

MICROBIOLOGIE, INFECTIOLOGIE ET IMMUNOLOGIE



CONFÉRENCE

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Localizing peptidoglycan synthesis for bacterial growth and morphogenesis

The diversity of shapes of organisms is one of the most fascinating aspects in the field of biology. While bacteria display a myriad of morphologies, the mechanisms that control morphogenesis and the evolution of bacterial morphology are not well understood. One mechanism that drives morphogenesis is the synthesis of peptidoglycan at specific subcellular sites, or zones. I will describe new methods of peptidoglycan labeling that allow the detection of sites of peptidoglycan synthesis in live cells and in real time, and their use to study the mechanisms of peptidoglycan synthesis. For example, these methods were used to show that pathogenic *Chlamydia* have peptidoglycan, ending 50 years of speculation and debate concerning the chlamydial anomaly, and to study the spatio-temporal dynamics of peptidoglycan synthesis at the site of cell division in *Bacillus subtilis*. I will describe the mechanisms that control morphological diversity in species related to *Caulobacter crescentus* that synthesize appendage-like extensions of the cell envelope at distinct sub-cellular positions. I will show that stepwise evolution of a specific domain of a developmental regulator led to the gain of a new function and localization of this protein, which drove the sequential transition in morphology. Our results indicate that evolution of protein function, co-option, and modularity are key elements in the evolution of bacterial morphology. In addition, I will show how evolutionary consideration of the mechanism of growth in the alphaproteobacteria led to the surprising discovery that polar growth, rather than the previously assumed binary fission, is the predominant mode of growth in a large group of the alphaproteobacteria that includes the plant pathogen *Agrobacterium tumefaciens* and the human pathogen *Brucella abortus*.

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