Conference or Workshop Item

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ISV22

Applying ecological principles to microbial systems: Partitioning core and satellite taxa from within bacterial communities

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It is well known that microbial ecology is both driven and limited by the increasing plethora of techniques used to assess microorganisms and their communities. In many cases this has led to an almost unhealthy obsession for using the latest methodologies, typically at the expense of the research questions being asked. It has been previously argued that new technologies will increasingly lead us down 'blind non-generalist and expensive alleyways' and microbial ecology will remain in a state of 'accumulating situation-bound statements' of limited predictive ability if studies are not directed and driven by ecological theory. Given the central and global importance of microorganisms in natural and engineered ecosystems, progress requires the acceptance, development, and application of ecological theory and principles. However, the application of theory is still in its infancy in microbial ecology. The potential of exploiting theories, models and principles from general ecology, coupled with ever improving molecular methodologies, could well provide invaluable insights into how microbial communities organise and change in space and time. In time, this increased knowledge of microbial community ecology will help us better understand and predict changes in the natural environment, allow manipulation of agricultural and industrial processes and give improved protection of human health.
In general terms, I will outline the importance of developing microbial ecological theory. More specifically, I will discuss my recent and ongoing work that seeks to use ecological insights for clinical benefit, by partitioning bacterial communities involved in the lung infections of cystic fibrosis patients into core and satellite species groups. From a fundamental perspective this work also demonstrates that a community is comprised of core and satellite species, and that partitioning the two groups from a (spatial or temporal) metacommunity reveals important aspects of species abundance distributions, which would otherwise be neglected with without such a distinction.

ISV23

Effects of space and ecosystem type on the structuring of marine microbial communities at the global scale

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Despite the importance of marine microbes for global ecosystem functioning, still little is known about the factors that contribute to the structuring of their communities in ocean water and sediments worldwide. This presentation proposes a community ecology approach to characterizing the main patterns of microbial diversity over large spatial scales and to quantifying the respective effects of major factors of variation. By synthesizing, visualizing and testing hypotheses on large molecular datasets, novel insights about microbial ecology at various spatial, temporal and taxonomic scales may be obtained with respect to the comparison of benthic and pelagic communities, the scales at which ocean realms are structured, the taxonomic scales of relevance to describe microbial diversity patterns, and the types of abiotic and biotic processes being most likely at play.

ISV24

Mechanisms of c-di-GMP mediated cell cycle control in Caulobacter crescentus

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The development of all living organisms depends on the generation of specialized cells in appropriate numbers. This requires tight regulation of proliferation-differentiation decisions by integrating cell fate determination processes with replication and cell division. Many bacteria use complex developmental strategies to optimize their survival. Like their eukaryotic counterparts, bacteria tightly coordinate morphogenetic programs with growth and division, be this to facilitate the transition between a replicative and a terminally differentiated cell form or to couple obligate cell differentiation events to cell proliferation. The gram-negative bacterium Caulobacter crescentus divides asymmetrically to produce two polarized daughters with distinct morphologies, behavior, and replicative potential. This enables Caulobacter to periodically switch between a motile, planktonic and a sessile, surface adherent life style. Recent studies have identified cyclic di-GMP as a key regulator of cell polarity and cell cycle progression in this organism. In particular, c-di-GMP facilitates the dynamic assembly and disassembly of polar organelles and couples these developmental processes to the underlying cell cycle. The seminar will summarize these findings and will highlight molecular and cellular aspects of c-di-GMP signaling components that contribute to the temporal and spatial control of the C. crescentus life cycle.

ISV25

Dynamic cyclic di-GMP signaling in Vibrio cholerae during infection

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Vibrio cholerae cycles between aquatic environments and the human small intestine. Its success as a pathogen depends in large part on surviving the transitions between these two disparate environments. Successful transition requires changes in gene expression and phenotypic changes, which we find are regulated in part by the bacterial second messenger c-di-GMP. In aquatic environments, *V. cholerae* forms biofilms - a state that requires high c-di-GMP concentration. Upon entry into the small intestine through ingestion of contaminated water or food, the concentration of c-di-GMP is lowered through activation of specific phosphodiesterases. This results in the repression of biofilm formation genes, which interfere with infection, and the simultaneous activation of virulence genes, which are needed for colonizing the epithelial surface in the small intestine. Late in infection, in response to changing nutrient and oxygen concentrations as the density of bacteria becomes high, the situation reverses whereby the concentration of c-di-GMP is raised through activation of diguanylate cyclases. This serves to prepare *V. cholerae* for the transition to life outside the host.

ISV26

From isolated molecules to intact cells: Structure of ribosomal arrangements in vitro and in situ

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X-ray crystallography and EM single particle analysis (SPA) have provided unprecedented insights into the molecular architecture of ribosomes and have been instrumental in elucidating key events during translation. Cryoelectron tomography (CET) can complement these techniques in that it allows the visualization of flexible molecular structures both *in vitro* and *in situ*, i.e., in the functional environment of intact cells. We have used CET to study the native 3D organizations of *Escherichia coli* ribosomes in polysomes and hibernating ribosomes (100S).
The quantitative evaluation of cryoelectron tomograms is challenging due to the extremely low signal-to-noise of cryoelectron tomograms. 3D averaging is a way to overcome the problem of low contrast in CET. First, we pursue the identification of ribosomes with a known structure by template matching; the macromolecular structure is used as a template for a local correlation with the tomogram. Secondly, we align subtomograms containing single ribosomal particles to a common origin and average them to reveal details of the interaction between the identified complexes. An *in situ* implementation of this approach, i.e. in the functional environment of intact cells, allowed us to obtain ribosomal atlases of *Spiroplasma melliferum* cells [1].
Applying CET and template matching to *in vitro* translation systems, we showed that *E. coli* ribosomes adopt two preferential relative orientations in densely-packed polysomes. These alternative manners of ribosomal pairing result in variable 3D polysomal organizations, i.e, pseudo-planar or pseudo-helical polysomes. In polysomes, the 30S subunits point inwards, possibly protecting mRNA from degradation, and the 50S subunits outwards, positioning the nascent chain exit sites of adjacent ribosomes away from each other. We hypothesize that these organizations disfavor interaction between the non-folded nascent chains avoiding protein misfolding [2].