High-speed and high-resolution AFM monitors membrane protein interactions

Adai Colom, Ignacio Casuso & Simon Scheuring
U1006 INSERM, Université Aix-Marseille, Campus Luminy, 13009 Marseille, France
adai.colom@inserm & simon.scheuring@inserm.fr

Membrane-mediated protein-protein and protein-lipid interactions, membrane protein localization, and related dynamics, modulate membrane protein function [1]. So far membrane structure and dynamics could not be studied altogether lacking the technique that analyzes unlabelled proteins at submolecular lateral and high temporal resolution. Here we used high-speed atomic force microscopy (HS-AFM, [2]) to characterize the movements and interactions of unlabelled porin OmpF (Fig. 1, [3]) and aquaporins (Fig. 2, [4]) in native membranes. First an introduction to AFM and its use in membrane biology will be given, followed by an introduction to the membrane proteins and the membrane structure as a current challenge in biology. Using HS-AFM, we are able to describe essential novel aspects that govern membrane protein assembly and membrane superstructure. Protein motion scales roughly with membrane crowding. However molecules display individuality of diffusion behavior ranging from fast moving to immobile molecules trapped by favorable protein-protein associations. We describe the molecular interaction and assembly rationales that we compare with coarse-grained molecular dynamics and Monte Carlo simulations. Furthermore, the development of a hybrid microscope combining high-speed atomic force microscopy and optical microscopy for the analysis of cells will be discussed. HS-AFM may open a novel research avenue that bridges structure of individual membrane proteins and supramolecular membrane architecture.

Figures:

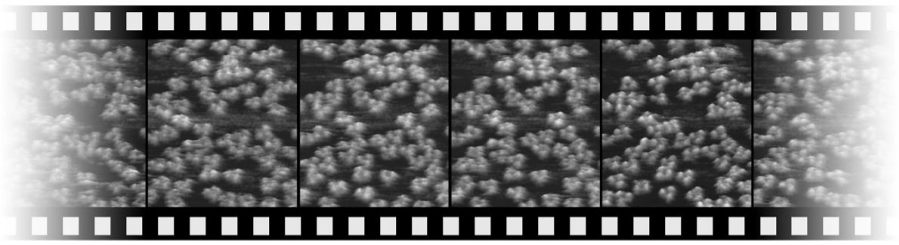

Fig. 1) HS-AFM movie frames (frame rate 477 ms) showing the motion of OmpF trimmers.

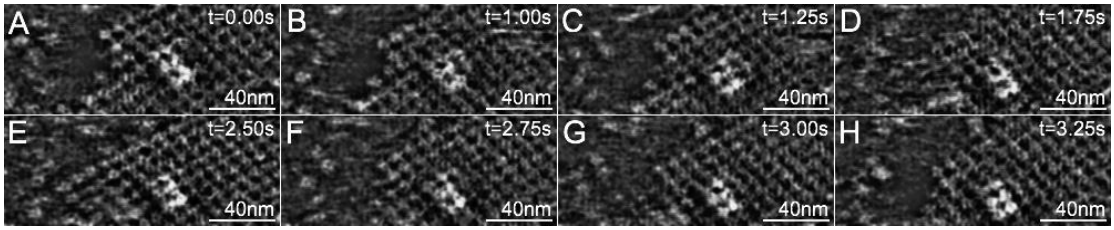

Fig. 2) HS-AFM movie frames (frame rate 250 ms) showing native AQP0 array assembly (A-E) and disassembly (E-H).

References:

[1] D.M. Engelman, Nature, 2005, 438, 578
[2] T. Ando, et al., Proceedings of the National Academy of Sciences, 2001, 98, 12468
[3] I. Casuso, et al., Nature Nanotechnology, 2012, 7 (8): 525-529
[4] A. Colom, et al., Journal of Molecular Biology, 2012, 423 (2): 249-256