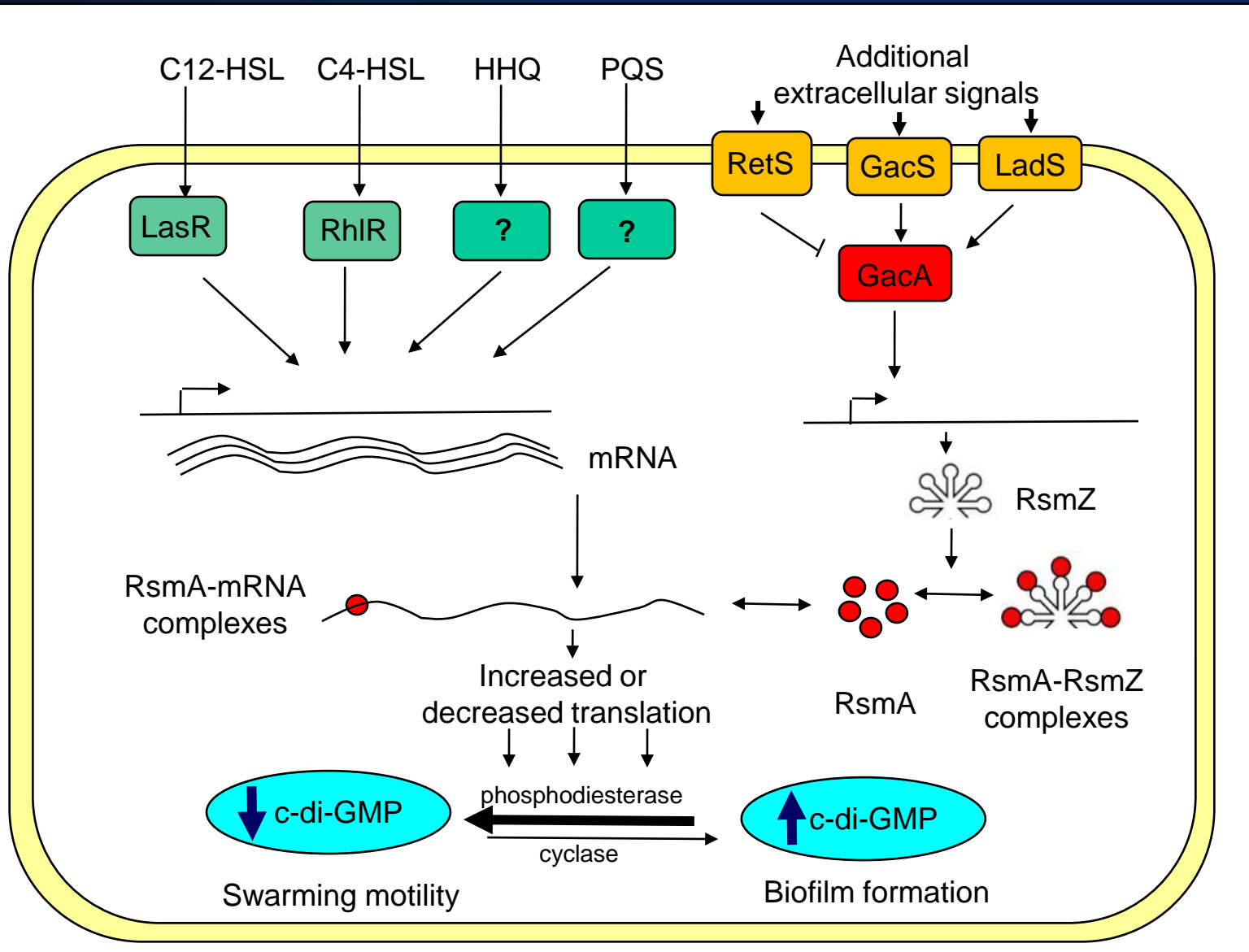
revertants

recombinants

RsmA mutant



Global Transcriptional & Post-Transcriptional QS-dependent Regulatory Networks in *P.aeruginosa*

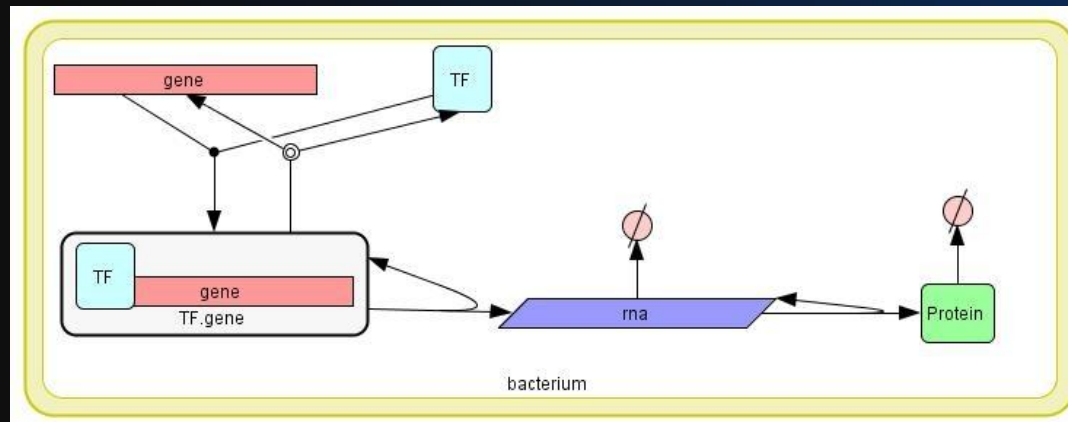


Modelling transcriptional regulation by quorum sensing

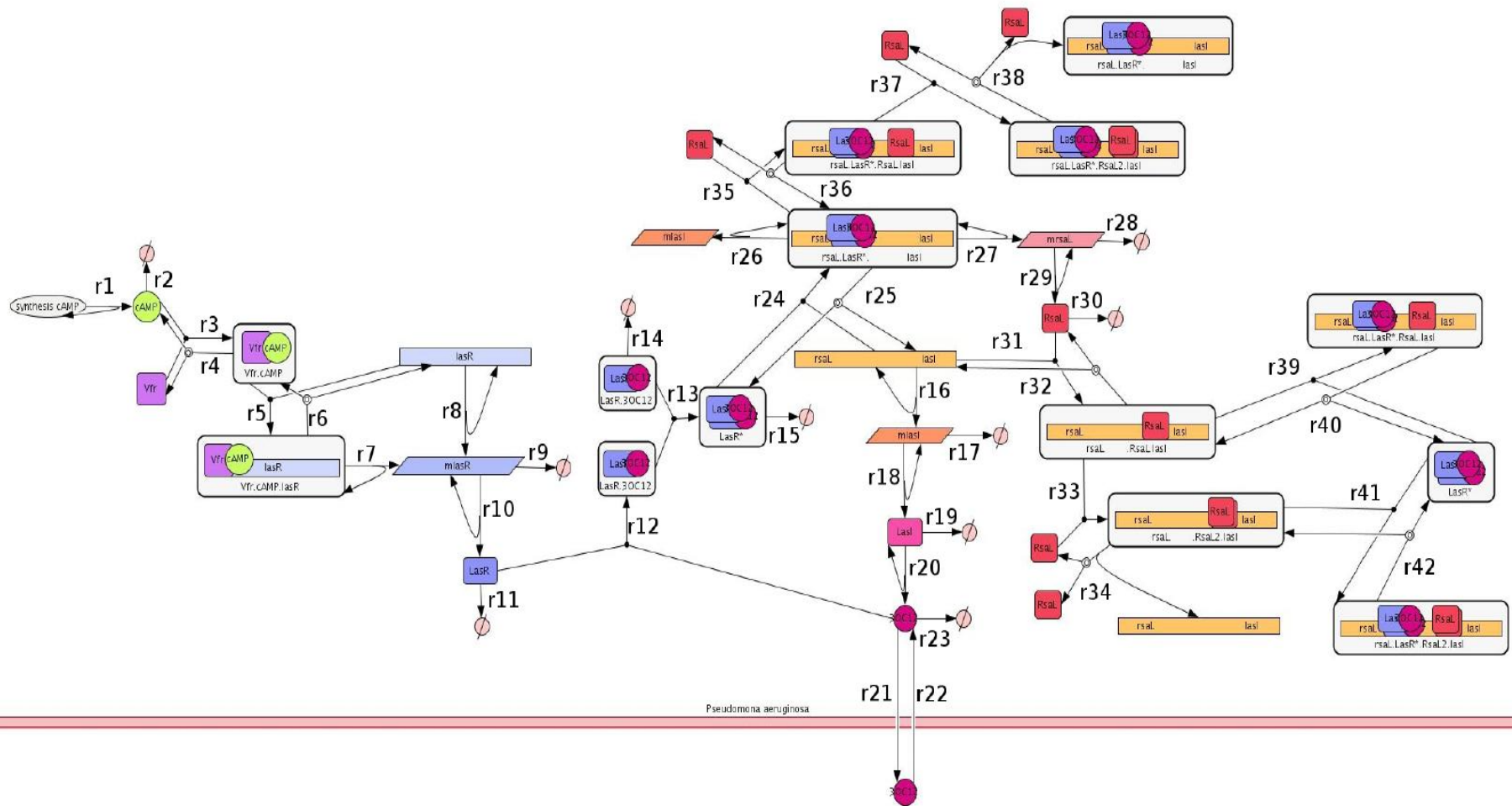
- Modelling is about making the correct simplifications:

Gene Regulation = Transcriptional Regulation

- For every gene in the model we are considering the following parameters:
 - Affinity of the different transcription factors.
 - Transcription rates for the possible promoter states.
 - Messenger RNA and protein half lives.
 - Synthesis rates
 - Diffusion rates



Modelling the las system



Conclusions

- Bacteria use quorum sensing signal molecules to coordinate changes in population behaviour.
- QS regulatory cascades are tightly interlinked to other transcriptional and post-transcriptional regulatory networks.
- We are starting to dissect the relationships between these networks using computational approaches.



The Nottingham Pseudomonas team

Chemistry

Ram Chhabra
Mary Bruce
Alex Truman
Cath Ortori
Dave Barrett

QS group

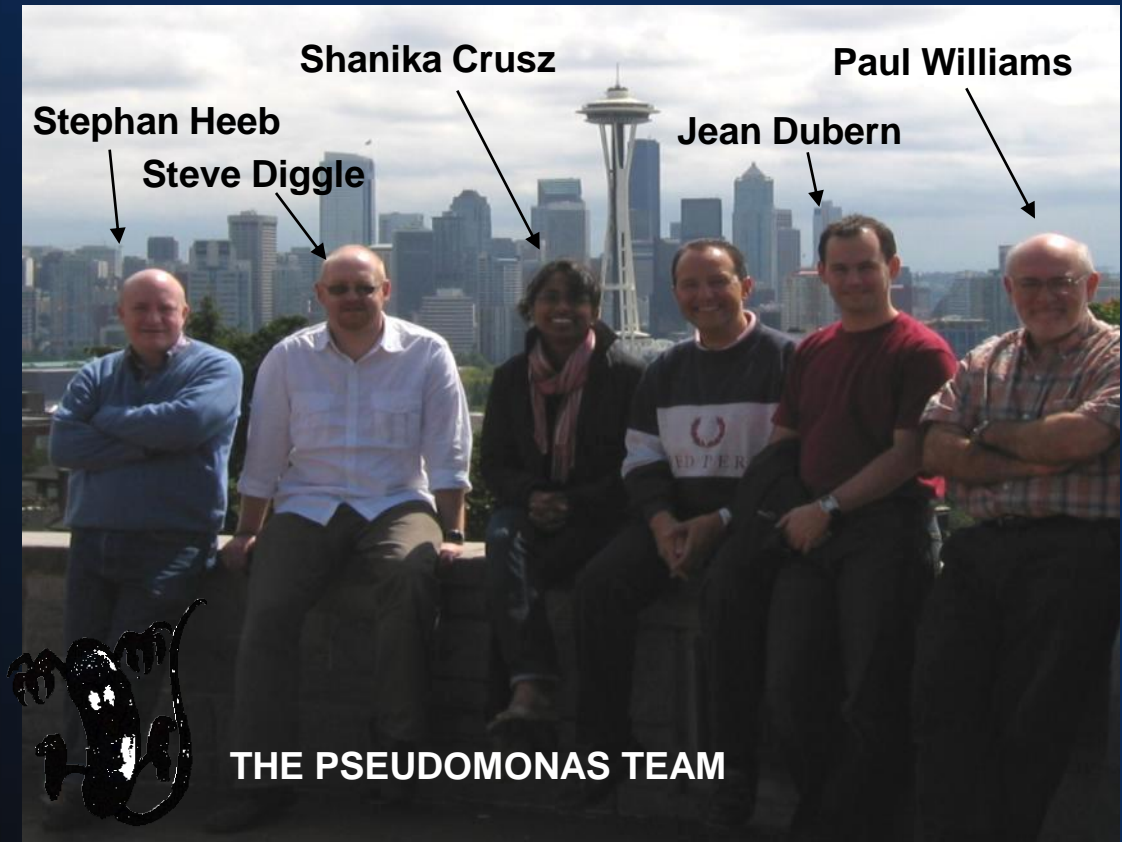
Steve Atkinson
Mathew Fletcher
Marco Messina
Karima Rhighetti
Christian Pustelny
Marco Grasso
Giordano Rampioni
Robert Goldstone
Matthew Twigg
Anne-Mai Prochnow
Monica Cartelle
Laura Tye
Owen Darch
Hannah Patrick

CF Unit

Alan Knox
Alan Smyth
Andrew Fogarty

Computer Sciences

Natalio Krasnogor
Francisco Romero
Jonathan Blakes



The quorum sensing site

www.nottingham.ac.uk/quorum

