Quantitative Studies of Intracellular Trafficking of Two Classes of Resident Golgi Apparatus Proteins

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ABSTRACT

The research presented in this dissertation consists of two primary parts. The initial focus centered on understanding the distribution of Golgi resident glycosyltransferases between the ER and Golgi at steady-state. Retrograde trafficking of these Golgi proteins has been demonstrated experimentally mandating the existence of a dynamic equilibrium between the Golgi apparatus and ER. Our published studies also included the development of a quantitative method for analysis of data collected using fluorescent microscopy. The second part of this dissertation presents results pertaining to the quantification of a unique Golgi resident protein that cycles in the late endosome bypass pathway. Using the published method of analysis and techniques developed during the initial project, the anterograde and retrograde transport kinetics of this Golgi protein were determined and used to develop a compartmental model for pH sensitive trafficking in the bypass pathway. The spatial Golgi distribution of the protein during retrograde transport to the Golgi following endosomal exit was also investigated. This research lies at the interface of experimental cell biology and quantitative computational analysis. These experiments combined more traditional experimental biological approaches with more recent computational approaches to understanding cellular mechanisms. Additionally, development of a quantitative method of analysis validated the use of fluorescent microscopy as a quantitative tool for studying intracellular proteins.

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