

## SELF-ORGANIZATION OF BACTERIAL CYTOSKELETON PROTEINS ON SURFACES

Marisela Vélez<sup>1</sup>, Pilar López Navajas<sup>2</sup>, Germán Rivas<sup>2</sup>

<sup>1</sup>Instituto Universitario de Ciencia de Materiales “Nicolás Cabrera”, Universidad  
Autónoma de Madrid

<sup>2</sup>Centro de Investigaciones Biológicas, Consejo Superior de Investigaciones Científicas

Cytoskeleton proteins are nanometer sized soluble proteins that play an essential role in maintaining cell shape. The polymerizing units are protein monomers or dimers, usually a few nanometers in diameter, that, in the presence of a phosphorylated nucleotide (ATP or GTP) are capable of self-organizing into larger structures that can incorporate up to a few hundred monomers. The polymers formed are usually dynamic structures that undergo continuous exchange of material with the soluble proteins available in the medium. The detailed interaction between the self-aggregating monomers or dimers, controlled partly by the phosphorylated state of the nucleotide, determines the rate and form of exchange. Actin and tubulin, two eukaryotic cytoskeletal proteins, have been extensively studied and characterized (1).

Bacterial cytoskeleton proteins have been described more recently and their self-aggregating properties have not yet been fully characterized. One of the bacterial cytoskeleton proteins, FtsZ, plays an essential role in cell division (2). It is a soluble 40 kD protein with GTPase activity that is structurally analogous to eukaryotic tubulin. This protein localizes on the inner side of the cytoplasmic membrane during bacterial cell division at the midcell point and forms a dynamic ring that is essential for the recruitment of other proteins the multiprotein complex called the septosome responsible of dividing the cell through the middle to form two new daughter cells.

We have used atomic force microscopy to characterize the shape and dynamic behaviour of individual *E. coli* FtsZ protein filaments formed on a mica surface. We describe their shape and observe the dynamic restructuring of the filaments as the nucleotide is being consumed (3). Filaments showed a strong tendency to curve and to interact laterally. Given that FtsZ interacts with the inner cytoplasmic membrane of the bacteria through its interaction with the membrane protein ZipA, we have also explored its behaviour on a mica surface covered with a lipid bilayer with the ZipA protein incorporated in the bilayer with a controlled orientation. FtsZ shows no affinity for lipid bilayers of different composition, but is able to attach and polymerize on a lipid surface in the presence of oriented ZipA.

- (1) Desai, A. and Mitchison, T.J. Microtubule Polymerization Dynamics Annu. Rev. Cell Dev. Biol. 1997. 13:83–117
- (2) Romberg, L. and Levin, P.A. Assembly Dynamics Of The Bacterial Cell Division Protein Ftsz: Poised At The Edge Of Stability. Annu. Rev. Microbiol. 2003. 57:125–54
- (3) Mingorance, J., Tadros, ., Vicente, M., González, J.M., Rivas, G., Vélez, M. Visualization of Single Escherichia coli FtsZ Filament Dynamics. with Atomic Force Microscopy. The Journal Of Biological Chemistry Vol. 280, No. 21, Issue of May 27, pp. 20909–20914, 2005