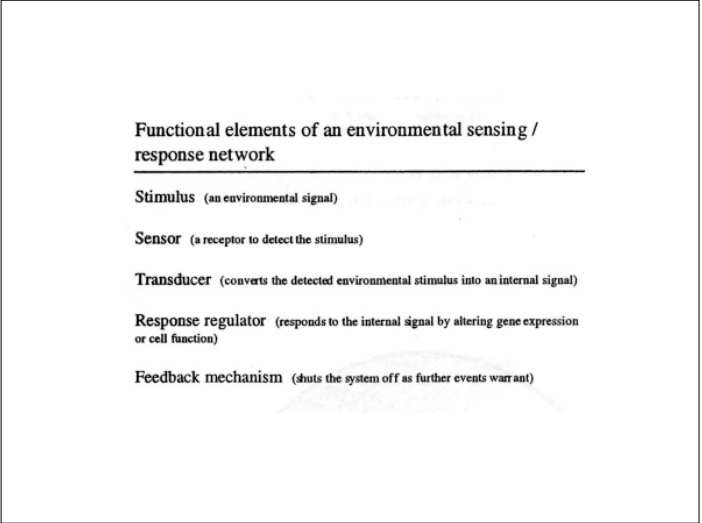
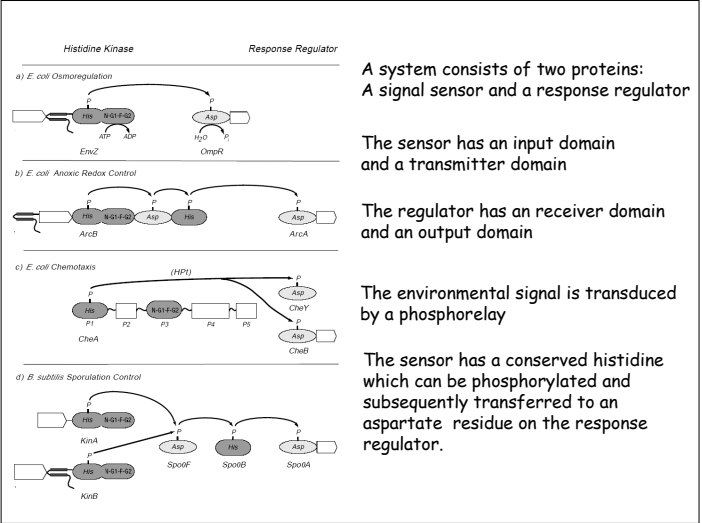


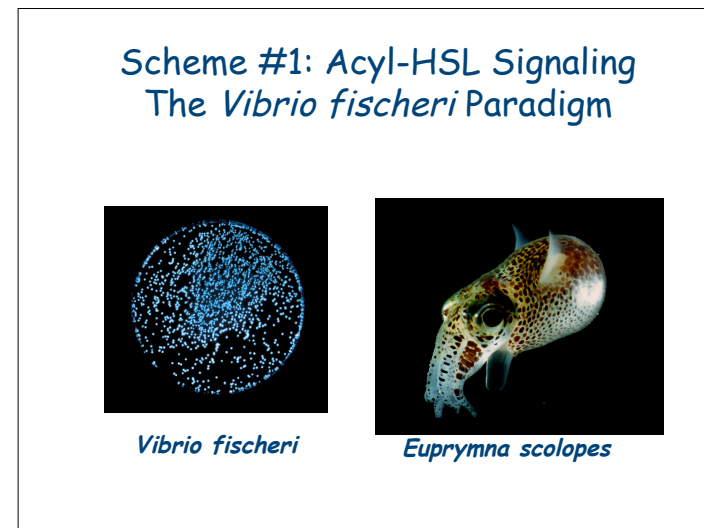
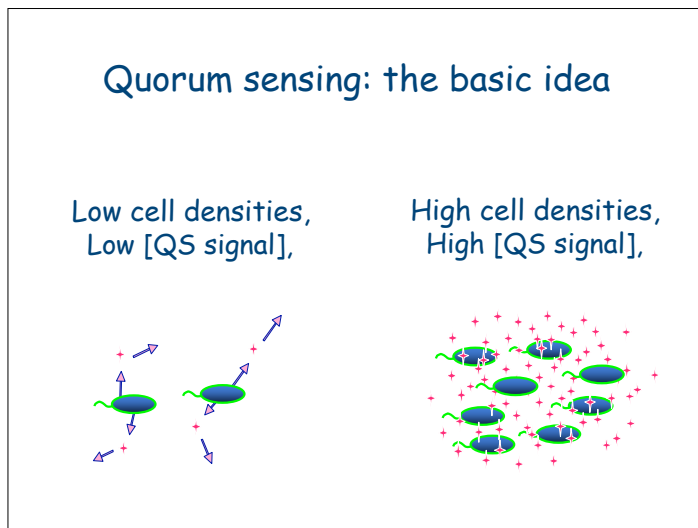
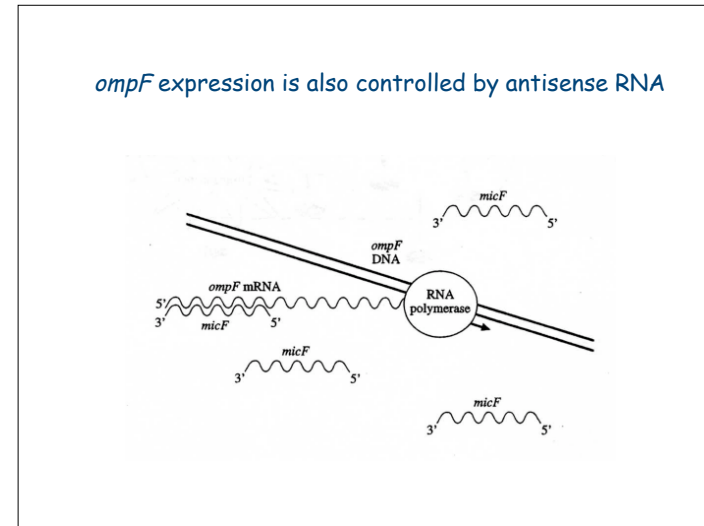
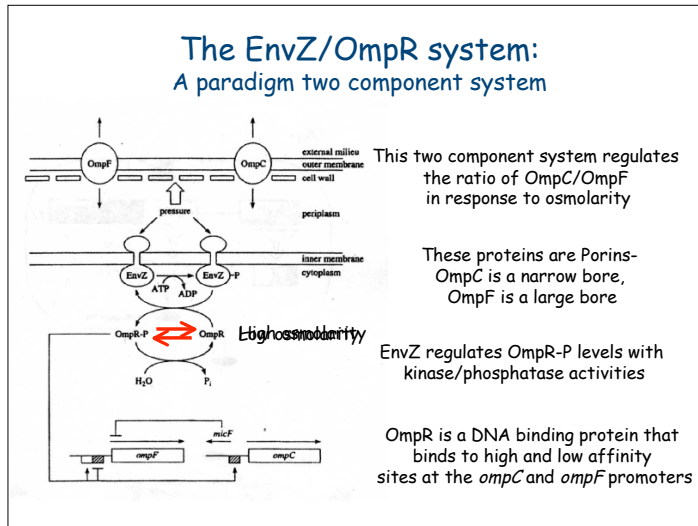
Environmental Sensing

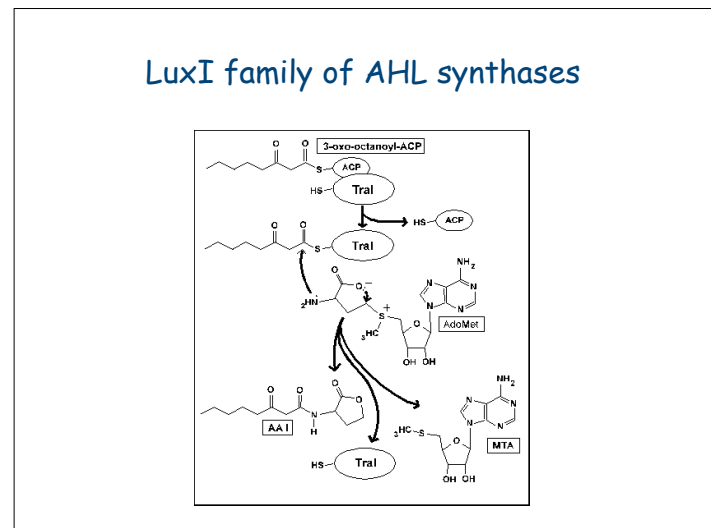
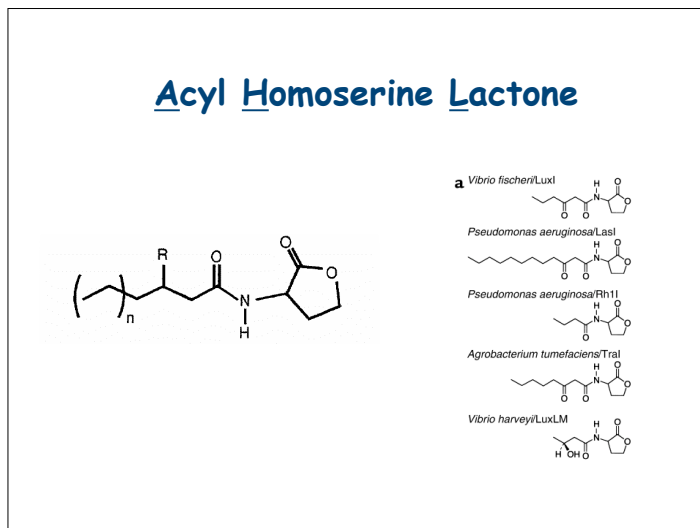
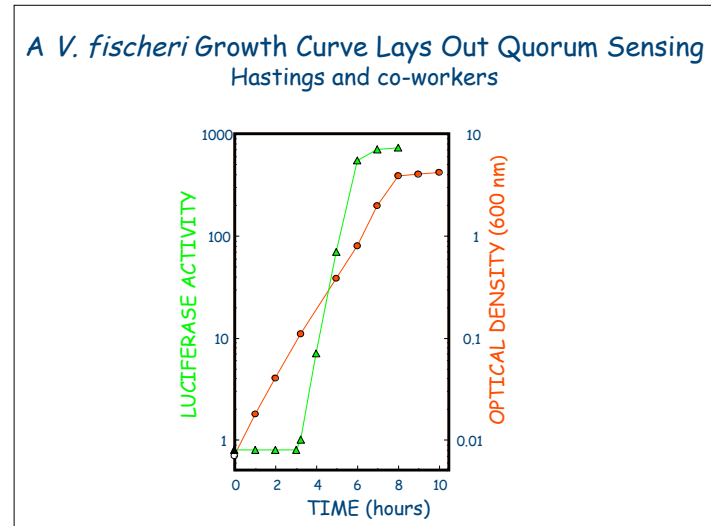
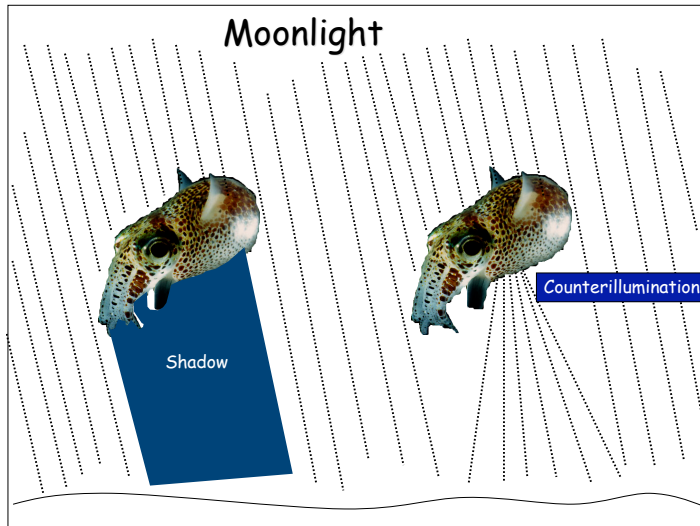


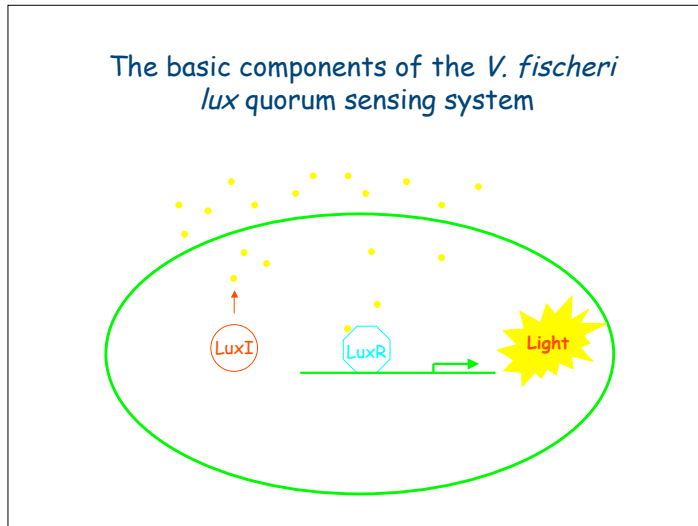
Two-Component Regulatory Systems and Phosphorelay Systems

- many genes and operons are turned on or off in response to environmental conditions
 - the regulatory proteins involved are part of a two-component signal which links external events to regulation of gene expression



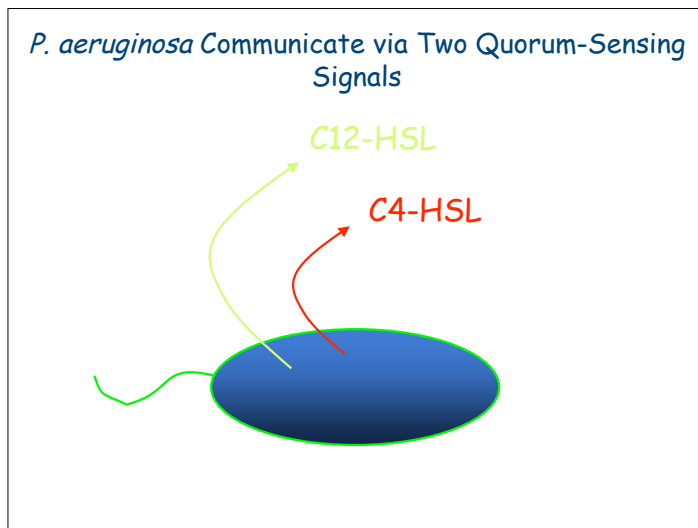




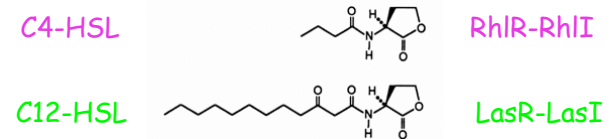


AHL signaling in different species

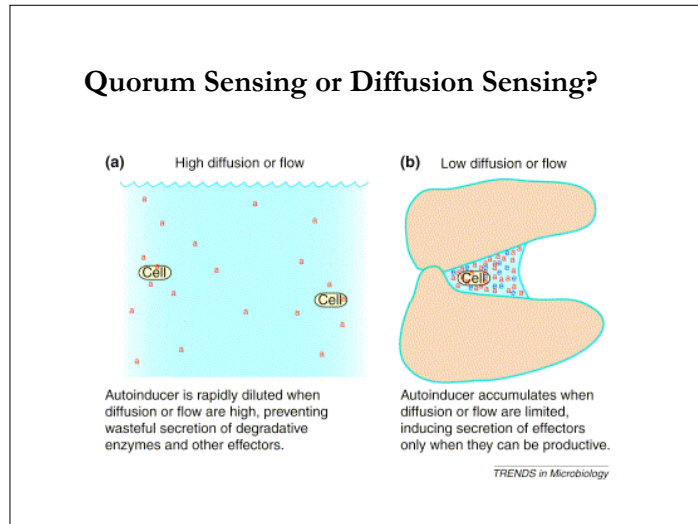
Species	QS-regulated function
<i>Burkholderia cepacia</i>	Secreted virulence factors
<i>Yersinia enterocolitica</i>	Cell aggregation
<i>Agrobacterium tumefaciens</i>	Conjugal plasmid transfer
<i>Erwinia carotovora</i>	Carbapenem antibiotics
<i>Aeromonas hydrophila</i>	Secreted virulence factors



P. aeruginosa AHL systems



LasR-LasI regulates RhIR-RhII.
 LasR-I is atop the quorum sensing cascade.



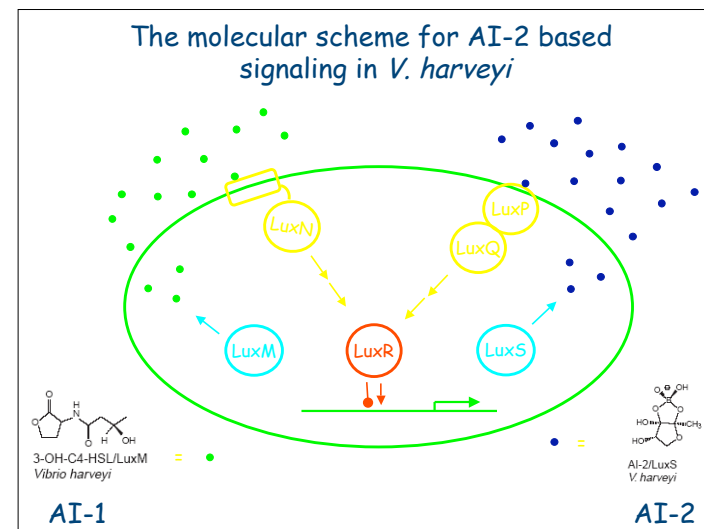
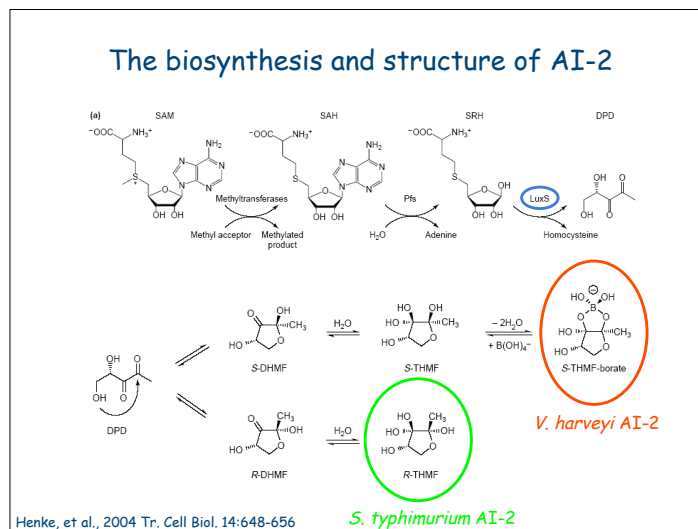
Scheme #2: AI-2 based signaling

Table 1
Bacteria that possess *luxS* genes

Widely distributed	<i>Actinobacillus pleuropneumoniae</i> <i>Bacillus anthracis</i> <i>Bacillus cereus</i> <i>Bacillus halodurans</i> <i>Bacillus subtilis</i> <i>Bifidobacterium longum</i> <i>Borrelia burgdorferi</i> <i>Campylobacter jejuni</i> <i>Clostridium acetabolyticum</i> <i>Clostridium difficile</i> <i>Clostridium perfringens</i> <i>Deinococcus radiodurans</i> <i>Enterococcus faecalis</i> <i>Enterococcus faecium</i> <i>Escherichia coli</i> <i>Haemophilus ducreyi</i> <i>Haemophilus influenzae</i> <i>Haemophilus somnus</i> <i>Helicobacter hepaticus</i>	<i>Helicobacter pylori</i> <i>Klebsiella pneumoniae</i> <i>Lactobacillus gasseri</i> <i>Lactobacillus plantarum</i> <i>Lactococcus lactis</i> <i>Lawsonella mesenteroides</i> <i>Lawsonella axensis</i> <i>Listeria monocytogenes</i> <i>Neisseria gonorrhoeae</i> <i>Neisseria meningitidis</i> <i>Oceanobacillus ihayensis</i> <i>Oenococcus oeni</i> <i>Pasteurella multocida</i> <i>Pasteurella multocida</i> <i>Porphyromonas gingivalis</i> <i>Proteus mirabilis</i> <i>Salmonella enterica</i>	<i>Salmonella paratyphi</i> <i>Salmonella typhi</i> <i>Salmonella typhimurium</i> <i>Shigella flexneri</i> <i>Sinorhizobium meliloti</i> <i>Staphylococcus aureus</i> <i>Streptococcus agalactiae</i> <i>Streptococcus gordonii</i> <i>Streptococcus mutans</i> <i>Streptococcus pneumoniae</i> <i>Streptococcus pyogenes</i> <i>Vibrio anguillarum</i> <i>Vibrio cholerae</i> <i>Vibrio parahaemolyticus</i> <i>Vibrio vulnificus</i> <i>Yersinia pestis</i>
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Characterized by *luxS* gene, which is involved in biosynthesis

AI-2 may be involved in inter-species quorum sensing.



Scheme #3: Most Gram-positive quorum sensing involves peptide signal molecules

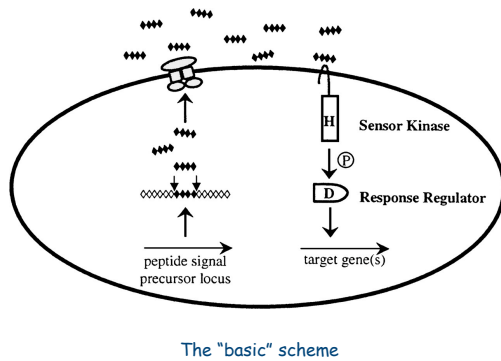
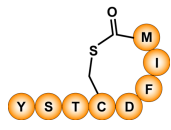


TABLE 2. Specific structures of peptide signal molecules*

Organism	Name of signal	AA Sequence of mature molecule	Length of unprocessed precursor (AA)
<i>Lactococcus lactis</i>	Nisin A	ITSISLCTPGCKTGALMG CNMKTATCHCSIHVSK ^b	57
<i>Lactobacillus plantarum</i>	IF (PhA)	KSSAYS LQMGATAI KQVKL LFKK WGW	48
<i>Streptococcus pneumoniae</i>	CSP (ComC)	EMRLSKFFRDFILQRKK	41
<i>S. gordonii</i>	CSP (ComC1)	DVRSNKIRLWVENIFFNKK	50
<i>Bacillus subtilis</i>	ComX pheromone	ADPITRQW ^b GDERGMT	55
	CSF (PhrC)		40
<i>Staphylococcus aureus</i>	AgrD	YSTCDFIM GVNACSSLF	44
<i>Enterococcus faecalis</i>	cCF10	LVTLVFV AITLFI	Not determined
	iCF10	LFSLVLAG	23
	cAD1	LFVVTLVG	Not determined
	iAD1		23
	GBAP	QNSPNIFGQWM	242

A Case study of Gram-positive quorum sensing: *S. aureus* agr system

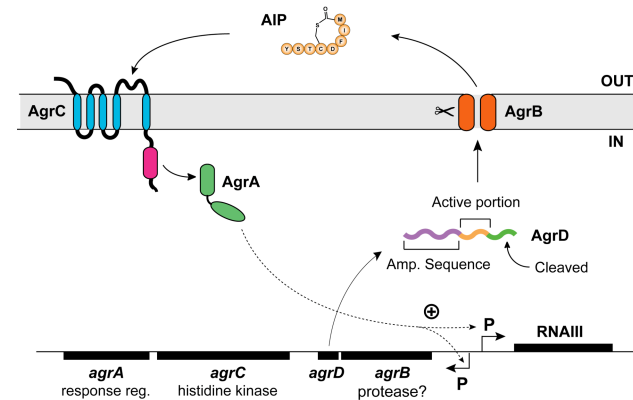


When the cell-density increases, signal reaches a critical threshold and:

Up-regulates extracellular virulence factors

Down-regulates cell surface virulence factors

Molecular scheme for *S. aureus* quorum sensing



Scheme #4: *Ralstonia solanacearum* uses
a volatile signaling molecule



3-OH palmitic acid methylester

Volatile signaling: The tip of the iceberg??

