containing putative GalT localisation signals in hybrid molecules. These studies have also demonstrated that wild type GalT is actively retained within the Golgi stack, and is not retrieved from the *trans*-Golgi network or later compartments. The mechanism of Golgi retention is currenly under investigation.

1. Teasdale, R. D., D'Agostaro, G., Gleeson, P. A. (1992) *J. Biol. Chem.*, **267**: 4084 – 96.
2. Burke, J., Pettitt, J. M., *et al.* (1992) *J. Biol. Chem.* **267**:2443 – 24440.

S14.4

Molecular Organization of the *Trans*-Golgi Apparatus: Evidence for Different Compartents of β-1,4-Galactosyl- and α-2,6-Sialyltransferase in HEPG2 Cells

H. Bosshart and E. G. Berger
Institute of Physiology, University of Zürich, CH-8057 Zürich, Switzerland

Colocalization by double immunofluorescence of β-1,4-galactosyltransferase (gal-T) and α-2,6-sialyltransferase (sialyl-T) suggested codistribution of both enzymes in the *trans*-Golgi apparatus. However, Golgi-disturbing agents such as monensin dissociated stainings for gal-T from sialyl-T: gal-T positive elements rounded up while sialyl-T distribution showed little change (Berger *et al.*, *J. Cell Biochem.*, 1993, in press). To further investigate the topographical relationship of gal-T and sialyl-T, both enzymes were sequentially immunoisolated from [^{35}S] methionine labelled HepG2 cells which were mechanically disrupted in absence of detergent. Two populations of Golgi-derived membrane vesicles were highly enriched in gal-T or sialyl-T, respectively. Pulse-chase experiments revealed different rates of intracellular transport for both enzymes as judged by acquisition of endo H resistance. Turnover for sialyl-T was very rapid when compared to gal-T. Upon CCCP treatment the compact juxtanuclear structure of gal-T positive Golgi elements broke down into small compact vesicles whereas the immunofluorescent pattern of sialyl-T remained unaffected. Correspondingly microsomes from CCCP preincubated cells subjected to velocity-controlled sucrose density gradient centrifugation displayed an accelerated sedimentation rate for sialyl-T whereas both enzymes cosedimented on control gradients.

Together these data support a model of topography for gal-T and sialyl-T in which these sequentially acting terminal glycosyltransferases are distributed to different Golgi subcompartments.

This work was supported by grant 31-30757.91 of the SNSF to EGB.

S14.5

RAB Proteins in *Lymnaea stagnalis*

I. van Die, M. Agterberg, J. Klumperman*, A. van Tetering, D. H. van den Eijnden and H. Ploegh
*Department of Medical Chemistry, v.d. Boechorststraat 7, and *Department of Biology, Boelelaan 1087, Vrije Universiteit, Amsterdam, The Netherlands.*

Rab proteins are small GTP-binding proteins with a molecular mass of 20 – 25 kDa, belonging to the Ras-superfamily. There is growing evidence indicating that these small GTP-binding proteins are involved in vesicular transport of (glyco)proteins along the secretory and endocytic pathways in eukaryotic cells.

The albumen gland (female accessory sex gland) and the central nervous system of *Lymnaea stagnalis* provide excellent model systems to study the secretory pathway in this animal.

In order to isolate *rab*-related cDNAs from *Lymnaea stagnalis we* have screened a lambda-zap cDNA library of the albumen gland with *rab*2 cDNA as a probe under low-stringency conditions. Three different cDNAs were isolated. Analysis of these cDNAs strongly suggest that we have isolated the *Lymnaea stagnalis* homologues of the mammalian Rab1 and Rab2. The third cDNA might represent the *Lymnaea* homologue of mouse-Rab 18, or a related, new member of the Rab-subfamily.

Peptide antisera were raised directed against the different *L. stagnalis* proteins and localization studies were performed by immuno electron microscopy.

S.15 MEDICAL ASPECTS OF GLYCOCONJUGATE RESEARCH

S15.1

Gangliosides as Risk Factors in Atherosclerosis

N. V. Prokazova and *L. D. Bergelson*
Institute of Experimental Cardiology, Academy of Medical Sciences, Moscow, Russia.

The ganglioside level in atherosclerotic lesions is considerably higher then in unaffected areas of the aorta, and atherosclerotic patients frequently are characterized by increased ganglioside concentrations in plasma. In this connection we studied the influence of gangliosides on the structure and functions of low density lipoproteins (LDL) and on some factors involved in the formation of atherosclerotic plaques. Preincubation of LDL with small amounts of gangliosides was found to cause structural changes of the LDL surface, to induce aggregation of LDL and to inhibit their binding to hepatic cells, thus possibly interfering with removal of cholesterol by the LDL-receptor mediated pathway [1,2]. Furthermore, gangliosides were found to stimulate LDL uptake by and accumulation of cholesterol and triglycerides in macrophages leading ultimately to formation of foam cells [3]. The ganglioside spectra of atherosclerotic intima cells were characterized by high levels of GD3, a marker of many fast growing cells and tissues [4]. GD3 (but not other aorta gangliosides) induced rapid adhesion, spreading and aggregation of platelets [5], suggesting that intimal GD3 exposed into the lumen after endothelial injury may be a factor responsible for platelet attachment to the damaged vessel wall. In combination, our data suggest that high ganglioside levels in plasma and aorta tissue may be a factor promoting processes involved in the development of atherosclerosis.