Feedbacks in quorum sensing: An evolutionary perspective

Ned Wingreen, Princeton KITP August 7, 2015

Outline

Introduction to quorum sensing

• The QS network in Vibrio harveyi

- Why so many feedbacks?
- Insights from evolution

Bacterial Quorum Sensing

Low cell density: low autoinducer (AI) concentration



Bacterial Quorum Sensing

High cell density: high Al concentration



Collective behaviors coordinated by quorum sensing



Vibrio harveyi

Bacteria are Multilingual

Species-specific signals

Universal signal

Acyl Homoserine Lactone (AHL)



Auto Inducing Polypeptide (AIP)

ADPITRQWGD

ComX (Bacillus subtilis)

AI-2



Quorum sensing is ubiquitous among bacteria





Vibrio cholerae

Biofilm formation

Bacillus subtilis

Bioluminescence



Vibrio harveyi

Quorum sensing network in V. harveyi



QS network has many internal feedbacks



Rutherford *et al., Genes & Dev* (2011) Shao & Bassler, *Mol Micro* (2012)

Engineered reporter strains



Single-cell measurements





AI-2(nM)

Teng et al. Mol Sys Biol (2011)

Each feedback does something...



LuxN feedback regulates receptor ratio

WT

Low Cell Density





WT



luxN expression

High Cell Density



Core feedbacks have little effect on noise



Feedback by LuxR controls inputoutput relation



LuxR feedback increases AI input dynamic range and decreases LuxR output dynamic range.

Quorum-sensing feedbacks and mutual information





Taillefumier & NSW PLoS Comp Biol (2015)

Feedbacks can optimize available information about cell density



Feedback from LuxR speeds Qrr production at HCD → LCD transition



Tu et al., Mol Micro (2008)

Simple model for network dynamics

E.g. equations for Qrrs and *luxR* / LuxR:

$$\begin{aligned} \frac{d[Qrr]}{dt} &= Q * V_{tscr} \left(\frac{[\text{LuxO} \sim \text{P}]}{K_M^{OP} + [\text{LuxO} \sim \text{P}]} \right) \left(\frac{K_I^A}{K_I^A + [\text{AphA}]} \right) \left(\frac{K_M^R + A_R^Q[\text{LuxR}]}{K_M^R + [\text{LuxR}]} \right) \\ &- k_{qn} [Qrr][luxN] \\ &- k_{qo} [Qrr][luxO] \\ &- k_{qr} [Qrr][luxR] \\ &- k_{qa} [Qrr][aphA] \end{aligned}$$
$$\begin{aligned} \frac{d[luxR]}{dt} &= V_{tsla} \left(\frac{K_M^A + A_A^R[\text{AphA}]}{K_M^A + [\text{AphA}]} \right) \left(\frac{K_I^R}{K_I^R + [\text{LuxR}]} \right) - k_{qr} [Qrr][luxR] - D_{mRNA}[luxR] \\ \\ \frac{d[\text{LuxR}]}{dt} &= V_{prot} [luxR] - D_{prot} [\text{LuxR}] \end{aligned}$$

Simulate transitions: LCD \rightarrow HCD and HCD \rightarrow LCD.

Model results for HCD→LCD transition



Network design accelerates HCD \rightarrow LCD response:

- Multiple Qrrs
- LuxR co-activation of Qrrs
- Qrr repression of LuxO
- Cap on total LuxR
- Negative feedback via AphA limits Qrr accumulation

AphA regulation correlates with multiplication of Qrrs

Group	Number of		<i>qrr</i> 1		
	qii genee		Region I	Region II	
la	1	/. fischeri ES114 /. fischeri MJ11 A. salmonicida LFI1238	TGACCCTTTA-AGCCAAAO TGACCCTTTA-AGCCAAAO TGACCCTTTA-AGCCAAAO	GGGTCA-CCTAGCCAACTGACGTTGTTAGTGA GGGTCA-CCTAGCCAACTGACGTTGTTAGTGA GGGTCA-CCTAGCCAACTGACGTTGTTAGTGA	
lb	1	P. angustum S14 P. sp.SKA34 P. damselae CIP 102761 P. leiognathi P. profundum SS9	TGACTCTTAAGTTAAO TGACTCTTAAGTTAAO TAACTCTTAC-TTAAO TGACTCTAAAATTTAO TGACTCTTAA-TGTAO	GAGTCAACCTAGCCAACTGACGTTGTTTGTGG GAGTCAACCTAGCCAACTGACGTTGTTTGTGG GAGTTAACCTAGCCAACTGACGTTGTTTGTGG GAGTCAACCTAGCCAACTGACGTTGTTTGTGG GAGTCAACCTAGCCAACTGACGTTGTTTGTGG	
II	4 or 5	G. hollisae CIP 101886 V. cholerae C6706 V. cholerae O395 V. harveyi ATCC BAA-1116 V. parahaemolyticus RIMD 2210633 V. splendidus LGP32 V. vulnificus CMCP6 V. vulnificus YJ016	TGACCCTTCTAC TGACCCGCAAC TGACCCGCAAC GGACCCCTCC CGACCCCTCC TGACCTTC-C CGACCCCTCC TGACCCTCTCC TGACCCCTCC TGACCCCTCC TGACCCCTCC	GGGTCA-CCTAGCCAACTGACGTTGTTGTGA GGGTCA-CCTAGCCAACTGACGTTGTTAGTGA GGGTCA-CCTAGCCAACTGACGTTGTTAGTGA GGGTCA-CCTAGCCAACTGACGTTGTTAGTGA GGGTCA-CCTAGCCAACTGACGTTGTTAGTGG GGGTCA-CCTAGCCAACTGACGTTGTTAGTGA GGGTCA-CCTAGCCAACTGACGTTGTTAGTGA GGGTCA-CCTAGCCAACTGACGTTGTTAGTGA	

В

А

		Region I	Region II		
V. harveyi Q	rr1 5'	GGACCCCU	CGGGUCACCUAG	CCAACUGACGUUGUU	AGUG 3'
Q	rr2 5'	CGACCCUUCUUAAGCCGA	-GGGUCACCUAG	CCAACUGACGUUGUU	AGUG 3'
Q	rr3 5'	UGACCCUUCUUAAGCCGA	-GGGUCACCUAG	CCAACUGACGUUGUU	AGUG 3'
Q	rr4 5'	AGACCCUUAUUAAGCCGA	-GGGUCACCUAG	CCAACUGACGUUGUU	AGUG 3'
Q	rr5 5'	UGACCCUU-UUAAGCCGA	-GGGUCACCUAG	CCAACUGACGUUGUU	AGUG 3'
V. fischeri Q	rr1 5'	UGACCCUUUAAGCCAA	AGGGUCACCUAG	CCAACUGACGUUGUU	AGUG 3'

Shao & Bassler Mol Micro (2012)

So why is the QS network so complex?

Lifecycle of bacteria in a biofilm



LuxN⁺ LuxPQ⁺ Al-1 Al-2 Dose Response

- Multiple autoinducers and feedbacks may allow multistage developmental program.
- Feedbacks can help cells focus on most relevant signal and respond quickly to HCD →LCD transitions.

Summary

- AphA/LuxR are the LCD/HCD master regulators in the Vibrio quorum-sensing network.
- Complex network architecture allows:
 - Increased information on cell density
 - "Attention" to specific signals
 - Fast response to HCD → LCD transition
- Interspecies comparison helps track network evolution.

Acknowledgments

Shu-wen Teng

Tao Long

Jose Mena

David Borenstein

Thibaud Taillefumier

Bonnie Bassler

Kim Tu Steve Rutherford Julia van Kessel Yi Shao

Jessie Schaffer

QUANTITATIVE

CENTER FOR

BIOLOGY









HHM HOWARD HUGHES MEDICAL INSTITUTE