

INVITED LECTURE T5

Structural studies of the transport protein particle (TRAPP)

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The human protein Bet3 is a component of the TRAPP tethering complex which is located at the Golgi membrane and is required for vesicular transport from the ER to the Golgi. Bet3 displays a novel dimeric architecture, and a fatty acid chain resides in a hydrophobic cleft (1). Biochemical studies proved that Bet3 palmitoylation is neither required for membrane attachment of Bet3 or TRAPP nor for yeast cell viability. The palmitoylation of Bet3 is independent of host-cell acyl transferases and stabilizes the protein *in vitro* and *in vivo* (2).

Structure analysis of Tpc6B, a second TRAPP component revealed a dimeric architecture reminiscent of Bet3, although the sequence match between both proteins is poor and Tpc6 is not palmitoylated (3). The structural similarity, which was pronounced at the subunit interface regions of Bet3 and Tpc6B, indicated the possible formation of Bet3-Tpc6B heterodimers. Pull-down and co-immunoprecipitation experiments supported this assumption. The crystal structure of a Bet3-Tpc6B complex revealed the expected heterodimeric arrangement and allowed the identification of surfaces likely to be involved in Golgi membrane attachment and in binding Mum2, a third TRAPP component (4).

1. Turnbull, A.P. et al. (2005) *EMBO J.* 24, 875-884.
2. Kümmel, D. et al. (2006) *Proc. Natl. Acad. Sci. USA* 103, 12701-12706.
3. Kümmel, D. et al. (2005) *EMBO Rep.* 6, 787-793.
4. Kümmel, D. et al. (2006) *J. Mol. Biol.* 361, 22-32.