Computational Approaches to Microbial Communication /Quorum sensing signalling

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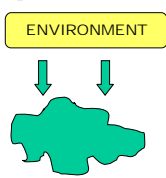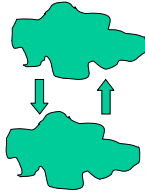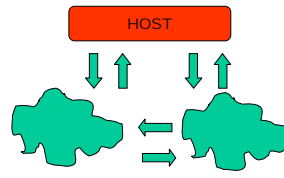
1. Synopsis

1. Microbes, such as bacteria have a large number of sensing systems that allow them to respond to molecules of the environment. Example: Chemotaxis

2. Microbes also respond to their own signals which allows them to sense their neighbors, to share public goods and to form complex communities. Example: Quorum sensing
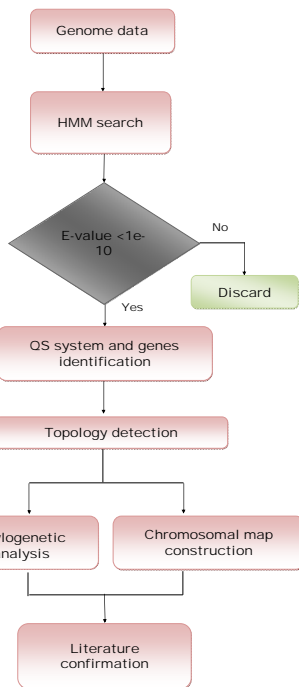
3. Interactions with host organism can build complex microfloras called microbiota or microbiomes. Example: Gut flora
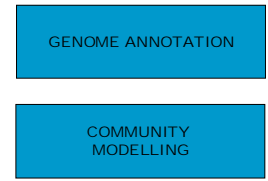
4. Two different approaches. *Genomics* identifies the building blocks and their interactions. *Modelling* uses a simplified picture in order to reproduce fundamental community behaviour.
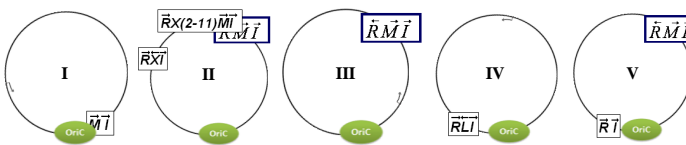
2. Automated Genome Annotation

Gene topologies

ID	Pattern	Gene topology
R1	$\vec{R}\vec{I}$	
R2	$\vec{R}\,\overleftarrow{I}$	
R3	$\overleftarrow{R}\vec{I}$	
R4	$\overleftarrow{I}\vec{R}$	
L1	$\vec{R}\overleftarrow{L}\vec{I}$	
M1	$\vec{R}\vec{M}\vec{I}$	
M2	$\vec{R}\vec{M}\overleftarrow{I}$	
X1	$\vec{R}\vec{X}\vec{I}$	
X2	$\vec{R}\overleftarrow{X}\vec{I}$	
X3	$\vec{R}\overleftarrow{X}\vec{I}$	
X4	$\vec{R}\vec{X}\vec{I}$	
X5	$\vec{R}\vec{X}\vec{I}$	
M3	$\vec{R}X(2-11)\vec{M}\vec{I}$	
M31	$\vec{M}\,\vec{I}$	
X6	$\vec{R}\vec{X}(7)\vec{I}$	
X7	$\overleftarrow{I}X(>7)\vec{R}$	

An automated computational pipeline (left) was created for analyzing AHL signalling genes in over 2670 complete and 7702 draft bacterial genomes as well as 16585 Individual GenBank sequences. The sequences revealed 17 distinct gene-topology groups present in Proteobacteria. The genes within a topology group are more related between species than between different topologies within the same organism.

3. Chromosomal maps

A computer program was written for visualizing the chromosomal location of the signalling genes. The arrangement of signalling genes is conserved within some taxons, i.e. we can distinguish a few major types (below), but the conservation is much less stringent than between topological clusters.
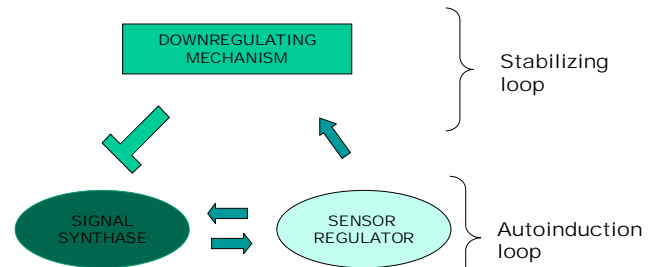

4. regulatory circuit architecture

A comprehensive survey of AHL signalling systems in several thousand genomes reveals a general framework called an incoherent feedforward loop, which stabilizes intercellular signalling against environmental disturbances. The downregulator mechanism can be a DNA binding protein, short RNA signals or an enzyme degrading the signal molecules

5. Phylogenetic tree of LuxI proteins
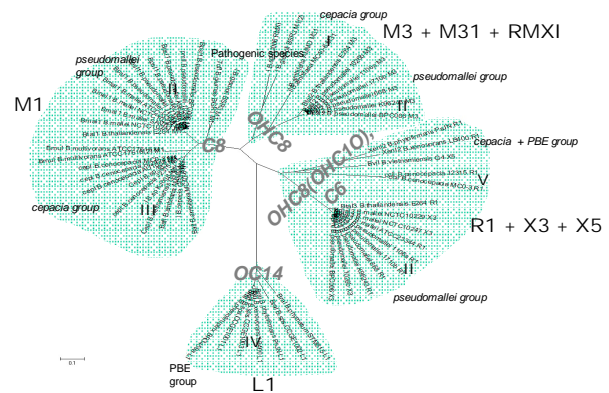
Phylogenetic tree was constructed for LuxI proteins of complete genomes in *Burkholderia* genomes. It shows the clustering of taxons according to topological groups . The numbers I, II, III, IV, and V indicates the arrangement of signaling genes as shown in section 3.

6. Agent-based computational models

Agent models are small computer programs that randomly move on an imaginary plane. Their only abilities are to emit and sense signal, then to turn on the production of a mutually beneficial material (public goods, such as proteases on the scheme at right), and then intensify movement as more food becomes available. The agent form spontaneous communities that are able to find food, to track external signals, to cooperate with non-communicating cells. But, cheater+ mutants that do not cooperate, can collapse a cooperating community.

1. Resting
2. Signal production
3. Public goods production
4. Swarming

Read: cheaters (non-cooperator mutants)
Blue: Cooperators (wt)

Healthy / Invaded community models / Collapsing

7. References

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