Golgi matrix proteins and the structural regulation of the Golgi apparatus

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The Golgi apparatus is an organelle situated at the center of the exocytic pathway. Newly synthesized proteins, oligosaccharides and lipids are transported to the Golgi apparatus from the endoplasmic reticulum (ER) and there they are processed, sorted and sent out for their final destinations. In mammalian cells, the Golgi apparatus has typical stacked cisternal structures and these are gathered around the perinuclear region. Exocytic material is transported through the Golgi apparatus by vesicles shuttling within the Golgi and between the Golgi and other exocytic organelles including the ER, endosomes, lysosomes and the plasma membrane. In spite of the extensive anterograde and retrograde vesicular flow, the identity and structure of the Golgi apparatus is apparently maintained. There are structural proteins, namely Golgi matrix proteins, that help to maintain the identity and structure of the Golgi apparatus including golgins, golgin binding proteins and subtypes of ankyrin and spectrin that function for the organization of actin-based membrane skeleton. We have shown that cis-Golgi matrix proteins, GM130 and GASP65 are directly incorporated into the preexisting Golgi matrix (Yoshimura et al., J. Cell Sci. 114 p4105, 2001). However, the precise mechanism of targeting and organization of Golgi matrix proteins are still obscure. To elucidate the molecular mechanism of the Golgi matrix organization, we aimed to (1) describe the dynamics of Golgi matrix proteins and to (2) identify novel Golgi membrane protein that functions for the anchor of the Golgi matrix proteins.

(1) When ER to Golgi transport was blocked, most of Golgi resident proteins were transported back into the ER. In contrast, the cis-Golgi matrix proteins were retained in punctate cytoplasmic structures, namely Golgi remnants. The medial-Golgi matrix proteins were partly retained in the Golgi remnants. These results suggested that cis-Golgi matrix proteins resisted retrograde transport flow and stayed as true residents in Golgi remnants after the inhibition of ER to Golgi transport (Yoshimura et al., submitted).

(2) A novel family of proteins with multiple transmembrane domains was identified form yeast interactome analysis database and 6 mammalian homologues were isolated. They were localized between the ER and Golgi apparatus and therefore named as Multispan membrane protein localized between the ER and the Golgi apparatus (MERG). Their over expression in the cells disrupted the Golgi apparatus suggesting their role in maintaining the Golgi structure (Shakoori et al., manuscript in preparation).