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.
# Table of Contents

Chapter 1 – Introduction  
1.1 Motivation  
1.2 Objective  
1.3 Specific Aims  
   1.3.1 Aim 1  
   1.3.2 Aim 2  
   1.3.3 Aim 3  
1.4 Dissertation Roadmap  

Chapter 2 – Literature Review  
2.1 Secretory Pathway  
   2.1.1 Endoplasmic Reticulum  
   2.1.2 Golgi Apparatus  
   2.1.3 Endosomes  
   2.1.4 Maturation versus Vesicular Transport Models  
2.2 Protein Labeling for Visualization  
   2.2.1 Immunofluorescence  
   2.2.2 Green Fluorescent Protein (GFP)  
   2.2.3 Vesicular Stomatitis Virus (VSV)  
2.3 Golgi Disturbing Agents  
   2.3.1 Nocodazole  
   2.3.2 Brefeldin A  
   2.3.3 Monensin and Bafilomycin  
2.4 Microscopy  
   2.4.1 Fluorescence Microscopy  
   2.4.2 Confocal Microscopy  
   2.4.3 Electron Microscopy  

3.1 Introduction
3.2 Materials and Methods 37
   3.2.1 Cell Culture 37
   3.2.2 Kinetic Modeling – Experimental Details 37
   3.2.3 Electron Microscopy 37
   3.2.4 Conventional Widefield Microscopy and Spinning Disk Confocal Microscopy 38
   3.2.5 Laser Scanning Confocal Microscopy 39
   3.2.6 Fluorescence Image Processing and Analysis 39
3.3 Results 41
   3.3.1 Golgi to ER exchange kinetics indicate an ~90:10 Golgi to ER distribution 41
   3.3.2 Immunogold electron microscopy indicates ~90:10 distribution of GalNAcT2-VSV between the Golgi Apparatus and ER 42
   3.3.3 Widefield fluorescence microscopy yields ~90:10 Golgi to ER steady-state distribution for Golgi glycosyltransferases 44
   3.3.4 Best-practice confocal microscopy also yields an approximately ~90:10 distribution 47
       A. Laser scanning confocal microscopy 47
       B. Spinning disk confocal microscopy 48
3.4 Discussion 49

Chapter 4 – Quantification of GPP130 Trafficking through Endosomes 61
4.1 Introduction 61
4.2 Materials and Methods 64
   4.2.1 Cell Culture 64
   4.2.2 Antibodies and Reagents 64
   4.2.3 Widefield and Spinning Disk Confocal Microscopy 64
   4.2.4 Laser Scanning Confocal Microscopy 65
   4.2.5 Monensin Induced GPP130 Redistribution and Washout 65
   4.2.6 Shiga toxin B-fragment Internalization 66
   4.2.7 Quantitative Analysis of GPP130 66
   4.2.8 Quantitative analysis of Shiga toxin 71
   4.2.9 Endosomal Markers: EEA1 and Cascade-blue dextran 71
4.2.10 Quantitative Analysis of LSM510 images  
4.2.11 Statistics  
4.3 Results  
4.3.1 GPP130 Golgi protein cycles between the endosomes and Golgi apparatus  
4.3.2 Monensin induces redistribution of GPP130 to endosomes  
4.3.3 Kinetic Analysis of GPP130 Cycling between Golgi and Endosomes  
4.3.4 Shiga toxin B-Fragment Traffics from Endosomes to Golgi  
4.3.5 Cisternal localization of retrograde trafficking GPP130 following monensin washout  
4.4 Discussion  

Chapter 5 – Conclusions and Future Directions  
5.1 Summary of Research  
5.2 Future Studies  
5.3 Conclusions  

Bibliography  

Appendix 1 – Stereology  
Appendix 2 – Electron Micrograph Analysis  
Appendix 3 – Pixel Shift  
Appendix 4 – Microscopy Terms  

Curriculum Vitae
TABLES AND FIGURES

Chapter 2

Table 1. Examples of Golgi Associated Proteins 21
Figure 1. Secretory Pathway in Eukaryotic Cells 22
Figure 2. Endosomal Sorting 24
Figure 3. Shiga toxin Internalization Pathway 25
Figure 4. Transport Models for the Golgi Apparatus 26
Figure 5. Antibody Detection 27
Figure 6. GalNAcT2-GFP protein 27
Figure 7. GFP Protein Distribution 28
Figure 8. Mitosis in the Eukaryotic cell 29
Figure 9. Effects of Golgi Disturbing Agents 30
Figure 10. Fluorescence excitation and emission diagram 31
Figure 11. Fluorescent Microscopy Diagram 32
Figure 12. Impact of Deconvolution on Visualized Signal 33
Figure 13. Confocal Microscopy 34

Chapter 3

Table 1. GalNAcT2-VSV relative protein distribution by immunogold labeling 52
Table 2. Percentage of glycosyltransferases found in the Golgi apparatus measured from single-plane widefield images 52
Table 3. Comparison of grayscale fluorescence intensity parameters by three fluorescence microscopy methods 53
Table 4. Percentage of glycosyltransferases found in the Golgi measured from laser scanning image stacks 53
Table 5. Percentage of glycosyltransferases found in the Golgi measured from spinning disk image stacks 54
Figure 1. Two compartment model for Golgi glycosyltransferase cycling 55
Figure 2. Electron micrographs of GalNAcT2-VSV HeLa cells with immunogold labeling and without 56
Figure 3. Golgi enzymes are found in the ER at lower concentrations by widefield light microscopy 57
Figure 4. Single-plane widefield images were analyzed before and after deconvolution using visual and calculated thresholds

Figure 5. Laser scanning confocal images

Figure 6. Spinning disk confocal images

Chapter 4

Table 1. Comparison of kinetic rate constants for protein transport between the Golgi and endosomes

Table 2. Distance Measurements for rab6, p115, and GPP130

Table 3. Secondary GPP130 Peak Analysis

Figure 1. Presence of light spread from adjacent focal planes can interfere with colocalization analysis

Figure 2. GalNAcT2-GFP cell stained with GPP130

Figure 3. Colocalization Mask used to Identify Golgi GPP130 signal

Figure 4. GPP130 Endosomal Staining is Distinguishable from Cytoplasm and Golgi Staining

Figure 5. Small GPP130 fraction is found in endosomes at steady-state by confocal fluorescent microscopy

Figure 6. Colocalization of redistributed GPP130 with Cascade blue-dextran, but not with another endosomal marker EEA1

Figure 7. Monensin treatment induces GPP130 redistribution to endosomes

Figure 8. Schematic diagram of GPP130 Intracellular Transport Model

Figure 9. Quantification of GPP130 in endosomes following monensin treatment

Figure 10. Extended monensin treatment results in accumulation of GPP130 in perinuclear endosomal populations

Figure 11. GPP130 returns to the Golgi apparatus following monensin washout

Figure 12. Quantification of GPP130 in endosomes following monensin washout

Figure 13. Shiga toxin B-fragment travels to the Golgi apparatus

Figure 14. Quantification of Shiga toxin B-fragment in endosomes following 19.5°C temperature block
Figure 15. Widefield analysis of Shiga toxin B-fragment in endosomes with and without monensin treatment

Figure 16. Distance Measurements for rab6 and GPP130 from LSM single-plane images

Figure 17. Distance Measurements for rab6 and p115 from LSM single-plane images

Appendix 1

Figure 1. Stereology

Figure 2. Stereology Grid

Appendix 3

Figure 1. Pixel Shift

Appendix 4

Table 1. Excitation and Emission wavelengths

Table 2. Refractive Index of Common Materials

Figure 1. Airy Disc