

P028 Polyglutamylation of microtubules regulates functions of microtubule-associated proteins

Benjamin Lacroix, Juliette van Dijk, Krzysztof Rogowski, Julie Miro, Carsten Janke

CRBM, CNRS, 34293 Montpellier, France

Polyglutamylation is a posttranslational modification that forms glutamate side chains of variable length on proteins. The best-studied substrates of polyglutamylation are tubulins, which are modified within their C-terminus, known to be the main binding site for many MAPs and motors. In cycling cells, interphase microtubules have a very low polyglutamylation level whereas during mitosis, a strong increase is observed on the mitotic spindle. Thus, functionally divergent microtubules could be distinguished by different polyglutamylation states. The question we address here is whether these polyglutamylation patterns could regulate the recruitment, interactions and/or functions of specific MAPs. We have identified different mammalian polyglutamylase enzymes that have distinct reaction specificities. By expressing selected enzymes in cultured cells, we can change the polyglutamylation pattern of the microtubules and study the effect on the localisation and function of MAPs *in vivo*. We demonstrate that the subcellular localisation of several cell cycle related MAPs is indeed determined by microtubule polyglutamylation. One of these proteins, katanin, is a microtubule severing protein with a role in cytokinesis. Our preliminary data show that both, the localisation and the activity of katanin depend on the degree of microtubule polyglutamylation. Taken together our results suggest that polyglutamylation could be a potent and highly selective regulator of specialised microtubule functions.