第10回細胞生物学セミナー

日時:平成25年11月27日(水)16:30~(1時間程度) 場所:手形キャンパス総合研究棟2階講義室

Eukaryotic cytosolic chaperonin CCT: the actin folding mechanism and cell biology in yeast

Prof Keith Willison, Institute of Chemical Biology, Department of Chemistry, Imperial College, South Kensington Campus, London, SW7 2AZ, UK Email: <u>keith.willison@imperial.ac.uk</u>

The chaperonin of the eukaryotic cytosol CCT performs an essential role in cells for the folding of newly translated actin and tubulin polypeptides. CCT is a double-ring ATPase machine constructed from 8 independent, but homologous, 60kDa protein subunits (Dekker et al; 2011). In the case of actin newly translated and experimentally unfolded actin polypeptides adopt similar, stable conformational ensembles, Ac_1 and l_3 respectively, which are kinetically and thermodynamically trapped under physiological conditions. The CCT machine binds these states of unfolded actin through a highly specific, mutual recognition mechanism and folds actin to a less kinetically stable but now productive folding intermediate I_2 by coupling its own nucleotide hydrolysis cycle to the phases of actin substrate maturation (Altschuler and Willison; 2008). We have assembled in vitro the yeast CCT-actin-PLP2 folding machine (McCormack et al; 2009) and have used a spectroscopic assay to monitor actin as it is folded by CCT (Stuart et al; 2011). In addition to actins and tubulins only a relatively small group of other proteins depend absolutely on CCT for their biogenesis. Several WD40-motif proteins are members of this group; the regulators of the anaphase promoting complex, Cdh1 and Cdc20; the Cdc55 phosphatase regulatory subunit and the TAF5 regulator of mediator complex (Dekker et al; 2008). We will describe a combination of yeast genetic approaches mass spectrometric approaches to the behaviour and quantification of substrate and co-factor proteins bound to yeast CCT and a set of ATP-site mutants (Amit et al; 2010). Co-variance analysis of the raw spectral signals shows strong correlations between expected binding partners such as Act1p and Plp2p (McCormack et al; 2009) and also reveals new couplings between CCT-binding proteins. CCT is intimately involved in co-ordinating cell cycle and cell growth control because it directly couples the rate of actin and tubulin biogenesis to the activities of critical regulators of these processes and a model will be discussed.

Altschuler, G.M. and Willison, K.R. (2008) Development of free-energy based models for Chaperonin Containing TCP-1 mediated folding of actin. *J.R. Soc.Interface*, **5**, 1391-1408

Amit, M., Weisberg, S.J., Nadler-Holly, M., McCormack, E.A., Feldmesser, E., Kaganovich, D., Willison, K.R. and Horovitz, A. (2010). Equivalent mutations in the eight subunits of the chaperonin CCT produce dramatically different cellular and gene expression phenotypes. *J.Mol.Biol*, 401, 532-543

Dekker, C., Stirling, P. C., McCormack, E. A., Filmore, H., Paul, A., Brost, R. L., Costanzo, M., Boone, C., Leroux, M. R. and Willison, K. R. (2008) The interaction network of the chaperonin CCT. *EMBO J*, **27**, 1827-1839

Dekker, C., Roe, S. M., McCormack, E. A., Beuron, F., Pearl, L.H. and Willison, K. R. (2011) The crystal structure of yeast CCT reveals the intrinsic asymmetry of eukaryotic cytosolic chaperonins. *EMBO J*, **30**, 3078-3090 Stuart, S.F., Leatherbarrow, R.F. and Willison, K.R. (2011) A two-step mechanism for the folding of actin by the

Stuart, S.F., Leatherbarrow, R.F. and Willison, K.R. (2011) A two-step mechanism for the folding of actin by the yeast cytosolic chaperonin. *J.Biol.Chem*, 286, 178-184

McCormack, E. A., Altschuler, G. M., Dekker, C., Filmore, H. and Willison, K. R. (2009) Yeast phosducin-like protein 2 acts as a stimulatory co-factor for the folding of actin by the chaperonin CCT via a ternary complex. *J.Mol.Biol*, **391**, 192-206

世話人:久保田広志(生命科学専攻)

Tel. 018-889-3053 E-mail hkubota@ipc.akita-u.ac.jp